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OM protein - protein search, using sw model

Run on: October 25, 2005, 20:58:51 / Search time 69.7126 Seconds
(without alignments)
55.479 Million cell updates/sec

Title: US-10-731-238-102
Sequence: 1 DFEEDTLPRV 10
Perfect score: 53

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:*

- 1: geneseqp1980s:*
- 2: geneseqp1990s:*
- 3: geneseqp2000s:*
- 4: geneseqp2001s:*
- 5: geneseqp2002s:*
- 6: geneseqp2003as:*
- 7: geneseqp2003bs:*
- 8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	53	100.0	10	2	AAW65758
2	53	100.0	11	2	AAW65742
3	53	100.0	22	2	AAW65669
4	53	100.0	37	1	AAW65677
5	53	100.0	37	4	AAW65678
6	53	100.0	38	1	AAW65679
7	53	100.0	134	2	AAW65680
8	53	100.0	139	2	AAW65681
9	53	100.0	961	6	AAW65682
10	53	100.0	978	4	AAW65683
11	53	100.0	1001	4	AAW65684
12	53	100.0	1018	1	AAW65685
13	53	100.0	1018	4	AAW65686
14	53	100.0	1018	4	AAW65687
15	53	100.0	1018	6	AAW65688
16	53	100.0	1018	6	AAW65689
17	53	100.0	1027	2	AAW65690
18	53	100.0	1038	6	AAW65691
19	53	100.0	1038	6	AAW65692
20	53	100.0	1038	6	AAW65693
21	53	100.0	1038	6	AAW65694
22	53	100.0	1038	6	AAW65695
23	53	100.0	1038	6	AAW65696
24	53	100.0	1038	6	AAW65697
25	53	100.0	1038	6	AAW65698

26	49	92.5	21	2	AAW65675	AAW65675 Fibronect
27	49	92.5	21	2	AAW65666	AAW65666 Fibronect
28	49	92.5	21	2	AAW65672	AAW65672 Fibronect
29	49	92.5	21	2	AAW65677	AAW65677 Fibronect
30	49	92.5	21	2	AAW65665	AAW65665 Fibronect
31	49	92.5	21	2	AAW65674	AAW65674 Fibronect
32	49	92.5	21	2	AAW65676	AAW65676 Fibronect
33	49	92.5	21	2	AAW65678	AAW65678 Fibronect
34	49	92.5	22	2	AAW65679	AAW65679 Fibronect
35	49	92.5	22	2	AAW65680	AAW65680 Fibronect
36	49	92.5	22	2	AAW65681	AAW65681 Fibronect
37	49	92.5	22	2	AAW65682	AAW65682 Fibronect
38	49	92.5	22	2	AAW65683	AAW65683 Fibronect
39	49	92.5	22	2	AAW65684	AAW65684 Fibronect
40	49	92.5	22	2	AAW65685	AAW65685 Fibronect
41	49	92.5	22	2	AAW65686	AAW65686 Fibronect
42	49	92.5	22	2	AAW65687	AAW65687 Fibronect
43	49	92.5	22	2	AAW65688	AAW65688 Fibronect
44	49	92.5	22	2	AAW65689	AAW65689 Fibronect
45	49	92.5	22	2	AAW65690	AAW65690 Fibronect

ALIGNMENTS

RESULT 1
ID AAW65758 standard; peptide; 10 AA.

AC AAW65758;

DT 16-OCT-1998 (first entry)

DE Fibronectin binding protein-derived peptide #102.

KW microbial surface components recognising adhesive matrix molecule;

KW MGRAMM; fibronectin; fibronectin-binding protein; antibody; epitope;

KW antibiotic; bacterial infection; antibiotic-resistant strain.

OS Synthetic.

PN Staphylococcus aureus.

PD W09831389-A2.

PF 23-JUL-1998.

PR 21-JAN-1998; 98WO-US001222.

PT 21-JAN-1997; 97US-0036139P.

PS (TEXA) UNIV TEXAS A & M SYSTEM.

PI Hoesek M, Patil JM, House-Pompeo KL, Speziale P, Joh D;

PT Mcgavin MJ;

PT WPI; 1998-413816/35.

PS Example 9, Page 111, 201pp: English.

The invention relates to antibodies that bind to a fibronectin-binding domain of a fibronectin-binding protein, and inhibit binding of the protein to fibronectin. Also claimed are: (1) isolated peptides of a fibronectin-binding protein that do not bind to fibronectin; (2) fusion protein containing at least one peptide of a fibronectin-binding protein linked to a second amino acid sequence; (3) nucleic acid encoding the isolated peptide of (1). Antibodies, the isolated peptides of (1) and the nucleic acids are all useful for immunisation (active or passive) and (by inhibiting binding of bacteria to fibronectin) for preventing or treating infection in humans or other animals, particularly by staphylococci or

CC streptococci, e.g. meningitis, otitis media, pneumonia, endocarditis,
 CC mastitis in cattle, abortion in horses and many others. Since the
 CC antibodies block binding of bacteria, they should be effective against
 CC antibiotic-resistant strains, and may replace antibiotic therapy or
 CC increase its effectiveness. Sequences AAW65744-58 represent peptides
 CC which were synthesised to span the D3 motif of *S. aureus* fibronectin
 CC binding protein A
 CC
 SQ Sequence 10 AA:
 Query Match 100.0%; Score 53; DB 2; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.0051;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DFEEDTLPKV 10
 DB 1 DFEEDTLPKV 10
 RESULT 2
 AAW65742
 ID AAW65742 standard; peptide; 11 AA.
 AC AAW65742;
 XX
 DT 16-OCT-1998 (first entry)
 DE Peptide #86.
 XX
 KM microbial surface components recognising adhesive matrix molecule;
 KM MSCRAMM; fibronectin; fibronectin-binding protein; antibody; epitope;
 KM antibiotic; bacterial infection; antibiotic-resistant strain.
 XX
 OS Synthetic.
 OS Staphylococcus aureus.
 XX
 PN MO9831389-A2.
 XX
 PD 23-JUL-1998.
 PF 21-JAN-1998; 98WO-US001222.
 XX
 PR 21-JAN-1997; 97US-0036139P.
 PA (TEXA) UNIV TEXAS A & M SYSTEM.
 XX
 PI Hoeek M, Patrl JM, House-Pompeo KL, Speziale P, Joh D;
 PI McGavin MJ;
 XX
 DR WPI; 1998-413816/35.
 XX
 PT Antibody that binds to fibronectin-binding protein, preventing its
 PT binding to fibronectin - used to treat or prevent bacterial infection,
 PT especially by Staphylococci and Streptococci.
 PS Example 9; Page 110; 201pp; English.
 CC The invention relates to antibodies that bind to a fibronectin-binding
 CC domain of a fibronectin-binding protein, and inhibit binding of the
 CC protein to fibronectin. Also claimed are: (1) isolated peptides of a
 CC fibronectin-binding protein that do not bind to fibronectin; (2) fusion
 CC protein containing at least one peptide of a fibronectin-binding protein
 CC linked to a second amino acid sequence; (3) nucleic acid encoding the
 CC isolated peptide of (1). Antibodies, the isolated peptides of (1) and the
 CC nucleic acids are all useful for immunisation (active or passive) and (by
 CC inhibiting binding of bacteria to fibronectin) for preventing or treating
 CC infection in humans or other animals, particularly by staphylococci or
 CC streptococci, e.g. meningitis, otitis media, pneumonia, endocarditis,
 CC mastitis in cattle, abortion in horses and many others. Since the
 CC antibodies block binding of bacteria, they should be effective against
 CC antibiotic-resistant strains, and may replace antibiotic therapy or
 CC increase its effectiveness. The present sequence is shown in the
 CC specification

XX
 SQ Sequence 11 AA:
 Query Match 100.0%; Score 53; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 0.0057;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DFEEDTLPKV 10
 DB 2 DFEEDTLPKV 11
 RESULT 3
 AAW65669
 ID AAW65669 standard; peptide; 22 AA.
 AC AAW65669;
 XX
 DT 16-OCT-1998 (first entry)
 DE Peptide #13.
 XX
 KM microbial surface components recognising adhesive matrix molecule;
 KM MSCRAMM; fibronectin; fibronectin-binding protein; antibody; epitope;
 KM antibiotic; bacterial infection; antibiotic-resistant strain.
 XX
 OS Synthetic.
 OS Staphylococcus aureus.
 XX
 PN MO9831389-A2.
 XX
 PD 23-JUL-1998.
 PF 21-JAN-1998; 98WO-US001222.
 XX
 PR 21-JAN-1997; 97US-0036139P.
 PA (TEXA) UNIV TEXAS A & M SYSTEM.
 XX
 PI Hoeek M, Patrl JM, House-Pompeo KL, Speziale P, Joh D;
 PI McGavin MJ;
 XX
 DR WPI; 1998-413816/35.
 XX
 PT Antibody that binds to fibronectin-binding protein, preventing its
 PT binding to fibronectin - used to treat or prevent bacterial infection,
 PT especially by Staphylococci and Streptococci.
 PS Example 3; Page 93; 201pp; English.
 CC The invention relates to antibodies that bind to a fibronectin-binding
 CC domain of a fibronectin-binding protein, and inhibit binding of the
 CC protein to fibronectin. Also claimed are: (1) isolated peptides of a
 CC fibronectin-binding protein that do not bind to fibronectin; (2) fusion
 CC protein containing at least one peptide of a fibronectin-binding protein
 CC linked to a second amino acid sequence; (3) nucleic acid encoding the
 CC isolated peptide of (1). Antibodies, the isolated peptides of (1) and the
 CC nucleic acids are all useful for immunisation (active or passive) and (by
 CC inhibiting binding of bacteria to fibronectin) for preventing or treating
 CC infection in humans or other animals, particularly by staphylococci or
 CC streptococci, e.g. meningitis, otitis media, pneumonia, endocarditis,
 CC mastitis in cattle, abortion in horses and many others. Since the
 CC antibodies block binding of bacteria, they should be effective against
 CC antibiotic-resistant strains, and may replace antibiotic therapy or
 CC increase its effectiveness. The present sequence is shown in the
 CC specification
 SQ Sequence 22 AA;
 Query Match 100.0%; Score 53; DB 2; Length 22;
 Best Local Similarity 100.0%; Pred. No. 0.012; Mismatches 0; Indels 0; Gaps 0;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DFEEDTLPKV 10

Db 13 DFEDTLPKV 22

RESULT 4
AAP82118 standard; protein; 37 AA.

XX AAP82118;

XX 25-MAR-2003 (revised)

DT 05-JUN-1990 (first entry)

XX Fibronectin binding protein.

XX Fibronectin binding protein; S.aureus; immunisation; mastitis; ruminants;
KM wound infection; diagnosis.

XX Staphylococcus aureus.

XX EP294349-A.

XX 07-DEC-1988.

XX 30-MAY-1988; 88EP-00850188.

XX 01-JUN-1987; 87SE-00002272.

XX (ALFA) ALFA LAVAL AGRIC INT AB.

XX Lindberg MK, Signas LC, Wadstrom TM, Froman G;

XX WPI: 1988-347978/49.

XX N-PSDB; AAN62056.

XX Hybrid DNA encoding Staphylococcus aureus fibronectin binding protein -
PT useful for immunisation and topical application to prevent staphylococcal
XX infections.

XX Claim 11, Page 12; 23pp; English.

XX The S.aureus fibronectin binding protein may be included in a hybrid
CC protein. The protein may be used to immunise ruminants against
CC staphylococcal mastitis, pref. when given at 0.5-5 microg/kg, using 3

CC doses at 1-3 week intervals; and for topical applicn. to prevent wound
CC infection, pref. using isotonic saline soln. of concn. 25-250 microg/mg.

CC The DNA encoding the binding protein and the hybrid protein may be
CC immobilised on a carrier and used to diagnose staphylococcal infections.
CC (Updated on 25-MAR-2003 to correct PA field.)

XX Sequence 37 AA;

Query Match 100.0%; Score 53; DB 1; Length 37;

Best Local Similarity 100.0%; Pred. No. 0.022; Mismatches 0; Indels 0; Gaps 0;

QY 1 DFEDTLPKV 10
Db 28 DFEDTLPKV 37

RESULT 5
AAP81958 standard; peptide; 37 AA.

XX AAP81958;

XX 22-JUN-2001 (first entry)

XX Fibronectin fragment and fibrin related peptide SEQ ID NO:1134.

XX Protection; endogenous therapeutic peptide; peptidase; conjugation;
KM blood component; modification; succinimidy; maleimido group; amino;

KM hydroxyl; thiol; hormone; growth factor; neurotransmitter.

XX Homo sapiens.

OS Synthetic.

XX WO200069900-A2.

XX 23-NOV-2000.

XX 17-MAY-2000; 2000WO-US013576.

XX 17-MAY-1999; 99US-0134406P.

XX 10-SEP-1999; 99US-0153406P.

XX 15-OCT-1999; 99US-0159783P.

XX (CONJ-) CONJUCHEM INC.

XX Bridon DP, Ezrin AM, Milner PG, Holmes DL, Thibaudau K;

XX WPI: 2001-112059/12.

XX Modifying and attaching therapeutic peptides to albumin prevents
PT peptidase degradation, useful for increasing length of in vivo activity.
XX Disclosure; Page 566; 733pp; English.

XX The present invention describes a modified therapeutic peptide (I)

CC comprising a therapeutically active amino acid region (III) and a
CC reactive group (II) (e.g. succinimidy and maleimido groups) attached to

CC a less therapeutically active amino acid region (IV), which covalently
CC bonds with amino/hydroxyl/thiol groups on blood components to form a

CC peptide stabilised therapeutic peptide composed of 3-50 amino acids.
CC (I) are useful for modifying therapeutic peptides e.g. hormones, growth

CC factors and neurotransmitters, to protect them from peptidase activity in
CC vivo for the treatment of various disorders. Endogenous therapeutic

CC peptides are not suitable as drug candidates as they require frequent
CC administration due to rapid degradation by peptidases in the body.

CC Modifying and attaching therapeutic peptides to albumin prevents or
CC reduces the action of peptidases to increase length of activity (half

CC life) and specificity as bonding to large molecules decreases.
CC intracellular uptake and interference with physiological processes.

CC AAP80829 to AAP92441 represent peptides which can be used in the
CC exemplification of the present invention

XX Sequence 37 AA;

Query Match 100.0%; Score 53; DB 4; Length 37;

Best Local Similarity 100.0%; Pred. No. 0.022; Mismatches 0; Indels 0; Gaps 0;

QY 1 DFEDTLPKV 10
Db 28 DFEDTLPKV 37

RESULT 6
AAP80662 standard; protein; 38 AA.

XX AAP80662;

XX 25-MAR-2003 (revised)

DT 07-OCT-1990 (first entry)

XX Protein with fibronectin binding ability.

XX Hybrid DNA molecule; fibronectin binding; mastitis; ruminants;
KM wound infection.

XX Staphylococcus aureus.

XX EP294349-A.

PD 07-DEC-1988.
 XX
 PF 30-MAY-1988; 88EP-00850188.
 XX
 PR 01-JUN-1987; 87SE-00002272.
 XX
 PA (ALFA) ALFA LAVAL AGRIC INT AB.
 XX
 PI Lindberg MK, Signas LC, Wedstrom TM, Froman G;
 XX WPI; 1988-347978/49.
 DR N-PSDB; AAN81099.
 XX
 PT Hybrid DNA encoding Staphylococcus aureus fibronectin binding protein -
 PT useful for immunisation and topical application to prevent staphylococcal
 PT infections.
 CC
 CC Claim 11; Page 12; 23pp; English.
 PS
 CC The peptide has fibronectin binding ability. It is useful for immunising
 CC ruminants against staphylococcal mastitis; pref. when used at 0.5-5
 CC micrograms/kg, using 3 doses given at 1-3 week intervals; for topical
 CC application to prevent wound infection, using an isotonic saline soln. of
 CC concn. 25-250 micrograms/ml; and, when immobilised on a carrier, for
 CC diagnosing staphylococcal infections. (Updated on 25-MAR-2003 to correct
 CC PF field.) (Updated on 25-MAR-2003 to correct PA field.)
 CC
 SQ Sequence 38 AA;

Query Match 100.0%; Score 53; DB 1; Length 38;
 Best Local Similarity 100.0%; Pred. No. 0.023;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DEEDTLPRV 10
 |||||
 DB 29 DEEDTLPRV 38

RESULT 7
 ID AAY29087 standard; protein; 134 AA.
 AC AAY29087;

XX 28-SEP-1999 (first entry)
 DT
 DE

S. aureus fibronectin binding protein A (FnBA) binding domain.

XX Bovine herpes virus-2; BHV-2; cytokine; immune response; immunogen; IL;
 XX interleukin; colony stimulating factor; CSF; interferon; IFN; TNF;
 KW tumour necrosis factor; recombinant virus; vaccine; mucosal disease;
 KW mastitis; breast cancer; stress-induced disease; binding domain; FnBA;
 KW fibronectin binding protein.

XX Staphylococcus aureus.

OS
 PN WO9916892-A1.

PD 08-APR-1999.

PF 29-SEP-1998; 98WO-GB002927.

PR 29-SEP-1997; 97GB-00020633.

XX (UWBR-) UNIV BRISTOL.

PI Bradley AJ, Duffas WPH;

DR WPI; 1999-255101/21.

XX N-PSDB; AAX91504.

XX New bovine herpes virus-2 vectors.

PS Example 2; Fig 8A-B; 130pp; English.
 XX
 CC The invention provides bovine herpes virus-2 (BHV-2) based vectors that
 CC comprise at least one cytokine-encoding DNA sequence. The expression of
 CC cytokines in mammals can up-regulate immune responses to the immunogens.
 CC The cytokine is selected from interleukins (IL), colony stimulating
 CC factors (CSF), interferons (IFN) and tumour necrosis factors (TNF). The
 CC BHV-2 based vector or recombinant virus can be used as vaccines. They can
 CC be used for preventing or treating a mucosal disease in a subject, e.g.
 CC ruminants, cattle, sheep, goats, cats, horses, or man, particularly
 CC mastitis in cows or breast cancers in humans. They can also be used for
 CC preventing or treating a stress-induced disease. The present sequence
 CC represents the binding domain of a previously published S. aureus
 CC fibronectin binding protein A (FnBA) sequence. The FnB binding domain
 CC gene sequence FnBAB, cloned for use in this invention has 97.8 percent
 CC identity when compared to the previously published FnBA and FnBB gene
 CC sequences
 CC
 SQ Sequence 134 AA;

Query Match 100.0%; Score 53; DB 2; Length 134;
 Best Local Similarity 100.0%; Pred. No. 0.092;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DEEDTLPRV 10
 |||||
 DB 105 DEEDTLPRV 114

RESULT 8
 ID AAM31556 standard; protein; 139 AA.
 AC AAM31556;

XX 27-AUG-2003 (revised)
 DT 25-MAR-2003 (revised)
 DT 21-MAY-1998 (first entry)
 XX

DE Fibronectin-binding MSCRAMM derivative pOD.

XX Fibronectin; pOD; collagen binding protein; sepsis; infection;
 KW microbial surface component recognising adhesive matrix molecule; MSCRAMM;
 KW adhesin; vaccine; immunisation; diagnosis; therapy; mastitis.

XX Staphylococcus aureus.

OS
 FH Key Location/Qualifiers

FT Peptide 1..12 /note="vector pOE30-derived peptide"

PN WO9743314-A2.

PD 20-NOV-1997.

PF 14-MAY-1997; 97WO-US008210.

PR 16-MAY-1996; 96US-0017678P.

PA (TEXA) UNIV TEXAS A & M SYSTEM.

XX (UABR-) UAB RES FOUND.

PI Hoeek M, Patti JM, House-Pompeo K, Schanam N, Symersky J;

DR WPI; 1998-008801/01.

XX Antibody that interacts with collagen binding domain of Staphylococcal

PT cna gene product - useful to prevent bacterial sepsis in animal infected

XX with Staphylococcus aureus.

PS Disclosure; Page 91; 143pp; English.

XX This protein comprises Staphylococcus aureus fibronectin-binding

CC microbial surface component recognising adhesive matrix molecule (MSCRAMM)
 CC -derivative PQD, plus a vector-derived N-terminal peptide. The invention
 CC relates to claimed nucleic acid sequences (see AA093436-38) encoding S.
 CC aureus collagen binding protein (CBP) epitopes M17, M31 and M55 (see
 CC AA01552-54) that confer protection against S. aureus infection. CBP
 CC protein and antigenic epitopes are contemplated for use in the treatment
 CC of pathological infections, especially to prevent bacterial adhesion to
 CC collagen. The epitopes are also contemplated for use in the preparation
 CC of vaccines and as carrier proteins in vaccine formulations, as well as
 CC in the formulation of compositions for the prevention of S. aureus
 CC infection. pCp33 and PQD (see AA01556) were used to raise anti-MSCRAMM
 CC polyclonal antibodies used in passive immunisation against bovine
 CC mastitis. (Updated on 25-MAR-2003 to correct PI field.) (Updated on 27-
 CC AUG-2003 to correct OS field.)

SO Sequence 139 AA:

Query Match 100.0%; Score 53; DB 2; Length 139;
 Best Local Similarity 100.0%; Pred. No. 0.096;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DFEEDTLPKV 10
 |||||
 DB 119 DFEEDTLPKV 128

RESULT 9

ABU15854 standard; protein: 961 AA.

AC ABU15854;
 DT 19-JUN-2003 (first entry)

DE Protein encoded by Prokaryotic essential gene #1381.

KM Antisense; prokaryotic essential gene; cell proliferation; drug design.
 OS Staphylococcus aureus.
 PN MO200277183-A2.

PD 03-OCT-2002.

PF 21-MAR-2002; 2002WO-US009107.

PR 21-MAR-2001; 2001US-00815242.

PR 06-SEP-2001; 2001US-00948993.

PR 25-OCT-2001; 2001US-0342923P.

PR 08-FEB-2002; 2002US-00072851.

PR 06-MAR-2002; 2002US-0362699P.

PA (ELIT-) ELITRA PHARM INC.

PI Wang J, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW,
 PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;
 PI N-PSDB; ACA19724.

PR WPI: 2001-029926/02.

PT New antisense nucleic acids, useful for identifying proteins or screening
 PT for homologous nucleic acids required for cellular proliferation to
 PT isolate candidate molecules for rational drug discovery programs.

PS Claim 25; SEQ ID NO 43778; 1766bp; English.

XX The invention relates to an isolated nucleic acid comprising any one of
 CC the 6213 antisense sequences given in the specification where expression
 CC of the nucleic acid inhibits proliferation of a cell. Also included are:
 CC (1) a vector comprising a promoter operably linked to the nucleic acid
 CC encoding a polypeptide whose expression is inhibited by the antisense
 CC nucleic acid; (2) a host cell containing the vector; (3) an isolated
 CC polypeptide or its fragment whose expression is inhibited by the

CC antisense nucleic acid; (4) an antibody capable of specifically binding
 CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular
 CC proliferation; (7) identifying a gene in an operon required for
 CC proliferation; (8) identifying a compound that influences the activity of
 CC the gene product or that has an activity against a biological pathway
 CC required for proliferation, or that inhibits cellular proliferation; (9)
 CC identifying a gene required for cellular proliferation or the biological
 CC pathway in which a proliferation-required gene or its gene product lies
 CC or a gene on which the test compound that inhibits proliferation of an
 CC organism acts; (9) manufacturing an antibiotic; (10) profiling a
 CC compound's activity; (11) a culture comprising strains in which the gene
 CC product is overexpressed or underexpressed; (12) determining the extent
 CC to which each of the strains is present in a culture or collection of
 CC strains; or (13) identifying the target of a compound that inhibits the
 CC proliferation of an organism. The antisense nucleic acids are useful for
 CC identifying proteins or screening for homologous nucleic acids required
 CC for cellular proliferation to isolate candidate molecules for rational
 CC drug discovery programs, or for screening homologous nucleic acids
 CC required for proliferation in cells other than S. aureus, S. typhimurium,
 CC K. pneumoniae or P. aeruginosa. The present sequence is encoded by one of
 CC the target prokaryotic essential genes. Note: The sequence data for this
 CC patent did not form part of the printed specification, but was obtained
 CC in electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences

SO Sequence 961 AA:

Query Match 100.0%; Score 53; DB 6; Length 961;
 Best Local Similarity 100.0%; Pred. No. 0.82;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DFEEDTLPKV 10
 |||||
 DB 796 DFEEDTLPKV 805

RESULT 10

AAU33960 standard; protein: 978 AA.

AC AAU33960;
 DT 14-FEB-2002 (first entry)

DE Staphylococcus aureus cellular proliferation protein #236.

KM Antisense; prokaryotic cellular proliferation protein; antibiotic;
 KW antibacterial; drug design.

OS Staphylococcus aureus.

PN MO200170955-A2.

PD 27-SEP-2001.

PF 21-MAR-2001; 2001WO-US009180.

PR 21-MAR-2000; 2000US-0191078P.

PR 23-MAY-2000; 2000US-0206848P.

PR 26-MAY-2000; 2000US-0207727P.

PR 23-OCT-2000; 2000US-0242578P.

PR 27-NOV-2000; 2000US-0253625P.

PR 22-DEC-2000; 2000US-0257931P.

PR 16-FEB-2001; 2001US-0269308P.

PA (ELIT-) ELITRA PHARM INC.

PI Haselbeck R, Ohlsen KL, Zyskind JW, Wall D, Trawick JD, Carr GJ;
 PI Yamamoto RT, Xu HH;
 PI WPI: 2001-611495/70.
 DR N-PSDB; AAS51819.

PT New polynucleotides for the identification and development of
PT antibiotics, comprise sequences of antisense nucleic acids.
XX
PS Example 3; SEQ ID NO 5456; 511pp; English.
XX
CC The invention relates to antisense inhibitors of genes essential to
CC prokaryotic cellular proliferation, their use in identifying the genes,
CC their use in the discovery of novel antibiotics, the essential genes
CC themselves and the encoded proteins. The prokaryotes used are *Escherichia*
CC coli, *Staphylococcus aureus*, *Salmonella typhi*, *Klebsiella pneumoniae*,
CC *Pseudomonas aeruginosa* and *Enterococcus faecalis*. The invention is also
CC useful for the identification of potential new targets for antibiotic
CC development. The antisense nucleic acids can also be used to identify
CC proteins used in proliferation, to express these proteins, and to obtain
CC antibodies capable of binding to the expressed proteins. The proteins can
CC be used to screen compounds in rational drug discovery programmes. The
CC antisense nucleic acid sequence is also useful to screen for homologous
CC nucleic acids which are required for cell proliferation in a wide variety
CC of organisms. The present sequence represents an essential prokaryotic
CC cellular proliferation protein. Note: The sequence data for this patent
CC did not form part of the printed specification, but was obtained in
CC electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
CC
SQ Sequence 978 AA;
XX
Query Match 100.0%; Score 53; DB 4; Length 978;
Best Local Similarity 100.0%; Pred. No. 0.84;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1 DFEEDTLPRV 10
|||
Db 827 DFEEDTLPRV 836
XX
RESULT 11
AAU37093
ID AAU37093 standard; protein; 1001 AA.
XX
AC AAU37093;
XX
DT 14-FEB-2002 (first entry)
XX
DE Staphylococcus aureus cellular proliferation protein #1263.
XX
DE Staphylococcus aureus cellular proliferation protein; antibiotic;
XX
KM antibacterial; drug design.
XX
OS Staphylococcus aureus.
XX
PN WO200170955-A2.
XX
PD 27-SEP-2001.
XX
PF 21-MAR-2001; 2001WO-US009180.
XX
PR 21-MAR-2000; 2000US-0191078P.
PR 23-MAY-2000; 2000US-0206848P.
PR 26-MAY-2000; 2000US-0207727P.
PR 23-OCT-2000; 2000US-0242578P.
PR 27-NOV-2000; 2000US-0253625P.
PR 22-DEC-2000; 2000US-0257931P.
PR 16-FEB-2001; 2001US-0269308P.
XX
PA (ELITR-) ELITRA PHARM INC.
XX
XX Haaslebeck R, Ohlsen KL, Zyskind JW, Wall D, Trawick JD, Carr GU,
PI Yamamoto RT, Xu HH;
XX
DR WPI: 2001-611495/70.
XX
DR N-PSDB; AAS54952.
XX
PT New polynucleotides for the identification and development of

PT antibiotics, comprise sequences of antisense nucleic acids.
XX
PS Example 3; SEQ ID NO 12686; 511pp; English.
XX
CC The invention relates to antisense inhibitors of genes essential to
CC prokaryotic cellular proliferation, their use in identifying the genes,
CC their use in the discovery of novel antibiotics, the essential genes
CC themselves and the encoded proteins. The prokaryotes used are *Escherichia*
CC coli, *Staphylococcus aureus*, *Salmonella typhi*, *Klebsiella pneumoniae*,
CC *Pseudomonas aeruginosa* and *Enterococcus faecalis*. The invention is also
CC useful for the identification of potential new targets for antibiotic
CC development. The antisense nucleic acids can also be used to identify
CC proteins used in proliferation, to express these proteins, and to obtain
CC antibodies capable of binding to the expressed proteins. The proteins can
CC be used to screen compounds in rational drug discovery programmes. The
CC antisense nucleic acid sequence is also useful to screen for homologous
CC nucleic acids which are required for cell proliferation in a wide variety
CC of organisms. The present sequence represents an essential prokaryotic
CC cellular proliferation protein. Note: The sequence data for this patent
CC did not form part of the printed specification, but was obtained in
CC electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
CC
SQ Sequence 1001 AA;
XX
Query Match 100.0%; Score 53; DB 4; Length 1001;
Best Local Similarity 100.0%; Pred. No. 0.86;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1 DFEEDTLPRV 10
|||
Db 850 DFEEDTLPRV 859
XX
RESULT 12
AAP82115
ID AAP82115 standard; protein; 1018 AA.
XX
AC AAP82115;
XX
DT 25-MAR-2003 (revised)
DT 05-JAN-1990 (first entry)
XX
DE Fibronectin binding protein.
XX
DE Fibronectin binding protein; S.aureus; immunisation; mastitis; ruminants;
XX
KM wound infection; diagnosis.
XX
OS Staphylococcus aureus.
XX
PN EP294349-A.
XX
PD 07-DEC-1988.
XX
PF 30-MAY-1988; 88EP-00850188.
XX
PR 01-JUN-1987; 87SE-00002272.
XX
PA (ALFA) ALFA LAVAL AGRIC INT AB.
XX
PI Lindberg MK, Signas LC, Wadstrom TW, Froman G;
XX
DR WPI: 1988-347978/49.
XX
DR P-PSDB; AAP82115.
XX
PT Hybrid DNA encoding Staphylococcus aureus fibronectin binding protein -
PT useful for immunisation and topical application to prevent staphylococcal
XX
PS infections.
XX
PS Disclosure; Fig. 8A:1-8A:2; 23pp; English.
XX
XX The S.aureus fibronectin binding protein may be included in a hybrid
CC protein. The protein may be used to immunise ruminants against

CC staphylococcal mastitis, pref. when given at 0.5-5 microg/kg, using 3
CC doses at 1-3 week intervals; and for topical applic. to prevent wound
CC infection, pref. using isotonic saline soln. of concn. 25-250 microg/mg.
CC The DNA encoding the binding protein and the hybrid protein may be
CC immobilised on a carrier and used to diagnose staphylococcal infections.
CC (Updated on 25-MAR-2003 to correct PA field.)
XX

SO Sequence 1018 AA;

Query Match 100.0%; Score 53; DB 1; Length 1018;
Best Local Similarity 100.0%; Pred. No. 0.88;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DFEEDTLPKV 10
|||||
Db 849 DFEEDTLPKV 858

RESULT 13
AAU37245

ID AAU37245 standard; protein; 1018 AA.

AC AAU37245;

DT 14-FEB-2002 (first entry)

DE Staphylococcus aureus cellular proliferation protein #A415.

KW Antisense; prokaryotic cellular proliferation protein; antibiotic;
antibacterial; drug design.

OS Staphylococcus aureus.

PN MO200170955-A2.

PD 27-SEP-2001.

PF 21-MAR-2001; 2001MO-US009180.

PR 21-MAR-2000; 2000US-0191078P.

PR 23-MAY-2000; 2000US-0206848P.

PR 26-MAY-2000; 2000US-0207727P.

PR 23-OCT-2000; 2000US-0242578P.

PR 27-NOV-2000; 2000US-0253625P.

PR 22-DEC-2000; 2000US-0257931P.

PR 16-FEB-2001; 2001US-0269308P.

(ELIT-) ELITRA PHARM INC.

PI Haselbeck R, Ohlsen KL, Zyskind JW, Wall D, Trawick JD, Carr GJ;

PI Yamamoto RT, Xu HH;

DR WPI; 2001-611495/70.

DR N-PSDB; AAS55104.

PT New polynucleotides for the identification and development of

PT antibiotics, comprise sequences of antisense nucleic acids.

PS Example 3; SEQ ID NO 12838; 511p; English.

XX The invention relates to antisense inhibitors of genes essential to
CC prokaryotic cellular proliferation, their use in identifying the genes,
CC their use in the discovery of novel antibiotics, the essential genes
CC themselves and the encoded proteins. The prokaryotes used are Escherichia
CC coli, Staphylococcus aureus, Salmonella typhi, Klebsiella pneumoniae,
CC Pseudomonas aeruginosa and Enterococcus faecalis. The invention is also
CC useful for the identification of potential new targets for antibiotic
CC development. The antisense nucleic acids can also be used to identify
CC proteins used in proliferation, to express these proteins, and to obtain
CC antibodies capable of binding to the expressed proteins. The proteins can
CC be used to screen compounds in rational drug discovery programmes. The
CC antisense nucleic acid sequence is also useful to screen for homologous
CC nucleic acids which are required for cell proliferation in a wide variety

CC of organisms. The present sequence represents an essential prokaryotic
CC cellular proliferation protein. Note: The sequence data for this patent
CC did not form part of the printed specification, but was obtained in
CC electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX

SO Sequence 1018 AA;

Query Match 100.0%; Score 53; DB 4; Length 1018;
Best Local Similarity 100.0%; Pred. No. 0.88;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DFEEDTLPKV 10
|||||
Db 849 DFEEDTLPKV 858

RESULT 14
AAU34301

ID AAU34301 standard; protein; 1018 AA.

AC AAU34301;

DT 14-FEB-2002 (first entry)

DE Staphylococcus aureus cellular proliferation protein #577.

KW Antisense; prokaryotic cellular proliferation protein; antibiotic;
antibacterial; drug design.

OS Staphylococcus aureus.

PN MO200170955-A2.

PD 27-SEP-2001.

PF 21-MAR-2001; 2001MO-US009180.

PR 21-MAR-2000; 2000US-0191078P.

PR 23-MAY-2000; 2000US-0206848P.

PR 26-MAY-2000; 2000US-0207727P.

PR 23-OCT-2000; 2000US-0242578P.

PR 27-NOV-2000; 2000US-0253625P.

PR 22-DEC-2000; 2000US-0257931P.

PR 16-FEB-2001; 2001US-0269308P.

(ELIT-) ELITRA PHARM INC.

PI Haselbeck R, Ohlsen KL, Zyskind JW, Wall D, Trawick JD, Carr GJ;

PI Yamamoto RT, Xu HH;

DR WPI; 2001-611495/70.

DR N-PSDB; AAS52160.

PT New polynucleotides for the identification and development of

PT antibiotics, comprise sequences of antisense nucleic acids.

PS Example 3; SEQ ID NO 5797; 511p; English.

XX The invention relates to antisense inhibitors of genes essential to
CC prokaryotic cellular proliferation, their use in identifying the genes,
CC their use in the discovery of novel antibiotics, the essential genes
CC themselves and the encoded proteins. The prokaryotes used are Escherichia
CC coli, Staphylococcus aureus, Salmonella typhi, Klebsiella pneumoniae,
CC Pseudomonas aeruginosa and Enterococcus faecalis. The invention is also
CC useful for the identification of potential new targets for antibiotic
CC development. The antisense nucleic acids can also be used to identify
CC proteins used in proliferation, to express these proteins. The proteins can
CC be used to screen compounds in rational drug discovery programmes. The
CC antisense nucleic acid sequence is also useful to screen for homologous
CC nucleic acids which are required for cell proliferation in a wide variety
CC of organisms. The present sequence represents an essential prokaryotic

CC cellular proliferation protein. Note: The sequence data for this patent
CC did not form part of the printed specification, but was obtained in
CC electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX

Sequence 1018 AA;

Query Match 100.0%; Score 53; DB 4; Length 1018;
Best Local Similarity 100.0%; Pred. No. 0.88;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DFEEDTLPKV 10
|||
Db 849 DFEEDTLPKV 858

RESULT 15

ABJ18922
ID ABJ18922 standard; protein; 1018 AA.

XX ABJ18922;

XX 06-MAR-2003 (first entry)

DE Pathogen specific antigen related staphylococcal protein SEQ ID No 68.

XX Antibacterial; virucide; fungicide; protozoacide; cytostatic; anti-HIV;
XX hyperimmune; serum-reactive; antigen; pathogen; tumour; allergen;
XX auto-immunity; vaccine; staphylococcal infection; antibody; cancer;
XX autoimmune disease; HIV; hepatitis.

OS Staphylococcus sp.

XX WO200259148-A2.

XX 01-AUG-2002.

XX 21-JAN-2002; 2002WO-EP000546.

XX 26-JAN-2001; 2001AT-00000130.

XX (CIST-) CISTEM BIOTECHNOLOGIES GMBH.

XX Meinke A, Nagy B, Von Ahnen U, Klade C, Henics T, Zauner W;
PI Minh DB, Vytvytska O, Eitz H, Dryla A, Weichart T, Hafner M,
PI Tempelmeier B;

XX WPI; 2003-075410/07.

PT Identifying, isolating and producing hyperimmune serum-reactive antigens
PT from a pathogen, for preparing vaccine or medicament for treating or
PT preventing e.g. staphylococcal infections, comprises providing antibody
PT preparation.

PS Example 7; Page 157; 252pp; English.

XX The invention relates to a novel method for identifying, isolating and
CC producing hyperimmune serum-reactive antigens from a pathogen, tumour,
CC allergen, a tissue or host prone to auto-immunity, where the antigens are
CC used in a vaccine, comprises providing antibody preparation from a plasma
CC pool of a type of animal, or individual sera with antibodies against the
CC specific pathogen, tumour, allergen, tissue or host prone to auto-
CC immunity. The hyperimmune serum-reactive antigens comprising any of the
CC 62 sequences of 53-2261 amino acids fully defined in the specification,
CC or their hyperimmune fragments are useful for the manufacture of a
CC pharmaceutical preparation, particularly a vaccine against staphylococcal
CC infections or colonisation against *S. aureus* or *S. epidermidis*. The
CC preparation of antibodies is useful for the manufacture of a medicament
CC for treating or preventing staphylococcal infections or colonisation
CC against *S. aureus* or *S. epidermidis*. The antibody preparations may also
CC be used for diagnostic and imaging purposes. Other conditions that can be
CC treated include cancer, autoimmune diseases or infections caused by viral
CC (e.g. HIV, hepatitis A, B or C), fungal or protozoan pathogens. This

CC sequence represents a staphylococcal protein relating to the method for
CC identifying and producing pathogen specific antigens of the invention
XX

Sequence 1018 AA;

Query Match 100.0%; Score 53; DB 6; Length 1018;
Best Local Similarity 100.0%; Pred. No. 0.88;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DFEEDTLPKV 10
|||
Db 849 DFEEDTLPKV 858

Search completed: October 25, 2005, 21:29:15
Job time : 70.7126 secs

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OM protein - protein search, using sw model

Run on: October 22, 2005, 08:04:46 ; Search time 11.6093 Seconds
(without alignments)
82.880 Million cell updates/sec

Title: US-10-731-238-100
Perfect score: 51
Sequence: 1 NSVDFEEDTL 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 793: *
1: pirl: *
2: pirl: *
3: pirl: *
4: pirl: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	51	100.0	940	2	S19702 fibronectin-binding
2	51	100.0	961	2	G90053 fibronectin-binding
3	51	100.0	1018	2	A32182 fibronectin-binding
4	51	100.0	1038	2	H90053 fibronectin-binding
5	38	74.5	275	2	D96826 fibronectin-binding
6	37	72.5	520	2	F70350 recombinant prote
7	36	70.6	345	2	A11448 gp18 (Bacteriophag
8	36	70.6	570	2	AB1581 DNA polymerase bet
9	36	70.6	829	2	S50246 STR4 protein - yea
10	35	68.6	165	2	S14477 glyceroldehydro-3-P
11	35	68.6	333	2	F90881 glyceroldehydro-3-P
12	35	68.6	333	2	C85737 glyceroldehydro-3-P
13	35	68.6	470	2	DB9890 cell division prot
14	35	68.6	476	2	S5085 exoenzymes regulat
15	35	68.6	488	2	T43789 H+-transporting tw
16	35	68.6	916	2	B84473 copII-like retroel
17	35	68.6	1011	2	JC8059 neuronal cell cycl
18	35	68.6	1251	2	A56677 hypotrichal prote
19	35	68.6	216	2	S58652 hypotrichal prote
20	34	66.7	249	2	G82808 hypotrichal prote
21	34	66.7	265	2	C83090 probable permease
22	34	66.7	348	2	S64041 nitrogen fixatio
23	34	66.7	387	2	B90533 hypotrichal prote
24	34	66.7	557	2	S61154 long-chain fatty-a
25	34	66.7	566	2	H84037 hypotrichal prote
26	34	66.7	665	2	T13744 hypotrichal prote
27	34	66.7	794	2	T17870 glycoprotein B pre
28	34	66.7	928	1	VBSEWC hypotrichal prote
29	34	66.7	1184	2	T46039 hypotrichal prote

30	34	66.7	1227	2	B96673 hypotrichal prote
31	34	66.7	1871	2	D96796 probable heat choc
32	34	66.7	4688	2	F82885 hypotrichal prote
33	33.5	65.7	190	2	F82610 hypotrichal prote
34	33	64.7	92	2	JN0906 cytoactin proteins
35	33	64.7	126	2	S75768 hypotrichal prote
36	33	64.7	176	2	T23025 hypotrichal prote
37	33	64.7	422	2	D75251 enolase - Delnoco
38	33	64.7	429	2	G97025 probable membrane
39	33	64.7	433	2	H70141 enolase (eno) homo
40	33	64.7	489	2	S51428 hypotrichal prote
41	33	64.7	575	2	S50962 hypotrichal prote
42	33	64.7	669	2	T07754 zeaxanthin epoxida
43	33	64.7	718	2	C90555 hypotrichal prote
44	33	64.7	751	2	T21967 hypotrichal prote
45	33	64.7	818	2	T02823 probable membrane

ALIGNMENTS

RESULT 1

S19702 fibronectin-binding protein B - Staphylococcus aureus
C/Species: Staphylococcus aureus
C/Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
R/Accession: S19702
R/Joensen, K.; Signaes, C.; Mueller, H.P.; Lindberg, M.
Eur. J. Biochem. 202, 1041-1048, 1991
A/Title: Two different genes encode fibronectin binding proteins in Staphylococcus aureus
A/Reference number: S19702; PMID:92111475; PMID:1837266
A/Accession: S19702
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-940 <JOB>
A/Cross-references: UNIPROT:Q53682; EMBL:X62992; NID:949040; PIDN:CAA44726.1; PID:G58156;
C/Keywords: fibronectin binding

Query Match

Best Local Similarity 100.0%; Score 51; DB 2; Length 940;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NSVDFEEDTL 10
DB 782 NSVDFEEDTL 791

RESULT 2

G90053 hypotrichal protein fmb (imported) - Staphylococcus aureus (strain N315)
C/Species: Staphylococcus aureus
C/Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C/Accession: G90053
R/Kuroda, M.; Ohba, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguchi, K.; Minamide, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.; Ima, A.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
A/Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.
A/Reference number: A89758; PMID:11418146
A/Accession: G90053
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-961 <KUR>
A/Cross-references: UNIPROT:Q99RD3; GB:BA000018; PID:913702452; PIDN:BA843593.1; GSPDB:GT
A/Experimental source: strain N315
C/Genetics:
A/Gene: fmb

Query Match

Best Local Similarity 100.0%; Score 51; DB 2; Length 961;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NSVDFEEDTL 10

|||||
Db 793 NSVDPEEDTL 802

RESULT 3

A32192

fibronectin-binding protein - Staphylococcus aureus

C1.Date: 31-Jul-1989 #sequence_revision 31-Jul-1989 #text_change 16-Feb-1997

C1.Species: Staphylococcus aureus

C1.Accession: A32192

R1.Signaee: C.; Raucel, G.; Joansson, K.; Lindgren, P.E.; Anantharamiah, G.M.; Hoecek, M

Proc. Natl. Acad. Sci. U.S.A. 86, 699-703, 1989

A1.Title: Nucleotide sequence of the gene for a fibronectin-binding protein from Staphylo

A1.Reference number: A32192; PMID:8908998; PMID:2521391

A1.Accession: A32192

A1.Status: preliminary

A1.Molecule type: DNA

A1.Residues: 1-1018 <SIG>

A1.Cross-references: GB:J04151

C1.Keywords: fibronectin binding

Query Match 100.0%; Score 51; DB 2; Length 1018;
Best Local Similarity 100.0%; Pred. No. 0.15;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NSVDPEEDTL 10
|||||
Db 846 NSVDPEEDTL 855

RESULT 4

H90053

hypothetical protein fnb [imported] - Staphylococcus aureus (strain N315)

C1.Species: Staphylococcus aureus

C1.Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004

C1.Accession: H90053

R1.Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Ogu

ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.;

C.; Shiba, T.; Hatori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.

Lancet 357, 1225-1240, 2001

A1.Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.

A1.Reference number: A89758; PMID:21311952; PMID:1148146

A1.Accession: H90053

A1.Status: preliminary

A1.Molecule type: DNA

A1.Residues: 1-1038 <KUP>

A1.Cross-references: UNIPROT:Q99R02; GB:BA000018; PID:G13702453; PIDN:BA843594.1; GSPDB:G

C1.Genetics:

A1.Gene: fnb

Query Match 100.0%; Score 51; DB 2; Length 1038;
Best Local Similarity 100.0%; Pred. No. 0.15;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NSVDPEEDTL 10
|||||
Db 842 NSVDPEEDTL 851

RESULT 5

D96826

hypothetical protein T8K14.7 [imported] - Arabidopsis thaliana

C1.Species: Arabidopsis thaliana (mouse-ear cress)

C1.Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004

C1.Accession: D96826

R1.Theologis, A.; Eckert, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,

Chin, C.W.; Chung, M.K.; Com, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;

ansen, N.F.; Hughes, B.; Huizer, L.

Nature 408, 816-820, 2000

A1.Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.

C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziani,

Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A1.Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, I
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A1.Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.

A1.Reference number: A8614; PMID:21016719; PMID:11130712

A1.Accession: D96826

A1.Status: preliminary

A1.Molecule type: DNA

A1.Residues: 1-275 <STO>

A1.Cross-references: UNIPROT:Q9SAL8; GB:AE005173; NID:g4835758; PIDN:AAD30225.1; GSPDB:GN

C1.Genetics:

A1.Gene: T8K14.7

A1.Map position: 1

Query Match 74.5%; Score 38; DB 2; Length 275;
Best Local Similarity 70.0%; Pred. No. 10;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 NSVDPEEDTL 10
|||:|||||
Db 38 NSYEFEDSL 47

RESULT 6

F70350

recombination protein RecN - Aquifex aeolicus

C1.Species: Aquifex aeolicus

C1.Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 09-Jul-2004

C1.Accession: F70350

R1.Decker, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.; Ove

V.

Nature 392, 353-358, 1998

A1.Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.

A1.Reference number: A70300; PMID:9819666; PMID:9537320

A1.Accession: F70350

A1.Status: preliminary; nucleic acid sequence not shown; translation not shown

A1.Molecule type: DNA

A1.Residues: 1-520 <ACF>

A1.Cross-references: UNIPROT:Q66834; GB:AE000695; NID:g2983180; PIDN:AAC06789.1; PID:g298;

A1.Experimental source: strain VPS

C1.Genetics:

A1.Gene: recN

C1.Superfamily: recN protein

Query Match 72.5%; Score 37; DB 2; Length 520;
Best Local Similarity 70.0%; Pred. No. 34;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 NSVDPEEDTL 10
|||||:
Db 310 NSVDPEEDSL 319

RESULT 7

AB1448

gpi8 (Bacteriophage A118) homolog 11n0121 [imported] - Listeria innocua (strain C11p1126;

C1.Species: Listeria innocua

C1.Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004

C1.Accession: AB1448

R1.Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloeker,

.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurgey, O.; Entian, K.D.; Fahn, H.;

D.; Jones, L.M.; Karet, U.

Science 294, 849-852, 2001

A1.Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkut, G.; Maduno, E.; Maitournam, A.; Mat

ok, C.; Schlueter, T.; Simoes, N.; Tietzer, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland,

A1.Title: Comparative genomes of Listeria species.

A1.Reference number: AB1077; PMID:21537279; PMID:11679669

A1.Accession: AB1448

A1.Status: preliminary

A1.Molecule type: DNA

A1.Residues: 1-345 <GLA>

A1.Cross-references: UNIPROT:Q92R14; GB:AL592022; PIDN:CAC95354.1; PID:g16412540; GSPDB:G

A1.Experimental source: strain C11p11262

C1.Genetics:

A:Gene: lin0121

Query Match 70.6%; Score 36; DB 2; Length 345;
Best Local Similarity 70.0%; Pred. No. 33;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 NSVDFEDTL 10
| | | | |
Db 197 NSVDFDIDL 206

RESULT 8

A:Accession: A11581

DNA polymerase beta, to B. subtilis yehC protein homolog lin1194 [imported] - Listeria

C:Species: Listeria innocua

C>Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004

C:Accession: A11581

R:Glaeser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloeker, J.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurgey, O.; Entian, K.D.; Fehl, H.; Jones, L.M.; Karst, U.

Science 294, 849-852, 2001

A:Authors: Krcft, J.; Kuhn, M.; Kunst, F.; Kurapat, G.; Madueno, E.; Maitounam, A.; Maok, C.; Schluter, T.; Simoes, N.; Tietze, A.; Vazquez-Boland, J.A.; Vose, H.; Wehland, A.; Title: Comparative genomics of Listeria species.

A:Reference number: AB1077; MUID:21537279; PMID:11679669

A:Accession: A11581

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-570 <GLA>

A:Cross-references: UNIPROT:Q92CH7; GB:AL592022; PIDN:CAC96425.1; PID:916413653; GSPDB:C

A:Experimental source: strain Clp11262

C:Genetics:

A:Gene: lin1194

C:Superfamily: DNA-dependent DNA polymerase beta chain yehC

Query Match 70.6%; Score 36; DB 2; Length 570;

Best Local Similarity 66.7%; Pred. No. 58;

Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 2 SVDFEDTL 10
| | | | |
Db 419 SLDFDDTL 427

RESULT 9

S50246

SIP4 protein - yeast (Saccharomyces cerevisiae)

N:Alternate names: protein J0922; protein YJ089w

C:Species: Saccharomyces cerevisiae

C>Date: 13-Jan-1995 #sequence_revision 10-Feb-1995 #text_change 16-Aug-2004

C:Accession: S50246; S56019; S56866

R:Lease, P.; Yang, X.; Carlson, M.

submitted to the EMBL Data Library, November 1994

A:Description: SIP4, a protein that interacts with the SNF1 protein kinase.

A:Reference number: S50246

A:Accession: S50246

A:Molecule type: DNA

A:Residues: 1-829 <LBS>

A:Cross-references: UNIPROT:P46954; EMBL:U17643; NID:G596254; PIDN:AAB04119.1; PID:95962

R:Mosger, T.; Schaff-Gerstenschlaeger, I.; Chaltatzis, N.; Baur, A.; Boles, E.; Fournie

Yearst 11, 681-689, 1995

A:Title: Sequence analysis of a 33.1 kb fragment from the left arm of Saccharomyces cere

ter domain and a putative alpha-2-SCB-alpha-2 binding site.

A:Reference number: S56016; MUID:96093911; PMID:7483841

A:Accession: S56019

A:Status: nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-655, 'N', 657-829 <MIO>

A:Cross-references: EMBL:X83502; NID:G929861; PIDN:CAA58479.1; PID:G929865

A>Note: the nucleotide sequence was submitted to the EMBL Data Library, December 1994

R:Mosger, T.; Schaff-Gerstenschlaeger, I.; Baur, A.; Boles, E.; Chaltatzis, N.; Fournie

submitted to the Protein Sequence Database, September 1995

A:Reference number: S56855

A:Accession: S56866

A:Molecule type: DNA

A:Residues: 1-655, 'N', 657-829 <MIW>

A:Cross-references: EMBL:Z49364; NID:g1008257; PIDN:CAA89382.1; PID:g1008258; MIPS:YJL08;

C:Genetics:

A:Gene: SGD:SIP4

A:Cross-references: SGD:S0003625; MIPS:YJL089w

A:Map position: 10L

C:Superfamily: GAL4 zinc binuclear cluster homology <GAL4>

F/41-78/Domain: GAL4 zinc binuclear cluster homology

Query Match 70.6%; Score 36; DB 2; Length 829;
Best Local Similarity 77.8%; Pred. No. 89;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 NSVDFEDTL 9
| | | | |
Db 771 NSVDFMTDT 779

RESULT 10

S14477

glyceraldehyde-3-phosphate dehydrogenase homolog - rat (fragment)

N:Alternate names: glyceraldehyde-3-phosphate dehydrogenase-like protein

C:Species: Rattus norvegicus (Norway rat)

C>Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 11-Jun-1999

C:Accession: S14477; A24915

R:Krawetz, S.A.; Connor, W.; Dixon, G.H.

submitted to the EMBL Data Library, October 1990

A:Reference number: S14477

A:Accession: S14477

A:Molecule type: mRNA

A:Residues: 1-165 <KRA1>

A:Cross-references: EMBL:X54798; NID:G57571; PIDN:CA38569.1; PID:G57572

R:Krawetz, S.A.; Connor, W.; Cannon, P.D.; Dixon, G.H.

DNA 5, 427-435, 1986

A:Title: A vector-primer-clone-sequence plasmid for the construction of cDNA libraries:

A:Reference number: A24915; MUID:87053179; PMID:3780374

A:Accession: A24915

A:Molecule type: mRNA

A:Residues: 1-52 <KRA2>

A:Cross-references: GB:M14166; NID:G204191; PIDN:AAA41178.1; PID:G204192

C:Genetics:

A:Gene: G3PD

C:Superfamily: glyceraldehyde-3-phosphate dehydrogenase

Query Match 68.6%; Score 35; DB 2; Length 165;
Best Local Similarity 77.8%; Pred. No. 22;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 SVDFEDTL 10
| | | | |
Db 57 SVDFEDSL 65

RESULT 11

F90881

glyceraldehyde-3-phosphate dehydrogenase C [imported] - Escherichia coli (strain O157:H7,

C:Species: Escherichia coli

C>Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 09-Jul-2004

C:Accession: F90881

R:Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.;

gasaawara, N.; Yasunaga, T.; Kuhnara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.

DNA Res. 8, 11-22, 2001

A:Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and genom

A:Reference number: A9629; MUID:21156231; PMID:11258796

A:Accession: F90881

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-333 <HNW>

A:Cross-references: UNIPROT:P58072; GB:BA000007; PIDN:BA835445.1; PID:913361488; GSPDB:GT

A:Experimental source: strain O157:H7, substrain RMD 0509952

C:Genetics:

A:Gene: EC62022
C:Superfamily: glyceralddehyde-3-phosphate dehydrogenase

Query Match 68.6%; Score 35; DB 2; Length 333;
Best Local Similarity 77.8%; Pred. No. 49;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 SVDFEEDTL 10
| | | | | | | | | |
Db 57 SVDFEEDSL 65

RESULT 12

C85737
glyceralddehyde-3-phosphate dehydrogenase [imported] - Escherichia coli (strain O157:H7,
C:Species: Escherichia coli
C:Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
C:Accession: C85737

P:Perla, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.U.; Mayhew
Miller, L.; Grobeck, E.J.; Davis, N.W.; Lim, A.; Dimlanta, E.; Potamouelis, K.; Apodaca,
Nature 409, 529-533, 2001
A:Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A:Reference number: A85480; PMID:21074935; PMID:11206551
A:Accession: C85737

A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-333 <STO>
A:Cross-References: UNIPROT:P58072; GB:AE005174; NID:g12515293; PIDN:AAG56359.1; GSPDB:C
A:Experimental source: strain O157:H7, substrain EDL933
C:Genetics:

A:Gene: gapc
C:Superfamily: glyceralddehyde-3-phosphate dehydrogenase

Query Match 68.6%; Score 35; DB 2; Length 333;
Best Local Similarity 77.8%; Pred. No. 49;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 SVDFEEDTL 10
| | | | | | | | | |
Db 57 SVDFEEDSL 65

RESULT 13

D89890
cell division protein [imported] - Staphylococcus aureus (strain N315)

C:Species: Staphylococcus aureus
C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C:Accession: D89890

R:Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguo
ma, A.; Mizutani-Uji, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.;
C.; Shiba, T.; Hatori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001

A:Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.
A:Reference number: A89758; PMID:21311952; PMID:11418146
A:Accession: D89890

A:Status: preliminary
A:Molecule type: DNA

A:Residues: 1-470 <KUR>

A:Cross-References: UNIPROT:Q9JUS9; GB:BA000018; PID:g13700984; PIDN:BA842280.1; GSPDB:C
A:Experimental source: strain N315
C:Genetics:

A:Gene: ftsA

Query Match 68.6%; Score 35; DB 2; Length 470;
Best Local Similarity 66.7%; Pred. No. 73;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 NSVDFEEDT 9
| : | | | | | | | |
Db 90 NEIDFEEDT 98

RESULT 14

F75085

exoenzyme regulatory protein aepa precursor PAB1657 - Pyrococcus abyssi (strain Orsay)

C:Species: Pyrococcus abyssi
C:Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004
C:Accession: F75085

R:anonymous, Genoscope
submitted to the EMBL Data Library, July 1999

A:Description: Pyrococcus abyssi genome sequence: insights into archaeal chromosome struc
A:Reference number: A75001

A:Accession: F75085

A:Status: preliminary
A:Molecule type: DNA

A:Residues: 1-476 <KAW>

A:Cross-References: UNIPROT:Q9JUR9; GB:A1248286; GB:A1096836; NID:g5458366; PIDN:CAB4998;
C:Genetics:

A:Gene: PAB1657

Query Match 68.6%; Score 35; DB 2; Length 476;
Best Local Similarity 87.5%; Pred. No. 74;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 SVDFEEDT 9
| | | | | | | | | |
Db 152 SKDFEEDT 159

RESULT 15

T43789
H+-transporting two-sector ATPase (EC 3.6.3.14) chain B, vacuolar [imported] - Citrus uni

C:Species: Citrus unshiu
C:Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 09-Jul-2004
C:Accession: T43789

R:Iiamoto, H.; Komatsu, A.; Omura, M.
submitted to the EMBL Data Library, February 1999

A:Description: Vacuolar H+-ATPase B subunit gene 1 in Citrus unshiu.
A:Reference number: 222659

A:Accession: T43789

A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA

A:Residues: 1-488 <YAM>
A:Cross-References: UNIPROT:Q9ZOS1; EMBL:AB024277; PIDN:BAAT5517.1
C:Genetics:

A:Note: CitVATP B-1

C:Superfamily: H+-transporting ATP synthase alpha chain; H+-transporting ATP synthase al
C:Keywords: ATP biosynthesis; hydrolyase

F:208-379/Domain: H+-transporting ATP synthase alpha chain homology <ATP>

Query Match 68.6%; Score 35; DB 2; Length 488;
Best Local Similarity 70.0%; Pred. No. 76;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 NSVDFEEDTL 10
| : | | | | | | | |
Db 6 NNVDMEEGTL 15

Search completed: October 22, 2005, 09:55:51
Job time : 12.6092 secs


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CC streptococci, e.g. meningitis, otitis media, pneumonia, endocarditis,
CC mastitis in cattle, abortion in horses and many others. Since the
CC antibodies block binding of bacteria, they should be effective against
CC antibiotic-resistant strains, and may replace antibiotic therapy or
CC increase its effectiveness. Sequences AAW65744-58 represent peptides
CC which were synthesised to span the D3 motif of S. aureus fibronectin
CC binding protein A
XX
SQ Sequence 10 AA;

Query Match          100.0%; Score 51; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.021;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NSVDPEEDTL 10
   |||||
DB 1 NSVDPEEDTL 10

RESULT 2
AAW65670
ID AAW65670 standard; peptide, 21 AA.
XX
AC AAW65670;
XX
DT 16-OCT-1998 (first entry)
XX
DE Fibronectin binding protein-derived peptide #14.
XX
KW microbial surface components recognising adhesive matrix molecule;
KW MSCRAMM; fibronectin; fibronectin-binding protein; antibody; epitope;
KW antibiotic; bacterial infection; antibiotic-resistant strain.
XX
OS Synthetic.
OS Staphylococcus aureus.
XX
PN WO9831389-A2.
XX
PD 23-JUL-1998.
XX
PF 21-JAN-1998; 98WO-US001222.
XX
PR 21-JAN-1997; 97US-0036139P.
XX
PA (TEXAS ) UNIV TEXAS A & M SYSTEM.
XX
PI Hoeoek M, Patti JM, House-Pompeo KL, Speziale P, Joh D;
PI McGavin MJ;
XX
DR MPI; 1998-413816/35.
XX
PT Antibody that binds to fibronectin-binding protein, preventing its
PT binding to fibronectin - used to treat or prevent bacterial infection,
PT especially by Staphylococci and Streptococci.
XX
PS Example 8; Page 100; 201pp; English.
XX
CC The invention relates to antibodies that bind to a fibronectin-binding
CC domain of a fibronectin-binding protein, and inhibit binding of the
CC protein to fibronectin. Also claimed are: (1) isolated peptides of a
CC fibronectin-binding protein that do not bind to fibronectin; (2) fusion
CC protein containing at least one peptide of a fibronectin-binding protein
CC linked to a second amino acid sequence; (3) nucleic acid encoding the
CC isolated peptide of (1). Antibodies, the isolated peptides of (1) and the
CC nucleic acids are all useful for immunisation (active or passive) and (by
CC inhibiting binding of bacteria to fibronectin) for preventing or treating
CC infection in humans or other animals, particularly by staphylococci or
CC streptococci, e.g. meningitis, otitis media, pneumonia, endocarditis,
CC mastitis in cattle, abortion in horses and many others. Since the
CC antibodies block binding of bacteria, they should be effective against
CC antibiotic-resistant strains, and may replace antibiotic therapy or
CC increase its effectiveness. Sequences AAW65670-90 represent a series of
CC synthetic peptides based on the D3 repeat of S. aureus fibronectin
CC

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```

CC binding protein A. They were synthesised to contain a proline residue at
CC each position throughout the sequence (ie a proline scan)
XX
SQ Sequence 21 AA;

Query Match          100.0%; Score 51; DB 2; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.047;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NSVDPEEDTL 10
   |||||
DB 10 NSVDPEEDTL 19

RESULT 3
AAW65689
ID AAW65689 standard; peptide, 21 AA.
XX
AC AAW65689;
XX
DT 16-OCT-1998 (first entry)
XX
DE Fibronectin binding protein-derived peptide #33.
XX
KW microbial surface components recognising adhesive matrix molecule;
KW MSCRAMM; fibronectin; fibronectin-binding protein; antibody; epitope;
KW antibiotic; bacterial infection; antibiotic-resistant strain.
XX
OS Synthetic.
OS Staphylococcus aureus.
XX
PN WO9831389-A2.
XX
PD 23-JUL-1998.
XX
PF 21-JAN-1998; 98WO-US001222.
XX
PR 21-JAN-1997; 97US-0036139P.
XX
PA (TEXAS ) UNIV TEXAS A & M SYSTEM.
XX
PI Hoeoek M, Patti JM, House-Pompeo KL, Speziale P, Joh D;
PI McGavin MJ;
XX
DR MPI; 1998-413816/35.
XX
PT Antibody that binds to fibronectin-binding protein, preventing its
PT binding to fibronectin - used to treat or prevent bacterial infection,
PT especially by Staphylococci and Streptococci.
XX
PS Example 8; Page 101; 201pp; English.
XX
CC The invention relates to antibodies that bind to a fibronectin-binding
CC domain of a fibronectin-binding protein, and inhibit binding of the
CC protein to fibronectin. Also claimed are: (1) isolated peptides of a
CC fibronectin-binding protein that do not bind to fibronectin; (2) fusion
CC protein containing at least one peptide of a fibronectin-binding protein
CC linked to a second amino acid sequence; (3) nucleic acid encoding the
CC isolated peptide of (1). Antibodies, the isolated peptides of (1) and the
CC nucleic acids are all useful for immunisation (active or passive) and (by
CC inhibiting binding of bacteria to fibronectin) for preventing or treating
CC infection in humans or other animals, particularly by staphylococci or
CC streptococci, e.g. meningitis, otitis media, pneumonia, endocarditis,
CC mastitis in cattle, abortion in horses and many others. Since the
CC antibodies block binding of bacteria, they should be effective against
CC antibiotic-resistant strains, and may replace antibiotic therapy or
CC increase its effectiveness. Sequences AAW65670-90 represent a series of
CC synthetic peptides based on the D3 repeat of S. aureus fibronectin
CC binding protein A. They were synthesised to contain a proline residue at
CC each position throughout the sequence (ie a proline scan)
XX
SQ Sequence 21 AA;

```

Query Match 100.0%; Score 51; DB 2; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.047;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NSVDPEEDTL 10
DB 10 NSVDPEEDTL 19

RESULT 4
AAW65690 standard; peptide; 21 AA.

AC AAW65690;

DT 16-OCT-1998 (first entry)

DE Fibronectin binding protein-derived peptide #34.

XX microbial surface components recognising adhesive matrix molecule;

KM MSCRAMM; fibronectin; fibronectin-binding protein; antibody; epitope;

KW antibiotic; bacterial infection; antibiotic-resistant strain.

XX Synthetic.

OS Staphylococcus aureus.

PN MO9831389-A2.

PD 23-JUL-1998.

PF 21-JAN-1998; 98WO-US001222.

PR 21-JAN-1997; 97US-0036139P.

XX (TEXA) UNIV TEXAS A & M SYSTEM.

PA Hoeek M, Patci JM, House-Pompeo KL, Speziale P, Joh D;

PI Mcgavln MJ;

DR WPI; 1998-413816/35.

XX Antibody that binds to fibronectin-binding protein, preventing its

PT binding to fibronectin - used to treat or prevent bacterial infection,

PT especially by Staphylococci and Streptococci.

PS Example 8; Page 101; 201pp; English.

XX The invention relates to antibodies that bind to a fibronectin-binding

CC domain of a fibronectin-binding protein, and inhibit binding of the

CC protein to fibronectin. Also claimed are: (1) isolated peptides of a

CC fibronectin-binding protein that do not bind to fibronectin; (2) fusion

CC protein containing at least one peptide of a fibronectin-binding protein

CC linked to a second amino acid sequence; (3) nucleic acid encoding the

CC isolated peptide of (1). Antibodies, the isolated peptides of (1) and the

CC nucleic acids are all useful for immunisation (active or passive) and (by

CC inhibiting binding of bacteria to fibronectin) for preventing or treating

CC infection in humans or other animals, particularly by staphylococci or

CC streptococci, e.g. meningitis, otitis media, pneumonia, endocarditis,

CC mastitis in cattle, abortion in horses and many others. Since the

CC antibodies block binding of bacteria, they should be effective against

CC antibiotic-resistant strains, and may replace antibiotic therapy or

CC increase its effectiveness. Sequences AAW65670-90 represent a series of

CC synthetic peptides based on the D3 repeat of S. aureus fibronectin

CC binding protein A. They were synthesised to contain a proline residue at

CC each position through the sequence (ie a proline scan)

CC

XX Sequence 21 AA;

SQ

Query Match 100.0%; Score 51; DB 2; Length 21;

Best Local Similarity 100.0%; Pred. No. 0.047;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NSVDPEEDTL 10

DB 10 NSVDPEEDTL 19

RESULT 6

DB 10 NSVDPEEDTL 19

RESULT 5
AAW65673 standard; peptide; 21 AA.

AC AAW65673;

DT 16-OCT-1998 (first entry)

DE Fibronectin binding protein-derived peptide #17.

XX microbial surface components recognising adhesive matrix molecule;

KM MSCRAMM; fibronectin; fibronectin-binding protein; antibody; epitope;

KW antibiotic; bacterial infection; antibiotic-resistant strain.

XX Synthetic.

OS Staphylococcus aureus.

PN MO9831389-A2.

PD 23-JUL-1998.

PF 21-JAN-1998; 98WO-US001222.

PR 21-JAN-1997; 97US-0036139P.

XX (TEXA) UNIV TEXAS A & M SYSTEM.

PA Hoeek M, Patci JM, House-Pompeo KL, Speziale P, Joh D;

PI Mcgavln MJ;

DR WPI; 1998-413816/35.

XX Antibody that binds to fibronectin-binding protein, preventing its

PT binding to fibronectin - used to treat or prevent bacterial infection,

PT especially by Staphylococci and Streptococci.

PS Example 8; Page 100; 201pp; English.

XX The invention relates to antibodies that bind to a fibronectin-binding

CC domain of a fibronectin-binding protein, and inhibit binding of the

CC protein to fibronectin. Also claimed are: (1) isolated peptides of a

CC fibronectin-binding protein that do not bind to fibronectin; (2) fusion

CC protein containing at least one peptide of a fibronectin-binding protein

CC linked to a second amino acid sequence; (3) nucleic acid encoding the

CC isolated peptide of (1). Antibodies, the isolated peptides of (1) and the

CC nucleic acids are all useful for immunisation (active or passive) and (by

CC inhibiting binding of bacteria to fibronectin) for preventing or treating

CC infection in humans or other animals, particularly by staphylococci or

CC streptococci, e.g. meningitis, otitis media, pneumonia, endocarditis,

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CC synthetic peptides based on the D3 repeat of S. aureus fibronectin

CC binding protein A. They were synthesised to contain a proline residue at

CC each position through the sequence (ie a proline scan)

CC

XX Sequence 21 AA;

SQ

Query Match 100.0%; Score 51; DB 2; Length 21;

Best Local Similarity 100.0%; Pred. No. 0.047;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NSVDPEEDTL 10

DB 10 NSVDPEEDTL 19

RESULT 6

AAW65671
ID AAW65671 standard; peptide; 21 AA.
XX
AC AAW65671;
XX
DT 16-OCT-1998 (first entry)
XX
DE Fibronectin binding protein-derived peptide #15.
XX
KW microbial surface components recognising adhesive matrix molecule;
KM MSCRAMM; fibronectin; fibronectin-binding protein; antibody; epitope;
XX antibiotic; bacterial infection; antibiotic-resistant strain.
XX
OS Synthetic.
OS Staphylococcus aureus.
XX
PN WO9831389-A2.
XX
PD 23-JUL-1998.
XX
PF 21-JAN-1998; 98MO-US001222.
XX
PR 21-JAN-1997; 97US-0036139P.
XX
XX (TEXA) UNIV TEXAS A & M SYSTEM.
XX
PI Hoeoek M, Patti JM, House-Pompeo KL, Speciale P, Joh D;
PI Mcgavin MJ;
XX
DR WPI; 1998-413816/35.
XX
PT Antibody that binds to fibronectin-binding protein, preventing its
PT binding to fibronectin - used to treat or prevent bacterial infection,
PT especially by Staphylococci and Streptococci.
XX
PS Example 8; Page 100; 201pp; English.
XX
CC The invention relates to antibodies that bind to a fibronectin-binding
CC domain of a fibronectin-binding protein, and inhibit binding of the
CC protein to fibronectin. Also claimed are: (1) isolated peptides of a
CC fibronectin-binding protein that do not bind to fibronectin; (2) fusion
CC protein containing at least one peptide of a fibronectin-binding protein
CC linked to a second amino acid sequence; (3) nucleic acid encoding the
CC isolated peptide of (1). Antibodies, the isolated peptides of (1) and the
CC nucleic acids are all useful for immunisation (active or passive) and (by
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CC streptococci, e.g. meningitis, otitis media, pneumonia, endocarditis,
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CC antibodies block binding of bacteria, they should be effective against
CC antibiotic-resistant strains, and may replace antibiotic therapy or
CC increase its effectiveness. Sequences AAW65670-90 represent a series of
CC synthetic peptides based on the D3 repeat of S. aureus fibronectin
CC binding protein A. They were synthesised to contain a proline residue at
CC each position through the sequence (ie a proline scan)
XX
SO Sequence 21 AA;
XX
Query Match 100.0%; Score 51; DB 2; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.047;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 NSVDPEEDTL 10
DB 10 NSVDPEEDTL 19
XX
RESULT 7
AAW65675
ID AAW65675 standard; peptide; 21 AA.
XX
AC AAW65675;
XX

DT 16-OCT-1998 (first entry)
XX
DE Fibronectin binding protein-derived peptide #19.
XX
KW microbial surface components recognising adhesive matrix molecule;
KM MSCRAMM; fibronectin; fibronectin-binding protein; antibody; epitope;
XX antibiotic; bacterial infection; antibiotic-resistant strain.
XX
OS Synthetic.
OS Staphylococcus aureus.
XX
PN WO9831389-A2.
XX
PD 23-JUL-1998.
XX
PF 21-JAN-1998; 98MO-US001222.
XX
PR 21-JAN-1997; 97US-0036139P.
XX
XX (TEXA) UNIV TEXAS A & M SYSTEM.
XX
PI Hoeoek M, Patti JM, House-Pompeo KL, Speciale P, Joh D;
PI Mcgavin MJ;
XX
DR WPI; 1998-413816/35.
XX
PT Antibody that binds to fibronectin-binding protein, preventing its
PT binding to fibronectin - used to treat or prevent bacterial infection,
PT especially by Staphylococci and Streptococci.
XX
PS Example 8; Page 100; 201pp; English.
XX
CC The invention relates to antibodies that bind to a fibronectin-binding
CC domain of a fibronectin-binding protein, and inhibit binding of the
CC protein to fibronectin. Also claimed are: (1) isolated peptides of a
CC fibronectin-binding protein that do not bind to fibronectin; (2) fusion
CC protein containing at least one peptide of a fibronectin-binding protein
CC linked to a second amino acid sequence; (3) nucleic acid encoding the
CC isolated peptide of (1). Antibodies, the isolated peptides of (1) and the
CC nucleic acids are all useful for immunisation (active or passive) and (by
CC inhibiting binding of bacteria to fibronectin) for preventing or treating
CC infection in humans or other animals, particularly by staphylococci or
CC streptococci, e.g. meningitis, otitis media, pneumonia, endocarditis,
CC mastitis in cattle, abortion in horses and many others. Since the
CC antibodies block binding of bacteria, they should be effective against
CC antibiotic-resistant strains, and may replace antibiotic therapy or
CC increase its effectiveness. Sequences AAW65670-90 represent a series of
CC synthetic peptides based on the D3 repeat of S. aureus fibronectin
CC binding protein A. They were synthesised to contain a proline residue at
CC each position through the sequence (ie a proline scan)
XX
SO Sequence 21 AA;
XX
Query Match 100.0%; Score 51; DB 2; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.047;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 NSVDPEEDTL 10
DB 10 NSVDPEEDTL 19
XX
RESULT 8
AAW65666
ID AAW65666 standard; peptide; 21 AA.
XX
AC AAW65666;
XX
DT 16-OCT-1998 (first entry)
XX
DE Fibronectin binding protein-derived peptide #10.
XX
KW microbial surface components recognising adhesive matrix molecule;
XX

KM MSCRAMM; fibronectin; fibronectin-binding protein; antibody; epitope;
 KM antibiotic; bacterial infection; antibiotic-resistant strain.
 XX
 OS Synthetic.
 OS Staphylococcus aureus.
 XX
 PN WO9831389-A2.
 XX
 PD 23-JUL-1998.
 XX
 PF 21-JAN-1998; 98WO-US001222.
 XX
 PR 21-JAN-1997; 97US-0036139P.
 XX
 PA (TEXA) UNIV TEXAS A & M SYSTEM.
 XX
 PI Hoeoek M, Patti JM, House-Pompeo KL, Speziale P, Joh D;
 PI McGavin MJ;
 XX
 DR WPI; 1998-413816/35.
 XX
 PT Antibody that binds to fibronectin-binding protein, preventing its
 PT binding to fibronectin - used to treat or prevent bacterial infection,
 PT especially by Staphylococci and Streptococci.
 XX
 PS Example 2; Page 92; 201pp; English.
 XX
 CC The invention relates to antibodies that bind to a fibronectin-binding
 CC domain of a fibronectin-binding protein, and inhibit binding of the
 CC protein to fibronectin. Also claimed are: (1) isolated peptides of a
 CC fibronectin-binding protein that do not bind to fibronectin; (2) fusion
 CC protein containing at least one peptide of a fibronectin-binding protein
 CC linked to a second amino acid sequence; (3) nucleic acid encoding the
 CC isolated peptide of (1). Antibodies, the isolated peptides of (1) and the
 CC nucleic acids are all useful for immunisation (active or passive) and (b)
 CC inhibiting binding of bacteria to fibronectin for preventing or treating
 CC infection in humans or other animals, particularly by staphylococci or
 CC streptococci, e.g. meningitis, otitis media, pneumonia, endocarditis,
 CC mastitis in cattle, abortion in horses and many others. Since the
 CC antibodies block binding of bacteria, they should be effective against
 CC antibiotic-resistant strains, and may replace antibiotic therapy or
 CC increase its effectiveness. Sequences AAW65659-68 represent synthetic
 CC epitopes from the fibronectin binding domains DU and DI-D4 of the S.
 CC aureus fnda gene
 CC
 SQ Sequence 21 AA;
 QY
 Query Match 100.0%; Score 51; DB 2; Length 21;
 Best Local Similarity 100.0%; Pred. No. 0.047;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 DB 1 NSVDFFEDTL 10
 10 NSVDFFEDTL 19
 ID AAW65688 standard; peptide: 21 AA.
 AAW65688
 AC AAW65688;
 XX
 DT 16-OCT-1998 (first entry)
 XX
 DE Fibronectin binding protein-derived peptide #32.
 XX
 KM microbial surface components recognising adhesive matrix molecule;
 KM MSCRAMM; fibronectin; fibronectin-binding protein; antibody; epitope;
 KM antibiotic; bacterial infection; antibiotic-resistant strain.
 XX
 OS Synthetic.
 OS Staphylococcus aureus.
 XX

PN WO9831389-A2.
 XX
 PD 23-JUL-1998.
 XX
 PF 21-JAN-1998; 98WO-US001222.
 XX
 PR 21-JAN-1997; 97US-0036139P.
 XX
 PA (TEXA) UNIV TEXAS A & M SYSTEM.
 XX
 PI Hoeoek M, Patti JM, House-Pompeo KL, Speziale P, Joh D;
 PI McGavin MJ;
 XX
 DR WPI; 1998-413816/35.
 XX
 PT Antibody that binds to fibronectin-binding protein, preventing its
 PT binding to fibronectin - used to treat or prevent bacterial infection,
 PT especially by Staphylococci and Streptococci.
 XX
 PS Example 8; Page 101; 201pp; English.
 XX
 CC The invention relates to antibodies that bind to a fibronectin-binding
 CC domain of a fibronectin-binding protein, and inhibit binding of the
 CC protein to fibronectin. Also claimed are: (1) isolated peptides of a
 CC fibronectin-binding protein that do not bind to fibronectin; (2) fusion
 CC protein containing at least one peptide of a fibronectin-binding protein
 CC linked to a second amino acid sequence; (3) nucleic acid encoding the
 CC isolated peptide of (1). Antibodies, the isolated peptides of (1) and the
 CC nucleic acids are all useful for immunisation (active or passive) and (b)
 CC inhibiting binding of bacteria to fibronectin for preventing or treating
 CC infection in humans or other animals, particularly by staphylococci or
 CC streptococci, e.g. meningitis, otitis media, pneumonia, endocarditis,
 CC mastitis in cattle, abortion in horses and many others. Since the
 CC antibodies block binding of bacteria, they should be effective against
 CC antibiotic-resistant strains, and may replace antibiotic therapy or
 CC increase its effectiveness. Sequences AAW65670-90 represent a series of
 CC synthetic peptides based on the D3 repeat of S. aureus fibronectin
 CC binding protein A. They were synthesised to contain a proline residue at
 CC each position through the sequence (ie a proline scan)
 CC
 SQ Sequence 21 AA;
 QY
 Query Match 100.0%; Score 51; DB 2; Length 21;
 Best Local Similarity 100.0%; Pred. No. 0.047;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 DB 1 NSVDFFEDTL 10
 10 NSVDFFEDTL 19
 ID AAW65672 standard; peptide: 21 AA.
 AAW65672
 AC AAW65672;
 XX
 DT 16-OCT-1998 (first entry)
 XX
 DE Fibronectin binding protein-derived peptide #16.
 XX
 KM microbial surface components recognising adhesive matrix molecule;
 KM MSCRAMM; fibronectin; fibronectin-binding protein; antibody; epitope;
 KM antibiotic; bacterial infection; antibiotic-resistant strain.
 XX
 OS Synthetic.
 OS Staphylococcus aureus.
 XX
 PN WO9831389-A2.
 XX
 PD 23-JUL-1998.
 XX
 PF 21-JAN-1998; 98WO-US001222.
 XX

XX 21-JAN-1997; 97US-0036139P.
PR (TEXA) UNIV TEXAS A & M SYSTEM.
XX
XX
PI Hoeoek M, Patti JM, House-Pompeo KL, Speziale P, Joh D;
PI Mcgavin MJ;
XX
XX WPI, 1998-413816/35.

DR
XX
XX Antibody that binds to fibronectin-binding protein, preventing its
PT binding to fibronectin - used to treat or prevent bacterial infection,
PT especially by Staphylococci and Streptococci.

XX Example 8; Page 100; 201pp; English.

XX The invention relates to antibodies that bind to a fibronectin-binding
CC domain of a fibronectin-binding protein, and inhibit binding of the
CC protein to fibronectin. Also claimed are: (1) isolated peptides of a
CC fibronectin-binding protein that do not bind to fibronectin; (2) fusion
CC protein containing at least one peptide of a fibronectin-binding protein
CC linked to a second amino acid sequence; (3) nucleic acid encoding the
CC isolated peptide of (1). Antibodies, the isolated peptides of (1) and the
CC nucleic acids are all useful for immunisation (active or passive) and (by
CC inhibiting binding of bacteria to fibronectin) for preventing or treating
CC infection in humans or other animals, particularly by staphylococci or
CC streptococci, e.g. meningitis, otitis media, pneumonia, endocarditis,
CC mastitis in cattle, abortion in horses and many others. Since the
CC antibodies block binding of bacteria, they should be effective against
CC antibiotic-resistant strains, and may replace antibiotic therapy or
CC increase its effectiveness. Sequences AAW65670-90 represent a series of
CC synthetic peptides based on the D3 repeat of S. aureus fibronectin
CC binding protein A. They were synthesised to contain a proline residue at
CC each position through the sequence (ie a proline scan)

XX Sequence 21 AA;

Query Match 100.0%; Score 51; DB 2; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.047;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NSVDPEEDTL 10
|||
DB 10 NSVDPEEDTL 19

RESULT 11

AAW65677 standard; peptide; 21 AA.

AAW65677;

16-OCT-1998 (first entry)

Fibronectin binding protein-derived peptide #21.

KM microbial surface components recognising adhesive matrix molecule;
KM MSCRAMM; fibronectin; fibronectin-binding protein; antibody; epitope;
KM antibiotic; bacterial infection; antibiotic-resistant strain.

OS Synthetic.
OS Staphylococcus aureus.

WO9831389-A2.

23-JUL-1998.

21-JAN-1998; 98WO-US001222.

21-JAN-1997; 97US-0036139P.

(TEXA) UNIV TEXAS A & M SYSTEM.

PI Hoeoek M, Patti JM, House-Pompeo KL, Speziale P, Joh D;
PI Mcgavin MJ;
XX
XX
DR WPI, 1998-413816/35.

PT Antibody that binds to fibronectin-binding protein, preventing its
PT binding to fibronectin - used to treat or prevent bacterial infection,
PT especially by Staphylococci and Streptococci.

XX Example 8; Page 100; 201pp; English.

XX The invention relates to antibodies that bind to a fibronectin-binding
CC domain of a fibronectin-binding protein, and inhibit binding of the
CC protein to fibronectin. Also claimed are: (1) isolated peptides of a
CC fibronectin-binding protein that do not bind to fibronectin; (2) fusion
CC protein containing at least one peptide of a fibronectin-binding protein
CC linked to a second amino acid sequence; (3) nucleic acid encoding the
CC isolated peptide of (1). Antibodies, the isolated peptides of (1) and the
CC nucleic acids are all useful for immunisation (active or passive) and (by
CC inhibiting binding of bacteria to fibronectin) for preventing or treating
CC infection in humans or other animals, particularly by staphylococci or
CC streptococci, e.g. meningitis, otitis media, pneumonia, endocarditis,
CC mastitis in cattle, abortion in horses and many others. Since the
CC antibodies block binding of bacteria, they should be effective against
CC antibiotic-resistant strains, and may replace antibiotic therapy or
CC increase its effectiveness. Sequences AAW65670-90 represent a series of
CC synthetic peptides based on the D3 repeat of S. aureus fibronectin
CC binding protein A. They were synthesised to contain a proline residue at
CC each position through the sequence (ie a proline scan)

XX Sequence 21 AA;

Query Match 100.0%; Score 51; DB 2; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.047;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NSVDPEEDTL 10
|||
DB 10 NSVDPEEDTL 19

RESULT 12

AAW65665 standard; peptide; 21 AA.

AAW65665;

16-OCT-1998 (first entry)

Fibronectin binding protein-derived peptide #9.

KM microbial surface components recognising adhesive matrix molecule;
KM MSCRAMM; fibronectin; fibronectin-binding protein; antibody; epitope;
KM antibiotic; bacterial infection; antibiotic-resistant strain.

OS Synthetic.
OS Staphylococcus aureus.

WO9831389-A2.

23-JUL-1998.

21-JAN-1998; 98WO-US001222.

21-JAN-1997; 97US-0036139P.

(TEXA) UNIV TEXAS A & M SYSTEM.

Hoeoek M, Patti JM, House-Pompeo KL, Speziale P, Joh D;
PI Mcgavin MJ;

WPI, 1998-413816/35.

PT Antibody that binds to fibronectin-binding protein, preventing its
 PT binding to fibronectin - used to treat or prevent bacterial infection,
 PT especially by Staphylococci and Streptococci.

XX Example 2; Page 92; 201pp; English.

CC The invention relates to antibodies that bind to a fibronectin-binding
 CC domain of a fibronectin-binding protein, and inhibit binding of the
 CC protein to fibronectin. Also claimed are: (1) isolated peptides of a
 CC fibronectin-binding protein that do not bind to fibronectin; (2) fusion
 CC protein containing at least one peptide of a fibronectin-binding protein
 CC linked to a second amino acid sequence; (3) nucleic acid encoding the
 CC isolated peptide of (1). Antibodies, the isolated peptides of (1) and (by
 CC nucleic acids are all useful for immunisation (active or passive) and (by
 CC inhibiting binding of bacteria to fibronectin) for preventing or treating
 CC infection in humans or other animals, particularly by staphylococci or
 CC streptococci, e.g. meningitis, otitis media, pneumonia, endocarditis,
 CC mastitis in cattle, abortion in horses and many others. Since the
 CC antibodies block binding of bacteria, they should be effective against
 CC antibiotic-resistant strains, and may replace antibiotic therapy or
 CC increase its effectiveness. Sequences AAM65670-68 represent synthetic
 CC epitopes from the fibronectin binding domains DU and D1-D4 of the S.
 CC aureus fnda gene

CC Sequence 21 AA;

Query Match 100.0%; Score 51; DB 2; Length 21;

Best Local Similarity 100.0%; Pred. No. 0.047;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NSVDFFEDTL 10
 |||||
 10 NSVDFFEDTL 19

RESULT 13
 ID AAM65674
 XX AAM65674 standard; peptide; 21 AA.

AC AAM65674;

XX 16-OCT-1998 (first entry)

XX Fibronectin binding protein-derived peptide #18.

DE microbial surface components recognising adhesive matrix molecule;

KM MSCRAMM; fibronectin; fibronectin-binding protein; antibody; epitope;

KM antibiotic; bacterial infection; antibiotic-resistant strain.

XX Synthetic.

OS Staphylococcus aureus.

XX WO9831389-A2.

XX 23-JUL-1998.

XX 21-JAN-1998; 98WO-US001222.

XX 21-JAN-1997; 97US-0036139P.

XX (TEXA) UNIV TEXAS A & M SYSTEM.

XX Hooeok M, Patti JM, House-Pompeo KL, Speziale P, Joh D;

XX Mcgavin MJ;

XX WPI; 1998-413816/35.

XX Antibody that binds to fibronectin-binding protein, preventing its

XX binding to fibronectin - used to treat or prevent bacterial infection,
 XX especially by Staphylococci and Streptococci.
 XX Example 8; Page 100; 201pp; English.

CC The invention relates to antibodies that bind to a fibronectin-binding
 CC domain of a fibronectin-binding protein, and inhibit binding of the
 CC protein to fibronectin. Also claimed are: (1) isolated peptides of a
 CC fibronectin-binding protein that do not bind to fibronectin; (2) fusion
 CC protein containing at least one peptide of a fibronectin-binding protein
 CC linked to a second amino acid sequence; (3) nucleic acid encoding the
 CC isolated peptide of (1). Antibodies, the isolated peptides of (1) and (by
 CC nucleic acids are all useful for immunisation (active or passive) and (by
 CC inhibiting binding of bacteria to fibronectin) for preventing or treating
 CC infection in humans or other animals, particularly by staphylococci or
 CC streptococci, e.g. meningitis, otitis media, pneumonia, endocarditis,
 CC mastitis in cattle, abortion in horses and many others. Since the
 CC antibodies block binding of bacteria, they should be effective against
 CC antibiotic-resistant strains, and may replace antibiotic therapy or
 CC increase its effectiveness. Sequences AAM65670-90 represent a series of
 CC synthetic peptides based on the D3 repeat of S. aureus fibronectin
 CC binding protein A. They were synthesised to contain a proline residue at
 CC each position through the sequence (ie a proline scan)

CC Sequence 21 AA;

Query Match 100.0%; Score 51; DB 2; Length 21;

Best Local Similarity 100.0%; Pred. No. 0.047;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NSVDFFEDTL 10
 |||||
 10 NSVDFFEDTL 19

RESULT 14
 ID AAM65676
 XX AAM65676 standard; peptide; 21 AA.

AC AAM65676;

XX 16-OCT-1998 (first entry)

XX Fibronectin binding protein-derived peptide #20.

DE microbial surface components recognising adhesive matrix molecule;

KM MSCRAMM; fibronectin; fibronectin-binding protein; antibody; epitope;

KM antibiotic; bacterial infection; antibiotic-resistant strain.

XX Synthetic.

OS Staphylococcus aureus.

XX WO9831389-A2.

XX 23-JUL-1998.

XX 21-JAN-1998; 98WO-US001222.

XX 21-JAN-1997; 97US-0036139P.

XX (TEXA) UNIV TEXAS A & M SYSTEM.

XX Hooeok M, Patti JM, House-Pompeo KL, Speziale P, Joh D;

XX Mcgavin MJ;

XX WPI; 1998-413816/35.

XX Antibody that binds to fibronectin-binding protein, preventing its

XX binding to fibronectin - used to treat or prevent bacterial infection,
 XX especially by Staphylococci and Streptococci.

XX Example 8; Page 100; 201pp; English.

XX The invention relates to antibodies that bind to a fibronectin-binding

XX domain of a fibronectin-binding protein, and inhibit binding of the
 XX protein to fibronectin. Also claimed are: (1) isolated peptides of a
 XX fibronectin-binding protein that do not bind to fibronectin; (2) fusion
 XX protein containing at least one peptide of a fibronectin-binding protein

CC linked to a second amino acid sequence; (3) nucleic acid encoding the
CC isolated peptide of (1). Antibodies, the isolated peptides of (1) and the
CC nucleic acids are all useful for immunisation (active or passive) and (by
CC inhibiting binding of bacteria to fibronectin) for preventing or treating
CC infection in humans or other animals, particularly by staphylococci or
CC streptococci, e.g. meningitis, otitis media, pneumonia, endocarditis,
CC mastitis in cattle, abortion in horses and many others. Since the
CC antibodies block binding of bacteria, they should be effective against
CC antibiotic-resistant strains, and may replace antibiotic therapy or
CC increase its effectiveness. Sequences AA65670-90 represent a series of
CC synthetic peptides based on the D3 repeat of *S. aureus* fibronectin
CC binding protein A. They were synthesised to contain a proline residue at
CC each position through the sequence (ie a proline scan)
XX
SQ Sequence 21 AA;

Query Match 100.0%; Score 51; DB 2; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.047;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 NSVDPEEDTL 10
|||
Db 10 NSVDPEEDTL 19

RESULT 15

AA21340 AAR21340 standard; peptide; 22 AA.

AC AAR21340;

DT 25-MAR-2003 (revised)

DT 15-JUN-1992 (first entry)

DE Fibronectin binding protein.

KW FnBP, wound infection reduction; vaccination; mastitis;

KW Staphylococcal infections; D3.

OS Synthetic.

PN WO9202555-A.

PD 20-FEB-1992.

PF 10-AUG-1990; 90SE-00002617.

PR 10-AUG-1990; 90SE-00002617.

PA (ALFA) ALFA LAVAL AGRIC INT AB.

PI Hook M, McGavin M, Raucel G;

PI WPI; 1992-080035/10.

PT New fibronectin binding peptide - combines with fusion peptide to form
PT large antigen, used in immunisation, diagnosis and for treating wounds.

PS Claim 1; Page 22; 33pp; English.

XX The sequence comprises amino acids 17-33 of a tandem repeat, designated
CC D3 of the fibronectin binding site of *Staphylococcus aureus* 8325-4 FnBP.
CC The N-terminal DK may be replaced with H or K, and the C-terminal LKP may
CC be replaced by either L, LP, or OH. The peptides were synthesised using
CC standard methods and purified using reverse phase HPLC. The appropriate
CC fractions were dialysed and lyophilised. Peptide sequencing was performed
CC and the peptides digested and chemically modified by dihydroxypropylation
CC of the amino side chain of lysine. The carboxylic side chains were
CC converted to glycine methyl esters. The phenyl side chains of tyrosine
CC residues were oxidised. Chemically modified peptide D3 was compared to
CC unmodified D3. Lysine and tyrosine modifications only partially
CC diminished its activity whereas modification of aspartic/glutamic
CC residues resulted in complete loss of activity. The peptide can be used

CC for the prevention or reduction of the risk of wound infection. The
CC peptide can be used to create a large antigen for vaccinating ruminants
CC against mastitis caused by *Staphylococcal* infections. It can also be used
CC to diagnose *Staphylococcal* infections using ELISA or DNA probes. (Updated
CC on 25-MAR-2003 to correct PA field.)
XX

SQ Sequence 22 AA;
Query Match 100.0%; Score 51; DB 2; Length 22;
Best Local Similarity 100.0%; Pred. No. 0.05;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 NSVDPEEDTL 10
|||
Db 11 NSVDPEEDTL 20

Search completed: October 25, 2005, 21:29:14
Job time : 69.7126 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 22, 2005, 08:04:46 ; Search time 11.6092 Seconds
(without alignments)
82.880 Million cell updates/sec

Title: US-10-731-238-101
Sequence: 1 VFEEEDTLPK 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_79:.*
1: pir1:.*
2: pir2:.*
3: pir3:.*
4: pir4:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	53	100.0	961	2	G90053
2	53	100.0	1018	2	A32192
3	53	100.0	1038	2	H90053
4	49	92.5	940	2	S19702
5	41	77.4	452	2	H86677
6	39	73.6	450	2	E95181
7	39	73.6	450	2	H98048
8	38	71.7	42	2	B82629
9	38	71.7	60	2	B82627
10	38	71.7	277	2	A64404
11	38	71.7	347	1	HPMS
12	38	71.7	518	2	S23692
13	38	71.7	831	2	T51185
14	37	69.8	234	2	T70473
15	37	69.8	795	2	F75154
16	37	69.8	798	2	B71196
17	36	67.9	216	2	S58652
18	36	67.9	867	2	D86393
19	36	67.9	1804	2	S56247
20	35	66.0	122	2	S34566
21	35	66.0	161	2	AE0162
22	35	66.0	257	2	A10393
23	35	66.0	330	2	S55733
24	35	66.0	391	2	S55732
25	35	66.0	394	2	B84830
26	35	66.0	424	2	AE2893
27	35	66.0	446	2	H97668
28	35	66.0	459	2	S66726
29	35	66.0	582	2	E84721

30	35	66.0	788	2	G81294	hypothetical prote
31	35	66.0	1492	2	T18560	DNA-directed DNA p
32	34	64.2	269	2	H84378	hypothetical prote
33	34	64.2	349	2	H82116	flagellar motor sw
34	34	64.2	368	2	T21748	hypothetical prote
35	34	64.2	404	2	A28404	S-antigen - bovine
36	34	64.2	459	2	AE3390	chiophen / furan o
37	34	64.2	465	2	H84930	H+-transporting tw
38	34	64.2	470	2	T45278	hypothetical prote
39	34	64.2	554	2	T13207	hypothetical prote
40	34	64.2	607	2	T40906	probable ATP-depen
41	34	64.2	665	2	T13744	hypothetical prote
42	34	64.2	794	2	T27870	hypothetical prote
43	34	64.2	865	2	T09050	AC13 antigen - hu
44	34	64.2	1009	2	T16604	hypothetical prote
45	34	64.2	1025	2	S69790	fibronectin-bindin

ALIGNMENTS

RESULT 1
G90053
hypothetical protein fnbB [imported] - Staphylococcus aureus (strain N315)
C/Species: Staphylococcus aureus
C/Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C/Accession: G90053
R/Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguci, ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.; I, C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
A/Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.
A/Reference number: A89758; WUID:21311952; PMID:11418146
A/Accession: G90053
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1961 <KUR>
A/Cross-references: UNIPROT:Q99R03; GB:BA000018; P1D:G13702452; P1DN:BA043593.1; GSPDB:G
A/Experimental source: strain N315
C/Genetics:
A/Gene: fnbB

Query Match 100.0%; Score 53; DB 2; Length 961;
Best Local Similarity 100.0%; Pred. No. 0.069;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 VFEEEDTLPK 10
Db 795 VFEEEDTLPK 804

RESULT 2
A32192
fibronectin-binding protein - Staphylococcus aureus
C/Species: Staphylococcus aureus
C/Date: 31-Jul-1989 #sequence_revision 31-Jul-1989 #text_change 16-Feb-1997
C/Accession: A32192
R/Signaes, C.; Raucel, G.; Joensen, K.; Lindgren, P.E.; Anantharamaiah, G.M.; Hoeoek, M.
Proc. Natl. Acad. Sci. U.S.A. 86, 699-703, 1989
A/Title: Nucleotide sequence of the gene for a fibronectin-binding protein from staphyloc
A/Reference number: A32192; MUID:89086998; PMID:2551391
A/Accession: A32192
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-1018 <SIG>
A/Cross-references: GB:J04151
C/Keywords: fibronectin binding

Query Match 100.0%; Score 53; DB 2; Length 1018;
Best Local Similarity 100.0%; Pred. No. 0.074;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 VFEEEDTLPK 10

|||||||
Db 848 VFEEBTLRK 857

RESULT 3

H90053

hypothetical protein fnb [imported] - Staphylococcus aureus (strain N315)

C:Species: Staphylococcus aureus

C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004

C:Accession: H90053

R:Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Ogunu, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kato, C.; Sekimizu, K.;

C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.

Lancet 357, 1225-1240, 2001

A:Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.

A:Reference number: A89758; PMID:21311952; PMID:11418146

A:Accession: H90053

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-1038 <K10>

A:Cross-references: UNIPROT:Q99RD2; GB:BA000018; PID:g13702453; PIDN:BA843594.1; GSPDB:G

A:Experimental source: strain N315

C:Genetics:

A:Gene: fnb

Query Match 100.0%; Score 53; DB 2; Length 1038;
Best Local Similarity 100.0%; Pred. No. 0.075; Indels 0; Gaps 0;
Matches 10; Conservative 0; Mismatches 0;

QY 1 VFEEBTLRK 10
:|||||||:
Db 844 VFEEBTLRK 853

RESULT 4

S19702

fibronectin-binding protein B - Staphylococcus aureus

C:Species: Staphylococcus aureus

C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004

C:Accession: S19702

R:Joensson, K.; Stignae, C.; Mueller, H. P.; Lindberg, M.

Eur. J. Biochem. 202, 1041-1048, 1991

A:Title: Two different genes encode fibronectin binding proteins in Staphylococcus aureus

A:Reference number: S19702; PMID:92111475; PMID:1837266

A:Accession: S19702

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-940 <J0E>

A:Cross-references: UNIPROT:Q53682; EMBL:X62992; NID:g49040; PIDN:CAA44726.1; PID:G58156

C:Keyword: fibronectin binding

Query Match 92.5%; Score 49; DB 2; Length 940;
Best Local Similarity 90.0%; Pred. No. 0.4; Indels 0; Gaps 0;
Matches 9; Conservative 1; Mismatches 0;

QY 1 VFEEBTLRK 10
:|||||||:
Db 784 VFEEBTLRK 793

RESULT 5

H86677

phosphoglucosamine mutase [imported] - Lactococcus lactis subsp. lactis (strain IL1403)

C:Species: Lactococcus lactis subsp. lactis

C:Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 09-Jul-2004

C:Accession: H86677

R:Polcic, A.; Winkler, P.; Mauger, S.; Jallion, O.; Malarme, K.; Weisenbach, J.; Ehrlich

Genome Res. 11, 731-753, 2001

A:Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis 88

A:Reference number: A86625; PMID:21235186; PMID:11337471

A:Accession: H86677

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-452 <STO>
A:Cross-references: UNIPROT:Q9CID9; GB:AE005176; PID:g12723300; PIDN:AAK04522.1; GSPDB:GT
A:Experimental source: strain IL1403
C:Genetics:
A:Gene: femp
C:Superfamily: phosphomannomutase

Query Match 77.4%; Score 41; DB 2; Length 452;
Best Local Similarity 70.0%; Pred. No. 6.1; Indels 1; Gaps 0;
Matches 7; Conservative 2; Mismatches 1;

QY 1 VFEEBTLRK 10
:|||||||:
Db 132 IDAEBTLRK 141

RESULT 6

E95181

hypothetical protein SP1559 [imported] - Streptococcus pneumoniae (strain TIGR4)

C:Species: Streptococcus pneumoniae

C:Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 09-Jul-2004

C:Accession: E95181

R:Tellet, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Heide

on, J.D.; Unayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapfel, I

nson, T.; Hickey, E.K.; Holt, I.E.

Science 293, 498-506, 2001

A:Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison,

A:Title: Complete genome sequence of a virulent isolate of Streptococcus pneumoniae.

A:Reference number: A95000; PMID:21357209; PMID:11463916

A:Accession: E95181

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-450 <KUR>

A:Cross-references: UNIPROT:Q97PP4; GB:AE005672; PIDN:AAK75646.1; PID:g14973050; GSPDB:GT

A:Experimental source: strain TIGR4

C:Genetics:

A:Gene: SP1559

C:Superfamily: phosphomannomutase

Query Match 73.6%; Score 39; DB 2; Length 450;
Best Local Similarity 70.0%; Pred. No. 15; Indels 1; Gaps 0;
Matches 7; Conservative 2; Mismatches 1;

QY 1 VFEEBTLRK 10
:|||||||:
Db 132 LBAEBTLRK 141

RESULT 7

H98048

phosphoacetylglucosamine mutase (EC 5.4.2.3) [imported] - Streptococcus pneumoniae (stra)

C:Species: Streptococcus pneumoniae

C:Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 09-Jul-2004

C:Accession: H98048

R:Hoskins, J.A.; Alborn Jr., W.; Arnold, J.; Blaszczak, L.; Burgett, S.; DeHoff, B.S.; E

e, R.; LeBlanc, D.J.; Lee, L.N.; Lefkowitz, E.J.; Lu, J.; Matsushima, P.; McAhren, S.; M

Y, P.; Sun, P.M.; Winkler, M.E.

J. Bacteriol. 183, 5709-5717, 2001

A:Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaaskunas, S.R.;

A:Title: Genome of the Bacterium Streptococcus pneumoniae strain R6.

A:Reference number: A97872; PMID:21429245; PMID:11544234

A:Accession: H98048

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-450 <KUR>

A:Cross-references: UNIPROT:Q8DP16; GB:AE007317; PIDN:AAL00221.1; PID:g15459071; GSPDB:GT

C:Genetics:

A:Gene: glmM

C:Superfamily: phosphomannomutase

C:Keywords: intramolecular transferase; isomerase

Query Match 73.6%; Score 39; DB 2; Length 450;
Best Local Similarity 70.0%; Pred. No. 15;

Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 1 VDPEDTLPR 10
Db 132 LDPEEDTLPR 141

RESULT 8

hypoetical protein XP1866 [imported] - Xylella fastidiosa (strain 945c)

C/Species: Xylella fastidiosa
C/Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
C/Accession: B82629
R:anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequen
Nature 406, 151-157, 2000
A/Title: The genome sequence of the plant pathogen Xylella fastidiosa.
A/Reference number: A82515; MUID:20365717; PMID:10910347
A/Note: for a complete list of authors see reference number A59328 below
A/Accession: B82629
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 142 <STM>
A/Cross-references: UNIPROT:Q9PC95; GB:AE004007; GB:AE003849; NID:g9106944; PIDN:AAFB467
A/Experimental source: strain 945c
R:Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; A
Brienes, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carer, H
as-Neto, E.; Docena, C.; El-Dorzy, H.; Facincani, A.P.; Ferreira, A.J.S.
submitted to Genbank, June 2000

A/Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franco, S.C.; Franco, M.C.; Frohm
J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Klieger, U.B.; Kurame, E.B.; Laiz
Chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, E
A/Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.;
Rodrigues, V.; Rosa, A.J. de M.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A
M.; Tshako, da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silveir
A/Reference number: A59328
A/Contents: annotation
C/Genetics:
A/Gene: XP1866

Query Match 71.7%; Score 38; DB 2; Length 42;
Best Local Similarity 70.0%; Pred. No. 1.7;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 1 VDPEDTLPR 10
Db 6 LDPEEDTLPR 15

RESULT 9

hypoetical protein XP1882 [imported] - Xylella fastidiosa (strain 945c)

C/Species: Xylella fastidiosa
C/Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
C/Accession: B82627
R:anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequen
Nature 406, 151-157, 2000
A/Title: The genome sequence of the plant pathogen Xylella fastidiosa.
A/Reference number: A82515; MUID:20365717; PMID:10910347
A/Note: for a complete list of authors see reference number A59328 below
A/Accession: B82627
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 160 <STM>
A/Cross-references: UNIPROT:Q9PC99; GB:AE004008; GB:AE003849; NID:g9106961; PIDN:AAFB466
A/Experimental source: strain 945c
R:Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; A
Brienes, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carer, H
as-Neto, E.; Docena, C.; El-Dorzy, H.; Facincani, A.P.; Ferreira, A.J.S.
submitted to Genbank, June 2000

A/Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franco, S.C.; Franco, M.C.; Frohm
J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Klieger, U.B.; Kurame, E.B.; Laiz

chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, E.
A/Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.;
Rodrigues, V.; Rosa, A.J. de M.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A
A/Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silveir
M.; Tshako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z
A/Reference number: A59328
A/Contents: annotation
C/Genetics:
A/Gene: XP1882

Query Match 71.7%; Score 38; DB 2; Length 60;
Best Local Similarity 70.0%; Pred. No. 2.6;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 1 VDPEDTLPR 10
Db 24 MDPEEDTLPR 33

RESULT 10

hypoetical protein MJ0833 - Methanococcus jannaschii

C/Species: Methanococcus jannaschii
C/Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 04-Mar-2000
C/Accession: A64404
R:Baill, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blake,
R.; Bult, C.J.; Overbeek, R.; Kirkness, E.F.; Weinstock, K.G.; Merrick, J.M.; Glodek, A.;
rson, J.D.; Sadow, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A.
Science 273, 1058-1073, 1996
A/Authors: Kaine, B.P.; Borodovsky, M.; Klink, H.P.; Fraser, C.M.; Smith, H.O.; Woese, C.
A/Title: Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschii.
A/Reference number: A64300; MUID:96337999; PMID:8688087
A/Accession: A64404

A/Status: preliminary; nucleic acid sequence not shown; translation not shown
A/Molecule type: DNA
A/Residues: 1277 <BL>
A/Cross-references: GB:067527; GB:L77117; NID:g1591519; PID:g1591521; TIGR:MJ0833; PID:g1
C/Genetics:
A/Map position: REV759071-758238
A/Start codon: TTG
C/Superfamily: Methanococcus jannaschii hypoetical protein MJ0833

Query Match 71.7%; Score 38; DB 2; Length 277;
Best Local Similarity 70.0%; Pred. No. 13;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 1 VDPEDTLPR 10
Db 58 ITPEDTLPR 67

RESULT 11

haptoglobin precursor - mouse

N/Contents: haptoglobin alpha chain, haptoglobin beta chain
C/Species: Mus musculus (house mouse)
C/Date: 23-Mar-1995 #sequence_revision 31-May-1996 #text_change 18-Jun-1999
C/Accession: A48918
R:Yang, F.; Linhan, L.A.; Friedrichs, W.E.; Lallay, P.A.; Sakaguchi, A.Y.; Bowman, B.H.
Genomics 18, 374-380, 1993
A/Title: Characterization of the mouse haptoglobin gene.
A/Reference number: A48918; MUID:94117006; PMID:8288241
A/Accession: A48918
A/Molecule type: mRNA
A/Residues: 1347 <YAN>
A/Cross-references: GB:567972; NID:g461137; PIDN:AA829697.1; PID:g461138
A/Note: Sequence extracted from NCBI backbone (NCBI:142156, NCBI:142157); sequence inc
C/Comment: The mature haptoglobin molecule is a dimer of heterodimers, the two chains of
C/Genetics:
A/Gene: Hp
A/Map position: 8

C:Superfamily: haptoglobin; complement factor H repeat homology; trypsin homology
C:Keywords: acute phase; glycoprotein; hemoglobin binding; heterotetramer; iron transport
F:1-18/Domain: signal sequence #status predicted <SIG>
F:19-101/Product: haptoglobin alpha chain #status predicted <ACH>
F:13-86/Domain: complement factor H repeat homology <FH2>
F:103-347/Product: haptoglobin beta chain #status predicted <BCH>
F:103-340/Domain: trypsin homology <TRY>
F:33/Dissulfide bonds: interchain #status predicted
F:52-86-90-207-250-281-292-322/Dissulfide bonds: #status predicted
F:148-182-250-264/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 71.7%; Score 38; DB 1; Length 347;
Best Local Similarity 60.0%; Pred. No. 17;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 VFPEEDTLPK 10
:||||:|
DB 26 MDEFDDSPK 35

RESULT 12
S23692
erythrocyte membrane-associated antigen (clone pF K16) - Plasmodium falciparum (fragment)
C:Species: Plasmodium falciparum
C:Date: 19-Mar-1997 #sequence_revision 12-Dec-1997 #text_change 09-Jul-2004
C:Accession: S23692
R:Kun, J.; Heselbach, J.; Schreiber, M.; Scherf, A.; Gysin, J.; Mattei, D.; Pereira da Res. Immunol. 142, 199-210, 1991
A:Title: Cloning and expression of genomic DNA sequences coding for putative erythrocyte
A:Reference number: S23684; MUID:91376328; PMID:1896607
A:Accession: S23692
A:Molecule type: DNA
A:Residues: 1-518 <KUN>
A:Cross-references: UNIPROT:Q9GVA9; EMBL:X53023
C:Keywords: surface antigen

Query Match 71.7%; Score 38; DB 2; Length 518;
Best Local Similarity 60.0%; Pred. No. 27;
Matches 6; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 VFPEEDTLPK 10
:||||:|
DB 407 VDYEENSLPR 416

RESULT 13
T51185
resistance protein RPP13 [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 28-Jul-2000 #sequence_revision 28-Jul-2000 #text_change 02-Sep-2000
C:Accession: T51185
R:Bitner-Eddy, P.D.; Crane, I.R.; Holub, E.B.; Beynon, J.L.
Plant J. 21, 177-186, 2000
A:Title: RPP13 is a simple locus in Arabidopsis thaliana for alleles that specify downy
A:Reference number: Z25333
A:Accession: T51185
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-831 <BIT>
A:Cross-references: EMBL:AF209731; PIDN:AAF42831.1
A:Experimental source: cultivar Rld
C:Genetics:
A:Gene: RPP13
A:Map position: 3
C:Superfamily: disease resistance protein RPS2; leucine-rich alpha-2-glycoprotein repeat

Query Match 71.7%; Score 38; DB 2; Length 831;
Best Local Similarity 66.7%; Pred. No. 45;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 VFPEEDTLPK 9
:||||:|
DB 739 ITFEEETMP 747

RESULT 14
T30473
late expression factor 1 - Lymantria dispar nuclear polyhedrosis virus
C:Species: Lymantria dispar nuclear polyhedrosis virus, LdNPV
C:Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
C:Accession: T30473
R:Kuzio, J.; Pearson, M.N.; Harwood, S.H.; Funk, C.J.; Evans, J.T.; Slavicek, J.M.; Rohm
Virology 253, 17-34, 1999
A:Title: Sequence and analysis of the genome of a baculovirus pathogenic for Lymantria di
A:Reference number: Z20836; MUID:99124785; PMID:9887315
A:Accession: T30473
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-234 <KUZ>
A:Cross-references: UNIPROT:Q9YMK4; EMBL:AF081810; NID:93822234; PIDN:AAC70309.1; PID:938
C:Superfamily: viral DNA primase, Ief-1

Query Match 69.8%; Score 37; DB 2; Length 234;
Best Local Similarity 70.0%; Pred. No. 17;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 VFPEEDTLPK 10
:||||:|
DB 81 VDPEEDTEPR 90

RESULT 15
F75154
cell division control protein 48, aaa family (cdc48-1) PAB2086 - Pyrococcus abyssi (strain
C:Species: Pyrococcus abyssi
C:Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004
C:Accession: F75154
R:anonymous, Genoscope
submitted to the EMBL Data Library, July 1999
A:Description: Pyrococcus abyssi genome sequence: insights into archaeal chromosome struc
A:Reference number: A75001
A:Accession: F75154
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-795 <KAN>
A:Cross-references: UNIPROT:Q9V1N2; GB:AJ248284; GB:AL096836; NID:95457730; PIDN:CAB4931.
A:Experimental source: strain Orsay
C:Genetics:
A:Gene: PAB2086
C:Superfamily: transitional endoplasmic reticulum ATPase; FtsH/SEC18/CDC48-type ATP-bind
F:530-737/Domain: FtsH/SEC18/CDC48-type ATP-binding domain homology <VAT>

Query Match 69.8%; Score 37; DB 2; Length 795;
Best Local Similarity 50.0%; Pred. No. 66;
Matches 5; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 VFPEEDTLPK 10
:||||:|
DB 469 IDPEAEETPR 478

Search completed: October 22, 2005, 09:55:52
Job time : 12.6092 secs

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OM protein - protein search, using sw model

Run on: October 22, 2005, 08:01:06 ; Search time 56.2069 Seconds
(without alignments)
91.106 Million cell updates/sec

Title: US-10-731-238-101
Perfect score: 53
Sequence: 1 VDFEEDLPK 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : Uniprot_03:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	53	100.0	961	2 Q99RD3	Q99RD3 staphylococ
2	53	100.0	961	2 Q7A3J8	Q7A3J8 staphylococ
3	53	100.0	965	2 Q6GDU5	Q6GDU5 staphylococ
4	53	100.0	1015	2 Q8NUY7	Q8NUY7 staphylococ
5	53	100.0	1015	2 Q6G6H3	Q6G6H3 staphylococ
6	53	100.0	1018	1 FNBA_STRAU	FNBA_STRAU
7	53	100.0	1038	2 Q99RD2	Q99RD2 staphylococ
8	53	100.0	1038	2 Q7A3J7	Q7A3J7 staphylococ
9	49	92.5	940	2 Q5J682	Q5J682 staphylococ
10	49	92.5	943	2 Q8NUH8	Q8NUH8 staphylococ
11	49	92.5	957	2 Q6G6H4	Q6G6H4 staphylococ
12	45	84.9	152	2 Q9AEP9	Q9AEP9 staphylococ
13	41	77.4	452	2 Q9CID9	Q9CID9 staphylococ
14	39	73.6	440	2 Q6BFT8	Q6BFT8 staphylococ
15	39	73.6	450	2 Q97PP4	Q97PP4 streptococ
16	39	73.6	450	2 Q8DPI6	Q8DPI6 streptococ
17	39	73.6	3298	2 Q9VB11	Q9VB11 streptococ
18	39	71.7	42	2 Q9PCB5	Q9PCB5 xyliella fae
19	38	71.7	60	2 Q9PC99	Q9PC99 xyliella fae
20	38	71.7	253	2 Q6FT09	Q6FT09 candida gla
21	38	71.7	277	1 Y833_MERJA	Y833_MERJA methanococ
22	38	71.7	347	1 HPT_MOUSE	HPT_MOUSE mus musculu
23	38	71.7	347	1 HPT_MOUSE	HPT_MOUSE mus caroli
24	38	71.7	347	1 HPT_MOUSE	HPT_MOUSE mus saxicol
25	38	71.7	347	1 HPT_MOUSE	HPT_MOUSE mus sp. hap
26	38	71.7	498	2 Q8VPP4	Q8VPP4 micrococ
27	38	71.7	514	2 Q9GVPA	Q9GVPA plasmodium
28	38	71.7	622	2 Q9GSC0	Q9GSC0 caenorhabdi
29	38	71.7	759	2 Q7R9A5	Q7R9A5 plasmodium
30	38	71.7	828	2 Q6RX39	Q6RX39 arabidopsis
31	38	71.7	829	2 Q6RX46	Q6RX46 arabidopsis

32	38	71.7	3165	2 Q81JL8	Q81JL8 plasmodium
33	37	69.8	190	2 Q72PK0	Q72PK0 leprospira
34	37	69.8	190	2 Q8F6S3	Q8F6S3 leprospira
35	37	69.8	234	2 Q9YMK4	Q9YMK4 lymantria d
36	37	69.8	397	1 ARGJ_THENE	ARGJ_THENE t arginine
37	37	69.8	430	2 Q6GJ77	Q6GJ77 xenopus lae
38	37	69.8	460	2 Q7NA94	Q7NA94 photorhabdu
39	37	69.8	482	2 Q76K22	Q76K22 streptococ
40	37	69.8	632	1 THIC_CHARVO	THIC_CHARVO chromobacte
41	37	69.8	795	2 Q9VIN2	Q9VIN2 pyrococcus
42	37	69.8	796	2 Q8TZW0	Q8TZW0 pyrococcus
43	37	69.8	798	2 Q59515	Q59515 pyrococcus
44	37	69.8	915	2 Q84VC7	Q84VC7 oryza sativ
45	37	69.8	919	2 Q818G7	Q818G7 oryza sativ

ALIGNMENTS

RESULT 1	PRELIMINARY;	PRT;	961 AA.
Q99RD3	Q99RD3		
AC	Q99RD3		
DT	01-JUN-2001 (T-EMBLrel. 17, Created)		
DT	01-JUN-2001 (T-EMBLrel. 17, Last sequence update)		
DT	01-JUN-2003 (T-EMBLrel. 24, Last annotation update)		
DE	Fibronectin-binding protein homolog.		
GN	Name=fndb; OrderedlocusNames=SAV2502;		
OS	Staphylococcus aureus (strain Mu50 / ATCC 700699).		
OC	Bacteria; Firmicutes; Bacillales; Staphylococcus.		
OX	NCBI_TaxID=158878;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=Mu50 / ATCC 700699;		
RC	MEDLINE=21311952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2;		
RA	Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,		
RA	Chii L., Oguchi A., Aoki K.-I., Nagai Y., Iino T.,		
RA	Kanamori M., Matsunaru H., Maruyama A., Murakami H., Hosoyama A.,		
RA	Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.I., Kaito C.,		
RA	Sekimizu K., Hatakeyama H., Kihara S., Goto S., Yabuzaki J.,		
RA	Kanehisa M., Yamauchi A., Oshima K., Furuya K., Yoshino C., Shiba T.,		
RA	Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.,		
RT	"Whole genome sequencing of methicillin-resistant Staphylococcus		
RT	aureus."		
RL	Lancet 357:1225-1240(2001).		
CC	-1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by		
CC	an amide bond (BY similarity).		
DR	EMBL; AP003365; BAB58664.1; -		
DR	PIR; G90053; G90053.		
DR	HSSP; Q53653; IN67.		
DR	GO; GO:0009986; C:cell surface; IEA.		
DR	GO; GO:0005618; C:cell wall; IEA.		
DR	GO; GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.		
DR	GO; GO:0016020; C:membrane; IEA.		
DR	GO; GO:0007155; P:cell adhesion; IEA.		
DR	InterPro; IPR008966; Adhes_Bact.		
DR	InterPro; IPR004237; Fn_bind.		
DR	InterPro; IPR005877; Gpos_YSRK.		
DR	InterPro; IPR001899; Gram_pos_anchor.		
DR	Pfam; PF02986; Fn_bind_1.		
DR	Pfam; PF00746; Gram_pos_anchor; 1.		
DR	Pfam; PF04650; YSRK_signal; 1.		
DR	TIGRFAMs; TIGR01167; LPTXG_anchor; 1.		
DR	TIGRFAMs; TIGR01168; YSRK_signal; 1.		
DR	PROSITE; PS50847; GRAM_POS_ANCHORING; 1.		
KW	Cell wall; Complete proteome; Peptidoglycan-anchor.		
SC	SEQUENCE 961 AA; 106010 MW; 364940F884EAA101 CRC64;		
Qy	Query Match	100.0%;	Score 53; DB 2; Length 961;
	Best Local Similarity	100.0%;	Pred. No. 0.38;
	Matches 10; Conservative 0;	Mismatches 0;	Indels 0; Gaps 0;
	1 VDFEEDLPK 10		


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DB      795 VFEEBTLRK 804
|||||
RESULT 2
O7A3J8      PRELIMINARY;      PRT;      961 AA.
AC      07A3J8;
ID      07A3J8;
DT      05-JUL-2004 (TREMBlrel. 27, Created)
DT      05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DE      FnbB protein.
DE      Name=fnbB; OrderedlocusNames=SA2290;
OS      Staphylococcus aureus (strain N315).
OC      Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX      NCBI_TaxId=158679;
RN      [1]
RP      SEQUENCE FROM N.A.
RA      MEDLINE=21311952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2;
RX      Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
RA      Cui L., Oguchi A., Aoki K.-I., Nagai Y., Iian J.-Q., Ito T.,
RA      Kanemori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,
RA      Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
RA      Sekimizu K., Hirakawa H., Kohara S., Goto S., Yabuzaki J.,
RA      Kanehisa M., Yamashita A., Oshino K., Furuya K., Yoshino C., Shiba T.,
RA      Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
RT      "Whole genome sequencing of methicillin-resistant Staphylococcus
RT      aureus."
RL      Lancet 357:1225-1240(2001).
RC      -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC      an amide bond (By similarity).
DR      EMBL: AP003137; BAB43593.1; -.
DR      GO: GO:0009986; C:cell surface; IEA.
DR      GO: GO:0005618; C:cell wall; IEA.
DR      GO: GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR      GO: GO:0016020; C:membrane; IEA.
DR      GO: GO:0007155; P:cell adhesion; IEA.
DR      InterPro: IPR008966; Adhes_bact.
DR      InterPro: IPR004237; Fn_bind.
DR      InterPro: IPR005877; Gpos_YsIRK.
DR      InterPro: IPR001899; Gram_pos_anchor.
DR      Pfam: PF02986; Fn_bind.1.
DR      Pfam: PF00746; Gram_pos_anchor.1.
DR      Pfam: PF04650; YsIRK_signal.1.
DR      TIGRFAMs: TIGR01167; LpxTG_anchor.1.
DR      TIGRFAMs: TIGR01168; YsIRK_signal.1.
DR      PROSITE: PS50847; GRAM_POS_ANCHORING.1.
DR      KEGG cell wall; Complete proteome; Peptidoglycan-anchor.
SQ      SEQUENCE 961 AA; 106010 MW; 364940F884EA4101 CRC64;

Query Match      100.0%; Score 53; DB 2; Length 961;
Best Local Similarity 100.0%; Pred. No. 0.38;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY      1 VFEEBTLRK 10
|||||
DB      795 VFEEBTLRK 804

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RX      PubMed=15213324; DOI=10.1073/pnas.0402521101;
RA      Holden M.T.G., Fell E.J., Lindsay J.A., Peacock S.J., Day N.P.J.,
RA      Enright M.C., Foster T.J., Moore C.E., Hurst L., Atkin R., Barron A.,
RA      Bason N., Bentley S.D., Chillingworth C., Chillingworth T.,
RA      Churcher C., Clark L., Cotton C., Cronin A., Doggett J., Dowd L.,
RA      Feltham T., Hance Z., Harris B., Hauser H., Holtroyd S., Jagsis K.,
RA      James K.D., Lennard N., Line A., Mayes R., Moule S., Mungall K.,
RA      Ormond D., Quail M.A., Rabinowitch E., Rutherford K.M., Sanders M.,
RA      Sharp S., Simmonds M., Stevens K., Whitehead S., Barrall B.G.,
RA      Spratt B.G., Parkhill J.;
RT      "Complete genomes of two clinical Staphylococcus aureus strains:
RT      evidence for the rapid evolution of virulence and drug resistance.";
RL      Proc. Natl. Acad. Sci. U.S.A. 101:9786-9791(2004).
CC      -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC      an amide bond (By similarity).
DR      EMBL: BX571856; CAG41560.1; -.
DR      GO: GO:0009986; C:cell surface; IEA.
DR      GO: GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR      GO: GO:0016020; C:membrane; IEA.
DR      GO: GO:0007155; P:cell adhesion; IEA.
DR      InterPro: IPR008966; Adhes_bact.
DR      InterPro: IPR004237; Fn_bind.
DR      InterPro: IPR005877; Gpos_YsIRK.
DR      InterPro: IPR001899; Gram_pos_anchor.
DR      Pfam: PF02986; Fn_bind.1.
DR      Pfam: PF00746; Gram_pos_anchor.1.
DR      Pfam: PF04650; YsIRK_signal.1.
DR      TIGRFAMs: TIGR01167; LpxTG_anchor.1.
DR      TIGRFAMs: TIGR01168; YsIRK_signal.1.
DR      PROSITE: PS50847; GRAM_POS_ANCHORING.1.
DR      KEGG cell wall; Complete proteome; Peptidoglycan-anchor.
SQ      SEQUENCE 965 AA; 105691 MW; 2982E132164D0551 CRC64;

Query Match      100.0%; Score 53; DB 2; Length 965;
Best Local Similarity 100.0%; Pred. No. 0.38;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY      1 VFEEBTLRK 10
|||||
DB      813 VFEEBTLRK 822

RESULT 4
O8NUU7      PRELIMINARY;      PRT;      1015 AA.
AC      O8NUU7;
ID      O8NUU7;
DT      01-OCT-2002 (TREMBlrel. 22, Created)
DT      01-OCT-2002 (TREMBlrel. 22, Last sequence update)
DE      Fnb protein.
DE      Name=fnb; OrderedlocusNames=MW2421;
OS      Staphylococcus aureus (strain MW2).
OC      Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX      NCBI_TaxId=196620;
RN      [1]
RP      SEQUENCE FROM N.A.
RA      STRAIN=MW2;
RA      MEDLINE=22040717; PubMed=12044378; DOI=10.1016/S0140-6736(02)08713-5;
RA      Baba T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Oguchi A.,
RA      Nagai Y., Iwama N., Asano K., Naimi T., Kuroda H., Cui L.,
RA      Yamamoto K., Hiramatsu K.;
RT      "Genome and virulence determinants of high virulence community-
RT      acquired MRSA."
RL      Lancet 359:1819-1827(2002).
CC      -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC      an amide bond (By similarity).
DR      EMBL: AP004830; BAB96286.1; -.
DR      GO: GO:0009986; C:cell surface; IEA.
DR      GO: GO:0005618; C:cell wall; IEA.
DR      GO: GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR      GO: GO:0016020; C:membrane; IEA.
DR      GO: GO:0007155; P:cell adhesion; IEA.
DR      InterPro: IPR008966; Adhes_bact.

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FT SITE 982 986 LPTG sorting signal (Potential).
 FT MOD_RES 985 985 Pentaglycyl murein peptidoglycan amidated
 FT chreonine (Potential).
 SQ SEQUENCE 1018 AA; 111780 MW; 581758020881F1F CRC64;

Query Match 100.0%; Score 53; DB 1; Length 1018;
 Best Local Similarity 100.0%; Pred. No. 0.4;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VDFEEDTLPK 10
 Db 848 VDFEEDTLPK 857

RESULT 7
 099RD2 PRELIMINARY; PRT; 1038 AA.
 AC 099RD2;
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Fibronectin-binding protein homolog.
 GN Name=fnb; OrderedLocustNames=SAV2503;
 OS Staphylococcus aureus (strain M50 / ATCC 700699).
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 OX NCBI_TaxID=158878;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=M50 / ATCC 700699;
 RX MEDLINE=21311952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2;
 RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
 RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Iian J.-O., Ito T.,
 RA Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosooyama A.,
 RA Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
 RA Sekimizu K., Hirakawa H., Kohara S., Goto S., Yabuzaki J.,
 RA Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
 RA Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.,
 RT "Whole genome sequencing of methicillin-resistant Staphylococcus
 aureus";
 RL Lancet 357:1225-1240(2001).
 CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
 an amide bond (By similarity).
 CEMBL AP00337; BAB594.1; -;
 DR EMBL; AP00337; BAB594.1; -;
 DR GO; GO:0009986; C:cell surface; IEA.
 DR GO; GO:0005618; C:cell wall; IEA.
 DR GO; GO:0005275; C:cell wall (sensu Gram-positive Bacteria); IEA.
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0007155; P:cell adhesion; IEA.
 DR InterPro: IPR008966; Adhes_bact.
 DR InterPro: IPR004237; Fn_bind.
 DR InterPro: IPR005877; Gpos_YsIRK.
 DR InterPro: IPR001899; Gram_pos_anchor.
 DR Pfam: PF02986; Fn_bind. 1.
 DR Pfam: PF00746; Gram_pos_anchor. 1.
 DR Pfam: PF04650; YsIRK_signal. 1.
 DR TIGRFA: TIGR01167; LPTG_anchor. 1.
 DR TIGRFA: TIGR01168; YsIRK_signal. 1.
 DR PROSITE: PS50847; GRAM_POS_ANCHORING. 1.
 KW Cell wall; Complete proteome; Peptidoglycan-anchor.
 SQ SEQUENCE 1038 AA; 113618 MW; 666BF6BF2BFEB12 CRC64;

Query Match 100.0%; Score 53; DB 2; Length 1038;
 Best Local Similarity 100.0%; Pred. No. 0.41;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VDFEEDTLPK 10
 Db 844 VDFEEDTLPK 853

RESULT 8
 07A3J7

ID 07A3J7 PRELIMINARY; PRT; 1038 AA.
 AC 07A3J7;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Fnb protein.
 GN Name=fnb; OrderedLocustNames=SA2291;
 OS Staphylococcus aureus (strain N315).
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 OX NCBI_TaxID=158879;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC MEDLINE=21311952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2;
 RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
 RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Iian J.-O., Ito T.,
 RA Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosooyama A.,
 RA Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
 RA Sekimizu K., Hirakawa H., Kohara S., Goto S., Yabuzaki J.,
 RA Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
 RA Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.,
 RT "Whole genome sequencing of methicillin-resistant Staphylococcus
 aureus";
 RL Lancet 357:1225-1240(2001).
 CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
 an amide bond (By similarity).
 CEMBL AP00337; BAB43594.1; -;
 DR EMBL; AP00337; BAB43594.1; -;
 DR GO; GO:0009986; C:cell surface; IEA.
 DR GO; GO:0005618; C:cell wall; IEA.
 DR GO; GO:0005275; C:cell wall (sensu Gram-positive Bacteria); IEA.
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0007155; P:cell adhesion; IEA.
 DR InterPro: IPR008966; Adhes_bact.
 DR InterPro: IPR004237; Fn_bind.
 DR InterPro: IPR005877; Gpos_YsIRK.
 DR InterPro: IPR001899; Gram_pos_anchor.
 DR Pfam: PF02986; Fn_bind. 1.
 DR Pfam: PF00746; Gram_pos_anchor. 1.
 DR Pfam: PF04650; YsIRK_signal. 1.
 DR TIGRFA: TIGR01167; LPTG_anchor. 1.
 DR TIGRFA: TIGR01168; YsIRK_signal. 1.
 DR PROSITE: PS50847; GRAM_POS_ANCHORING. 1.
 KW Cell wall; Complete proteome; Peptidoglycan-anchor.
 SQ SEQUENCE 1038 AA; 113618 MW; 666BF6BF2BFEB12 CRC64;

Query Match 100.0%; Score 53; DB 2; Length 1038;
 Best Local Similarity 100.0%; Pred. No. 0.41;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VDFEEDTLPK 10
 Db 844 VDFEEDTLPK 853

RESULT 9
 053682 PRELIMINARY; PRT; 940 AA.
 ID 053682;
 AC 053682;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Fibronectin binding protein B.
 GN Name=fnb;
 OS Staphylococcus aureus.
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 OX NCBI_TaxID=1280;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=8325-4;
 RX MEDLINE=92111475; PubMed=1837266;
 RA Jonsson K., Signas C., Muller H.P., Lindberg M.,
 RT "Two different genes encode fibronectin binding proteins in
 Staphylococcus aureus. The complete nucleotide sequence and
 characterization of the second gene.";

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DR InterPro: IPR004237; Fn_bind.
DR InterPro: IPR005877; Gpos_YsIRK.
DR InterPro: IPR001899; Gram_pos_anchor.
DR Pfam: PF02986; Fn_bind_1.
DR Pfam: PF00746; Gram_pos_anchor; 1.
DR Pfam: PF04650; YsIRK_signal; 1.
DR TIGRPFAM: TIGR01167; LPXTG_anchor; 1.
DR TIGRPFAM: TIGR01168; YsIRK_signal; 1.
DR PROSITE: PS50847; GRAM_POS_ANCHORING; 1.
KW Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ SEQUENCE 1015 AA; 11145 MW; D0F9281BB64D44D2 CRC64;

Query Match 100.0%; Score 53; DB 2; Length 1015;
Best Local Similarity 100.0%; Pred. No. 0.4;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VFEEPTLPK 10
DB 849 VFEEPTLPK 858

RESULT 5
Q6G6H3 PRELIMINARY; PRT; 1015 AA.
ID Q6G6H3;
AC Q6G6H3;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Fibronectin-binding protein.
OS OrderedLocustNames=5A52388;
GN Staphylococcus aureus (strain MSSA476).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
NCBI_TaxID=282459;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=1521324; DOI=10.1073/pnas.0402521101;
RA Holden M.T.G., Fell E.J., Lindsay J.A., Peacock S.J., Day N.P.J.,
RA Holten M.T.G., Foster T.J., Moore C.E., Hurst L., Atkin R., Barron A.,
RA Bason N., Bentley S.D., Chillingworth T.,
RA Churcher C., Clark L., Cotton C., Cronin A., Doggett J., Dowd L.,
RA Felwell T., Hance Z., Harris B., Hauser H., Holtroyd S., Jørgensen K.,
RA James K.D., Lennard N., Line A., Mayes R., Moule S., Mungall K.,
RA Ormond D., Quail M.A., Rabinowitch E., Rutherford K.M., Sanders M.,
RA Sharp S., Simmonds M., Stevens K., Whitehead S., Barrett B.G.,
RA Spratt B.G., Parkhill J.,
RT "Complete genomes of two clinical Staphylococcus aureus strains:
RT evidence for the rapid evolution of virulence and drug resistance."
RL Proc. Natl. Acad. Sci. U.S.A. 101:9786-9791(2004).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC an amide bond (By similarity).
EMBL BX571857; CAC44202.1; .
DR GO: GO:0009986; C:cell surface; IEA.
DR GO: GO:0005618; C:cell wall; IEA.
DR GO: GO:0009375; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO: GO:0016020; C:membrane; IEA.
DR GO: GO:0007155; P:cell adhesion; IEA.
DR InterPro: IPR008966; Adhes_bact.
DR InterPro: IPR004237; Fn_bind.
DR InterPro: IPR005877; Gpos_YsIRK.
DR InterPro: IPR001899; Gram_pos_anchor.
DR Pfam: PF02986; Fn_bind_1.
DR Pfam: PF00746; Gram_pos_anchor; 1.
DR Pfam: PF04650; YsIRK_signal; 1.
DR TIGRPFAM: TIGR01167; LPXTG_anchor; 1.
DR TIGRPFAM: TIGR01168; YsIRK_signal; 1.
DR PROSITE: PS50847; GRAM_POS_ANCHORING; 1.
KW Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ SEQUENCE 1015 AA; 11145 MW; D0F9281BB64D44D2 CRC64;

Query Match 100.0%; Score 53; DB 2; Length 1015;
Best Local Similarity 100.0%; Pred. No. 0.4;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 VFEEPTLPK 10
DB 849 VFEEPTLPK 858

RESULT 6
PDBA_STAAU STANDARD; PRT; 1018 AA.
ID PDBA_STAAU
AC P14738;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Fibronectin-binding protein precursor (FNBP).
GN Name=fnbp;
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
NCBI_TaxID=1280;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=NCTC 8325-4;
RX MEDLINE=89098998; PubMed=2521391;
RA Signaes C., Raucsi G., Joensson K., Lindgren P.-E.,
RA Anantharamiah G.M., Hoeck M., Lindberg M.;
RA "Nucleotide sequence of the gene for a fibronectin-binding protein
RT from Staphylococcus aureus: use of this peptide sequence in the
RT synthesis of biologically active peptides."
RT Proc. Natl. Acad. Sci. U.S.A. 86:699-703(1989).
RL -1- FUNCTION: The ability of bacteria to bind fibronectin has been
CC proposed as a virulence factor enabling bacteria to colonize wound
CC tissues and blood clots. Binding of plasma fibronectin to the
CC bacterial surface might block adhesion receptors on S. aureus, thus
CC representing an important defense mechanism against tissue
CC invasion.
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC an amide bond (Potential).
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC
CC EMBL J04151; AA26632.1; .
DR InterPro: IPR004237; Fn_bind.
DR InterPro: IPR005877; Gpos_YsIRK.
DR InterPro: IPR001899; Gram_pos_anchor.
DR Pfam: PF02986; Fn_bind_1.
DR Pfam: PF00746; Gram_pos_anchor; 1.
DR Pfam: PF04650; YsIRK_signal; 1.
DR TIGRPFAM: TIGR01167; LPXTG_anchor; 1.
DR TIGRPFAM: TIGR01168; YsIRK_signal; 1.
DR PROSITE: PS50847; GRAM_POS_ANCHORING; 1.
KW Cell adhesion; Cell wall; Peptidoglycan-anchor; Repeat; Signal;
KW Virulence.
KW SIGNAL 1 36
FT CHAIN 37 985 Fibronectin-binding protein.
FT PROPEP 986 1018 Removed by sortase (Potential).
FT REPEAT 545 574 B-1.
FT REPEAT 575 604 B-2.
FT DOMAIN 745 878 4 X approximate tandem repeats,
FT REPEAT 745 878 fibronectin-binding domain.
FT REPEAT 745 782 D-1.
FT REPEAT 783 820 D-2.
FT REPEAT 821 859 D-3.
FT REPEAT 860 878 D-4 (incomplete).
FT DOMAIN 879 948 5 X tandem repeats, Pro-rich (WR).
FT REPEAT 879 892 WR 1.
FT REPEAT 893 906 WR 2.
FT REPEAT 907 920 WR 3.
FT REPEAT 921 934 WR 4.
FT REPEAT 935 948 WR 5.

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RL Eur. J. Biochem. 202;1041-1048(1991).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC an amide bond (By similarity).
DR EMBL: X62992; CAA44726.1; -.
DR PIR: S19702; S19702.
DR HSP; Q53653; IN67.
DR GO: GO:0009986; C:cell surface; IEA.
DR GO: GO:0005618; C:cell wall; IEA.
DR GO: GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO: GO:0016020; C:membrane; IEA.
DR GO: GO:0007155; P:cell adhesion; IEA.
DR InterPro: IPR008966; Adhes_bact.
DR InterPro: IPR004237; Fn_bind.
DR InterPro: IPR005877; Gpos_YsIRK.
DR InterPro: IPR001899; Gram_pos_anchor.
DR Pfam: PF00746; Gram_pos_anchor; 1.
DR Pfam: PF04650; YsIRK_signal; 1.
DR TIGRFAMs: TIGR01167; LPXTG_anchor; 1.
DR TIGRFAMs: TIGR01168; YsIRK_signal; 1.
DR PROSITE: PS50847; GRAM_POS_ANCHORING; 1.
KW Cell wall; Peptidoglycan-anchor.
SQ SEQUENCE 940 AA; 10355 MW; E35FBBCA907A5345 CRC64;

Query Match 92.5%; Score 49; DB 2; Length 940;
Best Local Similarity 90.0%; Pred. No. 2.2;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 VFPEEDTLPK 10
Db 784 VFPEEDTLPK 793
|||||
PRT; 943 AA.

RESULT 10
ID 08NU8 PRELIMINARY; PRT; 943 AA.
AC 08NU8;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE FndB protein.
DE Name=fndB; OrderedlocusNames=MM2420;
OS Staphylococcus aureus (strain MM2).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
NCBI_TaxID=196620;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MM2;
RX MEDLINE=22040717; Pubmed=12044378; DOI=10.1016/S0140-6736(02)08713-5;
RA Baba T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Oguchi A.,
RA Nagai Y., Iwama N., Asano K., Naito T., Kuroda H., Cui L.,
RA Yamamoto K., Hiramatsu K.,
RT "Genome and virulence determinants of high virulence community-
acquired MRSA.";
RT Lancer 359:1819-1827(2002).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC an amide bond (By similarity).
EMBL: AP004830; BAB96285.1; -.
DR HSP; Q53653; IN67.
DR GO: GO:0009986; C:cell surface; IEA.
DR GO: GO:0005618; C:cell wall; IEA.
DR GO: GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO: GO:0016020; C:membrane; IEA.
DR GO: GO:0007155; P:cell adhesion; IEA.
DR InterPro: IPR008966; Adhes_bact.
DR InterPro: IPR004237; Fn_bind.
DR InterPro: IPR005877; Gpos_YsIRK.
DR InterPro: IPR001899; Gram_pos_anchor.
DR Pfam: PF00746; Gram_pos_anchor; 1.
DR Pfam: PF04650; YsIRK_signal; 1.
DR TIGRFAMs: TIGR01167; LPXTG_anchor; 1.
DR TIGRFAMs: TIGR01168; YsIRK_signal; 1.

DR PROSITE: PS50847; GRAM_POS_ANCHORING; 1.
KW Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ SEQUENCE 943 AA; 104537 MW; DA8A5F31947E1B6A CRC64;

Query Match 92.5%; Score 49; DB 2; Length 943;
Best Local Similarity 90.0%; Pred. No. 2.2;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 VFPEEDTLPK 10
Db 791 VFPEEDTLPK 800
|||||
PRT; 957 AA.

RESULT 11
ID 06G6H4 PRELIMINARY; PRT; 957 AA.
AC 06G6H4;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Fibronectin-binding protein.
DE Name=fndB; OrderedlocusNames=SAS2387;
OS Staphylococcus aureus (strain MSSA476).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
NCBI_TaxID=282459;
RN [1]
RP SEQUENCE FROM N.A.
RX Pubmed=15213324; DOI=10.1073/pnas.0402521101;
RA Holden M.T.G., Fell E.J., Lindsay J.A., Peacock S.J., Day N.P.J.,
RA Enright M.C., Foster T.J., Moore C.E., Hurst L., Ackin R., Barron A.,
RA Bason N., Bentley S.D., Chillingworth C., Chillingworth T.,
RA Churcher C., Clark L., Corton C., Cronin A., Doggett J., Dowd L.,
RA Felwell T., Hance Z., Harris B., Hauser H., Holtroyd S., Jagels K.,
RA James K.D., Leonard N., Line A., Mayes R., Moule S., Mungall K.,
RA Ormond D., Quail M.A., Rabinovitch E., Rutherford K.M., Sanders M.,
RA Sharp S., Simmonds M., Stevens K., Whitehead S., Barrett B.G.,
RA Spratt B.G., Parkhill J.,
RT "Complete genomes of two clinical Staphylococcus aureus strains:
evidence for the rapid evolution of virulence and drug resistance.";
RT Proc. Natl. Acad. Sci. U.S.A. 101:9786-9791(2004).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC an amide bond (By similarity).
EMBL: BX571857; CAG44201.1; -.
DR GO: GO:0009986; C:cell surface; IEA.
DR GO: GO:0005618; C:cell wall; IEA.
DR GO: GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO: GO:0016020; C:membrane; IEA.
DR GO: GO:0007155; P:cell adhesion; IEA.
DR InterPro: IPR008966; Adhes_bact.
DR InterPro: IPR004237; Fn_bind.
DR InterPro: IPR005877; Gpos_YsIRK.
DR InterPro: IPR001899; Gram_pos_anchor.
DR Pfam: PF00746; Gram_pos_anchor; 1.
DR Pfam: PF04650; YsIRK_signal; 1.
DR TIGRFAMs: TIGR01167; LPXTG_anchor; 1.
DR TIGRFAMs: TIGR01168; YsIRK_signal; 1.
DR PROSITE: PS50847; GRAM_POS_ANCHORING; 1.
KW Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ SEQUENCE 957 AA; 105980 MW; 28F8BA7FFFD3EAF CRC64;

Query Match 92.5%; Score 49; DB 2; Length 957;
Best Local Similarity 90.0%; Pred. No. 2.2;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 VFPEEDTLPK 10
Db 791 VFPEEDTLPK 800
|||||
PRT; 152 AA.

RESULT 12
ID 09AEP9 PRELIMINARY; PRT; 152 AA.

```
AC O9AEP9;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DE 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE Fibronectin-binding protein (Fragment).
GN Name=fnb;
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1280;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CMRSA-1;
RX MEDLINE=21246681; PubMed=11349044;
DOI=10.1128/IAI.69.6.3791-3799.2001;
R Rice K., Huebner M., Vaz D., McGavin M.J.;
RT "Variance in fibronectin binding and fmb locus polymorphisms in
RT Staphylococcus aureus: identification of antigenic variation in a
RT fibronectin binding protein adhesin of the epidemic CMRSA-1 strain of
RT methicillin-resistant S. aureus.";
RL Infect. Immun. 69:3791-3799(2001).
DR EMBL: AY029184; AAK31588.1; -.
FT NON_TER
FT NON_TER
SQ SEQUENCE 152 AA; 17193 MW; CFA3913C2B11C025 CRC64;

Query Match
Best Local Similarity 84.9%; Score 45; DB 2; Length 152;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 VFEDDTLPK 10
:|||||
141 IDVEDTLPK 150

RESULT 13
O9CID9 PRELIMINARY; PRT; 452 AA.
AC O9CID9;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DE 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE Phosphoglucosamine mutase.
GN Name=fmd; OrderedLocustNames=LP0424;
OS Lactococcus lactis (subsp. lactis) (Streptococcus lactis).
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae; Lactococcus.
OX NCBI_TaxID=1360;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=IL1403;
RX MEDLINE=21235186; PubMed=11337471; DOI=10.1101/gr.1697R;
RA Bolotin A., Wincker P., Manger S., Jallion O., Malarme K.,
RA Weissenbach J., Ehrlich S.D., Sorokin A.;
RT "The complete genome sequence of the lactic acid bacterium Lactococcus
RT lactis ssp. lactis IL1403.";
RL Genome Res. 11:731-753(2001).
DR EMBL: AB006279; AAK04522.1; -.
DR PIR: H86577; H86577
DR GO: GO:0016866; F:intramolecular transferase activity, phosph. .; IEA.
DR GO: GO:0005975; F:carbohydrate metabolism; IEA.
DR InterPro: IPR006352; GIMM.
DR InterPro: IPR005841; PG/PMM mutase.
DR InterPro: IPR005844; PG_PMM_ABAI.
DR InterPro: IPR005845; PG_PMM_ABAI.
DR InterPro: IPR005846; PG_PMM_ABAI.
DR InterPro: IPR005843; PG_PMM_C.
DR Pfam: PF02878; PGM_PMM_I; 1.
DR Pfam: PF02879; PGM_PMM_II; 1.
DR Pfam: PF02880; PGM_PMM_III; 1.
DR Pfam: PF00408; PGM_PMM_IV; 1.
DR PRINTS: PR00509; GPM_PMM.
DR TIGRfam: TIGR01455; GIMM; 1.
DR PROSITE: PS00710; PGM_PMM; 1.
KW Complete proteome.
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SQ SEQUENCE 452 AA; 48472 MW; 074B32FCSB7A5D63 CRC64;

Query Match
Best Local Similarity 77.4%; Score 41; DB 2; Length 452;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 VFEDDTLPK 10
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Db 132 IDVEDTLPR 141

RESULT 14
O6BFT8 PRELIMINARY; PRT; 440 AA.
AC O6BFT8;
DT 25-OCT-2004 (TREMBlrel. 28, Created)
DT 25-OCT-2004 (TREMBlrel. 28, Last sequence update)
DE 25-OCT-2004 (TREMBlrel. 28, Last annotation update)
DE Step II splicing factor SLU7, putative.
GN ORFNames=PTMB.284C;
OS Parametium tetraurelia.
OC Eukaryota; Alveolata; Ciliophora; Oligohymenophorea; Peniculida;
OC Parametium.
OX NCBI_TaxID=5888;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Stock d4-2;
RX PubMed=15296759; DOI=10.1016/j.cub.2004.07.029;
RA Zagulski M., Nowak J.K., Le Mouel A., Nowacki M., Migdalski A.,
RA Gromadka R., Noel B., Blanc I., Dessen P., Wincker P., Keller A.M.,
RA Cohen J., Meyer B., Sperling L.;
RT "High Coding Density on the Largest Parametium tetraurelia Somatic
RT Chromosome.";
RL Curr. Biol. 14:1397-1404(2004).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Stock d4-2;
RA Nowak J.K., Migdalski A., Gromadka R., Zagulski M.;
RT "Parametium megabase sequencing project.";
RL Submitted (JUL-2004) to the EMBL/Genbank/DBJ databases.
DR EMBL: CR548612; CAH03482.1; -.
DR GO: GO:0003676; F:nucleic acid binding; IEA.
DR InterPro: IPR001878; Znf_CCHC.
DR Pfam: PF00098; ZF-CCHC; 1.
DR PRINTS: PR00939; C2HCZNPINGER.
SQ SEQUENCE 440 AA; 51666 MW; 90DFD385D69F13FF CRC64;

Query Match
Best Local Similarity 73.6%; Score 39; DB 2; Length 440;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 VFEDDTLPK 10
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Db 329 VEYEDGLPK 338

RESULT 15
O97PP4 PRELIMINARY; PRT; 450 AA.
ID O97PP4;
AC O97PP4;
DT 01-OCT-2001 (TREMBlrel. 18, Created)
DT 01-OCT-2001 (TREMBlrel. 18, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE Phosphoglucosaminase/phosphomannomutase family protein.
GN OrderedLocustNames=SPI559;
OS Streptococcus pneumoniae.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1313;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC BAA-334 / TIGR4;
RX MEDLINE=21357209; PubMed=11463916; DOI=10.1126/science.1061217;
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RA Tettelein H., Nelson K.E., Paulsen I.T., Eisen J.A., Read T.D.,
 RA Peterson S.N., Heidelberg J.F., Deboy R.T., Haft D.H., Dodson R.J.,
 RA Durkin A.S., Gwinn M.L., Kolonay J.F., Nelson W.C., Peterson J.D.,
 RA Umayam L.A., White O., Salzberg S.L., Lewis M.R., Radune D.,
 RA Holtzapfel E.K., Knouri H.M., Wolf A.M., Utterback T.R., Hansen C.L.,
 RA McDonald L.A., Feldblyum T.V., Angiuoli S.V., Dickinson T.,
 RA Hickey E.K., Holt I.E., Loftus B.J., Yang F., Smith H.O., Venter J.C.,
 RA Dougherty B.A., Morrison D.A., Hollingshead S.K., Fraser C.M.,
 RA "Complete genome sequence of a virulent isolate of Streptococcus
 RT pneumoniae";
 RT Science 293:498-506(2001).
 DR EMBL; AB007451; AAK75646.1; -.
 DR PIR; E95181; E95181.
 DR TIGR; SPI559; -.
 DR GO; GO:0016868; P:intramolecular transferase activity, phosph. . .; IEA.
 DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
 DR InterPro; IPR006352; G1m.
 DR InterPro; IPR005841; PG/PWM_mutase.
 DR InterPro; IPR005844; PG_PWM_ABAI.
 DR InterPro; IPR005845; PG_PWM_ABAII.
 DR InterPro; IPR005846; PG_PWM_ABAIII.
 DR InterPro; IPR005843; PG_PWM_C.
 DR Pfam; PF02878; PGM_PWM_I; 1.
 DR Pfam; PF02879; PGM_PWM_II; 1.
 DR Pfam; PF02880; PGM_PWM_III; 1.
 DR Pfam; PF00408; PGM_PWM_IV; 1.
 DR PRINTS; PR00509; PGM_PWM.
 DR TIGRPFAM; TIGR01455; g1m; 1.
 DR PROSITE; PS00710; PGM_PWM; 1.
 DR Complete proteome.
 SQ SEQUENCE 450 AA; 48122 MW; 496B908FPAAD7AFB8 CRC64;

Query Match 73.6%; Score 39; DB 2; Length 450;
 Best Local Similarity 70.0%; Pred. No. 82;
 Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 QY 1 VDFEEDTLPR 10
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 Db 132 LDAEDTLPR 141

Search completed: October 22, 2005, 09:52:29
 Job time : 58.2069 secs

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GenCore version 5.1.6
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OM protein - protein search, using BW model

Run on: October 22, 2005, 12:39:57 : Search time 56.1494 Seconds
(without alignments)
74.354 Million cell updates/sec

Title: US-10-731-238-101

Perfect score: 53

Sequence: 1 VDFEEDTLPK 10

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 1862951 seqs, 417491010 residues

Total number of hits satisfying chosen parameters: 1862951

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database:

1: Published Applications_AA.*
2: /cgn2_6/prodata/2/pubppa/US07_PUBCOMB.pep.*
3: /cgn2_6/prodata/2/pubppa/PCT_NEW_PUB.pep.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	53	100.0	10	US-10-731-238-101	Sequence 101, App
2	53	100.0	11	US-10-731-238-86	Sequence 86, App1
3	53	100.0	21	US-10-731-238-9	Sequence 9, App1
4	53	100.0	21	US-10-731-238-10	Sequence 10, App1
5	53	100.0	21	US-10-731-238-14	Sequence 14, App1
6	53	100.0	21	US-10-731-238-15	Sequence 15, App1
7	53	100.0	21	US-10-731-238-16	Sequence 16, App1
8	53	100.0	21	US-10-731-238-17	Sequence 17, App1
9	53	100.0	21	US-10-731-238-18	Sequence 18, App1
10	53	100.0	21	US-10-731-238-19	Sequence 19, App1
11	53	100.0	21	US-10-731-238-20	Sequence 20, App1

12	53	100.0	21	US-10-731-238-21	Sequence 21, App1
13	53	100.0	21	US-10-731-238-22	Sequence 22, App1
14	53	100.0	21	US-10-731-238-23	Sequence 23, App1
15	53	100.0	21	US-10-731-238-24	Sequence 24, App1
16	53	100.0	22	US-10-731-238-13	Sequence 13, App1
17	53	100.0	37	US-11-066-697-1134	Sequence 1134, App
18	53	100.0	139	US-09-813-820-8	Sequence 8, App1
19	53	100.0	139	US-10-282-122A-43778	Sequence 43778, A
20	53	100.0	978	US-09-815-242-5456	Sequence 5456, App
21	53	100.0	1001	US-09-815-242-14686	Sequence 12686, A
22	53	100.0	1018	US-09-815-242-5797	Sequence 5797, App
23	53	100.0	1018	US-09-815-242-12838	Sequence 12838, A
24	53	100.0	1018	US-10-470-0488-68	Sequence 68, App1
25	53	100.0	1027	US-08-781-986A-5254	Sequence 5254, App
26	53	100.0	1027	US-10-328-624-5254	Sequence 5254, App
27	53	100.0	1038	US-10-282-122A-43827	Sequence 43827, A
28	49	92.5	10	US-10-731-238-102	Sequence 102, App1
29	49	92.5	21	US-10-731-238-24	Sequence 24, App1
30	49	92.5	388	US-08-901-062-1	Sequence 1, App1
31	49	92.5	8	US-08-781-986A-5251	Sequence 5251, App
32	49	92.5	559	US-10-328-624-5251	Sequence 5251, App
33	49	92.5	17	US-10-470-0488-69	Sequence 69, App1
34	49	92.5	948	US-10-470-0488-69	Sequence 69, App1
35	48	90.6	21	US-10-731-238-33	Sequence 33, App1
36	47	88.7	21	US-10-731-238-27	Sequence 27, App1
37	47	88.7	21	US-10-731-238-28	Sequence 28, App1
38	47	88.7	21	US-10-731-238-30	Sequence 30, App1
39	46	86.8	21	US-10-731-238-25	Sequence 25, App1
40	46	86.8	21	US-10-731-238-29	Sequence 29, App1
41	46	86.8	21	US-10-731-238-31	Sequence 31, App1
42	45	84.9	21	US-10-731-238-32	Sequence 32, App1
43	43	81.1	10	US-10-731-238-26	Sequence 26, App1
44	41	77.4	18	US-10-731-238-100	Sequence 100, App
45	41	77.4	15	US-10-369-493-18337	Sequence 18337, A

ALIGNMENTS

RESULT 1
US-10-731-238-101
Sequence 101, Application US/10731238
Publication No. US20050123552A1
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
Patti, Joseph M.
House-Pompeo, Karen L.
Speziale, Pietro
Joh, Danny
McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSER: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: US
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/731.238
FILING DATE: 10-Dec-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/010.317
FILING DATE: 21-Jan-1998
APPLICATION NUMBER: US 60/036.139

FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAMK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 101:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 101:
US-10-731-238-101

Query Match 100.0%; Score 53; DB 18; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0059;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VFEEEDTLPK 10
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1 VFEEEDTLPK 10

Db 1 VFEEEDTLPK 10

RESULT 2
US-10-731-238-86
Sequence 86, Application US/10731238
Publication No. US20050123552A1
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
Patti, Joseph M.
House-Pompeo, Karen L.
Speziale, Pietro
John, Danny
McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/731,238
FILING DATE: 10-Dec-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE: 21-Jan-1998
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAMK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 86:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>

TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 86:
US-10-731-238-86

Query Match 100.0%; Score 53; DB 18; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.0065;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VFEEEDTLPK 10
|||
1 VFEEEDTLPK 10

Db 1 VFEEEDTLPK 10

RESULT 3
US-10-731-238-9
Sequence 9, Application US/10731238
Publication No. US20050123552A1
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
Patti, Joseph M.
House-Pompeo, Karen L.
Speziale, Pietro
John, Danny
McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/731,238
FILING DATE: 10-Dec-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE: 21-Jan-1998
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAMK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 9:
US-10-731-238-9

Query Match 100.0%; Score 53; DB 18; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.013;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VFEEEDTLPK 10
|||
12 VFEEEDTLPK 21

Db 12 VFEEEDTLPK 21

RESULT 4
US-10-731-238-10
Sequence 10, Application US/10731238
Publication No. US20050123552A1
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
Patti, Joseph M.
House-Pompeo, Karen L.
Speziale, Pietro
Joh, Danny
McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/731,238
FILING DATE: 10-Dec-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE: 21-Jan-1998
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-Jan-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAMK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 10:
US-10-731-238-10
Query Match 100.0%; Score 53; DB 18; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.013;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 VDFEEDTLPK 10
Db 12 VDFEEDTLPK 21
RESULT 5
US-10-731-238-14
Sequence 14, Application US/10731238
Publication No. US20050123552A1
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
Patti, Joseph M.
House-Pompeo, Karen L.
Speziale, Pietro
Joh, Danny
McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
AND METHODS OF USE

NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/731,238
FILING DATE: 10-Dec-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE: 21-Jan-1998
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-Jan-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAMK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 14:
US-10-731-238-14
Query Match 100.0%; Score 53; DB 18; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.013;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 VDFEEDTLPK 10
Db 12 VDFEEDTLPK 21
RESULT 6
US-10-731-238-15
Sequence 15, Application US/10731238
Publication No. US20050123552A1
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
Patti, Joseph M.
House-Pompeo, Karen L.
Speziale, Pietro
Joh, Danny
McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30

1 CURRENT APPLICATION DATA:
2 APPLICATION NUMBER: US/10/731,238
3 FILING DATE: 10-Dec-2003
4 CLASSIFICATION: <Unknown>
5 PRIOR APPLICATION DATA:
6 APPLICATION NUMBER: US/09/010,317
7 FILING DATE: 21-Jan-1998
8 APPLICATION NUMBER: US 60/036,139
9 FILING DATE: 21-Jan-1997
10 ATTORNEY/AGENT INFORMATION:
11 NAME: Hibler, David W.
12 REGISTRATION NUMBER: 41,071
13 REFERENCE/DOCKET NUMBER: TAMK:189
14 TELECOMMUNICATION INFORMATION:
15 TELEPHONE: 512-418-3000
16 TELEFAX: 512-474-7577
17 INFORMATION FOR SEQ ID NO: 15:
18 SEQUENCE CHARACTERISTICS:
19 LENGTH: 21 amino acids
20 TYPE: amino acid
21 STRANDEDNESS: <Unknown>
22 TOPOLOGY: linear
23 SEQUENCE DESCRIPTION: SEQ ID NO: 15:
24 US-10-731-238-15
25
26 Query Match 100.0%; Score 53; DB 18; Length 21;
27 Best Local Similarity 100.0%; Pred. No. 0.013; 0; Indels 0; Gaps 0;
28 Matches 10; Conservative 0; Mismatches 0;
29
30 QY 1 VFEEEDTLPK 10
31 |||||
32 Db 12 VFEEEDTLPK 21
33
34 RESULT 7
35 US-10-731-238-16
36 Sequence 16, Application US/10731238
37 Publication No. US20050123552A1
38 GENERAL INFORMATION:
39 APPLICANT: Hook, Magnus
40 Patti, Joseph M.
41 House-Pompeo, Karen L.
42 Speziale, Pietro
43 Joh, Danny
44 McGavin, Martin J.
45 TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
46 NUMBER OF SEQUENCES: 105
47 CORRESPONDENCE ADDRESSES:
48 ADDRESSEE: Arnold, White & Durkee
49 STREET: P.O. Box 4433
50 CITY: Houston
51 STATE: TX
52 COUNTRY: USA
53 ZIP: 77210-4433
54 COMPUTER READABLE FORM:
55 MEDIUM TYPE: floppy disk
56 OPERATING SYSTEM: PC-DOS/MS-DOS
57 SOFTWARE: Patent in Release #1.0, Version #1.30
58 CURRENT APPLICATION DATA:
59 APPLICATION NUMBER: US/10/731,238
60 FILING DATE: 10-Dec-2003
61 CLASSIFICATION: <Unknown>
62 PRIOR APPLICATION DATA:
63 APPLICATION NUMBER: US/09/010,317
64 FILING DATE: 21-Jan-1998
65 APPLICATION NUMBER: US 60/036,139
66 FILING DATE: 21-Jan-1997
67 ATTORNEY/AGENT INFORMATION:
68 NAME: Hibler, David W.
69 REGISTRATION NUMBER: 41,071
70 REFERENCE/DOCKET NUMBER: TAMK:189

1 TELECOMMUNICATION INFORMATION:
2 TELEPHONE: 512-418-3000
3 TELEFAX: 512-474-7577
4 INFORMATION FOR SEQ ID NO: 16:
5 SEQUENCE CHARACTERISTICS:
6 LENGTH: 21 amino acids
7 TYPE: amino acid
8 STRANDEDNESS: <Unknown>
9 TOPOLOGY: linear
10 SEQUENCE DESCRIPTION: SEQ ID NO: 16:
11 US-10-731-238-16
12
13 Query Match 100.0%; Score 53; DB 18; Length 21;
14 Best Local Similarity 100.0%; Pred. No. 0.013;
15 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
16
17 QY 1 VFEEEDTLPK 10
18 |||||
19 Db 12 VFEEEDTLPK 21
20
21 RESULT 8
22 US-10-731-238-17
23 Sequence 17, Application US/10731238
24 Publication No. US20050123552A1
25 GENERAL INFORMATION:
26 APPLICANT: Hook, Magnus
27 Patti, Joseph M.
28 House-Pompeo, Karen L.
29 Speziale, Pietro
30 Joh, Danny
31 McGavin, Martin J.
32 TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
33 NUMBER OF SEQUENCES: 105
34 CORRESPONDENCE ADDRESSES:
35 ADDRESSEE: Arnold, White & Durkee
36 STREET: P.O. Box 4433
37 CITY: Houston
38 STATE: TX
39 COUNTRY: USA
40 ZIP: 77210-4433
41 COMPUTER READABLE FORM:
42 MEDIUM TYPE: floppy disk
43 OPERATING SYSTEM: PC-DOS/MS-DOS
44 SOFTWARE: Patent in Release #1.0, Version #1.30
45 CURRENT APPLICATION DATA:
46 APPLICATION NUMBER: US/10/731,238
47 FILING DATE: 10-Dec-2003
48 CLASSIFICATION: <Unknown>
49 PRIOR APPLICATION DATA:
50 APPLICATION NUMBER: US/09/010,317
51 FILING DATE: 21-Jan-1998
52 APPLICATION NUMBER: US 60/036,139
53 FILING DATE: 21-Jan-1997
54 ATTORNEY/AGENT INFORMATION:
55 NAME: Hibler, David W.
56 REGISTRATION NUMBER: 41,071
57 REFERENCE/DOCKET NUMBER: TAMK:189
58 TELECOMMUNICATION INFORMATION:
59 TELEPHONE: 512-418-3000
60 TELEFAX: 512-474-7577
61 INFORMATION FOR SEQ ID NO: 17:
62 SEQUENCE CHARACTERISTICS:
63 LENGTH: 21 amino acids
64 TYPE: amino acid
65 STRANDEDNESS: <Unknown>
66 TOPOLOGY: linear
67 SEQUENCE DESCRIPTION: SEQ ID NO: 17:
68 US-10-731-238-17
69
70 Query Match 100.0%; Score 53; DB 18; Length 21;

Best Local Similarity 100.0%; Pred. No. 0.013;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VDFEEDTLPK 10
Db 12 VDFEEDTLPK 21

RESULT 9

US-10-731-238-18

; Sequence 18, Application US/10731238
; Publication No. US20050123552A1
; GENERAL INFORMATION:

APPLICANT: Hook, Magnus

Patti, Joseph M.
House-Pompeo, Karen L.

Speziale, Pietro

John, Danny

McGavin, Martin J.

TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS

AND METHODS OF USE

NUMBER OF SEQUENCES: 105

CORRESPONDENCE ADDRESS:

ADDRESSEE: Arnold, White & Durkee

STREET: P.O. Box 4433

CITY: Houston

STATE: TX

COUNTRY: USA

ZIP: 77210-4433

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/731,238

FILING DATE: 10-Dec-2003

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/010,317

FILING DATE: 21-Jan-1998

APPLICATION NUMBER: US 60/036,139

FILING DATE: 21-JAN-1997

ATTORNEY/AGENT INFORMATION:

NAME: Hibler, David W.

REGISTRATION NUMBER: 41,071

REFERENCE/DOCKET NUMBER: TMK:189

TELECOMMUNICATION INFORMATION:

TELEPHONE: 512-418-3000

TELEFAX: 512-474-7577

INFORMATION FOR SEQ ID NO: 18:

SEQUENCE CHARACTERISTICS:

LENGTH: 21 amino acids

TYPE: amino acid

STRANDEDNESS: <Unknown>

TOPOLOGY: linear

SEQUENCE DESCRIPTION: SEQ ID NO: 18:

US-10-731-238-18

Query Match 100.0%; Score 53; DB 18; Length 21;

Best Local Similarity 100.0%; Pred. No. 0.013;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VDFEEDTLPK 10

Db 12 VDFEEDTLPK 21

RESULT 10

US-10-731-238-19

; Sequence 19, Application US/10731238

; Publication No. US20050123552A1

; GENERAL INFORMATION:

APPLICANT: Hook, Magnus

Patti, Joseph M.

House-Pompeo, Karen L.

Speziale, Pietro

John, Danny

McGavin, Martin J.

TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS

AND METHODS OF USE

NUMBER OF SEQUENCES: 105

CORRESPONDENCE ADDRESS:

ADDRESSEE: Arnold, White & Durkee

STREET: P.O. Box 4433

CITY: Houston

Query Match 100.0%; Score 53; DB 18; Length 21;

Best Local Similarity 100.0%; Pred. No. 0.013;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VDFEEDTLPK 10

Db 12 VDFEEDTLPK 21

RESULT 11

US-10-731-238-20

; Sequence 20, Application US/10731238

; Publication No. US20050123552A1

; GENERAL INFORMATION:

APPLICANT: Hook, Magnus

Patti, Joseph M.

House-Pompeo, Karen L.

Speziale, Pietro

John, Danny

McGavin, Martin J.

TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS

AND METHODS OF USE

NUMBER OF SEQUENCES: 105

CORRESPONDENCE ADDRESS:

ADDRESSEE: Arnold, White & Durkee

STREET: P.O. Box 4433

CITY: Houston

Query Match 100.0%; Score 53; DB 18; Length 21;

Best Local Similarity 100.0%; Pred. No. 0.013;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VDFEEDTLPK 10

Db 12 VDFEEDTLPK 21

RESULT 12

US-10-731-238-21

; Sequence 21, Application US/10731238

; Publication No. US20050123552A1

; GENERAL INFORMATION:

APPLICANT: Hook, Magnus

Patti, Joseph M.

House-Pompeo, Karen L.

Speziale, Pietro

John, Danny

McGavin, Martin J.

TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS

AND METHODS OF USE

NUMBER OF SEQUENCES: 105

CORRESPONDENCE ADDRESS:

ADDRESSEE: Arnold, White & Durkee

STREET: P.O. Box 4433

CITY: Houston

Query Match 100.0%; Score 53; DB 18; Length 21;

Best Local Similarity 100.0%; Pred. No. 0.013;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VDFEEDTLPK 10

Db 12 VDFEEDTLPK 21

RESULT 13

US-10-731-238-22

; Sequence 22, Application US/10731238

; Publication No. US20050123552A1

; GENERAL INFORMATION:

APPLICANT: Hook, Magnus

Patti, Joseph M.

House-Pompeo, Karen L.

Speziale, Pietro

John, Danny

McGavin, Martin J.

TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS

AND METHODS OF USE

NUMBER OF SEQUENCES: 105

CORRESPONDENCE ADDRESS:

ADDRESSEE: Arnold, White & Durkee

STREET: P.O. Box 4433

CITY: Houston

Query Match 100.0%; Score 53; DB 18; Length 21;

Best Local Similarity 100.0%; Pred. No. 0.013;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VDFEEDTLPK 10

Db 12 VDFEEDTLPK 21

RESULT 14

US-10-731-238-23

; Sequence 23, Application US/10731238

; Publication No. US20050123552A1

; GENERAL INFORMATION:

APPLICANT: Hook, Magnus

Patti, Joseph M.

House-Pompeo, Karen L.

Speziale, Pietro

John, Danny

McGavin, Martin J.

TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS

AND METHODS OF USE

NUMBER OF SEQUENCES: 105

CORRESPONDENCE ADDRESS:

ADDRESSEE: Arnold, White & Durkee

STREET: P.O. Box 4433

CITY: Houston

Query Match 100.0%; Score 53; DB 18; Length 21;

Best Local Similarity 100.0%; Pred. No. 0.013;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VDFEEDTLPK 10

Db 12 VDFEEDTLPK 21

RESULT 15

US-10-731-238-24

; Sequence 24, Application US/10731238

; Publication No. US20050123552A1

; GENERAL INFORMATION:

APPLICANT: Hook, Magnus

Patti, Joseph M.

House-Pompeo, Karen L.

Speziale, Pietro

John, Danny

McGavin, Martin J.

TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS

AND METHODS OF USE

NUMBER OF SEQUENCES: 105

CORRESPONDENCE ADDRESS:

ADDRESSEE: Arnold, White & Durkee

STREET: P.O. Box 4433

CITY: Houston

Query Match 100.0%; Score 53; DB 18; Length 21;

Best Local Similarity 100.0%; Pred. No. 0.013;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VDFEEDTLPK 10

Db 12 VDFEEDTLPK 21

RESULT 16

US-10-731-238-25

; Sequence 25, Application US/10731238

; Publication No. US20050123552A1

; GENERAL INFORMATION:

APPLICANT: Hook, Magnus

Patti, Joseph M.

House-Pompeo, Karen L.

Speziale, Pietro

John, Danny

McGavin, Martin J.

TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS

AND METHODS OF USE

NUMBER OF SEQUENCES: 105

CORRESPONDENCE ADDRESS:

ADDRESSEE: Arnold, White & Durkee

STREET: P.O. Box 4433

CITY: Houston

Query Match 100.0%; Score 53; DB 18; Length 21;

Best Local Similarity 100.0%; Pred. No. 0.013;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VDFEEDTLPK 10

Db 12 VDFEEDTLPK 21

RESULT 17

US-10-731-238-26

; Sequence 26, Application US/10731238

; Publication No. US20050123552A1

; GENERAL INFORMATION:

APPLICANT: Hook, Magnus

Patti, Joseph M.

House-Pompeo, Karen L.

Speziale, Pietro

John, Danny

McGavin, Martin J.

TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS

AND METHODS OF USE

NUMBER OF SEQUENCES: 105

CORRESPONDENCE ADDRESS:

ADDRESSEE: Arnold, White & Durkee

STREET: P.O. Box 4433

CITY: Houston

Query Match 100.0%; Score 53; DB 18; Length 21;

Best Local Similarity 100.0%; Pred. No. 0.013;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VDFEEDTLPK 10

Db 12 VDFEEDTLPK 21

RESULT 18

US-10-731-238-27

; Sequence 27, Application US/10731238

; Publication No. US20050123552A1

; GENERAL INFORMATION:

APPLICANT: Hook, Magnus

Patti, Joseph M.

House-Pompeo, Karen L.

Speziale, Pietro

John, Danny

McGavin, Martin J.

TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS

AND METHODS OF USE

NUMBER OF SEQUENCES: 105

CORRESPONDENCE ADDRESS:

ADDRESSEE: Arnold, White & Durkee

STREET: P.O. Box 4433

CITY: Houston

Query Match 100.0%; Score 53; DB 18; Length 21;

Best Local Similarity 100.0%; Pred. No. 0.013;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VDFEEDTLPK 10

Db 12 VDFEEDTLPK 21

RESULT 19

US-10-731-238-28

; Sequence 28, Application US/10731238

; Publication No. US20050123552A1

; GENERAL INFORMATION:

APPLICANT: Hook, Magnus

Patti, Joseph M.

House-Pompeo, Karen L.

Speziale, Pietro

John, Danny

McGavin, Martin J.

TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS

AND METHODS OF USE

NUMBER OF SEQUENCES: 105

CORRESPONDENCE ADDRESS:

ADDRESSEE: Arnold, White & Durkee

STREET: P.O. Box 4433

CITY: Houston

Query Match 100.0%; Score 53; DB 18; Length 21;

Best Local Similarity 100.0%; Pred. No. 0.013;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VDFEEDTLPK 10

Db 12 VDFEEDTLPK 21

RESULT 20

US-10-731-238-29

; Sequence 29, Application US/10731238

; Publication No. US20050123552A1

; GENERAL INFORMATION:

APPLICANT: Hook, Magnus

Patti, Joseph M.

House-Pompeo, Karen L.

Speziale, Pietro

John, Danny

McGavin, Martin J.

TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS

AND METHODS OF USE

NUMBER OF SEQUENCES: 105

CORRESPONDENCE ADDRESS:

ADDRESSEE: Arnold, White & Durkee

STREET: P.O. Box 4433

CITY: Houston

Query Match 100.0%; Score 53; DB 18; Length 21;

Best Local Similarity 100.0%; Pred. No. 0.013;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VDFEEDTLPK 10

Db 12 VDFEEDTLPK 21

RESULT 21

US-10-731-238-30

; Sequence 30, Application US/10731238

; Publication No. US20050123552A1

; GENERAL INFORMATION:

APPLICANT: Hook, Magnus

Patti, Joseph M.

House-Pompeo, Karen L.

Speziale, Pietro

John, Danny

McGavin, Martin J.

TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS

AND METHODS OF USE

NUMBER OF SEQUENCES: 105

CORRESPONDENCE ADDRESS:

ADDRESSEE: Arnold, White & Durkee

STREET: P.O. Box 4433

CITY: Houston

Query Match 100.0%; Score 53; DB 18; Length 21;

Best Local Similarity 100.0%; Pred. No. 0.013;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VDFEEDTLPK 10

STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA: US/10/731,238
APPLICATION NUMBER: US/10/731,238
FILING DATE: 10-Dec-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE: 21-Jan-1998
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAMK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 20:
US-10-731-238-20

Query Match 100.0%; Score 53; DB 18; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.013;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VFEEEDTLPK 10
12 VFEEEDTLPK 21

RESULT 12
US-10-731-238-21
Sequence 21, Application US/10731238
Publication No. US20050123552A1
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
Pattl, Joseph M.
House-Pompeo, Karen L.
Speziale, Pietro
John, Danny
McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA: US/10/731,238
APPLICATION NUMBER: US/10/731,238
FILING DATE: 10-Dec-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/010,317
FILING DATE: 21-Jan-1998
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAMK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 21:
US-10-731-238-21

Query Match 100.0%; Score 53; DB 18; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.013;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VFEEEDTLPK 10
12 VFEEEDTLPK 21

RESULT 13
US-10-731-238-22
Sequence 22, Application US/10731238
Publication No. US20050123552A1
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
Pattl, Joseph M.
House-Pompeo, Karen L.
Speziale, Pietro
John, Danny
McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA: US/10/731,238
APPLICATION NUMBER: US/10/731,238
FILING DATE: 10-Dec-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE: 21-Jan-1998
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAMK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:

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;          LENGTH: 21 amino acids
;          TYPE: amino acid
;          STRANDEDNESS: <Unknown>
;          TOPOLOGY: linear
;          SEQUENCE DESCRIPTION: SEQ ID NO: 22
US-10-731-238-22

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Query Match	100.0%;	Score 53;	DB 18;	Length 21;
Best Local Similarity	100.0%;	Pred. No. 0.013;		
Matches 10; Conservative	0;	Mismatches 0;	Indels 0;	Gaps 0;

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QY      1 VFEEEDTLPK 10
          |||||
Db      12 VFEEEDTLPK 21
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RESULT 14
US-10-731-238-23
; Sequence 23, Application US/10731238
; Publication No. US20050123552A1
; GENERAL INFORMATION:

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1 TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
2 AND METHODS OF USE
3
4 NUMBER OF SEQUENCES: 105
5
6 CORRESPONDENCE ADDRESS:
7 ADDRESSEE: Arnold, White & Durkee
8 STREET: P. O. Box 4433
9

TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 233
US-10-731-238-23

QY 1 VDFEEDTLPK 10
|||||

Db 12 VDFFEDTLPK 21

RESULT 15
US-10-711-238-34
Sequence 34, Application US/10731236
Publication No US20050123552A1
GENERAL INFORMATION:
APPLICANT: HOOK, Magnus
Pattl, Joseph M.
House-Pompeo, Karen L
Speziale, Pietro

TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
AND METHODS OF USE

NUMBER OF SEQUENCES: 105

CORRESPONDENCE ADDRESS:

ADDRESSEE: Arnold, White & Durkee

STREET: P.O. Box 4433

CITY: Houston

STATE: TX

COUNTRY: USA

ZIP: 77210-4433

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA: 06/06/93 09.00

Query Match	100.0%	Score 53	DB 18	Length 21
Best Local Similarity	100.0%	Pred. No. 0.013		
Matches 10	Conservative 0	Mismatches 0	Indels 0	Gaps 0

QY 1 VDFEEDTLPK 10
|||
|||
Db 12 VDFEEDTLPK 21

Search completed: October 22, 2005, 12:56:30
Job time : 56.1494 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 22, 2005, 07:41:53 ; Search time 17.2989 Seconds
(without alignments)
43.153 Million cell updates/sec

Title: US-10-731-238-101
Perfect score: 53
Sequence: 1 VDFEEDLPK 10

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database: Issued Patents_AA:*
1: /cgn2_6/prodata/1/aa/5A COMB pep.*
2: /cgn2_6/prodata/1/aa/5B COMB pep.*
3: /cgn2_6/prodata/1/aa/5A COMB pep.*
4: /cgn2_6/prodata/1/aa/5B COMB pep.*
5: /cgn2_6/prodata/1/aa/PCITUS COMB pep.*
6: /cgn2_6/prodata/1/aa/Backfile1 pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	53	100.0	10	4	US-09-010-317-101
2	53	100.0	11	4	US-09-010-317-86
3	53	100.0	21	4	US-09-010-317-9
4	53	100.0	21	4	US-09-010-317-10
5	53	100.0	21	4	US-09-010-317-14
6	53	100.0	21	4	US-09-010-317-15
7	53	100.0	21	4	US-09-010-317-16
8	53	100.0	21	4	US-09-010-317-17
9	53	100.0	21	4	US-09-010-317-18
10	53	100.0	21	4	US-09-010-317-19
11	53	100.0	21	4	US-09-010-317-20
12	53	100.0	21	4	US-09-010-317-21
13	53	100.0	21	4	US-09-010-317-22
14	53	100.0	21	4	US-09-010-317-23
15	53	100.0	21	4	US-09-010-317-34
16	53	100.0	22	4	US-09-010-317-13
17	53	100.0	37	1	US-08-234-622A-4
18	53	100.0	38	1	US-08-234-189-8
19	53	100.0	38	1	US-08-729-767-5
20	53	100.0	114	1	US-08-259-000-3
21	53	100.0	139	3	US-08-856-253-8
22	53	100.0	178	2	US-08-459-135A-12
23	53	100.0	178	2	US-08-495-559-10
24	53	100.0	1027	4	US-08-956-171E-5254
25	53	100.0	1027	4	US-08-781-986A-5254
26	49	92.5	10	4	US-09-010-317-102
27	49	92.5	21	4	US-09-010-317-24

28	49	92.5	130	2	US-08-459-135A-7	Sequence 7, Appl
29	49	92.5	130	2	US-08-459-135A-8	Sequence 8, Appl
30	49	92.5	130	3	US-08-495-559-7	Sequence 7, Appl
31	49	92.5	130	3	US-08-495-559-8	Sequence 8, Appl
32	49	92.5	174	2	US-08-459-135A-10	Sequence 10, Appl
33	49	92.5	174	2	US-08-459-135A-13	Sequence 13, Appl
34	49	92.5	174	3	US-08-495-559-10	Sequence 10, Appl
35	49	92.5	174	3	US-08-495-559-13	Sequence 13, Appl
36	49	92.5	176	3	US-08-495-559-6	Sequence 6, Appl
37	49	92.5	181	2	US-08-459-135A-6	Sequence 6, Appl
38	49	92.5	559	4	US-08-956-171E-5251	Sequence 5251, Ap
39	49	92.5	559	4	US-08-781-986A-5251	Sequence 5251, Ap
40	48	80.6	21	4	US-09-010-317-23	Sequence 23, Appl
41	47	88.7	21	4	US-09-010-317-27	Sequence 27, Appl
42	47	88.7	21	4	US-09-010-317-28	Sequence 28, Appl
43	47	88.7	21	4	US-09-010-317-30	Sequence 30, Appl
44	46	86.8	21	4	US-09-010-317-25	Sequence 25, Appl
45	46	86.8	21	4	US-09-010-317-29	Sequence 29, Appl

ALIGNMENTS

RESULT 1
US-09-010-317-101
Sequence 101, Application US/09010317
Patent No. 6685943
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
APPLICANT: Patti, Joseph M.
APPLICANT: House-Pompeo, Karen L.
APPLICANT: Speziale, Pietro
APPLICANT: Jon, Danny
APPLICANT: Mcgavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
TITLE OF INVENTION: AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAMK:169
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 101:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-09-010-317-101
Query Match 100.0%; Score 53; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0012;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VDFEEDTLPK 10
| | | | | | | | | |
Db 1 VDFEEDTLPK 10

RESULT 2
US-09-010-317-86
; Sequence 86, Application US/09010317
; Patent No. 6685943
; GENERAL INFORMATION:
; APPLICANT: Hook, Magnus
; APPLICANT: Patti, Joseph M.
; APPLICANT: House-Pompeo, Karen L.
; APPLICANT: Speziale, Pietro
; APPLICANT: Joh, Danny
; APPLICANT: McGavin, Martin J.
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
; TITLE OF INVENTION: AND METHODS OF USE
; NUMBER OF SEQUENCES: 105
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: TX
; COUNTRY: USA
; ZIP: 77210-4433
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/010,317
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/036,139
; FILING DATE: 21-JAN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Hibler, David W.
; REGISTRATION NUMBER: 41,071
; REFERENCE/DOCKET NUMBER: TANK:189
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 512-418-3000
; TELEFAX: 512-474-7577
; INFORMATION FOR SEQ ID NO: 86:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
US-09-010-317-86

Query Match 100.0%; Score 53; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.0014;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VDFEEDTLPK 10
| | | | | | | | | |
Db 1 VDFEEDTLPK 10

RESULT 3
US-09-010-317-9
; Sequence 9, Application US/09010317
; Patent No. 6685943
; GENERAL INFORMATION:
; APPLICANT: Hook, Magnus
; APPLICANT: Patti, Joseph M.
; APPLICANT: House-Pompeo, Karen L.
; APPLICANT: Speziale, Pietro

APPLICANT: Joh, Danny
APPLICANT: McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
TITLE OF INVENTION: AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TANK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-09-010-317-9

Query Match 100.0%; Score 53; DB 4; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.0028;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VDFEEDTLPK 10
| | | | | | | | | |
Db 12 VDFEEDTLPK 21

RESULT 4
US-09-010-317-10
; Sequence 10, Application US/09010317
; Patent No. 6685943
; GENERAL INFORMATION:
; APPLICANT: Hook, Magnus
; APPLICANT: Patti, Joseph M.
; APPLICANT: House-Pompeo, Karen L.
; APPLICANT: Speziale, Pietro
; APPLICANT: Joh, Danny
; APPLICANT: McGavin, Martin J.
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
; TITLE OF INVENTION: AND METHODS OF USE
; NUMBER OF SEQUENCES: 105
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: TX
; COUNTRY: USA
; ZIP: 77210-4433
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAMK:189
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-09-010-317-10

Query Match 100.0%; Score 53; DB 4; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.0028;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VFPEEDTLPK 10
DB 12 VFPEEDTLPK 21

RESULT 5
US-09-010-317-14
Sequence 14, Application US/09010317
Patent No. 6685943
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
APPLICANT: Patti, Joseph M.
APPLICANT: House-Pompeo, Karen L.
APPLICANT: Speziale, Pietro
APPLICANT: Jon, Danny
APPLICANT: McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
TITLE OF INVENTION: AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAMK:189
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 14:

SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-09-010-317-14

Query Match 100.0%; Score 53; DB 4; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.0028;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VFPEEDTLPK 10
DB 12 VFPEEDTLPK 21

RESULT 6
US-09-010-317-15
Sequence 15, Application US/09010317
Patent No. 6685943
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
APPLICANT: Patti, Joseph M.
APPLICANT: House-Pompeo, Karen L.
APPLICANT: Speziale, Pietro
APPLICANT: Jon, Danny
APPLICANT: McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
TITLE OF INVENTION: AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAMK:189
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-09-010-317-15

Query Match 100.0%; Score 53; DB 4; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.0028;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VFPEEDTLPK 10
DB 12 VFPEEDTLPK 21

RESULT 7
US-09-010-317-16
Sequence 16, Application US/09010317
Patent No. 6685943
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
APPLICANT: Patti, Joseph M.
APPLICANT: House-Pompeo, Karen L.
APPLICANT: Speziale, Pietro
APPLICANT: John, Danny
APPLICANT: McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
TITLE OF INVENTION: AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION NUMBER: US 60/036,139
APPLICATION NUMBER: 21-JAN-1997
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Habler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TANK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-09-010-317-16
Query Match 100.0%; Score 53; DB 4; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.0028;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 VFEEEDTLPK 10
Db 12 VFEEEDTLPK 21
RESULT 8
US-09-010-317-17
Sequence 17, Application US/09010317
Patent No. 6685943
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
APPLICANT: Patti, Joseph M.
APPLICANT: House-Pompeo, Karen L.
APPLICANT: Speziale, Pietro
APPLICANT: John, Danny
APPLICANT: McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
TITLE OF INVENTION: AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee

STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION NUMBER: US 60/036,139
APPLICATION NUMBER: 21-JAN-1997
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Habler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TANK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-09-010-317-17
Query Match 100.0%; Score 53; DB 4; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.0028;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 VFEEEDTLPK 10
Db 12 VFEEEDTLPK 21
RESULT 9
US-09-010-317-18
Sequence 18, Application US/09010317
Patent No. 6685943
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
APPLICANT: Patti, Joseph M.
APPLICANT: House-Pompeo, Karen L.
APPLICANT: Speziale, Pietro
APPLICANT: John, Danny
APPLICANT: McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
TITLE OF INVENTION: AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION NUMBER: US 60/036,139

FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-09-010-317-18

Query Match 100.0%; Score 53; DB 4; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.0028;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VFPEEDTLPK 10
Db 12 VFPEEDTLPK 21

RESULT 10
US-09-010-317-19
Sequence 19, Application US/09010317
Patent No. 6685943
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
APPLICANT: Patti, Joseph M.
APPLICANT: House-Pompeo, Karen L.
APPLICANT: Speziale, Pietro
APPLICANT: McGavin, Martin J.
APPLICANT: Mcgavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSER: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAMK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-09-010-317-19

Query Match 100.0%; Score 53; DB 4; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.0028;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VFPEEDTLPK 10
Db 12 VFPEEDTLPK 21

RESULT 11
US-09-010-317-20
Sequence 20, Application US/09010317
Patent No. 6685943
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
APPLICANT: Patti, Joseph M.
APPLICANT: House-Pompeo, Karen L.
APPLICANT: Speziale, Pietro
APPLICANT: Job, Danny
APPLICANT: McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSER: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAMK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-09-010-317-20

Query Match 100.0%; Score 53; DB 4; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.0028;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VFPEEDTLPK 10
Db 12 VFPEEDTLPK 21

RESULT 12
US-09-010-317-21
Sequence 21, Application US/09010317
Patent No. 6685943
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
APPLICANT: Patti, Joseph M.

APPLICANT: House-Pompeo, Karen L.
APPLICANT: Speziale, Pietro
APPLICANT: Joh, Danny
APPLICANT: McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
TITLE OF INVENTION: AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TANK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-09-010-317-21

Query Match 100.0%; Score 53; DB 4; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.0028;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VFEEEDTLPK 10
Db 12 VFEEEDTLPK 21

RESULT 13
US-09-010-317-22
Sequence 22, Application US/09010317
Patent No. 6685943
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
APPLICANT: Patil, Joseph M.
APPLICANT: House-Pompeo, Karen L.
APPLICANT: Speziale, Pietro
APPLICANT: Joh, Danny
APPLICANT: McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
TITLE OF INVENTION: AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TANK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-09-010-317-22

Query Match 100.0%; Score 53; DB 4; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.0028;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VFEEEDTLPK 10
Db 12 VFEEEDTLPK 21

RESULT 14
US-09-010-317-23
Sequence 23, Application US/09010317
Patent No. 6685943
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
APPLICANT: Patil, Joseph M.
APPLICANT: House-Pompeo, Karen L.
APPLICANT: Speziale, Pietro
APPLICANT: Joh, Danny
APPLICANT: McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
TITLE OF INVENTION: AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TANK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000

Search completed: October 22, 2005, 09:35:47
Job time : 17.2989 secs

TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-09-010-317-23

Query Match 100.0%; Score 53; DB 4; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.0028;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VDFEEDTLPK 10
Db 12 VDFEEDTLPK 21

RESULT 15
US-09-010-317-34
Sequence 34, Application US/09010317
Patent No. 6685943
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
APPLICANT: Patti, Joseph M.
APPLICANT: House-Pompeo, Karen L.
APPLICANT: Speziale, Pietro
APPLICANT: Joh, Danny
APPLICANT: McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
TITLE OF INVENTION: AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAMK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 34:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-09-010-317-34

Query Match 100.0%; Score 53; DB 4; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.0028;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VDFEEDTLPK 10
Db 12 VDFEEDTLPK 21

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OM protein - protein search, using sw model

Run on: October 25, 2005, 20:58:51 ; Search time 69.7156 Seconds
(without alignments)
55.479 Million cell updates/sec

Title: US-10-731-238-101
Perfect score: 53
Sequence: 1 VDFBPTLPK 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues
Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

- Database : A_Geneseq_16Dec04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	53	100.0	10	2	AAW65757 Fibrinect
2	53	100.0	11	2	AAW65742 Peptide #
3	53	100.0	21	2	AAW65670 Fibrinect
4	53	100.0	21	2	AAW65679 Fibrinect
5	53	100.0	21	2	AAW65690 Fibrinect
6	53	100.0	21	2	AAW65673 Fibrinect
7	53	100.0	21	2	AAW65671 Fibrinect
8	53	100.0	21	2	AAW65675 Fibrinect
9	53	100.0	21	2	AAW65666 Fibrinect
10	53	100.0	21	2	AAW65672 Fibrinect
11	53	100.0	21	2	AAW65677 Fibrinect
12	53	100.0	21	2	AAW65676 Fibrinect
13	53	100.0	21	2	AAW65674 Fibrinect
14	53	100.0	21	2	AAW65676 Fibrinect
15	53	100.0	21	2	AAW65678 Fibrinect
16	53	100.0	22	2	AAW65678 Fibrinect
17	53	100.0	22	2	AAW65669 Peptide #
18	53	100.0	37	1	AAW65669 Peptide #
19	53	100.0	37	1	AAW65669 Peptide #
20	53	100.0	38	1	AAW65669 Peptide #
21	53	100.0	134	2	AAW65669 Peptide #
22	53	100.0	139	2	AAW65669 Peptide #
23	53	100.0	961	6	AAW65669 Peptide #
24	53	100.0	978	4	AAW65669 Peptide #
25	53	100.0	1001	4	AAW65669 Peptide #

26	53	100.0	1018	1	AAW65757
27	53	100.0	1018	4	AAW65757
28	53	100.0	1018	4	AAW65757
29	53	100.0	1018	6	AAW65757
30	53	100.0	1018	6	AAW65757
31	53	100.0	1018	6	AAW65757
32	53	100.0	1018	6	AAW65757
33	53	100.0	1018	6	AAW65757
34	53	100.0	1018	6	AAW65757
35	53	100.0	1018	6	AAW65757
36	53	100.0	1018	6	AAW65757
37	53	100.0	1018	6	AAW65757
38	53	100.0	1018	6	AAW65757
39	53	100.0	1018	6	AAW65757
40	53	100.0	1018	6	AAW65757
41	53	100.0	1018	6	AAW65757
42	53	100.0	1018	6	AAW65757
43	53	100.0	1018	6	AAW65757
44	53	100.0	1018	6	AAW65757
45	53	100.0	1018	6	AAW65757

ALIGNMENTS

RESULT 1
ID AAW65757 standard; peptide; 10 AA.
XX AAW65757;
XX 16-OCT-1998 (first entry)
XX Fibrinectin binding protein-derived peptide #101.
XX DE microbial surface components recognising adhesive matrix molecule;
XX KM MCGRAMM; fibrinectin; fibrinectin-binding protein; antibody; epitope;
XX KW antiBiotic; bacterial infection; antibiotic-resistant strain.
XX OS Synthetic.
XX OS Staphylococcus aureus.
XX PN W09831389-A2.
XX PD 23-JUL-1998.
XX PF 21-JAN-1998; 98MO-US001222.
XX PR 21-JAN-1997; 97US-0036139P.
XX PA (TEXA) UNIV TEXAS A & M SYSTEM.
XX PI Hoeek M; Patl JM, House-Pompeo KL, Speziale P, Joh D;
XX PI McGavin MJ;
XX DR WPI; 1998-413816/35.
XX PT Antibody that binds to fibrinectin-binding protein, preventing its
XX PT binding to fibrinectin - used to treat or prevent bacterial infection,
XX PT especially by Staphylococci and Streptococci.
XX PS Example 9, Page 111; 201P; English.
XX CC The invention relates to antibodies that bind to a fibrinectin-binding
XX CC domain of a fibrinectin-binding protein, and inhibit binding of the
XX CC protein to a fibrinectin. Also claimed are: (1) isolated peptides of a
XX CC fibrinectin-binding protein that do not bind to fibrinectin; (2) fusion
XX CC protein containing at least one peptide of a fibrinectin-binding protein
XX CC linked to a second amino acid sequence; (3) nucleic acid encoding the
XX CC isolated peptide of (1). Antibodies, the isolated peptides of (1) and the
XX CC nucleic acids are all useful for immunisation (active or passive) and (by
XX CC inhibiting binding of bacteria to fibrinectin) for preventing or treating
XX CC infection in humans or other animals, particularly by staphylococci or


```

CC streptococci, e.g. meningitis, otitis media, pneumonia, endocarditis,
CC mastitis in cattle, abortion in horses and many others. Since the
CC antibodies block binding of bacteria, they should be effective against
CC antibiotic-resistant strains, and may replace antibiotic therapy or
CC increase its effectiveness. Sequences AAM65744-58 represent peptides
CC which were synthesised to span the D3 motif of S. aureus fibronectin
CC binding protein A
XX
SQ Sequence 10 AA;
XX
Query Match          100.0%; Score 53; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0096;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 VDFEEDTLPK 10
   |||||
DB 1 VDFEEDTLPK 10
XX
RESULT 2
ID AAM65742 standard; peptide; 11 AA.
XX
AC AAM65742;
XX
DT 16-OCT-1998 (first entry)
XX
DE Peptide #86.
XX
KW microbial surface components recognising adhesive matrix molecule;
KW MSCRAMM; fibronectin; fibronectin-binding protein; antibody; epitope;
KW antibiotic; bacterial infection; antibiotic-resistant strain.
XX
OS Synthetic.
OS Staphylococcus aureus.
XX
PN WO9831389-A2.
XX
PD 23-JUL-1998.
XX
PF 21-JAN-1998; 98WO-US001222.
XX
PR 21-JAN-1997; 97US-0036139P.
XX
PA (TEXA ) UNIV TEXAS A & M SYSTEM.
XX
PI Hoeoek M, Patti JM, House-Pompeo KL, Speziale P, Joh D;
PI McGavin MJ;
XX
PI Mcgavin MJ;
XX
DR WPI; 1998-413816/35.
XX
PT Antibody that binds to fibronectin-binding protein, preventing its
PT binding to fibronectin - used to treat or prevent bacterial infection,
PT especially by Staphylococci and Streptococci.
XX
PS Example 9; Page 110; 201pp; English.
XX
CC The invention relates to antibodies that bind to a fibronectin-binding
CC domain of a fibronectin-binding protein, and inhibit binding of the
CC protein to fibronectin. Also claimed are: (1) isolated peptides of a
CC fibronectin-binding protein that do not bind to fibronectin; (2) fusion
CC protein containing at least one peptide of a fibronectin-binding protein
CC linked to a second amino acid sequence; (3) nucleic acid encoding the
CC isolated peptide of (1). Antibodies, the isolated peptides of (1) and the
CC nucleic acids are all useful for immunisation (active or passive) and (by
CC inhibiting binding of bacteria to fibronectin) for preventing or treating
CC infection in humans or other animals, particularly by staphylococci or
CC streptococci, e.g. meningitis, otitis media, pneumonia, endocarditis,
CC mastitis in cattle, abortion in horses and many others. Since the
CC antibodies block binding of bacteria, they should be effective against
CC antibiotic-resistant strains, and may replace antibiotic therapy or
CC increase its effectiveness. The present sequence is shown in the
CC specification
QC

```

```

XX
SQ Sequence 11 AA;
XX
Query Match          100.0%; Score 53; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.011;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 VDFEEDTLPK 10
   |||||
DB 1 VDFEEDTLPK 10
XX
RESULT 3
ID AAM65670 standard; peptide; 21 AA.
XX
AC AAM65670;
XX
DT 16-OCT-1998 (first entry)
XX
DE Fibronectin binding protein-derived peptide #14.
XX
KW microbial surface components recognising adhesive matrix molecule;
KW MSCRAMM; fibronectin; fibronectin-binding protein; antibody; epitope;
KW antibiotic; bacterial infection; antibiotic-resistant strain.
XX
OS Synthetic.
OS Staphylococcus aureus.
XX
PN WO9831389-A2.
XX
PD 23-JUL-1998.
XX
PF 21-JAN-1998; 98WO-US001222.
XX
PR 21-JAN-1997; 97US-0036139P.
XX
PA (TEXA ) UNIV TEXAS A & M SYSTEM.
XX
PI Hoeoek M, Patti JM, House-Pompeo KL, Speziale P, Joh D;
PI McGavin MJ;
XX
DR WPI; 1998-413816/35.
XX
PT Antibody that binds to fibronectin-binding protein, preventing its
PT binding to fibronectin - used to treat or prevent bacterial infection,
PT especially by Staphylococci and Streptococci.
XX
PS Example 8; Page 100; 201pp; English.
XX
CC The invention relates to antibodies that bind to a fibronectin-binding
CC domain of a fibronectin-binding protein, and inhibit binding of the
CC protein to fibronectin. Also claimed are: (1) isolated peptides of a
CC fibronectin-binding protein that do not bind to fibronectin; (2) fusion
CC protein containing at least one peptide of a fibronectin-binding protein
CC linked to a second amino acid sequence; (3) nucleic acid encoding the
CC isolated peptide of (1). Antibodies, the isolated peptides of (1) and the
CC nucleic acids are all useful for immunisation (active or passive) and (by
CC inhibiting binding of bacteria to fibronectin) for preventing or treating
CC infection in humans or other animals, particularly by staphylococci or
CC streptococci, e.g. meningitis, otitis media, pneumonia, endocarditis,
CC mastitis in cattle, abortion in horses and many others. Since the
CC antibodies block binding of bacteria, they should be effective against
CC antibiotic-resistant strains, and may replace antibiotic therapy or
CC increase its effectiveness. Sequences AAM65670-90 represent a series of
CC synthetic peptides based on the D3 repeat of S. aureus fibronectin
CC binding protein A. They were synthesised to contain a proline residue at
CC each position through the sequence (ie a proline scan)
XX
SQ Sequence 21 AA;
XX
Query Match          100.0%; Score 53; DB 2; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.022;

```

```
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```

QY      1 VFEEEDTLPK 10
        |||||
Db      12 VFEEEDTLPK 21

```

RESULT 4	
AAW65679	
ID	AAW65679 standard; peptide; 21 AA

AC	AAW65679;
XX	
DT	16-OCT-1998 (first entry)

Fibronectin binding protein-derived peptide #23

KM microbial surface components recognising adhesive matrix molecule;
KM MSCRAMM; fibronectin; fibronectin-binding protein; antibody; epitope
KM antibiotic; bacterial infection; antibiotic-resistant strain.

OS	Synthetic.
OS	Staphylococcus aureus.

PN WO9831389-A2

PD 23-JUL-1998

PF 21-JAN-1998; 98WO-US001222.

PR 21-JAN-1997; 97US-0036139P.

PA (TEXA) UNIV TEXAS A & M SYSTEM.

PI Hoeoek M, Patti JM, House-Pompeo KL, Speciale P, Joh D,

DR WPI; 1998-413816/35

PT Antibody that binds to fibronectin-binding protein, preventing its binding to fibronectin - used to treat or prevent bacterial infection especially by *Staphylococci* and *Streptococci*.

PS Example 8; Page 100; 201pp; English.

The invention relates to antibodies that bind to a fibronectin-binding domain of a fibronectin-binding protein, and inhibit binding of the protein to fibronectin. Also claimed are: (1) isolated peptides of a fibronectin-binding protein that do not bind to fibronectin; (2) fusion protein containing at least one peptide of a fibronectin-binding protein linked to a second amino acid sequence; (3) nucleic acid encoding the isolated peptide of (1). Antibodies, the isolated peptides of (1) and the nucleic acids are all useful for immunisation (active or passive) and (b) inhibiting binding of bacteria to fibronectin for preventing or treating infection in humans or other animals, particularly for staphylococci or streptococci, e.g. meningitis, otitis media, pneumonia, endocarditis, mastitis in cattle, abortion in horses and many others. Since the antibodies block binding of bacteria, they should be effective against antibiotic-resistant strains, and may replace antibiotic therapy or increase its effectiveness. Sequences AAW5670-90 represent a series of synthetic peptides based on the D3 repeat of *S. aureus* fibronectin binding protein A. They were synthesised to contain a proline residue at each position through the sequence (ie a proline scan)

Sequence 21 AA;

Query Match 100.0%; Score 53; DB 2; Length 21;

```

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0.

```

```
QY      1 VDFEEDTLPK 10
         |||||
Db      12 VDFEEDTLPK 21
```

RESULT 5	
AAW65690	
ID	AAW65690 standard; peptide; 21 AA

AC AAW65690 ;

DT 16-OCT-1998 (first entry

DE Fibronectin binding protein-derived peptide #34

KW microbial surface components recognising adhesive matrix molecule;
KW MSCAM; fibronectin; fibronectin-binding protein; antibody; epitope
KW antibiotic; bacterial infection; antibiotic-resistant strain.

OS Synthetic.
OS Staphylococcus aureus

PN W09831389-A2.

PD 23-JUL-1998

PF 21-JAN-1998; 98WO-US001222.

PR 21-JAN-1997; 97US-0036139P.

PA (TEXA) UNIV TEXAS A & M SYSTEM.

PI Hoeoek M, Patti JM, House-Pompeo KL, Speciale P, Joh D,

WPI; 1998-413816/35

PT Antibody that binds to fibronectin-binding protein, preventing its binding to fibronectin - used to treat or prevent bacterial infection especially by *Staphylococci* and *Streptococci*.

Example 8; Page 101; 201pp; English

The invention relates to antibodies that bind to a fibronectin-binding domain of a fibronectin-binding protein, and inhibit binding of the protein to fibronectin. Also claimed are: (1) isolated peptides of a fibronectin-binding protein that do not bind to fibronectin; (2) fusion protein containing at least one peptide of a fibronectin-binding protein linked to a second amino acid sequence; (3) nucleic acid encoding the isolated peptide of (1). Antibodies, the isolated peptides of (1) and the nucleic acids are all useful for immunisation (active or passive) and inhibiting binding of bacteria to fibronectin for preventing or treating infection in humans or other animals, particularly by staphylococci or streptococci, e.g., meningitis, otitis media, pneumonia, endocarditis, mastitis in cattle, abortion in horses and many others. Since the antibodies block binding of bacteria, they should be effective against antibiotic-resistant strains, and may replace antibiotic therapy or increase its effectiveness. Sequences AA65670-80 represent a series of synthetic peptides based on the D3 repeat of S. aureus fibronectin binding protein A. They were synthesised to contain a proline residue at each position through the sequence (ie a proline scan).

Sequence 21 AA;

Query Match	100.0%;	Score 53;	DB 2;	Length 21
-------------	---------	-----------	-------	-----------

```
Matches    10; Conservative    0; Mismatches    0; Indels    0; Gaps    0;
```

```
QY      1 VDFEEDTLPK 10
         |||||
Db      12 VDFEEDTLPK 21
```

RESULT 6	
AAW65673	
ID	AAW65673 standard; peptide; 21 AA

```
XX AAW65673;
XX
XX 16-OCT-1998 (first entry)
XX
XX Fibronectin binding protein-derived peptide #17.
XX
XX microbial surface components recognising adhesive matrix molecule;
XX MSCRAMM; fibronectin; fibronectin-binding protein; antibody; epitope;
XX antibiotic; bacterial infection; antibiotic-resistant strain.
XX
XX Synthetic.
XX Staphylococcus aureus.
XX
XX WO9831389-A2.
XX
XX 23-JUL-1998.
XX
XX 21-JAN-1998; 98WO-US001222.
XX
XX 21-JAN-1997; 97US-0036139P.
XX
XX (TEXA ) UNIV TEXAS A & M SYSTEM.
XX
XX Hoeoek M, Patti JM, House-Pompeo KL, Speziale P, Joh D;
XX McGavin MJ;
XX WPI; 1998-413816/35.
XX
XX Antibody that binds to fibronectin-binding protein, preventing its
XX binding to fibronectin - used to treat or prevent bacterial infection,
XX especially by Staphylococci and Streptococci.
XX
XX Example 8; Page 100; 201pp; English.
XX
XX The invention relates to antibodies that bind to a fibronectin-binding
XX domain of a fibronectin-binding protein, and inhibit binding of the
XX protein to fibronectin. Also claimed are: (1) isolated peptides of a
XX fibronectin-binding protein that do not bind to fibronectin; (2) fusion
XX protein containing at least one peptide of a fibronectin-binding protein
XX linked to a second amino acid sequence; (3) nucleic acid encoding the
XX isolated peptide of (1). Antibodies, the isolated peptides of (1) and the
XX nucleic acids are all useful for immunisation (active or passive) and (by
XX inhibiting binding of bacteria to fibronectin) for preventing or treating
XX infection in humans or other animals, particularly by staphylococci or
XX streptococci, e.g. meningitis, otitis media, pneumonia, endocarditis,
XX mastitis in cattle, abortion in horses and many others. Since the
XX antibodies block binding of bacteria, they should be effective against
XX antibiotic-resistant strains, and may replace antibiotic therapy or
XX increase its effectiveness. Sequences AAW65670-90 represent a series of
XX synthetic peptides based on the D3 repeat of S. aureus fibronectin
XX binding protein A. They were synthesised to contain a proline residue at
XX each position through the sequence (ie a proline scan)
XX
XX Sequence 21 AA;
XX
XX Query Match 100.0%; Score 53; DB 2; Length 21;
XX Best Local Similarity 100.0%; Pred. No. 0.022;
XX Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 VDFEEDTLPK 10
XX |||||
XX 12 VDFEEDTLPK 21
XX
XX RESULT 7
XX AAW65671
XX ID AAW65671 standard; peptide; 21 AA.
XX
XX AAW65671;
XX
XX 16-OCT-1998 (first entry)
XX
```

```
DE Fibronectin binding protein-derived peptide #15.
XX
XX microbial surface components recognising adhesive matrix molecule;
XX MSCRAMM; fibronectin; fibronectin-binding protein; antibody; epitope;
XX antibiotic; bacterial infection; antibiotic-resistant strain.
XX
XX Synthetic.
XX Staphylococcus aureus.
XX
XX WO9831389-A2.
XX
XX 23-JUL-1998.
XX
XX 21-JAN-1998; 98WO-US001222.
XX
XX 21-JAN-1997; 97US-0036139P.
XX
XX (TEXA ) UNIV TEXAS A & M SYSTEM.
XX
XX Hoeoek M, Patti JM, House-Pompeo KL, Speziale P, Joh D;
XX McGavin MJ;
XX WPI; 1998-413816/35.
XX
XX Antibody that binds to fibronectin-binding protein, preventing its
XX binding to fibronectin - used to treat or prevent bacterial infection,
XX especially by Staphylococci and Streptococci.
XX
XX Example 8; Page 100; 201pp; English.
XX
XX The invention relates to antibodies that bind to a fibronectin-binding
XX domain of a fibronectin-binding protein, and inhibit binding of the
XX protein to fibronectin. Also claimed are: (1) isolated peptides of a
XX fibronectin-binding protein that do not bind to fibronectin; (2) fusion
XX protein containing at least one peptide of a fibronectin-binding protein
XX linked to a second amino acid sequence; (3) nucleic acid encoding the
XX isolated peptide of (1). Antibodies, the isolated peptides of (1) and the
XX nucleic acids are all useful for immunisation (active or passive) and (by
XX inhibiting binding of bacteria to fibronectin) for preventing or treating
XX infection in humans or other animals, particularly by staphylococci or
XX streptococci, e.g. meningitis, otitis media, pneumonia, endocarditis,
XX mastitis in cattle, abortion in horses and many others. Since the
XX antibodies block binding of bacteria, they should be effective against
XX antibiotic-resistant strains, and may replace antibiotic therapy or
XX increase its effectiveness. Sequences AAW65670-90 represent a series of
XX synthetic peptides based on the D3 repeat of S. aureus fibronectin
XX binding protein A. They were synthesised to contain a proline residue at
XX each position through the sequence (ie a proline scan)
XX
XX Sequence 21 AA;
XX
XX Query Match 100.0%; Score 53; DB 2; Length 21;
XX Best Local Similarity 100.0%; Pred. No. 0.022;
XX Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 VDFEEDTLPK 10
XX |||||
XX 12 VDFEEDTLPK 21
XX
XX RESULT 8
XX AAW65675
XX ID AAW65675 standard; peptide; 21 AA.
XX
XX AAW65675;
XX
XX 16-OCT-1998 (first entry)
XX
XX Fibronectin binding protein-derived peptide #19.
XX
XX microbial surface components recognising adhesive matrix molecule;
XX MSCRAMM; fibronectin; fibronectin-binding protein; antibody; epitope;
XX antibiotic; bacterial infection; antibiotic-resistant strain.
XX
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```
XX OS Synthetic.
XX OS Staphylococcus aureus.
XX PN WO9831389-A2.
XX PD 23-JUL-1998.
XX PF 21-JAN-1998; 98WO-US001222.
XX PR 21-JAN-1997; 97US-0036139P.
XX (TEXA ) UNIV TEXAS A & M SYSTEM.
XX PA Hoeek M, Patti JM, House-Pompeo KL, Speziale P, Joh D;
XX PI Mcgavin MJ;
XX PT WPI; 1998-413816/35.
XX DR
XX PS
XX PT Antibody that binds to fibronectin-binding protein, preventing its
XX binding to fibronectin - used to treat or prevent bacterial infection,
XX especially by Staphylococci and Streptococci.
XX
XX PS Example 8; Page 100; 201pp; English.
XX
XX CC The invention relates to antibodies that bind to a fibronectin-binding
XX domain of a fibronectin-binding protein, and inhibit binding of the
XX protein to fibronectin. Also claimed are: (1) isolated peptides of a
XX fibronectin-binding protein that do not bind to fibronectin; (2) fusion
XX protein containing at least one peptide of a fibronectin-binding protein
XX linked to a second amino acid sequence; (3) nucleic acid encoding the
XX isolated peptide of (1). Antibodies, the isolated peptides of (1) and (b)
XX nucleic acids are all useful for immunisation (active or passive) and (b)
XX inhibiting binding of bacteria to fibronectin) for preventing or treating
XX infection in humans or other animals, particularly by staphylococci or
XX streptococci, e.g. meningitis, otitis media, pneumonia, endocarditis,
XX mastitis in cattle, abortion in horses and many others. Since the
XX antibodies block binding of bacteria, they should be effective against
XX antibiotic-resistant strains, and may replace antibiotic therapy or
XX increase its effectiveness. Sequences AAW65670-90 represent a series of
XX synthetic peptides based on the D3 repeat of S. aureus fibronectin
XX binding protein A. They were synthesised to contain a proline residue at
XX each position through the sequence (ie a proline scan)
XX
XX SQ Sequence 21 AA:
XX
XX QY
XX DB 1 VFEEEDTLPK 10
XX 12 VFEEEDTLPK 21
XX
XX RESULT 9
XX AAW65666 standard; peptide; 21 AA.
XX
XX AC AAW65666;
XX DT 16-OCT-1998 (first entry)
XX DE Fibronectin binding protein-derived peptide #10.
XX
XX KW microbial surface components recognising adhesive matrix molecule;
XX MSCRAMM; fibronectin; fibronectin-binding protein; antibody; epitope;
XX antibiotic; bacterial infection; antibiotic-resistant strain.
XX
XX OS Synthetic.
XX OS Staphylococcus aureus.
XX PN WO9831389-A2.
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XX PD 23-JUL-1998.
XX PF 21-JAN-1998; 98WO-US001222.
XX PR 21-JAN-1997; 97US-0036139P.
XX (TEXA ) UNIV TEXAS A & M SYSTEM.
XX PA Hoeek M, Patti JM, House-Pompeo KL, Speziale P, Joh D;
XX PI Mcgavin MJ;
XX PT WPI; 1998-413816/35.
XX DR
XX PS
XX PT Antibody that binds to fibronectin-binding protein, preventing its
XX binding to fibronectin - used to treat or prevent bacterial infection,
XX especially by Staphylococci and Streptococci.
XX
XX PS Example 2; Page 92; 201pp; English.
XX
XX CC The invention relates to antibodies that bind to a fibronectin-binding
XX domain of a fibronectin-binding protein, and inhibit binding of the
XX protein to fibronectin. Also claimed are: (1) isolated peptides of a
XX fibronectin-binding protein that do not bind to fibronectin; (2) fusion
XX protein containing at least one peptide of a fibronectin-binding protein
XX linked to a second amino acid sequence; (3) nucleic acid encoding the
XX isolated peptide of (1). Antibodies, the isolated peptides of (1) and (b)
XX nucleic acids are all useful for immunisation (active or passive) and (b)
XX inhibiting binding of bacteria to fibronectin) for preventing or treating
XX infection in humans or other animals, particularly by staphylococci or
XX streptococci, e.g. meningitis, otitis media, pneumonia, endocarditis,
XX mastitis in cattle, abortion in horses and many others. Since the
XX antibodies block binding of bacteria, they should be effective against
XX antibiotic-resistant strains, and may replace antibiotic therapy or
XX increase its effectiveness. Sequences AAW65659-68 represent synthetic
XX epitopes from the fibronectin binding domains DV and DI-D4 of the S.
XX aureus fnda gene
XX
XX SQ Sequence 21 AA:
XX
XX QY
XX DB 1 VFEEEDTLPK 10
XX 12 VFEEEDTLPK 21
XX
XX RESULT 10
XX AAW65672 standard; peptide; 21 AA.
XX
XX AC AAW65672;
XX DT 16-OCT-1998 (first entry)
XX DE Fibronectin binding protein-derived peptide #16.
XX
XX KW MSCRAMM; fibronectin; fibronectin-binding protein; antibody; epitope;
XX antibiotic; bacterial infection; antibiotic-resistant strain.
XX
XX OS Synthetic.
XX OS Staphylococcus aureus.
XX PN WO9831389-A2.
XX PD 23-JUL-1998.
XX PF 21-JAN-1998; 98WO-US001222.
XX PR 21-JAN-1997; 97US-0036139P.
```

XX (TEXA) UNIV TEXAS A & M SYSTEM.
PA Hoecek M, Patti JM, House-Pompeo KL, Speciale P, Joh D;
XX Mcgavin MJ;
PI MPI; 1998-413816/35.
XX
DR
XX Antibody that binds to fibronectin-binding protein, preventing its
PT binding to fibronectin - used to treat or prevent bacterial infection,
PT especially by Staphylococci and Streptococci.
XX
PS Example 8; Page 100; 201pp; English.
XX
CC The invention relates to antibodies that bind to a fibronectin-binding
CC domain of a fibronectin-binding protein, and inhibit binding of the
CC protein to fibronectin. Also claimed are: (1) isolated peptides of a
CC fibronectin-binding protein that do not bind to fibronectin; (2) fusion
CC protein containing at least one peptide of a fibronectin-binding protein
CC linked to a second amino acid sequence; (3) nucleic acid encoding the
CC isolated peptide of (1). Antibodies, the isolated peptides of (1) and the
CC nucleic acids are all useful for immunisation (active or passive) and (by
CC inhibiting binding of bacteria to fibronectin) for preventing or treating
CC infection in humans or other animals, particularly by staphylococci or
CC streptococci, e.g. meningitis, otitis media, pneumonia, endocarditis,
CC mastitis in cattle, abortion in horses and many others. Since the
CC antibodies block binding of bacteria, they should be effective against
CC antibiotic-resistant strains, and may replace antibiotic therapy or
CC increase its effectiveness. Sequences AAW65670-90 represent a series of
CC synthetic peptides based on the D3 repeat of S. aureus fibronectin
CC binding protein A. They were synthesised to contain a proline residue at
CC each position through the sequence (ie a proline scan)
XX
SQ Sequence 21 AA;

Query Match 100.0%; Score 53; DB 2; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.022;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VFPEEDTLRK 10
|||
DB 12 VFPEEDTLRK 21

RESULT 11

AAW65677 standard; peptide; 21 AA.

AAW65677;

16-OCT-1998 (first entry)

Fibronectin binding protein-derived peptide #21.

microbial surface components recognising adhesive matrix molecule;

MSCRAMM; fibronectin; fibronectin-binding protein; antibody; epitope;

antibiotic; bacterial infection; antibiotic-resistant strain.

Synthetic.

Staphylococcus aureus.

WO9831389-A2.

23-JUL-1998.

21-JAN-1998; 98WO-US001222.

21-JAN-1997; 97US-0036139P.

(TEXA) UNIV TEXAS A & M SYSTEM.

Hoecek M, Patti JM, House-Pompeo KL, Speciale P, Joh D;
Mcgavin MJ;

XX MPI; 1998-413816/35.
XX
DR
XX Antibody that binds to fibronectin-binding protein, preventing its
PT binding to fibronectin - used to treat or prevent bacterial infection,
PT especially by Staphylococci and Streptococci.
XX
PS Example 8; Page 100; 201pp; English.
XX
CC The invention relates to antibodies that bind to a fibronectin-binding
CC domain of a fibronectin-binding protein, and inhibit binding of the
CC protein to fibronectin. Also claimed are: (1) isolated peptides of a
CC fibronectin-binding protein that do not bind to fibronectin; (2) fusion
CC protein containing at least one peptide of a fibronectin-binding protein
CC linked to a second amino acid sequence; (3) nucleic acid encoding the
CC isolated peptide of (1). Antibodies, the isolated peptides of (1) and the
CC nucleic acids are all useful for immunisation (active or passive) and (by
CC inhibiting binding of bacteria to fibronectin) for preventing or treating
CC infection in humans or other animals, particularly by staphylococci or
CC streptococci, e.g. meningitis, otitis media, pneumonia, endocarditis,
CC mastitis in cattle, abortion in horses and many others. Since the
CC antibodies block binding of bacteria, they should be effective against
CC antibiotic-resistant strains, and may replace antibiotic therapy or
CC increase its effectiveness. Sequences AAW65670-90 represent a series of
CC synthetic peptides based on the D3 repeat of S. aureus fibronectin
CC binding protein A. They were synthesised to contain a proline residue at
CC each position through the sequence (ie a proline scan)
XX
SQ Sequence 21 AA;

Query Match 100.0%; Score 53; DB 2; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.022;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VFPEEDTLRK 10
|||
DB 12 VFPEEDTLRK 21

RESULT 12

AAW65665 standard; peptide; 21 AA.

AAW65665;

16-OCT-1998 (first entry)

Fibronectin binding protein-derived peptide #9.

microbial surface components recognising adhesive matrix molecule;

MSCRAMM; fibronectin; fibronectin-binding protein; antibody; epitope;

antibiotic; bacterial infection; antibiotic-resistant strain.

Synthetic.

Staphylococcus aureus.

WO9831389-A2.

23-JUL-1998.

21-JAN-1998; 98WO-US001222.

21-JAN-1997; 97US-0036139P.

(TEXA) UNIV TEXAS A & M SYSTEM.

Hoecek M, Patti JM, House-Pompeo KL, Speciale P, Joh D;
Mcgavin MJ;

XX MPI; 1998-413816/35.
XX
DR
XX Antibody that binds to fibronectin-binding protein, preventing its
PT binding to fibronectin - used to treat or prevent bacterial infection,
PT

PT especially by Staphylococci and Streptococci.
 XX
 PS Example 2; Page 92; 201pp; English.

CC The invention relates to antibodies that bind to a fibronectin-binding
 CC domain of a fibronectin-binding protein, and inhibit binding of the
 CC protein to fibronectin. Also claimed are: (1) isolated peptides of a
 CC fibronectin-binding protein that do not bind to fibronectin; (2) fusion
 CC protein containing at least one peptide of a fibronectin-binding protein
 CC linked to a second amino acid sequence; (3) nucleic acid encoding the
 CC isolated peptide of (1). Antibodies, the isolated peptides of (1) and the
 CC nucleic acids are all useful for immunisation (active or passive) and (by
 CC inhibiting binding of bacteria to fibronectin) for preventing or treating
 CC infection in humans or other animals, particularly by staphylococci or
 CC streptococci, e.g. meningitis, otitis media, pneumonia, endocarditis,
 CC mastitis in cattle, abortion in horses and many others. Since the
 CC antibodies block binding of bacteria, they should be effective against
 CC antibiotic-resistant strains, and may replace antibiotic therapy or
 CC increase its effectiveness. Sequences AAW65670-68 represent synthetic
 CC epitopes from the fibronectin binding domains DU and D1-D4 of the S.
 CC aureus fnba gene

XX Sequence 21 AA:

Query Match 100.0%; Score 53; DB 2; Length 21;
 Best Local Similarity 100.0%; Pred. No. 0.022;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 VDFEEDTLRK 10
 |||||
 DB 12 VDFEEDTLRK 21

RESULT 13

ID AAW65674 standard; peptide; 21 AA.

XX AAW65674;

XX 16-OCT-1998 (first entry)

XX Fibronectin binding protein-derived peptide #18.

XX microbial surface components recognising adhesive matrix molecule;

KW MSCRAMM; fibronectin; fibronectin-binding protein; antibody; epitope;

KW antibiotic; bacterial infection; antibiotic-resistant strain.

XX Synthetic.

OS Staphylococcus aureus.

XX MO9831389-A2.

XX 23-JUL-1998.

XX 21-JAN-1998; 98WO-US001222.

XX 21-JAN-1997; 97US-0036139P.

XX (TEXA) UNIV TEXAS A & M SYSTEM.

XX Hoeoek M, Patti JM, House-Pompeo KL, Speziale P, Joh D;

XX Mcgavln MJ;

XX WPI; 1998-413816/35.

XX Antibody that binds to fibronectin-binding protein, preventing its

XX binding to fibronectin - used to treat or prevent bacterial infection,

XX especially by Staphylococci and Streptococci.

CC protein to fibronectin. Also claimed are: (1) isolated peptides of a
 CC fibronectin-binding protein that do not bind to fibronectin; (2) fusion
 CC protein containing at least one peptide of a fibronectin-binding protein
 CC linked to a second amino acid sequence; (3) nucleic acid encoding the
 CC isolated peptide of (1). Antibodies, the isolated peptides of (1) and the
 CC nucleic acids are all useful for immunisation (active or passive) and (by
 CC inhibiting binding of bacteria to fibronectin) for preventing or treating
 CC infection in humans or other animals, particularly by staphylococci or
 CC streptococci, e.g. meningitis, otitis media, pneumonia, endocarditis,
 CC mastitis in cattle, abortion in horses and many others. Since the
 CC antibodies block binding of bacteria, they should be effective against
 CC antibiotic-resistant strains, and may replace antibiotic therapy or
 CC increase its effectiveness. Sequences AAW65670-90 represent a series of
 CC synthetic peptides based on the D3 repeat of S. aureus fibronectin
 CC binding protein A. They were synthesised to contain a proline residue at
 CC each position throughout the sequence (ie a proline scan)

XX Sequence 21 AA:

Query Match 100.0%; Score 53; DB 2; Length 21;
 Best Local Similarity 100.0%; Pred. No. 0.022;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 VDFEEDTLRK 10
 |||||
 DB 12 VDFEEDTLRK 21

RESULT 14

ID AAW65676 standard; peptide; 21 AA.

XX AAW65676;

XX 16-OCT-1998 (first entry)

XX Fibronectin binding protein-derived peptide #20.

XX microbial surface components recognising adhesive matrix molecule;

KW MSCRAMM; fibronectin; fibronectin-binding protein; antibody; epitope;

KW antibiotic; bacterial infection; antibiotic-resistant strain.

XX Synthetic.

OS Staphylococcus aureus.

XX MO9831389-A2.

XX 23-JUL-1998.

XX 21-JAN-1998; 98WO-US001222.

XX 21-JAN-1997; 97US-0036139P.

XX (TEXA) UNIV TEXAS A & M SYSTEM.

XX Hoeoek M, Patti JM, House-Pompeo KL, Speziale P, Joh D;

XX Mcgavln MJ;

XX WPI; 1998-413816/35.

XX Antibody that binds to fibronectin-binding protein, preventing its

XX binding to fibronectin - used to treat or prevent bacterial infection,

XX especially by Staphylococci and Streptococci.

XX Example 8; Page 100; 201pp; English.

XX The invention relates to antibodies that bind to a fibronectin-binding

XX domain of a fibronectin-binding protein, and inhibit binding of the

XX protein to fibronectin. Also claimed are: (1) isolated peptides of a

XX fibronectin-binding protein that do not bind to fibronectin; (2) fusion

XX protein containing at least one peptide of a fibronectin-binding protein

XX linked to a second amino acid sequence; (3) nucleic acid encoding the

XX isolated peptide of (1). Antibodies, the isolated peptides of (1) and the

CC nucleic acids are all useful for immunisation (active or passive) and (by
 CC inhibiting binding of bacteria to fibronectin) for preventing or treating
 CC infection in humans or other animals, particularly by staphylococci or
 CC streptococci, e.g. meningitis, otitis media, pneumonia, endocarditis,
 CC mastitis in cattle, abortion in horses and many others. Since the
 CC antibodies block binding of bacteria, they should be effective against
 CC antibiotic-resistant strains, and may replace antibiotic therapy or
 CC increase its effectiveness. Sequences AAW65670-90 represent a series of
 CC synthetic peptides based on the D3 repeat of *S. aureus* fibronectin
 CC binding protein A. They were synthesised to contain a proline residue at
 CC each position through the sequence (ie a proline scan)

CC Sequence 21 AA:

Query Match 100.0%; Score 53; DB 2; Length 21;
 Best Local Similarity 100.0%; Pred. No. 0.022;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VDFEEDTLPK 10
 |||||
 DB 12 VDFEEDTLPK 21

RESULT 15

AAW65678
 ID AAW65678 standard; peptide; 21 AA.

AC AAW65678;

DT 16-OCT-1998 (first entry)

DE Fibronectin binding protein-derived peptide #22.

XX microbial surface components recognising adhesive matrix molecule;
 KM MSCRAMM; fibronectin; fibronectin-binding protein; antibody; epitope;
 KW antibiotic; bacterial infection; antibiotic-resistant strain.

OS Synthetic.
 OS Staphylococcus aureus.

PN WO9831389-A2.

PD 23-JUL-1998.

PF 21-JAN-1998; 98WO-US001222.

PR 21-JAN-1997; 97US-0036139P.

PA (TEXA) UNIV TEXAS A & M SYSTEM.

PI Hoegek M, Patti JM, House-Pompeo KL, Speziale P, Joh D;
 PI Mcgarvin MJ;

XX WPI; 1998-413816/35.

XX Antibody that binds to fibronectin-binding protein, preventing its
 PT binding to fibronectin - used to treat or prevent bacterial infection,
 PT especially by Staphylococci and Streptococci.

XX Example 8; Page 100; 201pp; English.

XX The invention relates to antibodies that bind to a fibronectin-binding
 CC domain of a fibronectin-binding protein, and inhibit binding of the
 CC protein to fibronectin. Also claimed are: (1) isolated peptides of a
 CC fibronectin-binding protein that do not bind to fibronectin; (2) fusion
 CC protein containing at least one peptide of a fibronectin-binding protein
 CC linked to a second amino acid sequence; (3) nucleic acid encoding the
 CC isolated peptide of (1). Antibodies, the isolated peptides of (1) and the
 CC nucleic acids are all useful for immunisation (active or passive) and (by
 CC inhibiting binding of bacteria to fibronectin) for preventing or treating
 CC infection in humans or other animals, particularly by staphylococci or
 CC streptococci, e.g. meningitis, otitis media, pneumonia, endocarditis,
 CC mastitis in cattle, abortion in horses and many others. Since the

CC antibodies block binding of bacteria, they should be effective against
 CC antibiotic-resistant strains, and may replace antibiotic therapy or
 CC increase its effectiveness. Sequences AAW65670-90 represent a series of
 CC synthetic peptides based on the D3 repeat of *S. aureus* fibronectin
 CC binding protein A. They were synthesised to contain a proline residue at
 CC each position through the sequence (ie a proline scan)

CC Sequence 21 AA:

Query Match 100.0%; Score 53; DB 2; Length 21;
 Best Local Similarity 100.0%; Pred. No. 0.022;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VDFEEDTLPK 10
 |||||
 DB 12 VDFEEDTLPK 21

Search completed: October 25, 2005, 21:29:14
 Job time : 69.7126 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 22, 2005, 08:01:06 ; Search time 56.2069 Seconds
(without alignments)
91.106 Million cell updates/sec

Title: US-10-731-238-100
Perfect score: 51
Sequence: 1 NSVDFFEDTL 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : Uniprot_03:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	51	100.0	940	2	Q53682
2	51	100.0	943	2	Q8NUH8
3	51	100.0	957	2	Q6G6H4
4	51	100.0	961	2	Q99RD3
5	51	100.0	961	2	Q7A3J8
6	51	100.0	965	2	Q6GDU5
7	51	100.0	1015	2	Q8NUV7
8	51	100.0	1015	2	Q6G6H3
9	51	100.0	1038	1	FNBA STNAU
10	51	100.0	1038	2	Q99RD2
11	51	100.0	1038	2	Q7A3J7
12	41	80.4	885	2	Q9VNX1
13	41	80.4	885	2	Q8Q2P8
14	40	78.4	140	2	Q8V2H5
15	40	78.4	141	2	Q8V2H5
16	40	78.4	557	2	Q72756
17	40	78.4	557	2	Q8QMN3
18	39	76.5	152	2	Q9AEP9
19	38	74.5	275	2	Q9SAJ8
20	38	74.5	579	2	Q9LUV6
21	37	72.5	265	2	Q70E89
22	37	72.5	281	2	Q9LS15
23	37	72.5	407	2	Q8J0A6
24	37	72.5	417	2	Q6BWM5
25	37	72.5	430	2	Q66J77
26	37	72.5	438	2	Q82GB7
27	37	72.5	520	1	RECNA AQUAE
28	37	72.5	529	2	Q6BWE3
29	37	72.5	597	2	Q8T3W3
30	37	72.5	1920	2	Q6BNV7
31	37	72.5	3446	2	Q86AC8

32	36	70.6	89	2	Q846S0	Q846S0 myxococcus
33	36	70.6	96	2	Q6L1B5	Q6L1B5 picophilus
34	36	70.6	230	2	Q81E19	Q81E19 bacillus ce
35	36	70.6	232	2	Q63BW9	Q63BW9 bacillus ce
36	36	70.6	232	2	Q738Z0	Q738Z0 bacillus ce
37	36	70.6	232	2	Q6HJEO	Q6HJEO bacillus th
38	36	70.6	235	2	Q81R35	Q81R35 bacillus an
39	36	70.6	262	2	Q979Y9	Q979Y9 thermoplas
40	36	70.6	345	2	Q92F14	Q92F14 listeria in
41	36	70.6	506	2	Q8TKM1	Q8TKM1 methanosarc
42	36	70.6	509	2	Q62180	Q62180 burkholderi
43	36	70.6	534	1	PYRG_METAC	Q8TKW5 methanosarc
44	36	70.6	534	1	PYRG_METMA	Q8G018 methanosarc
45	36	70.6	570	2	Q92CH7	Q92CH7 listeria in

ALIGNMENTS

RESULT 1	Q53682	PRELIMINARY;	PRT;	940 AA.
ID	Q53682			
AC	Q53682			
DT	01-NOV-1996 (TREMblrel. 01, Created)			
DT	01-NOV-1996 (TREMblrel. 01, Last sequence update)			
DT	01-MAR-2004 (TREMblrel. 26, Last annotation update)			
DE	Fibronectin binding protein B.			
GN	Name=fnbB;			
OS	Staphylococcus aureus.			
OC	Bacteria; Firmicutes; Bacillales; Staphylococcus.			
OX	NCBI_TaxID=1280;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=8325-4;			
RX	MEDLINE=92111475; PubMed=1837266;			
RA	Jonsson K., Signas C., Muller H.P., Lindberg M.;			
RT	Two different genes encode fibronectin binding proteins in			
RT	Staphylococcus aureus. The complete nucleotide sequence and			
RT	characterization of the second gene."			
RL	Eur. J. Biochem. 202:1041-1048 (1991).			
CC	-1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by			
CC	an amide bond (By similarity).			
DR	EMBL; X62992; CAA44726.1; ..			
DR	PIR; S19702; S19702.			
DR	HSSP; Q53682; 1N67.			
DR	GO; GO:0009986; C:cell surface; IEA.			
DR	GO; GO:0005618; C:cell wall; IEA.			
DR	GO; GO:0009775; C:cell wall (sensu Gram-positive Bacteria); IEA.			
DR	GO; GO:0016020; C:membrane; IEA.			
DR	GO; GO:0007155; P:cell adhesion; IEA.			
DR	InterPro; IPR008966; Adhes_Dact.			
DR	InterPro; IPR004237; Fn_Bind.			
DR	InterPro; IPR005877; Gpos_YsIRK.			
DR	InterPro; IPR001899; Gram_pos_anchor.			
DR	Pfam; PF02986; Fn_Bind; 2.			
DR	Pfam; PF00746; Gram_pos_anchor; 1.			
DR	Pfam; PF04650; YsIRK_signal; 1.			
DR	TIGRFAMs; TIGR01167; LPXTG_anchor; 1.			
DR	TIGRFAMs; TIGR01168; YsIRK_signal; 1.			
DR	PROSITE; PSS0847; GRAM_POS_ANCHORING; 1.			
KW	Cell wall; peptidoglycan-anchor. E35FBBCA907AE345 CRC64;			
SQ	SEQUENCE 940 AA; 103555 MW; E35FBBCA907AE345 CRC64;			
Query Match	100.0%; Score 51; DB 2; Length 940;			
Best Local Similarity	100.0%; Pred. No. 1.1;			
Matches	10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
QY	1 NSVDFFEDTL 10			
Db	782 NSVDFFEDTL 791			
RESULT 2				


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08N008      PRELIMINARY;      PRT;      943 AA.
AC 08N008;
DT 01-OCT-2002 (TREMBlrel. 22, Created)
DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Fndb protein.
GN Name=fndb; OrderedLocusNames=MM2420;
OS Staphylococcus aureus (strain MM2).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxId=196620;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MM2;
RX MEDLINE=22040717; PubMed=12044378; DOI=10.1016/S0140-6736(02)08713-5;
RA Baba T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Oguchi A.,
RA Nagai Y., Iwano N., Asano K., Naimi T., Kuroda H., Cui L.,
RA Yamamoto K., Hiramatsu K.;
RT "Genome and virulence determinants of high virulence community-
RT acquired MRSA.";
RL Lancel 359.1819-1827(2002).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC an amide bond (By similarity).
EMBL; AP004830; BAB96285.1; -.
DR HSSP; O53653; 1N67.
DR GO; GO:0009986; C:cell surface; IEA.
DR GO; GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0007155; P:cell adhesion; IEA.
DR InterPro; IPR008966; Adhes_bact.
DR InterPro; IPR004237; Fn_bind.
DR InterPro; IPR005877; Gpos_YsIRK.
DR Pfam; PF02986; Fn_bind_1.
DR Pfam; PF02986; Fn_bind_1.
DR Pfam; PF00746; Gram_pos_anchor_1.
DR TIGRFAMs; TIGR01167; LpxTG_anchor; 1.
DR TIGRFAMs; TIGR01168; YsIRK_signal; 1.
DR PROSITE; PS50847; GRAM_POS_ANCHORING; 1.
KW CELL wall; Complete proteome; Peptidoglycan-anchor.
SQ SEQUENCE 943 AA; 104537 MW; DA6A5F31947E1B6A CRC64;

Query Match      100.0%; Score 51; DB 2; Length 943;
Best Local Similarity 100.0%; Pred. No. 1.1;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 NSVDFEEDTL 10
      |||||
DB      789 NSVDFEEDTL 798

RESULT 3
O6G6H4      PRELIMINARY;      PRT;      957 AA.
AC 06G6H4;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE Fibronectin-binding protein.
GN Name=fndb; OrderedLocusNames=SA52387;
OS Staphylococcus aureus (strain MSSA476).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxId=282459;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=15213324; DOI=10.1073/pnas.0402521101;
RA Holden M.T.G., Fell E.J., Lindsey J.A., Peacock S.D., Day N.P.J.,
RA Enright M.C., Foster T.J., Moore C.E., Hurst L., Acklin R., Barron A.,
RA Bason N., Bentley S.D., Chillingworth C., Chillingworth T., Dowd L.,
RA Churcher C., Clark L., Cotton C., Cronin A., Doggett J., Dowd L.,
RA Felwell T., Hance Z., Harris B., Hauser H., Holtroyd S., Jagsels K.,
RA James K.D., Lennard N., Line A., Mayes R., Moule S., Mungall K.,

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RA Ormond D., Quail M.A., Rabinowitch E., Rutherford K.M., Sanders M.,
RA Sharp S., Simmonds M., Stevens K., Whitehead S., Barrell B.G.,
RA Spratt B.G., Parkhill J.;
RT "Complete genomes of two clinical Staphylococcus aureus strains:
RT evidence for the rapid evolution of virulence and drug resistance.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:9786-9791(2004).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC an amide bond (By similarity).
EMBL; BX571857; CNG44201.1; -.
DR GO; GO:0009986; C:cell surface; IEA.
DR GO; GO:0005618; C:cell wall; IEA.
DR GO; GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0007155; P:cell adhesion; IEA.
DR InterPro; IPR008966; Adhes_bact.
DR InterPro; IPR004237; Fn_bind.
DR InterPro; IPR005877; Gpos_YsIRK.
DR InterPro; IPR001899; Gram_pos_anchor.
DR Pfam; PF02986; Fn_bind_1.
DR Pfam; PF00746; Gram_pos_anchor_1.
DR TIGRFAMs; TIGR01167; LpxTG_anchor; 1.
DR TIGRFAMs; TIGR01168; YsIRK_signal; 1.
DR PROSITE; PS50847; GRAM_POS_ANCHORING; 1.
KW Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ SEQUENCE 957 AA; 105980 MW; 28F8BA7FDFD3EAF CRC64;

Query Match      100.0%; Score 51; DB 2; Length 957;
Best Local Similarity 100.0%; Pred. No. 1.1;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 NSVDFEEDTL 10
      |||||
DB      789 NSVDFEEDTL 798

RESULT 4
O99RD3      PRELIMINARY;      PRT;      961 AA.
AC 099RD3;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE Fibronectin-binding protein homolog.
GN Name=fndb; OrderedLocusNames=SAV2502;
OS Staphylococcus aureus (strain Mu50 / ATCC 700699).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxId=158878;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=Mu50 / ATCC 700699;
RX MEDLINE=21311952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2;
RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Lian J.-Q., Ito T.,
RA Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hoshoyama A.,
RA Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaio C.,
RA Sekimizu K., Hiramatsu H., Kuhara S., Goto S., Yabuuchi Y.,
RA Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
RA Hattori M., Ogatawara N., Hayashi H., Hiramatsu K.;
RT "Whole genome sequencing of methicillin-resistant Staphylococcus
RT aureus.";
RL Lancel 357.1225-1240(2001).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC an amide bond (By similarity).
EMBL; AP003365; BAB58664.1; -.
DR PIR; G90053; G90053.
DR HSSP; O53653; 1N67.
DR GO; GO:0009986; C:cell surface; IEA.
DR GO; GO:0005618; C:cell wall; IEA.
DR GO; GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0007155; P:cell adhesion; IEA.
DR InterPro; IPR008966; Adhes_bact.

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DR InterPro: IPR004237; Fn_bind.
 DR InterPro: IPR005877; Gpos_Ysirk.
 DR InterPro: IPR001899; Gram_pos_anchor.
 DR Pfam: PF02986; Fn_bind; 1.
 DR Pfam: PF00746; Gram_pos_anchor; 1.
 DR Pfam: PF04650; Ysirk_signal; 1.
 DR TIGRFAMs: TIGR01167; Lpxtg_anchor; 1.
 DR TIGRFAMs: TIGR01168; Ysirk_signal; 1.
 DR PROSITE: PS50847; GRAM_POS_ANCHORING; 1.
 DR Cell wall; Complete proteome; Peptidoglycan-anchor.
 KW SEQUENCE 961 AA; 106010 MW; 364940F84EA4101 CRC64;

Query Match 100.0%; Score 51; DB 2; Length 961;
 Best Local Similarity 100.0%; Pred. No. 1.1;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NSVDPEEDTL 10
 Db 793 NSVDPEEDTL 802

RESULT 5
 Q7A3J8 PRELIMINARY; PRT; 961 AA.
 ID 07A3J8
 AC 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE FmbB protein.
 OS Name=fmbB; OrderedLocustNames=SA2290;
 GN Staphylococcus aureus (strain N315).
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 OX NCBI_TaxID=158879;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21311952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2;
 RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
 RA Chii L., Oguchi A., Aoki K.-I., Nagai Y., Iian J.-O., Ito T.,
 RA Kanamori M., Matsunaru H., Maruyama A., Murakami H., Hosoyama A.,
 RA Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
 RA Sekizawa K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
 RA Kanehisa M., Yanaohta A., Oshima K., Furuya K., Yoshino C., Shiba T.,
 RA Hattori M., Ogasawara N., Hayashi H., Hiratake K.,
 RA "Whole genome sequencing of methicillin-resistant Staphylococcus
 aureus."
 RT Lancel 357:1225-1240(2001).
 RL -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
 CC an amide bond (By similarity).
 DR EMBL: AP003137; BAB3593.1; -.
 DR GO: GO:0009986; C:cell surface; IEA.
 DR GO: GO:0005618; C:cell wall; IEA.
 DR GO: GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
 DR GO: GO:0016020; C:membrane; IEA.
 DR GO: GO:0007155; P:cell adhesion; IEA.
 DR InterPro: IPR008966; Adhes_bact.
 DR InterPro: IPR004237; Fn_bind.
 DR InterPro: IPR005877; Gpos_Ysirk.
 DR InterPro: IPR001899; Gram_pos_anchor.
 DR Pfam: PF02986; Fn_bind; 1.
 DR Pfam: PF00746; Gram_pos_anchor; 1.
 DR Pfam: PF04650; Ysirk_signal; 1.
 DR TIGRFAMs: TIGR01167; Lpxtg_anchor; 1.
 DR TIGRFAMs: TIGR01168; Ysirk_signal; 1.
 DR PROSITE: PS50847; GRAM_POS_ANCHORING; 1.
 DR Cell wall; Complete proteome; Peptidoglycan-anchor.
 KW SEQUENCE 961 AA; 106010 MW; 364940F84EA4101 CRC64;

Query Match 100.0%; Score 51; DB 2; Length 961;
 Best Local Similarity 100.0%; Pred. No. 1.1;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NSVDPEEDTL 10
 Db 793 NSVDPEEDTL 802

Db 793 NSVDPEEDTL 802

RESULT 6
 Q6GDUS PRELIMINARY; PRT; 965 AA.
 ID Q6GDUS
 AC Q6GDUS
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Fibronectin-binding protein.
 GN Name=fmbA; OrderedLocustNames=SA22580;
 OS Staphylococcus aureus (strain MRSA252).
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 OX NCBI_TaxID=282458;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX PubMed=15213324; DOI=10.1073/pnas.0402521101;
 RA Holden M.T.G., Fell E.J., Lindsey J.A., Peacock S.J., Day N.P.J.,
 RA Enright M.C., Foster T.J., Moore C.E., Hurst L., Actin R.,
 RA Bason N., Bentley S.D., Chillingworth C., Chillingworth T.,
 RA Churcher C., Clark L., Corton C., Cronin A., Doggett J., Dowd L.,
 RA Felwell T., Hance Z., Harris B., Hauser H., Holtroyd S., Jagels K.,
 RA James K.D., Lennard N., Line A., Mayes R., Moule S., Mungall K.,
 RA Ormond D., Quail M.A., Rabinowitz R., Rutherford K.M., Sanders M.,
 RA Sharp S., Simmonds M., Stevens K., Whitehead S., Barrett B.G.,
 RA Spratt B.G., Parkhill J.,
 RA "Complete genomes of two clinical Staphylococcus aureus strains:
 RT evidence for the rapid evolution of virulence and drug resistance."
 Proc. Natl. Acad. Sci. U.S.A. 101:9786-9791(2004).
 RL -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
 CC an amide bond (By similarity).
 DR EMBL: BX571856; CMG41560.1; -.
 DR GO: GO:0009986; C:cell surface; IEA.
 DR GO: GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
 DR GO: GO:0016020; C:membrane; IEA.
 DR GO: GO:0007155; P:cell adhesion; IEA.
 DR InterPro: IPR008966; Adhes_bact.
 DR InterPro: IPR004237; Fn_bind.
 DR InterPro: IPR005877; Gpos_Ysirk.
 DR InterPro: IPR001899; Gram_pos_anchor.
 DR Pfam: PF02986; Fn_bind; 1.
 DR Pfam: PF00746; Gram_pos_anchor; 1.
 DR Pfam: PF04650; Ysirk_signal; 1.
 DR TIGRFAMs: TIGR01167; Lpxtg_anchor; 1.
 DR TIGRFAMs: TIGR01168; Ysirk_signal; 1.
 DR PROSITE: PS50847; GRAM_POS_ANCHORING; 1.
 DR Cell wall; Complete proteome; Peptidoglycan-anchor.
 KW SEQUENCE 965 AA; 105691 MW; 2982E132164D0551 CRC64;

Query Match 100.0%; Score 51; DB 2; Length 965;
 Best Local Similarity 100.0%; Pred. No. 1.1;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NSVDPEEDTL 10
 Db 811 NSVDPEEDTL 820

RESULT 7
 Q8NUU7 PRELIMINARY; PRT; 1015 AA.
 ID Q8NUU7
 AC Q8NUU7
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Fmb protein.
 GN Name=fmb; OrderedLocustNames=MM2421;
 OS Staphylococcus aureus (strain MM2).
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 OX NCBI_TaxID=196620;
 RN [1]
 RP SEQUENCE FROM N.A.

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RC STRAIN=WM2;
RX MEDLINE=22040717; PubMed=12044378; DOI=10.1016/S0140-6736(02)08713-5;
RA Baba T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Ouchi A.,
RA Nagai Y., Iwano N., Asano K., Naimi T., Kuroda H., Cui L.,
RA Yamamoto K., Hiramatsu K.;
RT "Genome and virulence determinants of high virulence community-
RT acquired MRSA.";
RL Lancet 359:1819-1827(2002).
CC -|- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC an amide bond (By similarity).
CC EMBL: AP004830; BAB96286.1; -.
DR GO: GO:0009986; C:cell surface; IEA.
DR GO: GO:0005618; C:cell wall; IEA.
DR GO: GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO: GO:0016020; C:membrane; IEA.
DR GO: GO:0007135; P:cell adhesion; IEA.
DR InterPro: IPR008966; Adhes_bact.
DR InterPro: IPR004237; Fn_bind.
DR InterPro: IPR005877; Gpos_YsIRK.
DR InterPro: IPR001899; Gram_pos_anchor.
DR Pfam: PF02986; Fn_bind; 1.
DR Pfam: PF00746; Gram_pos_anchor; 1.
DR Pfam: PF04650; YsIRK_signal; 1.
DR TIGRFAMs: TIGR01167; LPXTG_anchor; 1.
DR TIGRFAMs: TIGR01168; YsIRK_signal; 1.
DR PROSITE: PS50847; GRAM_POS_ANCHORING; 1.
KW Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ SEQUENCE 1015 AA; 111145 MW; D0F9281BB64d44D2 CRC64;

Query Match 100.0%; Score 51; DB 2; Length 1015;
Best Local Similarity 100.0%; Pred. No. 1.2;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NSVDPEEDTL 10
DB 847 NSVDPEEDTL 856

RESULT 8
ID Q6G6H3 PRELIMINARY; PRT; 1015 AA.
AC Q6G6H3;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Fibronectin-binding protein.
GN OrderedLocustNames=SA52388;
OS Staphylococcus aureus (strain MSSA476).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=282459;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=15213324; DOI=10.1073/pnas.0402521101;
RA Holden M.T.G., Fell E.J., Lindsey J.A., Peacock S.J., Day N.P.J.,
RA Enright M.C., Foster T.J., Moore C.E., Hurst L., Atkin R., Barron A.,
RA Bason N., Bentley S.D., Chillingworth C., Chillingworth T.,
RA Churcher C., Clark L., Corton C., Cronin A., Doggett J., Dowd L.,
RA Felwell T., Hance Z., Harris B., Hauser H., Holtroyd S., Jagels K.,
RA James K.D., Lennard N., Line A., Mayes R., Moule S., Mungall K.,
RA Sharp S., Simmonds M., Stevens K., Whitehead S., Barrett B.G.,
RA Spratt B.G., Parkhill J.;
RT "Complete genomes of two clinical Staphylococcus aureus strains:
RT evidence for the rapid evolution of virulence and drug resistance.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:9786-9791(2004).
CC -|- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC an amide bond (By similarity).
CC EMBL: BX571857; CAG44202.1; -.
DR GO: GO:0009986; C:cell surface; IEA.
DR GO: GO:0005618; C:cell wall; IEA.
DR GO: GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO: GO:0016020; C:membrane; IEA.
DR GO: GO:0007155; P:cell adhesion; IEA.

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DR InterPro: IPR008966; Adhes_bact.
DR InterPro: IPR004237; Fn_bind.
DR InterPro: IPR005877; Gpos_YsIRK.
DR InterPro: IPR001899; Gram_pos_anchor.
DR Pfam: PF02986; Fn_bind; 1.
DR Pfam: PF00746; Gram_pos_anchor; 1.
DR Pfam: PF04650; YsIRK_signal; 1.
DR TIGRFAMs: TIGR01167; LPXTG_anchor; 1.
DR TIGRFAMs: TIGR01168; YsIRK_signal; 1.
DR PROSITE: PS50847; GRAM_POS_ANCHORING; 1.
KW Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ SEQUENCE 1015 AA; 111145 MW; D0F9281BB64d44D2 CRC64;

Query Match 100.0%; Score 51; DB 2; Length 1015;
Best Local Similarity 100.0%; Pred. No. 1.2;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NSVDPEEDTL 10
DB 847 NSVDPEEDTL 856

RESULT 9
ID FNBA STAU STANDARD; PRT; 1018 AA.
AC FNBA STAU STANDARD; PRT; 1018 AA.
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Fibronectin-binding protein precursor (FNBP).
GN Name=FNBP;
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1280;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=NCTC 8325-4;
RX MEDLINE=89098998; PubMed=2521391;
RA Signes C., Raucot G., Joensson K., Lindgren P.-E.,
RA Anantharamiah G.M., Hoocek M., Lindberg M.;
RT "Nucleotide sequence of the gene for a fibronectin-binding protein
RT from Staphylococcus aureus: use of this peptide sequence in the
RT synthesis of biologically active peptides.";
RL Proc. Natl. Acad. Sci. U.S.A. 86:699-703(1989).
CC -|- FUNCTION: The ability of bacteria to bind fibronectin has been
CC proposed as a virulence factor enabling bacteria to colonize wound
CC tissues and blood clots. Binding of plasma fibronectin to the
CC bacterial surface might block adhesion receptors on S.aureus, thus
CC representing an important defense mechanism against tissue
CC invasion.
CC -|- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC an amide bond (Potential).
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@sib-sib.ch).
CC
CC EMBL: J04151; AAA6632.1; -.
DR InterPro: IPR004237; Fn_bind.
DR InterPro: IPR005877; Gpos_YsIRK.
DR InterPro: IPR001899; Gram_pos_anchor.
DR Pfam: PF02986; Fn_bind; 1.
DR Pfam: PF00746; Gram_pos_anchor; 1.
DR Pfam: PF04650; YsIRK_signal; 1.
DR TIGRFAMs: TIGR01167; LPXTG_anchor; 1.
DR TIGRFAMs: TIGR01168; YsIRK_signal; 1.
DR PROSITE: PS50847; GRAM_POS_ANCHORING; 1.
KW Cell adhesion; Cell wall; Peptidoglycan-anchor; Repeat; Signal;
KW Virulence.

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FT SIGNAL 1 36
FT CHAIN 37 985 Fibronectin-binding protein.
FT PROPEP 986 1018 Removed by sortase (Potential).
FT REPEAT 545 574 B-1.
FT REPEAT 575 604 B-2.
FT DOMAIN 745 878 4 X approximate tandem repeats,
FT REPEAT 745 878 fibronectin-binding domain.
FT REPEAT 745 878 D-1.
FT REPEAT 821 859 D-2.
FT REPEAT 860 878 D-3.
FT DOMAIN 879 948 5 X tandem repeats, Pro-rich (WR).
FT REPEAT 879 892 WR 1.
FT REPEAT 893 906 WR 2.
FT REPEAT 907 920 WR 3.
FT REPEAT 921 934 WR 4.
FT REPEAT 935 948 WR 5.
FT SITE 982 986 LpxTG sorting signal (Potential).
FT MOD_RES 985 985 Pentaglycyl murein peptidoglycan amidated
SQ SEQUENCE 1018 AA; 111780 MW; 58175E020E81F1F CRC64;
chreonine (Potential).

Query Match 100.0%; Score 51; DB 1; Length 1018;
Best Local Similarity 100.0%; Pred. No. 1.2;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NSVDPEEDTL 10
DB 846 NSVDPEEDTL 855

RESULT 10
Q99RD2 PRELIMINARY; PRT; 1038 AA.
ID Q99RD2;
AC Q99RD2;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Fibronectin-binding protein homolog.
GN Name=fnb; OrderedLocustNames=SAV503;
OS Staphylococcus aureus (strain Mu50 / ATCC 700699).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=158878;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Mu50 / ATCC 700699;
RX MEDLINE=21311952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2;
RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Iian J.-O., Ito T.,
RA Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,
RA Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
RA Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuaki J.,
RA Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
RA Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
RT "Whole genome sequencing of methicillin-resistant Staphylococcus
aureus."
RT Lancet 357:1225-1240(2001).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
an amide bond (By similarity).
CC EMBL; AP003365; BAB58665.1; -.
DR PIR; H90053; H90053.
DR GO; GO:0009986; C:cell surface; IEA.
DR GO; GO:0005618; C:cell wall; IEA.
DR GO; GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0007155; P:cell adhesion; IEA.
DR InterPro; IPR008966; Adhes_bact.
DR InterPro; IPR004237; Fn_bind.
DR InterPro; IPR005877; Gpos_YsIRK.
DR InterPro; IPR001899; Gram_pos_anchor.
DR Pfam; PF02986; Fn_bind; 1.
DR Pfam; PF00746; Gram_pos_anchor; 1.
DR Pfam; PF04650; YsIRK_signal; 1.
DR Pfam; PF00746; Gram_pos_anchor; 1.
DR Pfam; PF04650; YsIRK_signal; 1.
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DR TIGRFAMs; TIGR01167; LpxTG_anchor; 1.
DR TIGRFAMs; TIGR01168; YsIRK_signal; 1.
DR PROSITE; PS50847; GRAM_POS_ANCHORING; 1.
DR Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ SEQUENCE 1038 AA; 113618 MW; 666BF6BF2BFBB12 CRC64;

Query Match 100.0%; Score 51; DB 2; Length 1038;
Best Local Similarity 100.0%; Pred. No. 1.2;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NSVDPEEDTL 10
DB 842 NSVDPEEDTL 851

RESULT 11
Q7A3J7 PRELIMINARY; PRT; 1038 AA.
ID Q7A3J7;
AC Q7A3J7;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Fnb protein.
GN Name=fnb; OrderedLocustNames=SA2291;
OS Staphylococcus aureus (strain N315).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=158879;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=21311952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2;
RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Iian J.-O., Ito T.,
RA Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,
RA Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
RA Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuaki J.,
RA Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
RA Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
RT "Whole genome sequencing of methicillin-resistant Staphylococcus
aureus."
RT Lancet 357:1225-1240(2001).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
an amide bond (By similarity).
CC EMBL; AP003337; BAB43594.1; -.
DR GO; GO:0009986; C:cell surface; IEA.
DR GO; GO:0005618; C:cell wall; IEA.
DR GO; GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0007155; P:cell adhesion; IEA.
DR InterPro; IPR008966; Adhes_bact.
DR InterPro; IPR004237; Fn_bind.
DR InterPro; IPR005877; Gpos_YsIRK.
DR InterPro; IPR001899; Gram_pos_anchor.
DR Pfam; PF02986; Fn_bind; 1.
DR Pfam; PF00746; Gram_pos_anchor; 1.
DR Pfam; PF04650; YsIRK_signal; 1.
DR TIGRFAMs; TIGR01167; LpxTG_anchor; 1.
DR TIGRFAMs; TIGR01168; YsIRK_signal; 1.
DR PROSITE; PS50847; GRAM_POS_ANCHORING; 1.
DR Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ SEQUENCE 1038 AA; 113618 MW; 666BF6BF2BFBB12 CRC64;

Query Match 100.0%; Score 51; DB 2; Length 1038;
Best Local Similarity 100.0%; Pred. No. 1.2;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NSVDPEEDTL 10
DB 842 NSVDPEEDTL 851

RESULT 12
Q9GNCO PRELIMINARY; PRT; 885 AA.
ID Q9GNCO
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AC 09GNC0;
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE DNA polymerase eta (Dpol-eta) (SD05329p).
GN Name=DNApol-eta; Synonym=POLH, drad30A;
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydriidae; Drosophilidae; Drosophila.
OX NCBI_TaxId=7227;
RN [1]
RP SEQUENCE FROM N.A.
RA Oshige M., Kimura S., Takara K., Sakaguchi K.;
RA Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA MEDLINE=2126760; PubMed=11297519; DOI=10.1074/jbc.M009822200;
RA Ishikawa T., Umetsu N., Mizukoshi T., Iwai S., Iwasaki H.,
RA Maestani C., Hanoka F., Ueda R., Ohmori H., Todo T.;
RA "Mutagenic and nonmutagenic bypass of DNA lesions by Drosophila DNA
RT polymerases dpol-eta and dpol-epsilon".
RT J. Biol. Chem. 276:15155-15163(2001).
RN [3]
RP SEQUENCE FROM N.A.
RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
RA Champe M., Chavez C., Dorset V., Farfan D., Frise E., George R.,
RA Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J.,
RA Nunoo J., Pacleb J., Paragae V., Park S., Phuenavong S., Wan K.,
RA Yu C., Lewis S.E., Rubin G.M., Celinker S.;
RA Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB036766; BAB20905.1; -;
DR EMBL; AB049433; BAB15799.1; -;
DR EMBL; AY058771; AAL14000.1; -;
DR HSSP; P96022; 1K1S.
DR Flybase; FBgn0037141; DNAPol-eta.
DR GO; GO:0015999; P:eta DNA polymerase activity; IDA.
DR GO; GO:0019985; P:bypass DNA synthesis; IDA.
DR InterPro; IPR001126; UMC_1like.
DR Pfam; PF00817; IMS; 1.
DR PROSITE; PS50173; UMC_1.
SQ SEQUENCE 885 AA; 98986 MW; 79AD7F7548464568 CRC64;
QY Query Match 80.4%; Score 41; DB 2; Length 885;
Beet Local Similarity 88.9%; Pred. No. 77;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 NSVFDEEDT 9
ID 09VNX1 PRELIMINARY; PRT; 885 AA.
AC 09VNX1;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE CG7143-PA.
GN Name=DNApol-eta; ORFName=CG7143;
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydriidae; Drosophilidae; Drosophila.
OX NCBI_TaxId=7227;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;
RA Adams M.D., Celinker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,

RA Brandon R.C., Rogers Y.H., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Gabor G.L.,
RA Abtill J.F., Agbayani A., An H.J., Andrews-Frankoch C., Baldwin D.,
RA Ballew R.W., Basu A., Bendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhanderi D., Bolshakov S.,
RA Borova D., Botchan M.R., Bouck J., Brokstein P., Brothier P.,
RA Burris J.K., Busan D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Padua B., Deicher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Foster C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glaeser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.H., Ibeagwam C.,
RA Jatali M., Kalush F., Karpen G.H., Ke Z., Kennison J.R., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Laspo P., Lei Y., Lavitcky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milahina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nuskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reibert K., Remington K., Saunders R.D., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tecor C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.Y., Waasatman D.A., Weinstein G.M., Weissbach J.,
RA Williams S.E., Wheeler D.A., Krommiller B., Carlson J.W., Halpern A.,
RA Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
RT Science 287:2185-2195(2000).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=22426065; PubMed=12537568;
RA Celinker S.E., Wheeler D.A., Krommiller B., Carlson J.W., Halpern A.,
RA Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A.,
RA George R.A., Hoskins R.A., Lavery T., Muzny D.M., Nelson C.R.,
RA Pacleb J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,
RA Svirskas R., Taber P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,
RA Weinstein G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.;
RT "Finishing a whole-genome shotgun: Release 3 of the Drosophila
RT melanogaster euchromatic genome sequence.";
RT Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=22426070; PubMed=12537573;
RA Kaminker J.S., Bergman C.M., Krommiller B., Carlson J., Svirskas R.,
RA Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,
RA Ashburner M., Celinker S.E.;
RT "The transposable elements of the Drosophila melanogaster euchromatin:
RT a genome perspective.";
RT Genome Biol. 3:RESEARCH0084-RESEARCH0084(2002).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=22426069; PubMed=12537572;
RA Mista S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
RA Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochuk S.E.,
RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,
RA Betencourt B.R., Celinker S.E., de Grey A.D., Drysdale R.A.,
RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.O.,
RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
RA Lewis S.E.;
RT "Annotation of the Drosophila melanogaster euchromatic genome: a
RT systematic review.";
RT Genome Biol. 3:RESEARCH0083-RESEARCH0083(2002).
RN [5]
RP SEQUENCE FROM N.A.
RX Flybase; (SEP-2002) to the EMBL/GenBank/DBJ databases.
RT Submitted

RP SEQUENCE FROM N.A.
 RG Playase:
 RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB003596; AAF51794.1; -.
 DR HSSP; P96022; IKIS.
 DR InTact; Q9VNX1; -.
 DR Playase; Fgno0037141; DNAPol-eta.
 DR GO; GO:0015999; F-eta DNA polymerase activity; IDA.
 DR GO; GO:0019985; P-byrase DNA synthesis; IDA.
 DR InterPro; IPR001126; UMUC_like.
 DR Pfam; PF00817; IMS; 1.
 DR PROSITE; PS50173; UMUC; 1.
 SQ SEQUENCE 885 AA; 99026 MW; 79AD67CA651AC68 CRC64;

Query Match 80.4%; Score 41; DB 2; Length 885;
 Best Local Similarity 88.9%; Pred. No. 77;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 NSVDPEEDT 9
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 Db 604 NSVDPEEDT 612

RESULT 14
 O8QPZ8 PRELIMINARY; PRT; 140 AA.
 AC O8QPZ8;
 DT 01-JUN-2002 (T-EMBLrel. 21, Created)
 DT 01-JUN-2002 (T-EMBLrel. 21, Last sequence update)
 DT 01-MAR-2003 (T-EMBLrel. 23, Last annotation update)
 DE CML199R.
 GN Name=CML199R;
 OS Camelipox virus (strain CMS).
 OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
 OC Orthopoxvirus.
 OX NCBI_TaxID=203172;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CMS;
 RX PubMed=11907336;
 RA Gubser C., Smith G.L.;
 RT "The sequence of camelipox virus shows it is most closely related to variola virus, the cause of smallpox."
 RL J. Gen. Virol. 83:855-872(2002).
 DR EMBL; AY009089; AAG37709.1; -.
 DR InterPro; IPR011043; Gal_oxid_central.
 DR InterPro; IPR006652; Kelch_rep.
 DR Pfam; PF01344; Kelch_1; 2.
 DR SMART; SM00612; Kelch; 2.
 SQ SEQUENCE 140 AA; 16301 MW; 7C7E1DFA9DB787F CRC64;

Query Match 78.4%; Score 40; DB 2; Length 140;
 Best Local Similarity 77.8%; Pred. No. 16;
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 NSVDPEEDT 9
 |||
 Db 83 NSIDMEEDT 91

RESULT 15
 O8VZHS PRELIMINARY; PRT; 141 AA.
 AC O8VZHS;
 DT 01-MAR-2002 (T-EMBLrel. 20, Created)
 DT 01-MAR-2002 (T-EMBLrel. 20, Last sequence update)
 DT 01-MAR-2003 (T-EMBLrel. 23, Last annotation update)
 DE Kelch-like protein.
 OS Camelipox virus (strain M-96).
 OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
 OC Orthopoxvirus.
 OX NCBI_TaxID=203173;
 RN [1]

RP SEQUENCE FROM N.A.
 RX MEDLINE=22031204; PubMed=12033760; DOI=10.1006/viro.2001.1343;
 RA Alfonso C.L., Tulman E.R., Lu Z., Zaak L., Sandybaev N.T.,
 RA Kerembekova U.Z., Zaitsev V.L., Kutilsh G.F., Rock D.L.;
 RT "The genome of camelipox virus."
 DR Virology 295:1-9(2002).
 DR EMBL; AF438165; AAL73911.1; -.
 DR Pfam; PF01344; Kelch_1; 2.
 DR SMART; SM00612; Kelch; 2.
 SQ SEQUENCE 141 AA; 16204 MW; EA6B5AFA9DBE88BD CRC64;

Query Match 78.4%; Score 40; DB 2; Length 141;
 Best Local Similarity 77.8%; Pred. No. 17;
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 NSVDPEEDT 9
 |||
 Db 83 NSIDMEEDT 91

Search completed: October 22, 2005, 09:52:27
 Job time : 57.2069 secs

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OM protein - protein search, using sw model

Run on: October 22, 2005, 12:39:57 ; Search time 56.1494 Seconds
(Without alignments)
74.354 Million cell updates/sec

Title: US-10-731-238-100
Perfect score: 51
Sequence: 1 NSVDPEEDTL 10

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 1862951 seqs, 417491010 residues

Total number of hits satisfying chosen parameters: 1862951

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database:

1: Published Applications AA:
2: /cgn2_6/prodata/2/pubppaa/US07_PUBCOMB.pep.*
3: /cgn2_6/prodata/2/pubppaa/PCT_NEW_PUB.pep.*
4: /cgn2_6/prodata/2/pubppaa/US06_NEW_PUB.pep.*
5: /cgn2_6/prodata/2/pubppaa/US06_PUBCOMB.pep.*
6: /cgn2_6/prodata/2/pubppaa/US07_NEW_PUB.pep.*
7: /cgn2_6/prodata/2/pubppaa/PCTUS_PUBCOMB.pep.*
8: /cgn2_6/prodata/2/pubppaa/US08_NEW_PUB.pep.*
9: /cgn2_6/prodata/2/pubppaa/US08_PUBCOMB.pep.*
10: /cgn2_6/prodata/2/pubppaa/US09_PUBCOMB.pep.*
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12: /cgn2_6/prodata/2/pubppaa/US09_NEW_PUB.pep.*
13: /cgn2_6/prodata/2/pubppaa/US10_PUBCOMB.pep.*
14: /cgn2_6/prodata/2/pubppaa/US10B_PUBCOMB.pep.*
15: /cgn2_6/prodata/2/pubppaa/US10C_PUBCOMB.pep.*
16: /cgn2_6/prodata/2/pubppaa/US10D_PUBCOMB.pep.*
17: /cgn2_6/prodata/2/pubppaa/US10E_PUBCOMB.pep.*
18: /cgn2_6/prodata/2/pubppaa/US10F_NEW_PUB.pep.*
19: /cgn2_6/prodata/2/pubppaa/US11_PUBCOMB.pep.*
20: /cgn2_6/prodata/2/pubppaa/US11A_PUBCOMB.pep.*
21: /cgn2_6/prodata/2/pubppaa/US60_NEW_PUB.pep.*
22: /cgn2_6/prodata/2/pubppaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	51	100.0	10	US-10-731-238-100	Sequence 100, Appl
2	51	100.0	21	US-10-731-238-9	Sequence 9, Appl
3	51	100.0	21	US-10-731-238-10	Sequence 10, Appl
4	51	100.0	21	US-10-731-238-14	Sequence 14, Appl
5	51	100.0	21	US-10-731-238-15	Sequence 15, Appl
6	51	100.0	21	US-10-731-238-16	Sequence 16, Appl
7	51	100.0	21	US-10-731-238-17	Sequence 17, Appl
8	51	100.0	21	US-10-731-238-18	Sequence 18, Appl
9	51	100.0	21	US-10-731-238-19	Sequence 19, Appl
10	51	100.0	21	US-10-731-238-20	Sequence 20, Appl
11	51	100.0	21	US-10-731-238-21	Sequence 21, Appl

12	51	100.0	21	US-10-731-238-32	Sequence 32, Appl
13	51	100.0	21	US-10-731-238-33	Sequence 33, Appl
14	51	100.0	21	US-10-731-238-34	Sequence 34, Appl
15	51	100.0	22	US-10-731-238-13	Sequence 13, Appl
16	51	100.0	37	US-11-066-697-1134	Sequence 1134, Ap
17	51	100.0	37	US-09-813-820-8	Sequence 8, Appl
18	51	100.0	388	US-08-901-062-1	Sequence 1, Appl
19	51	100.0	559	US-08-781-986A-5251	Sequence 5251, Ap
20	51	100.0	559	US-10-329-624-5251	Sequence 5251, Ap
21	51	100.0	948	US-10-470-048B-424	Sequence 424, Ap
22	51	100.0	948	US-10-470-048B-69	Sequence 69, Appl
23	51	100.0	978	US-10-282-122A-43778	Sequence 43778, A
24	51	100.0	978	US-09-815-242-5456	Sequence 5456, Ap
25	51	100.0	1001	US-09-815-242-5797	Sequence 5797, Ap
26	51	100.0	1018	US-09-815-242-5797	Sequence 5797, Ap
27	51	100.0	1018	US-09-815-242-12838	Sequence 12838, A
28	51	100.0	1018	US-10-470-048B-68	Sequence 68, Appl
29	51	100.0	1027	US-08-781-986A-5254	Sequence 5254, Ap
30	51	100.0	1027	US-10-329-624-5254	Sequence 5254, Ap
31	51	100.0	1038	US-10-282-122A-43827	Sequence 43827, A
32	51	92.2	14	US-10-731-238-61	Sequence 61, Appl
33	47	92.2	21	US-10-731-238-31	Sequence 31, Appl
34	46	90.2	21	US-10-731-238-23	Sequence 23, Appl
35	45	88.2	21	US-10-731-238-22	Sequence 22, Appl
36	45	88.2	21	US-10-731-238-24	Sequence 24, Appl
37	45	88.2	21	US-10-731-238-27	Sequence 27, Appl
38	45	88.2	21	US-10-731-238-28	Sequence 28, Appl
39	45	88.2	21	US-10-731-238-30	Sequence 30, Appl
40	44	86.3	21	US-10-731-238-25	Sequence 25, Appl
41	44	86.3	21	US-10-731-238-29	Sequence 29, Appl
42	42	82.4	10	US-10-731-238-99	Sequence 99, Appl
43	41	80.4	10	US-10-731-238-104	Sequence 104, Appl
44	41	80.4	10	US-10-731-238-101	Sequence 101, Appl
45	41	80.4	11	US-10-731-238-86	Sequence 86, Appl

ALIGNMENTS

RESULT 1
US-10-731-238-100
Sequence 100, Application US/10731238
Publication No. US20050123552A1

GENERAL INFORMATION:
APPLICANT: Hook, Magnus

Patel, Joseph M.
House-Pompeo, Karen L.
Speziale, Pietro
Joh, Danny

TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
AND METHODS OF USE

NUMBER OF SEQUENCES: 105

CORRESPONDENCE ADDRESS:

ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433

CITY: Houston
STATE: TX

COUNTRY: USA
ZIP: 77210-4433

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/731.238

FILING DATE: 10-Dec-2003
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/010.317

FILING DATE: 21-Jan-1998
APPLICATION NUMBER: US 60/036.139

FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAMK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 100:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 100:
US-10-731-238-100

Query Match 100.0%; Score 51; DB 18; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.019;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NSVDFFEDTL 10
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1 NSVDFFEDTL 10

Db 1 NSVDFFEDTL 10

RESULT 2
US-10-731-238-9
Sequence 9, Application US/10731238
Publication No. US20050123552A1
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
Pattl, Joseph M.
House-Pompeo, Karen L.
Speziale, Pietro
Joh, Danny
McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/731,238
FILING DATE: 10-Dec-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE: 21-Jan-1998
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAMK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>

TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 9:
US-10-731-238-9

Query Match 100.0%; Score 51; DB 18; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.042;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NSVDFFEDTL 10
|||
10 NSVDFFEDTL 19

Db 10 NSVDFFEDTL 19

RESULT 3
US-10-731-238-10
Sequence 10, Application US/10731238
Publication No. US20050123552A1
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
Pattl, Joseph M.
House-Pompeo, Karen L.
Speziale, Pietro
Joh, Danny
McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/731,238
FILING DATE: 10-Dec-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE: 21-Jan-1998
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAMK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 10:
US-10-731-238-10

Query Match 100.0%; Score 51; DB 18; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.042;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NSVDFFEDTL 10
|||
10 NSVDFFEDTL 19

Db 10 NSVDFFEDTL 19

RESULT 4
US-10-731-238-14
Sequence 14, Application US/10731238
Publication No. US20050123552A1
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
Pacti, Joseph M.
House-Pompeo, Karen L.
Speziale, Pietro
Joh, Danny
McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/731,238
FILING DATE: 10-Dec-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE: 21-Jan-1998
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAMK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 14:
US-10-731-238-14
Query Match 100.0%; Score 51; DB 18; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.042;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 NSVDFFEDTL 10
Db 10 NSVDFFEDTL 19
RESULT 5
US-10-731-238-15
Sequence 15, Application US/10731238
Publication No. US20050123552A1
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
Pacti, Joseph M.
House-Pompeo, Karen L.
Speziale, Pietro
Joh, Danny
McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
AND METHODS OF USE

NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/731,238
FILING DATE: 10-Dec-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE: 21-Jan-1998
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAMK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 15:
US-10-731-238-15
Query Match 100.0%; Score 51; DB 18; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.042;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 NSVDFFEDTL 10
Db 10 NSVDFFEDTL 19
RESULT 6
US-10-731-238-16
Sequence 16, Application US/10731238
Publication No. US20050123552A1
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
Pacti, Joseph M.
House-Pompeo, Karen L.
Speziale, Pietro
Joh, Danny
McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30

1 CURRENT APPLICATION DATA:
2 APPLICATION NUMBER: US/10/731,238
3 FILING DATE: 10-Dec-2003
4 CLASSIFICATION: <Unknown>
5 PRIOR APPLICATION DATA:
6 APPLICATION NUMBER: US/09/010,317
7 FILING DATE: 21-Jan-1998
8 APPLICATION NUMBER: US 60/036,139
9 FILING DATE: 21-Jan-1997
10 ATTORNEY/AGENT INFORMATION:
11 NAME: Hibler, David W.
12 REGISTRATION NUMBER: 41,071
13 REFERENCE/DOCKET NUMBER: TAMK:189
14 TELECOMMUNICATION INFORMATION:
15 TELEPHONE: 512-418-3000
16 TELEFAX: 512-474-7577
17 INFORMATION FOR SEQ ID NO: 16:
18 SEQUENCE CHARACTERISTICS:
19 LENGTH: 21 amino acids
20 TYPE: amino acid
21 STRANDEDNESS: <Unknown>
22 TOPOLOGY: linear
23 SEQUENCE DESCRIPTION: SEQ ID NO: 16:
24 US-10-731-238-16
25
26 Query Match 100.0%; Score 51; DB 18; Length 21;
27 Best Local Similarity 100.0%; Pred. No. 0.042;
28 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
29
30 QY 1 NSVDFFEDTL 10
31 |||||||
32 Db 10 NSVDFFEDTL 19
33
34 RESULT 7
35 US-10-731-238-17
36 Sequence 17, Application US/10731238
37 Publication No. US20050123552A1
38 GENERAL INFORMATION:
39 APPLICANT: Hook, Magnus
40 Patell, Joseph M.
41 House-Pompeo, Karen L.
42 Speciale, Pietro
43 Joh, Danny
44
45 TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
46 AND METHODS OF USE
47
48 NUMBER OF SEQUENCES: 105
49 CORRESPONDENCE ADDRESS:
50 ADDRESSEE: Arnold, White & Durkee
51 STREET: P.O. Box 4433
52 CITY: Houston
53 STATE: TX
54 COUNTRY: USA
55 ZIP: 77210-4433
56 COMPUTER READABLE FORM:
57 MEDIUM TYPE: Floppy disk
58 OPERATING SYSTEM: PC-DOS/MS-DOS
59 SOFTWARE: PatentIn Release #1.0, Version #1.30
60 CURRENT APPLICATION DATA:
61 APPLICATION NUMBER: US/10/731,238
62 FILING DATE: 10-Dec-2003
63 CLASSIFICATION: <Unknown>
64 PRIOR APPLICATION DATA:
65 APPLICATION NUMBER: US/09/010,317
66 FILING DATE: 21-Jan-1998
67 APPLICATION NUMBER: US 60/036,139
68 FILING DATE: 21-Jan-1997
69 ATTORNEY/AGENT INFORMATION:
70 NAME: Hibler, David W.
71 REGISTRATION NUMBER: 41,071
72 REFERENCE/DOCKET NUMBER: TAMK:189
73 TELECOMMUNICATION INFORMATION:
74 TELEPHONE: 512-418-3000
75 TELEFAX: 512-474-7577
76 INFORMATION FOR SEQ ID NO: 18:
77 SEQUENCE CHARACTERISTICS:
78 LENGTH: 21 amino acids
79 TYPE: amino acid
80 STRANDEDNESS: <Unknown>
81 TOPOLOGY: linear
82 SEQUENCE DESCRIPTION: SEQ ID NO: 18:
83 US-10-731-238-18
84
85 Query Match 100.0%; Score 51; DB 18; Length 21;
86 Best Local Similarity 100.0%; Pred. No. 0.042;
87 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 TELECOMMUNICATION INFORMATION:
2 TELEPHONE: 512-418-3000
3 TELEFAX: 512-474-7577
4 INFORMATION FOR SEQ ID NO: 17:
5 SEQUENCE CHARACTERISTICS:
6 LENGTH: 21 amino acids
7 TYPE: amino acid
8 STRANDEDNESS: <Unknown>
9 TOPOLOGY: linear
10 SEQUENCE DESCRIPTION: SEQ ID NO: 17:
11 US-10-731-238-17
12
13 Query Match 100.0%; Score 51; DB 18; Length 21;
14 Best Local Similarity 100.0%; Pred. No. 0.042;
15 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
16
17 QY 1 NSVDFFEDTL 10
18 |||||||
19 Db 10 NSVDFFEDTL 19
20
21 RESULT 8
22 US-10-731-238-18
23 Sequence 18, Application US/10731238
24 Publication No. US20050123552A1
25 GENERAL INFORMATION:
26 APPLICANT: Hook, Magnus
27 Patell, Joseph M.
28 House-Pompeo, Karen L.
29 Speciale, Pietro
30 Joh, Danny
31
32 TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
33 AND METHODS OF USE
34
35 NUMBER OF SEQUENCES: 105
36 CORRESPONDENCE ADDRESS:
37 ADDRESSEE: Arnold, White & Durkee
38 STREET: P.O. Box 4433
39 CITY: Houston
40 STATE: TX
41 COUNTRY: USA
42 ZIP: 77210-4433
43 COMPUTER READABLE FORM:
44 MEDIUM TYPE: Floppy disk
45 OPERATING SYSTEM: PC-DOS/MS-DOS
46 SOFTWARE: PatentIn Release #1.0, Version #1.30
47 CURRENT APPLICATION DATA:
48 APPLICATION NUMBER: US/10/731,238
49 FILING DATE: 10-Dec-2003
50 CLASSIFICATION: <Unknown>
51 PRIOR APPLICATION DATA:
52 APPLICATION NUMBER: US/09/010,317
53 FILING DATE: 21-Jan-1998
54 APPLICATION NUMBER: US 60/036,139
55 FILING DATE: 21-Jan-1997
56 ATTORNEY/AGENT INFORMATION:
57 NAME: Hibler, David W.
58 REGISTRATION NUMBER: 41,071
59 REFERENCE/DOCKET NUMBER: TAMK:189
60 TELECOMMUNICATION INFORMATION:
61 TELEPHONE: 512-418-3000
62 TELEFAX: 512-474-7577
63 INFORMATION FOR SEQ ID NO: 18:
64 SEQUENCE CHARACTERISTICS:
65 LENGTH: 21 amino acids
66 TYPE: amino acid
67 STRANDEDNESS: <Unknown>
68 TOPOLOGY: linear
69 SEQUENCE DESCRIPTION: SEQ ID NO: 18:
70 US-10-731-238-18
71
72 Query Match 100.0%; Score 51; DB 18; Length 21;
73 Best Local Similarity 100.0%; Pred. No. 0.042;
74 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Best Local Similarity 100.0%; Pred. No. 0.042;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NSVDPEEDTL 10
|||||
Db 10 NSVDPEEDTL 19

RESULT 9

US-10-731-238-19

; Sequence 19, Application US/10731238
; Publication No. US20050123552A1
; GENERAL INFORMATION:

APPLICANT: Hook, Magnus

Pattl, Joseph M.
House-Pompeo, Karen L.

Speziale, Pietro

Joh, Danny

McGavin, Martin J.

TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
AND METHODS OF USE

NUMBER OF SEQUENCES: 105

CORRESPONDENCE ADDRESS:

ADDRESSEE: Arnold, White & Durkee

STREET: P.O. Box 4433

CITY: Houston

STATE: TX

COUNTRY: USA

ZIP: 77210-4433

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/731,238

FILING DATE: 10-Dec-2003

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/010,317

FILING DATE: 21-Jan-1998

APPLICATION NUMBER: US 60/036,139

FILING DATE: 21-JAN-1997

ATTORNEY/AGENT INFORMATION:

NAME: Hibler, David W.

REGISTRATION NUMBER: 41,071

REFERENCE/DOCKET NUMBER: TAMK:189

TELECOMMUNICATION INFORMATION:

TELEPHONE: 512-418-3000

TELEFAX: 512-474-7577

INFORMATION FOR SEQ ID NO: 19:

SEQUENCE CHARACTERISTICS:

LENGTH: 21 amino acids

TYPE: amino acid

STRANDEDNESS: <Unknown>

TOPOLOGY: linear

SEQUENCE DESCRIPTION: SEQ ID NO: 19:

US-10-731-238-19

Query Match 100.0%; Score 51; DB 18; Length 21;

Best Local Similarity 100.0%; Pred. No. 0.042;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NSVDPEEDTL 10

Db 10 NSVDPEEDTL 19

RESULT 10

US-10-731-238-20

; Sequence 20, Application US/10731238
; Publication No. US20050123552A1
; GENERAL INFORMATION:

APPLICANT: Hook, Magnus

Pattl, Joseph M.
House-Pompeo, Karen L.

Speziale, Pietro

Joh, Danny

McGavin, Martin J.

TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
AND METHODS OF USE

NUMBER OF SEQUENCES: 105

CORRESPONDENCE ADDRESS:

ADDRESSEE: Arnold, White & Durkee

STREET: P.O. Box 4433

CITY: Houston

STATE: TX

COUNTRY: USA

ZIP: 77210-4433

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/731,238

FILING DATE: 10-Dec-2003

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/010,317

FILING DATE: 21-Jan-1998

APPLICATION NUMBER: US 60/036,139

FILING DATE: 21-JAN-1997

ATTORNEY/AGENT INFORMATION:

NAME: Hibler, David W.

REGISTRATION NUMBER: 41,071

REFERENCE/DOCKET NUMBER: TAMK:189

TELECOMMUNICATION INFORMATION:

TELEPHONE: 512-418-3000

TELEFAX: 512-474-7577

INFORMATION FOR SEQ ID NO: 20:

SEQUENCE CHARACTERISTICS:

LENGTH: 21 amino acids

TYPE: amino acid

STRANDEDNESS: <Unknown>

TOPOLOGY: linear

SEQUENCE DESCRIPTION: SEQ ID NO: 20:

US-10-731-238-20

Query Match 100.0%; Score 51; DB 18; Length 21;

Best Local Similarity 100.0%; Pred. No. 0.042;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NSVDPEEDTL 10

Db 10 NSVDPEEDTL 19

RESULT 11

US-10-731-238-21

; Sequence 21, Application US/10731238
; Publication No. US20050123552A1
; GENERAL INFORMATION:

APPLICANT: Hook, Magnus

Pattl, Joseph M.
House-Pompeo, Karen L.

Speziale, Pietro

Joh, Danny

McGavin, Martin J.

TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
AND METHODS OF USE

NUMBER OF SEQUENCES: 105

CORRESPONDENCE ADDRESS:

ADDRESSEE: Arnold, White & Durkee

STREET: P.O. Box 4433

CITY: Houston

STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA: US/10/731,238
APPLICATION NUMBER: US/10/731,238
FILING DATE: 10-Dec-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE: 21-Jan-1998
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAMK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 21:
US-10-731-238-21

Query Match 100.0%; Score 51; DB 18; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.042;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NSVDFFEDTL 10
|||
DB 10 NSVDFFEDTL 19

RESULT 12
US-10-731-238-32
Sequence 32, Application US/10731238
Publication No. US20050123552A1
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
Patel, Joseph M.
House-Pompeo, Karen L.
Speziale, Pietro
Job, Danny
McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA: US/10/731,238
APPLICATION NUMBER: US/10/731,238
FILING DATE: 10-Dec-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/010,317
FILING DATE: 21-Jan-1998
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAMK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 32:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 32:
US-10-731-238-32

Query Match 100.0%; Score 51; DB 18; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.042;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NSVDFFEDTL 10
|||
DB 10 NSVDFFEDTL 19

RESULT 13
US-10-731-238-33
Sequence 33, Application US/10731238
Publication No. US20050123552A1
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
Patel, Joseph M.
House-Pompeo, Karen L.
Speziale, Pietro
Job, Danny
McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA: US/10/731,238
APPLICATION NUMBER: US/10/731,238
FILING DATE: 10-Dec-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE: 21-Jan-1998
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAMK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:

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;          LENGTH: 21 amino acids
;          TYPE: amino acid
;          STRANDEDNESS: <Unknown>
;          TOPOLOGY: linear
;          SEQUENCE DESCRIPTION: SEQ ID NO: 33
US-10-731-238-33

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Query Match	100.0%;	Score 51;	DB 18;	Length 21;
Best Local Similarity	100.0%;	Pred. No. 0.042;		
Matches 10;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

RESULT 14
US-10-731-238-34
; Sequence 34, Application US/10731238
; Publication No. US20050123552A1
; GENERAL INFORMATION:
; APPLICANT: Mitsubishi Electric Corporation
; INVENTOR: Mitsubishi Electric Corporation
; ATTORNEY: Mitsubishi Electric Corporation

TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433

TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 34
US-10-731-238-34

Db 10 NSVDFEEDTL 19

RESULT 15
US-10-731-238-13
; Sequence 13, Application US/10731238
; Publication No. US20050123552A1
; GENERAL INFORMATION:
; APPLICANT: Hook, Magnus
; Inventor: Hook, Magnus
; Attorney: Hook, Magnus

TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/731,238

Query Match	100.0%	Score 51	DB 18	Length 22
Best Local Similarity	100.0%	Pred. No. 0.045		
Matches 10	Conservative 0	Mismatches 0	Indels 0	Gaps 0

Search completed: October 22, 2005, 12:56:30
Job time : 57.1494 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 22, 2005, 07:41:53 ; Search time 17.2989 Seconds
(without alignments)
43.153 Million cell updates/sec

Title: US-10-731-238-100
Sequence: 1 NSVDFEDTL 10

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database: Issued Patents AA:
1: /cgn2_6/prodata/1/aa/5A COMB.pep.*
2: /cgn2_6/prodata/1/aa/5B COMB.pep.*
3: /cgn2_6/prodata/1/aa/6A COMB.pep.*
4: /cgn2_6/prodata/1/aa/6B COMB.pep.*
5: /cgn2_6/prodata/1/aa/PCITUS COMB.pep.*
6: /cgn2_6/prodata/1/aa/backfile1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	51	100.0	10	4	US-09-010-317-100
2	51	100.0	21	4	US-09-010-317-9
3	51	100.0	21	4	US-09-010-317-10
4	51	100.0	21	4	US-09-010-317-14
5	51	100.0	21	4	US-09-010-317-15
6	51	100.0	21	4	US-09-010-317-16
7	51	100.0	21	4	US-09-010-317-17
8	51	100.0	21	4	US-09-010-317-18
9	51	100.0	21	4	US-09-010-317-19
10	51	100.0	21	4	US-09-010-317-20
11	51	100.0	21	4	US-09-010-317-21
12	51	100.0	21	4	US-09-010-317-32
13	51	100.0	21	4	US-09-010-317-33
14	51	100.0	21	4	US-09-010-317-34
15	51	100.0	22	4	US-09-010-317-13
16	51	100.0	37	1	US-08-234-622A-4
17	51	100.0	38	1	US-08-234-189-8
18	51	100.0	38	1	US-08-729-767-5
19	51	100.0	114	1	US-08-259-000-3
20	51	100.0	130	2	US-08-459-135A-7
21	51	100.0	130	2	US-08-459-135A-8
22	51	100.0	130	3	US-08-495-559-7
23	51	100.0	130	3	US-08-495-559-8
24	51	100.0	139	3	US-08-856-253-8
25	51	100.0	174	2	US-08-459-135A-10
26	51	100.0	174	2	US-08-459-135A-13
27	51	100.0	174	3	US-08-495-559-10

28	51	100.0	174	3	US-08-495-559-13	Sequence 13, Appl
29	51	100.0	176	3	US-08-495-559-6	Sequence 6, Appl
30	51	100.0	178	2	US-08-459-135A-12	Sequence 12, Appl
31	51	100.0	178	3	US-08-495-559-12	Sequence 12, Appl
32	51	100.0	181	2	US-08-459-135A-6	Sequence 6, Appl
33	51	100.0	559	4	US-08-956-171E-5251	Sequence 5251, Ap
34	51	100.0	559	4	US-08-781-986A-5251	Sequence 5251, Ap
35	51	100.0	1027	4	US-08-956-171E-5254	Sequence 5254, Ap
36	51	100.0	1027	4	US-08-781-986A-5254	Sequence 5254, Ap
37	47	92.2	19	4	US-09-010-317-61	Sequence 61, Appl
38	47	92.2	14	4	US-08-234-622A-1	Sequence 1, Appl
39	47	92.2	21	4	US-09-010-317-31	Sequence 31, Appl
40	46	90.2	21	4	US-09-010-317-23	Sequence 23, Appl
41	45	88.2	21	4	US-09-010-317-22	Sequence 22, Appl
42	45	88.2	21	4	US-09-010-317-24	Sequence 24, Appl
43	45	88.2	21	4	US-09-010-317-27	Sequence 27, Appl
44	45	88.2	21	4	US-09-010-317-28	Sequence 28, Appl
45	45	88.2	21	4	US-09-010-317-30	Sequence 30, Appl

ALIGNMENTS

RESULT 1
US-09-010-317-100
Sequence 100, Application US/09010317
Patent No. 6685943
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
APPLICANT: Patti, Joseph M.
APPLICANT: House-Pompeo, Karen L.
APPLICANT: Speziale, Pietro
APPLICANT: Joh, Danny
APPLICANT: McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
TITLE OF INVENTION: AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Releasee #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAMK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 100:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-09-010-317-100
Query Match 100.0%; Score 51; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0037;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NSVDFFEDTL 10
|||||

Db 1 NSVDFFEDTL 10

RESULT 2
US-09-010-317-9
Sequence 9, Application US/09010317

Patent No. 6685943

GENERAL INFORMATION:

APPLICANT: Hook, Magnus

APPLICANT: Patti, Joseph M.

APPLICANT: House-Pompeo, Karen L.

APPLICANT: Speziale, Pietro

APPLICANT: McGavin, Martin J.

TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS

TITLE OF INVENTION: AND METHODS OF USE

NUMBER OF SEQUENCES: 105

CORRESPONDENCE ADDRESS:

ADDRESSEE: Arnold, White & Durkee

STREET: P.O. Box 4433

CITY: Houston

STATE: TX

COUNTRY: USA

ZIP: 77210-4433

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Releasee #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/010,317

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 60/036,139

FILING DATE: 21-JAN-1997

ATTORNEY/AGENT INFORMATION:

NAME: Hblber, David W.

REGISTRATION NUMBER: 41,071

REFERENCE/DOCKET NUMBER: TANK:189

TELECOMMUNICATION INFORMATION:

TELEPHONE: 512-418-3000

TELEFAX: 512-474-7577

INFORMATION FOR SEQ ID NO: 9:

SEQUENCE CHARACTERISTICS:

LENGTH: 21 amino acids

TYPE: amino acid

STRANDEDNESS:

TOPOLOGY: linear

US-09-010-317-9

Query Match 100.0%; Score 51; DB 4; Length 21;

Best Local Similarity 100.0%; Pred. No. 0.0082;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NSVDFFEDTL 10
|||||

Db 10 NSVDFFEDTL 19

RESULT 3

US-09-010-317-10

Sequence 10, Application US/09010317

Patent No. 6685943

GENERAL INFORMATION:

APPLICANT: Hook, Magnus

APPLICANT: Patti, Joseph M.

APPLICANT: House-Pompeo, Karen L.

APPLICANT: Speziale, Pietro

APPLICANT: McGavin, Martin J.

TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS

TITLE OF INVENTION: AND METHODS OF USE

NUMBER OF SEQUENCES: 105

CORRESPONDENCE ADDRESS:

ADDRESSEE: Arnold, White & Durkee

STREET: P.O. Box 4433

CITY: Houston

STATE: TX

COUNTRY: USA

ZIP: 77210-4433

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

APPLICANT: Joh, Danny

APPLICANT: McGavin, Martin J.

TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS

TITLE OF INVENTION: AND METHODS OF USE

NUMBER OF SEQUENCES: 105

CORRESPONDENCE ADDRESS:

ADDRESSEE: Arnold, White & Durkee

STREET: P.O. Box 4433

CITY: Houston

STATE: TX

COUNTRY: USA

ZIP: 77210-4433

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Releasee #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/010,317

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 60/036,139

FILING DATE: 21-JAN-1997

ATTORNEY/AGENT INFORMATION:

NAME: Hblber, David W.

REGISTRATION NUMBER: 41,071

REFERENCE/DOCKET NUMBER: TANK:189

TELECOMMUNICATION INFORMATION:

TELEPHONE: 512-418-3000

TELEFAX: 512-474-7577

INFORMATION FOR SEQ ID NO: 10:

SEQUENCE CHARACTERISTICS:

LENGTH: 21 amino acids

TYPE: amino acid

STRANDEDNESS:

TOPOLOGY: linear

US-09-010-317-10

Query Match 100.0%; Score 51; DB 4; Length 21;

Best Local Similarity 100.0%; Pred. No. 0.0082;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NSVDFFEDTL 10
|||||

Db 10 NSVDFFEDTL 19

RESULT 4

US-09-010-317-14

Sequence 14, Application US/09010317

Patent No. 6685943

GENERAL INFORMATION:

APPLICANT: Hook, Magnus

APPLICANT: Patti, Joseph M.

APPLICANT: House-Pompeo, Karen L.

APPLICANT: Speziale, Pietro

APPLICANT: Joh, Danny

APPLICANT: McGavin, Martin J.

TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS

TITLE OF INVENTION: AND METHODS OF USE

NUMBER OF SEQUENCES: 105

CORRESPONDENCE ADDRESS:

ADDRESSEE: Arnold, White & Durkee

STREET: P.O. Box 4433

CITY: Houston

STATE: TX

COUNTRY: USA

ZIP: 77210-4433

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TANK:189
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-09-010-317-14

Query Match 100.0%; Score 51; DB 4; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.0082;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NSVDPEEDTL 10
DB 10 NSVDPEEDTL 19

RESULT 5
US-09-010-317-15
Sequence 15, Application US/09010317
Patent No. 6685943
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
APPLICANT: Patti, Joseph M.
APPLICANT: House-Pompeo, Karen L.
APPLICANT: Speziale, Pietro
APPLICANT: John, Danny
APPLICANT: McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
TITLE OF INVENTION: AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TANK:189
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 15:

SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-09-010-317-15

Query Match 100.0%; Score 51; DB 4; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.0082;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NSVDPEEDTL 10
DB 10 NSVDPEEDTL 19

RESULT 6
US-09-010-317-16
Sequence 16, Application US/09010317
Patent No. 6685943
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
APPLICANT: Patti, Joseph M.
APPLICANT: House-Pompeo, Karen L.
APPLICANT: Speziale, Pietro
APPLICANT: John, Danny
APPLICANT: McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
TITLE OF INVENTION: AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TANK:189
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-09-010-317-16

Query Match 100.0%; Score 51; DB 4; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.0082;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NSVDPEEDTL 10
DB 10 NSVDPEEDTL 19

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RESULT 7
US-09-010-317-17
: Sequence 17, Application US/09010317
: Patent No. 6685943
: GENERAL INFORMATION:
: APPLICANT: Hook, Magnus
: APPLICANT: Patti, Joseph M.
: APPLICANT: House-Pompeo, Karen L.
: APPLICANT: Speciale, Pietro
: APPLICANT: Joh, Danny
: APPLICANT: McGavin, Martin J.
: TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
: NUMBER OF SEQUENCES: 105
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Arnold, White & Durkee
: STREET: P.O. Box 4433
: CITY: Houston
: STATE: TX
: COUNTRY: USA
: ZIP: 77210-4433
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/010.317
: FILING DATE:
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 60/036.139
: FILING DATE: 21-JAN-1997
: ATTORNEY/AGENT INFORMATION:
: NAME: Hibler, David W.
: REGISTRATION NUMBER: 41,071
: REFERENCE/DOCKET NUMBER: TAMK:189
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 512-474-7577
: TELEFAX: 512-474-3000
: INFORMATION FOR SEQ ID NO: 17:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 21 amino acids
: TYPE: amino acid
: STRANDEDNESS:
: TOPOLOGY: linear
US-09-010-317-17

Query Match      100.0%; Score 51; DB 4; Length 21;
Beet Local Similarity 100.0%; Pred. No. 0.0082;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 NSVDFFEDTL 10
       |||||
Db      10 NSVDFFEDTL 19

RESULT 8
US-09-010-317-18
: Sequence 18, Application US/09010317
: Patent No. 6685943
: GENERAL INFORMATION:
: APPLICANT: Hook, Magnus
: APPLICANT: Patti, Joseph M.
: APPLICANT: House-Pompeo, Karen L.
: APPLICANT: Speciale, Pietro
: APPLICANT: Joh, Danny
: APPLICANT: McGavin, Martin J.
: TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
: NUMBER OF SEQUENCES: 105
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Arnold, White & Durkee

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: STREET: P.O. Box 4433
: CITY: Houston
: STATE: TX
: COUNTRY: USA
: ZIP: 77210-4433
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/010.317
: FILING DATE:
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 60/036.139
: FILING DATE: 21-JAN-1997
: ATTORNEY/AGENT INFORMATION:
: NAME: Hibler, David W.
: REGISTRATION NUMBER: 41,071
: REFERENCE/DOCKET NUMBER: TAMK.189
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 512-418-3000
: TELEFAX: 512-474-7577
: INFORMATION FOR SEQ ID NO: 18:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 21 amino acids
: TYPE: amino acid
: STRANDEDNESS:
: TOPOLOGY: linear
: US-09-010-317-18
:
: Query Match 100.0%; Score 51; DB 4; Length 21;
: Best Local Similarity 100.0%; Pred. No. 0.0082;
: Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
:
: QY 1 NSVDPEEDTL 10
: ||||||||
: Db 10 NSVDPEEDTL 19
:
: RESULT 9
: US-09-010-317-19
: Sequence 19, Application US/09010317
: Patent No. 6685943
: GENERAL INFORMATION:
: APPLICANT: Hook, Magnus
: APPLICANT: Patti, Joseph M.
: APPLICANT: House-Pompeo, Karen L.
: APPLICANT: Speziale, Pietro
: APPLICANT: John, Danny
: APPLICANT: McGavin, Martin J.
: TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
: NUMBER OF SEQUENCES: 105
: CORRESPONDENCE ADDRESS:
: ADDRESSES: Arnold, White & Durkee
: STREET: P.O. Box 4433
: CITY: Houston
: STATE: TX
: COUNTRY: USA
: ZIP: 77210-4433
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/010.317
: FILING DATE:
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 60/036.139

```

FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAMK:189
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-09-010-317-19

Query Match 100.0%; Score 51; DB 4; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.0082;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NSVDPEEDTL 10
Db 10 NSVDPEEDTL 19

RESULT 10
US-09-010-317-20
Sequence 20, Application US/09010317
Patent No. 6685943
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
APPLICANT: Patti, Joseph M.
APPLICANT: House-Pompeo, Karen L.
APPLICANT: Speziale, Pietro
APPLICANT: Jon, Danny
APPLICANT: McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
TITLE OF INVENTION: AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAMK:189
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-09-010-317-20

Query Match 100.0%; Score 51; DB 4; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.0082;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NSVDPEEDTL 10
Db 10 NSVDPEEDTL 19

RESULT 11
US-09-010-317-21
Sequence 21, Application US/09010317
Patent No. 6685943
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
APPLICANT: Patti, Joseph M.
APPLICANT: House-Pompeo, Karen L.
APPLICANT: Speziale, Pietro
APPLICANT: Jon, Danny
APPLICANT: McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
TITLE OF INVENTION: AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAMK:189
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-09-010-317-21

Query Match 100.0%; Score 51; DB 4; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.0082;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NSVDPEEDTL 10
Db 10 NSVDPEEDTL 19

RESULT 12
US-09-010-317-32
Sequence 32, Application US/09010317
Patent No. 6685943
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
APPLICANT: Patti, Joseph M.

APPLICANT: House-Pompeo, Karen L.
APPLICANT: Speziale, Pietro
APPLICANT: John, Danny
APPLICANT: McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
TITLE OF INVENTION: AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TANK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 32:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-09-010-317-32

Query Match 100.0%; Score 51; DB 4; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.0082;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NSVDFEEDTL 10
Db 10 NSVDFEEDTL 19

RESULT 13
US-09-010-317-33
Sequence 33, Application US/09010317
Patent No. 6685943
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
APPLICANT: Patti, Joseph M.
APPLICANT: House-Pompeo, Karen L.
APPLICANT: Speziale, Pietro
APPLICANT: John, Danny
APPLICANT: McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
TITLE OF INVENTION: AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TANK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-09-010-317-33

Query Match 100.0%; Score 51; DB 4; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.0082;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NSVDFEEDTL 10
Db 10 NSVDFEEDTL 19

RESULT 14
US-09-010-317-34
Sequence 34, Application US/09010317
Patent No. 6685943
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
APPLICANT: Patti, Joseph M.
APPLICANT: House-Pompeo, Karen L.
APPLICANT: Speziale, Pietro
APPLICANT: John, Danny
APPLICANT: McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
TITLE OF INVENTION: AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TANK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000

Search completed: October 22, 2005, 09:35:47
Job time : 18.2989 secs

TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 34:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-09-010-317-34

Query Match 100.0%; Score 51; DB 4; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.0082;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NSVDPEEDTL 10
|||
10 NSVDPEEDTL 19

RESULT 15

US-09-010-317-13
Sequence 13, Application US/09010317
Patent No. 6685943
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
APPLICANT: Patti, Joseph M.
APPLICANT: House-Pompeo, Karen L.
APPLICANT: Speziale, Pietro
APPLICANT: Joh, Danny
APPLICANT: Mcgavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
TITLE OF INVENTION: AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAMK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 22 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-09-010-317-13

Query Match 100.0%; Score 51; DB 4; Length 22;
Best Local Similarity 100.0%; Pred. No. 0.0086;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NSVDPEEDTL 10
|||
10 NSVDPEEDTL 19

Db

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GenCore version 5.1.6
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OM protein - protein search, using bw model

Run on: October 22, 2005, 07:41:53 ; Search time 17.2989 Seconds
(without alignments)
43.153 Million cell updates/sec

Title: US-10-731-238-102

Sequence: 1 DFEEDTPKLV 10L

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Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
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2: /cgn2_6/prodata/1/aa/5B.COMB.pep:*
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6: /cgn2_6/prodata/1/aa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	53	100.0	40	US-09-010-317-102	Sequence 102, App
2	53	100.0	11	US-09-010-317-86	Sequence 86, Appl
3	53	100.0	22	US-09-010-317-13	Sequence 13, Appl
4	53	100.0	37	US-08-234-622A-4	Sequence 4, Appl
5	53	100.0	38	US-08-234-189-8	Sequence 8, Appl
6	53	100.0	38	US-08-729-767-5	Sequence 5, Appl
7	53	100.0	114	US-08-259-000-3	Sequence 3, Appl
8	53	100.0	139	US-08-856-253-8	Sequence 8, Appl
9	53	100.0	178	US-08-459-135A-12	Sequence 12, Appl
10	53	100.0	1027	US-08-956-171E-5254	Sequence 5254, Ap
11	53	100.0	1027	US-08-781-986A-5254	Sequence 5254, Ap
12	53	100.0	1027	US-08-010-317-101	Sequence 101, App
13	49	92.5	21	US-09-010-317-9	Sequence 9, Appl
14	49	92.5	21	US-09-010-317-10	Sequence 10, Appl
15	49	92.5	21	US-09-010-317-14	Sequence 14, Appl
16	49	92.5	21	US-09-010-317-15	Sequence 15, Appl
17	49	92.5	21	US-09-010-317-16	Sequence 16, Appl
18	49	92.5	21	US-09-010-317-17	Sequence 17, Appl
19	49	92.5	21	US-09-010-317-18	Sequence 18, Appl
20	49	92.5	21	US-09-010-317-19	Sequence 19, Appl
21	49	92.5	21	US-09-010-317-20	Sequence 20, Appl
22	49	92.5	21	US-09-010-317-21	Sequence 21, Appl
23	49	92.5	21	US-09-010-317-22	Sequence 22, Appl
24	49	92.5	21	US-09-010-317-23	Sequence 23, Appl
25	49	92.5	21	US-09-010-317-24	Sequence 24, Appl
26	49	92.5	21	US-09-010-317-24	Sequence 24, Appl
27	49	92.5	21	US-09-010-317-34	Sequence 34, Appl

28	49	92.5	130	2	US-08-459-135A-7	Sequence 7, Appl
29	49	92.5	130	2	US-08-459-135A-8	Sequence 8, Appl
30	49	92.5	130	3	US-08-495-559-7	Sequence 7, Appl
31	49	92.5	130	3	US-08-495-559-8	Sequence 8, Appl
32	49	92.5	174	2	US-08-459-135A-10	Sequence 10, Appl
33	49	92.5	174	2	US-08-459-135A-13	Sequence 13, Appl
34	49	92.5	174	3	US-08-495-559-10	Sequence 10, Appl
35	49	92.5	174	3	US-08-495-559-13	Sequence 13, Appl
36	49	92.5	176	3	US-08-495-559-6	Sequence 6, Appl
37	49	92.5	181	2	US-08-459-135A-6	Sequence 6, Appl
38	49	92.5	559	4	US-08-956-171E-5251	Sequence 5251, Ap
39	49	92.5	559	4	US-08-781-986A-5251	Sequence 5251, Ap
40	44	83.0	21	4	US-09-010-317-33	Sequence 33, Appl
41	44	81.1	21	4	US-09-010-317-25	Sequence 25, Appl
42	43	81.1	21	4	US-09-010-317-27	Sequence 27, Appl
43	43	81.1	21	4	US-09-010-317-28	Sequence 28, Appl
44	43	81.1	21	4	US-09-010-317-30	Sequence 30, Appl
45	42	79.2	21	4	US-09-010-317-29	Sequence 29, Appl

ALIGNMENTS

RESULT 1
US-09-010-317-102
Sequence 102, Application US/09010317
Patent No. 6685943
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
APPLICANT: Patti, Joseph M.
APPLICANT: House-Pompeo, Karen L.
APPLICANT: Speziale, Pietro
APPLICANT: John, Danny
APPLICANT: McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
TITLE OF INVENTION: AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESSES:
ADDRESSER: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAMK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 102:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-09-010-317-102
Query Match 100.0%; Score 53; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.001;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DFEEDTLPRV 10
| | | | | | | | | |
Db 1 DFEEDTLPRV 10

RESULT 2
US-09-010-317-86
; Sequence 86, Application US/09010317
; Patent No. 6685943
; GENERAL INFORMATION:
; APPLICANT: Hook, Magnus
; APPLICANT: Patti, Joseph M.
; APPLICANT: House-Pompeo, Karen L.
; APPLICANT: Speziale, Pietro
; APPLICANT: McGavin, Martin J.
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
; TITLE OF INVENTION: AND METHODS OF USE
; NUMBER OF SEQUENCES: 105
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: TX
; COUNTRY: USA
; ZIP: 77210-4433
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/010,317
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/036,139
; FILING DATE: 21-JAN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Hibler, David W.
; REGISTRATION NUMBER: 41,071
; REFERENCE/DOCKET NUMBER: TANK:189
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 512-418-3000
; TELEFAX: 512-474-7577
; INFORMATION FOR SEQ ID NO: 86:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
US-09-010-317-86

Query Match 100.0%; Score 53; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.0011;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DFEEDTLPRV 10
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Db 2 DFEEDTLPRV 11

RESULT 3
US-09-010-317-13
; Sequence 13, Application US/09010317
; Patent No. 6685943
; GENERAL INFORMATION:
; APPLICANT: Hook, Magnus
; APPLICANT: Patti, Joseph M.
; APPLICANT: House-Pompeo, Karen L.
; APPLICANT: Speziale, Pietro

APPLICANT: Joh, Danny
APPLICANT: McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
TITLE OF INVENTION: AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TANK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 22 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-09-010-317-13

Query Match 100.0%; Score 53; DB 4; Length 22;
Best Local Similarity 100.0%; Pred. No. 0.0024;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DFEEDTLPRV 10
| | | | | | | | | |
Db 13 DFEEDTLPRV 22

RESULT 4
US-08-234-622A-4
; Sequence 4, Application US/08234622A
; Patent No. 5460014
; GENERAL INFORMATION:
; APPLICANT: HOOK, Magnus
; APPLICANT: MCGAVIN, Martin
; APPLICANT: RAUCCI, Giuseppe
; TITLE OF INVENTION: A FIBRONECTIN BINDING PEPTIDE
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Doane, Swecker & Mathis
; STREET: P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22113-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/234,622A
; FILING DATE: 28-APR-1994

CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: SE 9002617-0
FILING DATE: 10-AUG-1990
PRIOR APPLICATION DATA: WO PCT/SE91/00534
APPLICATION NUMBER: WO PCT/SE91/00534
FILING DATE: 09-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: Meuch, Donna M
REGISTRATION NUMBER: 36,607
REFERENCE/DOCKET NUMBER: 012885-044
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 37 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-234-622A-4

Query Match 100.0%; Score 53; DB 1; Length 37;
Best Local Similarity 100.0%; Pred. No. 0.0042;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DFEEDTLPKV 10
DB 28 DFEEDTLPKV 37

RESULT 5
US-08-294-189-8
Sequence 8, Application US/08294189
Patent No. 5707822
GENERAL INFORMATION:
APPLICANT: Fischetti, Vincent A.
APPLICANT: Rakonjac, Jasna
APPLICANT: Robbins, John
TITLE OF INVENTION: GENE SERUM OPACITY FACTOR
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack Avenue
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/294,189
FILING DATE: 22-AUG-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-118
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 487-5800
TELEFAX: 201 343-1684
TELEX: 133521
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: peptide

ORIGINAL SOURCE:
ORGANISM: Streptococcus pyogenes
STRAIN: D734
INDIVIDUAL ISOLATE: 22
IMMEDIATE SOURCE:
CLONE: 8AU3a
US-08-294-189-8

Query Match 100.0%; Score 53; DB 1; Length 38;
Best Local Similarity 100.0%; Pred. No. 0.0043;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DFEEDTLPKV 10
DB 22 DFEEDTLPKV 31

RESULT 6
US-08-729-767-5
Sequence 5, Application US/08729767
Patent No. 5770702
GENERAL INFORMATION:
APPLICANT: HOOK, Magnus
APPLICANT: LINDBERG, Martin Kjell
APPLICANT: SIGNAS, Lars Christer
APPLICANT: WADSTROM, Torkel Mikael
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN AS WELL AS
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Burns, Doane, Swecker & Machis, L.L.P.
STREET: P.O. Box 1404
CITY: Alexandria
STATE: Virginia
COUNTRY: United States
ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/729,767
FILING DATE: 07-OCT-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/259,000
FILING DATE: 13-JUN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/007,817
FILING DATE: 22-JAN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/201,028
FILING DATE: 01-JUN-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: SE 8702272-9
FILING DATE: 01-JUN-1987
ATTORNEY/AGENT INFORMATION:
NAME: McGowan, Malcolm K.
REGISTRATION NUMBER: 39,300
REFERENCE/DOCKET NUMBER: 012889-036
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-729-767-5

Query Match 100.0%; Score 53; DB 1; Length 38;
Best Local Similarity 100.0%; Pred. No. 0.0043;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 DFEEDTLPRV 10
DB 29 DFEEDTLPRV 38

RESULT 7
US-08-259-000-3
; Sequence 3, Application US/08259000
; Patent No. 5571514
; GENERAL INFORMATION:
; APPLICANT: HOOK, Magnus
; APPLICANT: LINDBERG, Martin Kjell
; APPLICANT: SIGNAS, Lars Christer
; APPLICANT: MADSTROM, Torkel Mikael
; APPLICANT: FROMAN, Gunnar
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN AS WELL AS
; TITLE OF INVENTION: ITS PREPARATION
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Doane, Swecker & Mathis
; STREET: P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Releasee #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/259,000
; FILING DATE: 13-JUN-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: SE 8702272-9
; FILING DATE: 01-JUN-1987
; ATTORNEY/AGENT INFORMATION:
; NAME: Meuth, Donna M
; REGISTRATION NUMBER: 36,607
; REFERENCE/DOCKET NUMBER: 012885-062
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ. ID NO. 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 114 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-259-000-3

Query Match 100.0%; Score 53; DB 1; Length 114;
Best Local Similarity 100.0%; Pred. No. 0.014;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 DFEEDTLPRV 10
DB 105 DFEEDTLPRV 114

RESULT 8
US-08-856-253-8
; Sequence 8, Application US/08856253
; Patent No. 6288214
; GENERAL INFORMATION:
; APPLICANT: Hook, Magnus

; APPLICANT: Patti, Joseph M.
; APPLICANT: House-Pompeo, Karen
; APPLICANT: Schanem, Narayana
; APPLICANT: Symersky, Jindrich
; TITLE OF INVENTION: COLLAGEN BINDING PROTEIN COMPOSITIONS
; TITLE OF INVENTION: AND METHODS OF USE
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: U.S.
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Releasee #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/856,253
; FILING DATE: Concurrently Herewith
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/017,678
; FILING DATE: 16-MAY-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Kitchell, Barbara S.
; REGISTRATION NUMBER: 33,928
; REFERENCE/DOCKET NUMBER: TANK:193
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (512) 418-3000
; TELEFAX: (512) 474-7577
; INFORMATION FOR SEQ. ID NO. 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 139 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
US-08-856-253-8

Query Match 100.0%; Score 53; DB 3; Length 139;
Best Local Similarity 100.0%; Pred. No. 0.017;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 DFEEDTLPRV 10
DB 119 DFEEDTLPRV 128

RESULT 9
US-08-459-135A-12
; Sequence 12, Application US/08459135A
; Patent No. 5955078
; GENERAL INFORMATION:
; APPLICANT: BURNHAM, Martin Karl Russel
; APPLICANT: CHOPRA, Ian
; APPLICANT: CRITCHLEY, Ian Alfred
; APPLICANT: KNOWLES, David Justin Charles
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN: MONOCLONAL ANTIBODY AND THEIR US
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corporation
; STREET: 709 Swedeland Road
; CITY: King of Prussia
; STATE: PA
; COUNTRY: U.S.A.
; ZIP: 19406-0939
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: Fastseq, Version 2.0

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;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/459,135A
;; FILING DATE: 02-JUN-1995
;; CLASSIFICATION: 435
;; PRIORITY APPLICATION DATA: PCT/GB/94/00215
;; APPLICATION NUMBER: 435
;; FILING DATE: 04-Feb-1994
;; CLASSIFICATION: 435
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Gimm, Edward R
;; REGISTRATION NUMBER: 38,891
;; REFERENCE/DOCKET NUMBER: P30591C2
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 610-270-4478
;; TELEFAX: 610-270-5090
;; TELEX:
;; INFORMATION FOR SEQ ID NO: 12:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 178 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: Protein
;; US-08-459-135A-12

Query Match 100.0%; Score 53; DB 2; Length 178;
Best Local Similarity 100.0%; Pred. No. 0.023;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DFEEDTLPKV 10
Db 105 DFEEDTLPKV 114

RESULT 10
US-08-495-559-12
; Sequence 12, Application US/08495559A
; Patent No. 6054572
; GENERAL INFORMATION:
; APPLICANT: BURHAM, Martin Karl Russel
; APPLICANT: CHOPRA, Ian
; APPLICANT: CRITCHLEY, Ian Alfred
; APPLICANT: KNOWLES, David Justin Charles
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN: MONOCLONAL
; TITLE OF INVENTION: ANTIBODY AND THEIR USE IN PREVENTING BACTERIAL ADHESION
; FILE REFERENCE: P30591
; CURRENT APPLICATION NUMBER: US/08/495,559A
; CURRENT FILING DATE: 1995-08-03
; EARLIER APPLICATION NUMBER: GB 9302289.5
; EARLIER FILING DATE: 1993-02-05
; EARLIER APPLICATION NUMBER: GB 9321592.9
; EARLIER FILING DATE: 1993-10-20
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 12
; LENGTH: 178
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
; US-08-495-559-12

Query Match 100.0%; Score 53; DB 3; Length 178;
Best Local Similarity 100.0%; Pred. No. 0.023;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DFEEDTLPKV 10
Db 105 DFEEDTLPKV 114

RESULT 11
US-08-956-171E-5254
; Sequence 5254, Application US/08956171E
; Patent No. 6593114

;;
;; GENERAL INFORMATION:
;; APPLICANT: Charles Kunsch
;; Gil H. Choi
;; Patrick S. Dillon
;; Craig A. Rosen
;; Steven C. Barash
;; Michael R. Fannon
;; TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
;; NUMBER OF SEQUENCES: 5256
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Human Genome Sciences, Inc.
;; STREET: 9410 Key West Avenue
;; CITY: Rockville
;; STATE: Maryland
;; COUNTRY: USA
;; ZIP: 20850
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Diskette, 3.50 inch, 1.4MB storage
;; OPERATING SYSTEM: MSDOS version 6.2
;; SOFTWARE: ASCII Text
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/956,171E
;; FILING DATE: 20-Oct-1997
;; CLASSIFICATION: <Unknown>
;; PRIORITY APPLICATION DATA:
;; APPLICATION NUMBER: 60/009,861
;; FILING DATE: January 5, 1996
;; APPLICATION NUMBER: 08/781,986
;; FILING DATE: January 3, 1997
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Mark J. Hyman
;; REGISTRATION NUMBER: 46,789
;; REFERENCE/DOCKET NUMBER: PB248P1
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (240) 314-1224
;; TELEFAX: (301) 309-8439
;; INFORMATION FOR SEQ ID NO: 5254:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 1027 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; SEQUENCE DESCRIPTION: SEQ ID NO: 5254:
;; US-08-956-171E-5254

Query Match 100.0%; Score 53; DB 4; Length 1027;
Best Local Similarity 100.0%; Pred. No. 0.15;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DFEEDTLPKV 10
Db 858 DFEEDTLPKV 867

RESULT 12
US-08-781-986A-5254
; Sequence 5254, Application US/08781986A
; Patent No. 6737248
; GENERAL INFORMATION:
; APPLICANT: Charles Kunsch
; TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
; NUMBER OF SEQUENCES: 5255
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4MB storage

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COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/781,986A
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Benson, Bob
REGISTRATION NUMBER: 30,446
REFERENCE/DOCKET NUMBER: PB248PP
TELEPHONE: (301) 309-8504
TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 5254:
SEQUENCE CHARACTERISTICS:
LENGTH: 1027 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-781-986A-5254

Query Match          100.0%; Score 53; DB 4; Length 1027;
Best Local Similarity 100.0%; Pred. No. 0.15;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 DFEEDTLPKV 10
Db      858 DFEEDTLPKV 867

RESULT 13
US-09-010-317-101
Sequence 101, Application US/09010317
Patent No. 6685943
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
APPLICANT: Patti, Joseph M.
APPLICANT: House-Pompeo, Karen L.
APPLICANT: Speziale, Pietro
APPLICANT: Joh, Danny
APPLICANT: McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSER: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAMK:189
TELECOMMUNICATION INFORMATION:
```

```
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 101:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-09-010-317-101

Query Match          92.5%; Score 49; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0057;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 DFEEDTLPK 9
Db      2 DFEEDTLPK 10

RESULT 14
US-09-010-317-9
Sequence 9, Application US/09010317
Patent No. 6685943
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
APPLICANT: Patti, Joseph M.
APPLICANT: House-Pompeo, Karen L.
APPLICANT: Speziale, Pietro
APPLICANT: Joh, Danny
APPLICANT: McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSER: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAMK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-09-010-317-9

Query Match          92.5%; Score 49; DB 4; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.013;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 DFEEDTLPK 9
Db      1 DFEEDTLPK 9
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Db 13 DFEBDTLPK 21

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RESULT 15
US-09-010-317-10
; Sequence 10, Application US/09010317
; Patent No. 6685943
; GENERAL INFORMATION:
; APPLICANT: Hook, Magnus
; APPLICANT: Patti, Joseph M.
; APPLICANT: House-Pompeo, Karen L.
; APPLICANT: Speziale, Pietro
; APPLICANT: Joh, Danny
; APPLICANT: McGavin, Martin J.
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
; TITLE OF INVENTION: AND METHODS OF USE
; NUMBER OF SEQUENCES: 105
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: TX
; COUNTRY: USA
; ZIP: 77210-4433
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/010,317
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/036,139
; FILING DATE: 21-JAN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Hibler, David W.
; REGISTRATION NUMBER: 41,071
; REFERENCE/DOCKET NUMBER: TAMK:189
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 512-418-3000
; TELEFAX: 512-474-7577
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; US-09-010-317-10

Query Match 92.5%; Score 49; DB 4; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.013;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 DFEBDTLPK 9
| | | | |
| | | | |
Db 13 DFEBDTLPK 21

Search completed: October 22, 2005, 09:35:47
Job time : 17.2989 secs

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GenCore version 5.1.6
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OM protein - protein search, using BW model

Run on: October 22, 2005, 12:39:57 : Search time 56.1494 Seconds
(without alignments)
74.354 Million cell updates/sec

Title: US-10-731-238-102

Perfect score: 53

Sequence: 1 DFEEDTLPRV 10

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 1862951 seqs, 417491010 residues

Total number of hits satisfying chosen parameters: 1862951

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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3: /cgnt_6/prodata/2/pubppa/US06_NEW_PUB.pep.*
4: /cgnt_6/prodata/2/pubppa/US07_PUBCOMB.pep.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	53	100.0	10	US-10-731-238-102	Sequence 102, App
2	53	100.0	11	US-10-731-238-86	Sequence 86, App
3	53	100.0	22	US-10-731-238-13	Sequence 13, App
4	53	100.0	37	US-11-066-697-1134	Sequence 1134, App
5	53	100.0	139	US-09-813-820-8	Sequence 8, App
6	53	100.0	961	US-10-282-122A-43778	Sequence 43778, A
7	53	100.0	978	US-09-815-242-5456	Sequence 5456, App
8	53	100.0	1001	US-09-815-242-12686	Sequence 12686, A
9	53	100.0	1018	US-09-815-242-5797	Sequence 5797, App
10	53	100.0	1018	US-09-815-242-12838	Sequence 12838, A
11	53	100.0	1018	US-10-470-0488-68	Sequence 68, App

12	53	100.0	1027	US-08-781-986A-5254	Sequence 5254, App
13	53	100.0	1027	US-10-329-624-5254	Sequence 5254, App
14	53	100.0	1038	US-10-282-122A-43827	Sequence 43827, A
15	49	92.5	10	US-10-731-238-101	Sequence 101, App
16	49	92.5	21	US-10-731-238-9	Sequence 9, App
17	49	92.5	21	US-10-731-238-10	Sequence 10, App
18	49	92.5	21	US-10-731-238-14	Sequence 14, App
19	49	92.5	21	US-10-731-238-15	Sequence 15, App
20	49	92.5	21	US-10-731-238-16	Sequence 16, App
21	49	92.5	21	US-10-731-238-17	Sequence 17, App
22	49	92.5	21	US-10-731-238-18	Sequence 18, App
23	49	92.5	21	US-10-731-238-19	Sequence 19, App
24	49	92.5	21	US-10-731-238-20	Sequence 20, App
25	49	92.5	21	US-10-731-238-21	Sequence 21, App
26	49	92.5	21	US-10-731-238-22	Sequence 22, App
27	49	92.5	21	US-10-731-238-23	Sequence 23, App
28	49	92.5	21	US-10-731-238-24	Sequence 24, App
29	49	92.5	21	US-10-731-238-34	Sequence 34, App
30	49	92.5	388	US-08-901-062-1	Sequence 1, App
31	49	92.5	559	US-08-781-986A-5251	Sequence 5251, App
32	49	92.5	559	US-10-329-624-5251	Sequence 5251, App
33	49	92.5	940	US-10-470-048B-424	Sequence 424, App
34	49	92.5	948	US-10-470-048B-69	Sequence 69, App
35	44	83.0	21	US-10-731-238-33	Sequence 33, App
36	43	81.1	21	US-10-731-238-25	Sequence 25, App
37	43	81.1	21	US-10-731-238-27	Sequence 27, App
38	43	81.1	21	US-10-731-238-28	Sequence 28, App
39	43	81.1	21	US-10-731-238-30	Sequence 30, App
40	42	79.2	21	US-10-731-238-29	Sequence 29, App
41	42	79.2	21	US-10-731-238-31	Sequence 31, App
42	41	77.4	21	US-10-731-238-32	Sequence 32, App
43	39	73.6	21	US-10-731-238-26	Sequence 26, App
44	39	73.6	438	US-10-369-493-1427	Sequence 1427, A
45	39	73.6	438	US-10-369-493-14717	Sequence 14717, A

ALIGNMENTS

RESULT 1
US-10-731-238-102
Sequence 102, Application US/10731238
Publication No. US20050123552A1
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
Patel, Joseph M.
House-Pompeo, Karen L.
Speziale, Pietro
Job, Danny
McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/731.238
FILING DATE: 10-Dec-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/010.317
FILING DATE: 21-Jan-1998
APPLICATION NUMBER: US 60/036,139

FILED DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAMK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 102:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 102:
US-10-731-238-102
Query Match 100.0%; Score 53; DB 18; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0041;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 DPEEDTLPRV 10
DB 1 DPEEDTLPRV 10
RESULT 2
US-10-731-238-86
Sequence 86, Application US/10731238
Publication No. US20050123552A1
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
Patti, Joseph M.
House-Pompeo, Karen L.
Speziale, Pietro
Joh, Danny
McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Releasee #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/731,238
FILING DATE: 10-Dec-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE: 21-Jan-1998
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAMK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 86:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>

TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 86:
US-10-731-238-86
Query Match 100.0%; Score 53; DB 18; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.0045;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 DPEEDTLPRV 10
DB 2 DPEEDTLPRV 11
RESULT 3
US-10-731-238-13
Sequence 13, Application US/10731238
Publication No. US20050123552A1
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
Patti, Joseph M.
House-Pompeo, Karen L.
Speziale, Pietro
Joh, Danny
McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Releasee #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/731,238
FILING DATE: 10-Dec-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE: 21-Jan-1998
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAMK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 22 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 13:
US-10-731-238-13
Query Match 100.0%; Score 53; DB 18; Length 22;
Best Local Similarity 100.0%; Pred. No. 0.0098;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 DPEEDTLPRV 10
DB 13 DPEEDTLPRV 22

RESULT 4
US-11-066-697-1134
Sequence 1134, Application US/11066697
Publication No. US20050187159A1
GENERAL INFORMATION:
APPLICANT: Bridon, Dominique P.
APPLICANT: Ezrin, Alan M.
APPLICANT: Milner, Peter G.
APPLICANT: Holmes, Darren L.
APPLICANT: Thibaudau, Karen
TITLE OF INVENTION: PROTECTION OF ENDOGENOUS THERAPEUTIC PEPTIDES FROM
TITLE OF INVENTION: PEPTIDASE ACTIVITY THROUGH CONJUGATION TO BLOOD
FILE REFERENCE: 500862002301
CURRENT APPLICATION NUMBER: US/11/066,697
CURRENT FILING DATE: 2005-02-25
PRIOR APPLICATION NUMBER: 09/657,276
PRIOR FILING DATE: 2000-09-07
PRIOR APPLICATION NUMBER: 60/153,406
PRIOR FILING DATE: 1999-09-10
PRIOR APPLICATION NUMBER: 60/159,783
PRIOR FILING DATE: 1999-10-15
NUMBER OF SEQ ID NOS: 1617
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 1134
LENGTH: 37
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE: Description of Artificial Sequence: Synthetic
OTHER INFORMATION: Peptide
US-11-066-697-1134
Query Match 100.0%; Score 53; DB 20; Length 37;
Best Local Similarity 100.0%; Pred. No. 0.017;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 DFEEDTLPRV 10
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Db 28 DFEEDTLPRV 37
RESULT 5
US-09-813-820-8
Sequence 8, Application US/09813820
Patent No. US20020102262A1
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
Patel, Joseph M.
House-Pompeo, Karen
Sthanam, Narayana
Symserey, Jindrich
TITLE OF INVENTION: COLLAGEN BINDING PROTEIN COMPOSITIONS
AND METHODS OF USE
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: Texas
COUNTRY: U.S.
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/813,820
FILING DATE: 22-Mar-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/856,253

FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Kitchell, Barbara S.
REGISTRATION NUMBER: 33,928
REFERENCE/DOCKET NUMBER: TANK:193
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
TELEFAX: (512) 474-7577
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 139 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
US-09-813-820-8
SEQUENCE DESCRIPTION: SEQ ID NO: 8:
Query Match 100.0%; Score 53; DB 9; Length 139;
Best Local Similarity 100.0%; Pred. No. 0.076;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 DFEEDTLPRV 10
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Db 119 DFEEDTLPRV 128
RESULT 6
US-10-282-122A-43778
Sequence 43778, Application US/10282122A
Publication No. US20040029129A1
GENERAL INFORMATION:
APPLICANT: Wang, Lianguo
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Heselbeck, Robert
APPLICANT: Ohlsen, Kari
APPLICANT: Zyekind, Judith
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John
APPLICANT: Carr, Grant
APPLICANT: Yamamoto, Robert
APPLICANT: Forsyth, R.
APPLICANT: Xu, H.
TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REFERENCE: ELITRA.034A
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/230,335
PRIOR FILING DATE: 2000-09-06
PRIOR APPLICATION NUMBER: 60/230,347
PRIOR FILING DATE: 2000-09-09
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/267,636
PRIOR FILING DATE: 2001-02-09
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 78614
SOFTWARE: Patentin version 3.1
SEQ ID NO 43778
LENGTH: 961
TYPE: PRT

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; ORGANISM: Staphylococcus aureus
US-10-282-122A-43778

Query Match      100.0%; Score 53; DB 15; Length 961;
Best Local Similarity 100.0%; Pred. No. 0.64;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 DFEEDLPRV 10
DB      796 DFEEDLPRV 805

RESULT 7
US-09-815-242-5456
; Sequence 5456, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Karl L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Cair, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; FILE REFERENCE: ELITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5456
; LENGTH: 978
; TYPE: PRF
; ORGANISM: Staphylococcus aureus
US-09-815-242-5456

Query Match      100.0%; Score 53; DB 9; Length 978;
Best Local Similarity 100.0%; Pred. No. 0.66;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB      827 DFEEDLPRV 836

RESULT 8
US-09-815-242-12686
; Sequence 12686, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Karl L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Cair, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; FILE REFERENCE: ELITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5797
; LENGTH: 1018

APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; FILE REFERENCE: ELITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5797
; LENGTH: 1018
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TYPE: PRT
ORGANISM: Staphylococcus aureus
US-09-815-242-5797

Query Match 100.0%; Score 53; DB 9; Length 1018;
Best Local Similarity 100.0%; Pred. No. 0.69;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DFEEDTLPKV 10
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Db 849 DFEEDTLPKV 858

RESULT 10
US-09-815-242-12838
Sequence 12838, Application US/09815242
Patent No. US2002061569A1

GENERAL INFORMATION:
APPLICANT: Habelbeck, Robert
APPLICANT: Ohlsen, Karl L.
APPLICANT: Zyskind, Judith W.
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John D.
APPLICANT: Carr, Grant J.
APPLICANT: Yamamoto, Robert T.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in
FILE REFERENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21

PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 12838
LENGTH: 1018
TYPE: PRT
ORGANISM: Staphylococcus aureus
US-09-815-242-12838

Query Match 100.0%; Score 53; DB 9; Length 1018;
Best Local Similarity 100.0%; Pred. No. 0.69;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DFEEDTLPKV 10
|||||
Db 849 DFEEDTLPKV 858

RESULT 11
US-10-470-048B-68
Sequence 68, Application US/10470048B
Publication No. US2005003744A1
GENERAL INFORMATION:
APPLICANT: MEINKE ET AL.

TITLE OF INVENTION: A METHOD FOR IDENTIFICATION, ISOLATION AND PRODUCTION OF
TITLE OF INVENTION: ANTIGENS TO A SPECIFIC PATHOGEN
FILE REFERENCE: SONN.035US
CURRENT APPLICATION NUMBER: US/10/470,048B
CURRENT FILING DATE: 2003-07-25

NUMBER OF SEQ ID NOS: 603
SOFTWARE: Patentin version 3.1
SEQ ID NO 68
LENGTH: 1018
TYPE: PRT
ORGANISM: Staphylococcus aureus
US-10-470-048B-68

Query Match 100.0%; Score 53; DB 17; Length 1018;
Best Local Similarity 100.0%; Pred. No. 0.69;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DFEEDTLPKV 10
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Db 849 DFEEDTLPKV 858

RESULT 12
US-08-781-986A-5254
Sequence 5254, Application US/08781986A
Publication No. US20030054436A1

GENERAL INFORMATION:
APPLICANT: Charles Kunsch
TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
NUMBER OF SEQUENCES: 5255
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COUNTRY: USA
ZIP: 20850

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4MB storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2

SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/781,986A
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:

ATTORNEY/AGENT INFORMATION:
NAME: Benson, Bob
REGISTRATION NUMBER: 30,446
REFERENCE/DOCKET NUMBER: PB248PP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 5254:
SEQUENCE CHARACTERISTICS:
LENGTH: 1027 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-781-986A-5254

Query Match 100.0%; Score 53; DB 8; Length 1027;
Best Local Similarity 100.0%; Pred. No. 0.69;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DFEEDTLPKV 10
|||||
Db 858 DFEEDTLPKV 867

RESULT 13
US-10-329-624-5254
Sequence 5254, Application US/10329624
Publication No. US20040043037A1

```

GENERAL INFORMATION:
APPLICANT: Charles Kunsch
            Gil H. Choi
            Patrick S. Dillon
            Craig A. Rosen
            Steven C. Barash
            Michael R. Fannon
TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
NUMBER OF SEQUENCES: 5256
CORRESPONDENCE ADDRESS:
    ADDRESSEE: Human Genome Sciences, Inc.
    STREET: 9410 Key West Avenue
    CITY: Rockville
    STATE: Maryland
    COUNTRY: USA
    ZIP: 20850
COMPUTER READABLE FORM:
    MEDIUM TYPE: Diskette, 3.50 inch, 1.4mb storage
    COMPUTER: HP Vectra 486/33
    OPERATING SYSTEM: MSDOS version 6.2
    SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
    APPLICATION NUMBER: US/10/329,624
    FILING DATE: 27-Dec-2002
PRIOR APPLICATION DATA:
    APPLICATION NUMBER: 08/956,171
    FILING DATE: October 20, 1997
    APPLICATION NUMBER: 60/009,861
    FILING DATE: January 5, 1996
    APPLICATION NUMBER: 08/781,986
    FILING DATE: January 3, 1997
ATTORNEY/AGENT INFORMATION:
    NAME: Mark J. Hyman
    REGISTRATION NUMBER: 46,789
    REFERENCE/DOCKET NUMBER: PB248PID1
TELECOMMUNICATION INFORMATION:
    TELEPHONE: (240) 314-1224
    TELEFAX: (301) 309-8439
    INFORMATION FOR SEQ ID NO: 5254:
        SEQUENCE CHARACTERISTICS:
            LENGTH: 1027 amino acids
            TYPE: amino acid
            STRANDEDNESS: single
            TOPOLOGY: linear
        MOLECULE TYPE: protein
        SEQUENCE DESCRIPTION: SEQ ID NO: 5254:
US-10-329-624-5254
Query Match          100.0%; Score 53; DB 15; Length 1027;
Best Local Similarity 100.0%; Pred. No. 0.69;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      1 DFEEDTLPKV 10
        |||||
Db      858 DFEEDTLPKV 867

```

```

APPLICANT: Xu, H.
TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REFERENCE: ELITR 034A
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
PRIORITY APPLICATION NUMBER: 60/191,078
PRIORITY FILING DATE: 2000-03-21
PRIORITY APPLICATION NUMBER: 60/206,848
PRIORITY FILING DATE: 2000-05-23
PRIORITY APPLICATION NUMBER: 60/207,727
PRIORITY FILING DATE: 2000-05-26
PRIORITY APPLICATION NUMBER: 60/230,335
PRIORITY FILING DATE: 2000-09-06
PRIORITY APPLICATION NUMBER: 60/230,347
PRIORITY FILING DATE: 2000-09-09
PRIORITY APPLICATION NUMBER: 60/242,578
PRIORITY FILING DATE: 2000-10-23
PRIORITY APPLICATION NUMBER: 60/253,625
PRIORITY FILING DATE: 2000-11-27
PRIORITY APPLICATION NUMBER: 60/257,931
PRIORITY FILING DATE: 2000-12-22
PRIORITY APPLICATION NUMBER: 60/267,636
PRIORITY FILING DATE: 2001-02-09
PRIORITY APPLICATION NUMBER: 60/269,308
PRIORITY FILING DATE: 2001-02-16
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 78614
SOFTWARE: PatentIn version 3.1
SEQ ID NO 43827
LENGTH: 1038
TYPE: PRT
ORGANISM: Staphylococcus aureus
US-10-282-122A-43827

Query Match          100.0%; Score 53; DB 15; Length 1038;
Best Local Similarity 100.0%; Pred. No. 0.7;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0.

QY      1 DFEEDTLPKV 10
        |||||||
Db       845 DFEEDTLPKV 854

RESULT 15
US-10-731-238-101
; Sequence 101, Application US/10731238
; Publication No. US2005012352A1
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
            Patti, Joseph M.
            House-Pompeo, Karen L.
            Speciale, Pietro
            John, Danny
            McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/731,238
FILING DATE: 10-Dec-2003
CLASSIFICATION: <Unknown>

```

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE: 21-Jan-1998
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAMK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 101:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 101:
US-10-731-238-101

Query Match 92.5%; Score 49; DB 18; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.023;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 DFEEDTLPK 9
Db 2 DFEEDTLPK 10

Search completed: October 22, 2005, 12:56:30
Job time : 56.1494 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 22, 2005, 08:04:46 ; Search time 11.6092 seconds
(without alignments)

82.880 Million cell updates/sec

Title: US-10-731-238-102

Perfect score: 53

Sequence: 1 DFEDTLPKV 10

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	53	100.0	961	2	G90053	hypothetical prote
2	53	100.0	1018	2	A32192	fibronectin-bindin
3	53	100.0	1038	2	H90053	hypothetical prote
4	49	92.5	940	2	S19702	fibronectin-bindin
5	39	73.6	424	2	AE2893	UDP-glucose/GDP-ma
6	39	73.6	446	2	H97668	probable UDP-gluc
7	38	71.7	450	2	E95181	hypothetical prote
8	38	71.7	450	2	H98048	phosphoacetylgluco
9	38	71.7	452	2	H86677	phosphoglucosamine
10	37	69.8	42	2	B82629	hypothetical prote
11	37	69.8	60	2	B82627	hypothetical prote
12	37	69.8	347	1	HPMS	haptoglobin precur
13	36	67.9	277	1	A64404	hypothetical prote
14	36	67.9	383	1	S42003	sterol 24-C-methyl
15	36	67.9	449	2	A35762	mannosyltransferas
16	36	67.9	582	2	E84721	probable calcium-d
17	36	67.9	831	2	T51185	resistance protein
18	36	67.9	867	2	D86193	hypothetical prote
19	35	66.0	269	2	H84378	hypothetical prote
20	35	66.0	518	2	S35692	erythrocyte membra
21	35	66.0	562	2	H88071	protein ZK1340.3 l
22	35	66.0	881	2	F72397	pyruvate, phosphat
23	35	66.0	1090	2	C86450	peroxisomal assemb
24	35	66.0	1165	2	A48667	probable RNA helic
25	35	66.0	1220	2	A56236	amloridine-sensitiv
26	35	66.0	1420	1	A4361	probable membrane
27	35	65.1	1804	2	S66247	RNA-directed RNA p
28	34.5	65.1	878	1	RXK51B	hypothetical 13.7k
29	34	64.2	122	2	S34566	

30	34	64.2	157	2	B69538	conserved hypothet
31	34	64.2	206	2	A81281	probable cellulaufa
32	34	64.2	224	2	T07006	L-lactate dehydrog
33	34	64.2	234	2	T30473	late expression fa
34	34	64.2	346	2	T07005	L-lactate dehydrog
35	34	64.2	347	2	T07063	L-lactate dehydrog
36	34	64.2	368	2	T21748	hypothetical prote
37	34	64.2	404	2	A28404	S-antigen - bovine
38	34	64.2	483	2	T42952	hypothetical prote
39	34	64.2	528	1	MMBV8B	58k protein - bart
40	34	64.2	574	2	T30133	hypothetical prote
41	34	64.2	574	2	T29747	hypothetical prote
42	34	64.2	607	2	T40906	probable ATP-depen
43	34	64.2	730	2	B83540	hemolytic phosphol
44	34	64.2	730	2	A26391	phospholipase C (B
45	34	64.2	749	2	S61643	probable membrane

ALIGNMENTS

RESULT 1
G90053
hypothetical protein fabb [imported] - Staphylococcus aureus (strain N315)
C/Species: Staphylococcus aureus
C/Date: 10-May-2001 #sequence_revision 10-May-2001 #ext_change 09-Jul-2004
C/Accession: G90053
R/Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Chu, L.; Oguci
ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.; I
C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiratsuku, K.
Lancet 357, 1225-1240, 2001
A/Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.
A/Reference number: A89758; PMID:11418146
A/Accession: G90053
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-961 <R>
A/Cross-references: UNIPROT:Q99RD3; GB:BA000018; PID:g13702452; PIDN:BA843593.1; GSPDB:G
A/Experimental source: strain N315
C/Genetics:
A/Gene: fabb

Query Match 100.0%; Score 53; DB 2; Length 961;
Best Local Similarity 100.0%; Pred. No. 0.05; Mismatches 0; Indels 0; Gaps 0;
Matches 10; Conservative 0;

QY 1 DFEDTLPKV 10
DB 796 DFEDTLPKV 805

RESULT 2

A32192
fibronectin-binding protein - Staphylococcus aureus
C/Species: Staphylococcus aureus
C/Date: 31-Jul-1989 #sequence_revision 31-Jul-1989 #ext_change 16-Feb-1997
C/Accession: A32192
R/Sigman, C.; Raucel, G.; Joensson, K.; Lindgren, P.E.; Anantharamaiah, G.M.; Hoeck, M.
Proc. Natl. Acad. Sci. U.S.A. 86, 699-703, 1989
A/Title: Nucleotide sequence of the gene for a fibronectin-binding protein from Staphylo
A/Reference number: A32192; PMID:8908998; PMID:2521391
A/Accession: A32192
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-1018 <SIG>
A/Cross-references: GB:J04151
C/Keywords: fibronectin binding

Query Match 100.0%; Score 53; DB 2; Length 1018;
Best Local Similarity 100.0%; Pred. No. 0.054; Mismatches 0; Indels 0; Gaps 0;
Matches 10; Conservative 0;

QY 1 DFEDTLPKV 10

Db 849 DFEEDTLPRV 858

RESULT 3

H90053

hypothetical protein fnb [imported] - Staphylococcus aureus (strain N315)

C:Species: Staphylococcus aureus

C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004

C:Accession: H90053

R:Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguc

ma, A.; Mizutani, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.;

C.; Shiba, T.; Hatori, M.; Ogasawara, N.; Hayashi, H.; Hiramoto, K.

Science 357, 1225-1240, 2001

A:Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.

A:Reference number: A89758; MUID:21311952; PMID:11418146

A:Accession: H90053

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-1038 <KUR>

A:Cross-references: UNIPROT:Q99RD2; GB:BA000018; PID:g13702453; PIDN:BA843594.1; GSPDB:G

A:Experimental source: strain N315

C:Genetics:

A:Gene: fnb

Query Match 100.0%; Score 53; DB 2; Length 1038;

Best Local Similarity 100.0%; Pred. No. 0.055;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DFEEDTLPRV 10

Db 845 DFEEDTLPRV 854

RESULT 4

S19702

fibronectin-binding protein B - Staphylococcus aureus

C:Species: Staphylococcus aureus

C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004

C:Accession: S19702

R:Joensen, K.; Signaes, C.; Mueller, H.P.; Lindberg, M.

Eur. J. Biochem. 202, 1041-1048, 1991

A:Title: Two different genes encode fibronectin binding proteins in Staphylococcus aureus

A:Reference number: S19702; MUID:92111475; PMID:1837266

A:Accession: S19702

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-940 <JOE>

A:Cross-references: UNIPROT:Q53682; EMBL:X62992; NID:G49040; PIDN:CAA44726.1; PID:G58156

C:Keywords: fibronectin binding

Query Match 92.5%; Score 49; DB 2; Length 940;

Best Local Similarity 90.0%; Pred. No. 0.3;

Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DFEEDTLPRV 10

Db 765 DFEEDTLPRV 794

RESULT 5

A82893

UDP-glucose/GDP-mannose dehydrogenase Atu2582 [imported] - Agrobacterium tumefaciens (str

C:Species: Agrobacterium tumefaciens

C:Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 16-Aug-2004

C:Accession: A82893

R:Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, I

erage, G.; Gilllet, W.; Grant, C.; Guenther, D.; Kuyavlin, T.; Levy, R.; Li, M.; McClell

; Karp, P.; Romero, P.; Zhang, S.

Science 294, 2317-2323, 2001

A:Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,

ster, E.W.

A:Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.

A:Reference number: A82577; MUID:21608550; PMID:11743193

A:Accession: A82893

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-424 <KUR>

A:Cross-references: UNIPROT:Q8UCB6; GB:AE008688; PIDN:AAL43563.1; PID:g17741077; GSPDB:G

A:Experimental source: strain C58 (Dupont)

C:Genetics:

A:Gene: Atu2582

A:Map position: circular chromosome

C:Superfamily: GDPmannose dehydrogenase

Query Match 73.6%; Score 39; DB 2; Length 424;

Best Local Similarity 70.0%; Pred. No. 11;

Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 DFEEDTLPRV 10

Db 155 DFEETSTIRPV 164

RESULT 6

H97668

probable UDP-glucose/GDP-mannose dehydrogenase wbpa PA3159 [imported] - Agrobacterium tum

C:Species: Agrobacterium tumefaciens

C:Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 09-Jul-2004

C:Accession: H97668

R:Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman,

A.; Liu, F.; Molism, C.; Allinger, M.; Dougherty, D.; Scott, C.; Lappas, C.; Markels, B.;

Science 294, 2323-2328, 2001

A:Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tume

A:Reference number: A97359; MUID:21608551; PMID:11743194

A:Accession: H97668

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-446 <KUR>

A:Cross-references: UNIPROT:O8UCB6; GB:AE007869; PIDN:AAK88305.1; PID:g15157777; GSPDB:G

C:Genetics:

A:Gene: AGR C 4677

A:Map position: circular chromosome

C:Superfamily: UDP-N-acetyl-D-mannosaminuronic acid dehydrogenase

Query Match 73.6%; Score 39; DB 2; Length 446;

Best Local Similarity 70.0%; Pred. No. 12;

Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 DFEEDTLPRV 10

Db 177 DFEETSTIRPV 186

RESULT 7

E95181

hypothetical protein SPI559 [imported] - Streptococcus pneumoniae (strain TIGR4)

C:Species: Streptococcus pneumoniae

C:Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 09-Jul-2004

C:Accession: E95181

R:Retzlaff, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Held

on, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapple, I

neon, T.; Hickey, E.K.; Holt, I.E.

Science 293, 498-506, 2001

A:Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison,

A:Title: Complete Genome Sequence of a virulent isolate of Streptococcus pneumoniae.

A:Reference number: A85000; MUID:21357209; PMID:11463916

A:Accession: E95181

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-450 <KUR>

A:Cross-references: UNIPROT:Q97PP4; GB:AE005672; PIDN:AAK75646.1; PID:g14973050; GSPDB:G

A:Experimental source: strain TIGR4

C:Genetics:

A:Gene: SPI559

C:Superfamily: phosphomannomutase

Query Match 71.7% Score 38; DB 2; Length 450;
Best Local Similarity 77.8%; Pred. No. 19;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 DFEEDTLPK 9
| | | | |
133 DAEEDTLPR 141

RESULT 8

H98048
phosphoacetylglucosamine mutase [EC 5.4.2.3] [imported] - Streptococcus pneumoniae (strain
C:Species: Streptococcus pneumoniae
C:Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 09-Jul-2004
C:Accession: H98048
R:Authors: J.A.; Albom Jr., W.; Arnold, J.; Blaszcak, L.; Burgett, S.; Dehoff, B.S.; E
e, R.; Leblanc, D.J.; Lee, L.N.; Lefkowitz, E.D.; Lu, J.; Matsushima, P.; McAhren, S.; M
y, P.; Sun, P.M.; Winkler, M.E.
J. Bacteriol. 183, 5709-5717, 2001
A:Title: Genome of the Bacterium Streptococcus pneumoniae Strain R6.
A:Reference number: A97872; MUID:21429245; PMID:11544234
A:Accession: H98048
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-450 <KUR>
A:Cross-references: UNIPROT:Q8DPI6; GB:AE007317; PIDN:AAU00221.1; PID:G15459071; GSPDB:C
C:Genetics:
A:Gene: glmM
C:Superfamily: phosphomannomutase
C:Keywords: intramolecular transferase; isomerase

Query Match 71.7% Score 38; DB 2; Length 450;
Best Local Similarity 77.8%; Pred. No. 19;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 DFEEDTLPK 9
| | | | |
133 DAEEDTLPR 141

RESULT 9

H86677
phosphoglucosamine mutase [imported] - Lactococcus lactis subsp. lactis (strain IL1403)
C:Species: Lactococcus lactis subsp. lactis
C:Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 09-Jul-2004
C:Accession: H86677
R:Boletín, A.; Winkler, P.; Manger, S.; Jallón, O.; Malarme, K.; Weissenbach, J.; Ehrlich
Genome Res. 11, 731-753, 2001
A:Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis se
A:Reference number: A86625; MUID:21235186; PMID:11337471
A:Accession: H86677
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-452 <STO>
A:Cross-references: UNIPROT:Q9C1D9; GB:AE005176; PID:G12723300; PIDN:AAK04522.1; GSPDB:C
C:Genetics:
A:Gene: femD
C:Superfamily: phosphomannomutase

Query Match 71.7% Score 38; DB 2; Length 452;
Best Local Similarity 77.8%; Pred. No. 19;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 DFEEDTLPK 9
| | | | |
133 DAEEDTLPR 141

RESULT 10

B82629

hypothetical protein xrl866 [imported] - Xylella fastidiosa (strain 9a5c)

C:Species: Xylella fastidiosa

C:Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004

C:Accession: B82629

R:Anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequenc

Nature 406, 151-157, 2000

A:Title: The genome sequence of the plant pathogen Xylella fastidiosa.

A:Reference number: A82515; MUID:20365717; PMID:10910347

A:Note: for a complete list of authors see reference number A59328 below

A:Accession: B82629

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-442 <STM>

A:Cross-references: UNIPROT:Q9PC95; GB:AE004007; GB:AE003849; NID:G9106944; PIDN:AAF84672

A:Experimental source: strain 9a5c

R:Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; A

Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carter, H.

as-Neto, E.; Docena, C.; El-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S.

submitted to GenBank, June 2000

A:Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franco, S.C.; Franco, M.C.; Frohme

J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.B.; Laigre

chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Martino, C.L.; Marques, M.V.; Martins, B.

A:Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.;

F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A.

Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasak

A:Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silveir

M.; Tshako, M.H.; Valada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z

A:Reference number: A59328

A:Contents: annotation

C:Genetics:

RESULT 11

B82627

hypothetical protein xrl892 [imported] - Xylella fastidiosa (strain 9a5c)

C:Species: Xylella fastidiosa

C:Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004

C:Accession: B82627

R:Anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequenc

Nature 406, 151-157, 2000

A:Title: The genome sequence of the plant pathogen Xylella fastidiosa.

A:Reference number: A82515; MUID:20365717; PMID:10910347

A:Note: for a complete list of authors see reference number A59328 below

A:Accession: B82627

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-60 <STM>

A:Cross-references: UNIPROT:Q9PC99; GB:AE004008; GB:AE003849; NID:G9106961; PIDN:AAF8468

A:Experimental source: strain 9a5c

R:Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; A

Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carter, H.

as-Neto, E.; Docena, C.; El-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S.

A:Gene: XF1882

Query Match 69.8%; Score 37; DB 2; Length 60;

Best Local Similarity 77.8%; Pred. No. 3.1;

Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 DFEEDTLPK 9
|||
DB 25 DFEEDTLPK 33

RESULT 12

HPMS

haptooglobin precursor - mouse

N:Contains: haptooglobin alpha chain; haptooglobin beta chain

C:Species: Mus musculus (house mouse)

C>Date: 23-Mar-1995 #sequence_revision 31-May-1996 #text_change 18-Jun-1999

C:Accession: A48918

R:Yang, F.; Linhan, L.A.; Friedrichs, W.E.; Lalley, P.A.; Sakaguchi, A.Y.; Bowman, B.H.

Genomics 18, 374-380, 1993

A>Title: Characterization of the mouse haptooglobin gene.

A:Reference number: A48918; MUID:94117006; PMID:8288241

A:Accession: A48918

A:Molecule type: mRNA

A:Residues: 1-347 <YAN>

A:Cross-references: GB:S67972; NID:9461137; PIDN:AAB29697.1; PID:9461138

A>Note: sequence extracted from NCBI backbone (NCBIN:142156; NCBIP:142157); sequence ind

C:Comment: The mature haptooglobin molecule is a dimer of heterodimers, the two chains of

C:Comment: Haptooglobin is a plasma glycoprotein; haptooglobin forms a complex with hemogl

C:Genetics:

A:Gene: Hp

A:Map position: 8

C:Superfamily: haptooglobin; complement factor H repeat homology; trypsin homology

C:Keywords: acute phase; glycoprotein; hemoglobin binding; heterocetimer; iron transpor

F:1-18/Domain: signal sequence #status predicted <SIG>

F:19-101/Product: haptooglobin alpha chain #status predicted <ACH>

F:33-86/Domain: complement factor H repeat homology <FH2>

F:103-347/Product: haptooglobin beta chain #status predicted <BCH>

F:103-340/Domain: trypsin homology <TRY>

F:33/Disulfide bonds: interchain #status predicted

F:52-86, 90-207, 250-281, 292-322/Disulfide bonds: #status predicted

F:148,182,256,264/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match

Best Local Similarity 69.8%; Score 37; DB 1; Length 347;

Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 DFEEDTLPK 9
|||
DB 27 DFEEDTLPK 35

RESULT 13

A64404

hypothetical protein M00833 - Methanococcus jannaschii

C:Species: Methanococcus jannaschii

C>Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 04-Mar-2000

C:Accession: A64404

R:Bult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blake,

; Reisch, C.I.; Overbeek, R.; Kirkness, E.F.; Weinstock, K.G.; Merrick, J.M.; Glodok, A.;

reen, J.D.; Sadow, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A.

Science 273, 1058-1073, 1996

A:Authors: Kaine, B.P.; Borodovsky, M.; Klank, H.P.; Fraser, C.M.; Smith, H.O.; Moese, C

A>Title: Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschii

A:Reference number: A64300; MUID:96337999; PMID:8688087

A:Accession: A64404

A:Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Cross-references: GB:U67527; GB:L77117; NID:91591519; PID:91591521; TIGR:M0833; PID:9

C:Genetics:

A:Map position: REV759071-758238

A:Start codon: TTG

C:Superfamily: Methanococcus jannaschii hypothetical protein M00833

Query Match 67.9%; Score 36; DB 2; Length 277;

Best Local Similarity 87.5%; Pred. No. 27;

Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 FEEDTLPK 9
|||
DB 60 FEEDTLPK 67

RESULT 14

S42003

sterol 24-C-methyltransferase (EC 2.1.1.41) - yeast (Saccharomyces cerevisiae)

N:Alternate names: PDR4-region bioc homology; protein YW9571.10c; protein YML008c

C:Species: Saccharomyces cerevisiae

C>Date: 03-Feb-1994 #sequence_revision 27-Jan-1995 #text_change 09-Jul-2004

C:Accession: S42003; PE0402; S5511; S17001; S35982

R:Hardwick, K.G.; Pelham, H.R.B.

Yeast 10, 265-269, 1994

A>Title: SED6 is identical to ERG6, and encodes a putative methyltransferase required for

A:Reference number: S42003; MUID:94262330; PMID:8203167

A:Accession: S42003

A:Molecule type: DNA

A:Residues: 1-383 <HAR>

A:Cross-references: UNIPROT:P25087; EMBL:X74249; NID:9396514; PIDN:CAA52308.1; PID:939651

A>Note: the authors translated the codon ACT for residue 322 as Ala

R:Hussein, M.; Lenard, J.

Gene 101, 149-152, 1991

A>Title: Characterization of PDR4, a Saccharomyces cerevisiae gene that confers pleiotrop

A:Reference number: JE0416; MUID:91285426; PMID:2060792

A:Accession: PE0402

A:Molecule type: DNA

A:Residues: 1-258 <HUS>

A:Cross-references: GB:X53830; NID:94121; PIDN:CAA37826.1; PID:94122

A>Note: the authors suggested that this protein is unrelated to the pleiotropic drug res

nown to be a transcriptional activator (see PIR:S16706)

R:Gentles, S.; Bowman, S.

submitted to the EMBL Data Library, June 1995

A:Reference number: S55102

A:Accession: S55111

A:Molecule type: DNA

A:Residues: 1-383 <GEN>

A:Cross-references: EMBL:Z49810; NID:9854472; PIDN:CAA89944.1; PID:9854482; GSPDB:GN0001;

A:Experimental source: strain AB972

C:Genetics:

A:Gene: SGD:ERG6; SED6; MIPS:YML008c

A:Cross-references: SGD:S0004467; MIPS:YML008c

A:Map position: 13L

C:Superfamily: 24-sterol C-methyltransferase; bioc homology

C:Keywords: methyltransferase; S-adenosylmethionine

F:120-224/Domain: bioc homology <BIOC>

QY 1 DFEEDTLPKV 10
|||
DB 182 DFEEDTLPKV 191

RESULT 15

A35762

mannosyltransferase (EC 2.4.1.-) ALG1 - yeast (Saccharomyces cerevisiae)

N:Alternate names: protein YBR0906; protein YBR110w

C:Species: Saccharomyces cerevisiae

C>Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 09-Jul-2004

C:Accession: A35762; S48275; S45978; S44690

R:Albright, C.F.; Robbina, P.W.

J. Biol. Chem. 265, 7042-7049, 1990

A>Title: The sequence and transcript heterogeneity of the yeast gene ALG1, an essential n

A:Reference number: A35762; MUID:90216743; PMID:2182636

A:Accession: A35762
 A:Molecule type: DNA
 A:Residues: 1-449 <ALB>
 A:Cross-references: UNIPROT:P16661; EMBL:J05416; NID:G171049; PIDN:AAA6322.1; PID:G1710
 R:Manhaupt, G.; Stucka, R.; Ehle, S.; Vetter, I.; Feldmann, H.
 Yeast 10, 1363-1381, 1994
 A:Title: Analysis of a 70 kb region on the right arm of yeast chromosome II.
 A:Reference number: S48255; MUID:95208357; PMID:7900426
 A:Accession: S48275
 A:Status: nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-449 <MAN>
 A:Cross-references: EMBL:X78993; NID:G476045; PIDN:CAA55613.1; PID:G476066
 A:Note: the nucleotide sequence was submitted to the EMBL Data Library, April 1994
 R:Feldmann, H.; Manhaupt, G.; Schwarzlose, C.; Vetter, I.
 submitted to the Protein Sequence Database, August 1994
 A:Reference number: S45927
 A:Accession: S45978
 A:Molecule type: DNA
 A:Residues: 1-449 <FE2>
 A:Cross-references: EMBL:Z35979; NID:G536376; PID:G536377; MIPS:YBR110W
 C:Genetics:
 A:Gene: SGD:ALG1
 A:Cross-references: SGD:S0000314; MIPS:YBR110W
 A:Map position: 2R
 C:Keywords: glycoprotein; glycosyltransferase; hexosyltransferase; transmembrane protein
 F:5-31/Domain: transmembrane #status predicted <TM1>
 F:104-123/Domain: transmembrane #status predicted <TM2>
 F:143-159/Domain: transmembrane #status predicted <TM3>
 F:180-196/Domain: transmembrane #status predicted <TM4>

Query Match 67.3%; Score 36; DB 2; Length 449;
 Best Local Similarity 66.7%; Pred. No. 46;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 FEEDTLPKV 10
 : |||||:
 : |||||:
 Db 74 YVEDTLPKI 82

Search completed: October 22, 2005, 09:55:53
 Job time : 12.6092 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: October 22, 2005, 08:01:06 ; Search time 56.2069 Seconds
(without alignments)
91.106 Million cell updates/sec

Title: US-10-731-238-102
Perfect score: 53
Sequence: 1 DFEEDTLPKV 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Uniprot_03:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	53	100.0	961	2 Q99RD3	Q99ID3 staphylococ
2	53	100.0	961	2 Q7A3J8	Q7A3J8 staphylococ
3	53	100.0	965	2 Q6GDJ5	Q6GDJ5 staphylococ
4	53	100.0	1015	2 Q8NUU7	Q8NUU7 staphylococ
5	53	100.0	1015	2 Q6G6H3	Q6G6H3 staphylococ
6	53	100.0	1018	1 FNBA_STAAU	P14738 staphylococ
7	53	100.0	1038	2 Q99RD2	Q99ID2 staphylococ
8	53	100.0	1038	2 Q7A3J7	Q7A3J7 staphylococ
9	49	92.5	940	2 Q53682	Q53682 staphylococ
10	49	92.5	943	2 Q8NUU8	Q8NUU8 staphylococ
11	49	92.5	957	2 Q6G6H4	Q6G6H4 staphylococ
12	46	86.8	152	2 Q9AEP9	Q9AEP9 staphylococ
13	39	73.6	424	2 Q8UCB6	Q8UCB6 agrobacteri
14	39	73.6	446	2 Q7CWO5	Q7CWO5 agrobacteri
15	39	73.6	1096	2 Q8P6R2	Q8P6R2 xanthomonas
16	38	71.7	253	2 Q6FT09	Q6FT09 candida gla
17	38	71.7	253	2 Q6FT09	Q6FT09 streptococ
18	38	71.7	450	2 Q97PP4	Q97PP4 streptococ
19	38	71.7	450	2 Q8DP16	Q8DP16 streptococ
20	38	71.7	452	2 Q9CID9	Q9CID9 lactococcus
21	38	71.7	482	2 Q76K22	Q76K22 streptococ
22	38	71.7	622	2 Q9GSC0	Q9GSC0 caenorhabdi
23	38	71.7	3298	2 Q9VBI1	Q9VBI1 drosophila
24	37	69.8	42	2 Q9PCB5	Q9PCB5 xylella fas
25	37	69.8	60	2 Q9PC39	Q9PC39 xylella fas
26	37	69.8	177	2 Q8VL45	Q8VL45 actinobacil
27	37	69.8	177	2 Q8VLA2	Q8VLA2 actinobacil
28	37	69.8	177	2 Q8VLA4	Q8VLA4 actinobacil
29	37	69.8	177	2 Q8VOB1	Q8VOB1 actinobacil
30	37	69.8	177	2 Q8VDB2	Q8VDB2 actinobacil
31	37	69.8	190	2 Q72PK0	Q72PK0 leptospira
	37	69.8	190	2 Q8F6S3	Q8F6S3 leptospira

32	37	69.8	292	2 Q740C2	Q740C2 mycobacteri
33	37	69.8	347	1 HPT_MOUSE	Q61646 mus musculu
34	37	69.8	347	1 HPT_MOUSE	Q60574 mus cervoli
35	37	69.8	347	1 HPT_MOUSE	Q62558 mus saxicol
36	37	69.8	347	2 Q63927	Q63927 mus sp. hap
37	37	69.8	428	2 Q6C0M4	Q6C0M4 kluyveromyc
38	37	69.8	436	2 Q7MY92	Q7MY92 photorhabdu
39	37	69.8	460	2 Q7NA94	Q7NA94 chromobacte
40	37	69.8	632	1 THIC_CHRYO	Q7P1B8 chromobacte
41	37	69.8	915	2 Q84VC7	Q84VC7 oryza sativ
42	37	69.8	919	2 Q8L8G7	Q8L8G7 oryza sativ
43	37	69.8	1446	2 Q86AC8	Q86AC8 dictyostell
44	36	67.9	277	1 Y833_METJA	Q58243 methanococc
45	36	67.9	292	2 Q8NLP7	Q8NLP7 corynebacte

ALIGNMENTS

RESULT 1
Q99RD3 ID Q99RD3 PRELIMINARY; PRT; 961 AA.
AC Q99RD3;
DT 01-JUN-2001 (TREMblrel. 17, Last sequence update)
DT 01-JUN-2001 (TREMblrel. 24, Last annotation update)
DT 01-JUN-2003 (TREMblrel. 24, Last annotation update)
DE Fibronectin-binding protein homolog.
GN Name=fnbB; OrderedLocustNames=SAV2502;
OS Staphylococcus aureus (strain Mu50 / ATCC 700699).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxId=158878;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Mu50 / ATCC 700699;
RX MEDLINE=2111952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2;
RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Iino J.-O., Ito T.,
RA Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hoshiyama A.,
RA Mizutani-Uji Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
RA Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuuchi J.,
RA Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
RA Hattori M., Ogasawara N., Hayashi H., Hiratsuka K.;
RT "Whole genome sequencing of methicillin-resistant Staphylococcus
RT aureus.";
RL Lancet 357.1225-1240(2001).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC an amide bond (By similarity).
DR EMBL: AP003365; BAB58664.1; -.
DR PIR: G90053; G90053.
DR HSSP: Q53653; IN67.
DR GO: GO:0009986; C:cell surface; IEA.
DR GO: GO:0005618; C:cell wall; IEA.
DR GO: GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO: GO:0016020; C:membrane; IEA.
DR GO: GO:007135; P:cell adhesion; IEA.
DR InterPro: IPR008966; Adhes_bact.
DR InterPro: IPR004237; Fn_bind.
DR InterPro: IPR005877; Gpos_YsIRK.
DR InterPro: IPR001899; Gram_pos_anchor.
DR Pfam: PF02986; Fn_bind_1.
DR Pfam: PF00746; Gram_pos_anchor_1.
DR Pfam: PF04650; YsIRK_signal_1.
DR TIGRPFAM: TIGR01167; LPXTG_anchor_1.
DR TIGRPFAM: TIGR01168; YsIRK_signal_1.
DR PROSITE: PS50847; GRAM_POS_ANCHORING; 1.
KW Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ SEQUENCE 961 AA; 106010 MW; 364940F884EA4101 CRC64;
Query Match 100.0%; Score 53; DB 2; Length 961;
Best Local Similarity 100.0%; Pred. No. 0.3;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db          |||||
           796 DFEEDLPRV 805

RESULT 2
AC 07A3J8      PRELIMINARY;      PRT;      961 AA.
ID 07A3J8:
DT 05-JUL-2004 (TEMBLrel. 27, Created)
DT 05-JUL-2004 (TEMBLrel. 27, Last annotation update)
DE Fnb protein.
GN Name=fnb: OrderedLocNames=SA2290;
OS Staphylococcus aureus (strain N315).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxId=158879;
RN [1]
RX SEQUENCE FROM N.A.
MEDLINE=21311952; PubMed=1418146; DOI=10.1016/S0140-6736(00)04403-2;
RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Lian J.-Q., Ito T.,
RA Kanemori M., Matsumaru H., Maruyama A., Murakami H., Hoshiyama A.,
RA Mizutani-U Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
RA Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
RA Kanehisa M., Yamashita A., Oshida K., Furuya K., Yoshino C., Shiba T.,
RA Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
RT "Whole genome sequencing of methicillin-resistant Staphylococcus
RT aureus."
RL Lancet 357.1225-1240(2001).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC an amide bond (By similarity).
DR EMBL: AP003137; BAB43593.1; -.
DR GO: GO:0009986; C:cell surface; IEA.
DR GO: GO:0005618; C:cell wall; IEA.
DR GO: GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO: GO:0016020; C:membrane; IEA.
DR GO: GO:0007155; P:cell adhesion; IEA.
DR InterPro: IPR008966; Adhes_bact.
DR InterPro: IPR004237; Fn_bind.
DR InterPro: IPR005877; Gpos_YsIRK.
DR InterPro: IPR001899; Gram_pos_anchor.
DR Pfam: PF02986; Fn_bind. 1.
DR Pfam: PF00746; Gram_pos_anchor. 1.
DR Pfam: PF04650; YsIRK_signal. 1.
DR TIGRFAMs: TIGR01167; LpxTG_anchor. 1.
DR TIGRFAMs: TIGR01168; YsIRK_signal. 1.
DR PROSITE: PS50847; GRAM_POS_ANCHORING. 1.
DR Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ SEQUENCE 961 AA; 106010 MW; 364940F884EA4101 CRC64;

Query Match          100.0%; Score 53; DB 2; Length 961;
Best Local Similarity 100.0%; Pred. No. 0.3;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DFEEDLPRV 10
   |||||
Db 796 DFEEDLPRV 805

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RX PubMed=15213324; DOI=10.1073/pnas.0402521101;
RA Holden M.T.G., Fell E.J., Lindsey J.A., Peacock S.J., Day N.P.J.,
RA Enright M.C., Foster T.O., Moore C.E., Hurst L., Atkin R., Barron A.,
RA Baeson N., Bentley S.D., Chillingworth C., Chillingworth T.,
RA Churcher C., Clark L., Corton C., Cronin A., Doggett J., Dowd L.,
RA Felwell T., Hance Z., Harris B., Hauser H., Holroyd S., Jaggel K.,
RA James K.D., Lennard N., Line A., Mayes R., Moule S., Mungall K.,
RA Ormond D., Quail M.A., Rabinowitch E., Rutherford K.M., Sanders M.,
RA Sharp S., Simmonds M., Stevens K., Whitehead S., Barrell B.G.,
RA Spratt B.G., Parkhill J.;
RT "Complete genomes of two clinical Staphylococcus aureus strains:
RT evidence for the rapid evolution of virulence and drug resistance.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:9786-9791(2004).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC an amide bond (By similarity).
DR EMBL: BX571856; CAG41560.1; -.
DR GO: GO:0009986; C:cell surface; IEA.
DR GO: GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO: GO:0016020; C:membrane; IEA.
DR GO: GO:0007155; P:cell adhesion; IEA.
DR InterPro: IPR008966; Adhes_bact.
DR InterPro: IPR004237; Fn_bind.
DR InterPro: IPR005877; Gpos_YsIRK.
DR InterPro: IPR001899; Gram_pos_anchor.
DR Pfam: PF02986; Fn_bind. 1.
DR Pfam: PF00746; Gram_pos_anchor. 1.
DR Pfam: PF04650; YsIRK_signal. 1.
DR TIGRFAMs: TIGR01167; LpxTG_anchor. 1.
DR TIGRFAMs: TIGR01168; YsIRK_signal. 1.
DR PROSITE: PS50847; GRAM_POS_ANCHORING. 1.
DR Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ SEQUENCE 965 AA; 105691 MW; 2982E132164D0551 CRC64;

Query Match          100.0%; Score 53; DB 2; Length 965;
Best Local Similarity 100.0%; Pred. No. 0.3;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DFEEDLPRV 10
   |||||
Db 814 DFEEDLPRV 823

RESULT 4
AC 08NUU7      PRELIMINARY;      PRT;      1015 AA.
ID 08NUU7:
DT 01-OCT-2002 (TEMBLrel. 22, Created)
DT 01-OCT-2002 (TEMBLrel. 22, Last annotation update)
DE Fnb protein.
GN Name=fnb: OrderedLocNames=MW2421;
OS Staphylococcus aureus (strain MW2).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxId=196620;
RN [1]
RX SEQUENCE FROM N.A.
STRAIN=MW2;
MEDLINE=22040717; PubMed=12044378; DOI=10.1016/S0140-6736(02)08713-5;
RA Baba T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Oguchi A.,
RA Nagai Y., Iwama N., Asano K., Naimi T., Kuroda H., Cui L.,
RA Yamamoto K., Hiramatsu K.;
RT "Genome and virulence determinants of high virulence community-
RT acquired MRSA."
RL Lancet 359:1819-1827(2002).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC an amide bond (By similarity).
DR EMBL: AP004830; BAB36286.1; -.
DR GO: GO:0009986; C:cell surface; IEA.
DR GO: GO:0005618; C:cell wall; IEA.
DR GO: GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO: GO:0016020; C:membrane; IEA.
DR GO: GO:0007155; P:cell adhesion; IEA.
DR InterPro: IPR008966; Adhes_bact.

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DR InterPro: IPR004237; Fn_bind.
DR InterPro: IPR005877; GpoS_Ysirk.
DR InterPro: IPR001899; Gram_pos_anchor.
DR Pfam: PF02986; Fn_bind. 1.
DR Pfam: PF00746; Gram_pos_anchor; 1.
DR Pfam: PF04650; Ysirk_signal; 1.
DR TIGRFAMs: TIGR01167; LPXTG_anchor; 1.
DR TIGRFAMs: TIGR01168; Ysirk_signal; 1.
DR PROSITE: PS50847; GRAM_POS_ANCHORING; 1.
KW Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ SEQUENCE 1015 AA; 11145 MW; DDF9281BB64D44D2 CRC64;

Query Match 100.0%; Score 53; DB 2; Length 1015;
Best Local Similarity 100.0%; Pred. No. 0.32;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DFEEDTLPRV 10
DB 850 DFEEDTLPRV 859

RESULT 5
ID 06G6H3 PRELIMINARY; PRT; 1015 AA;
AC 06G6H3;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Fibronectin-binding protein.
GN OrderedLocuNames=SA52388;
OS Staphylococcus aureus (strain MSSA476).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
NC NCBI_Taxid=282459;
RX [1]
RA SEQUENCE FROM N.A.
RP PubMed=1521324; DOI=10.1073/pnas.0402521101;
RX Holdren M.T.G., Fell E.J., Lindsay J.A., Peacock S.J., Day N.P.J.,
RA Burdett M.C., Foster T.J., Moore C.E., Hurst L., Atkin R., Barron A.,
RA Bason N., Bentley S.D., Chillingworth T.,
RA Churcher C., Clark L., Cotton C., Cronin A., Doggett J., Dowd L.,
RA Felwell T., Hance Z., Harris B., Hauser H., Holtroyd S., Jørgensen K.,
RA James K.D., Lennard N., Line A., Mayes R., Moule S., Mungall K.,
RA Ommond D., Quail M.A., Rabinowitsch E., Rutherford K.M., Sanders M.,
RA Sharp S., Simmonds M., Stevens K., Whitehead S., Barrett B.G.,
RA Spratt B.G., Parkhill J.;
RT "Complete genomes of two clinical Staphylococcus aureus strains:
RT evidence for the rapid evolution of virulence and drug resistance.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:9786-9791(2004).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC an amide bond (By similarity).
EMBL: BX571857; CACG44202.1; -
DR GO: GO:0009986; C:cell surface; IEA.
DR GO: GO:0005618; C:cell wall; IEA.
DR GO: GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO: GO:0016020; C:membrane; IEA.
DR GO: GO:0007155; P:cell adhesion; IEA.
DR InterPro: IPR008965; Adhes_bact.
DR InterPro: IPR004237; Fn_bind.
DR InterPro: IPR005877; GpoS_Ysirk.
DR InterPro: IPR001899; Gram_pos_anchor.
DR Pfam: PF02986; Fn_bind. 1.
DR Pfam: PF00746; Gram_pos_anchor; 1.
DR Pfam: PF04650; Ysirk_signal; 1.
DR TIGRFAMs: TIGR01167; LPXTG_anchor; 1.
DR TIGRFAMs: TIGR01168; Ysirk_signal; 1.
DR PROSITE: PS50847; GRAM_POS_ANCHORING; 1.
KW Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ SEQUENCE 1015 AA; 11145 MW; DDF9281BB64D44D2 CRC64;

Query Match 100.0%; Score 53; DB 2; Length 1015;
Best Local Similarity 100.0%; Pred. No. 0.32;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 DFEEDTLPRV 10
DB 850 DFEEDTLPRV 859

RESULT 6
ID FNBA_STRAU STANDARD; PRT; 1018 AA.
AC FNBA_STRAU
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Fibronectin-binding protein precursor (FNBP).
GN Name=FNBA;
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
NC NCBI_Taxid=1280;
RX [1]
RA SEQUENCE FROM N.A.
RP STRAIN=NCTC 8325-4;
RX MEDLINE=8908998; PubMed=2521391;
RA Signaes C., Raucsi G., Joensen K., Lindgren P.-E.,
RA Anantharamaiah G.M., Hoeoek M., Lindberg M.;
RT "Nucleotide sequence of the gene for a fibronectin-binding protein
RT from Staphylococcus aureus: use of this peptide sequence in the
RT synthesis of biologically active peptides.";
RL Proc. Natl. Acad. Sci. U.S.A. 86:689-703(1989).
CC -1- FUNCTION: The ability of bacteria to bind fibronectin has been
CC proposed as a virulence factor enabling bacteria to colonize wound
CC tissues and blood clots. Binding of plasma fibronectin to the
CC bacterial surface might block adhesion receptors on S. aureus, thus
CC representing an important defense mechanism against tissue
CC invasion.
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC an amide bond (Potential).
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@sib-sib.ch).
CC -----
EMBL: J04151; AAA26632.1; -
DR InterPro: IPR004237; Fn_bind.
DR InterPro: IPR005877; GpoS_Ysirk.
DR InterPro: IPR001899; Gram_pos_anchor.
DR Pfam: PF02986; Fn_bind. 1.
DR Pfam: PF00746; Gram_pos_anchor; 1.
DR Pfam: PF04650; Ysirk_signal; 1.
DR TIGRFAMs: TIGR01167; LPXTG_anchor; 1.
DR TIGRFAMs: TIGR01168; Ysirk_signal; 1.
DR PROSITE: PS50847; GRAM_POS_ANCHORING; 1.
KW Cell adhesion; Cell wall; Peptidoglycan-anchor; Repeat; Signal;
KW virulence.
FT SIGNAL 1 36
FT CHAIN 37 985
FT PROPEP 986 1018
FT REPEAT 545 574
FT REPEAT 575 604
FT DOMAIN 745 878
FT REPEAT 745 782
FT REPEAT 783 820
FT REPEAT 821 859
FT REPEAT 860 878
FT DOMAIN 879 948
FT REPEAT 879 892
FT REPEAT 893 906
FT REPEAT 907 920
FT REPEAT 921 934
FT REPEAT 935 948
FT REPEAT 948 948

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FT SITE 982 966 LPXTG sorting signal (Potential).
PT MOD_RES 985 985 Pentaglycyl murin peptidoglycan amidated
  threonine (Potential).
SQ SEQUENCE 1018 AA; 111780 MW; 5817580208B1F1F CRC64;

Query Match
Best Local Similarity 100.0%; Score 53; DB 1; Length 1018;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DFEEDTLPRV 10
DB 849 DFEEDTLPRV 854

RESULT 7
ID 099RD2 PRELIMINARY; PRT; 1038 AA.
AC 099RD2;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Fibronectin-binding protein homolog.
GN Name=fnb; OrderedlocusNames=SAV2503;
OS Staphylococcus aureus (strain Mu50 / ATCC 700699).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=158878;

[1]
SEQUENCE FROM N.A.
RP STRAIN=MU50 / ATCC 700699;
RX MEDLINE=21311952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2;
RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
  Cui L., Oguchi A., Aoki K.-I., Nagai Y., Iian J.-Q., Ito T.,
  Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,
  Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
  Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
  Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
  Hattori M., Ogasawara N., Hayaishi H., Hiramatsu K.;
RT "Whole genome sequencing of methicillin-resistant Staphylococcus
  aureus.";
RL Lancet 357:1225-1240(2001).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
  an amide bond (By similarity).
EMBL, AP003137; BAB43594.1; -.
DR GO; GO:0009986; C:cell surface; IEA.
DR GO; GO:0005618; C:cell wall; IEA.
DR GO; GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0007155; P:cell adhesion; IEA.
DR InterPro; IPR008966; Adhes_bact.
DR InterPro; IPR004237; Fn_bind.
DR InterPro; IPR005877; Gpos_YsIRK.
DR InterPro; IPR001899; Gram_pos_anchor.
DR Pfam; PF02986; Fn_bind.1.
DR Pfam; PF04650; Gram_pos_anchor; 1.
DR TIGRFAMs; TIGR01167; LPXTG_signal; 1.
DR TIGRFAMs; TIGR01168; YsIRK_signal; 1.
DR PROSITE; PS50847; GRAM_POS_ANCHORING; 1.
SQ SEQUENCE 1038 AA; 113618 MW; 666BF6BF2BFEB12 CRC64;

Query Match
Best Local Similarity 100.0%; Score 53; DB 2; Length 1038;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DFEEDTLPRV 10
DB 845 DFEEDTLPRV 854

RESULT 8
Q7A3J7

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ID Q7A3J7 PRELIMINARY; PRT; 1038 AA.
AC Q7A3J7;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Fnb protein.
GN Name=fnb; OrderedlocusNames=SA2291;
OS Staphylococcus aureus (strain N315).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=158879;

[1]
SEQUENCE FROM N.A.
RP MEDLINE=21311952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2;
RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
  Cui L., Oguchi A., Aoki K.-I., Nagai Y., Iian J.-Q., Ito T.,
  Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,
  Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
  Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
  Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
  Hattori M., Ogasawara N., Hayaishi H., Hiramatsu K.;
RT "Whole genome sequencing of methicillin-resistant Staphylococcus
  aureus.";
RL Lancet 357:1225-1240(2001).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
  an amide bond (By similarity).
EMBL, AP003137; BAB43594.1; -.
DR GO; GO:0009986; C:cell surface; IEA.
DR GO; GO:0005618; C:cell wall; IEA.
DR GO; GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0007155; P:cell adhesion; IEA.
DR InterPro; IPR008966; Adhes_bact.
DR InterPro; IPR004237; Fn_bind.
DR InterPro; IPR005877; Gpos_YsIRK.
DR InterPro; IPR001899; Gram_pos_anchor.
DR Pfam; PF02986; Fn_bind.1.
DR Pfam; PF04650; Gram_pos_anchor; 1.
DR TIGRFAMs; TIGR01167; LPXTG_signal; 1.
DR TIGRFAMs; TIGR01168; YsIRK_signal; 1.
DR PROSITE; PS50847; GRAM_POS_ANCHORING; 1.
SQ SEQUENCE 1038 AA; 113618 MW; 666BF6BF2BFEB12 CRC64;

Query Match
Best Local Similarity 100.0%; Score 53; DB 2; Length 1038;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DFEEDTLPRV 10
DB 845 DFEEDTLPRV 854

RESULT 9
ID Q53682 PRELIMINARY; PRT; 940 AA.
AC Q53682;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Fibronectin binding protein B.
GN Name=fnbB;
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1280;

[1]
SEQUENCE FROM N.A.
RP STRAIN=8325-4;
RX MEDLINE=92111475; PubMed=1837266;
RA Jonsson K., Sigfus C., Muller H.P., Lindberg M.;
RT "Two different genes encode fibronectin binding proteins in
  Staphylococcus aureus. The complete nucleotide sequence and
  characterization of the second gene.";

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RL Bur. J. Biochem. 202:1041-1048(1991).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC an amide bond (By similarity).
DR EMBL: X62992; CAA4726.1; -.
DR FIR: S19702; S19702.
DR HSSP: Q53653; 1N67.
DR GO: GO:0009986; C:cell surface; IEA.
DR GO: GO:0005618; C:cell wall; IEA.
DR GO: GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO: GO:0016020; C:membrane; IEA.
DR GO: GO:0007155; P:cell adhesion; IEA.
DR InterPro: IPR008966; Adhes_bact.
DR InterPro: IPR004237; Fn_bind.
DR InterPro: IPR005877; Gpos_Ysirk.
DR InterPro: IPR001899; Gram_pos_anchor.
DR Pfam: PF02986; Fn_bind_2.
DR Pfam: PF00746; Gram_pos_anchor; 1.
DR Pfam: PF04650; Ysirk_signal; 1.
DR TIGRFAMs: TIGR01167; LPXTG_anchor; 1.
DR TIGRFAMs: TIGR01168; Ysirk_signal; 1.
DR PROSITE: PSS0847; GRAM_POS_ANCHORING; 1.
KW Cell wall; Peptidoglycan-anchor.
SQ SEQUENCE 940 AA; 103555 MW; E35FBBCA907AE345 CRC64;

Query Match
Best Local Similarity 92.5%; Score 49; DB 2; Length 940;
Best Local Similarity 90.0%; Pred. No. 1.8;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DFEEDTLPKV 10
Db 785 DFEEDTLPOV 794

RESULT 10
ID Q8NU8 PRELIMINARY; PRT; 943 AA.
AC Q8NU8;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE FndB protein.
GN Name=fndB; OrderedlocusNames=MM2420;
OS Staphylococcus aureus (strain MM2).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
NC NCBI_TaxID=196620;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MM2;
RX MEDLINE=22040717; PubMed=12044378; DOI=10.1016/S0140-6736(02)08713-5;
RA Baba T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Oguchi A.,
RA Nagai Y., Iwano N., Amano K., Naito T., Kuroda H., Cui L.,
RA Yamamoto K., Hiramatsu K.
RT "genome and virulence determinants of high virulence community-
RT acquired MRSA."
RL Lancer 359:1819-1827(2002).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC an amide bond (By similarity).
DR EMBL: AP004830; BAB96285.1; -.
DR HSSP: Q53653; 1N67.
DR GO: GO:0009986; C:cell surface; IEA.
DR GO: GO:0005618; C:cell wall; IEA.
DR GO: GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO: GO:0016020; C:membrane; IEA.
DR GO: GO:0007155; P:cell adhesion; IEA.
DR InterPro: IPR008966; Adhes_bact.
DR InterPro: IPR004237; Fn_bind.
DR InterPro: IPR005877; Gpos_Ysirk.
DR InterPro: IPR001899; Gram_pos_anchor.
DR Pfam: PF02986; Fn_bind_1.
DR Pfam: PF00746; Gram_pos_anchor; 1.
DR Pfam: PF04650; Ysirk_signal; 1.
DR TIGRFAMs: TIGR01167; LPXTG_anchor; 1.
DR TIGRFAMs: TIGR01168; Ysirk_signal; 1.

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DR PROSITE: PSS0847; GRAM_POS_ANCHORING; 1.
KW Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ SEQUENCE 943 AA; 104537 MW; DA8A5F31947E1B6A CRC64;

Query Match
Best Local Similarity 92.5%; Score 49; DB 2; Length 943;
Best Local Similarity 90.0%; Pred. No. 1.8;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DFEEDTLPKV 10
Db 792 DFEEDTLPOV 801

RESULT 11
ID Q6G6H4 PRELIMINARY; PRT; 957 AA.
AC Q6G6H4;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Fibronectin-binding protein.
GN Name=fndB; OrderedlocusNames=SAS2387;
OS Staphylococcus aureus (strain MSSA476).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
NC NCBI_TaxID=282459;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=15213324; DOI=10.1073/pnas.0402521101;
RA Holden M.T.G., Fell E.J., Lindsay J.A., Peacock S.J., Day N.P.J.,
RA Burdett M.C., Foster T.J., Moore C.E., Hurst L., Acklin R., Barron A.,
RA Bason N., Bentley S.D., Chillingworth C., Chillingworth T.,
RA Churcher C., Clark L., Cotton C., Cronin A., Doggett J., Dowd L.,
RA Felwell T., Hance Z., Harris B., Hauser H., Holtroyd S., Jagsels K.,
RA James K.D., Leonard N., Line A., Mayes R., Moule S., Mungall K.,
RA Ormond D., Quail M.A., Rabinowitsch B., Rutherford K.M., Sanders M.,
RA Sharp S., Simmonds M., Stevens K., Whitehead S., Barrett B.G.,
RA Spratt B.G., Parkhill J.
RT "Complete genomes of two clinical Staphylococcus aureus strains:
RT evidence for the rapid evolution of virulence and drug resistance."
RL Proc. Natl. Acad. Sci. U.S.A. 101:9786-9791(2004).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC an amide bond (By similarity).
DR EMBL: BX571857; CAG44201.1; -.
DR GO: GO:0009986; C:cell surface; IEA.
DR GO: GO:0005618; C:cell wall; IEA.
DR GO: GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO: GO:0016020; C:membrane; IEA.
DR GO: GO:0007155; P:cell adhesion; IEA.
DR InterPro: IPR008966; Adhes_bact.
DR InterPro: IPR004237; Fn_bind.
DR InterPro: IPR005877; Gpos_Ysirk.
DR InterPro: IPR001899; Gram_pos_anchor.
DR Pfam: PF02986; Fn_bind_1.
DR Pfam: PF00746; Gram_pos_anchor; 1.
DR Pfam: PF04650; Ysirk_signal; 1.
DR TIGRFAMs: TIGR01167; LPXTG_anchor; 1.
DR TIGRFAMs: TIGR01168; Ysirk_signal; 1.
DR PROSITE: PSS0847; GRAM_POS_ANCHORING; 1.
KW Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ SEQUENCE 957 AA; 105980 MW; 28F8BA7FFFD3EAF CRC64;

Query Match
Best Local Similarity 92.5%; Score 49; DB 2; Length 957;
Best Local Similarity 90.0%; Pred. No. 1.8;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DFEEDTLPKV 10
Db 792 DFEEDTLPOV 801

RESULT 12
ID Q9AEP9 PRELIMINARY; PRT; 152 AA.

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AC 09AEP9;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DE 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Fibronectin-binding protein (Fragment).
GN Name=fnb;
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxId=1280;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CMRSA-1;
RX MEDLINE=21246681; PubMed=11349044;
DOI=10.1128/IAI.69.6.3791-3799.2001;
RA Rice K., Huesca M., Vaz D., McGavin M.J.;
RT Variance in Fibronectin binding and fnb locus polymorphisms in
RT Staphylococcus aureus: identification of antigenic variation in a
RT fibronectin binding protein adhesin of the epidemic CMRSA-1 strain of
RT methicillin-resistant S. aureus."
RL Infect. Immun. 69:3791-3799(2001).
DR EMBL, AY029184; AAK31588.1; -.
FT NON_TER 1
FT TER 152
SQ SEQUENCE 152 AA; 17193 MW; CFA3913C2B11C025 CRC64;

Query Match
Best Local Similarity 90.0%; Score 46; DB 2; Length 152;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DEEDTLPRV 10
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    |||
    |||
Db 142 DFEDTLPRV 151

RESULT 13
O8UCB6 PRELIMINARY; PRT; 424 AA.
AC O8UCB6;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DE 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE UDP-glucose/GDP-mannose dehydrogenase.
OS OrderedlocusNames=Atcu2582;
GN Agrobacterium tumefaciens (strain C58 / ATCC 33970).
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Rhizobiaceae; Rhizobium/Agrobacterium group; Agrobacterium.
OX NCBI_TaxId=176299;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Dupont;
RX MEDLINE=21608550; PubMed=11743193; DOI=10.1126/science.1066804;
Wood D.W., Setubal J.C., Kaul R., Monks D.E., Kitalima J.P.,
Wood K.V., Zhou Y., Chen L., Wood G.E., Almeida N.F. Jr., Woo L.,
Chen Y., Paulsen I.T., Eisen J.A., Karp P.D., Boyee D. Sr.,
Chapman P., Clendenning J., Deaerhug J., Gillet W., Grant C.,
Kutyavin T., Levy R., Li M.-J., McClelland E., Palmeri A.,
Raymond C., Rouse G., Saenphimachak C., Wu Z., Romero P., Gordon D.,
Zhang S., Yoo H., Tao Y., Biddle P., Jung M., Krespan W., Perry M.,
Gordon-Kamm B., Liao L., Kim S., Hendrick C., Zhao Z.-Y., Dolan M.,
Chumley F., Tingey S.V., Tomb J.-F., Gordon M.P., Olson M.V.,
Nester E.W.;
RA "The genome of the natural genetic engineer Agrobacterium tumefaciens
RA C58."
RL Science 294:2317-2323(2001).
DR EMBL, AE009204; AAL43563.1; -.
DR PIR, AE2893; AE2893.
DR PIR, H97668; H97668.
GO GO:0006118; P-electron transport; IEA.
DR pfam, PF00984; UDPG_MGDP_dh.1.
DR pfam, PF03720; UDPG_MGDP_dh.1.
DR pfam, PF03721; UDPG_MGDP_dh.N.1.
KW Complete proteome.
SQ SEQUENCE 424 AA; 46225 MW; BD48C6629BDBCB36 CRC64;
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Query Match
Best Local Similarity 70.0%; Score 39; DB 2; Length 424;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 DEEDTLPRV 10
    |||
    |||
    |||
Db 155 DFETSTIPRV 164

RESULT 14
O7CWO5 PRELIMINARY; PRT; 446 AA.
ID O7CWO5
AC O7CWO5;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE AGR C 4677P.
GN OrderedlocusNames=AGR_C_4677;
OS Agrobacterium tumefaciens (strain C58 / ATCC 33970).
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Rhizobiaceae; Rhizobium/Agrobacterium group; Agrobacterium.
OX NCBI_TaxId=176299;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Cereon;
RX MEDLINE=21608551; PubMed=11743194; DOI=10.1126/science.1066803;
Goodner B., Hinkle G., Gattung S., Miller N., Blanchard M.,
Quoiolo B., Goldman B.S., Cao Y., Askenazi M., Halling C., Mullin L.,
RA Houmel K., Gordon J., Vaudin M., Iartchouk O., Epp A., Liu F.,
RA Wollam C., Allinger M., Doughy D., Scott C., Lappas C., Markelz B.,
RA Flanagan C., Crowell C., Gursen J., Lomo C., Sear C., Strub G.,
Cielo C., Slater S.;
RT "Genome sequence of the plant pathogen and biotechnology agent
RT Agrobacterium tumefaciens C58."
RL Science 294:2323-2328(2001).
DR EMBL, AE008171; AAK8305.1; -.
DR GO:0006118; P-electron transport; IEA.
DR InterPro, IPR008927; 60GDH_C_like.
DR InterPro, IPR00205; NAD_BS.
DR InterPro, IPR011732; UDPG_MGDP_dh.
DR pfam, PF00984; UDPG_MGDP_dh.1.
DR pfam, PF03720; UDPG_MGDP_dh.C.1.
DR pfam, PF03721; UDPG_MGDP_dh.N.1.
SQ SEQUENCE 446 AA; 48481 MW; 451FB8280B52D250 CRC64;

Query Match
Best Local Similarity 73.6%; Score 39; DB 2; Length 446;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 DEEDTLPRV 10
    |||
    |||
    |||
Db 177 DFETSTIPRV 186

RESULT 15
O8P6R2 PRELIMINARY; PRT; 1096 AA.
ID O8P6R2
AC O8P6R2;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE HsdR protein.
GN OrderedlocusNames=XCC2905;
OS Xanthomonas campestris (pv. campestris).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
OC Xanthomonadaceae; Xanthomonas.
OX NCBI_TaxId=340;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 33913 / NCPPB 528;
RX MEDLINE=22022145; PubMed=12024217; DOI=10.1038/417459a;
da Silva A.C.R., Ferro J.A., Reinach F.C., Farah C.S., Furlan L.R.,
```

RA Quaggio R.B., Monteiro-Vitorello C.B., Van Sluys M.A., Almeida N.F.,
 RA Alves L.M.C., do Amaral A.M., Bertolini M.C., Camargo L.B.A.,
 RA Camarotte G., Camarvan F., Cardoso J., Chambergo F., Chapina L.P.,
 RA Ciccarelli R.M.B., Coutinho L.L., Cursino-Santos J.R., El-Dorry H.,
 RA Faria J.B., Ferreira A.J.S., Ferreira R.C.C., Ferro M.I.T.,
 RA Fomighieri E.F., Franco M.C., Greggio C.C., Gruber A.,
 RA Katuyama A.M., Kishi L.T., Leite R.P., Lemos E.G.M., Lemos M.V.F.,
 RA Locali E.C., Machado M.A., Madeira A.M.B.N., Martinez-Rosai N.M.,
 RA Martins E.C., Melanda J., Menck C.F.M., Miyaki C.Y., Moon D.H.,
 RA Moreira L.M., Novo M.T.M., Okura V.K., Oliveira M.C., Oliveira V.R.,
 RA Pereira H.A., Rossi A., Sena J.A.D., Silva C., de Souza R.F.,
 RA Spínola L.A.F., Takita M.A., Tamura R.E., Teixeira E.C., Tezza R.I.D.,
 RA Trindade dos Santos M., Truffi D., Tsai S.M., White F.F.,
 RA Setubal J.C., Kitzajima J.P.;
 RT "Comparison of the genomes of two Xanthomonas pathogens with differing
 RT host specificities";
 RL Nature 417:459-463(2002).
 DR EMBL: AE012404; AAM42177.1; -.
 DR GO: GO:0005524; P:ATP binding; IEA.
 DR GO: GO:0009035; F:Type I site-specific deoxyribonuclease acti. . .; IEA.
 DR GO: GO:0015668; F:Type III site-specific deoxyribonuclease ac. . .; IEA.
 DR GO: GO:0009307; P:DNA restriction; IEA.
 DR InterPro: IPR011545; DEAD/DEAH_N.
 DR InterPro: IPR007409; DUF450.
 DR InterPro: IPR004473; Hsdr.
 DR InterPro: IPR006935; ResIII.
 DR Pfam: PF04313; HSDR_N; 1.
 DR Pfam: PF04851; ResIII; 1.
 DR SMART: SM00487; DEXDC; 1.
 DR TIGRPFAM: TIGR00348; hsdR; 1.
 KM Complete proteome.
 SQ SEQUENCE 1096 AA; 122445 MW; 03FAE92D8DCB2F30 CRC64;

Query Match 73.6%; Score 39; DB 2; Length 1096;

Best Local Similarity 70.0%; Pred. No. 1.9e+02;

Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 DFEEDTLPRV 10

DB 633 DVDEDTLPEV 642

Search completed: October 22, 2005, 09:52:29
 Job time : 56.2069 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model
Run on: October 25, 2005, 20:58:51 ; Search time 97.5977 Seconds
(without alignments)
55.479 Million cell updates/sec

Title: US-10-731-238-105
Sequence: 1 SPEEDBEDPKPKYK_14
Perfect score: 76

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues
Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: Genesegp_16Dec04:*
2: genesegp1980s:*
3: genesegp1990s:*
4: genesegp2000s:*
5: genesegp2001s:*
6: genesegp2002s:*
7: genesegp2003as:*
8: genesegp2003bs:*
9: genesegp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	76	100.0	14	2	AAW65761
2	76	100.0	38	1	AAW65761 Peptide #
3	76	100.0	38	1	AAW65761 Peptide #
4	76	100.0	38	2	AAW65761 Peptide #
5	76	100.0	38	2	AAW65761 Peptide #
6	76	100.0	38	2	AAW65761 Peptide #
7	76	100.0	38	2	AAW65761 Peptide #
8	76	100.0	38	2	AAW65761 Peptide #
9	76	100.0	38	2	AAW65761 Peptide #
10	76	100.0	38	2	AAW65761 Peptide #
11	76	100.0	38	2	AAW65761 Peptide #
12	76	100.0	38	2	AAW65761 Peptide #
13	76	100.0	38	2	AAW65761 Peptide #
14	76	100.0	38	2	AAW65761 Peptide #
15	76	100.0	38	2	AAW65761 Peptide #
16	76	100.0	38	2	AAW65761 Peptide #
17	76	100.0	38	2	AAW65761 Peptide #
18	76	100.0	38	2	AAW65761 Peptide #
19	76	100.0	38	2	AAW65761 Peptide #
20	76	100.0	38	2	AAW65761 Peptide #
21	76	100.0	38	2	AAW65761 Peptide #
22	76	100.0	38	2	AAW65761 Peptide #
23	76	100.0	38	2	AAW65761 Peptide #
24	76	100.0	38	2	AAW65761 Peptide #
25	76	100.0	38	2	AAW65761 Peptide #

26	76	100.0	948	6	ADA89470
27	76	100.0	948	6	ADA89470
28	76	100.0	948	6	ADA89470
29	76	100.0	948	6	ADA89470
30	76	100.0	948	6	ADA89470
31	76	100.0	948	6	ADA89470
32	76	100.0	948	6	ADA89470
33	76	100.0	948	6	ADA89470
34	76	100.0	948	6	ADA89470
35	76	100.0	948	6	ADA89470
36	76	100.0	948	6	ADA89470
37	76	100.0	948	6	ADA89470
38	76	100.0	948	6	ADA89470
39	76	100.0	948	6	ADA89470
40	76	100.0	948	6	ADA89470
41	76	100.0	948	6	ADA89470
42	76	100.0	948	6	ADA89470
43	76	100.0	948	6	ADA89470
44	76	100.0	948	6	ADA89470
45	76	100.0	948	6	ADA89470

ALIGNMENTS

RESULT 1
ID AAW65761 standard; peptide; 14 AA.
XX
AC AAW65761;
XX
DT 16-OCT-1998 (first entry)
XX
DE Peptide #105.
XX
KW microbial surface components recognising adhesive matrix molecule;
KW MSCRAMM; fibronectin-binding protein; antibody; epitope;
KW antibiotic; bacterial infection; antibiotic-resistant strain.
XX
OS Synthetic.
OS Staphylococcus aureus.
XX
PN W09831369-A2.
XX
PD 23-JUL-1998.
XX
PF 21-JAN-1998; 98WO-US001222.
XX
PR 21-JAN-1997; 97US-0036139P.
XX
XX (TEXA) UNIV TEXAS A & M SYSTEM.
XX
XX Hoeok M, Patti JM, House-Pompeo KL, Speziale P, Joh D;
XX Mcgavin MJ;
XX WPI; 1998-413816/35.
XX
XX Antibody that binds to fibronectin-binding protein, preventing its
XX binding to fibronectin - used to treat or prevent bacterial infection,
XX especially by Staphylococci and Streptococci.
XX
XX Disclosure, Page 173; 201pp; English.
XX
XX The invention relates to antibodies that bind to a fibronectin-binding
XX domain of a fibronectin-binding protein, and inhibit binding of the
XX protein to fibronectin. Also claimed are: (1) isolated peptides of a
XX fibronectin-binding protein that do not bind to fibronectin; (2) fusion
XX protein containing at least one peptide of a fibronectin-binding protein
XX linked to a second amino acid sequence; (3) nucleic acid encoding the
XX isolated peptide of (1). Antibodies, the isolated peptides of (1) and the
XX nucleic acids are all useful for immunisation (active or passive) and (by
XX inhibiting binding of bacteria to fibronectin) for preventing or treating
XX infection in humans or other animals, particularly by staphylococci or

CC streptococci, e.g. meningitis, otitis media, pneumonia, endocarditis,
CC mastitis in cattle, abortion in horses and many others. Since the
CC antibodies block binding of bacteria, they should be effective against
CC antibiotic-resistant strains, and may replace antibiotic therapy or
CC increase its effectiveness. The present sequence is shown in the
CC specification
XX

SD Sequence 14 AA;

Query Match 100.0%; Score 76; DB 2; Length 14;
Best Local Similarity 100.0%; Pred. No. 6.8e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SPEEDTEEDKPKYE 14
DB 1 SPEEDTEEDKPKYE 14

RESULT 2

AA80660
ID AAP80660 standard; protein; 38 AA.

XX AAP80660;

XX 25-MAR-2003 (revised)

DT 07-OCT-1990 (first entry)

XX Protein with fibronectin binding ability.

DE Hybrid DNA molecule; fibronectin binding; mastitis; ruminants;
XX wound infection.

XX Staphylococcus aureus.

OS EP294349-A.

XX 07-DEC-1988.

XX 30-MAY-1988; 88EP-00850188.

XX 01-JUN-1987; 87SE-00002272.

XX (ALFA) ALFA LAVAL AGRIC INT AB.

XX Lindberg MK, Signas LC, Wadstrom TM, Froman G;

XX WPI; 1988-347978/49.

DR N-PSDB; AAN81097.

XX Hybrid DNA encoding Staphylococcus aureus fibronectin binding protein -
XX useful for immunisation and topical application to prevent staphylococcal
XX infections.

XX Claim 11; Page 12; 23pp; English.

XX The peptide has fibronectin binding ability. It is useful for immunising
XX ruminants against staphylococcal mastitis, pref. when used at 0.5-5
XX micrograms/kg, using 3 doses given at 1-3 week intervals; for topical
XX application to prevent wound infection, using an isotonic saline soln. of
XX concn. 25-250 micrograms/ml; and, when immobilised on a carrier, for
XX diagnosing staphylococcal infections. (Updated on 25-MAR-2003 to correct
XX PF field.) (Updated on 25-MAR-2003 to correct PA field.)
XX

SD Sequence 38 AA;

Query Match 100.0%; Score 76; DB 1; Length 38;
Best Local Similarity 100.0%; Pred. No. 0.00019;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SPEEDTEEDKPKYE 14
DB 8 SPEEDTEEDKPKYE 21

RESULT 3
AA82116
ID AAP82116 standard; protein; 38 AA.

XX AAP82116;

XX 25-MAR-2003 (revised)

DT 05-JAN-1990 (first entry)

XX Fibronectin binding protein.

DE Fibronectin binding protein.

XX Fibronectin binding protein; S. aureus; immunisation; mastitis; ruminants;

XX wound infection; diagnosis.

XX Staphylococcus aureus.

OS EP294349-A.

XX 07-DEC-1988.

XX 30-MAY-1988; 88EP-00850188.

XX 01-JUN-1987; 87SE-00002272.

XX (ALFA) ALFA LAVAL AGRIC INT AB.

XX Lindberg MK, Signas LC, Wadstrom TM, Froman G;

XX WPI; 1988-347978/49.

DR N-PSDB; AAN82054.

XX Hybrid DNA encoding Staphylococcus aureus fibronectin binding protein -
XX useful for immunisation and topical application to prevent staphylococcal
XX infections.

XX Claim 11; Page 12; 23pp; English.

XX The S. aureus fibronectin binding protein may be included in a hybrid
XX protein. The protein may be used to immunise ruminants against
XX staphylococcal mastitis, pref. when given at 0.5-5 microg/kg, using 3
XX doses at 1-3 week intervals; and for topical applicn. to prevent wound
XX infection, pref. using isotonic saline soln. of concn. 25-250 microg/mg.
XX The DNA encoding the binding protein and the hybrid protein may be
XX immobilised on a carrier and used to diagnose staphylococcal infections.
XX (Updated on 25-MAR-2003 to correct PA field.)
XX

SD Sequence 38 AA;

Query Match 100.0%; Score 76; DB 1; Length 38;
Best Local Similarity 100.0%; Pred. No. 0.00019;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SPEEDTEEDKPKYE 14
DB 8 SPEEDTEEDKPKYE 21

RESULT 4

AAW65662
ID AAW65662 standard; peptide; 38 AA.

XX AAW65662;

XX 16-OCT-1998 (first entry)

XX Fibronectin binding protein-derived peptide #6.

XX microbial surface components recognising adhesive matrix molecule;

XX MSCRAMM; fibronectin; fibronectin-binding protein; antibody; epitope;

XX antibiotic; bacterial infection; antibiotic-resistant strain.
XX Synthetic.

OS Staphylococcus aureus.
 XX
 PN MO9831389-A2.
 XX
 PD 23-JUL-1998.
 XX
 PF 21-JAN-1998; 98WO-US001222.
 XX
 PR 21-JAN-1997; 97US-0036139P.
 XX
 PA (TEXA) UNIV TEXAS A & M SYSTEM.
 PI Hoeoek M, Patli JM, House-Pompeo KL, Speziale P, Joh D,
 PI Mcgavin MJ;
 XX WPI; 1998-413816/35.
 DR
 XX
 PT Antibody that binds to fibronectin-binding protein, preventing its
 PT binding to fibronectin - used to treat or prevent bacterial infection,
 PT especially by Staphylococci and Streptococci.
 PS
 XX Example 2; Page 92; 201pp; English.
 CC The invention relates to antibodies that bind to a fibronectin-binding
 CC domain of a fibronectin-binding protein, and inhibit binding of the
 CC protein to fibronectin. Also claimed are: (1) isolated peptides of a
 CC fibronectin-binding protein that do not bind to fibronectin; (2) fusion
 CC protein containing at least one peptide of a fibronectin-binding protein
 CC linked to a second amino acid sequence; (3) nucleic acid encoding the
 CC isolated peptide of (1). Antibodies, the isolated peptides of (1) and the
 CC nucleic acids are all useful for immunisation (active or passive) and (by
 CC inhibiting binding of bacteria to fibronectin) for preventing or treating
 CC infection in humans or other animals, particularly by staphylococci or
 CC streptococci, e.g. meningitis, otitis media, pneumonia, endocarditis,
 CC mastitis in cattle, abortion in horses and many others. Since the
 CC antibodies block binding of bacteria, they should be effective against
 CC antibiotic-resistant strains, and may replace antibiotic therapy or
 CC increase its effectiveness. Sequences AAW65659-68 represent synthetic
 CC epitopes from the fibronectin binding domains DU and DI-D4 of the S.
 CC aureus fmda gene
 CC
 XX
 SQ Sequence 38 AA;
 CC
 XX
 Query Match 100.0%; Score 76; DB 2; Length 38;
 Best Local Similarity 100.0%; Pred. No. 0.00019;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 SPEEDTEEDKPKYE 14
 |||||
 DB 7 SPEEDTEEDKPKYE 20
 |||||
 RESULT 5
 ID AAW65699 standard; peptide; 38 AA.
 XX
 AC AAW65699;
 XX
 DT 16-OCT-1998 (first entry)
 XX
 DE Fibronectin binding protein-derived peptide #43.
 XX
 KM microbial surface components recognising adhesive matrix molecule;
 KM MSCRAMM; fibronectin; fibronectin-binding protein; antibody; epitope;
 KM antibiotic; bacterial infection; antibiotic-resistant strain.
 XX
 OS Synthetic.
 OS Staphylococcus aureus.
 XX
 PN MO9831389-A2.
 XX
 PD 23-JUL-1998.
 XX

PF 21-JAN-1998; 98WO-US001222.
 XX
 PR 21-JAN-1997; 97US-0036139P.
 XX
 PA (TEXA) UNIV TEXAS A & M SYSTEM.
 XX
 PI Hoeoek M, Patli JM, House-Pompeo KL, Speziale P, Joh D;
 PI Mcgavin MJ;
 XX WPI; 1998-413816/35.
 DR
 XX
 PT Antibody that binds to fibronectin-binding protein, preventing its
 PT binding to fibronectin - used to treat or prevent bacterial infection,
 PT especially by Staphylococci and Streptococci.
 PS
 XX Example 8; Page 102; 201pp; English.
 CC The invention relates to antibodies that bind to a fibronectin-binding
 CC domain of a fibronectin-binding protein, and inhibit binding of the
 CC protein to fibronectin. Also claimed are: (1) isolated peptides of a
 CC fibronectin-binding protein that do not bind to fibronectin; (2) fusion
 CC protein containing at least one peptide of a fibronectin-binding protein
 CC linked to a second amino acid sequence; (3) nucleic acid encoding the
 CC isolated peptide of (1). Antibodies, the isolated peptides of (1) and the
 CC nucleic acids are all useful for immunisation (active or passive) and (by
 CC inhibiting binding of bacteria to fibronectin) for preventing or treating
 CC infection in humans or other animals, particularly by staphylococci or
 CC streptococci, e.g. meningitis, otitis media, pneumonia, endocarditis,
 CC mastitis in cattle, abortion in horses and many others. Since the
 CC antibodies block binding of bacteria, they should be effective against
 CC antibiotic-resistant strains, and may replace antibiotic therapy or
 CC increase its effectiveness. Sequences AAW65691-700 represent a series of
 CC synthetic peptides based on the DI region of S. aureus fibronectin
 CC binding protein A. They were synthesised to contain mutations
 CC
 XX
 SQ Sequence 38 AA;
 CC
 XX
 Query Match 100.0%; Score 76; DB 2; Length 38;
 Best Local Similarity 100.0%; Pred. No. 0.00019;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 SPEEDTEEDKPKYE 14
 |||||
 DB 7 SPEEDTEEDKPKYE 20
 |||||
 RESULT 6
 ID AAW65661 standard; peptide; 38 AA.
 XX
 AC AAW65661;
 XX
 DT 16-OCT-1998 (first entry)
 XX
 DE Fibronectin binding protein-derived peptide #5.
 XX
 KM microbial surface components recognising adhesive matrix molecule;
 KM MSCRAMM; fibronectin; fibronectin-binding protein; antibody; epitope;
 KM antibiotic; bacterial infection; antibiotic-resistant strain.
 XX
 OS Synthetic.
 OS Staphylococcus aureus.
 XX
 PN MO9831389-A2.
 XX
 PD 23-JUL-1998.
 XX
 PF 21-JAN-1998; 98WO-US001222.
 XX
 PR 21-JAN-1997; 97US-0036139P.
 XX
 PA (TEXA) UNIV TEXAS A & M SYSTEM.
 XX

PI Hoeoek M, Patti JM, House-Pompeo KL, Speziale P, Joh D;
 PI Mcgavin MJ;
 DR WPI, 1998-413816/35.
 XX
 XX Antibody that binds to fibronectin-binding protein, preventing its
 PT binding to fibronectin - used to treat or prevent bacterial infection,
 PR especially by Staphylococci and Streptococci.
 PS
 XX Example 2; Page 92; 201pp; English.
 CC The invention relates to antibodies that bind to a fibronectin-binding
 CC domain of a fibronectin-binding protein, and inhibit binding of the
 CC protein to fibronectin. Also claimed are: (1) isolated peptides of a
 CC fibronectin-binding protein that do not bind to fibronectin; (2) fusion
 CC protein containing at least one peptide of a fibronectin-binding protein
 CC linked to a second amino acid sequence; (3) nucleic acid encoding the
 CC isolated peptide of (1). Antibodies, the isolated peptides of (1) and the
 CC nucleic acids are all useful for immunisation (active or passive) and (by
 CC inhibiting binding of bacteria to fibronectin) for preventing or treating
 CC infection in humans or other animals, particularly by staphylococci or
 CC streptococci, e.g. meningitis, otitis media, pneumonia, endocarditis,
 CC mastitis in cattle, abortion in horses and many others. Since the
 CC antibodies block binding of bacteria, they should be effective against
 CC antibiotic-resistant strains, and may replace antibiotic therapy or
 CC increase its effectiveness. Sequences AAM65569-68 represent synthetic
 CC epitopes from the fibronectin binding domains DU and DI-D4 of the S.
 CC aureus fmbA gene
 CC
 XX
 SQ Sequence 38 AA;
 QY
 Query Match 100.0%; Score 76; DB 2; Length 38;
 Best Local Similarity 100.0%; Pred. No. 0.00019;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 DB 1 SPEEDTEEDKPKYE 14
 7 SPEEDTEEDKPKYE 20
 RESULT 7
 AAM65712
 ID AAM65712 standard; peptide; 39 AA.
 AC AAM65712;
 XX
 XX 16-OCT-1998 (first entry)
 DT
 DE Fibronectin binding protein-derived peptide #56.
 XX
 XX microblal surface components recognising adhesive matrix molecule;
 KW MSCRAMM; fibronectin; fibronectin-binding protein; antibody; epitope;
 KW antibiotic; bacterial infection; antibiotic-resistant strain.
 XX
 OS Synthetic.
 OS Staphylococcus aureus.
 OS
 PN WO9831389-A2.
 XX
 PD 23-JUL-1998.
 XX
 PF 21-JAN-1998; 98WO-US001222.
 XX
 PR 21-JAN-1997; 97US-0036139P.
 XX
 PA (TEXA) UNIV TEXAS A & M SYSTEM.
 XX
 PI Hoeoek M, Patti JM, House-Pompeo KL, Speziale P, Joh D;
 PI Mcgavin MJ;
 XX WPI, 1998-413816/35.
 DR
 XX Antibody that binds to fibronectin-binding protein, preventing its

PT binding to fibronectin - used to treat or prevent bacterial infection,
 PT especially by Staphylococci and Streptococci.
 PS
 XX Example 8; Page 104; 201pp; English.
 CC The invention relates to antibodies that bind to a fibronectin-binding
 CC domain of a fibronectin-binding protein, and inhibit binding of the
 CC protein to fibronectin. Also claimed are: (1) isolated peptides of a
 CC fibronectin-binding protein that do not bind to fibronectin; (2) fusion
 CC protein containing at least one peptide of a fibronectin-binding protein
 CC linked to a second amino acid sequence; (3) nucleic acid encoding the
 CC isolated peptide of (1). Antibodies, the isolated peptides of (1) and the
 CC nucleic acids are all useful for immunisation (active or passive) and (by
 CC inhibiting binding of bacteria to fibronectin) for preventing or treating
 CC infection in humans or other animals, particularly by staphylococci or
 CC streptococci, e.g. meningitis, otitis media, pneumonia, endocarditis,
 CC mastitis in cattle, abortion in horses and many others. Since the
 CC antibodies block binding of bacteria, they should be effective against
 CC antibiotic-resistant strains, and may replace antibiotic therapy or
 CC increase its effectiveness. The present sequence is shown in the
 CC specification
 CC
 XX
 SQ Sequence 39 AA;
 QY
 Query Match 100.0%; Score 76; DB 2; Length 39;
 Best Local Similarity 100.0%; Pred. No. 0.00019;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 DB 1 SPEEDTEEDKPKYE 14
 7 SPEEDTEEDKPKYE 20
 RESULT 8
 AAM65713
 ID AAM65713 standard; peptide; 39 AA.
 AC AAM65713;
 XX
 XX 16-OCT-1998 (first entry)
 DT
 DE Fibronectin binding protein-derived peptide #57.
 XX
 XX microblal surface components recognising adhesive matrix molecule;
 KW MSCRAMM; fibronectin; fibronectin-binding protein; antibody; epitope;
 KW antibiotic; bacterial infection; antibiotic-resistant strain.
 XX
 OS Synthetic.
 OS Staphylococcus aureus.
 OS
 PN WO9831389-A2.
 XX
 PD 23-JUL-1998.
 XX
 PF 21-JAN-1998; 98WO-US001222.
 XX
 PR 21-JAN-1997; 97US-0036139P.
 XX
 PA (TEXA) UNIV TEXAS A & M SYSTEM.
 XX
 PI Hoeoek M, Patti JM, House-Pompeo KL, Speziale P, Joh D;
 PI Mcgavin MJ;
 XX WPI, 1998-413816/35.
 DR
 XX Antibody that binds to fibronectin-binding protein, preventing its
 PT binding to fibronectin - used to treat or prevent bacterial infection,
 PR especially by Staphylococci and Streptococci.
 PS
 XX Example 8; Page 104; 201pp; English.
 CC The invention relates to antibodies that bind to a fibronectin-binding
 CC domain of a fibronectin-binding protein, and inhibit binding of the

CC protein to fibronectin. Also claimed are: (1) isolated peptides of a
 CC fibronectin-binding protein that do not bind to fibronectin; (2) fusion
 CC protein containing at least one peptide of a fibronectin-binding protein
 CC linked to a second amino acid sequence; (3) nucleic acid encoding the
 CC isolated peptide of (1). Antibodies, the isolated peptides of (1) and the
 CC nucleic acids are all useful for immunisation (active or passive) and (by
 CC inhibiting binding of bacteria to fibronectin) for preventing or treating
 CC infection in humans or other animals, particularly by staphylococci or
 CC streptococci, e.g. meningitis, otitis media, pneumonia, endocarditis,
 CC mastitis in cattle, abortion in horses and many others. Since the
 CC antibodies block binding of bacteria, they should be effective against
 CC antibiotic-resistant strains, and may replace antibiotic therapy or
 CC increase its effectiveness. The present sequence is shown in the
 CC specification

SO Sequence 39 AA;

Query Match 100.0%; Score 76; DB 2; Length 39;

Best Local Similarity 100.0%; Pred. No. 0.00019; Mismatches 0; Indels 0; Gaps 0;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 SPEEDTEDEKPKYE 14
 Db 7 SPEEDTEDEKPKYE 20

RESULT 9

AA858806 standard; protein; 130 AA.

AA858806;

25-MAR-2003 (revised)

30-MAR-1995 (first entry)

Fibronectin binding domain D1-D4(709-838(P838T)).

Fibronectin binding protein; Fbp; fibronectin binding domain;

monoclonal antibody; Mab; adhesion; Gram-positive bacterium; bacteremia;

Escherichia coli.

Staphylococcus aureus.

MO9418327-A1.

18-AUG-1994.

04-FEB-1994; 94MO-GB000215.

05-FEB-1993; 93GB-00002289.

20-OCT-1993; 93GB-00021592.

(SMIK) SMITHKLINE BEECHAM PLC.

Burnham MKR, Chopra I, Critchley IA, Knowles DJC;

WPI; 1994-279748/34.

Fibronectin binding protein and monoclonal antibodies specific for Fbp -

useful to prevent adherence of Gram-positive bacteria to indwelling

devices or wounds.

Disclosure; Page 30; 40pp; English.

Polypeptides corresponding to residues G709-T886 plus PRIVPT, G709-

P838(P838T) and G709-P838 (AA858805-07, respectively) of S. aureus J2385

(NCIMB 40532) Fbp type A fibronectin binding domain D1-D4 region

(AA858808) were expressed in E. coli BL21(DE4) and used to raise Mabs

specific for Fbp. (Updated on 25-MAR-2003 to correct PN field.)

Best Local Similarity 100.0%; Pred. No. 0.00067; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SPEEDTEDEKPKYE 14
 Db 8 SPEEDTEDEKPKYE 21

RESULT 10

AA858807 standard; protein; 130 AA.

AA858807;

25-MAR-2003 (revised)

30-MAR-1995 (first entry)

Fibronectin binding domain D1-D4(709-838).

Fibronectin binding protein; Fbp; fibronectin binding domain;

monoclonal antibody; Mab; adhesion; Gram-positive bacterium; bacteremia;

Escherichia coli.

Staphylococcus aureus.

MO9418327-A1.

18-AUG-1994.

04-FEB-1994; 94MO-GB000215.

05-FEB-1993; 93GB-00002289.

20-OCT-1993; 93GB-00021592.

(SMIK) SMITHKLINE BEECHAM PLC.

Burnham MKR, Chopra I, Critchley IA, Knowles DJC;

WPI; 1994-279748/34.

Fibronectin binding protein and monoclonal antibodies specific for Fbp -

useful to prevent adherence of Gram-positive bacteria to indwelling

devices or wounds.

Disclosure; Page 30; 40pp; English.

Polypeptides corresponding to residues G709-T886 plus PRIVPT, G709-

P838(P838T) and G709-P838 (AA858805-07, respectively) of S. aureus J2385

(NCIMB 40532) Fbp type A fibronectin binding domain D1-D4 region

(AA858808) were expressed in E. coli BL21(DE4) and used to raise Mabs

specific for Fbp. (Updated on 25-MAR-2003 to correct PN field.)

Sequence 130 AA;

Query Match 100.0%; Score 76; DB 2; Length 130;

Best Local Similarity 100.0%; Pred. No. 0.00067; Mismatches 0; Indels 0; Gaps 0;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SPEEDTEDEKPKYE 14
 Db 8 SPEEDTEDEKPKYE 21

RESULT 11

AA891202 standard; peptide; 130 AA.

AA891202;

13-NOV-1996 (first entry)

D1-D4 fibronectin binding domains.

```

KM Fibronectin; oral hygiene; gingivitis; gum disease; adhesion;
KM periodontitis; oral pathogens; caries; calculus; candidiasis; oral surgery;
KM tissue regeneration; irrigation; toothpaste; dentifrice; mouthwash;
KM lozenge.
XX
XX Staphylococcus aureus.
XX
XX WO9604003-A1.
XX
XX 15-FEB-1996.
XX
XX 18-JUL-1995; 95WO-EP02825.
XX
XX 05-AUG-1994; 94GB-00015902.
XX
XX (SMITK ) SMITHKLINE BEECHAM PLC.
XX
XX Barnett P, Critchley IA, Dodd I;
XX
XX WPI; 1996-129122/13.
XX
XX Prevention of adherence of oral pathogens in the oral cavity, partic.
XX tooth surfaces - by application of a fibronectin binding protein or
XX polypeptide or a monoclonal antibody or fragment against it.
XX
XX Claim 5; Page 32; 41pp; English.
XX
XX Adherence of oral pathogens, particularly to tooth surfaces, can be
XX prevented by application of a fibronectin binding protein or polypeptide.
XX The fibronectin binding protein or polypeptide is useful in the
XX manufacture of oral hygiene compositions, eg. toothpaste, liquid
XX dentifrice, mouthwash or lozenge. They are useful to prevent the plaque-
XX related development of carious lesions, gingivitis, calculus or
XX periodontal disease and to combat oral cavity infections, e.g.
XX candidiasis. They may also be useful in oral surgery e.g. in guided
XX tissue regeneration procedures to prevent subsequent bacterial infection,
XX and for irrigation of periodontal pockets. This sequence corresponds to
XX amino acids 709-838 of the D1-D4 fibronectin binding domain of
XX Staphylococcus aureus
XX
XX SQ Sequence 130 AA;
XX
XX Query Match 100.0%; Score 76; DB 2; Length 130;
XX Best Local Similarity 100.0%; Pred. No. 0.00067;
XX Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 SPEEDTEEDKPKYE 14
XX |||||
XX 8 SPEEDTEEDKPKYE 21
XX
XX RESULT 12
XX ID AAR91201 standard; peptide; 130 AA.
XX
XX AC AAR91201;
XX
XX DT 13-NOV-1996 (first entry)
XX
XX DE D1-D4 fibronectin binding domains.
XX
XX DE D1-D4 fibronectin binding domains.
XX
XX DE Fibronectin; oral hygiene; gingivitis; gum disease; adhesion;
XX KM periodontitis; oral pathogens; caries; calculus; candidiasis; oral surgery;
XX KM tissue regeneration; irrigation; toothpaste; dentifrice; mouthwash;
XX KM lozenge.
XX
XX OS Staphylococcus aureus.
XX
XX OS WO9604003-A1.
XX
XX PN 15-FEB-1996.
XX
XX PD 18-JUL-1995; 95WO-EP02825.
XX
XX PF

```

```

XX
XX 05-AUG-1994; 94GB-00015902.
XX
XX (SMITK ) SMITHKLINE BEECHAM PLC.
XX
XX Barnett P, Critchley IA, Dodd I;
XX
XX WPI; 1996-129122/13.
XX
XX Prevention of adherence of oral pathogens in the oral cavity, partic.
XX tooth surfaces - by application of a fibronectin binding protein or
XX polypeptide or a monoclonal antibody or fragment against it.
XX
XX Claim 5; Page 31-32; 41pp; English.
XX
XX Adherence of oral pathogens, particularly to tooth surfaces, can be
XX prevented by application of a fibronectin binding protein or polypeptide.
XX The fibronectin binding protein or polypeptide is useful in the
XX manufacture of oral hygiene compositions, eg. toothpaste, liquid
XX dentifrice, mouthwash or lozenge. They are useful to prevent the plaque-
XX related development of carious lesions, gingivitis, calculus or
XX periodontal disease and to combat oral cavity infections, e.g.
XX candidiasis. They may also be useful in oral surgery e.g. in guided
XX tissue regeneration procedures to prevent subsequent bacterial infection,
XX and for irrigation of periodontal pockets. This sequence corresponds to
XX amino acids 709-838 of the D1-D4 fibronectin binding domain of
XX Staphylococcus aureus with a P838T substitution
XX
XX SQ Sequence 130 AA;
XX
XX Query Match 100.0%; Score 76; DB 2; Length 130;
XX Best Local Similarity 100.0%; Pred. No. 0.00067;
XX Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 SPEEDTEEDKPKYE 14
XX |||||
XX 8 SPEEDTEEDKPKYE 21
XX
XX Db
XX
XX RESULT 13
XX ID AAY29089 standard; protein; 134 AA.
XX
XX AC AAY29089;
XX
XX DT 28-SEP-1999 (first entry)
XX
XX DE Cloned fibronectin binding protein binding domain (FnDAB) sequence.
XX
XX DE Bovine herpes virus-2; BHV-2; cytokine; immune response; immunogen; IL;
XX KM interleukin; colony stimulating factor; CSF; interferon; IFN; TNF;
XX KM tumour necrosis factor; recombinant virus; vaccine; mucosal disease;
XX KM mastitis; breast cancer; stress-induced disease; binding domain; FnDAB;
XX KM fibronectin binding protein.
XX
XX OS Staphylococcus aureus.
XX
XX OS WO916892-A1.
XX
XX PN 08-APR-1999.
XX
XX PD 29-SEP-1998; 98WO-GB002927.
XX
XX PR 29-SEP-1997; 97GB-00020633.
XX
XX (UYBR-) UNITV BRISTOL.
XX
XX PA Bradley AJ, Duffas WP;
XX
XX PI WPI; 1999-255101/21.
XX
XX DR N-PSDB; AAX91506.
XX
XX PT New bovine herpes virus-2 vectors.

```

XX Example 2; Fig 8A-B; 130bp; English.

PS The invention provides bovine herpes virus-2 (BHV-2) based vectors that
CC comprise at least one cytokine-encoding DNA sequence. The expression of
CC cytokines in mammals can up-regulate immune responses to the immunogens.
CC The cytokine is selected from interleukins (IL), colony stimulating
CC factors (CSF), interferons (IFN) and tumour necrosis factors (TNF). The
CC BHV-2 based vector or recombinant virus can be used as vaccines. They can
CC be used for preventing or treating a mucosal disease in a subject, e.g.
CC ruminants, cattle, sheep, goats, dogs, cats, horses, or man, particularly
CC mastitis in cows or breast cancers in humans. They can also be used for
CC preventing or treating a stress-induced disease. The present sequence
CC represents a S. aureus fibronectin binding protein binding domain
CC sequence FNBA, the gene cloned for use in this invention. The gene has
CC 97.8 percent identity when compared to the previously published sequences
CC FNBA and FNBB
XX

XX Sequence 134 AA;

Query Match 100.0%; Score 76; DB 2; Length 134;
Best Local Similarity 100.0%; Pred. No. 0.00069;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SPEEDTEEDKPKYE 14
|||
DB 8 SFEDTEEDKPKYE 21

RESULT 14

AAAY29088
ID AAY29088 standard; protein; 134 AA.

XX AAY29088;

XX 28-SEP-1999 (first entry)

XX S. aureus fibronectin binding protein B (FnBB) binding domain.

XX Bovine herpes virus-2; BHV-2; cytokine; immune response; immunogen; IL;
XX Interleukin; colony stimulating factor; CSF; interferon; IFN; TNF;
XX tumour necrosis factor; recombinant virus; vaccine; mucosal disease;
XX mastitis; breast cancer; stress-induced disease; binding domain; FNBB;
XX fibronectin binding protein.

XX Staphylococcus aureus.

XX WO916892-A1.

XX 08-APR-1999.

XX 29-SEP-1998; 98WO-GB002927.

XX 29-SEP-1997; 97GB-00020633.

XX (UYBR-) UNIV BRISTOL.

XX Bradley AJ, Duffas WPH;

XX WPI; 1999-255101/21.

XX N-PSDB; AAX91505.

XX New bovine herpes virus-2 vectors.

XX Example 2; Fig 8A-B; 130bp; English.

XX The invention provides bovine herpes virus-2 (BHV-2) based vectors that
CC comprise at least one cytokine-encoding DNA sequence. The expression of
CC cytokines in mammals can up-regulate immune responses to the immunogens.
CC The cytokine is selected from interleukins (IL), colony stimulating
CC factors (CSF), interferons (IFN) and tumour necrosis factors (TNF). The
CC BHV-2 based vector or recombinant virus can be used as vaccines. They can
CC be used for preventing or treating a mucosal disease in a subject, e.g.

CC ruminants, cattle, sheep, goats, dogs, cats, horses, or man, particularly
CC mastitis in cows or breast cancers in humans. They can also be used for
CC preventing or treating a stress-induced disease. The present sequence
CC represents the binding domain of a previously published S. aureus
CC fibronectin binding protein B (FNBB) sequence. The FNBB binding domain
CC gene sequence FNBA, cloned for use in this invention has 97.8 percent
CC identity when compared to the previously published FNBA and FNBB gene
CC sequences
XX

XX Sequence 134 AA;

Query Match 100.0%; Score 76; DB 2; Length 134;
Best Local Similarity 100.0%; Pred. No. 0.00069;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SPEEDTEEDKPKYE 14
|||
DB 8 SFEDTEEDKPKYE 21

RESULT 15

AAAY29087
ID AAY29087 standard; protein; 134 AA.

XX AAY29087;

XX 28-SEP-1999 (first entry)

XX S. aureus fibronectin binding protein A (FNBA) binding domain.

XX Bovine herpes virus-2; BHV-2; cytokine; immune response; immunogen; IL;
XX Interleukin; colony stimulating factor; CSF; interferon; IFN; TNF;
XX tumour necrosis factor; recombinant virus; vaccine; mucosal disease;
XX mastitis; breast cancer; stress-induced disease; binding domain; FNBA;
XX fibronectin binding protein.

XX Staphylococcus aureus.

XX WO916892-A1.

XX 08-APR-1999.

XX 29-SEP-1998; 98WO-GB002927.

XX 29-SEP-1997; 97GB-00020633.

XX (UYBR-) UNIV BRISTOL.

XX Bradley AJ, Duffas WPH;

XX WPI; 1999-255101/21.

XX N-PSDB; AAX91504.

XX New bovine herpes virus-2 vectors.

XX Example 2; Fig 8A-B; 130bp; English.

XX The invention provides bovine herpes virus-2 (BHV-2) based vectors that
CC comprise at least one cytokine-encoding DNA sequence. The expression of
CC cytokines in mammals can up-regulate immune responses to the immunogens.
CC The cytokine is selected from interleukins (IL), colony stimulating
CC factors (CSF), interferons (IFN) and tumour necrosis factors (TNF). The
CC BHV-2 based vector or recombinant virus can be used as vaccines. They can
CC be used for preventing or treating a mucosal disease in a subject, e.g.
CC ruminants, cattle, sheep, goats, dogs, cats, horses, or man, particularly
CC mastitis in cows or breast cancers in humans. They can also be used for
CC preventing or treating a stress-induced disease. The present sequence
CC represents the binding domain of a previously published S. aureus
CC fibronectin binding protein A (FNBA) sequence. The FNBB binding domain
CC gene sequence FNBA, cloned for use in this invention has 97.8 percent
CC identity when compared to the previously published FNBA and FNBB gene
CC sequences
XX

sq Sequence 134 AA;

Query Match 100.0%; Score 76; DB 2; Length 134;

Best Local Similarity 100.0%; Pred. No. 0.00069; Mismatches 0; Indels 0; Gaps 0;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SPEEDTEEDPKYE 14

Db 8 SPEEDTEEDPKYE 21

Search completed: October 25, 2005, 21:29:15
Job time : 97.5977 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 22, 2005, 07:41:53 ; Search time 24.2184 Seconds
(without alignments)
43.153 Million cell updates/sec

Title: US-10-731-238-105

Sequence: 1 SFEDTEBDKPKYE 14

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*

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- 2: /cgn2_6/ptodata/1/1aa/5B COMB .pep:*
- 3: /cgn2_6/ptodata/1/1aa/6A COMB .pep:*
- 4: /cgn2_6/ptodata/1/1aa/6B COMB .pep:*
- 5: /cgn2_6/ptodata/1/1aa/PTUG COMB .pep:*
- 6: /cgn2_6/ptodata/1/1aa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	76	100.0	14	US-09-010-317-105	Sequence 105, App
2	76	100.0	38	US-08-234-622A-2	Sequence 2, Appl
3	76	100.0	38	US-08-729-767-3	Sequence 3, Appl
4	76	100.0	38	US-09-010-317-5	Sequence 5, Appl
5	76	100.0	38	US-09-010-317-6	Sequence 6, Appl
6	76	100.0	38	US-09-010-317-43	Sequence 43, Appl
7	76	100.0	39	US-09-010-317-56	Sequence 56, Appl
8	76	100.0	39	US-09-010-317-57	Sequence 57, Appl
9	76	100.0	114	US-08-259-000-3	Sequence 8, Appl
10	76	100.0	130	US-08-459-135A-7	Sequence 7, Appl
11	76	100.0	130	US-08-459-135A-8	Sequence 8, Appl
12	76	100.0	130	US-08-495-559-7	Sequence 7, Appl
13	76	100.0	130	US-08-495-559-8	Sequence 8, Appl
14	76	100.0	139	US-08-856-253-8	Sequence 8, Appl
15	76	100.0	174	US-08-459-135A-10	Sequence 10, Appl
16	76	100.0	174	US-08-459-135A-13	Sequence 13, Appl
17	76	100.0	174	US-08-495-559-10	Sequence 10, Appl
18	76	100.0	174	US-08-495-559-13	Sequence 13, Appl
19	76	100.0	176	US-08-495-559-6	Sequence 6, Appl
20	76	100.0	178	US-08-459-135A-12	Sequence 12, Appl
21	76	100.0	178	US-08-495-559-12	Sequence 12, Appl
22	76	100.0	181	US-08-459-135A-6	Sequence 6, Appl
23	76	100.0	559	US-08-956-171E-5251	Sequence 5251, Ap
24	76	100.0	559	US-08-781-986A-5251	Sequence 5251, Ap
25	76	100.0	1027	US-08-956-171E-5254	Sequence 5254, Ap
26	76	100.0	1027	US-08-781-986A-5254	Sequence 5254, Ap
27	72	94.7	38	US-08-234-622A-3	Sequence 3, Appl

ALIGNMENTS

28	72	94.7	38	1	US-08-729-767-4	Sequence 4, Appl
29	72	94.7	38	4	US-09-010-317-7	Sequence 7, Appl
30	72	94.7	38	4	US-09-010-317-8	Sequence 8, Appl
31	72	94.7	38	4	US-09-010-317-49	Sequence 49, Appl
32	70	92.1	38	4	US-09-010-317-36	Sequence 36, Appl
33	70	92.1	38	4	US-09-010-317-37	Sequence 37, Appl
34	70	92.1	38	4	US-09-010-317-39	Sequence 39, Appl
35	70	92.1	38	4	US-09-010-317-40	Sequence 40, Appl
36	70	92.1	38	4	US-09-010-317-41	Sequence 41, Appl
37	69	90.8	38	4	US-09-010-317-38	Sequence 38, Appl
38	69	90.8	38	4	US-09-010-317-42	Sequence 42, Appl
39	66	86.8	38	4	US-09-010-317-35	Sequence 35, Appl
40	66	86.8	38	4	US-09-010-317-46	Sequence 46, Appl
41	66	86.8	38	4	US-09-010-317-47	Sequence 47, Appl
42	65	85.5	38	4	US-09-010-317-48	Sequence 48, Appl
43	64	84.2	38	4	US-09-010-317-44	Sequence 44, Appl
44	62	81.6	38	4	US-09-010-317-45	Sequence 45, Appl
45	60	78.9	12	4	US-09-010-317-62	Sequence 62, Appl

RESULT 1
US-09-010-317-105
Sequence 105, Application US/09010317
Patent No. 6685943
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
APPLICANT: Patti, Joseph M.
APPLICANT: House-Pompeo, Karen L.
APPLICANT: Speziale, Pietro
APPLICANT: McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
TITLE OF INVENTION: AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAMK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 105:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-09-010-317-105
Query Match 100.0%; Score 76; DB 4; Length 14;
Best Local Similarity 100.0%; Pred. No. 2e-05;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SPEEDTEEDKPKYE 14
| | | | | | | | | | | | | | | |

Db 1 SPEEDTEEDKPKYE 14

RESULT 2
US-08-234-622A-2
; Sequence 2, Application US/08234622A
; Patent No. 5440014
; GENERAL INFORMATION:
; APPLICANT: HOOK, Magnus
; APPLICANT: MCGAVIN, Martin
; APPLICANT: RAUCCI, Giuseppe
; TITLE OF INVENTION: A FIBRONECTIN BINDING PEPTIDE
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Doane, Swecker & Mathis
; STREET: P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/234,622A
; FILING DATE: 28-APR-1994
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: SE 9002617-0
; FILING DATE: 10-AUG-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/SE91/00534
; FILING DATE: 09-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Weuth, Donna M
; REGISTRATION NUMBER: 36,607
; REFERENCE/DOCKET NUMBER: 012885-044
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 38 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-234-622A-2

Query Match 100.0%; Score 76; DB 1; Length 38;
Best Local Similarity 100.0%; Pred. No. 5.5e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SPEEDTEEDKPKYE 14
| | | | | | | | | | | | | | | |

Db 7 SPEEDTEEDKPKYE 20

RESULT 3
US-08-729-767-3
; Sequence 3, Application US/08729767
; Patent No. 5770702
; GENERAL INFORMATION:
; APPLICANT: HOOK, Magnus
; APPLICANT: LINDBERG, Martin Kjell
; APPLICANT: SIGNAS, Lars Christer
; APPLICANT: WADSTROM, Torkel Mikael

APPLICANT: FROMAN, Gunnar
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN AS WELL AS
; TITLE OF INVENTION: ITS PREPARATION
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Doane, Swecker & Mathis, L.L.P.
; STREET: P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/729,767
; FILING DATE: 07-OCT-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/259,000
; FILING DATE: 13-JUN-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/007,817
; FILING DATE: 22-JAN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/201,028
; FILING DATE: 01-JUN-1988
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: SE 8702272-9
; FILING DATE: 01-JUN-1987
; ATTORNEY/AGENT INFORMATION:
; NAME: McGowan, Malcolm K.
; REGISTRATION NUMBER: 39,300
; REFERENCE/DOCKET NUMBER: 012889-036
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 38 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-729-767-3

Query Match 100.0%; Score 76; DB 1; Length 38;
Best Local Similarity 100.0%; Pred. No. 5.5e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SPEEDTEEDKPKYE 14
| | | | | | | | | | | | | | | |

Db 8 SPEEDTEEDKPKYE 21

RESULT 4
US-09-010-317-5
; Sequence 5, Application US/09010317
; Patent No. 6685943
; GENERAL INFORMATION:
; APPLICANT: Hook, Magnus
; APPLICANT: Patti, Joseph M.
; APPLICANT: House-Pompeo, Karen L.
; APPLICANT: Speciale, Pietro
; APPLICANT: Joh, Danny
; APPLICANT: McGavin, Martin J.
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
; NUMBER OF SEQUENCES: 105
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee

STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAMK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-09-010-317-5

Query Match 100.0%; Score 76; DB 4; Length 38;
Best Local Similarity 100.0%; Pred. No. 5.5e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 SPEEDTEEDPKPYE 14
Db 7 SPEEDTEEDPKPYE 20

RESULT 5
US-09-010-317-6
Sequence 6, Application US/09010317
Patent No. 6685943
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
APPLICANT: Patli, Joseph M.
APPLICANT: House-Pompeo, Karen L.
APPLICANT: Speziale, Pietro
APPLICANT: Joh, Danny
APPLICANT: Mcgavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
TITLE OF INVENTION: AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/036,139

FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAMK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-09-010-317-6

Query Match 100.0%; Score 76; DB 4; Length 38;
Best Local Similarity 100.0%; Pred. No. 5.5e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SPEEDTEEDPKPYE 14
Db 7 SPEEDTEEDPKPYE 20

RESULT 6
US-09-010-317-43
Sequence 43, Application US/09010317
Patent No. 6685943
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
APPLICANT: Patli, Joseph M.
APPLICANT: House-Pompeo, Karen L.
APPLICANT: Speziale, Pietro
APPLICANT: Joh, Danny
APPLICANT: Mcgavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
TITLE OF INVENTION: AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAMK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 43:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-09-010-317-43

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/259,000
FILING DATE: 13-JUN-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: SE 8702272-9
FILING DATE: 01-JUN-1987
ATTORNEY/AGENT INFORMATION:
NAME: Meuth, Donna M
REGISTRATION NUMBER: 36,607
REFERENCE/DOCKET NUMBER: 012885-062
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-5620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 114 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-259-000-3

Query Match 100.0%; Score 76; DB 1; Length 114;
Best Local Similarity 100.0%; Pred. No. 0.00017;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SPEEDTEEDPKYE 14
DB 8 SPEEDTEEDPKYE 21

RESULT 10
US-08-459-135A-7
Sequence 7, Application US/08459135A
Patent No. 5955078
GENERAL INFORMATION:
APPLICANT: BURHAM, Martin Karl Russel
APPLICANT: CHOPRA, Ian
APPLICANT: CRITCHLEY, Ian Alfred
APPLICANT: KNOWLES, David Justin Charles
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN: MONOCLONAL ANTIBODY AND THEIR US
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Smithkline Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
STATE: PA
COUNTRY: U.S.A.
ZIP: 19406-0939
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: Fastseq, Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/459,135A
FILING DATE: 02-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB/94/00215
FILING DATE: 04-Feb-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Gimmil, Edward R
REGISTRATION NUMBER: 38,891
REFERENCE/DOCKET NUMBER: P30591C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-4478
TELEFAX: 610-270-5090
TELEX:

INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 130 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-459-135A-7

Query Match 100.0%; Score 76; DB 2; Length 130;
Best Local Similarity 100.0%; Pred. No. 0.0002;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SPEEDTEEDPKYE 14
DB 8 SPEEDTEEDPKYE 21

RESULT 11
US-08-459-135A-8
Sequence 8, Application US/08459135A
Patent No. 5955078
GENERAL INFORMATION:
APPLICANT: BURHAM, Martin Karl Russel
APPLICANT: CHOPRA, Ian
APPLICANT: CRITCHLEY, Ian Alfred
APPLICANT: KNOWLES, David Justin Charles
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN: MONOCLONAL ANTIBODY AND THEIR US
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Smithkline Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
STATE: PA
COUNTRY: U.S.A.
ZIP: 19406-0939
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: Fastseq, Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/459,135A
FILING DATE: 02-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB/94/00215
FILING DATE: 04-Feb-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Gimmil, Edward R
REGISTRATION NUMBER: 38,891
REFERENCE/DOCKET NUMBER: P30591C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-4478
TELEFAX: 610-270-5090
TELEX:

INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 130 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-459-135A-8

Query Match 100.0%; Score 76; DB 2; Length 130;
Best Local Similarity 100.0%; Pred. No. 0.0002;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SPEEDTEEDPKYE 14
DB 8 SPEEDTEEDPKYE 21

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RESULT 12
US-08-495-559-7
Sequence 7, Application US/08495559A
Patent No. 6054572
GENERAL INFORMATION:
APPLICANT: BURMAN, Martin Karl Russel
APPLICANT: CHOPRA, Ian
APPLICANT: CRITCHLEY, Ian Alfred
APPLICANT: KNOWLES, David Juetin Charles
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN: MONOCLONAL
FILE REFERENCE: P30591
CURRENT APPLICATION NUMBER: US/08/495,559A
EARLIER FILING DATE: 1995-08-03
EARLIER APPLICATION NUMBER: GB 9302289.5
EARLIER FILING DATE: 1993-02-05
EARLIER APPLICATION NUMBER: GB 9321592.9
EARLIER FILING DATE: 1993-10-20
NUMBER OF SEQ ID NOS: 13
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 7
LENGTH: 130
TYPE: PRT
ORGANISM: Staphylococcus aureus
US-08-495-559-7

Query Match      100.0%; Score 76; DB 3; Length 130;
Best Local Similarity 100.0%; Pred. No. 0.0002;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0.

QY      1 SPEEDTEEDKPKYE 14
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DB       8 SPEEDTEEDKPKYE 21

RESULT 13
US-08-495-559-8
Sequence 8, Application US/08495559A
Patent No. 6054572
GENERAL INFORMATION:
APPLICANT: BURMAN, Martin Karl Russel
APPLICANT: CHOPRA, Ian
APPLICANT: CRITCHLEY, Ian Alfred
APPLICANT: KNOWLES, David Juetin Charles
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN: MONOCLONAL
FILE REFERENCE: P30591
CURRENT APPLICATION NUMBER: US/08/495,559A
EARLIER FILING DATE: 1995-08-03
EARLIER APPLICATION NUMBER: GB 9302289.5
EARLIER FILING DATE: 1993-02-05
EARLIER APPLICATION NUMBER: GB 9321592.9
EARLIER FILING DATE: 1993-10-20
NUMBER OF SEQ ID NOS: 13
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 8
LENGTH: 130
TYPE: PRT
ORGANISM: Staphylococcus aureus
US-08-495-559-8

Query Match      100.0%; Score 76; DB 3; Length 130;
Best Local Similarity 100.0%; Pred. No. 0.0002;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0.

QY      1 SPEEDTEEDKPKYE 14
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DB       8 SPEEDTEEDKPKYE 21

RESULT 14
US-08-856-253-8
Sequence 8, Application US/08856253

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Patent No. 6288214
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
APPLICANT: Patti, Joseph M.
APPLICANT: House-Pompeo, Karen
APPLICANT: Narayanam, Narayana
APPLICANT: Symersky, Jindrich
TITLE OF INVENTION: COLLAGEN BINDING PROTEIN COMPOSITIONS
TITLE OF INVENTION: AND METHODS OF USE
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: Texas
COUNTRY: U.S.
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/856,253
FILING DATE: Concurrently Herewith
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/017,678
FILING DATE: 16-MAY-1996
ATTORNEY/AGENT INFORMATION:
NAME: Kirchell, Barbara S.
REGISTRATION NUMBER: 33,928
REFERENCE/DOCKET NUMBER: TMK:193
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
TELEFAX: (512) 474-7577
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 139 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-08-856-253-8

Query Match 100.0%; Score 76; DB 3; Length 139;
Best Local Similarity 100.0%; Pred. NO. 0.00021;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SPEEDTEDEKPYE 14
| | | | | | | | | | | | | | | | | | | | | |
DB 22 SPEEDTEDEKPYE 35

RESULT 15
US-08-459-135A-10
; Sequence 10, Application US/08459135A
; Patent No. 5955078
; GENERAL INFORMATION:
; APPLICANT: BURNHAM, Martin Karl Russel
; APPLICANT: CHOPRA, Ian
; APPLICANT: CRITCHLEY, Ian Alfred
; APPLICANT: KNOWLES, David Justin Charles
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN: MONOCLONAL ANTIBODY AND THEIR USE
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Smithline Beecham Corporation
; STREET: 709 Swedeland Road
; CITY: King of Prussia
; STATE: PA
; COUNTRY: U.S.A.
; ZIP: 19406-0939
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette

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COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: Pastseq, Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/459,135A
FILING DATE: 02-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB/94/00215
FILING DATE: 04-Feb-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Gimmil, Edward R.
REGISTRATION NUMBER: 38,891
REFERENCE/DOCKET NUMBER: P30591C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-4478
TELEFAX: 610-270-5090
TELEX:
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 174 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULAR TYPE: Protein
US-08-459-135A-10

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Best Local Similarity 100.0%; Pred. No. 0.00026;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 8 SFEDTEEDKKPYE 21

Search completed: October 22, 2005, 09:35:47
Job time : 24.2184 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 22, 2005, 12:39:57 ; Search time 78.6092 Seconds
(without alignments)
74.354 Million cell updates/sec

Title: US-10-731-238-105
Perfect score: 76
Sequence: 1 SPEEDTEBDPKRYE 14

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1862951 seqs, 417491010 residues
Total number of hits satisfying chosen parameters: 1862951

Minimum DB seq length: 0
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Post-Processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

Published Applications AA:
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2: /cgn2_6/prodata/2/pubppaa/PCT_NEW_PUB.pep:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	76	100.0	38	US-10-731-238-5	Sequence 5, Appl
3	76	100.0	38	US-10-731-238-6	Sequence 6, Appl
4	76	100.0	38	US-10-731-238-43	Sequence 43, Appl
5	76	100.0	39	US-10-731-238-56	Sequence 56, Appl
6	76	100.0	39	US-10-731-238-57	Sequence 57, Appl
7	76	100.0	139	US-09-813-820-8	Sequence 8, Appl
8	76	100.0	388	US-08-901-062-1	Sequence 1, Appl
9	76	100.0	559	US-08-781-986A-5251	Sequence 5251, Ap
10	76	100.0	559	US-10-329-624-5251	Sequence 5251, Ap
11	76	100.0	767	US-09-815-242-5899	Sequence 5899, Ap

12	76	100.0	767	9	US-09-815-242-13140	Sequence 13140, A
13	76	100.0	940	17	US-10-470-048B-424	Sequence 424, App
14	76	100.0	948	17	US-10-470-048B-69	Sequence 69, Appl
15	76	100.0	961	15	US-10-282-122A-43778	Sequence 43778, A
16	76	100.0	978	9	US-09-815-242-5456	Sequence 5456, Ap
17	76	100.0	1001	9	US-09-815-242-12686	Sequence 12686, A
18	76	100.0	1018	9	US-09-815-242-5797	Sequence 5797, Ap
19	76	100.0	1018	9	US-09-815-242-12838	Sequence 12838, A
20	76	100.0	1018	17	US-10-470-048B-68	Sequence 68, Appl
21	76	100.0	1027	8	US-08-781-986A-5254	Sequence 5254, Ap
22	76	100.0	1027	15	US-10-329-624-5254	Sequence 5254, A
23	76	100.0	1038	15	US-10-282-122A-43827	Sequence 43827, A
24	76	100.0	1038	14	US-10-287-821-1	Sequence 1, Appl
25	72	94.7	31	14	US-10-731-238-7	Sequence 2, Appl
26	72	94.7	31	14	US-10-731-238-7	Sequence 7, Appl
27	72	94.7	38	18	US-10-731-238-8	Sequence 8, Appl
28	72	94.7	38	18	US-10-731-238-49	Sequence 49, Appl
29	72	94.7	38	18	US-10-731-238-46	Sequence 46, Appl
30	70	92.1	38	18	US-10-731-238-37	Sequence 37, Appl
31	70	92.1	38	18	US-10-731-238-39	Sequence 39, Appl
32	70	92.1	38	18	US-10-731-238-40	Sequence 40, Appl
33	70	92.1	38	18	US-10-731-238-41	Sequence 41, Appl
34	69	90.8	38	18	US-10-731-238-38	Sequence 38, Appl
35	69	90.8	38	18	US-10-731-238-42	Sequence 42, Appl
36	66	86.8	38	18	US-10-731-238-35	Sequence 35, Appl
37	66	86.8	38	18	US-10-731-238-46	Sequence 46, Appl
38	66	86.8	38	18	US-10-731-238-47	Sequence 47, Appl
39	65	85.5	38	18	US-10-731-238-48	Sequence 48, Appl
40	64	84.2	38	18	US-10-731-238-44	Sequence 44, Appl
41	62	81.6	38	18	US-10-731-238-45	Sequence 45, Appl
42	60	78.9	12	18	US-10-731-238-62	Sequence 62, Appl
43	60	78.9	38	18	US-10-731-238-60	Sequence 60, Appl
44	56	71.7	10	18	US-10-731-238-68	Sequence 68, Appl
45	54	71.1	10	18	US-10-731-238-67	Sequence 67, Appl

ALIGNMENTS

RESULT 1
US-10-731-238-105
Sequence 105, Application US/10731238
Publication No. US20050123552A1
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
Pattli, Joseph M.
House-Pompeo, Karen L.
Speziale, Pietro
Job, Danny
McGavin, Martin J.
TITLE OF INVENTION: FIBROBLAST BINDING PROTEIN COMPOSITIONS
AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSER: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/731,238
FILING DATE: 10-Dec-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE: 21-Jan-1998
APPLICATION NUMBER: US 60/036,139

FILED DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAMK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 105:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 105:
US-10-731-238-105

Query Match 100.0%; Score 76; DB 18; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.00013;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SPEEDTEEDKPKYE 14
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Db 1 SPEEDTEEDKPKYE 14

RESULT 2
US-10-731-238-5
Sequence 5, Application US/10731238
Publication No. US20050123552A1
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
Patti, Joseph M.
House-Pompeo, Karen L.
Speziale, Pietro
Joh, Danny
McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Releasee #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/731,238
FILING DATE: 10-Dec-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE: 21-Jan-1998
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAMK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>

TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-10-731-238-5

Query Match 100.0%; Score 76; DB 18; Length 38;
Best Local Similarity 100.0%; Pred. No. 0.00038;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SPEEDTEEDKPKYE 14
| | | | | | | | | | | | | | | |
Db 7 SPEEDTEEDKPKYE 20

RESULT 3
US-10-731-238-6
Sequence 6, Application US/10731238
Publication No. US20050123552A1
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
Patti, Joseph M.
House-Pompeo, Karen L.
Speziale, Pietro
Joh, Danny
McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Releasee #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/731,238
FILING DATE: 10-Dec-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE: 21-Jan-1998
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAMK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-10-731-238-6

Query Match 100.0%; Score 76; DB 18; Length 38;
Best Local Similarity 100.0%; Pred. No. 0.00038;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SPEEDTEEDKPKYE 14
| | | | | | | | | | | | | | | |
Db 7 SPEEDTEEDKPKYE 20

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RESULT 4
US-10-731-238-43
; Sequence 43, Application US/10731238
; Publication No. US20050123552A1
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
             Patti, Joseph M.
             House-Pompeo, Karen L.
             Speziale, Pietro
             Joh, Danny
             McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSER: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/731,238
FILING DATE: 10-Dec-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE: 21-Jan-1998
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-Jan-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAMK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 43:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 43:
US-10-731-238-43
Query Match      100.0%; Score 76; DB 18; Length 38;
Best Local Similarity 100.0%; Pred. No. 0.00039;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 SPEEDTEEDKPKYE 14
    |||||||
    7 SPEEDTEEDKPKYE 20
Db

RESULT 5
US-10-731-238-56
; Sequence 56, Application US/10731238
; Publication No. US20050123552A1
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
             Patti, Joseph M.
             House-Pompeo, Karen L.
             Speziale, Pietro
             Joh, Danny
             McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
AND METHODS OF USE
```

```
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSER: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/731,238
FILING DATE: 10-Dec-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE: 21-Jan-1998
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-Jan-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAMK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 56:
SEQUENCE CHARACTERISTICS:
LENGTH: 39 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 56:
US-10-731-238-56
Query Match      100.0%; Score 76; DB 18; Length 39;
Best Local Similarity 100.0%; Pred. No. 0.00039;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 SPEEDTEEDKPKYE 14
    |||||||
    7 SPEEDTEEDKPKYE 20
Db

RESULT 6
US-10-731-238-57
; Sequence 57, Application US/10731238
; Publication No. US20050123552A1
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
             Patti, Joseph M.
             House-Pompeo, Karen L.
             Speziale, Pietro
             Joh, Danny
             McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSER: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
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;/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/10/731,238
/ FILING DATE: 10-Dec-2003
/ CLASSIFICATION: <Unknown>
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US/09/010,317
/ FILING DATE: 21-Jan-1998
/ APPLICATION NUMBER: US 60/036,139
/ FILING DATE: 21-Jan-1997
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Hibler, David W.
/ REGISTRATION/DOCKET NUMBER: 41,071
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 512-418-3000
/ TELEFAX: 512-474-7577
/ INFORMATION FOR SEQ ID NO: 57:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 39 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: <Unknown>
/ TOPOLOGY: linear
/ SEQUENCE DESCRIPTION: SEQ ID NO: 57:
/ US-10-731-238-57
/ Query Match 100.0%; Score 76; DB 18; Length 39;
/ Best Local Similarity 100.0%; Pred. No. 0.00039;
/ Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
/ QY 1 SPEEDTEEDKPKYE 14
/ |||||
/ Db 7 SPEEDTEEDKPKYE 20
/ RESULT 7
/ US-09-813-820-8
/ Sequence 8, Application US/09813820
/ Patent No. US20020102262A1
/ GENERAL INFORMATION:
/ APPLICANT: Hook, Magnus
/ Patti, Joseph M.
/ House-Pompeo, Karen
/ Sthanam, Narayana
/ Symeraky, Jindrich
/ TITLE OF INVENTION: COLLAGEN BINDING PROTEIN COMPOSITIONS
/ NUMBER OF SEQUENCES: 8
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Arnold, White & Durkee
/ STREET: P.O. Box 4433
/ CITY: Houston
/ STATE: Texas
/ COUNTRY: U.S.
/ ZIP: 77210
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/813,820
/ FILING DATE: 22-Mar-2001
/ CLASSIFICATION: <Unknown>
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/856,253
/ FILING DATE: <Unknown>
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Kitchell, Barbara S.
/ REGISTRATION/DOCKET NUMBER: 33,928
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (512) 418-3000
/ TELEFAX: (512) 474-7577

;/ INFORMATION FOR SEQ ID NO: 8:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 139 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: <Unknown>
/ TOPOLOGY: linear
/ SEQUENCE DESCRIPTION: SEQ ID NO: 8:
/ US-09-813-820-8
/ Query Match 100.0%; Score 76; DB 9; Length 139;
/ Best Local Similarity 100.0%; Pred. No. 0.0014;
/ Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
/ QY 1 SPEEDTEEDKPKYE 14
/ |||||
/ Db 22 SPEEDTEEDKPKYE 35
/ RESULT 8
/ US-08-901-062-1
/ Sequence 1, Application US/08901062
/ Publication No. US20020025324A1
/ GENERAL INFORMATION:
/ APPLICANT: SEALS, JONATHAN R.
/ TITLE OF INVENTION: RECOMBINANT BIVALENT BACTERIAL VACCINE
/ NUMBER OF SEQUENCES: 2
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: HALE AND DORR LLP
/ STREET: 60 State Street
/ CITY: Boston
/ STATE: MA
/ COUNTRY: United States Of America
/ ZIP: 02109
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/901,062
/ FILING DATE: 25-JUL-1997
/ CLASSIFICATION: 424
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Baker, Hollie L.
/ REGISTRATION NUMBER: 31,321
/ REFERENCE/DOCKET NUMBER: 106941.153
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (617) 526-6000
/ TELEFAX: (617) 526-5000
/ INFORMATION FOR SEQ ID NO: 1:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 388 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ HYPOTHETICAL: NO
/ ANTI-SENSE: NO
/ US-08-901-062-1
/ Query Match 100.0%; Score 76; DB 8; Length 388;
/ Best Local Similarity 100.0%; Pred. No. 0.0042;
/ Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
/ QY 1 SPEEDTEEDKPKYE 14
/ |||||
/ Db 271 SPEEDTEEDKPKYE 284
/ RESULT 9
/ US-08-781-986A-5251
/ Sequence 5251, Application US/08781986A

Publication No. US20030054436A1
GENERAL INFORMATION:
APPLICANT: Charles Kunsch
TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
NUMBER OF SEQUENCES: 5255
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COUNTRY: USA
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/781,986A
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Benson, Bob
REGISTRATION NUMBER: 30,446
REFERENCE/DOCKET NUMBER: PB248PP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 5251:
SEQUENCE CHARACTERISTICS:
LENGTH: 559 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-781-986A-5251

Query Match 100.0%; Score 76; DB 8; Length 559;
Best Local Similarity 100.0%; Pred. No. 0.0061;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SPEEDTEEDPKPYE 14
Db 307 SPEEDTEEDPKPYE 320

RESULT 10
US-10-329-624-5251
Sequence 5251, Application US/10329624
Publication No. US20040043037A1
GENERAL INFORMATION:
APPLICANT: Charles Kunsch
Gil H. Choi
Patrick S. Dillon
Craig A. Rosen
Steven C. Barash
Michael R. Fannon
TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
NUMBER OF SEQUENCES: 5256
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COUNTRY: USA
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2

SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/329,624
FILING DATE: 27-Dec-2002
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/956,171
FILING DATE: October 20, 1997
APPLICATION NUMBER: 60/009,861
FILING DATE: January 5, 1996
APPLICATION NUMBER: 08/781,986
FILING DATE: January 3, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Mark J. Hyman
REGISTRATION NUMBER: 46,789
REFERENCE/DOCKET NUMBER: PB248P1D1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (240) 314-1224
TELEFAX: (301) 309-8439
INFORMATION FOR SEQ ID NO: 5251:
SEQUENCE CHARACTERISTICS:
LENGTH: 559 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 5251:
US-10-329-624-5251

Query Match 100.0%; Score 76; DB 15; Length 559;
Best Local Similarity 100.0%; Pred. No. 0.0061;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SPEEDTEEDPKPYE 14
Db 307 SPEEDTEEDPKPYE 320

RESULT 11
US-09-815-242-5899
Sequence 5899, Application US/09815242
Patent No. US20020061569A1
GENERAL INFORMATION:
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Karl L.
APPLICANT: Zysek, Judith W.
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John D.
APPLICANT: Carr, Grant J.
APPLICANT: Yamamoto, Robert T.
TITLE OF INVENTION: Identification of Essential Genes in
FILE REFERENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 5899
LENGTH: 767

```

; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-09-815-242-5899

Query Match
Best Local Similarity 100.0%; Score 76; DB 9; Length 767;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SPEEDTEEDKPKYE 14
DB 688 SPEEDTEEDKPKYE 701

RESULT 12
US-09-815-242-13140
; Sequence 13140, Application US/09815242
; Patent No. US2002061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Karl L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; TITLE OF INVENTION: Prokaryotes
; FILE REFERENCE: ELITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13140
; LENGTH: 767
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-09-815-242-13140

Query Match
Best Local Similarity 100.0%; Score 76; DB 9; Length 767;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SPEEDTEEDKPKYE 14
DB 688 SPEEDTEEDKPKYE 701

RESULT 13
US-10-470-048B-424
; Sequence 424, Application US/10470048B
; Publication No. US2005003744A1
; GENERAL INFORMATION:
; APPLICANT: MEINKE ET AL.
; TITLE OF INVENTION: A METHOD FOR IDENTIFICATION, ISOLATION AND PRODUCTION OF
; FILE REFERENCE: SONN:035US
; CURRENT APPLICATION NUMBER: US/10/470,048B
; CURRENT FILING DATE: 2003-07-25
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; NUMBER OF SEQ ID NOS: 603
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 424
; LENGTH: 940
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-10-470-048B-424

Query Match
Best Local Similarity 100.0%; Score 76; DB 17; Length 940;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SPEEDTEEDKPKYE 14
DB 688 SPEEDTEEDKPKYE 701

RESULT 14
US-10-470-048B-69
; Sequence 69, Application US/10470048B
; Publication No. US2005003744A1
; GENERAL INFORMATION:
; APPLICANT: MEINKE ET AL.
; TITLE OF INVENTION: A METHOD FOR IDENTIFICATION, ISOLATION AND PRODUCTION OF
; FILE REFERENCE: SONN:035US
; CURRENT APPLICATION NUMBER: US/10/470,048B
; CURRENT FILING DATE: 2003-07-25
; NUMBER OF SEQ ID NOS: 603
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 69
; LENGTH: 948
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-10-470-048B-69

Query Match
Best Local Similarity 100.0%; Score 76; DB 17; Length 948;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SPEEDTEEDKPKYE 14
DB 696 SPEEDTEEDKPKYE 709

RESULT 15
US-10-282-122A-43778
; Sequence 43778, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangnu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Karl
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
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; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 43778
; LENGTH: 961
; TYPE: PRF
; ORGANISM: Staphylococcus aureus
US-10-282-122A-43778

Query Match 100.0%; Score 76; DB 15; Length 961;
Best Local Similarity 100.0%; Pred. No. 0.011;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SPEEDTEEDPKYE 14
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DB 699 SPEEDTEEDPKYE 712

Search completed: October 22, 2005, 12:56:31
Job time : 79.6092 secs

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OM protein - protein search, using SW model

Run on: October 22, 2005, 08:04:46 ; Search time 16.2529 Seconds
(without alignments)
82.880 Million cell updates/sec

Title: US-10-731-238-105
Perfect score: 76
Sequence: 1 SPEEDTEEDKPKYE 14

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Length	DB	ID	Description
1	76	100.0	940	2	S19702 fibronectin-binding
2	76	100.0	961	2	G90053 fibronectin-binding
3	76	100.0	1018	2	A32192 fibronectin-binding
4	76	100.0	1038	2	H90053 fibronectin-binding
5	47	61.8	1074	2	T01906 fibronectin-binding
6	44	57.9	448	2	S39348 26S ATP/ubiquitin-
7	44	57.9	467	2	F90989 sensor protein for
8	44	57.9	467	2	A85835 sensor protein (fo
9	44	57.9	467	2	B64974 sensory kinase Bae
10	44	57.9	697	2	T16908 fibronectin-binding
11	43	56.6	152	2	D64169 methylglyoxal synt
12	43	56.6	653	2	T15665 fibronectin-binding
13	43	56.6	784	2	T45971 fibronectin-binding
14	43	56.6	845	2	A45669 neurofilament trip
15	42	55.3	56	2	S74259 tropomyosin T 3, fast
16	42	55.3	67	2	S48660 tropomyosin T 1, fast
17	42	55.3	258	2	I53021 tropomyosin T - human
18	42	55.3	261	2	T02107 fibronectin-binding
19	42	55.3	283	2	T16644 fibronectin-binding
20	42	55.3	517	1	A39038 1-caldesmon, nonmu
21	42	55.3	689	4	S30392 fibronectin-binding
22	42	55.3	771	1	A33430 h-caldesmon - chick
23	42	55.3	849	2	S00030 neurofilament trip
24	41.5	54.6	700	2	T24092 fibronectin-binding
25	41.5	54.6	783	2	F88808 protein R09E10.3
26	41	53.9	51	2	I66796 fetal tropomyosin T 3
27	41	53.9	56	2	I33073 fetal tropomyosin T 2
28	41	53.9	193	2	H69938 conserved hypother
29	41	53.9	298	2	T47760 fibronectin-binding

30	41	53.9	371	2	A55302 probable transcrip
31	41	53.9	467	2	AG0771 probable two-compo
32	41	53.9	470	2	T49175 fibronectin-binding
33	41	53.9	548	2	T27542 fibronectin-binding
34	41	53.9	633	2	S45877 uracil transport p
35	41	53.9	890	2	S44150 coat protein - str
36	41	53.9	952	2	S64473 translocation initia
37	41	53.9	1192	2	A71623 probable secreted
38	41	53.9	2257	2	T33152 fibronectin-binding
39	40	52.6	205	2	T18811 probable chloride
40	40	52.6	209	2	H69901 general stress pro
41	40	52.6	240	2	T25191 fibronectin-binding
42	40	52.6	316	2	T11021 farnesyltransferas
43	40	52.6	435	2	S69035 fibronectin-binding
44	40	52.6	446	2	T01524 zinc finger protei
45	40	52.6	550	2	B82074 1-aspartate oxidas

ALIGNMENTS

RESULT 1
S19702 fibronectin-binding protein B - Staphylococcus aureus
C/Species: Staphylococcus aureus
C/Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
R/Accession: S19702
R/Accession: K.; Signaes, C.; Mueller, H.P.; Lindberg, M.
Eur. J. Biochem. 202, 1041-1048, 1991
A/Title: Two different genes encode fibronectin binding proteins in Staphylococcus aureus
A/Reference number: S19702, PMID:92111475, PMID:1837266
A/Accession: S19702
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-940 <JOB>
A/Cross-references: UNIPROT:Q53682; EMBL:X62992; NID:G49040; PIDD:CAA44726.1; PID:G58156;
C/Keywords: fibronectin binding

Query Match 100.0%; Score 76; DB 2; Length 940;
Best Local Similarity 100.0%; Pred. No. 0.00067;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SPEEDTEEDKPKYE 14
Db 688 SPEEDTEEDKPKYE 701

RESULT 2

G90053 fibronectin-binding protein fmbB [imported] - Staphylococcus aureus (strain N315)
C/Species: Staphylococcus aureus
C/Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C/Accession: G90053
R/Kuroda, M.; Ohba, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguchi, A.; Mizutani, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kato, C.; Sekimizu, K.; Imae, A.; Shibata, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
A/Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.
A/Reference number: A89758; PMID:11418146

A/Accession: G90053
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-961 <KUR>
A/Cross-references: UNIPROT:Q99RD3; GB:BA000018; PID:G13702452; PIDD:BA843593.1; GSPDB:G13702452
A/Experimental source: strain N315
C/Genetics:
A/Genes: fmbB

Query Match 100.0%; Score 76; DB 2; Length 961;
Best Local Similarity 100.0%; Pred. No. 0.00068;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SPEEDTEEDKPKYE 14

DB 699 SPEEDTEEDPKPYE 712

RESULT 3

A32192
fibronectin-binding protein - Staphylococcus aureus
C:Species: Staphylococcus aureus
C:Date: 31-Jul-1989 #sequence_revision 31-Jul-1989 #text_change 16-Feb-1997
C:Accession: A32192
R:Signaas, C.; Raucel, G.; Joensen, K.; Lindgren, P.E.; Anantharamaiah, G.M.; Hoeoek, M.
Proc. Natl. Acad. Sci. U.S.A. 86, 699-703, 1989
A:Title: Nucleotide sequence of the gene for a fibronectin-binding protein from Staphylococcus aureus
A:Reference number: A32192; MUID:89038998; PMID:2521391
A:Accession: A32192
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1018 <SIG>
A:Cross-references: GB:J04151
C:Keywords: fibronectin binding

Query Match 100.0%; Score 76; DB 2; Length 1018;

Best Local Similarity 100.0%; Pred. No. 0.00073;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SPEEDTEEDPKPYE 14

DB 752 SPEEDTEEDPKPYE 765

RESULT 4

H90053
hypothetical protein fmb [imported] - Staphylococcus aureus (strain N315)
C:Species: Staphylococcus aureus
C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C:Accession: H90053
R:Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguc
ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.;
C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
A:Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.
A:Reference number: A89758; MUID:21311952; PMID:11418146
A:Accession: H90053
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1038 <KUN>
A:Cross-references: UNIPROT:Q99RD2; GB:BA000018; PID:G13702453; PIDN:BA843594.1; GSPDB:G
A:Experimental source: strain N315
C:Genetics:
A:Gene: fmb

Query Match 100.0%; Score 76; DB 2; Length 1038;

Best Local Similarity 100.0%; Pred. No. 0.00074;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SPEEDTEEDPKPYE 14

DB 748 SPEEDTEEDPKPYE 761

RESULT 5

T01906
hypothetical protein T12H20.3 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear crebs)
C:Date: 26-Feb-1999 #sequence_revision 26-Feb-1999 #text_change 09-Jul-2004
C:Accession: T01906
R:Corrton, M.; Graves, T.; Suterer, C.; Modde, T.
submitted to the EMBL Data Library, July 1998
A:Description: The sequence of A. thaliana T12H20.
A:Reference number: Z14453
A:Accession: T01906
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA

A:Residues: 1-1074 <COT>
A:Cross-references: UNIPROT:O82491; EMBL:AF080119; NID:G3600029; PID:G3600033
A:Experimental source: cultivar Columbia
C:Genetics:
A:Map position: 4
A:Note: T12H20.3

Query Match 61.8%; Score 47; DB 2; Length 1074;

Best Local Similarity 66.7%; Pred. No. 25;

Matches 8; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 SPEEDTEEDPKPYE 12

DB 459 SPEEDTEEDPKPYE 470

RESULT 6

S39348
26S ATP/ubiquitin-dependent proteinase chain S4 - fission yeast (Schizosaccharomyces pombe)
C:Species: Schizosaccharomyces pombe
C:Date: 18-Feb-1994 #sequence_revision 23-Feb-1996 #text_change 09-Jul-2004
C:Accession: S39348; T40421
R:Gordon, C.; McGurk, G.; Dillon, P.; Rosen, C.; Hastie, N.D.
Nature 366, 355-357, 1993
A:Title: Defective mitosis due to a mutation in the gene for a fission yeast 26S protease
A:Reference number: S39348; MUID:94067321; PMID:8247131
A:Accession: S39348
A:Status: nucleic acid sequence not shown
A:Molecule type: DNA
A:Residues: 1-448 <GOR>
A:Cross-references: UNIPROT:P36612; EMBL:Z29366; NID:G442507; PIDN:CAA82554.1; PID:G44250
R:McDougal, R.C.; Rajandream, M.A.; Barrell, B.G.; Brown, S.; Harte, D.
submitted to the EMBL Data Library, October 1999
A:Reference number: Z21927
A:Accession: T40421
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-448 <MCD>
A:Cross-references: EMBL:AL121863; PIDN:CA58406.1; GSPDB:GN00067; SPDB:SPBC4.07C
A:Experimental source: strain 972h-; cosmid c4
C:Genetics:
A:Gene: SPBC4.07C
A:Map position: 2
A:Introns: 1/3
C:Superfamily: ATP-dependent 26S proteinase; FtsH/SEC18/CDC48-type ATP-binding domain hom
C:Keywords: ATP; nucleotide binding; nucleus; Pilcop
F:205-416/Domain: FtsH/SEC18/CDC48-type ATP-binding domain homology <VATP>
F:232-239/Region: nucleotide-binding motif A (P-loop)

Query Match 57.9%; Score 44; DB 2; Length 448;

Best Local Similarity 58.3%; Pred. No. 29;

Matches 7; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 3 EEDTEEDPKPYE 14

DB 21 KKDQKDKPKPYE 32

RESULT 7

F90989
sensor protein for Baer [imported] - Escherichia coli (strain O157:H7, substrain R1MD 05C)
C:Species: Escherichia coli
C:Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 09-Jul-2004
C:Accession: F90989
R:Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.;
gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shingawa, H.
DNA Res. 8, 11-22, 2001
A:Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and genom
A:Reference number: A99629; MUID:21156231; PMID:11258796
A:Accession: F90989
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-467 <HAY>

A:Cross-references: UNIPROT:Q8X712; GB:BA000007; PIDN:BAE36309.1; PID:G13362355; GSPDB:G
 A:Experimental source: strain O157:H7, substrain RIMD 0509952
 C:Species: Escherichia coli
 C:Accession: A85835
 A:Gene: EC82886

Query Match 57.9%; Score 44; DB 2; Length 467;
 Best Local Similarity 72.7%; Pred. No. 31;
 Matches 8; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 SPEEDTEEDKP 11
 DB 84 SFEHDSSEDKP 94

RESULT 8

Sensor protein (for Baer) [imported] - Escherichia coli (strain O157:H7, substrain EDL93
 A:Accession: A85835
 C:Species: Escherichia coli
 C:Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
 C:Accession: A85835
 R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew
 Miller, L.; Grothbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca,
 Nature 409, 529-533, 2001
 A:Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
 A:Reference number: A85480; MUID:21074935; PMID:11206551
 A:Accession: A85835
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-467 <STO>
 A:Cross-references: UNIPROT:Q8X712; GB:AE005174; NID:G12516284; PIDN:AA657141.1; GSPDB:G
 A:Experimental source: strain O157:H7, substrain EDL933
 C:Genetics:
 A:Gene: baes

Query Match 57.9%; Score 44; DB 2; Length 467;
 Best Local Similarity 72.7%; Pred. No. 31;
 Matches 8; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 SPEEDTEEDKP 11
 DB 84 SFEHDSSEDKP 94

RESULT 9

Sensory kinase Baes (EC 2.7.3.-) - Escherichia coli (strain K-12)
 N:Alternate names: signal transduction protein
 C:Species: Escherichia coli
 C:Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 09-Jul-2004
 C:Accession: B64974; JX0282
 R:Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Co
 A.; Rose, D.J.; Mau, B.; Shaoh, Y.
 Science 277, 1453-1462, 1997
 A:Title: The complete genome sequence of Escherichia coli K-12.
 A:Reference number: A64720; MUID:97426617; PMID:9278503
 A:Accession: B64974
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-467 <BLAT>
 A:Cross-references: UNIPROT:P30847; GB:AE000297; GB:U00096; NID:G1788382; PIDN:AACT5139
 A:Experimental source: strain K-12, substrain MG1655
 R:Nagaoka, S.; Ishige, K.; Mizuno, T.
 J. Biochem. 114, 350-357, 1993
 A:Title: Novel members of the two-component signal transduction genes in Escherichia coli
 A:Reference number: JX0282; MUID:94110256; PMID:8282723
 A:Accession: JX0282
 A:Molecule type: DNA
 A:Residues: 1-413, 'VPAT', 'VPA', 422-467 <NAG>
 A:Cross-references: GB:D14054; NID:G216530; PIDN:BA03140.1; PID:dl003646; PID:G216532
 C:Genetics:
 A:Gene: baes
 C:Keywords: autophosphorylation; phosphohistidine; phosphoprotein; phosphotransferase; P
 F,12-32/Domain: transmembrane #status predicted <TM>

F,168-186/Domain: transmembrane #status predicted <TM>
 F,219-458/Domain: sensor histidine kinase homology <SHK>
 F,250/Binding site: phosphate (His) (covalent) (by autophosphorylation) #status predicted

Query Match 57.9%; Score 44; DB 2; Length 467;
 Best Local Similarity 72.7%; Pred. No. 31;
 Matches 8; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 SPEEDTEEDKP 11
 DB 84 SFEHDSSEDKP 94

RESULT 10

Hypothetical protein T20B12.8 - Caenorhabditis elegans
 A:Accession: T16908
 C:Species: Caenorhabditis elegans
 C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 16-Aug-2004
 C:Accession: T16908
 R:Du, Z.
 submitted to the EMBL Data Library, June 1994
 A:Description: The sequence of C. elegans cosmid T20B12.
 A:Reference number: S46772
 A:Accession: T16908
 A:Status: preliminary; translated from GB/EMBL/DDBJ
 A:Molecule type: DNA
 A:Residues: 1-697 <DU>
 A:Cross-references: UNIPROT:P41848; EMBL:U010401; NID:G500713; PID:G500721; PIDN:AAA19061
 C:Genetics:
 A:Gene: CSP:T20B12.8
 A:Initiators: 79/3; 292/2; 601/3
 C:Superfamily: HMG box homology

Query Match 57.9%; Score 44; DB 2; Length 697;
 Best Local Similarity 61.5%; Pred. No. 47;
 Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 2 FEEDTEEDKPKYE 14
 DB 603 WEKAEDEKSRYE 615

RESULT 11

Methylglyoxal synthase (EC 4.2.3.3) - Haemophilus influenzae (strain Rd KW20)
 C:Species: Haemophilus influenzae
 C:Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 09-Jul-2004
 C:Accession: D64169
 R:Fleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kesteven, A.
 J.; Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman, J.
 D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhmann, J.L.; Geoghegan, N.S.M.
 Science 269, 496-512, 1995
 A:Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter, A.
 A:Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.
 A:Reference number: A64000; MUID:95350630; PMID:7542800
 A:Accession: D64169
 A:Status: nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-152 <TIGR>
 A:Cross-references: UNIPROT:P45120; GB:U32803; GB:L42023; NID:G1574162; PIDN:AACT2887.1;
 C:Genetics:
 A:Gene: mgsA
 C:Superfamily: methylglyoxal synthase
 C:Keywords: carbon-oxygen lyase

Query Match 56.6%; Score 43; DB 2; Length 152;
 Best Local Similarity 61.5%; Pred. No. 13;
 Matches 8; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 2 FEEDTEEDKPKYE 14
 DB 132 FEQVEIVDPYE 144

RESULT 12

T15665

hypothetical protein C27F2.1 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C>Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #ext_change 09-Jul-2004

C:Accession: T15665

R:Kirsten, J.

Submitted to the EMBL Data Library, November 1995

A:Description: The sequence of C. elegans cosmid C27F2.

A:Reference number: Z18385

A:Accession: T15665

A:Status: preliminary; translated from GB/EMBL/DDbJ

A:Molecule type: DNA

A:Residues: 1-653 <NIR>

A:Cross-references: UNIPROT:Q18263; EMBL:U04049; NID:G1065504; PID:G1065511; PIDN:AAA814

C:Genetics:

A:Gene: CESP:C27F2.1

A:Introns: 12/2: 97/3: 138/3: 171/1: 261/3: 302/1: 349/2: 373/3: 398/1: 434/2: 536/2: 56

C:Superfamily: Caenorhabditis elegans hypothetical protein C27F2.1

Query Match

56.6%; Score 43; DB 2; Length 653;

Best Local Similarity 66.7%; Pred. No. 63;

Matches 10; Conservative 1; Mismatches 2; Indels 2; Gaps 1;

QY 2 FEEDTEEDK--PKYE 14

DB 66 FEEDDEEEKKAPKVE 80

RESULT 13

T45971

hypothetical protein F9D24.20 - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)

C>Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #ext_change 09-Jul-2004

C:Accession: T45971

R:D'Angelio, M.; Vezzi, A.; Modesto, D.; Pigazzi, M.; Valle, G.; Mewes, H.W.; Lemcke, K.;

Submitted to the Protein Sequence Database, January 2000

A:Reference number: Z23011

A:Accession: T45971

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-784 <DN>

A:Cross-references: UNIPROT:Q9M2K5; EMBL:AL137081

A:Experimental source: cultivar Columbia; BAC clone F9D24

C:Genetics:

A:Map position: 3

A:Note: F9D24.20

C:Superfamily: Arabidopsis thaliana hypothetical protein F9D24.20

Query Match

56.6%; Score 43; DB 2; Length 784;

Best Local Similarity 66.7%; Pred. No. 76;

Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 3 EEDTEEDKPKYE 14

DB 460 EEDTEEDTEKHE 471

RESULT 14

A45669

neurofilament triplet M protein - rat

C:Species: Rattus norvegicus (Norway rat)

C>Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #ext_change 09-Jul-2004

C:Accession: A45669; S25712; A42393

R:Napolitano, E.W.; Chin, S.S.M.; Colman, D.R.; Liem, R.K.H.

J. Neurosci. 7, 2590-2599, 1987

A:Title: Complete amino acid sequence and in vitro expression of rat NF-M, the middle mo

A:Reference number: A45669

A:Accession: A45669; MUID:87282618; PMID:2441012

A:Status: preliminary; not compared with conceptual translation

A:Molecule type: mRNA

A:Residues: 1-845 <NAP>

A:Cross-references: UNIPROT:P12839; EMBL:M18628; NID:G205687; PIDN:AAA41696.1; PID:G20568

R:Kelly, B.M.; Gillespie, C.S.; Sherman, D.L.; Brophy, P.J.

J. Cell Biol. 118, 397-410, 1992

A:Title: Schwann cells of the myelin-forming phenotype express neurofilament protein NF-M

A:Reference number: S25712; MUID:92332596; PMID:1321159

A:Accession: S25712

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-17,19-21,'P',23-204,'L',206-500,'E',501-845 <KE>

A:Cross-references: EMBL:U12152; NID:G56751; PIDN:CAA78136.1; PID:G56752

R:Xu, Z.S.; Liu, W.S.; Willard, M.B.

J. Biol. Chem. 267, 4467-4471, 1992

A:Title: Identification of six phosphorylation sites in the COOH-terminal tail region of

A:Reference number: A42393; MUID:92165797; PMID:1537832

A:Accession: A42393

A:Status: preliminary; not compared with conceptual translation

A:Molecule type: nucleic acid

A:Residues: 411-500,'E',501-843,'D' <XU1>

A:Note: sequence extracted from NCBI backbone (NCBIP:83873)

C:Superfamily: cytoskeletal keratin

Query Match

56.6%; Score 43; DB 2; Length 845;

Best Local Similarity 50.0%; Pred. No. 82;

Matches 7; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 1 SEEDTEEDKPKYE 14

DB 686 SLEKDTKEKPKQOQ 699

RESULT 15

S74259

tropoinin T 3, fast skeletal muscle, fetal - human (fragment)

C:Species: Homo sapiens (man)

C>Date: 13-Mar-1997 #sequence_revision 13-Mar-1997 #ext_change 09-Jul-2004

C:Accession: S74259

R:Briggs, M.M.; Maready, M.; Schmidt, J.M.; Schachar, F.

FEBS Lett. 350, 37-40, 1994

A:Title: Identification of a fetal exon in the human fast Tropoinin T gene.

A:Reference number: S48660; MUID:94341369; PMID:8062920

A:Accession: S74259

A:Molecule type: mRNA

A:Residues: 1-56 <BRI>

A:Cross-references: UNIPROT:P45378; EMBL:U14642; NID:G557025; PIDN:AAA50360.1; PID:G55702

C:Superfamily: tropoinin T

C:Keywords: alternative splicing; phosphoprotein; skeletal muscle

Query Match

55.3%; Score 42; DB 2; Length 56;

Best Local Similarity 70.0%; Pred. No. 6.6;

Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 EEDTEEDKPK 12

DB 31 EEDAEERKPR 40

Search completed: October 22, 2005, 09:55:54
Job time: 17.2529 secs

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OW protein - protein search, using SW model

Run on: October 22, 2005, 08:01:06 ; Search time 78.6897 Seconds
(without alignments)
91.106 Million cell updates/sec

Title: US-10-731-238-105
Perfect score: 76
Sequence: 1 SFEDTEEDPKPYE 14

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues
Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Uniprot_03:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	76	100.0	152	2	Q9AEP9	Q9AEP9 staphylococ
2	76	100.0	940	2	Q53682	Q53682 staphylococ
3	76	100.0	943	2	Q8NUB8	Q8NUB8 staphylococ
4	76	100.0	957	2	Q6G6H4	Q6G6H4 staphylococ
5	76	100.0	961	2	Q99RD3	Q99RD3 staphylococ
6	76	100.0	961	2	Q7A3J8	Q7A3J8 staphylococ
7	76	100.0	965	2	Q6GDU5	Q6GDU5 staphylococ
8	76	100.0	1015	2	Q8NUU7	Q8NUU7 staphylococ
9	76	100.0	1015	2	Q6G6H3	Q6G6H3 staphylococ
10	76	100.0	1038	1	FNBA_STAU	P14738 staphylococ
11	76	100.0	1038	2	Q99RD2	Q99RD2 staphylococ
12	76	100.0	1038	2	Q7A3J7	Q7A3J7 staphylococ
13	49	64.5	293	2	Q8GKQ3	Q8GKQ3 enterococu
14	49	64.5	299	2	P71446	P71446 lactococcus
15	49	64.5	829	2	Q72CT7	Q72CT7 desulfovibr
16	48	63.2	820	1	SVL_CHLVC	Q82247 chlamydomon
17	47	61.8	1074	2	Q82491	Q82491 arabidopsis
18	46	60.5	586	2	Q6QJ78	Q6QJ78 zea mays (m
19	45	59.2	317	2	Q98LE0	Q98LE0 rhizobium 1
20	45	59.2	359	2	Q64T22	Q64T22 bacteroides
21	45	59.2	569	2	Q8SR48	Q8SR48 encephalito
22	45	59.2	572	2	Q7YZ17	Q7YZ17 scypha sp.
23	45	59.2	1213	2	Q6C8W7	Q6C8W7 yarrowia 11
24	44	57.9	164	2	Q7RT09	Q7RT09 plasmodium
25	44	57.9	274	2	Q8RNB7	Q8RNB7 bradyrhizob
26	44	57.9	448	1	PR54_SCHPO	P36612 escherichia
27	44	57.9	467	1	BAES_ECOLI	P30847 escherichia
28	44	57.9	467	2	Q8H8K6	Q8H8K6 oxyza sativ
29	44	57.9	467	2	Q8X712	Q8X712 escherichia
30	44	57.9	467	2	Q83M11	Q83M11 shigella fl
31	44	57.9	548	2	Q7MHN0	Q7MHN0 vibrio vuln

32	44	57.9	574	2	Q7YZ15	Q7YZ15 nematostell
33	44	57.9	697	1	SSRP_CABEL	P41848 caenorhabdi
34	44	57.9	858	2	O18466	O18466 hirudo medi
35	43	56.6	152	1	M5SA_HAETIN	P45120 haemophilus
36	43	56.6	235	2	Q6QAN3	Q6QAN3 megachile r
37	43	56.6	310	2	Q8CBA4	Q8CBA4 mus muscula
38	43	56.6	311	2	Q8SY78	Q8SY78 drosophila
39	43	56.6	311	2	Q9Y106	Q9Y106 drosophila
40	43	56.6	466	2	Q6GN22	Q6GN22 xenopus lae
41	43	56.6	502	2	Q8NFC6	Q8NFC6 homo sapien
42	43	56.6	552	2	Q6S9B4	Q6S9B4 hexamita in
43	43	56.6	552	2	Q6S9B5	Q6S9B5 hexamita in
44	43	56.6	619	2	Q6SU21	Q6SU21 manheimia
45	43	56.6	660	2	Q6FXN2	Q6FXN2 candida gla

ALIGNMENTS

RESULT 1
ID Q9AEP9 PRELIMINARY; PRT; 152 AA.
AC Q9AEP9;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Fibronectin-binding protein (Fragment).
GN Name=fnb;
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1280;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CMRSA-1;
RX DOI=10.1128/IAI.69.6.3791-3799.2001;
RA Rice K., Huesca M., Vaz D., McGavin M.J.;
RT "Variance in fibronectin binding and fnb locus polymorphisms in
RT Staphylococcus aureus: identification of antigenic variations in a
RT fibronectin binding protein adhesin of the epidemic CMRSA-1 strain of
RT methicillin-resistant S. aureus.";
RL Infect. Immun. 69:3791-3799(2001).
DR EMBL: AY029184; AK31588.1; -.
FT NON_TER
FT NON_TER
SQ SEQUENCE 152 AA; 17193 MW; CFA3913C2B11C025 CRC64;
Query Match 100.0%; Score 76; DB 2; Length 152;
Best Local Similarity 100.0%; Pred. No. 0.0014;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 SFEDTEEDPKPYE 14
Db 7 SFEDTEEDPKPYE 20
RESULT 2
ID Q53682 PRELIMINARY; PRT; 940 AA.
AC Q53682;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Fibronectin binding protein B.
GN Name=fnbB;
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1280;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=8325-4;
RX MEDLINE=92111475; PubMed=1837266;
RA Jonsson K., Signas C., Muller H.P., Lindberg M.;

DR	Pfam; PF04650; YSIRK_signal; 1.
DR	TIGRFAMs; TIGR01167; LPTXG_anchor; 1.
DR	TIGRFAMs; TIGR01168; YSIRK_signal; 1.
DR	PROSITE; PS50847; GRAM_POS_ANCHORING; 1.
KW	Cell wall; Complete proteome; Peptidoglycan-anchor.
SO	SEQUENCE 943 AA; 104537 MW; DA8A5F31947E1B6A CRC64;

Qy	Query Match	100.0%;	Score 76;	DB 2;	Length 943;
	Best Local Similarity	100.0%;	Pred. No. 0.01;		
Matches	14; Conservative	0;	Mismatches	0;	Indels 0; Gaps 0;

Db	1 SPEEDTEEDKPXYE 14
	695 SPEEDTEEDKPXYE 708

RESULT 4

O6G6H4	PRELIMINARY;	PRT;	957 AA.
ID	O6G6H4		
AC	O6G6H4;		
DT	05-JUL-2004 (TRMBLrel. 27, Created)		
DT	05-JUL-2004 (TRMBLrel. 27, Last sequence update)		
DT	05-JUN-2004 (TRMBLrel. 27, Last annotation update)		
DE	Fibronectin-binding protein.		
CN	Name=fndB; OrderedLocNames=SAS3387;		
OS	Staphylococcus aureus (strain MSSA476).		
OC	Bacteria; Firmicutes; Bacillales; Staphylococcus.		
OX	NCBI_TaxID=282459;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RX	PUMed=15213324; DOI=10.1073/pnas.0402521101;		
RA	Holden M.T.G., Fell E.J., Lindsay J.A., Peacock S.J., Day N.P.J.,		
RA	Enright M.C., Foster T.J., Moore C.E., Hurst L., Atkin R., Barron A.,		
RA	Bacon N., Bentley S.D., Chillingworth C., Chillingworth T.,		
RA	Churcher C., Clark L., Corton C., Cronin A., Doggett J., Dowd L.,		
RA	Feltwell T., Hance Z., Harris B., Hauser H., Holtroyd S., Jegede K.,		
RA	James K.D., Lemard N., Line A., Mayes R., Moule S., Mungall K.,		
RA	Ormond D., Simmonds M., Rabdinowitsch E., Rutherford K.W., Sanders M.,		
RA	Sharp S., Simmonds M., Stevens K., Whitehead S., Barrell B.G.,		
RA	Spratt B.G., Parkhill J.;		
RT	"Complete genomes of two clinical <i>Staphylococcus aureus</i> strains:		
RT	evidence for the rapid evolution of virulence and drug resistance."		
RL	Proc. Natl. Acad. Sci. U.S.A. 101:9786-9791(2004).		
CC	-1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by		
CC	an amide bond (By similarity).		
CC	EMBL: BX571857; CAG44201.1;-		
DR	GO: GO:0009986; C:cell surface; IEA.		
DR	GO: GO:0005618; C:cell wall; IEA.		
DR	GO: GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.		
DR	GO: GO:0016020; C:membrane; IEA.		
DR	GO: GO:0007155; P:cell adhesion; IEA.		
DR	InterPro: IPR008966; Adhes_bact.		
DR	InterPro: IPR004237; Fn_bind		
DR	InterPro: IPR005877; GPoS_YSIRK.		
DR	InterPro: IPR001899; Gram_pos_anchor.		
DR	Pfam; PF02986; Fn_bind; 1.		
DR	Pfam; PF00746; Gram_pos_anchor; 1.		
DR	Pfam; PF04650; YSIRK_signal; 1.		
DR	TIGRFAMs; TIGR01167; LPTXG_anchor; 1.		
DR	TIGRFAMs; TIGR01168; YSIRK_signal; 1.		
DR	PROSITE; PS50847; GRAM_POS_ANCHORING; 1.		
KW	Cell wall; Complete proteome; Peptidoglycan-anchor.		
SO	SEQUENCE 957 AA; 105980 MW; 28F8BA7FFDPD3EAF CRC64;		

Qy	Query Match	100.0%;	Score 76;	DB 2;	Length 957;
	Best Local Similarity	100.0%;	Pred. NO. 0.01;		
Matches	14; Conservative	0;	Mismatches	0;	Indels 0; Gaps 0;

Db	1 SPEEDTEEDKPXYE 14
	695 SPEEDTEEDKPXYE 708

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RESULT 5
099R03 PRELIMINARY; PRT; 961 AA.
ID 099R03;
AC 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE Fibronectin-binding protein homolog.
GN Name=fnb3; OrderedLocuNames=SAV2502;
OS Staphylococcus aureus (strain M50 / ATCC 700699).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxId=158878;
[1]
RN SEQUENCE FROM N.A.
RC STRAIN=M50 / ATCC 700699;
RA MEDLINE=21311952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2;
RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Iino T.,
RA Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,
RA Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
RA Sekimizu K., Hirakawa H., Kohara S., Goto S., Yabuuchi J.,
RA Kanehisa M., Yamashita A., Oshima K., Hara K., Yoshino C., Shiba T.,
RA Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
RT "Whole genome sequencing of methicillin-resistant Staphylococcus
RT aureus."
RL Lancet 357:1225-1240(2001).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC an amide bond (By similarity).
EMBL; AP003365; BAB58664.1; -.
DR PIR; G90053; G90053.
DR HSSP; Q53653; IN67.
DR GO; GO:0009986; C:cell surface; IEA.
DR GO; GO:0005618; C:cell wall; IEA.
DR GO; GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0007155; P:cell adhesion; IEA.
DR InterPro; IPR008966; Adhes_bact.
DR InterPro; IPR004237; Fn_bind.
DR InterPro; IPR005877; Gpos_YsIRK.
DR InterPro; IPR001899; Gram_pos_anchor.
DR Pfam; PF02986; Fn_bind; 1.
DR Pfam; PF00746; Gram_pos_anchor; 1.
DR Pfam; PF04650; YsIRK_signal; 1.
DR TIGRPFAMs; TIGR01167; LPTXG_anchor; 1.
DR TIGRPFAMs; TIGR01168; YsIRK_signal; 1.
DR POSITE; PS50847; GRAM_POS_ANCHORING; 1.
DR Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ SEQUENCE 961 AA; 106010 MW; 364940F884EA4101 CRC64;

Query Match 100.0%; Score 76; DB 2; Length 961;
Best Local Similarity 100.0%; Pred. No. 0.01;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Iino T.,
RA Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,
RA Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
RA Sekimizu K., Hirakawa H., Kohara S., Goto S., Yabuuchi J.,
RA Kanehisa M., Yamashita A., Oshima K., Hara K., Yoshino C., Shiba T.,
RA Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
RT "Whole genome sequencing of methicillin-resistant Staphylococcus
RT aureus."
RL Lancet 357:1225-1240(2001).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC an amide bond (By similarity).
EMBL; AP003365; BAB58664.1; -.
DR GO; GO:0009986; C:cell surface; IEA.
DR GO; GO:0005618; C:cell wall; IEA.
DR GO; GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0007155; P:cell adhesion; IEA.
DR InterPro; IPR008966; Adhes_bact.
DR InterPro; IPR004237; Gpos_YsIRK.
DR InterPro; IPR005877; Gpos_YsIRK.
DR InterPro; IPR001899; Gram_pos_anchor.
DR Pfam; PF02986; Fn_bind; 1.
DR Pfam; PF00746; Gram_pos_anchor; 1.
DR Pfam; PF04650; YsIRK_signal; 1.
DR TIGRPFAMs; TIGR01167; LPTXG_anchor; 1.
DR TIGRPFAMs; TIGR01168; YsIRK_signal; 1.
DR POSITE; PS50847; GRAM_POS_ANCHORING; 1.
DR Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ SEQUENCE 961 AA; 106010 MW; 364940F884EA4101 CRC64;

Query Match 100.0%; Score 76; DB 2; Length 961;
Best Local Similarity 100.0%; Pred. No. 0.01;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SPEEDTEBDKPKYE 14
DB 699 SPEEDTEBDKPKYE 712

RESULT 7
06GDU5 PRELIMINARY; PRT; 965 AA.
ID 06GDU5;
AC 06GDU5;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE Fibronectin-binding protein.
GN Name=fnb3; OrderedLocuNames=SA2580;
OS Staphylococcus aureus (strain M5A252).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxId=282458;
[1]
RN SEQUENCE FROM N.A.
RC PubMed=15213324; DOI=10.1073/pnas.040252101;
RA Holden M.T.G., Fell E.J., Lindsay J.A., Peacock S.J., Day N.P.J.,
RA Enright M.C., Foster T.J., Moore C.E., Hurst L., Atkin R., Barron A.,
RA Bason N., Bentley S.D., Chillingworth C., Chillingworth T.,
RA Churcher C., Clark L., Corton C., Cronin A., Doggett J., Dowd L.,
RA Felwell T., Hance Z., Harris B., Hauser H., Holtroyd S., Jørgensen K.,
RA James K.D., Lennard N., Line A., Mayes R., Mole S., Mungall K.,
RA Ormond D., Quail M.A., Rabinowitsch E., Rutherford K.M., Sanders M.,
RA Sharp S., Simmonds M., Stevens K., Whitehead S., Barrett B.G.,
RA Spratt B.G., Parkhill J.;
RT "Complete genomes of two clinical Staphylococcus aureus strains:
RT evidence for the rapid evolution of virulence and drug resistance."
RT Proc. Natl. Acad. Sci. U.S.A. 101:9786-9791(2004).
RL -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC an amide bond (By similarity).
EMBL; BX571856; CAG41560.1; -.
DR GO; GO:0009986; C:cell surface; IEA.
DR GO; GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO; GO:0016020; C:membrane; IEA.

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DR GO:0007155; P:cell adhesion; IEA.
DR InterPro: IPR008966; Adhes_bact.
DR InterPro: IPR004237; Fn_bind.
DR InterPro: IPR005877; Gpos_YsIRK.
DR InterPro: IPR001899; Gram_pos_anchor.
DR Pfam: PF02986; Fn_bind; 1.
DR Pfam: PF00746; Gram_pos_anchor; 1.
DR Pfam: PF04650; YsIRK_signal; 1.
DR TIGRFAMs: TIGR01167; LpxTG_anchor; 1.
DR TIGRFAMs: TIGR01168; YsIRK_signal; 1.
DR PROSITE: PS50847; GRAM_POS_ANCHORING; 1.
DR Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ SEQUENCE 965 AA; 105691 MW; 2982E312164D0551 CRC64;

Query Match 100.0%; Score 76; DB 2; Length 965;
Best Local Similarity 100.0%; Pred. No. 0.01;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 SPEEDTEEDPKPYE 14
pb 753 SPEEDTEEDPKPYE 766

RESULT 8
ID 08NU7 PRELIMINARY; PRT; 1015 AA.
AC 08NU7;
DT 01-OCT-2002 (TRENBLrel. 22, Created)
DT 01-OCT-2002 (TRENBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
DE Fnb protein.
GN Name:fnb; OrderedLocustNames=MM2421;
OS Staphylococcus aureus (strain MM2);
OC Bacteria; Firmicutes; Bacilliales; Staphylococcus.
OX NCBI_TaxID=196620;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=22040717; PubMed=12044378; DOI=10.1016/S0140-6736(02)08713-5;
RA Baba T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Oguchi A.,
RA Nagai Y., Iwano N., Asano K., Naimi T., Kuroda H., Cui L.,
RA Yamamoto K., Hiramatsu K.;
RT "Genome and virulence determinants of high virulence community-acquired MRSA.";
RL Lancet 359:1819-1827(2002).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by an amide bond (By similarity).
EMBL: AP004830; BAB96286.1; -.
DR GO:0009986; C:cell surface; IEA.
DR GO:0005618; C:cell wall; IEA.
DR GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO:0016020; C:membrane; IEA.
DR GO:007155; P:cell adhesion; IEA.
DR InterPro: IPR008966; Adhes_bact.
DR InterPro: IPR004237; Fn_bind.
DR InterPro: IPR005877; Gpos_YsIRK.
DR InterPro: IPR001899; Gram_pos_anchor.
DR Pfam: PF02986; Fn_bind; 1.
DR Pfam: PF00746; Gram_pos_anchor; 1.
DR Pfam: PF04650; YsIRK_signal; 1.
DR TIGRFAMs: TIGR01167; LpxTG_anchor; 1.
DR TIGRFAMs: TIGR01168; YsIRK_signal; 1.
DR PROSITE: PS50847; GRAM_POS_ANCHORING; 1.
DR Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ SEQUENCE 1015 AA; 111145 MW; D0F9281BB64D4D2 CRC64;

Query Match 100.0%; Score 76; DB 2; Length 1015;
Best Local Similarity 100.0%; Pred. No. 0.01;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 SPEEDTEEDPKPYE 14
pb 753 SPEEDTEEDPKPYE 766

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RESULT 9
ID 06G6H3 PRELIMINARY; PRT; 1015 AA.
AC 06G6H3;
DT 05-JUL-2004 (TRENBLrel. 27, Created)
DT 05-JUL-2004 (TRENBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TRENBLrel. 27, Last annotation update)
DE Fibronectin-binding protein.
GN OrderedLocustNames=SA52388;
OS Staphylococcus aureus (strain MSSA476).
OC Bacteria; Firmicutes; Bacilliales; Staphylococcus.
OX NCBI_TaxID=282459;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=15213324; DOI=10.1073/pnas.0402521101;
RA Holden M.T.G., Fell E.J., Lindsay J.A., Peacock S.J., Day N.P.J.,
RA Enright M.C., Foster T.J., Moore C.E., Hurst L., Atkin R., Barron A.,
RA Bason N., Bentley S.D., Chillingworth C., Chillingworth T.,
RA Churcher C., Clark L., Cronin A., Doggett J., Dowd L.,
RA Felwell T., Hance Z., Harris B., Hauser H., Holroyd S., Jagels K.,
RA James K.D., Lennard N., Line A., Mays R., Moule S., Mungall K.,
RA Ormond D., Quail M.A., Rabinowitsch E., Rutherford K.M., Sanders M.,
RA Sharp S., Simmonds M., Stevens K., Whitehead S., Barrall B.G.,
RA Spratt B.G., Parthill J.;
RT "Complete genomes of two clinical Staphylococcus aureus strains: evidence for the rapid evolution of virulence and drug resistance.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:9786-9791(2004).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by an amide bond (By similarity).
EMBL: BX571857; CAG44202.1; -.
DR GO:0009986; C:cell surface; IEA.
DR GO:0005618; C:cell wall; IEA.
DR GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO:0016020; C:membrane; IEA.
DR GO:007155; P:cell adhesion; IEA.
DR InterPro: IPR008966; Adhes_bact.
DR InterPro: IPR004237; Fn_bind.
DR InterPro: IPR005877; Gpos_YsIRK.
DR InterPro: IPR001899; Gram_pos_anchor.
DR Pfam: PF02986; Fn_bind; 1.
DR Pfam: PF00746; Gram_pos_anchor; 1.
DR Pfam: PF04650; YsIRK_signal; 1.
DR TIGRFAMs: TIGR01167; LpxTG_anchor; 1.
DR TIGRFAMs: TIGR01168; YsIRK_signal; 1.
DR PROSITE: PS50847; GRAM_POS_ANCHORING; 1.
DR Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ SEQUENCE 1015 AA; 111145 MW; D0F9281BB64D4D2 CRC64;

Query Match 100.0%; Score 76; DB 2; Length 1015;
Best Local Similarity 100.0%; Pred. No. 0.01;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 SPEEDTEEDPKPYE 14
DB 753 SPEEDTEEDPKPYE 766

RESULT 10
ID FNBA STAAU STANDARD; PRT; 1018 AA.
AC FNBA STAAU;
DT 01-APR-1990 (rel. 14, Created)
DT 01-APR-1990 (rel. 14, Last sequence update)
DT 25-OCT-2004 (rel. 45, Last annotation update)
DE Fibronectin-binding protein precursor (FBNP).
GN Name:fnbA;
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacilliales; Staphylococcus.
OX NCBI_TaxID=1280;
RN [1]
RP SEQUENCE FROM N.A.

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RC STRAIN=NCTC 8325-4;
 RX MEDLINE=89098998; PubMed=2521391;
 RA Signaes C., Raucel G., Jonsson K., Lindgren P.-E.,
 RA Anantharaman G.M., Hoeck M., Lindberg M.,
 RT "Nucleotide sequence of the gene for a fibronectin-binding protein
 from *Staphylococcus aureus*: use of this peptide sequence in the
 RT synthesis of biologically active peptides.";
 RL Proc. Natl. Acad. Sci. U.S.A. 86:699-703(1989).
 CC -1- FUNCTION: The ability of bacteria to bind fibronectin has been
 CC proposed as a virulence factor enabling bacteria to colonize wound
 CC tissues and blood clots. Binding of plasma fibronectin to the
 CC bacterial surface might block adhesion receptors on *S. aureus*, thus
 CC representing an important defense mechanism against tissue
 CC invasion.
 CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
 CC an amide bond (potential).
 CC -----
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 CC -----
 CC EMBL: J04151; AAA26632.1; -;
 CC InterPro: IPR004237; Fn_bind
 CC InterPro: IPR005877; Gpos_YsIRK.
 CC InterPro: IPR001899; Gram_pos_anchor.
 CC Pfam: PF02986; Fn_bind; 1.
 CC Pfam: PF00746; Gram_pos_anchor; 1.
 CC Pfam: PF04650; YsIRK_signal; 1.
 CC TIGRfam: TIGR01167; LPXTG_anchor; 1.
 CC TIGRfam: TIGR01168; YsIRK_signal; 1.
 CC PROSITE: PS50847; GRAM_POS_ANCHORING; 1.
 CC Cell adhesion; Cell wall; Peptidoglycan-anchor; Repeat; Signal;
 CC virulence.
 CC KM
 CC FT SIGNAL 1 36
 CC FT CHAIN 37 985
 CC FT PROPE 986 1018
 CC FT REPEAT 545 574
 CC FT REPEAT 575 604
 CC FT DOMAIN 745 878
 CC FT REPEAT 745 782
 CC FT REPEAT 783 820
 CC FT REPEAT 821 859
 CC FT REPEAT 860 878
 CC FT DOMAIN 879 948
 CC FT REPEAT 879 892
 CC FT REPEAT 893 906
 CC FT REPEAT 907 920
 CC FT REPEAT 921 934
 CC FT REPEAT 935 948
 CC FT SITE 982 986
 CC FT MOD_RES 985 985
 CC SQ SEQUENCE 1018 AA; 111760 MW; 58175E0020B81F1F CR664;
 CC
 CC Query Match 100.0%; Score 76; DB 1; Length 1018;
 CC Best Local Similarity 100.0%; Pred. No. 0.011;
 CC Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Fibronectin-binding protein homolog.
 GN Name=fnb; OrderedLocustNames=SAV2503;
 OS *Staphylococcus aureus* (strain Mu50 / ATCC 700699).
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 OX NCBI_TaxId=158878;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC STRAIN=MU50 / ATCC 700699;
 RX MEDLINE=2111952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2;
 RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
 RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Iino J.-O., Ito T.,
 RA Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,
 RA Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
 RA Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuuchi J.,
 RA Kanehisa M., Yamashita A., Oshima K., Haraoka K., Shiba T.,
 RA Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
 RT "Whole genome sequencing of methicillin-resistant *Staphylococcus*
 RT *aureus*.";
 RL Lancet 357:1225-1240(2001).
 CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
 CC an amide bond (By similarity).
 CC -----
 CC EMBL: AB003365; BAB58665.1; -;
 CC PIR: H90053; H90053.
 CC GO: GO:0009986; Cell surface; IEA.
 CC GO: GO:0005618; Cell wall; IEA.
 CC GO: GO:0009275; Cell wall (sensu Gram-positive Bacteria); IEA.
 CC GO: GO:0016020; C-membrane; IEA.
 CC GO: GO:0007155; P-cell adhesion; IEA.
 CC InterPro: IPR008966; Adhes_bact.
 CC InterPro: IPR004237; Fn_bind
 CC InterPro: IPR005877; Gpos_YsIRK.
 CC InterPro: IPR001899; Gram_pos_anchor.
 CC Pfam: PF02986; Fn_bind; 1.
 CC Pfam: PF00746; Gram_pos_anchor; 1.
 CC Pfam: PF04650; YsIRK_signal; 1.
 CC TIGRfam: TIGR01167; LPXTG_anchor; 1.
 CC TIGRfam: TIGR01168; YsIRK_signal; 1.
 CC PROSITE: PS50847; GRAM_POS_ANCHORING; 1.
 CC Cell wall; Complete proteome; Peptidoglycan-anchor.
 CC SQ SEQUENCE 1038 AA; 113618 MW; 666BF6BF2BFEB12 CR664;
 CC
 CC Query Match 100.0%; Score 76; DB 2; Length 1038;
 CC Best Local Similarity 100.0%; Pred. No. 0.011;
 CC Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 12
 ID Q7A3J7 PRELIMINARY; PRT; 1038 AA.
 AC Q7A3J7;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Fnb protein.
 GN Name=fnb; OrderedLocustNames=SA2291;
 OS *Staphylococcus aureus* (strain N315).
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 OX NCBI_TaxId=158879;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC MEDLINE=21311952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2;
 RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
 RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Iino J.-O., Ito T.,
 RA Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,
 RA Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
 RA Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuuchi J.,
 RA Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,

RA Hattori M., Ogasawara N., Hayaishi H., Hiramatsu K.;
 RT "Whole genome sequencing of methicillin-resistant *Staphylococcus*
 RT aureus".
 RL Lancet 357:1225-1240(2001).
 CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
 CC an amide bond (By similarity).
 DR EMBL: AP003137; BAB43594.1; -.
 DR GO: GO:0009986; C:cell surface; IEA.
 DR GO: GO:0005618; C:cell wall; IEA.
 DR GO: GO:0009275; C:cell wall (benu Gram-positive Bacteria); IEA.
 DR GO: GO:0016020; C:membrane; IEA.
 DR GO: GO:007155; P:cell adhesion; IEA.
 DR InterPro: IPR008966; Adhes_bact.
 DR InterPro: IPR004237; Fn_bind.
 DR InterPro: IPR005877; Gpox_Ysirk.
 DR InterPro: IPR001899; Gram_pos_anchor.
 DR Pfam: PF02986; Fn_bind; 1.
 DR Pfam: PF00746; Gram_pos_anchor; 1.
 DR Pfam: PF04650; Ysirk_signal; 1.
 DR TIGRFAM: TIGR01167; Lpxg_anchor; 1.
 DR TIGRFAM: TIGR01168; Ysirk_signal; 1.
 DR TIGRFAM: PS50847; GRAM_POS_ANCHORING; 1.
 DR PROSITE: PS00178; AA_TRNA_LIGASE_I; 1.
 KW Cell wall, Complete proteome, Peptidoglycan-anchor.
 SQ SEQUENCE 1038 AA; 113618 MW; 666B6BF2BFEB12 CRC64;

Query Match 100.0%; Score 76; DB 2; Length 1038;
 Best Local Similarity 100.0%; Pred. No. 0.011; Mismatches 0; Indels 0; Gaps 0;
 Matches 14; Conservative 0;

OY 1 SPEEDTEEDKPKYE 14
 DB 748 SPEEDTEEDKPKYE 761

RESULT 13
 Q8GK03 PRELIMINARY; PRT; 293 AA.

AC Q8GK03;
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE SfeI restriction endonuclease.
 GN Name=SfeIR;
 OS Enterococcus faecalis (Streptococcus faecalis).
 OC Bacteria; Firmicutes; Lactobacillales; Enterococcaceae; Enterococcus.
 NC NCBI_Taxid=1351;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=SE72;
 RA Okhapkina S., Neresova N., Golikova L., Seregina E., Sosnovtsev S.,
 RA Abdurashitov M., Degtyarev S.;
 RT "Comparison of the Homologous SfeI and LlaBI Restriction and
 RT Modification Systems";
 RT Mol. Biol. 36:333-337(2002).
 DR EMBL: AY151403; AAN71749.1; -.
 DR GO: GO:0004519; P:endonuclease activity; IEA.
 SQ SEQUENCE 293 AA; 34043 MW; F9BE463A8A0187B7 CRC64;

Query Match 64.5%; Score 49; DB 2; Length 293;
 Best Local Similarity 75.0%; Pred. No. 30;
 Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 3 EEDTEEDKPKYE 14
 DB 217 EODLEEDKPKYE 228

RESULT 14
 ID P71446 PRELIMINARY; PRT; 299 AA.
 AC P71446;
 DT 01-FEB-1997 (TrEMBLrel. 02, Created)

DT 01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE LlaBI protein.
 GN Name=LlaBI;
 OS Lactococcus lactis.
 OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae; Lactococcus.
 NC NCBI_Taxid=1358;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=H56;
 RX MEDLINE=96387774; PubMed=8795244;
 RA Nyengaard N.R., Falkenberg-Klock J., Josephsen J.;
 RT "Cloning and characterization of the restriction-modification system
 RT LlaBI, a phage resistance system from *L. lactis* subsp. cremoris
 RT H56";
 RT Appl. Environ. Microbiol. 62:3494-3498(1996).
 DR EMBL: X97263; CAAG5918.1; -.
 SQ SEQUENCE 299 AA; 34587 MW; 6CCBE4490192C91 CRC64;

Query Match 64.5%; Score 49; DB 2; Length 299;
 Best Local Similarity 75.0%; Pred. No. 31;
 Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 3 EEDTEEDKPKYE 14
 DB 217 EODLEEDKPKYE 228

RESULT 15
 Q72CT7 PRELIMINARY; PRT; 829 AA.

AC Q72CT7;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Leucyl-tRNA synthetase (EC 6.1.1.4).
 GN Name=leus; OrderedLocustNames=DVU1196;
 OS Desulfovibrio vulgaris (strain Hildenborough / ATCC 29579 / NCIMB
 OS 8303).
 OC Bacteria; Proteobacteria; Deltaproteobacteria; Desulfovibrionales;
 OC Desulfovibrionaceae; Desulfovibrio.
 NC NCBI_Taxid=882;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX PubMed=15077118; DOI=10.1038/nbt959;
 RA Heidelberg J.F., Seshadri R., Haveman S.A., Hemme C.L., Paulsen I.T.,
 RA Kolony J.F., Eisen J.A., Ward N.L., Methe B.A., Binkac L.M.,
 RA Daugherty S.C., DeBoy R.T., Dodson R.J., Durkin A.S., Madupu R.,
 RA Nelson W.C., Sullivan S.A., Fouts D.E., Haft D.H., Selengut J.,
 RA Peterson J.D., Davidson T.M., Zafar N., Zhou L., Radune D.,
 RA Dimitrov G., Hance M., Tran K., Khouri H.M., Gill J., Utterback T.R.,
 RA Feldblyum T.V., Wall J.D., Voordouw G., Fraser C.M.;
 RT "The genome sequence of the anaerobic, sulfate-reducing bacterium
 RT Desulfovibrio vulgaris Hildenborough";
 RT Nat. Biotechnol. 22:554-559(2004).
 DR EMBL: AE017313; AAS95674.1; -.
 DR TIGR: DVU1196; -.
 DR GO: GO:0005524; P:ATP binding; IEA.
 DR GO: GO:0004823; P:leucine-tRNA ligase activity; IEA.
 DR GO: GO:0006429; P:leucyl-tRNA aminoacylation; IEA.
 DR InterPro: IPR002302; Leu-tRNA synthetase.
 DR InterPro: IPR002300; tRNA-synt_1a.
 DR InterPro: IPR001412; tRNA-synt_1.
 DR InterPro: IPR009080; tRNA-synt_1a_bind.
 DR InterPro: IPR009008; ValRS_Tiers_edit.
 DR Pfam: PF00133; tRNA-synt_1; 1.
 DR PRINTS: PR00985; TRNASYNTHLEU.
 DR TIGRFAM: TIGR00396; leus_bact; 1.
 DR PROSITE: PS00178; AA_TRNA_LIGASE_I; 1.
 KW Complete proteome.
 SQ SEQUENCE 829 AA; 93979 MW; 075C5C6BED149142 CRC64;

Query Match 64.5%; Score 49; DB 2; Length 829;

- Best Local Similarity 75.0%; Pred. No. 91;
Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 2 FREDTREDKKKY 13
|: ||| |||
Db 22 FQCDTREADKKKY 33

Search completed: October 22, 2005, 09:52:31
Job time : 80.6897 secs

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OM protein - protein search, using SW model

Run on: October 25, 2005, 18:43:07 ; Search time 53.469 Seconds
(without alignments)
137,434 Million cell updates/sec

Title: US-10-731-238-12
Perfect score: 104
Sequence: 1 GNEGQQTPEPTPIPV 19

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :
A_Geneseq_16Dec04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	104	100.0	19	2	AAW65668
2	96	92.3	19	2	AAW65667
3	96	92.3	134	2	AAW29087
4	96	92.3	1018	2	AAW82115
5	96	92.3	1018	4	AAU37245
6	96	92.3	1018	4	AAU34301
7	96	92.3	1018	6	ABU18922
8	96	92.3	1018	6	ABM72537
9	96	92.3	1027	2	AAW89806
10	96	92.3	1027	2	AAW89806
11	91	87.5	134	2	AAW29088
12	91	87.5	134	2	AAW29088
13	91	87.5	559	2	AAW89803
14	91	87.5	940	2	AAW89803
15	91	87.5	940	6	ABU19111
16	91	87.5	948	6	ADA89470
17	91	87.5	948	6	ABU18923
18	91	87.5	948	6	ABM72536
19	90	86.5	19	2	AAW65707
20	89	85.6	19	2	AAW65709
21	85	81.7	961	6	ABU15854
22	85	81.7	978	4	AAU33960
23	85	81.7	1001	4	AAU37093
24	85	81.7	1038	6	ABU15903
25	80	76.9	101	2	AAW90939

26	80	76.9	124	2	AAW90940	AAW90940 D3D4 poly
27	80	76.9	128	2	AAW90941	AAW90941 D3D4 poly
28	80	76.9	162	2	AAW90942	AAW90942 D3D4 poly
29	80	76.9	164	2	AAW90938	AAW90938 D3D4 poly
30	80	76.9	174	2	AAW88808	AAW88808 Fbp fibro
31	80	76.9	174	2	AAW91203	AAW91203 D1-D4 fib
32	80	76.9	181	2	AAW88805	AAW88805 Fibronect
33	80	76.9	181	2	AAW91200	AAW91200 D1-D4 fib
34	69	66.3	130	2	AAW88807	AAW88807 Fibronect
35	69	66.3	130	2	AAW91202	AAW91202 D1-D4 fib
36	62	59.6	113	2	AAW90937	AAW90937 D3D4 poly
37	62	59.6	130	2	AAW88806	AAW88806 Fibronect
38	62	59.6	130	2	AAW91201	AAW91201 D1-D4 fib
39	49	47.1	206	7	ADP04471	ADP04471 Bacterial
40	49	47.1	874	6	ABU17261	ABU17261 Protein e
41	49	47.1	877	6	ADA36875	ADA36875 Actinocba
42	49	47.1	1136	7	ADP11278	ADP11278 Novel hum
43	49	47.1	1172	5	ABG93308	ABG93308 C. albica
44	49	47.1	1201	8	ADN21296	ADN21296 Bacterial
45	49	47.1	1427	7	ADJ71067	ADJ71067 Human hea

ALIGNMENTS

RESULT 1
AAW65668
ID AAW65668 standard; peptide; 19 AA.

XX AC AAW65668;

DT 16-OCT-1998 (first entry)

DE Fibronectin binding protein-derived peptide #12.

KM microRNA; fibronectin; fibronectin-binding protein; antibody; epitope;

KW MSCRAMM; fibronectin; fibronectin-binding protein; antibody; epitope;

KW antibiotic; bacterial infection; antibiotic-resistant strain.

XX Synthetic.

OS Staphylococcus aureus.

PN W09831389-A2.

XX 21-JAN-1998; 98MO-US001222.

PR 21-JAN-1997; 97US-0036139P.

XX (TEXA) UNIV TEXAS A & M SYSTEM.

XX Hoeoek M, Patil JM, House-Pompeo KL, Speziale P, Joh D;

PI Mcgavin MJ;

DR WPI; 1998-413816/35.

XX Antibody that binds to fibronectin-binding protein, preventing its

PT binding to fibronectin - used to treat or prevent bacterial infection,

PT especially by Staphylococci and Streptococci.

PS Example 2; Page 92; 201pp; English.

XX The invention relates to antibodies that bind to a fibronectin-binding
CC domain of a fibronectin-binding protein, and inhibit binding of the
CC protein to fibronectin. Also claimed are: (1) isolated peptides of a
CC fibronectin-binding protein that do not bind to fibronectin; (2) fusion
CC protein containing at least one peptide of a fibronectin-binding protein
CC linked to a second amino acid sequence; (3) nucleic acid encoding the
CC isolated peptide of (1). Antibodies, the isolated peptides of (1) and the
CC nucleic acids are all useful for immunisation (active or passive) and (by
CC inhibiting binding of bacteria to fibronectin) for preventing or treating
CC infection in humans or other animals, particularly by staphylococci or

CC streptococci, e.g. meningitis, otitis media, pneumonia, endocarditis,
 CC mastitis in cattle, abortion in horses and many others. Since the
 CC antibodies block binding of bacteria, they should be effective against
 CC antibiotic-resistant strains, and may replace antibiotic therapy or
 CC increase its effectiveness. Sequences AAW65659-68 represent synthetic
 CC epitopes from the fibronectin binding domains DU and DI-D4 of the S.
 CC aureus fnba gene
 XX

Sequence 19 AA;
 SQ

Query Match 100.0%; Score 104; DB 2; Length 19;
 Best Local Similarity 100.0%; Pred. No. 5.9e-08;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GONEGQQTIPEDTTPPIVP 19
 |||||
 DB 1 GONEGQQTIPEDTTPPIVP 19

RESULT 2
 AAW65667
 ID AAW65667 standard; peptide; 19 AA.
 XX
 AC AAW65667;
 XX
 DT 16-OCT-1998 (first entry)
 XX
 DE Fibronectin binding protein-derived peptide #11.
 XX
 KW microbial surface components recognising adhesive matrix molecule;
 KW MSCRAMM; fibronectin; fibronectin-binding protein; antibody; epitope;
 KW antibiotic; bacterial infection; antibiotic-resistant strain.
 XX
 OS Synthetic.
 OS Staphylococcus aureus.
 XX
 PN WO9831389-A2.
 XX
 PD 23-JUL-1998.
 XX
 PF 21-JAN-1998; 98WO-US001222.
 XX
 PR 21-JAN-1997; 97US-0036139P.
 XX
 PA (TEXA) UNIV TEXAS A & M SYSTEM.
 XX
 PI Hoecek M, Patti JM, House-Pompeo KL, Speciale P, Joh D;
 PI McGavin MJ;
 XX
 DR MPI: 1998-413816/35.
 XX

Antibody that binds to fibronectin-binding protein, preventing its
 binding to fibronectin - used to treat or prevent bacterial infection,
 especially by Staphylococci and Streptococci.
 PS
 Example 2; Page 92; 201pp; English.

The invention relates to antibodies that bind to a fibronectin-binding
 domain of a fibronectin-binding protein, and inhibit binding of the
 protein to fibronectin. Also claimed are: (1) isolated peptides of a
 fibronectin-binding protein that do not bind to fibronectin; (2) fusion
 protein containing at least one peptide of a fibronectin-binding protein
 linked to a second amino acid sequence; (3) nucleic acid encoding the
 isolated peptide of (1). Antibodies, the isolated peptides of (1) and the
 nucleic acids are all useful for immunisation (active or passive) and (by
 inhibiting binding of bacteria to fibronectin) for preventing or treating
 infection in humans or other animals, particularly by staphylococci or
 streptococci, e.g. meningitis, otitis media, pneumonia, endocarditis,
 mastitis in cattle, abortion in horses and many others. Since the
 antibodies block binding of bacteria, they should be effective against
 antibiotic-resistant strains, and may replace antibiotic therapy or
 increase its effectiveness. Sequences AAW65659-68 represent synthetic
 epitopes from the fibronectin binding domains DU and DI-D4 of the S.

CC aureus fnba gene
 XX

Sequence 19 AA;
 SQ

Query Match 92.3%; Score 96; DB 2; Length 19;
 Best Local Similarity 94.7%; Pred. No. 8.3e-07;
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GONEGQQTIPEDTTPPIVP 19
 |||||
 DB 1 GONEGQQTIPEDTTPPIVP 19

RESULT 3
 AAY29087
 ID AAY29087 standard; protein; 134 AA.
 XX
 AC AAY29087;
 XX
 DT 28-SEP-1999 (first entry)
 XX
 DE S. aureus fibronectin binding protein A (Fnba) binding domain.
 XX
 KW Bovine herpes virus-2; BHV-2; cytokine; immune response; immunogen; IL;
 KW interleukin; colony stimulating factor; CSF; interferon; IFN; TNF;
 KW tumour necrosis factor; recombinant virus; vaccine; mucosal disease;
 KW mastitis; breast cancer; stress-induced disease; binding domain; Fnba;
 KW fibronectin binding protein.
 XX
 OS Staphylococcus aureus.
 OS
 PN WO9916892-A1.
 XX
 PD 08-APR-1999.
 XX
 PF 29-SEP-1998; 98WO-GB002927.
 XX
 PR 29-SEP-1997; 97GB-00020633.
 XX
 PA (UYBR-) UNIV BRISTOL.
 XX
 PI Bradley AJ, Duffas WP;
 XX
 DR MPI: 1999-255101/21.
 XX
 DR N-PSDB; AAX91504.
 XX
 PT New bovine herpes virus-2 vectors.
 XX
 PS Example 2; Fig 8A-B; 130pp; English.
 XX

The invention provides bovine herpes virus-2 (BHV-2) based vectors that
 comprise at least one cytokine-encoding DNA sequence. The expression of
 CC cytokines in mammals can up-regulate immune responses to the immunogens.
 CC The cytokine is selected from interleukins (IL), colony stimulating
 CC factors (CSF), interferons (IFN) and tumour necrosis factors (TNF). The
 CC BHV-2 based vector or recombinant virus can be used as vaccines. They can
 CC be used for preventing or treating a mucosal disease in a subject, e.g.
 CC tumourants, cattle, sheep, goats, dogs, cats, horses, or man, particularly
 CC mastitis in cows or breast cancers in humans. They can also be used for
 CC preventing or treating a stress-induced disease. The present sequence
 CC represents the binding domain of a previously published S. aureus
 CC fibronectin binding protein A (Fnba) sequence. The Fnba binding domain
 CC gene sequence FNBA8, cloned for use in this invention has 97.8 percent
 CC identity when compared to the previously published Fnba and Fnbb gene
 CC sequences
 XX

Sequence 134 AA;
 SQ

Query Match 92.3%; Score 96; DB 2; Length 134;
 Best Local Similarity 94.7%; Pred. No. 7.1e-06;
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GONEGQQTIPEDTTPPIVP 19

Db 116 GONEGQOTIEBTTPIVP 134

RESULT 4

AA082115 standard; protein; 1018 AA.

AA082115;

25-MAR-2003 (revised)

05-JUN-1990 (first entry)

Fibronectin binding protein.

Fibronectin binding protein; S.aureus; immunisation; mastitis; ruminants;

wound infection; diagnosis.

Staphylococcus aureus.

EP294349-A.

07-DEC-1988.

30-MAY-1988; 88BP-00850188.

01-JUN-1987; 87SE-00002272.

(ALFA) ALFA LAVAL AGRIC INT AB.

Lindberg MK, Signas LC, Wadstrom TM, Froman G;

WPI: 1988-347978/49.

P-PSDB; AA082115.

Hybrid DNA encoding Staphylococcus aureus fibronectin binding protein -

useful for immunisation and topical application to prevent staphylococcal

infections.

Disclosure; Fig. 8A:1-8A:2; 23pp; English.

The S.aureus fibronectin binding protein may be included in a hybrid

protein. The protein may be used to immunise ruminants against

staphylococcal mastitis, pref. when given at 0.5-5 microg/kg, using 3

doses at 1-3 week intervals; and for topical applicn. to prevent wound

infection, pref. using isotonic saline soln. of concn. 25-250 microg/mg.

The DNA encoding the binding protein and the hybrid protein may be

immobilised on a carrier and used to diagnose staphylococcal infections.

(Updated on 25-MAR-2003 to correct PA field.)

Sequence 1018 AA;

Query Match 92.3%; Score 96; DB 1; Length 1018;

Best Local Similarity 94.7%; Pred. No. 6.6e-05;

Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

1 GONEGQOTIEBTTPIVP 19

860 GONEGQOTIEBTTPIVP 878

AAU37245 standard; protein; 1018 AA.

AAU37245;

14-FEB-2002 (first entry)

Staphylococcus aureus cellular proliferation protein #1415.

Antisense; prokaryotic cellular proliferation protein; antibiotic;

antibacterial; drug design.

Staphylococcus aureus.

WO200170955-A2.

27-SEP-2001.

21-MAR-2001; 2001WO-US009180.

21-MAR-2000; 2000US-0191078P.

23-MAY-2000; 2000US-0206848P.

26-MAY-2000; 2000US-0207727P.

23-OCT-2000; 2000US-0242578P.

27-NOV-2000; 2000US-0253625P.

22-DEC-2000; 2000US-0257931P.

16-FEB-2001; 2001US-0269308P.

(ELIT-) ELITRA PHARM INC.

Haselbeck R, Ohlsen KL, Zyskind JW, Wall D, Trawick JD, Carr GJ;

Yamamoto RT, Xu HH;

WPI: 2001-61495/70.

N-PSDB; AAS55104.

New polynucleotides for the identification and development of

antibiotics, comprise sequences of antisense nucleic acids.

Example 3; SEQ ID NO 12838; 511pp; English.

The invention relates to antisense inhibitors of genes essential to

prokaryotic cellular proliferation, their use in identifying the genes,

their use in the discovery of novel antibiotics, the essential genes

themselves and the encoded proteins. The prokaryotes used are Escherichia

coli, Staphylococcus aureus, Salmonella typhi, Klebsiella pneumoniae,

Pseudomonas aeruginosa and Enterococcus faecalis. The invention is also

useful for the identification of potential new targets for antibiotic

development. The antisense nucleic acids can also be used to identify

proteins used in proliferation, to express these proteins, and to obtain

antibodies capable of binding to the expressed proteins. The proteins can

be used to screen compounds in rational drug discovery programmes. The

antisense nucleic acid sequence is also useful to screen for homologous

nucleic acids which are required for cell proliferation in a wide variety

of organisms. The present sequence represents an essential prokaryotic

cellular proliferation protein. Note: The sequence data for this patent

did not form part of the printed specification, but was obtained in

electronic format directly from WIPO at

ftp.wipo.int/pub/published_pct_sequences

Sequence 1018 AA;

Query Match 92.3%; Score 96; DB 4; Length 1018;

Best Local Similarity 94.7%; Pred. No. 6.6e-05;

Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

1 GONEGQOTIEBTTPIVP 19

860 GONEGQOTIEBTTPIVP 878

AAU34301 standard; protein; 1018 AA.

AAU34301;

14-FEB-2002 (first entry)

Staphylococcus aureus cellular proliferation protein #577.

Antisense; prokaryotic cellular proliferation protein; antibiotic;

antibacterial; drug design.

```

OS Staphylococcus aureus.
XX
XX WO200170955-A2.
XX
XX
XX 27-SEP-2001.
XX
XX
XX 21-MAR-2001; 2001WO-US009180.
XX
XX
XX 21-MAR-2000; 2000US-0191078P.
XX 23-MAY-2000; 2000US-0206848P.
XX 26-MAY-2000; 2000US-0207727P.
XX 23-OCT-2000; 2000US-0242578P.
XX 27-NOV-2000; 2000US-0253625P.
XX 22-DEC-2000; 2000US-0257931P.
XX 16-FEB-2001; 2001US-0269308P.
XX
XX (ELITR-) ELITRA PHARM INC.
XX
XX
XX Haselbeck R, Ohlsen KL, Zyskind JW, Wall D, Trawick JD, Carr GJ,
XX Yamamoto RT, Xu HH;
XX WPI; 2001-611495/70.
XX
XX N-PSDB; AAS52160.
XX
XX New polynucleotides for the identification and development of
XX antibiotics, comprise sequences of antisense nucleic acids.
XX
XX Example 3; SEQ ID NO 5797; 511pp; English.
XX
XX The invention relates to antisense inhibitors of genes essential to
XX prokaryotic cellular proliferation, their use in identifying the genes,
XX their use in the discovery of novel antibiotics, the essential genes
XX themselves and the encoded proteins. The prokaryotes used are Escherichia
XX coli, Staphylococcus aureus, Salmonella typhi, Klebsiella pneumoniae,
XX Pseudomonas aeruginosa and Enterococcus faecalis. The invention is also
XX useful for the identification of potential new targets for antibiotic
XX development. The antisense nucleic acids can also be used to identify
XX proteins used in proliferation, to express these proteins, and to obtain
XX antibodies capable of binding to the expressed proteins. The proteins can
XX be used to screen compounds in rational drug discovery programmes. The
XX antisense nucleic acid sequence is also useful to screen for homologous
XX nucleic acids which are required for cell proliferation in a wide variety
XX of organisms. The present sequence represents an essential prokaryotic
XX cellular proliferation protein. Note: The sequence data for this patent
XX did not form part of the printed specification, but was obtained in
XX electronic format directly from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 1018 AA;
XX
XX
XX Query Match 92.3%; Score 96; DB 4; Length 1018;
XX Best Local Similarity 94.7%; Pred. No. 6.6e-05;
XX Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX 1 GONEGQQTIEBDTTPPIVP 19
XX |||||
XX 860 GONEGQQTIEBDTTPPIVP 878
XX
XX
XX RESULT 7
XX ABJ18922
XX ID ABJ18922 standard; protein; 1018 AA.
XX
XX AC ABJ18922;
XX
XX DT 06-MAR-2003 (first entry)
XX
XX DE Pathogen specific antigen related staphylococcal protein SEQ ID No 68.
XX
XX KW Antibacterial; virucide; fungicide; protozoacide; cytostatic; anti-HIV;
XX hyperimmune; serum-reactive; antigen; pathogen; tumour; allergen;
XX auto-immunity; vaccine; staphylococcal infection; antibody; cancer;
XX autoimmune disease; HIV; hepatitis.
XX
XX

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XX
XX OS Staphylococcus sp.
XX
XX XX WO200259148-A2.
XX
XX
XX 01-AUG-2002.
XX
XX
XX 21-JAN-2002; 2002WO-EP000546.
XX
XX
XX 26-JAN-2001; 2001AT-00000130.
XX
XX
XX (CIST-) CISTEM BIOTECHNOLOGIES GMBH.
XX
XX
XX Meike A, Nagy E, Von Ahsen U, Klade C, Henics T, Zauner W;
XX Minh D, Vytvytka O, Etc H, Dryla A, Weichart T, Hafner M,
XX Tempelmeier B;
XX WPI; 2003-075410/07.
XX
XX
XX PT Identifying, isolating and producing hyperimmune serum-reactive antigens
XX from a pathogen, for preparing vaccine or medicament for treating or
XX preventing e.g. staphylococcal infections, comprises providing antibody
XX preparation.
XX
XX
XX Example 7; Page 157; 252pp; English.
XX
XX
XX The invention relates to a novel method for identifying, isolating and
XX producing hyperimmune serum-reactive antigens from a pathogen, tumour,
XX allergen, a tissue or host prone to auto-immunity, where the antigens are
XX used in a vaccine, comprises providing antibody preparation from a plasma
XX pool of a type of animal, or individual sera with antibodies against the
XX specific pathogen, tumour, allergen, tissue or host prone to auto-
XX immunity. The hyperimmune serum-reactive antigens comprising any of the
XX 62 sequences of 53-261 amino acids fully defined in the specification,
XX or their hyperimmune fragments are useful for the manufacture of a
XX pharmaceutical preparation, particularly a vaccine against staphylococcal
XX infections or colonisation against S. aureus or S. epidermidis. The
XX preparation of antibodies is useful for the manufacture of a medicament
XX for treating or preventing staphylococcal infections or colonisation
XX against S. aureus or S. epidermidis. The antibody preparations may also
XX be used for diagnostic and imaging purposes. Other conditions that can be
XX treated include cancer, autoimmune diseases or infections caused by viral
XX (e.g. HIV, hepatitis A, B or C), fungal or protozoan pathogens. This
XX sequence represents a staphylococcal protein relating to the method for
XX identifying and producing pathogen specific antigens of the invention
XX
XX
XX Sequence 1018 AA;
XX
XX
XX Query Match 92.3%; Score 96; DB 6; Length 1018;
XX Best Local Similarity 94.7%; Pred. No. 6.6e-05;
XX Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX 1 GONEGQQTIEBDTTPPIVP 19
XX |||||
XX 860 GONEGQQTIEBDTTPPIVP 878
XX
XX
XX RESULT 8
XX ABM72537
XX ID ABM72537 standard; protein; 1018 AA.
XX
XX AC ABM72537;
XX
XX DT 20-NOV-2003 (first entry)
XX
XX DE Staphylococcus aureus protein #1777.
XX
XX KW Antibacterial; vaccine; gene therapy; infection; sepsis; diagnosis;
XX enzymatic assay; antibiotic target.
XX
XX OS Staphylococcus aureus.
XX
XX
XX WO200294868-A2.
XX

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XX 26-NOV-2002.
 XX
 PF 27-MAR-2002; 2002WC-1B002637.
 XX
 PR 27-MAR-2001; 2001GB-00007661.
 XX
 PA (CHIR-) CHIRON SPA.
 XX
 PI Maignant V, Mora M, Scarselli M;
 XX
 DR WPI; 2003-120786/11.
 XX
 N-PSDB; ACF74097.
 PT New Staphylococcus aureus infection, useful as a vaccine for treating or
 PT preventing Staphylococcal infection, specifically an infection caused by
 PT S. aureus, e.g. sepsis.
 XX
 PS Claim 1; SEQ ID NO 3554; 49pp; English.
 XX
 CC The invention relates to novel genes and encoded proteins from
 CC Staphylococcus aureus. A composition comprising the S. aureus protein, a
 CC nucleic acid encoding the protein, or an antibody to the protein, is
 CC useful as a pharmaceutical, particularly as a vaccine for treating or
 CC preventing infection due to Staphylococcus bacteria, specifically an
 CC infection caused by S. aureus. The composition is particularly useful for
 CC treating or preventing sepsis in a patient. The composition can also be
 CC used for diagnostics. The protein is also used in an assay for enzymatic
 CC studies and as a target for antibiotics. This sequence represents one of
 CC the novel S. aureus proteins of the invention
 XX
 SQ Sequence 1018 AA;

Query Match 92.3%; Score 96; DB 6; Length 1018;
 Best Local Similarity 94.7%; Pred. No. 6.6e-05;
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GONEGQOTIPEDTTPPIVP 19
 |||||
 DB 860 GONEGQOTIPEDTTPPIVP 878

RESULT 9

AAW89806
 ID AAW89806 standard; protein; 1027 AA.

AC AAW89806;
 XX

DT 16-MAR-1999 (first entry)
 XX

DE Staphylococcus aureus protein SEQ ID #5254.

KM Computer readable medium; vaccine; S.aureus infection; immunodetection;
 KM cellulitis; eyelid infection; food poisoning; osteomyelitis; therapy;
 KM skin infection; surgical wound infection; scalded skin syndrome;
 KM toxic shock syndrome.
 XX

OS Staphylococcus aureus.
 XX

PN EP786519-A2.
 XX

PD 30-JUL-1997.
 XX

PF 07-JAN-1997; 97EP-00100117.
 XX

PR 05-JAN-1996; 96US-0009861P.
 XX

PA (HUMA-) HUMAN GENOME SCI INC.
 XX

PI Kunach CA, Choi GH, Barash SC, Dillon PJ, Fannon MR, Rosen CA;
 XX

DR WPI; 1997-374922/35.
 XX

PT polynucleotide(s) and proteins derived from Staphylococcus aureus -
 PT stored on computer readable medium and used in the production of anti-
 PT S.aureus vaccines.
 XX
 XX

PS Claim 23; Page 3263-3267; 3271pp; English.

CC This sequence represents a Staphylococcus aureus protein sequence of the
 CC invention. The DNA sequences encoding the S aureus proteins are recorded
 CC on a computer readable medium, preferably, selected from a floppy or hard
 CC disk, random access memory (RAM), read-only memory (ROM) or CD-ROM.
 CC Homology searches using the S.aureus DNA sequences allows putative
 CC functions to be assigned so that protein-encoding or regulatory regions
 CC of commercial, therapeutic or industrial importance can be obtained.
 CC Specifically, sequences which are likely to encode antigens have been
 CC identified and these polypeptides can be used in a vaccine composition
 CC against S.aureus infection. The polypeptides can also be used in a kit
 CC for the immunodetection of S.aureus in a sample. S.aureus is implicated
 CC in numerous human diseases, including cellulitis, eyelid infections, food
 CC poisoning, osteomyelitis, skin and surgical wound infections, scalded
 CC skin syndrome, toxic shock syndrome, etc. Organisms transformed with the
 CC DNA sequences can be used for recombinant production of the polypeptides.
 CC The new DNA sequences (and their fragments) are useful as primers or
 CC probes for isolating homologues of any of the 5191 S.aureus DNA sequences
 CC contained on the computer readable medium
 XX

SQ Sequence 1027 AA;

Query Match 92.3%; Score 96; DB 2; Length 1027;
 Best Local Similarity 94.7%; Pred. No. 6.6e-05;
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GONEGQOTIPEDTTPPIVP 19
 |||||
 DB 869 GONEGQOTIPEDTTPPIVP 887

RESULT 10

AAV29089
 ID AAV29089 standard; protein; 134 AA.

AC AAV29089;
 XX

DT 28-SEP-1999 (first entry)
 XX

DE Cloned fibronectin binding protein binding domain (FnBAB) sequence.

KM Bovine herpes virus-2; BHV-2; cytokine; immune response; immunogen; IL;
 KM interleukin; colony stimulating factor; CSF; interferon; IFN; TNF;
 KM tumour necrosis factor; recombinant virus; vaccine; mucosal disease;
 KM mastitis; breast cancer; stress-induced disease; binding domain; FnBAB;
 KM fibronectin binding protein.
 XX

OS Staphylococcus aureus.
 XX

PN W09916892-A1.
 XX

PD 08-APR-1999.
 XX

PF 29-SEP-1998; 98WO-G8002927.
 XX

PR 29-SEP-1997; 97GB-00020633.
 XX

PA (UYBR-) UNIV BRISTOL.
 XX

PI Bradley AJ, Duffas WPH;
 XX

XX WPI; 1999-255101/21.
 XX

DR N-PSDB; AAX91506.
 XX

PT New bovine herpes virus-2 vectors.
 XX

PS Example 2; Fig 8A-B, 130pp; English.
 XX

CC The invention provides bovine herpes virus-2 (BHV-2) based vectors that
 CC comprise at least one cytokine-encoding DNA sequence. The expression of
 CC cytokines in mammals can up-regulate immune responses to the immunogens.
 CC The cytokine is selected from interleukins (IL), colony stimulating
 CC factors (CSF), interferons (IFN) and tumour necrosis factors (TNF). The
 CC BHV-2 based vector or recombinant virus can be used as vaccines. They can
 CC be used for preventing or treating a mucosal disease in a subject, e.g.
 CC ruminants, cattle, sheep, goats, cats, horses, or man, particularly
 CC mastitis in cows or breast cancers in humans. They can also be used for
 CC preventing or treating a stress-induced disease. The present sequence
 CC represents a S. aureus fibronectin binding protein binding domain
 CC sequence FNBA, the gene cloned for use in this invention. The gene has
 CC 97.8 percent identity when compared to the previously published sequences
 CC FNBA and FNBB
 CC
 XX
 SQ Sequence 134 AA;

Query Match 87.5%; Score 91; DB 2; Length 134;
 Best Local Similarity 89.5%; Pred. No. 3.7e-05;
 Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GONEGQQTTEEDTTPPIVP 19
 | ||||| ||||| |||||
 DB 116 GHNEGQQTTEEDTTPPIVP 134

RESULT 11

AAI29088
 ID AAY29088 standard; protein; 134 AA.

XX AAY29088;
 XX

DT 28-SEP-1999 (first entry)

XX S. aureus fibronectin binding protein B (FNBB) binding domain.

XX Bovine herpes virus-2; BHV-2; cytokine; immune response; immunogen; IL;
 XX interleukin; colony stimulating factor; CSF; interferon; IFN; TNF;
 XX tumour necrosis factor; recombinant virus; vaccine; mucosal disease;
 XX mastitis; breast cancer; stress-induced disease; binding domain; FNBB;
 XX fibronectin binding protein.

XX Staphylococcus aureus.

XX WO916892-A1.

XX 08-APR-1999.

XX 29-SEP-1998; 98WO-GB002927.

XX 29-SEP-1997; 97GB-00020633.

XX (UYBR-) UNIV BRISTOL.

XX Bradley AJ, Duffas WPJ;

XX MPI: 1999-255101/21.

XX N-PSDB; AAX91505.

XX New bovine herpes virus-2 vectors.

XX Example 2; Fig 8A-B; 130pp; English.

XX The invention provides bovine herpes virus-2 (BHV-2) based vectors that
 CC comprise at least one cytokine-encoding DNA sequence. The expression of
 CC cytokines in mammals can up-regulate immune responses to the immunogens.
 CC The cytokine is selected from interleukins (IL), colony stimulating
 CC factors (CSF), interferons (IFN) and tumour necrosis factors (TNF). The
 CC BHV-2 based vector or recombinant virus can be used as vaccines. They can
 CC be used for preventing or treating a mucosal disease in a subject, e.g.
 CC ruminants, cattle, sheep, goats, cats, horses, or man, particularly
 CC mastitis in cows or breast cancers in humans. They can also be used for
 CC preventing or treating a stress-induced disease. The present sequence

CC represents the binding domain of a previously published S. aureus
 CC fibronectin binding protein B (FNBB) sequence. The FNBB binding domain
 CC gene sequence FNBA, cloned for use in this invention has 97.8 percent
 CC identity when compared to the previously published FNBA and FNBB gene
 CC sequences
 CC
 XX
 SQ Sequence 134 AA;

Query Match 87.5%; Score 91; DB 2; Length 134;
 Best Local Similarity 89.5%; Pred. No. 3.7e-05;
 Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GONEGQQTTEEDTTPPIVP 19
 | ||||| ||||| |||||
 DB 116 GHNEGQQTTEEDTTPPIVP 134

RESULT 12

AAW69803
 ID AAW69803 standard; protein; 559 AA.

XX AAW69803;
 XX

DT 16-MAR-1999 (first entry)

XX Staphylococcus aureus protein SEQ ID #5251.

XX Computer readable medium; vaccine; S. aureus infection; immunodetection;
 XX cellulitis; eyelid infection; food poisoning; osteomyelitis; therapy;
 XX skin infection; surgical wound infection; scalded skin syndrome;
 XX toxic shock syndrome.

XX Staphylococcus aureus.

XX EP786519-A2.

XX 30-JUL-1997.

XX 07-JAN-1997; 97EP-00100117.

XX 05-JAN-1996; 96US-0009861P.

XX (HUMA-) HUMAN GENOME SCI INC.

XX Kunsch CA, Choi GH, Barash SC, Dillon PJ, Fannon MR, Rosen CA;

XX MPI: 1997-374922/35.

XX Polynucleotide(s) and proteins derived from Staphylococcus aureus -
 XX stored on computer readable medium and used in the production of anti-
 XX S. aureus vaccines.

XX Claim 23; Page 3259-3261; 3271pp; English.

XX This sequence represents a Staphylococcus aureus protein sequence of the
 CC invention. The DNA sequences encoding the S. aureus proteins are recorded
 CC on a computer readable medium, preferably selected from a floppy or hard
 CC disk, random access memory (RAM), read-only memory (ROM) or CD-ROM.
 CC Homology searches using the S. aureus DNA sequences allows putative
 CC functions to be assigned so that protein-encoding or regulatory regions
 CC of commercial, therapeutic or industrial importance can be obtained.
 CC Specifically, sequences which are likely to encode antigens have been
 CC identified and these polypeptides can be used in a vaccine composition
 CC against S. aureus infection. The polypeptides can also be used in a kit
 CC for the immunodetection of S. aureus in a sample. S. aureus is implicated
 CC in numerous human diseases, including cellulitis, eyelid infections, food
 CC poisoning, osteomyelitis, skin and surgical wound infections, scalded
 CC skin syndrome, toxic shock syndrome, etc. Organisms transformed with the
 CC DNA sequences can be used for recombinant production of the polypeptides.
 CC The new DNA sequences (and their fragments) are useful as primers or
 CC probes for isolating homologues of any of the 5191 S. aureus DNA sequences
 CC contained on the computer readable medium

RESULT 15
ADA89470
ID ADA89470 standard; protein; 948 AA.
XX
AC ADA89470;
XX
DT 20-NOV-2003 (first entry)
XX
DE Staphylococcus aureus antigenic protein #9.
XX
KW antigenic protein; vaccine; Staphylococcus aureus; pathogenic organism;
KW antibacterial; neuroprotective; immunosuppressive; antiinflammatory;
KW antifungal; immunostimulant; ophthalmological; pathogenic microbe;
KW bacteraemia; septic shock; organ infection; skin infection;
KW bacterial basal colonisation; bacterial eye infection; septicaemia;
KW tuberculosis; food poisoning; blood infection; peritonitis; endocarditis;
KW sepsis; meningitis; pneumonia; stomach ulcer; gonorrhoea; toxic shock;
KW necrotising fasciitis; impetigo; histoplasmosis; Lyme disease;
KW gastro-enteritis; dysentery; shigellosis; skin disorder.
XX
OS Staphylococcus aureus.
XX
PN WO2003011899-A2.
XX
PD 13-FEB-2003.
XX
PF 02-AUG-2002; 2002WO-GB003606.
XX
PR 02-AUG-2001; 2001GB-00018825.
PR 09-JAN-2002; 2002GB-00000349.
XX
PA (UYSH-) UNIV SHEFFIELD.
PA (BIOS-) BIOSYNEXUS INC.
XX
PI Foster S, Mond J, Clarke S, McDowell P, Brummel K;
XX
DR MPI; 2003-256434/25.
XX
PT New antigenic polypeptides from Staphylococcus aureus or S. epidermidis,
PT useful as a vaccine for immunizing humans against e.g. bacteraemia, septic
PT shock, septicaemia, tuberculosis, meningitis, pneumonia, gonorrhoea or
PT impetigo.
XX
PS Claim 4; Page 124-125; 189pp; English.
XX
CC The present invention describes an antigenic protein or its part, which
CC is for use as a vaccine. The antigenic protein is encoded by an isolated
CC DNA molecule of Staphylococcus aureus or S. epidermidis partial gene
CC sequences (designated dnasA and dna SE, respectively; and which encodes a
CC protein expressed by a pathogenic organism. Also described: (1) a vaccine
CC composition comprising at least one antigenic protein; (2) a method of
CC immunising an animal against a disease or condition caused by a
CC pathogenic microbe by administering the antigenic protein or the vaccine;
CC (3) an antibody or its binding part obtainable by the method above; (4)
CC preparing a hybridoma cell line producing monoclonal antibodies; (5) a
CC hybridoma cell line produced by the method of (4); and (6) identifying
CC opsonic antigens expressed by a pathogenic microbe. The antigenic
CC proteins have antibacterial, neuroprotective, immunosuppressive,
CC antiinflammatory, antifungal, immunostimulant and ophthalmological
CC activities, and can be used in vaccines. The antigenic proteins or
CC vaccines can be used for immunising an animal (specifically a human)
CC against a disease or condition caused by a pathogenic microbe, e.g.
CC bacteraemia, septic shock, organ infection, skin infection, bacterial
CC basal colonisation, bacterial eye infections, septicaemia, tuberculosis,
CC bacteria-associated food poisoning, blood infections, peritonitis,
CC endocarditis, sepsis, meningitis, pneumonia, stomach ulcers, gonorrhoea,
CC strep throat, streptococcal-associated toxic shock, necrotising
CC fasciitis, impetigo, histoplasmosis, Lyme disease, gastro-enteritis,
CC dysentery, shigellosis, S. aureus-associated septicaemia, food-poisoning,
CC skin disorders, S. epidermidis-associated septicaemia, peritonitis or
CC endocarditis. The present sequence represents a S. aureus antigenic
CC protein sequence from the present invention.
XX

SQ Sequence 948 AA;
Query Match 87.5%; Score 91; DB 6; Length 948;
Best Local Similarity 89.5%; Pred. No. 0.00032;
Matches 17; Conservative 0; Mismatches 2; Indels 0;
Gaps 0;
QY 1 GONEGQQTIEEDTTPPIVP 19
| | | | | | | | | | | | | | | | | | | | | |
DB 804 GNEGQQTIEEDTTPPIVP 822

Search completed: October 25, 2005, 19:38:17
Job time : 56.519 secs

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OM protein - protein search, using sw model

Run on: October 22, 2005, 02:23:36 ; Search time 14.4181 Seconds
(without alignments)
98.371 Million cell updates/sec

Title: US-10-731-238-12
Perfect score: 104
Sequence: 1 GONEGQQTPEPTPIPV 19

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues
Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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3: /cgn2_6/prodata/1/iaa/5A-COMB.pep: *
4: /cgn2_6/prodata/1/iaa/5B-COMB.pep: *
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	104	100.0	19	US-09-010-317-12	Sequence 12, Appl
2	96	92.3	19	US-09-010-317-11	Sequence 11, Appl
3	96	92.3	178	US-08-459-135A-12	Sequence 12, Appl
4	96	92.3	178	US-08-495-559-12	Sequence 12, Appl
5	96	92.3	1027	US-08-956-171E-5254	Sequence 5254, Ap
6	96	92.3	1027	US-08-781-986A-5254	Sequence 5254, Ap
7	91	87.5	174	US-08-459-135A-13	Sequence 13, Appl
8	91	87.5	174	US-08-495-559-13	Sequence 13, Appl
9	91	87.5	559	US-08-956-171E-5251	Sequence 5251, Ap
10	91	87.5	559	US-08-781-986A-5251	Sequence 5251, Ap
11	90	86.5	19	US-09-010-317-51	Sequence 51, Appl
12	89	85.6	19	US-09-010-317-52	Sequence 52, Appl
13	89	85.6	19	US-09-010-317-53	Sequence 53, Appl
14	80	76.9	174	US-08-459-135A-10	Sequence 10, Appl
15	80	76.9	174	US-08-495-559-10	Sequence 10, Appl
16	80	76.9	176	US-08-459-559-6	Sequence 6, Appl
17	80	76.9	181	US-08-459-135A-6	Sequence 6, Appl
18	69	66.3	130	US-08-459-135A-8	Sequence 8, Appl
19	69	66.3	130	US-08-495-559-8	Sequence 8, Appl
20	62	59.6	130	US-08-459-135A-7	Sequence 7, Appl
21	62	59.6	130	US-08-495-559-7	Sequence 7, Appl
22	49	47.1	206	US-09-543-681A-4756	Sequence 4756, Ap
23	49	47.1	877	US-09-328-352-8162	Sequence 8162, Ap
24	47	45.2	38	US-09-010-317-46	Sequence 46, Appl
25	46	44.2	38	US-09-010-317-46	Sequence 46, Appl
26	46	44.2	228	US-09-270-767-46270	Sequence 46270, A
27	46	44.2	2736	US-09-252-991A-30227	Sequence 30227, A

28	45.5	43.8	486	4	US-09-489-039A-14195	Sequence 14195, A
29	45	43.3	38	1	US-08-729-767-4	Sequence 4, Appl
30	45	43.3	90	4	US-09-248-796A-21460	Sequence 21460, A
31	45	43.3	114	1	US-08-259-000-3	Sequence 3, Appl
32	45	43.3	139	3	US-08-856-253-8	Sequence 8, Appl
33	45	43.3	401	4	US-09-248-796A-25547	Sequence 25547, A
34	45	43.3	514	4	US-09-252-991A-25281	Sequence 25281, A
35	45	43.3	3838	4	US-09-949-015-10853	Sequence 10853, A
36	44	42.3	38	1	US-08-729-767-3	Sequence 3, Appl
37	44	42.3	38	4	US-09-010-317-41	Sequence 41, Appl
38	44	42.3	150	4	US-09-270-767-32833	Sequence 32833, A
39	44	42.3	150	4	US-09-270-767-48050	Sequence 48050, A
40	44	42.3	257	4	US-09-567-458A-2	Sequence 2, Appl
41	43.5	41.8	338	4	US-09-270-767-43303	Sequence 43303, A
42	43	41.3	38	4	US-09-010-317-42	Sequence 42, Appl
43	43	41.3	99	3	US-09-025-596-61	Sequence 61, Appl
44	43	41.3	99	4	US-09-073-661-61	Sequence 61, Appl
45	43	41.3	99	4	US-10-100-785-61	Sequence 61, Appl

ALIGNMENTS

RESULT 1
US-09-010-317-12
Sequence 12, Application US/09010317
Patent No. 6685943
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
APPLICANT: Patti, Joseph M.
APPLICANT: House-Pompeo, Karen L.
APPLICANT: Speziale, Pietro
APPLICANT: John, Danny
APPLICANT: McLaughlin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
TITLE OF INVENTION: AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSER: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hidler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAMK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 12:
LENGTH: 19 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-09-010-317-12
Query Match 100.0%; Score 104; DB 4; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.4e-08;

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Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GONEGQOTIPEDTTPPIV 19
Db 1 GONEGQOTIPEDTTPPIV 19

RESULT 2
US-09-010-317-11
; Sequence 11, Application US/09010317
; Patent No. 6685943
; GENERAL INFORMATION:
; APPLICANT: Hook, Magnus
; APPLICANT: Patti, Joseph W.
; APPLICANT: House-Pompeo, Karen L.
; APPLICANT: Speziale, Pietro
; APPLICANT: Jch, Danny
; APPLICANT: McGavin, Martin J.
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
; TITLE OF INVENTION: AND METHODS OF USE
; NUMBER OF SEQUENCES: 105
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: TX
; COUNTRY: USA
; ZIP: 77210-4433
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/010,317
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/036,139
; FILING DATE: 21-JAN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Hibley, David W.
; REGISTRATION NUMBER: 41,071
; REFERENCE/DOCKET NUMBER: TANK:189
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 512-418-3000
; TELEFAX: 512-474-7577
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 19 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; US-09-010-317-11

Query Match 92.3%; Score 96; DB 4; Length 19;
Best Local Similarity 94.7%; Pred. No. 3.2e-07;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GONEGQOTIPEDTTPPIV 19
Db 1 GONEGQOTIPEDTTPPIV 19

RESULT 3
US-08-459-135A-12
; Sequence 12, Application US/08459135A
; Patent No. 5955078
; GENERAL INFORMATION:
; APPLICANT: BURHAM, Martin Karl Russel
; APPLICANT: CHOPRA, Ian
; APPLICANT: CRITCHLEY, Ian Alfred
; APPLICANT: KNOWLES, David Justin Charles

; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN: MONOCLONAL ANTIBODY AND THEIR USE IN PREVENTING BACTERIAL ADHESION
; TITLE OF INVENTION: ANTIBODY AND THEIR USE IN PREVENTING BACTERIAL ADHESION
; FILE REFERENCE: P30591
; CURRENT APPLICATION NUMBER: US/08/495,559A
; CURRENT FILING DATE: 1995-08-03
; EARLIER APPLICATION NUMBER: GB 9302289.5
; EARLIER FILING DATE: 1993-02-05
; EARLIER APPLICATION NUMBER: GB 9321592.9
; EARLIER FILING DATE: 1993-10-20
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 12
; LENGTH: 178
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
; US-08-495-559-12

; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN: MONOCLONAL ANTIBODY AND THEIR USE
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corporation
; STREET: 709 Swedeland Road
; CITY: King of Prussia
; STATE: PA
; COUNTRY: U.S.A.
; ZIP: 19406-0939
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq, Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/459,135A
; FILING DATE: 02-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB/94/00215
; FILING DATE: 04-Feb-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Gimm, Edward R
; REGISTRATION NUMBER: 38,891
; REFERENCE/DOCKET NUMBER: P30591C2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-270-4478
; TELEFAX: 610-270-5090
; TELEX:
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 178 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Protein
; US-08-459-135A-12

Query Match 92.3%; Score 96; DB 2; Length 178;
Best Local Similarity 94.7%; Pred. No. 3.4e-06;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GONEGQOTIPEDTTPPIV 19
Db 116 GONEGQOTIPEDTTPPIV 134

RESULT 4
US-08-495-559-12
; Sequence 12, Application US/08495559A
; Patent No. 6054572
; GENERAL INFORMATION:
; APPLICANT: BURHAM, Martin Karl Russel
; APPLICANT: CHOPRA, Ian
; APPLICANT: CRITCHLEY, Ian Alfred
; APPLICANT: KNOWLES, David Justin Charles
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN: MONOCLONAL ANTIBODY AND THEIR USE IN PREVENTING BACTERIAL ADHESION
; TITLE OF INVENTION: ANTIBODY AND THEIR USE IN PREVENTING BACTERIAL ADHESION
; FILE REFERENCE: P30591
; CURRENT APPLICATION NUMBER: US/08/495,559A
; CURRENT FILING DATE: 1995-08-03
; EARLIER APPLICATION NUMBER: GB 9302289.5
; EARLIER FILING DATE: 1993-02-05
; EARLIER APPLICATION NUMBER: GB 9321592.9
; EARLIER FILING DATE: 1993-10-20
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 12
; LENGTH: 178
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
; US-08-495-559-12
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Query Match 92.3%; Score 96; DB 3; Length 178;
Best Local Similarity 94.7%; Pred. No. 3.4e-06;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GONEGQOTIEBTTPIVP 19
DB 116 GONEGQOTIEBTTPIVP 134

RESULT 5
US-08-956-171E-5254
; Sequence 5254, Application US/08956171E
; Patent No. 6593114

GENERAL INFORMATION:

APPLICANT: Charles Kunesh

Gill H. Choi

Patrick S. Dillon

Craig A. Rosen

Steven C. Barash

Michael R. Fannon

TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences

NUMBER OF SEQUENCES: 5256

CORRESPONDENCE ADDRESS:

ADDRESSEE: Human Genome Sciences, Inc.

STREET: 9410 Key West Avenue

CITY: Rockville

STATE: Maryland

COUNTRY: USA

ZIP: 20850

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.50 inch, 1.4mb storage

COMPUTER: HP Vectra 486/33

OPERATING SYSTEM: MSDOS version 6.2

SOFTWARE: ASCII Text

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/956,171E

FILING DATE: 20-Oct-1997

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 60/009,861

FILING DATE: January 5, 1996

APPLICATION NUMBER: 08/781,986

FILING DATE: January 3, 1997

ATTORNEY/AGENT INFORMATION:

NAME: Mark J. Hyman

REGISTRATION NUMBER: 46,789

REFERENCE/DOCKET NUMBER: PB248P1

TELECOMMUNICATION INFORMATION:

TELEPHONE: (240) 314-1224

TELEFAX: (301) 309-8439

INFORMATION FOR SEQ ID NO: 5254:

SEQUENCE CHARACTERISTICS:

LENGTH: 1027 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 5254:

US-08-956-171E-5254

Query Match 92.3%; Score 96; DB 4; Length 1027;

Best Local Similarity 94.7%; Pred. No. 2.2e-05;

Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GONEGQOTIEBTTPIVP 19

DB 869 GONEGQOTIEBTTPIVP 887

RESULT 6

US-08-781-986A-5254

; Sequence 5254, Application US/08781986A

Patent No. 6737248

GENERAL INFORMATION:

APPLICANT: Charles Kunesh

TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences

NUMBER OF SEQUENCES: 5255

CORRESPONDENCE ADDRESS:

ADDRESSEE: Human Genome Sciences, Inc.

STREET: 9410 Key West Avenue

CITY: Rockville

STATE: Maryland

COUNTRY: USA

ZIP: 20850

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.50 inch, 1.4mb storage

COMPUTER: HP Vectra 486/33

OPERATING SYSTEM: MSDOS version 6.2

SOFTWARE: ASCII Text

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/781,986A

FILING DATE:

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER:

ATTORNEY/AGENT INFORMATION:

NAME: Benson, Bob

REGISTRATION NUMBER: 30,446

REFERENCE/DOCKET NUMBER: PB248PP

TELECOMMUNICATION INFORMATION:

TELEPHONE: (301) 309-8504

TELEFAX: (301) 309-8512

INFORMATION FOR SEQ ID NO: 5254:

SEQUENCE CHARACTERISTICS:

LENGTH: 1027 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-781-986A-5254

Query Match 92.3%; Score 96; DB 4; Length 1027;
Best Local Similarity 94.7%; Pred. No. 2.2e-05;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GONEGQOTIEBTTPIVP 19
DB 869 GONEGQOTIEBTTPIVP 887

RESULT 7
US-08-459-135A-13
; Sequence 13, Application US/08459135A
; Patent No. 5955078

GENERAL INFORMATION:

APPLICANT: BURHAM, Martin Karl Russel

APPLICANT: CHOPRA, Ian

APPLICANT: CRITCHLEY, David Justin Charles

TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN: MONOCLONAL ANTIBODY AND THEIR US

NUMBER OF SEQUENCES: 15

CORRESPONDENCE ADDRESS:

ADDRESSEE: SmithKline Beecham Corporation

STREET: 709 Swedeland Road

CITY: King of Prussia

STATE: PA

COUNTRY: U.S.A.

ZIP: 19406-0939

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: Fastseq, Version 2.0

CURRENT APPLICATION DATA:

RESULT 9
US-08-956-171E-5251
; Sequence 5251, Application US/08956171E
; Patent No. 6593114
; GENERAL INFORMATION:

```

APPLICANT: Charles Kunsch
           Gil H. Choi
           Patrick S. Dillon
           Craig A. Rosen
           Steven C. Barash
           Michael R. Fannon
TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
NUMBER OF SEQUENCES: 5256
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COUNTRY: USA
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4mb storage
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/956,171E
FILING DATE: 20-Oct-1997
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/009,861
FILING DATE: January 5, 1996
APPLICATION NUMBER: 08/781,986
FILING DATE: January 3, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Mark J. Hyman
REGISTRATION NUMBER: 46,789
REFERENCE/DOCKET NUMBER: PB248P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (240) 314-1224
TELEFAX: (301) 309-8439
INFORMATION FOR SEQ ID NO: 5251:
SEQUENCE CHARACTERISTICS:
LENGTH: 559 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 5251:
US-08-956-171E-5251
Query Match          87.5%; Score 91; DB 4; Length 559;
Best Local Similarity 89.5%; Pred. No. 5.8e-05;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY      1 GONEGQQTPEPTTPPIVP 19
        | ||||| ||||| |||||
DB      415 GHNEGQQTIEDTTPPIVP 433
RESULT 10
US-08-781-986A-5251
; Sequence 5251, Application US/08781986A
; Patent No. 6737248
; GENERAL INFORMATION:
APPLICANT: Charles Kunsch
TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
NUMBER OF SEQUENCES: 5255
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COUNTRY: USA
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4mb storage
COMPUTER: HP Vectra 486/33

```

OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/781,986A
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Benson, Bob
REGISTRATION NUMBER: 30,446
REFERENCE/DOCKET NUMBER: PB248PP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 5251:
SEQUENCE CHARACTERISTICS:
LENGTH: 559 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-781-986A-5251

Query Match: 87.5%; Score 91; DB 4; Length 559;
Best Local Similarity 89.5%; Pred. No. 5,8e-05;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GONEGQOTIEPTTPPIV 19
DB 415 GHNEGQOTIEPTTPPIV 433

RESULT 11
US-09-010-317-51
Sequence 51, Application US/09010317
Patent No. 6685943
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
APPLICANT: Patti, Joseph M.
APPLICANT: House-Pompeo, Karen L.
APPLICANT: Speziale, Pietro
APPLICANT: John, Danny
APPLICANT: McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
TITLE OF INVENTION: AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESSES:
ADDRESSES: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAMK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000

TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 51:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-09-010-317-51

Query Match: 86.5%; Score 90; DB 4; Length 19;
Best Local Similarity 89.5%; Pred. No. 2,2e-06;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GONEGQOTIEPTTPPIV 19
DB 1 GONEGQOTIEPTTPPIV 19

RESULT 12
US-09-010-317-52
Sequence 52, Application US/09010317
Patent No. 6685943
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
APPLICANT: Patti, Joseph M.
APPLICANT: House-Pompeo, Karen L.
APPLICANT: Speziale, Pietro
APPLICANT: John, Danny
APPLICANT: McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
TITLE OF INVENTION: AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESSES:
ADDRESSES: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAMK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 52:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-09-010-317-52

Query Match: 85.6%; Score 89; DB 4; Length 19;
Best Local Similarity 89.5%; Pred. No. 3e-06;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GONEGQOTIEPTTPPIV 19
DB 1 GONEGQOTIEPTTPPIV 19

RESULT 13
US-09-010-317-53
Sequence 53, Application US/09010317
Patent No. 6685943
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
APPLICANT: Patcl, Joseph M.
APPLICANT: House-Pompeo, Karen L.
APPLICANT: Speziale, Pietro
APPLICANT: Jch, Danny
APPLICANT: McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSER: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hbljer, David W.
REGISTRATION NUMBER: 41,071
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 53:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-09-010-317-53

Query Match 85.6%; Score 89; DB 4; Length 19;
Best Local Similarity 89.5%; Pred. No. 3e-06;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GONEGQQTPEEDTTPPIVP 19
DB 1 GONEGQQTPEEDTTPPIVP 19

RESULT 14
US-08-459-135A-10
Sequence 10, Application US/08459135A
Patent No. 5955078
GENERAL INFORMATION:
APPLICANT: BURHAM, Martin Karl Russel
APPLICANT: CHOPRA, Ian
APPLICANT: CRITCHLEY, Ian Alfred
APPLICANT: KNOWLES, David Justin Charles
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN: MONOCLONAL ANTIBODY AND THEIR US
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSER: SmithKline Beecham Corporation
STREET: 709 Swedeland Road

CITY: King of Prussia
STATE: PA
COUNTRY: U.S.A.
ZIP: 19406-0939
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: Fastseq, Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/459,135A
FILING DATE: 02-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB/94/00215
FILING DATE: 04-Feb-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Gimm, Edward R
REGISTRATION NUMBER: 38,891
REFERENCE/DOCKET NUMBER: P30591C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-4478
TELEFAX: 610-270-5090
TELEX:
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 174 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: Protein
US-08-459-135A-10

Query Match 76.9%; Score 80; DB 2; Length 174;
Best Local Similarity 78.9%; Pred. No. 0.00059;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GONEGQQTPEEDTTPPIVP 19
DB 116 GONEGQQTPEEDTTPPIVP 134

RESULT 15
US-08-495-559-10
Sequence 10, Application US/08495559A
Patent No. 6054572
GENERAL INFORMATION:
APPLICANT: BURHAM, Martin Karl Russel
APPLICANT: CHOPRA, Ian
APPLICANT: CRITCHLEY, Ian Alfred
APPLICANT: KNOWLES, David Justin Charles
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN: MONOCLONAL
TITLE OF INVENTION: ANTIBODY AND THEIR USE IN PREVENTING BACTERIAL ADHESION
FILE REFERENCE: P30591
CURRENT APPLICATION NUMBER: US/08/495,559A
CURRENT FILING DATE: 1995-08-03
EARLIER APPLICATION NUMBER: GB 9302289.5
EARLIER FILING DATE: 1993-02-05
EARLIER APPLICATION NUMBER: GB 9321592.9
EARLIER FILING DATE: 1993-10-20
NUMBER OF SEQ ID NOS: 13
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 10
LENGTH: 174
TYPE: PRT
ORGANISM: Staphylococcus aureus
US-08-495-559-10

Query Match 76.9%; Score 80; DB 3; Length 174;
Best Local Similarity 78.9%; Pred. No. 0.00059;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GONEGQQTPEEDTTPPIVP 19

Wed Oct 26 15:01:51 2005

us-10-731-238-12.rat

Page 7

Db 116 GHNEGQOTIBEDTTPPP 134

Search completed: October 22, 2005, 03:51:10
Job time : 15.4181 secs

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GenCore version 5.1.6
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OM protein - protein search, using BW model

Run on: October 22, 2005, 10:49:15 ; Search time 53.5951 Seconds
(without alignments)
148.005 Million cell updates/sec

Title: US-10-731-238-12
Perfect score: 104
Sequence: 1 GQNEGQRTPEPTPIPV 19

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 1862951 seqs, 417491010 residues

Total number of hits satisfying chosen parameters: 1862951

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA:
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	104	100.0	19	US-10-731-238-12	Sequence 11, Appl
2	96	92.3	19	US-10-731-238-11	Sequence 12, Appl
3	96	92.3	1018	US-09-815-242-5797	Sequence 5797, Ap
4	96	92.3	1018	US-09-815-242-1288	Sequence 1288, A
5	96	92.3	1018	US-10-470-048B-68	Sequence 68, Appl
6	96	92.3	1027	US-08-781-986A-5254	Sequence 5254, Ap
7	96	92.3	1027	US-10-329-624-5254	Sequence 5254, Ap
8	96	92.3	1027	US-08-781-986A-5251	Sequence 5251, Ap
9	91	87.5	559	US-10-329-624-5251	Sequence 5251, Ap
10	91	87.5	559	US-10-329-624-5251	Sequence 5251, Ap
11	91	87.5	559	US-10-329-624-5251	Sequence 5251, Ap
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22	91	87.5	559	US-10-329-624-5251	Sequence 5251, Ap

12	90	86.5	19	US-10-731-238-51	Sequence 51, Appl
13	89	85.6	19	US-10-731-238-52	Sequence 52, Appl
14	89	85.6	19	US-10-731-238-53	Sequence 53, Appl
15	85	81.7	961	US-10-282-122A-43778	Sequence 43778, A
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22	49	47.1	101	US-10-425-115-210044	Sequence 45185, A
23	49	47.1	874	US-10-282-122A-45185	Sequence 574, App
24	49	47.1	1172	US-10-451-467A-574	Sequence 3949, App
25	49	47.1	1201	US-10-369-493-3949	Sequence 2873, App
26	49	47.1	1427	US-10-408-765A-2873	Sequence 1470, App
27	48	46.2	1460	US-10-408-765A-1400	Sequence 38821, A
28	48	46.2	218	US-10-450-763-38821	Sequence 38821, A
29	48	46.2	344	US-10-116-275-327	Sequence 327, App
30	48	46.2	347	US-10-105-823-188	Sequence 188, App
31	48	46.2	347	US-10-105-823-188	Sequence 33982, A
32	48	46.2	347	US-10-116-275-327	Sequence 347, App
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37	47	45.2	157	US-11-097-143-38406	Sequence 38406, A
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39	47	45.2	343	US-11-097-143-39570	Sequence 39570, A
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42	47	45.2	836	US-10-878-652-7	Sequence 7, Appl
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44	46	44.2	36	US-11-097-143-4959	Sequence 4959, Ap
45	46	44.2	336	US-11-097-143-24198	Sequence 24198, A

ALIGNMENTS

RESULT 1
US-10-731-238-12
; Sequence 12, Application US/10731238
; Publication NO. US20050123552A1
; GENERAL INFORMATION:
; APPLICANT: Hook, Magnus
; Patti, Joseph M.
; House-Pompeo, Karen L.
; Speziale, Pietro
; John, Danny
; McGavin, Martin J.
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
; AND METHODS OF USE
; NUMBER OF SEQUENCES: 105
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: TX
; COUNTRY: USA
; ZIP: 77210-4433
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/731.238
; FILING DATE: 10-Dec-2003
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/010.317
; FILING DATE: 21-Jan-1998
; APPLICATION NUMBER: US 60/036.139

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      FILING DATE: 21-JAN-1997
      ATTORNEY/AGENT INFORMATION:
        NAME: Hibler, David W.
        REGISTRATION NUMBER: 41,071
        REFERENCE/DOCKET NUMBER: TANK:189
      TELECOMMUNICATION INFORMATION:
        TELEPHONE: 512-418-3000
        TELEFAX: 512-474-7577
      INFORMATION FOR SEQ ID NO: 12:
        SEQUENCE CHARACTERISTICS:
          LENGTH: 19 amino acids
          TYPE: amino acid
          STRANDEDNESS: <Unknown>
          TOPOLOGY: linear
      US-10-731-238-12
      SEQUENCE DESCRIPTION: SEQ ID NO: 12:
      Query Match      100.0%; Score 104; DB 18; Length 19;
      Best Local Similarity 100.0%; Pred. No. 6.3e-08;
      Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0.

QY      1 GONEGQQTIPEDTTPPIVP 19
      |||||||
Db      1 GONEGQQTIPEDTTPPIVP 19

RESULT 2
US-10-731-238-11
; Sequence 11, Application US/10731238
; Publication No. US20050123552A1
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
          Patti, Joseph M.
          House-Pompeo, Karen L.
          Speziale, Pietro
          Joh, Danny
          McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P. O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/731,238
FILING DATE: 10-Dec-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE: 21-Jan-1998
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TANK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
  LENGTH: 19 amino acids
  TYPE: amino acid
  STRANDEDNESS: <Unknown>

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; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 11:
; US-10-731-238-11

Query Match          92.3%; Score 96; DB 18; Length 19;
Best Local Similarity 94.7%; Pred. No. 8.7e-07;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0.

OY      1 GONEGQQTIEDTTPPIVP 19
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Db      1 GONEGQQTIEDTTPPIVP 19

RESULT 3
US-09-815-242-5797
; Sequence 5797, Application US/09815242
; Patent No. US20020061569A1
GENERAL INFORMATION:
APPLICANT: Haeselbeck, Robert
APPLICANT: Ohlsen, Kari L.
APPLICANT: Zyskind, Judith W.
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John D.
APPLICANT: Carr, Grant J.
APPLICANT: Yamamoto, Robert T.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in
FILE REFERENCE: ELITRA.01A
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 5797
LENGTH: 1018
TYPE: PRT
ORGANISM: Staphylococcus aureus
US-09-815-242-5797

Query Match          92.3%; Score 96; DB 9; Length 1018;
Best Local Similarity 94.7%; Pred. No. 7e-05;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0.

OY      1 GONEGQQTIEDTTPPIVP 19
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Db      860 GONEGQQTIEDTTPPIVP 878

RESULT 4
US-09-815-242-12838
; Sequence 12838, Application US/09815242
; Patent No. US20020061569A1
GENERAL INFORMATION:
APPLICANT: Haeselbeck, Robert
APPLICANT: Ohlsen, Kari L.
APPLICANT: Zyskind, Judith W.
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John D.
APPLICANT: Carr, Grant J.

```

RESULT 6
 US-08-781-986A-5254
 ; Sequence 5254, Application US/08781986A
 ; Publication NO. US20030054436A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Charles Kunsch
 ; TITLE OF INVENTION: Straphylococcus aureus Polymnucleotides and Sequences

FILING DATE: 27-Dec-

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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/956,171
FILING DATE: October 20, 1997
APPLICATION NUMBER: 60/009,861
FILING DATE: January 5, 1996
APPLICATION NUMBER: 08/781,986
FILING DATE: January 3, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Mark J. Hyman
REGISTRATION NUMBER: 46,789
REFERENCE/DOCKET NUMBER: PB248P1D1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (240) 314-1224
TELEFAX: (301) 309-8439
INFORMATION FOR SEQ ID NO: 5254:
SEQUENCE CHARACTERISTICS:
LENGTH: 1027 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 5254:
US-10-329-624-5254

Query Match 92.3%; Score 96; DB 15; Length 1027;
Best Local Similarity 94.7%; Pred. No. 7.1e-05;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GONEGQQTIEEDTTPPIVP 19
DB 869 GONEGQQTIEEDTTPPIVP 887

RESULT 8
US-08-781-986A-5251
Sequence 5251, Application US/08781986A
Publication No. US20030054436A1
GENERAL INFORMATION:
APPLICANT: Charles Kunach
TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
NUMBER OF SEQUENCES: 5255
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COUNTRY: USA
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/781,986A
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Benson, Bob
REGISTRATION NUMBER: 30,446
REFERENCE/DOCKET NUMBER: PB248PP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 5251:
SEQUENCE CHARACTERISTICS:
LENGTH: 559 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear

MOLECULE TYPE: protein
US-08-781-986A-5251

Query Match 87.5%; Score 91; DB 8; Length 559;
Best Local Similarity 89.5%; Pred. No. 0.00019;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GONEGQQTIEEDTTPPIVP 19
DB 415 GONEGQQTIEEDTTPPIVP 433

RESULT 9
US-10-329-624-5251
Sequence 5251, Application US/10329624
Publication No. US20040043037A1
GENERAL INFORMATION:
APPLICANT: Charles Kunach
Gill H. Choi
Patrick S. Dillon
Craig A. Rosen
Steven C. Barash
Michael R. Fannon
TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
NUMBER OF SEQUENCES: 5256
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COUNTRY: USA
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/329,624
FILING DATE: 27-Dec-2002
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/956,171
FILING DATE: October 20, 1997
APPLICATION NUMBER: 60/009,861
FILING DATE: January 5, 1996
APPLICATION NUMBER: 08/781,986
FILING DATE: January 3, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Mark J. Hyman
REGISTRATION NUMBER: 46,789
REFERENCE/DOCKET NUMBER: PB248P1D1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (240) 314-1224
TELEFAX: (301) 309-8439
INFORMATION FOR SEQ ID NO: 5251:
SEQUENCE CHARACTERISTICS:
LENGTH: 559 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 5251:
US-10-329-624-5251

Query Match 87.5%; Score 91; DB 15; Length 559;
Best Local Similarity 89.5%; Pred. No. 0.00019;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GONEGQQTIEEDTTPPIVP 19
DB 415 GONEGQQTIEEDTTPPIVP 433

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RESULT 10
US-10-470-048B-424
; Sequence 424, Application US/10470048B
; Publication No. US20050037444A1
; GENERAL INFORMATION:
; APPLICANT: MEINKE ET AL.
; TITLE OF INVENTION: A METHOD FOR IDENTIFICATION, ISOLATION AND PRODUCTION OF
; FILE REFERENCE: SONN:035US
; CURRENT FILING DATE: 2003-07-25
; NUMBER OF SEQ ID NOS: 603
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 424
; LENGTH: 940
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-10-470-048B-424

Query Match      87.5%; Score 91; DB 17; Length 940;
Best Local Similarity 89.5%; Pred. No. 0.00033;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 GONEGQQTIEPDTTPPIV 19
      ||||| ||||| |||||
Db      796 GHNEGQQTIEPDTTPPIV 814

RESULT 11
US-10-470-048B-69
; Sequence 69, Application US/10470048B
; Publication No. US20050037444A1
; GENERAL INFORMATION:
; APPLICANT: MEINKE ET AL.
; TITLE OF INVENTION: A METHOD FOR IDENTIFICATION, ISOLATION AND PRODUCTION OF
; FILE REFERENCE: SONN:035US
; CURRENT FILING DATE: 2003-07-25
; NUMBER OF SEQ ID NOS: 603
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 69
; LENGTH: 948
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-10-470-048B-69

Query Match      87.5%; Score 91; DB 17; Length 948;
Best Local Similarity 89.5%; Pred. No. 0.00034;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 GONEGQQTIEPDTTPPIV 19
      ||||| ||||| |||||
Db      804 GHNEGQQTIEPDTTPPIV 822

RESULT 12
US-10-731-238-51
; Sequence 51, Application US/10731238
; Publication No. US20050123552A1
; GENERAL INFORMATION:
; APPLICANT: Hook, Magnus
;               Patti, Joseph M.
;               House-Pompeo, Karen L.
;               Speziale, Pietro
;               Joh, Danny
;               McGavin, Martin J.
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
; AND METHODS OF USE
; NUMBER OF SEQUENCES: 105
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P. O. Box 4433
```

```
      CITY: Houston
      STATE: TX
      COUNTRY: USA
      ZIP: 77210-4433
      COMPUTER READABLE FORM:
      MEDIUM TYPE: Floppy disk
      COMPUTER: IBM PC compatible
      OPERATING SYSTEM: PC-DOS/MS-DOS
      SOFTWARE: Patentin Release #1.0, Version #1.30
      CURRENT APPLICATION DATA:
      APPLICATION NUMBER: US/10/731,238
      FILING DATE: 10-Dec-2003
      CLASSIFICATION: <Unknown>
      PRIOR APPLICATION DATA:
      APPLICATION NUMBER: US/09/010,317
      FILING DATE: 21-Jan-1998
      APPLICATION NUMBER: US 60/036,139
      FILING DATE: 21-JAN-1997
      ATTORNEY/AGENT INFORMATION:
      NAME: Hidler, David W.
      REGISTRATION NUMBER: 41,071
      REFERENCE/DOCKET NUMBER: TAMK:189
      TELECOMMUNICATION INFORMATION:
      TELEPHONE: 512-418-3000
      TELEFAX: 512-474-7577
      INFORMATION FOR SEQ ID NO: 51:
      SEQUENCE CHARACTERISTICS:
      LENGTH: 19 amino acids
      TYPE: amino acid
      STRANDEDNESS: <Unknown>
      TOPOLOGY: linear
      SEQUENCE DESCRIPTION: SEQ ID NO: 51:
US-10-731-238-51

Query Match      86.5%; Score 90; DB 18; Length 19;
Best Local Similarity 89.5%; Pred. No. 6.3e-06;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 GONEGQQTIEPDTTPPIV 19
      ||||| ||||| |||||
Db      1 GONEGQQTIEPDTTPPIV 19

RESULT 13
US-10-731-238-52
; Sequence 52, Application US/10731238
; Publication No. US20050123552A1
; GENERAL INFORMATION:
; APPLICANT: Hook, Magnus
;               Patti, Joseph M.
;               House-Pompeo, Karen L.
;               Speziale, Pietro
;               Joh, Danny
;               McGavin, Martin J.
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
; AND METHODS OF USE
; NUMBER OF SEQUENCES: 105
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P. O. Box 4433
; CITY: Houston
; STATE: TX
; COUNTRY: USA
; ZIP: 77210-4433
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/731,238
; FILING DATE: 10-Dec-2003
; CLASSIFICATION: <Unknown>
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE: 21-Jan-1998
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-Jan-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAMK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 52:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 52:
US-10-731-238-52

Query Match 85.6%; Score 89; DB 18; Length 19;
Best Local Similarity 89.5%; Pred. No. 8.7e-06;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GONEGQQTPEPTTPPIVP 19
Db 1 GONEGQQTPEPTTPPIVP 19

RESULT 14
US-10-731-238-53
Sequence 53, Application US/10731238
Publication No. US20050123552A1
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
Patti, Joseph M.
House-Pompeo, Karen L.
Speziale, Pietro
Joh, Danny
McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/731,238
FILING DATE: 10-Dec-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE: 21-Jan-1998
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-Jan-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAMK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 53:

SEQUENCE CHARACTERISTICS:
LENGTH: 19 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 53:
US-10-731-238-53

Query Match 85.6%; Score 89; DB 18; Length 19;
Best Local Similarity 89.5%; Pred. No. 8.7e-06;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GONEGQQTPEPTTPPIVP 19
Db 1 GONEGQQTPEPTTPPIVP 19

RESULT 15
US-10-282-122A-43778
Sequence 43778, Application US/10282122A
Publication No. US20040029129A1
GENERAL INFORMATION:
APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari
APPLICANT: Zyeckind, Judith
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John
APPLICANT: Carr, Grant
APPLICANT: Yamamoto, Robert
APPLICANT: Foreyth, R.
APPLICANT: Xu, H.
TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REFERENCE: ELITRA.034A
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/230,335
PRIOR FILING DATE: 2000-09-06
PRIOR APPLICATION NUMBER: 60/230,347
PRIOR FILING DATE: 2000-09-09
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/267,636
PRIOR FILING DATE: 2001-02-09
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 78614
SOFTWARE: PatentIn version 3.1
SEQ ID NO 43778
LENGTH: 961
TYPE: prt
ORGANISM: *Staphylococcus aureus*
US-10-282-122A-43778

Query Match 81.7%; Score 85; DB 15; Length 961;
Best Local Similarity 84.2%; Pred. No. 0.0024;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GONEGQQTPEPTTPPIVP 19

Db 807 GONEGQTIIBDTTPPTPP 825

Search completed: October 22, 2005, 11:34:38
Job time : 60.5951 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 22, 2005, 02:23:36 ; Search time 9.54204 Seconds
(without alignments)
191.586 Million cell updates/sec

Title: US-10-731-238-12

Perfect score: 104

Sequence: 1 GONEGQQTIEDTTPPIVP 19

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	96	92.3	1018	2 A32192	fibronectin-binding
2	91	87.5	940	2 S19702	fibronectin-binding
3	85	81.7	961	2 G90053	hypothetical prote
4	85	81.7	1038	2 H90053	hypothetical prote
5	53	51.0	367	2 A13319	choleylglycine hyd
6	49	47.1	307	1 S75769	hypothetical prote
7	49	47.1	488	2 A41961	chitinase (EC 3.2.
8	48	46.2	218	2 T17259	hypothetical prote
9	48	46.2	344	1 TVMSB	transforming prote
10	48	46.2	344	1 S21063	transforming prote
11	48	46.2	347	1 TVHUB	transforming prote
12	48	46.2	576	2 T46385	hypothetical prote
13	48	46.2	622	2 S71342	calnexin precursor
14	47.5	45.7	1200	2 T17404	hyalin - sea urchi
15	47	45.2	121	2 T03103	hypothetical prote
16	47	45.2	485	2 F70464	hypothetical prote
17	47	45.2	741	2 I51657	suppressor of yeast
18	47	45.2	836	2 JEO248	ATP-binding caset
19	46	44.2	179	2 C86292	PNH2.13 protein -
20	46	44.2	264	2 A28942	pancreatic elasta
21	46	44.2	655	2 T00768	polydendylate-bind
22	46	44.2	1526	2 A44406	DNA topoisomerase
23	46	44.2	2468	2 A83412	hypothetical prote
24	45	43.3	311	2 T12500	hypothetical prote
25	45	43.3	368	2 S62412	2-dehydro-3-deoxy
26	45	43.3	418	2 S38125	hypothetical prote
27	45	43.3	514	2 B83360	hypothetical prote
28	44.5	42.8	558	2 G85430	hypothetical prote
29	44.5	42.8	3624	2 AD0835	large repetitive p

30	44	42.3	250	1 A49053	CD27 antigen precu
31	44	42.3	257	1 MGNZBR	major surface glyc
32	44	42.3	336	2 T2767	hypothetical prote
33	44	42.3	342	2 B96668	protein FIN19.3 (I
34	44	42.3	1086	2 JC7736	C3G protein, long
35	43.5	41.8	653	2 A82334	DNA mismatch repa
36	43	41.3	224	2 D72861	Acortf-91 protein -
37	43	41.3	263	2 A42890	hypothetical prote
38	43	41.3	282	2 D97666	molybdate-binding
39	43	41.3	286	2 S72384	hypothetical prote
40	43	41.3	393	2 S06259	major outer membra
41	43	41.3	449	2 T29425	4-carboxymuconolac
42	43	41.3	478	2 B72543	hypothetical prote
43	43	41.3	591	2 A47662	two-component sens
44	43	41.3	504	2 T03806	hypothetical prote
45	43	41.3	3300	2 D70575	probable PPE prote

ALIGNMENTS

RESULT 1
A32192
fibronectin-binding protein B - Staphylococcus aureus
C/Species: Staphylococcus aureus
C/Date: 31-Jul-1989 #sequence_revision 31-Jul-1989 #ext_change 16-Feb-1997
C/Accession: A32192
R/Signaes: C.; Raucel, G.; Joensen, K.; Lindgren, P.E.; Anantharamiah, G.M.; Hoecek, M.
Proc. Natl. Acad. Sci. U.S.A. 86, 699-703, 1989
A/Title: Nucleotide sequence of the gene for a fibronectin-binding protein from Staphyloc
A/Reference number: A32192; MUID:8908998; PMID:2521391
A/Accession: A32192
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-1018 <SIG>
C/Keywords: fibronectin binding

Query Match 92.3%; Score 96; DB 2; Length 1018;
Best Local Similarity 94.7%; Pred. No. 1.7e-06;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GONEGQQTIEDTTPPIVP 19
DB 860 GONEGQQTIEDTTPPIVP 878

RESULT 2
S19702
fibronectin-binding protein B - Staphylococcus aureus
C/Species: Staphylococcus aureus
C/Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #ext_change 09-Jul-2004
R/Joensen, K.; Signaes, C.; Mueller, H.P.; Lindberg, M.
Eur. J. Biochem. 202, 1041-1048, 1991
A/Title: Two different genes encode fibronectin binding proteins in Staphylococcus aureu
A/Reference number: S19702; MUID:92111475; PMID:1837266
A/Accession: S19702
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-940 <JOB>
C/Keywords: fibronectin binding

Query Match 87.5%; Score 91; DB 2; Length 940;
Best Local Similarity 89.5%; Pred. No. 9.2e-06;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GONEGQQTIEDTTPPIVP 19
DB 796 GONEGQQTIEDTTPPIVP 814

```
RESULT 3
G90053
hypothetical protein fnbB [imported] - Staphylococcus aureus (strain N315)
C:Species: Staphylococcus aureus
C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C:Accession: G90053
R:Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguc
ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.;
C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
A:Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.
A:Reference number: A89758; MUID:21311952; PMID:11418146
A:Accession: G90053
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-961 <KUR>
A:Cross-references: UNIPROT:Q99RD3; GB:BA000018; PID:G13702452; PIDN:BA843593.1; GSPDB:G
A:Experimental source: strain N315
C:Genetics:
A:Gene: fnbB

Query Match      81.7%  Score 85;  DB 2;  Length 961;
Best Local Similarity 84.2%  Pred. No. 7.8e-05;
Matches 16;  Conservative 0;  Mismatches 3;  Indels 0;  Gaps 0;

QY      1 GONEGQRTPEPTTPPV 19
      |||||
Db      807 GONEGQRTPEPTTPP 825

RESULT 4
H90053
hypothetical protein fnbB [imported] - Staphylococcus aureus (strain N315)
C:Species: Staphylococcus aureus
C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C:Accession: H90053
R:Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguc
ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.;
C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
A:Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.
A:Reference number: A89758; MUID:21311952; PMID:11418146
A:Accession: H90053
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1038 <KUR>
A:Cross-references: UNIPROT:Q99RD2; GB:BA000018; PID:G13702453; PIDN:BA843594.1; GSPDB:G
A:Experimental source: strain N315
C:Genetics:
A:Gene: fnbB

Query Match      81.7%  Score 85;  DB 2;  Length 1038;
Best Local Similarity 84.2%  Pred. No. 8.5e-05;
Matches 16;  Conservative 0;  Mismatches 3;  Indels 0;  Gaps 0;

QY      1 GONEGQRTPEPTTPPV 19
      |||||
Db      856 GONEGQRTPEPTTPP 874

RESULT 5
A13319
cholo[yl]glycine hydrolase (EC 3.5.1.24) [imported] - Brucella melitensis (strain 16M)
C:Species: Brucella melitensis
C:Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 09-Jul-2004
C:Accession: A13319
R:Delvecchio, V.G.; Kaparatel, V.; Redkar, R.J.; Patra, G.; Mujeer, C.; Loe, T.; Ivanova,
Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
A:Title: The genome sequence of the facultative intracellular pathogen Brucella melitensis
A:Reference number: AD2252; PMID:11756688
A:Accession: A13319
A:Status: preliminary
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A:Molecule type: DNA
A:Residues: 1-367 <KUR>
A:Cross-references: UNIPROT:Q8Y1A2; GB:AE008917; PIDN:AAL51724.1; PID:G17982460; GSPDB:G
A:Experimental source: strain 16M
C:Genetics:
A:Gene: BME10543
A:Map position: I
A:Superfamily: cholo[yl]glycine hydrolase
C:Keywords: hydrolase

Query Match      51.0%  Score 53;  DB 2;  Length 367;
Best Local Similarity 62.5%  Pred. No. 2.1;
Matches 10;  Conservative 0;  Mismatches 6;  Indels 0;  Gaps 0;

QY      1 GONEGQRTPEPTTPP 16
      |||||
Db      249 GQAGMHCIPGDTTPP 264

RESULT 6
S75769
hypothetical protein gl10540 - Synechocystis sp. (strain PCC 6803)
C:Species: Synechocystis sp.
A:Variety: PCC 6803
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C:Accession: S75769
R:Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.;
O. K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda,
DNA Res. 3, 109-136, 1996
A:Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis
S.
A:Reference number: S74322; MUID:97061201; PMID:8905231
A:Accession: S75769
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-307 <KAN>
A:Cross-references: UNIPROT:Q55410; EMBL:D64003; GB:AB001339; NID:G1001200; PIDN:BAAL0504
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
C:Superfamily: Methanobacterium phosphate-binding protein pbs

Query Match      47.1%  Score 49;  DB 1;  Length 307;
Best Local Similarity 50.0%  Pred. No. 6.9;
Matches 9;  Conservative 2;  Mismatches 7;  Indels 0;  Gaps 0;

QY      1 GONEGQRTPEPTTPPV 18
      |||||
Db      214 GQGANFQTPMDATTPP 231

RESULT 7
A41961
chitinase (EC 3.2.1.14) D - Bacillus circulans
C:Species: Bacillus circulans
C:Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C:Accession: A41961
R:Watanabe, T.; Oyanagi, W.; Suzuki, K.; Ohnishi, K.; Tanaka, H.
J. Bacteriol. 174, 408-414, 1992
A:Title: Structure of the gene encoding chitinase D of Bacillus circulans WL-12 and possi
A:Reference number: A41961; MUID:9210506; PMID:1729234
A:Accession: A41961
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: nucleic acid; protein
A:Residues: 1-488 <WAT>
A:Cross-references: UNIPROT:P27050
A:Experimental source: WL-12
A:Note: sequence extracted from NCBI backbone (NCBI:75502)
C:Superfamily: Streptomyces chitinase ch1A
C:Keywords: glycosidase; hydrolase; polysaccharide degradation

Query Match      47.1%  Score 49;  DB 2;  Length 488;
Best Local Similarity 52.6%  Pred. No. 12;
Matches 10;  Conservative 1;  Mismatches 8;  Indels 0;  Gaps 0;
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FT REPEAT 545 574 B-1.
FT REPEAT 575 604 B-2.
FT DOMAIN 745 878 4 X approximate tandem repeats,
  fibronectin-binding domain.
FT REPEAT 745 782 D-1.
FT REPEAT 783 820 D-2.
FT REPEAT 821 859 D-3.
FT REPEAT 860 878 D-4 (incomplete).
FT DOMAIN 879 948 5 X tandem repeats, Pro-rich (WR).
FT REPEAT 879 892 WR 1.
FT REPEAT 893 906 WR 2.
FT REPEAT 907 920 WR 3.
FT REPEAT 921 934 WR 4.
FT REPEAT 935 948 WR 5.
FT SITE 982 986 LpXTG sorting signal (Potential).
FT MOD_RES 985 985 Pentaglycyl murein peptidoglycan amidated
  chreonine (Potential).
SQ SEQUENCE 1018 AA; 111780 MW; 58175E020E81F1F CRC64;

Query Match 92.3%; Score 96; DB 1; Length 1018;
Best Local Similarity 94.7%; Pred. No. 9.7e-06;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GONEGQQTIEDTTPPIVP 19
  |||||
  860 GONEGQQTIEDTTPPIVP 878

Db

RESULT 2
ID 053682 PRELIMINARY; PRT; 940 AA.
AC 053682;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Fibronectin binding protein B.
GN Name=fnbB;
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1280;
CC EMBL; X62992; CAA44726.1; -.
CC SEQUENCE FROM N.A.
RC STRAIN=8325-4;
RX MEDLINE=8325-4;
RA Jonsson K., Sionas C., Muller H.P., Lindberg M.;
RT "Two different genes encode fibronectin binding proteins in
  Staphylococcus aureus. The complete nucleotide sequence and
  characterization of the second gene."
RT Eur. J. Biochem. 202;104:1048(1991).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
  an amide bond (By similarity).
CC EMBL; X62992; CAA44726.1; -.
DR PIR; S19702; S19702.
DR HSSP; 053653; 1N67.
DR GO; GO:0008986; C:cell surface; IEA.
DR GO; GO:0005618; C:cell wall; IEA.
DR GO; GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:007155; P:cell adhesion; IEA.
DR InterPro; IPR008966; Adhes_bact.
DR InterPro; IPR004237; Fn_bind.
DR InterPro; IPR005877; Gpos_YsIRK.
DR InterPro; IPR001899; Gram_pos_anchor.
DR Pfam; PF02986; Fn_bind; 2.
DR Pfam; PF00746; Gram_pos_anchor; 1.
DR Pfam; PF04650; YsIRK_signal; 1.
DR TIGRFAMs; TIGR01167; LpXTG_anchor; 1.
DR TIGRFAMs; TIGR01168; YsIRK_signal; 1.
DR PROSITE; PS50847; GRAM_POS_ANCHORING; 1.
DR PROSITE; PS50847; GRAM_POS_ANCHORING; 1.
KM Cell wall; Peptidoglycan-anchor.
SQ SEQUENCE 940 AA; 103555 MW; E35FBBCA907A5345 CRC64;

Query Match 87.5%; Score 91; DB 2; Length 940;
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Best Local Similarity 89.5%; Pred. No. 5.2e-05;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GONEGQQTIEDTTPPIVP 19
  |||||
  796 GNEGQQTIEDTTPPIVP 814

Db

RESULT 3
ID 099RD3 PRELIMINARY; PRT; 961 AA.
AC 099RD3;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Fibronectin-binding protein homolog.
GN Name=fnbB; Ordered locus names=SAV2502;
OS Staphylococcus aureus (strain Mu50 / ATCC 700699).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=158878;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Mu50 / ATCC 700699;
RX MEDLINE=21311952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2;
RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
  Cui L., Oguchi A., Aoki K.-I., Nagai Y., Iian J.-O., Ito T.,
  Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hoshiyama A.,
  Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
  Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
  Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
  Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
RT "Whole genome sequencing of methicillin-resistant Staphylococcus
  aureus."
RL Lancet 357;1225-1240(2001).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
  an amide bond (By similarity).
CC EMBL; AP003365; BAB58664.1; -.
DR PIR; G90053; G90053.
DR HSSP; 053653; 1N67.
DR GO; GO:0008986; C:cell surface; IEA.
DR GO; GO:0005618; C:cell wall; IEA.
DR GO; GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:007155; P:cell adhesion; IEA.
DR InterPro; IPR008966; Adhes_bact.
DR InterPro; IPR004237; Fn_bind.
DR InterPro; IPR005877; Gpos_YsIRK.
DR InterPro; IPR001899; Gram_pos_anchor.
DR Pfam; PF02986; Fn_bind; 1.
DR Pfam; PF00746; Gram_pos_anchor; 1.
DR Pfam; PF04650; YsIRK_signal; 1.
DR TIGRFAMs; TIGR01167; LpXTG_anchor; 1.
DR TIGRFAMs; TIGR01168; YsIRK_signal; 1.
DR PROSITE; PS50847; GRAM_POS_ANCHORING; 1.
KM Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ SEQUENCE 961 AA; 106010 MW; 364940F884EA4101 CRC64;

Query Match 81.7%; Score 85; DB 2; Length 961;
Best Local Similarity 84.2%; Pred. No. 0.00044;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GONEGQQTIEDTTPPIVP 19
  |||||
  807 GONEGQQTIEDTTPPIVP 825

Db

RESULT 4
ID 07A3J8 PRELIMINARY; PRT; 961 AA.
AC 07A3J8;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
```

```
DE FnbB protein.
GN Name=fnbB: OrderedLocuNames=SA2290;
OS Staphylococcus aureus (strain NJ15).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=158879;
RN
RP SEQUENCE FROM N.A.
RX MEDLINE=21311952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2;
RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
RA Chi L., Oguchi A., Aoki K.-I., Nagai Y., Iian J.-O., Ito T.,
RA Kanamori M., Matsunaru H., Maruyama A., Murakami H., Hoshiyama A.,
RA Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue K.-I., Kaito C.,
RA Sekimizu K., Hiramatsu H., Kuhara S., Goto S., Yabuuchi J.,
RA Kamehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
RA Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
RT "whole genome sequencing of methicillin-resistant Staphylococcus
aureus."
RL Lancet 357:1225-1240(2001).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
an amide bond (By similarity).
EMBL: AP003137; BAB43593.1; -.
DR GO: GO:0009986; C:cell surface; IEA.
DR GO: GO:0005618; C:cell wall; IEA.
DR GO: GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO: GO:0016020; C:membrane; IEA.
DR GO: GO:0007155; P:cell adhesion; IEA.
DR InterPro: IPR008966; Adhes_bact.
DR InterPro: IPR004237; Fn_bind.
DR InterPro: IPR005877; Gpos_YsIRK.
DR InterPro: IPR001899; Gram_pos_anchor.
DR Pfam: PF02986; Fn_bind.1.
DR Pfam: PF04650; YsIRK_signal; 1.
DR TIGRFAMs: TIGR01167; LPXTG_anchor; 1.
DR TIGRFAMs: TIGR01168; YsIRK_signal; 1.
DR PROSITE: PS50847; GRAM_POS_ANCHORING; 1.
KM Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ SEQUENCE 961 AA; 106010 MW; 364940F884EA4101 CRC64;

Query Match 81.7%; Score 85; DB 2; Length 961;
Best Local Similarity 84.2%; Pred. No. 0.00045;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GONEGGQTIPEDTTPPIVP 19
DB 807 GONEGGQTIPEDTTPPIVP 825

RESULT 5
OG6DUS PRELIMINARY; PRT; 965 AA.
ID OG6DUS;
AC 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE Fibronectin-binding protein.
GN Name=fnbA: OrderedLocuNames=SA2580;
OS Staphylococcus aureus (strain MRSA2525).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=282458;
RN
RP SEQUENCE FROM N.A.
RX PubMed=15213324; DOI=10.1073/pnas.0402521101;
RA Holden M.T.G., Feil E.J., Lindsay J.A., Peacock S.J., Day N.P.J.,
RA Enright M.C., Foster T.J., Moore C.E., Hurst L., Atkin R., Barron A.,
RA Baeson N., Bentley S.D., Chillingworth C., Chillingworth T.,
RA Churcher C., Clark L., Cotton C., Cronin A., Doggett J., Dowd L.,
RA Felwell T., Hens Z., Harris B., Hauser H., Holroyd S., Jagsels K.,
RA James K.D., Leonard N., Line A., Mayes R., Moutle S., Mungall K.,
RA Ormond D., Quail M.A., Rabinowitch B., Rutherford K.M., Sanders M.,
RA Sharp S., Simmonds M., Stevens K., Whitehead S., Barrall B.G.,
RA Spratt B.G., Partridge J.;
RT "Complete genomes of two clinical Staphylococcus aureus strains;
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RT evidence for the rapid evolution of virulence and drug resistance."
RL Proc. Natl. Acad. Sci. U.S.A. 101:9786-9791(2004).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
an amide bond (By similarity).
EMBL: BX571856; CAG41560.1; -.
DR GO: GO:0009986; C:cell surface; IEA.
DR GO: GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO: GO:0016020; C:membrane; IEA.
DR GO: GO:0007155; P:cell adhesion; IEA.
DR InterPro: IPR008966; Adhes_bact.
DR InterPro: IPR004237; Fn_bind.
DR InterPro: IPR001899; Gram_pos_anchor.
DR Pfam: PF02986; Fn_bind.1.
DR Pfam: PF04650; YsIRK_signal; 1.
DR TIGRFAMs: TIGR01167; LPXTG_anchor; 1.
DR TIGRFAMs: TIGR01168; YsIRK_signal; 1.
DR PROSITE: PS50847; GRAM_POS_ANCHORING; 1.
KM Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ SEQUENCE 965 AA; 105691 MW; 29628132164D0551 CRC64;

Query Match 81.7%; Score 85; DB 2; Length 965;
Best Local Similarity 84.2%; Pred. No. 0.00045;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GONEGGQTIPEDTTPPIVP 19
DB 825 GONEGGQTIPEDTTPPIVP 843

RESULT 6
OG8NUV7 PRELIMINARY; PRT; 1015 AA.
ID OG8NUV7;
AC 08-NOV-2002 (TREMBlrel. 22, Created)
DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
DT 01-OCT-2002 (TREMBlrel. 25, Last annotation update)
DE FnbB protein.
GN Name=fnb; OrderedLocuNames=MM2421;
OS Staphylococcus aureus (strain MM2).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=196620;
RN
RP SEQUENCE FROM N.A.
RX STRAIN=MM2;
RA MEDLINE=22040717; PubMed=12044378; DOI=10.1016/S0140-6736(02)08713-5;
RA Baba T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Oguchi A.,
RA Nagai Y., Iwama N., Amano K., Naito T., Kuroda H., Cui L.,
RA Yamamoto K., Hiramatsu K.;
RT "Genome and virulence determinants of high virulence community-
acquired MRSA."
RL Lancet 359:1819-1827(2002).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
an amide bond (By similarity).
EMBL: AP004830; BAB96286.1; -.
DR GO: GO:0009986; C:cell surface; IEA.
DR GO: GO:0005618; C:cell wall; IEA.
DR GO: GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO: GO:0016020; C:membrane; IEA.
DR GO: GO:0007155; P:cell adhesion; IEA.
DR InterPro: IPR008966; Adhes_bact.
DR InterPro: IPR004237; Fn_bind.
DR InterPro: IPR005877; Gpos_YsIRK.
DR InterPro: IPR001899; Gram_pos_anchor.
DR Pfam: PF02986; Fn_bind.1.
DR Pfam: PF04650; YsIRK_signal; 1.
DR TIGRFAMs: TIGR01167; LPXTG_anchor; 1.
DR TIGRFAMs: TIGR01168; YsIRK_signal; 1.
DR PROSITE: PS50847; GRAM_POS_ANCHORING; 1.
KM Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ SEQUENCE 1015 AA; 111145 MW; D0F9261B864D4D2 CRC64;
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Query Match      81.7%; Score 85; DB 2; Length 1015;
Best Local Similarity 84.2%; Pred. No. 0.00047;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      1 GONEGQOTIEBDTTPPTP 19
Db      861 GONEGQOTIEBDTTPPTP 879

RESULT 7
ID Q6G6H3 PRELIMINARY; PRT; 1015 AA.
AC Q6G6H3;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DE Fibronectin-binding protein.
GN OrderedlocusNames=SA52388;
OS Staphylococcus aureus (strain MSSA476).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
CX NCBI_TaxId=282459;
RN (1)
RP SEQUENCE FROM N.A.
RX PubMed=15213324; DOI=10.1073/pnas.0402521101;
RA Holden M.T.G., Fell E.J., Lindsay J.A., Peacock S.J., Day N.P.J.,
RA Enright M.C., Foster T.J., Moore C.E., Hurst L., Actin R., Barron A.,
RA Baason N., Bentley S.D., Chillingworth C., Chillingworth T.,
RA Churcher C., Clark L., Corton C., Cronin A., Doggett J., Dowd L.,
RA Felwell T., Hance Z., Harris B., Hauser H., Holtroyd S., Jagels K.,
RA James K.D., Lennard N., Line A., Mayes R., Moule S., Mungall K.,
RA Omond D., Quail M.A., Rabinowitch E., Rutherford K.M., Sanders M.,
RA Sharp S., Simmonds M., Stevens K., Whitehead S., Barrett B.G.,
RA Spratt B.G., Parkhill J.
RT "Complete genomes of two clinical Staphylococcus aureus strains:
RT evidence for the rapid evolution of virulence and drug resistance."
RT Proc. Natl. Acad. Sci. U.S.A. 101:9786-9791(2004).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC an amide bond (By similarity).
EMBL BX571857; CNG44202.1; -.
DR GO; GO:0009986; C:cell surface; IEA.
DR GO; GO:0005618; C:cell wall; IEA.
DR GO; GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0007155; P:cell adhesion; IEA.
DR InterPro; IPR008866; Adhes_Bact.
DR InterPro; IPR004237; Fn_bind.
DR InterPro; IPR005877; Gpos_YsIRK.
DR InterPro; IPR001899; Gram_pos_anchor.
DR Pfam; PF02986; Fn_bind; 1.
DR Pfam; PF04650; YsIRK_signal; 1.
DR TIGRFAMs; TIGR01167; LPTXG_anchor; 1.
DR TIGRFAMs; TIGR01168; YsIRK_signal; 1.
DR PROSITE; PS50847; GRAM_POS_ANCHORING; 1.
DR Cell wall; Complete proteome; Peptidoglycan-anchor.
KW SEQUENCE 1015 AA; 11145 MW; DDF92818B64442 CRC64;
SQ

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DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE Fibronectin-binding protein homolog.
GN Name=fnb; OrderedlocusNames=SA12503;
OS Staphylococcus aureus (strain Mu50 / ATCC 700699).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
CX NCBI_TaxId=158878;
RN (1)
RP SEQUENCE FROM N.A.
RX STRAIN=Mu50 / ATCC 700699;
RC MEDLINE=21311952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2;
RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Iken J.-Q., Ito T.,
RA Kanamori M., Matsumaru H., Murakami H., Miyazawa A.,
RA Mizutani-Uji Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaio C.,
RA Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
RA Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
RA Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
RT "Whole genome sequencing of methicillin-resistant Staphylococcus
RT aureus."
RT Lancet 357:1225-1240(2001).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC an amide bond (By similarity).
EMBL AP003365; BAB58665.1; -.
DR PIR; H90053; H90053.
DR GO; GO:0009986; C:cell surface; IEA.
DR GO; GO:0005618; C:cell wall; IEA.
DR GO; GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0007155; P:cell adhesion; IEA.
DR InterPro; IPR008866; Adhes_Bact.
DR InterPro; IPR004237; Fn_bind.
DR InterPro; IPR005877; Gpos_YsIRK.
DR InterPro; IPR001899; Gram_pos_anchor.
DR Pfam; PF02986; Fn_bind; 1.
DR Pfam; PF00746; Gram_pos_anchor; 1.
DR Pfam; PF04650; YsIRK_signal; 1.
DR TIGRFAMs; TIGR01167; LPTXG_anchor; 1.
DR TIGRFAMs; TIGR01168; YsIRK_signal; 1.
DR PROSITE; PS50847; GRAM_POS_ANCHORING; 1.
DR Cell wall; Complete proteome; Peptidoglycan-anchor.
KW SEQUENCE 1038 AA; 113618 MW; 666BF6B2BFBB12 CRC64;
SQ

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Query Match      81.7%; Score 85; DB 2; Length 1015;
Best Local Similarity 84.2%; Pred. No. 0.00047;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      1 GONEGQOTIEBDTTPPTP 19
Db      861 GONEGQOTIEBDTTPPTP 879

RESULT 8
ID Q99RD2 PRELIMINARY; PRT; 1038 AA.
AC Q99RD2;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
RT

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DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE Fibronectin-binding protein homolog.
GN Name=fnb; OrderedlocusNames=SA12503;
OS Staphylococcus aureus (strain Mu50 / ATCC 700699).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
CX NCBI_TaxId=158878;
RN (1)
RP SEQUENCE FROM N.A.
RX MEDLINE=21311952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2;
RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Iken J.-Q., Ito T.,
RA Kanamori M., Matsumaru H., Murakami H., Miyazawa A.,
RA Mizutani-Uji Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaio C.,
RA Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
RA Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
RA Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
RT "Whole genome sequencing of methicillin-resistant Staphylococcus
RT aureus."
RT Lancet 357:1225-1240(2001).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC an amide bond (By similarity).
EMBL AP003365; BAB58665.1; -.
DR PIR; H90053; H90053.
DR GO; GO:0009986; C:cell surface; IEA.
DR GO; GO:0005618; C:cell wall; IEA.
DR GO; GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0007155; P:cell adhesion; IEA.
DR InterPro; IPR008866; Adhes_Bact.
DR InterPro; IPR004237; Fn_bind.
DR InterPro; IPR005877; Gpos_YsIRK.
DR InterPro; IPR001899; Gram_pos_anchor.
DR Pfam; PF02986; Fn_bind; 1.
DR Pfam; PF00746; Gram_pos_anchor; 1.
DR Pfam; PF04650; YsIRK_signal; 1.
DR TIGRFAMs; TIGR01167; LPTXG_anchor; 1.
DR TIGRFAMs; TIGR01168; YsIRK_signal; 1.
DR PROSITE; PS50847; GRAM_POS_ANCHORING; 1.
DR Cell wall; Complete proteome; Peptidoglycan-anchor.
KW SEQUENCE 1038 AA; 113618 MW; 666BF6B2BFBB12 CRC64;
SQ

```

RT "Whole genome sequencing of methicillin-resistant *Staphylococcus aureus*";
 RL Lancel 357.11225-1240(2001).
 CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by an amide bond (By similarity).
 DR EMBL; AF003137; BAB43594.1; -.
 DR GO; GO:0009986; C:cell surface; IEA.
 DR GO; GO:0005618; C:cell wall; IEA.
 DR GO; GO:0009375; C:cell wall (sensu Gram-positive Bacteria); IEA.
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0007155; P:cell adhesion; IEA.
 DR InterPro; IPR008966; Adhes_Dact.
 DR InterPro; IPR004237; Fn_bind.
 DR InterPro; IPR005877; Gpos_YsIRK.
 DR InterPro; IPR001899; Gram_pos_anchor.
 DR Pfam; PF02986; Fn_bind; 1.
 DR Pfam; PF00746; Gram_pos_anchor; 1.
 DR Pfam; PF04650; YsIRK_signal; 1.
 DR TIGRFAMs; TIGR01167; LPXTG_anchor; 1.
 DR TIGRFAMs; TIGR01168; YsIRK_signal; 1.
 DR PROSITE; PS50847; GRAM_POS_ANCHORING; 1.
 KW Cell wall; Complete proteome; Peptidoglycan-anchor.
 SQ SEQUENCE 1038 AA; 113618 MW; 666BF6BF2BFEB12 CRC64;
 Query Match 81.7%; Score 85; DB 2; Length 1038;
 Best Local Similarity 84.2%; Pred. No. 0.00049;
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1 GONEGQOTIEPTPTTP 19
 DB 856 GONEGQOTIEPTTPPP 874
 RESULT 10
 ID Q6G6H4 PRELIMINARY; PRT; 957 AA.
 AC Q6G6H4;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DE Fibronectin-binding protein.
 GN Name=fnbB; OrderedLocustNames=SAS2387;
 OS *Staphylococcus aureus* (strain MSSA476).
 OC Bacteria; Firmicutes; Bacillales; *Staphylococcus*.
 NCBI_TaxID=282459;
 [1]
 RP SEQUENCE FROM N.A.
 RX PubMed=15213324; DOI=10.1073/pnas.0402521101;
 RA Holden M.T.G., Fell E.J., Lindsey J.A., Peacock S.J., Day N.P.J.,
 RA Bright M.C., Foster T.J., Moore C.E., Hurst L., Atkin R., Barron A.,
 RA Baeson N., Bentley S.D., Chillingworth C., Chillingworth T.,
 RA Churcher C., Clark L., Cotton C., Cronin A., Doggett J., Dowd L.,
 RA Fellwell T., Hance Z., Harris B., Hauser H., Holtroyd S., Jagsels K.,
 RA James K.D., Lennard N., Line A., Mayes R., Moule S., Mungall K.,
 RA Ommond D., Quail M.A., Rabinowitsch E., Rutherford K.M., Sanders M.,
 RA Sharp S., Simmonds M., Stevens K., Whitehead S., Barrell B.G.,
 RA Spratt B.G., Parkhill J.,
 RT "Complete genomes of two clinical *Staphylococcus aureus* strains:
 evidence for the rapid evolution of virulence and drug resistance.";
 RL Proc. Natl. Acad. Sci. U.S.A. 101:9786-9791(2004).
 CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by an amide bond (By similarity).
 DR EMBL; BX571857; CAG4201.1; -.
 DR GO; GO:0009986; C:cell surface; IEA.
 DR GO; GO:0005618; C:cell wall; IEA.
 DR GO; GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0007155; P:cell adhesion; IEA.
 DR InterPro; IPR008966; Adhes_Dact.
 DR InterPro; IPR004237; Fn_bind.
 DR InterPro; IPR005877; Gpos_YsIRK.
 DR InterPro; IPR001899; Gram_pos_anchor.
 DR Pfam; PF02986; Fn_bind; 1.

DR Pfam; PF00746; Gram_pos_anchor; 1.
 DR Pfam; PF04650; YsIRK_signal; 1.
 DR TIGRFAMs; TIGR01167; LPXTG_anchor; 1.
 DR TIGRFAMs; TIGR01168; YsIRK_signal; 1.
 DR PROSITE; PS50847; GRAM_POS_ANCHORING; 1.
 KW Cell wall; Complete proteome; Peptidoglycan-anchor.
 SQ SEQUENCE 957 AA; 105980 MW; 28F8BA7FFDFD3EAF CRC64;
 Query Match 76.9%; Score 80; DB 2; Length 957;
 Best Local Similarity 73.7%; Pred. No. 0.0026;
 Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 QY 1 GONEGQOTIEPTPTTP 19
 DB 803 GONEGQOTIEPTTPPP 821
 RESULT 11
 ID Q8NU08 PRELIMINARY; PRT; 943 AA.
 AC Q8NU08;
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE FnbB protein.
 GN Name=fnbB; OrderedLocustNames=MM2420;
 OS *Staphylococcus aureus* (strain MM2).
 OC Bacteria; Firmicutes; Bacillales; *Staphylococcus*.
 NCBI_TaxID=196620;
 [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=MM2;
 RX MEDLINE=22040717; PubMed=12044378; DOI=10.1016/S0140-6736(02)08713-5;
 RA Baba T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Oguchi A.,
 RA Nagai Y., Iwama N., Amano K., Naimi T., Kuroda H., Cui L.,
 RA Yamamoto K., Hiratsugu K.,
 RT "Genome and virulence determinants of high virulence community-acquired MRSA".
 RL Lancel 359.1819-1827(2002).
 CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by an amide bond (By similarity).
 DR EMBL; AP004830; BAB96285.1; -.
 DR HSPS; Q53653; IN67.
 DR GO; GO:0009986; C:cell surface; IEA.
 DR GO; GO:0005618; C:cell wall; IEA.
 DR GO; GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0007155; P:cell adhesion; IEA.
 DR InterPro; IPR008966; Adhes_Dact.
 DR InterPro; IPR004237; Fn_bind.
 DR InterPro; IPR005877; Gpos_YsIRK.
 DR InterPro; IPR001899; Gram_pos_anchor.
 DR Pfam; PF02986; Fn_bind; 1.
 DR Pfam; PF00746; Gram_pos_anchor; 1.
 DR Pfam; PF04650; YsIRK_signal; 1.
 DR TIGRFAMs; TIGR01167; LPXTG_anchor; 1.
 DR TIGRFAMs; TIGR01168; YsIRK_signal; 1.
 DR PROSITE; PS50847; GRAM_POS_ANCHORING; 1.
 KW Cell wall; Complete proteome; Peptidoglycan-anchor.
 SQ SEQUENCE 943 AA; 104537 MW; DA85F31947E1B6A CRC64;
 Query Match 67.3%; Score 70; DB 2; Length 943;
 Best Local Similarity 73.7%; Pred. No. 0.087;
 Matches 14; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
 QY 1 GONEGQOTIEPTPTTP 19
 DB 803 GONEGQOTIEPTTPPP 821
 RESULT 12
 ID Q8FZL2 PRELIMINARY; PRT; 333 AA.

AC Q8FZL2; 01-MAR-2003 (TReMBLrel. 23, Created)
 DT 01-MAR-2003 (TReMBLrel. 23, Last sequence update)
 DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)
 GN CholoYlglycine hydrolase family protein.
 DE OrderedLocuNames=BR1468;
 OS Brucella suis.
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
 OC Brucellaceae; Brucella.
 OK NCBI_TaxID=29461;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=J330 / Biovar 1;
 RX MEDLINE=22247741; PubMed=12271122; DOI=10.1073/pnas.192319099;
 RA Paulsen I.T., Seshadri R., Nelson K.E., Eisen J.A., Heidelberg J.F.,
 Read T.D., Dodson R.J., Umayam L.A., Brinkac L.M., Beanan M.J.,
 Daugherty S.C., DeBoy R.T., Durkin A.S., Kolonay J.F., Madupu R.,
 Nelson W.C., Ayodeji B., Krahl M., Shetty J., Malek J.A.,
 Van Aken S.E., Riedmuller S., Tettelin H., Gill S.R., White O.,
 Salzberg S.L., Hoover D.L., Lindler L.E., Hailing S.M., Boyle S.M.,
 Fraser C.M.;
 RA "The Brucella suis genome reveals fundamental similarities between
 animal and plant pathogens and symbionts."
 RT Proc. Natl. Acad. Sci. U.S.A. 99:13148-13153(2002).
 DR EMBL; AE014442; AAN30379.1; -.
 DR HSSP; P12256; 2PVA.
 DR TIGR; BR1468; -.
 DR InterPro; IPR003199; Chgly_hydrolase.
 DR Pfam; PF02275; CBMH; 1.
 DR Complete proteome.
 SQ SEQUENCE 333 AA; 36865 MW; 50B0980CDB0792F7 CRC64;

Query Match 51.0%; Score 53; DB 2; Length 333;
 Best Local Similarity 62.5%; Pred. No. 11;
 Matches 10; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 GONEGQOTIPEDTTP 16
 DB 215 GQAGMHGIPGDTTP 230

RESULT 13
 Q8YIA2 PRELIMINARY; PRT; 367 AA.
 AC Q8YIA2;
 DT 01-MAR-2002 (TReMBLrel. 20, Created)
 DT 01-MAR-2002 (TReMBLrel. 20, Last sequence update)
 DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)
 GN CHOLOYLGLYCINE HYDROLASE (EC 3.5.1.24).
 DE OrderedLocuNames=BMEI0543;
 OS Brucella melitensis.
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
 OC Brucellaceae; Brucella.
 OK NCBI_TaxID=29459;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=16M / ATCC 23456 / Biotype 1;
 RX MEDLINE=20020109; PubMed=11756688; DOI=10.1073/pnas.221575398;
 RA DelVecchio V.G., Kapral V., Redkar R.J., Patra G., Mijer C., Los T.,
 Ivanova N., Anderson I., Bhattacharya A., Lykakis A., Reznik G.,
 Jablonksi L., Larsen N., D'Souza M., Bernal A., Mazur I., Goltsman E.,
 Selkov E., Elker P.H., Hagius S., O'Callaghan D., Letesson J.-J.,
 Haeflorn R., Kyrides N.C., Overbeek R.;
 RA "The genome sequence of the facultative intracellular pathogen
 Brucella melitensis."
 RT Proc. Natl. Acad. Sci. U.S.A. 99:443-448(2002).
 DR EMBL; AE009496; AAL51724.1; -.
 DR PIR; A13319; A13319.
 DR HSSP; P12256; 2PVA.
 DR MEROPS; CS9 001; -.
 DR GO; GO:0045302; F:choloYlglycine hydrolase activity; IEA.
 DR Pfam; PF02275; CBMH; 1.
 DR Complete proteome.

SQ SEQUENCE 367 AA; 40337 MW; 2B21A795961E3B87 CRC64;

Query Match 51.0%; Score 53; DB 2; Length 367;
 Best Local Similarity 62.5%; Pred. No. 12;
 Matches 10; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 GONEGQOTIPEDTTP 16
 DB 249 GQAGMHGIPGDTTP 264

RESULT 14
 Q96PV3 PRELIMINARY; PRT; 441 AA.
 AC Q96PV3;
 DT 01-DEC-2001 (TReMBLrel. 19, Created)
 DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)
 DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
 DE KIAA1935 protein (Fragment).
 GN Name=KIAA1935;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OK NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=21456161; PubMed=11572484;
 RA Nagase T., Kikuno R., Ohara O.;
 RT "Prediction of the coding sequences of unidentified human genes. XXI.
 RT The complete sequences of 60 new cDNA clones from brain which code for
 RT large proteins."
 RL DNA Res. 8:179-187(2001).
 DR EMBL; AB067522; BAB67828.1; -.
 FT NON_TER 1 441
 FT NON_TER 1 441
 FT NON_TER 441 441
 SQ SEQUENCE 441 AA; 47250 MW; B7B085B5EC09F4F CRC64;

Query Match 50.0%; Score 52; DB 2; Length 441;
 Best Local Similarity 42.1%; Pred. No. 21;
 Matches 8; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

QY 1 GONEGQOTIPEDTTP 19
 DB 58 GRTDQGSAPQADBPPLP 76

RESULT 15
 Q81YR3 PRELIMINARY; PRT; 571 AA.
 AC Q81YR3;
 DT 01-MAR-2003 (TReMBLrel. 23, Created)
 DT 01-MAR-2004 (TReMBLrel. 26, Last sequence update)
 DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)
 DE KIAA1935 protein (Fragment).
 GN Name=KIAA1935;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OK NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 Altschul S.F., Zeeberg B., Buelow K.H., Scheffer C.F., Bhat N.K.,
 Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 Brownstein M.J., Ueda T.B., Toshiyuki S., Cartinci P., Prange C.,
 Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullen S.J.,
 Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Pahey J., Helton E., Ketterman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.W., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smalhus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN (2)
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Strausberg R.;
DR Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
EMBL BC035076; AAH35076.2; -.
FT NON_TER 1
SQ SEQUENCE 571 AA; 61967 MW; 6C1FD65914BAEF98 CRC64;

Query Match 50.0%; Score 52; DB 2; Length 571;
Best Local Similarity 42.1%; Pred. No. 28;
Matches 8; Conservative 5; Mismatches 6; Indels 0; Gaps 0;
QY 1 GQNEGQOTIPEDTTPPIVP 19
|: :|||: |:|:|
DB 63 GERTDGGQSAPOADEPPLPP 81

Search completed: October 22, 2005, 04:09:49
Job time : 51.5332 secs

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GenCore version 5.1.6
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OM protein - protein search, using bw model

Run on: October 25, 2005, 18:43:07 ; Search time 59.0973 Seconds
(without alignments)
137.434 Million cell updates/sec

Title: US-10-731-238-14
Sequence: 1 PPSYQFGHNSYDFEDTLPK 21

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:*

- 1: geneseqp19808:*
- 2: geneseqp19908:*
- 3: geneseqp20008:*
- 4: geneseqp20018:*
- 5: geneseqp20028:*
- 6: geneseqp20038:*
- 7: geneseqp20048:*
- 8: geneseqp20058:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	119	100.0	21	2	AAW65670 Fibronec
2	112	94.1	21	2	AAW65665 Fibronec
3	112	94.1	22	2	AAW65679 Fibronec
4	112	94.1	37	4	AAW65680 Fibronec
5	112	94.1	38	1	AAW65682 Fibronec
6	112	94.1	134	2	AAW65686 Fibronec
7	112	94.1	139	2	AAW65688 Fibronec
8	112	94.1	1018	1	AAW65690 Fibronec
9	112	94.1	1018	4	AAW65692 Fibronec
10	112	94.1	1018	4	AAW65694 Fibronec
11	112	94.1	1018	6	AAW65696 Fibronec
12	112	94.1	1018	6	AAW65698 Fibronec
13	112	94.1	1018	6	AAW65700 Fibronec
14	112	94.1	1018	6	AAW65702 Fibronec
15	112	94.1	1018	6	AAW65704 Fibronec
16	112	94.1	1018	6	AAW65706 Fibronec
17	112	94.1	1018	6	AAW65708 Fibronec
18	112	94.1	1018	6	AAW65710 Fibronec
19	112	94.1	1018	6	AAW65712 Fibronec
20	112	94.1	1018	6	AAW65714 Fibronec
21	112	94.1	1018	6	AAW65716 Fibronec
22	112	94.1	1018	6	AAW65718 Fibronec
23	112	94.1	1018	6	AAW65720 Fibronec
24	112	94.1	1018	6	AAW65722 Fibronec
25	112	94.1	1018	6	AAW65724 Fibronec

26	105	88.2	21	2	AAW65685
27	105	88.2	21	2	AAW65671
28	105	88.2	21	2	AAW65687
29	105	88.2	21	2	AAW65681
30	105	88.2	77	2	AAW65689
31	105	88.2	101	2	AAW65693
32	105	88.2	113	2	AAW65697
33	105	88.2	124	2	AAW65701
34	105	88.2	128	2	AAW65705
35	105	88.2	130	2	AAW65709
36	105	88.2	130	2	AAW65713
37	105	88.2	130	2	AAW65717
38	105	88.2	130	2	AAW65721
39	105	88.2	134	2	AAW65725
40	105	88.2	162	2	AAW65729
41	105	88.2	164	2	AAW65733
42	105	88.2	174	2	AAW65737
43	105	88.2	174	2	AAW65741
44	105	88.2	181	2	AAW65745
45	105	88.2	181	2	AAW65749

ALIGNMENTS

RESULT 1
AAW65670 standard; peptide; 21 AA.

AC AAW65670;

DT 16-OCT-1998 (first entry)

DE Fibronecin binding protein-derived peptide #14.

KW microbially surface components recognising adhesive matrix molecule;

KW MSCRAMM; fibronecin; fibronecin-binding protein; antibody; epitope;

KW antibiotic; bacterial infection; antibiotic-resistant strain.

OS Synthetic.

OS Staphylococcus aureus.

PN W09831389-A2.

XX 23-JUL-1998.

XX 21-JAN-1998; 98MO-US001222.

XX 21-JAN-1997; 97US-0036139P.

XX (TEXA) UNIV TEXAS A & M SYSTEM.

XX Hoeck M, Patti JW, House-Pompeo KL, Speziale P, Joh D;

XX Megavlin MJ;

XX WPI; 1998-413816/35.

XX Example 8, Page 100; 201P; English.

XX The invention relates to antibodies that bind to a fibronecin-binding

XX domain of a fibronecin-binding protein, and inhibit binding of the

XX protein to a fibronecin. Also claimed are: (1) isolated peptides of a

XX fibronecin-binding protein that do not bind to fibronecin; (2) fusion

XX protein containing at least one peptide of a fibronecin-binding protein

XX linked to a second amino acid sequence; (3) nucleic acid encoding the

XX isolated peptide of (1). Antibodies, the isolated peptides of (1) and the

XX nucleic acids are all useful for immunisation (active or passive) and (by

XX inhibiting binding of bacteria to fibronecin) for preventing or treating

XX infection in humans or other animals, particularly by staphylococci or

CC streptococci, e.g. meningitis, otitis media, pneumonia, endocarditis,
 CC mastitis in cattle, abortion in horses and many others. Since the
 CC antibodies block binding of bacteria, they should be effective against
 CC antibiotic-resistant strains, and may replace antibiotic therapy or
 CC increase its effectiveness. Sequences AAW65670-90 represent a series of
 CC synthetic peptides based on the D3 repeat of *S. aureus* fibronectin
 CC binding protein A. They were synthesised to contain a proline residue at
 CC each position through the sequence (ie a proline scan)
 XX
 SQ Sequence 21 AA:
 QY
 Query Match 100.0%; Score 119; DB 2; Length 21;
 Best Local Similarity 100.0%; Pred. No. 3.9e-11;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Db 1 PSYQFGHNSVDFEEDTLPK 21
 1 PSYQFGHNSVDFEEDTLPK 21
 RESULT 2
 AAW65665 standard; peptide; 21 AA.
 AC AAW65665;
 XX
 DT 16-OCT-1998 (first entry)
 XX
 DE Fibronectin binding protein-derived peptide #9.
 XX
 DE Microbial surface components recognising adhesive matrix molecule;
 KM MSCRAMM; fibronectin; fibronectin-binding protein; antibody; epitope;
 KM antibiotic; bacterial infection; antibiotic-resistant strain.
 XX
 OS Synthetic.
 OS Staphylococcus aureus.
 OS
 PN WO9831389-A2.
 XX
 PD 23-JUL-1998.
 XX
 PF 21-JAN-1998; 98WO-US001222.
 XX
 PR 21-JAN-1997; 97US-0036139P.
 XX
 PA (TEXA) UNITV TEXAS A & M SYSTEM.
 XX
 PI Hoeoek M, Patli JM, House-Pompeo KL, Speziale P, Joh D;
 PI McGavin MJ;
 XX
 DR WPI; 1998-413816/35.
 XX
 XX Antibody that binds to fibronectin-binding protein, preventing its
 PT binding to fibronectin - used to treat or prevent bacterial infection,
 PT especially by Staphylococci and Streptococci.
 PR
 PS Example 2; Page 92; 201pp; English.
 XX
 CC The invention relates to antibodies that bind to a fibronectin-binding
 CC domain of a fibronectin-binding protein, and inhibit binding of the
 CC protein to a fibronectin. Also claimed are: (1) isolated peptides of a
 CC fibronectin-binding protein that do not bind to fibronectin; (2) fusion
 CC protein containing at least one peptide of a fibronectin-binding protein
 CC linked to a second amino acid sequence; (3) nucleic acid encoding the
 CC isolated peptide of (1). Antibodies, the isolated peptides of (1) and the
 CC nucleic acids are all useful for immunisation (active or passive) and (b)
 CC inhibiting binding of bacteria to fibronectin) for preventing or treating
 CC infection in humans or other animals, particularly by staphylococci or
 CC streptococci, e.g. meningitis, otitis media, pneumonia, endocarditis,
 CC mastitis in cattle, abortion in horses and many others. Since the
 CC antibodies block binding of bacteria, they should be effective against
 CC antibiotic-resistant strains, and may replace antibiotic therapy or
 CC increase its effectiveness. Sequences AAW65659-68 represent synthetic

CC epitopes from the fibronectin binding domains DU and D1-D4 of the *S.*
 CC aureus fnbA gene
 XX
 SQ Sequence 21 AA;
 QY
 Query Match 94.1%; Score 112; DB 2; Length 21;
 Best Local Similarity 100.0%; Pred. No. 4.8e-10;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Db 2 PSYQFGHNSVDFEEDTLPK 21
 2 PSYQFGHNSVDFEEDTLPK 21
 RESULT 3
 AAR21340 standard; peptide; 22 AA.
 ID AAR21340
 XX
 AC AAR21340;
 XX
 DT 25-MAR-2003 (revised)
 DT 15-JUN-1992 (first entry)
 XX
 DE Fibronectin binding protein.
 XX
 KM FbBP; wound infection reduction; vaccination; mastitis;
 KM Staphylococcal infections; D3.
 XX
 OS Synthetic.
 OS
 PN WO9202555-A.
 XX
 PD 20-FEB-1992.
 XX
 PF 10-AUG-1990; 90SE-00002617.
 XX
 PR 10-AUG-1990; 90SE-00002617.
 XX
 PA (ALFA) ALFA LAVAL AGRIC INT AB.
 XX
 PI Hook M, McGavin M, Raucel G;
 PI
 DR WPI; 1992-080035/10.
 XX
 PT New fibronectin binding peptide - combines with fusion peptide to form
 PT large antigen, used in immunisation, diagnosis and for treating wounds.
 XX
 PS Claim 1; Page 22; 33pp; English.
 XX
 CC The sequence comprises amino acids 17-33 of a tandem repeat, designated
 CC D3 of the fibronectin binding site of *Staphylococcus aureus* 8325-4 FbBP.
 CC The N-terminal DK may be replaced with H or K, and the C-terminal LKP may
 CC be replaced by either L, LP, or OH. The peptides were synthesised using
 CC standard methods and purified using reverse phase HPLC. The appropriate
 CC fractions were dialysed and lyophilised. Peptide sequencing was performed
 CC and the peptides digested and chemically modified by dihydroxypropylation
 CC of the amino side chain of lysine. The carboxylic side chains were
 CC converted to glycine methyl esters. The phenyl side chains of tyrosine
 CC residues were oxidised. Chemically modified peptide D3 was compared to
 CC unmodified D3. Lysine and tyrosine modifications only partially
 CC diminished its activity whereas modification of aspartic/glutamic
 CC residues resulted in complete loss of activity. The peptide can be used
 CC for the prevention or reduction of the risk of wound infection. The
 CC peptide can be used to create a large antigen for vaccinating ruminants
 CC against mastitis caused by *Staphylococcal* infections. It can also be used
 CC to diagnose *Staphylococcal* infections using ELISA or DNA probes. (Updated
 CC on 25-MAR-2003 to correct PA field.)
 XX
 SQ Sequence 22 AA:
 QY
 Query Match 94.1%; Score 112; DB 2; Length 22;
 Best Local Similarity 100.0%; Pred. No. 5e-10;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PSYQFGHNSVDFEEDTLPK 21
 |||||
 DB 3 PSYQFGHNSVDFEEDTLPK 22

RESULT 4
 AAB91958
 ID AAB91958 standard; peptide; 37 AA.

XX AAB91958;
 AC
 XX

DT 22-JUN-2001 (first entry)
 XX

DE Fibronectin fragment and fibrin related peptide SEQ ID NO:1134.

XX Protection; endogenous therapeutic peptide; peptidase; conjugation;
 KW blood component; modification; succinimide; maleimide group; amino;
 KM hydroxyl; thiol; hormone; growth factor; neurotransmitter.
 XX

OS Homo sapiens.
 OS Synthetic.
 XX

PN WO200069900-A2.
 XX

PD 23-NOV-2000.
 XX

PF 17-MAY-2000; 2000MO-US013576.
 XX

PR 17-MAY-1999; 99US-0134406P.
 XX

PR 10-SEP-1999; 99US-0153406P.
 XX

PR 15-OCT-1999; 99US-0159783P.
 XX

PA (CON1-) CONDUCHEM INC.
 XX

PI Bridon DP, Ezrin AM, Milner PG, Holmes DL, Thibaudau K;
 XX

DR WPI; 2001-112059/12.
 XX

PT Modifying and attaching therapeutic peptides to albumin prevents
 PT peptidase degradation, useful for increasing length of in vivo activity.
 XX

PS Disclosure; Page 566; 733pp; English.
 XX

CC The present invention describes a modified therapeutic peptide (I)
 CC comprising a therapeutically active amino acid region (III) and a
 CC reactive group (II) (e.g. succinimide and maleimide groups) attached to
 CC a less therapeutically active amino acid region (IV), which covalently
 CC bonds with amino/hydroxyl/thiol groups on blood components to form a
 CC peptide stabilised therapeutic peptide composed of 3-50 amino acids.
 CC (I) are useful for modifying therapeutic peptides e.g. hormones, growth
 CC factors and neurotransmitters, to protect them from peptidase activity in
 CC vivo for the treatment of various disorders. Endogenous therapeutic
 CC peptides are not suitable as drug candidates as they require frequent
 CC administration due to rapid degradation by peptidases in the body.
 CC Modifying and attaching therapeutic peptides to albumin prevents or
 CC reduces the action of peptidases to increase length of activity (half
 CC life) and specifically as bonding to large molecules decreases
 CC intracellular uptake and interference with physiological processes.
 CC AAB90829 to AAB92441 represent peptides which can be used in the
 CC exemplification of the present invention
 XX

SQ Sequence 37 AA;
 XX

Query Match 94.1%; Score 112; DB 4; Length 37;
 Best Local Similarity 100.0%; Pred. No. 8.7e-10;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PSYQFGHNSVDFEEDTLPK 21
 |||||
 DB 17 PSYQFGHNSVDFEEDTLPK 36

RESULT 5
 AAB80662
 ID AAB80662 standard; protein; 38 AA.
 XX

AC AAB80662;
 XX

DT 25-MAR-2003 (revised)
 XX

DT 07-OCT-1990 (first entry)
 XX

DE Protein with fibronectin binding ability.
 XX

XX Hybrid DNA molecule; fibronectin binding; mastitis; ruminants;
 KW wound infection.
 XX

OS Staphylococcus aureus.
 XX

PN EP294349-A.
 XX

PD 07-DEC-1988.
 XX

PF 30-MAY-1988; 88EP-00850188.
 XX

PR 01-JUN-1987; 87SE-0002272.
 XX

PA (ALFA) ALFA LAVAL AGRIC INT AB.
 XX

PI Iandberg MK, Signas LC, Wadstrom TM, Froman G;
 XX

DR WPI; 1988-347978/49.
 XX

DR N-PSDB; AAN81099.
 XX

PT Hybrid DNA encoding Staphylococcus aureus fibronectin binding protein -
 PT useful for immunisation and topical application to prevent staphylococcal
 PT infections.
 XX

PS Claim 11; Page 12; 23pp; English.
 XX

CC The peptide has fibronectin binding ability. It is useful for immunising
 CC CC ruminants against staphylococcal mastitis, pref. when used at 0.5-5
 CC micrograms/kg, using 3 doses given at 1-3 week intervals; for topical
 CC application to prevent wound infection, using an isotonic saline soln. of
 CC concn. 25-250 micrograms/ml; and, when immobilised on a carrier, for
 CC diagnosing staphylococcal infections. (Updated on 25-MAR-2003 to correct
 CC PF field.) (Updated on 25-MAR-2003 to correct PA field.)
 CC

SQ Sequence 38 AA;
 XX

Query Match 94.1%; Score 112; DB 1; Length 38;
 Best Local Similarity 100.0%; Pred. No. 9e-10;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PSYQFGHNSVDFEEDTLPK 21
 |||||
 DB 18 PSYQFGHNSVDFEEDTLPK 37

RESULT 6
 AAY29087
 ID AAY29087 standard; protein; 134 AA.
 XX

AC AAY29087;
 XX

DT 28-SEP-1999 (first entry)
 XX

DE S. aureus fibronectin binding protein A (FnBA) binding domain.
 XX

XX Bovine herpes virus-2; BHV-2; cytokine; immune response; immunogen; IL;
 KW interleukin; colony stimulating factor; CSF; interferon; IFN; TNF;
 KW tumour necrosis factor; recombinant virus; vaccine; mucosal disease;
 KW mastitis; breast cancer; stress-induced disease; binding domain; FnBA;
 KW fibronectin binding protein.
 XX

OS Staphylococcus aureus.
 XX

XX	PN	W09916892-A1.
XX	PD	08-APR-1999.
XX	PF	29-SEP-1998; 98WO-GB002927.
XX	PR	29-SEP-1997; 97GB-00020633.
XX	PA	(UYBR-) UNIV BRISTOL.
XX	P1	Bradley AJ, Duffas WPJ;
XX	DR	WPI; 1999-255101/21.
XX	DR	N-PSDB; AAX91504.
XX	PT	New bovine herpes virus-2 vectors.
XX	PS	Example 2; Fig 8A-B; 130pp; English.
XX	CC	The invention provides bovine herpes virus-2 (BHV-2) based vectors that
XX	CC	comprise at least one cytokine-encoding DNA sequence. The expression of
XX	CC	cytokines in mammals can up-regulate immune responses to the immunogens.
XX	CC	The cytokine is selected from interleukins (IL), colony stimulating
XX	CC	factors (CSF), interferons (IFN) and tumour necrosis factors (TNF). The
XX	CC	BHV-2 based vector or recombinant virus can be used as vaccines. They can
XX	CC	be used for preventing or treating a mucosal disease in a subject, e.g.
XX	CC	ruminants, cattle, sheep, goats, dogs, cats, horses, or man, particularly
XX	CC	mastitis in cows or breast cancers in humans. They can also be used for
XX	CC	preventing or treating a stress-induced disease. The present sequence
XX	CC	represents the binding domain of a previously published S. aureus
XX	CC	fibronectin binding protein A (FnBA) sequence. The Fnb binding domain
XX	CC	gene sequence FNAB, cloned for use in this invention has 97.8 percent
XX	CC	identity when compared to the previously published FnBA and FnBB gene
XX	CC	sequences
XX	SO	Sequence 134 AA;
QY		Query Match 94.1%; Score 112; DB 2; Length 134;
DB		Best Local Similarity 100.0%; Pred. No. 3.5e-09;
		Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
		2 PSYQGGHNSVDFEEDTLPK 21
		94 PSYQGGHNSVDFEEDTLPK 113
RESULT 7		
AAW31556		
ID	AAW31556	standard; protein; 139 AA.
XX	AC	AAW31556;
XX	DT	27-AUG-2003 (revised)
XX	DT	25-MAR-2003 (revised)
XX	DT	21-MAY-1998 (first entry)
XX	DE	Fibronectin-binding MSCRAMM derivative POD.
XX	KW	Fibronectin; POD; collagen binding protein; sepsis; infection;
KW	KM	microbial surface component recognising adhesive matrix molecule; MSCRAMM;
KW	adhesin; vaccine; immunisation; diagnosis; therapy; mastitis.	
OS	Staphylococcus aureus.	
XX	XX	
FH	Key	Location/Qualifiers
FT	Peptide	1..12
FT		/note= "vector pQE30-derived peptide"
XX	PN	W09743314-A2.
XX	PD	20-NOV-1997.
XX		

```

PF 14-MAY-1997; 97MO-USO08210.
PR 16-MAY-1996; 96US-0017678P.
XX (TEXTA ) UNIV TEXAS A & M SYSTEM.
PA (UABR-) UAB RES FOUND.
XX
PI Hoeseok M, Patil JM, House-Pompeo K, Sthanam N, Symersky J;
XX WPI; 1998-008801/01.
DR
PT Antibody that interacts with collagen binding domain of Staphylococcal
PT cna gene product - useful to prevent bacterial sepsis in animal infected
PT with Staphylococcus aureus.
XX
PS Disclosure; Page 91; 143pp; English.
XX
XX This protein comprises Staphylococcus aureus fibronectin-binding
CC microbial surface component recognizing adhesive matrix molecule (MSCRAMM)
CC derivative pOD, plus a vector-derived N-terminal peptide. The invention
CC relates to claimed nucleic acid sequences (see AAT93436-38) encoding S-
CC aureus collagen binding protein (CBP) epitopes M17, M31 and M55 (see
CC AAT931552-54) that confer protection against S. aureus infection. CBP
CC protein and antigenic epitopes are contemplated for use in the treatment
CC of pathological infections, especially to prevent bacterial adhesion to
CC collagen. The epitopes are also contemplated for use in the preparation
CC of vaccines and as carrier proteins in vaccine formulations, as well as
CC in the formulation of compositions for the prevention of S. aureus
CC infection. pCF33 and pOD (see AAT931556) were used to raise anti-MSCRAMM
CC polyclonal antibodies used in passive immunisation against bovine
CC mastitis. (Updated on 25-MAR-2003 to correct PI field.) (Updated on 27-
CC AUG-2003 to correct OS field.)
XX
SQ Sequence 139 AA:
XX
XX Query Match 94.1%; Score 112; DB 2; Length 139;
XX Best Local Similarity 100.0%; Pred. NO.3.6e-09;
XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0.
XX
QY 2 PSYQFGHNSVDFEDTLPR 21
XX |||||
DB 108 PSYQFGHNSVDFEDTLPR 127
XX
RESULT 8
AID ID AAF82115 standard; protein; 1018 AA.
XX
XX AAF82115;
AC
XX AAF82115;
AC
XX 25-MAR-2003 (revised)
DT 05-JAN-1990 (first entry)
XX
XX Fibronectin binding protein.
DE
XX Fibronectin binding protein; S.aureus; immunisation; mastitis; ruminants;
KM wound infection; diagnosis.
XX
XX Staphylococcus aureus.
OS
XX EP294349-A.
PN
XX 07-DEC-1988.
PD
XX 30-MAY-1988; 88EP-00850188.
PF
XX 01-JUN-1987; 87SR-00002272.
PR
XX (ALFA ) ALFA LAVAL AGRIC INT AB.
PA
XX Lindberg MK, Signas LC, Wadstrom TM, Froman G;
PI WPI; 1988-347978/49.
XX

```

DR P-PSDB; AAP92115.
XX
XX Hybrid DNA encoding Staphylococcus aureus fibronectin binding protein -
PT useful for immunisation and topical application to prevent staphylococcal
PT infections.
PS
PS Disclosure; Fig. 8A: 1-8A.2; 23pp; English.
XX
XX The S.aureus fibronectin binding protein may be included in a hybrid
CC protein. The protein may be used to immunise ruminants against
CC staphylococcal mastitis, pref. when given at 0.5-5 microg/kg, using 3
CC doses at 1-3 week intervals; and for topical applicn. to prevent wound
CC infection, pref. using isotonic saline soln. of concn. 25-250 microg/mg.
CC The DNA encoding the binding protein and the hybrid protein may be
CC immobilised on a carrier and used to diagnose staphylococcal infections.
CC (Updated on 25-MAR-2003 to correct PA field.)
XX
SQ Sequence 1018 AA;
Query Match 94.1%; Score 112; DB 1; Length 1018;
Best Local Similarity 100.0%; Pred. No. 3e-08;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 2 PSYQFGHNSVDFEEDTLPK 21
Db 838 PSYQFGHNSVDFEEDTLPK 857
RESULT 9
AAU37245
ID AAU37245 standard; protein; 1018 AA.
XX
XX AAU37245;
AC
XX
DT 14-FEB-2002 (first entry)
XX
XX Staphylococcus aureus cellular proliferation protein #1415.
DE
XX Antisense; prokaryotic cellular proliferation protein; antibiotic;
KM antibacterial; drug design.
XX
XX Staphylococcus aureus.
OS
XX MO200170955-A2.
PN
XX 27-SEP-2001.
PD
XX 21-MAR-2001; 2001WO-US009180.
PF
XX 21-MAR-2000; 2000US-0191078P.
PR 21-MAR-2000; 2000US-0191078P.
XX 23-MAY-2000; 2000US-0206848P.
PR 26-MAY-2000; 2000US-0207727P.
XX 23-OCT-2000; 2000US-0242578P.
PR 27-NOV-2000; 2000US-0253625P.
XX 22-DEC-2000; 2000US-0257931P.
PR 16-FEB-2001; 2001US-0269308P.
XX
XX (ELIT-) ELITRA PHARM INC.
PA
XX Haseelbeck R, Ohlsen KL, Zyekind JW, Wall D, Trawick JD, Carr GJ;
PI Yamamoto RT, Xu HH;
PI WPI; 2001-611495/70.
XX N-PSDB; AAS55104.
DR
XX N-PSDB; AAS55104.
DR
XX New polynucleotides for the identification and development of
PT antibiotics, comprise sequences of antisense nucleic acids.
XX
XX Example 3; SEQ ID NO 12838; 511pp; English.
PS
XX The invention relates to antisense inhibitors of genes essential to
CC prokaryotic cellular proliferation, their use in identifying the genes,
CC their use in the discovery of novel antibiotics, the essential genes

CC themselves and the encoded proteins. The prokaryotes used are Escherichia
CC coli, Staphylococcus aureus, Salmonella typhi, Klebsiella pneumoniae,
CC Pseudomonas aeruginosa and Enterococcus faecalis. The invention is also
CC useful for the identification of potential new targets for antibiotic
CC development. The antisense nucleic acids can also be used to identify
CC proteins used in proliferation, to express these proteins, and to obtain
CC antibodies capable of binding to the expressed proteins. The proteins can
CC be used to screen compounds in rational drug discovery programmes. The
CC antisense nucleic acid sequence is also useful to screen for homologous
CC nucleic acids which are required for cell proliferation in a wide variety
CC of organisms. The present sequence represents an essential prokaryotic
CC cellular proliferation protein. Note: The sequence data for this patent
CC did not form part of the printed specification, but was obtained in
CC electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pcc_sequences
XX
SQ Sequence 1018 AA;
Query Match 94.1%; Score 112; DB 4; Length 1018;
Best Local Similarity 100.0%; Pred. No. 3e-08;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 2 PSYQFGHNSVDFEEDTLPK 21
Db 838 PSYQFGHNSVDFEEDTLPK 857
RESULT 10
AAU34301
ID AAU34301 standard; protein; 1018 AA.
XX
XX AAU34301;
AC
XX
DT 14-FEB-2002 (first entry)
XX
XX Staphylococcus aureus cellular proliferation protein #577.
DE
XX Antisense; prokaryotic cellular proliferation protein; antibiotic;
KM antibacterial; drug design.
XX
XX Staphylococcus aureus.
OS
XX MO200170955-A2.
PN
XX 27-SEP-2001.
PD
XX 21-MAR-2001; 2001WO-US009180.
PF
XX 21-MAR-2000; 2000US-0191078P.
PR 21-MAR-2000; 2000US-0191078P.
XX 23-MAY-2000; 2000US-0206848P.
PR 26-MAY-2000; 2000US-0207727P.
XX 23-OCT-2000; 2000US-0242578P.
PR 27-NOV-2000; 2000US-0253625P.
XX 22-DEC-2000; 2000US-0257931P.
PR 16-FEB-2001; 2001US-0269308P.
XX
XX (ELIT-) ELITRA PHARM INC.
PA
XX Haseelbeck R, Ohlsen KL, Zyekind JW, Wall D, Trawick JD, Carr GJ;
PI Yamamoto RT, Xu HH;
PI WPI; 2001-611495/70.
XX N-PSDB; AAS52160.
DR
XX N-PSDB; AAS52160.
DR
XX New polynucleotides for the identification and development of
PT antibiotics, comprise sequences of antisense nucleic acids.
XX
XX Example 3; SEQ ID NO 5797; 511pp; English.
PS
XX The invention relates to antisense inhibitors of genes essential to
CC prokaryotic cellular proliferation, their use in identifying the genes,
CC their use in the discovery of novel antibiotics, the essential genes
CC themselves and the encoded proteins. The prokaryotes used are Escherichia

CC coli, *Staphylococcus aureus*, *Salmonella typhi*, *Klebsiella pneumoniae*,
CC *Pseudomonas aeruginosa* and *Enterococcus faecalis*. The invention is also
CC useful for the identification of potential new targets for antibiotic
CC development. The antisense nucleic acids can also be used to identify
CC proteins used in proliferation, to express these proteins, and to obtain
CC antibodies capable of binding to the expressed proteins. The proteins can
CC be used to screen compounds in rational drug discovery programmes. The
CC antisense nucleic acid sequence is also useful to screen for homologous
CC nucleic acids which are required for cell proliferation in a wide variety
CC of organisms. The present sequence represents an essential prokaryotic
CC cellular proliferation protein. Note: The sequence data for this patent
CC did not form part of the printed specification, but was obtained in
CC electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 1018 AA;
XX
Query Match 94.1%; Score 112; DB 4; Length 1018;
Best Local Similarity 100.0%; Pred. No. 3e-08;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 PSYQFGHNSVDFEEDTLPK 21
DB 838 PSYQFGHNSVDFEEDTLPK 857
XX
RESULT 11
ABJ18922
ID ABJ18922 standard; protein; 1018 AA.
XX
AC ABJ18922;
XX
DT 06-MAR-2003 (first entry)
XX
DE Pathogen specific antigen related staphylococcal protein SEQ ID No 68.
XX
XX Antibacterial; virucide; fungicide; protozoacide; cytostatic; anti-HIV;
XX hyperimmune; serum-reactive; antigen; pathogen; tumour; allergen;
XX auto-immunity; vaccine; staphylococcal infection; antibody; cancer;
XX autoimmune disease; HIV; hepatitis.
XX
XX *Staphylococcus* sp.
XX
XX OS
XX PN WO200259148-A2.
XX
XX PD 01-AUG-2002.
XX
XX PF 21-JAN-2002; 2002WO-EP000546.
XX
XX PR 26-JAN-2001; 2001AT-00000130.
XX
XX (CIST-) CISTEM BIOTECHNOLOGIES GMBH.
XX
XX PI Meinke A, Nagy E, Von Ahnen U, Klade C, Henics T, Zauner W;
XX Minh DB, Vytvytska O, Etz H, Dryla A, Weischart T, Hafner M;
XX Tempelmeier B;
XX
XX WPI; 2003-075410/07.
XX
XX Identifying, isolating and producing hyperimmune serum-reactive antigens
XX from a pathogen, for preparing vaccine or medicament for treating or
XX preventing e.g. staphylococcal infections, comprises providing antibody
XX preparation.
XX
XX Example 7; Page 157; 252pp; English.
XX
XX PS The invention relates to a novel method for identifying, isolating and
XX CC producing hyperimmune serum-reactive antigens from a pathogen, tumour,
XX CC allergen, a tissue or host prone to auto-immunity, where the antigens are
XX CC used in a vaccine, comprises providing antibody preparation from a plasma
XX CC pool of a type of animal, or individual sera with antibodies against the
XX CC specific pathogen, tumour, allergen, tissue or host prone to auto-
XX CC immunity. The hyperimmune serum-reactive antigens comprising any of the

CC 62 sequences of 53-2261 amino acids fully defined in the specification,
CC or their hyperimmune fragments are useful for the manufacture of a
CC pharmaceutical preparation, particularly a vaccine against staphylococcal
CC infections or colonisation against *S. aureus* or *S. epidermidis*. The
CC preparation of antibodies is useful for the manufacture of a medicament
CC for treating or preventing staphylococcal infections or colonisation
CC against *S. aureus* or *S. epidermidis*. The antibody preparations may also
CC be used for diagnostic and imaging purposes. Other conditions that can be
CC treated include cancer, autoimmune diseases or infections caused by viral
CC (e.g. HIV, hepatitis A, B or C), fungal or protozoan pathogens. This
CC sequence represents a staphylococcal protein relating to the method for
CC identifying and producing pathogen specific antigens of the invention
XX
SQ Sequence 1018 AA;
XX
Query Match 94.1%; Score 112; DB 6; Length 1018;
Best Local Similarity 100.0%; Pred. No. 3e-08;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 PSYQFGHNSVDFEEDTLPK 21
DB 838 PSYQFGHNSVDFEEDTLPK 857
XX
RESULT 12
ABM72537
ID ABM72537 standard; protein; 1018 AA.
XX
AC ABM72537;
XX
XX DT 20-NOV-2003 (first entry)
XX
XX DE *Staphylococcus aureus* protein #1777.
XX
XX XX Antibacterial; vaccine; gene therapy; infection; sepsis; diagnosis;
XX KM enzymatic assay; antibiotic target.
XX
XX OS
XX XX *Staphylococcus aureus*.
XX
XX PN WO200294868-A2.
XX
XX XX 28-NOV-2002.
XX
XX PD 27-MAR-2002; 2002WO-IB002637.
XX
XX PF 27-MAR-2001; 2001GB-00007661.
XX
XX PR (CHIR-) CHIRON SPA.
XX
XX PA
XX PI Masignani V, Mora M, Scarselli M;
XX
XX XX WPI; 2003-120786/11.
XX
XX DR N-PSDB; ACF74097.
XX
XX PT New *Staphylococcus aureus* protein, useful as a vaccine for treating or
XX PT preventing staphylococcal infection, specifically an infection caused by
XX PT *S. aureus*, e.g. sepsis.
XX
XX PS Claim 1; SEQ ID NO 3554; 49pp; English.
XX
XX XX The invention relates to novel genes and encoded proteins from
XX CC *Staphylococcus aureus*. A composition comprising the *S. aureus* protein, a
XX CC nucleic acid encoding the protein, or an antibody to the protein, is
XX CC useful as a pharmaceutical, particularly as a vaccine for treating or
XX CC preventing infection due to *Staphylococcus* bacteria, specifically an
XX CC infection caused by *S. aureus*. The composition is particularly useful for
XX CC treating or preventing sepsis in a patient. The composition can also be
XX CC used for diagnostics. The protein is also used in an assay for enzymatic
XX CC studies and as a target for antibiotics. This sequence represents one of
XX CC the novel *S. aureus* proteins of the invention
XX
SQ Sequence 1018 AA;

Query Match 94.1%; Score 112; DB 6; Length 1018;
Best Local Similarity 100.0%; Pred. No. 3e-08;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PSYOGGHSVDFEEDTLPK 21
DB 838 PSYOGGHSVDFEEDTLPK 857

RESULT 13
AAW89806 standard; protein; 1027 AA.

AAW89806;

16-MAR-1999 (first entry)

Staphylococcus aureus protein SEQ ID #5254.

Computer readable medium; vaccine; S.aureus infection; immunodetection;
cellulitis; eyelid infection; food poisoning; osteomyelitis; therapy;
skin infection; surgical wound infection; scalded skin syndrome;
toxic shock syndrome.

Staphylococcus aureus.

EP786519-A2.

30-JUL-1997.

07-JAN-1997; 97EP-00100117.

05-JAN-1996; 96US-0009861P.

(HUMA-) HUMAN GENOME SCT INC.

Kunsch CA, Choi GH, Barash SC, Dillon PJ, Fannon MR, Rosen CA;

WPI; 1997-374922/35.

polynucleotide(s) and proteins derived from Staphylococcus aureus -
stored on computer readable medium and used in the production of anti-
S.aureus vaccines.

Claim 23; Page 3263-3267; 3271pp; English.

This sequence represents a Staphylococcus aureus protein sequence of the
invention. The DNA sequences encoding the S.aureus proteins are recorded
on a computer readable medium, preferably selected from a floppy or hard
disk, random access memory (RAM), read-only memory (ROM) or CD-ROM.
Homology searches using the S.aureus DNA sequences allows putative
functions to be assigned so that protein-encoding or regulatory regions
of commercial, therapeutic or industrial importance can be obtained.
Specifically, sequences which are likely to encode antigens have been
identified and these polypeptides can be used in a vaccine composition
against S.aureus infection. The polypeptides can also be used in a kit
for the immunodetection of S.aureus in a sample. S.aureus is implicated
in numerous human diseases, including cellulitis, eyelid infections, food
poisoning, osteomyelitis, skin and surgical wound infections, scalded
skin syndrome, toxic shock syndrome, etc. Organisms transformed with the
DNA sequences can be used for recombinant production of the polypeptides.
The new DNA sequences (and their fragments) are useful as primers or
probes for isolating homologues of any of the 5191 S.aureus DNA sequences
contained on the computer readable medium

Sequence 1027 AA;

Query Match 94.1%; Score 112; DB 2; Length 1027;

Best Local Similarity 100.0%; Pred. No. 3.1e-08;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PSYOGGHSVDFEEDTLPK 21
|||||

DB 847 PSYOGGHSVDFEEDTLPK 866

RESULT 14

ABU15854
ID ABU15854 standard; protein; 961 AA.

ABU15854;

19-JUN-2003 (first entry)

Protein encoded by prokaryotic essential gene #1381.

Antisense; prokaryotic essential gene; cell proliferation; drug design.

Staphylococcus aureus.

WO200277183-A2.

03-OCT-2002.

21-MAR-2002; 2002WO-US009107.

21-MAR-2001; 2001US-00815242.

06-SEP-2001; 2001US-00948993.

25-OCT-2001; 2001US-0342323P.

08-FEB-2002; 2002US-00072851.

06-MAR-2002; 2002US-0326599P.

(ELIT-) ELITRA PHARM INC.

WPI; 2003-029926/02.

N-PSDB; ACA19724.

New antisense nucleic acids, useful for identifying proteins or screening
for homologous nucleic acids required for cellular proliferation to
isolate candidate molecules for rational drug discovery programs.

Claim 25; SEQ ID NO 43778; 1766pp; English.

The invention relates to an isolated nucleic acid comprising any one of
the 6213 antisense sequences given in the specification where expression
of the nucleic acid inhibits proliferation of a cell. Also included are:
(1) a vector comprising a promoter operably linked to the nucleic acid
encoding a polypeptide whose expression is inhibited by the antisense
nucleic acid; (2) a host cell containing the vector; (3) an isolated
polypeptide or its fragment whose expression is inhibited by the
antisense nucleic acid; (4) an antibody capable of specifically binding
the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular
proliferation or the activity of a gene in an operon required for
proliferation; (7) identifying a compound that influences the activity of
the gene product or that has an activity against a biological pathway
required for proliferation, or that inhibits cellular proliferation; (8)
identifying a gene required for cellular proliferation or the biological
pathway in which a proliferation-required gene or its gene product lies
or a gene on which the test compound that inhibits proliferation of an
organism acts; (9) manufacturing an antibiotic; (10) profiling a
compound's activity; (11) a culture comprising strains in which the gene
product is overexpressed or underexpressed; (12) determining the extent
to which each of the strains is present in a culture or collection of
strains; or (13) identifying the target of a compound that inhibits the
proliferation of an organism. The antisense nucleic acids are useful for
identifying proteins or screening for homologous nucleic acids required
for cellular proliferation to isolate candidate molecules for rational
drug discovery programs, or for screening homologous nucleic acids
required for proliferation in cells other than S. aureus, S. typhimurium,
K. pneumoniae or P. aeruginosa. The present sequence is encoded by one of
the target prokaryotic essential genes. Note: The sequence data for this
patent did not form part of the printed specification, but was obtained
in electronic format directly from WIPO at

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CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 961 AA;
Query Match 91.6%; Score 109; DB 6; Length 961;
Best Local Similarity 95.0%; Pred. No. 8.3e-08;
Matches 19; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 PSYFGGHNSVDFEEDTLPK 21
   |:|||||
DB 785 PNYQFGHNSVDFEEDTLPK 804

RESULT 15
AAU33960
ID AAU33960 standard; protein; 978 AA.
XX
AC AAU33960;
XX
DT 14-FEB-2002 (first entry)
XX
DE Staphylococcus aureus cellular proliferation protein #236.
XX
KW Antisense; prokaryotic cellular proliferation protein; antibiotic;
XX antibacterial; drug design.
XX
OS Staphylococcus aureus.
XX
PN WO200170955-A2.
XX
PD 27-SEP-2001.
XX
PF 21-MAR-2001; 2001WO-US009180.
XX
PR 21-MAR-2000; 2000US-0191078P.
XX PR 23-MAY-2000; 2000US-0206848P.
XX PR 26-MAY-2000; 2000US-0207727P.
XX PR 23-OCT-2000; 2000US-0242578P.
XX PR 27-NOV-2000; 2000US-0253625P.
XX PR 22-DEC-2000; 2000US-0257931P.
XX PR 16-FEB-2001; 2001US-0269308P.
XX
PA (ELIT-) ELITRA PHARM INC.
XX
PI Haselbeck R, Ohlsen KL, Zyekind JM, Wall D, Trawick JD, Carr GJ;
PI Yamamoto RT, Xu HH;
XX
DR N-PSDB; AAS51819.
XX
PT New polynucleotides for the identification and development of
XX antibiotics, comprise sequences of antisense nucleic acids.
XX
PS Example 3; SEQ ID NO 5456; 511p; English.
XX
CC The invention relates to antisense inhibitors of genes essential to
CC prokaryotic cellular proliferation, their use in identifying the genes,
CC their use in the discovery of novel antibiotics, the essential genes
CC themselves and the encoded proteins. The prokaryotes used are Escherichia
CC coli, Staphylococcus aureus, Salmonella typhi, Klebsiella pneumoniae,
CC Pseudomonas aeruginosa and Enterococcus faecalis. The invention is also
CC useful for the identification of potential new targets for antibiotic
CC development. The antisense nucleic acids can also be used to identify
CC proteins used in proliferation, to express these proteins, and to obtain
CC antibodies capable of binding to the expressed proteins. The proteins can
CC be used to screen compounds in rational drug discovery programmes. The
CC antisense nucleic acid sequence is also useful to screen for homologous
CC nucleic acids which are required for cell proliferation in a wide variety
CC of organisms. The present sequence represents an essential prokaryotic
CC cellular proliferation protein. Note: The sequence data for this patent
CC did not form part of the printed specification, but was obtained in
CC electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences

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XX
SQ Sequence 978 AA;
Query Match 91.6%; Score 109; DB 4; Length 978;
Best Local Similarity 95.0%; Pred. No. 8.5e-08;
Matches 19; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 PSYFGGHNSVDFEEDTLPK 21
   |:|||||
DB 816 PNYQFGHNSVDFEEDTLPK 835

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Search completed: October 25, 2005, 19:38:26
 Job time : 68.1473 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 22, 2005, 02:23:36 ; Search time 15.9358 Seconds
(without alignments)
98.371 Million cell updates/sec

Title: US-10-731-238-14

Sequence: 1 PPSYQFGHNSVDFEEDLPK 21

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database: Issued Patents AA:*
1: /cgn2_6/ptodata/1/iaa/5A COMB pep.*
2: /cgn2_6/ptodata/1/iaa/5B COMB pep.*
3: /cgn2_6/ptodata/1/iaa/6A COMB pep.*
4: /cgn2_6/ptodata/1/iaa/6B COMB pep.*
5: /cgn2_6/ptodata/1/iaa/PCTUS COMB pep.*
6: /cgn2_6/ptodata/1/iaa/backfilee1 pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	119	100.0	21	4	US-09-010-317-14
2	112	94.1	21	4	US-09-010-317-9
3	112	94.1	37	1	US-08-234-622A-4
4	112	94.1	38	1	US-08-294-189-8
5	112	94.1	38	1	US-08-729-767-5
6	112	94.1	139	3	US-08-259-000-3
7	112	94.1	139	3	US-08-856-253-8
8	112	94.1	178	2	US-08-459-135A-12
9	112	94.1	178	2	US-08-495-559-12
10	112	94.1	1027	4	US-08-956-171E-5254
11	112	94.1	1027	4	US-08-781-986A-5254
12	107	89.9	21	4	US-09-010-317-16
13	107	89.9	21	4	US-09-010-317-23
14	107	89.9	21	4	US-09-010-317-33
15	106	89.1	21	4	US-09-010-317-18
16	106	89.1	21	4	US-09-010-317-24
17	106	89.1	21	4	US-09-010-317-27
18	106	89.1	21	4	US-09-010-317-28
19	106	89.1	21	4	US-09-010-317-30
20	105	88.2	21	4	US-09-010-317-15
21	105	88.2	21	4	US-09-010-317-25
22	105	88.2	21	4	US-09-010-317-29
23	105	88.2	21	4	US-09-010-317-31
24	105	88.2	130	2	US-08-459-135A-7
25	105	88.2	130	2	US-08-459-135A-8
26	105	88.2	130	3	US-08-495-559-7
27	105	88.2	130	3	US-08-495-559-8

28	105	88.2	174	2	US-08-459-135A-10	Sequence 10, Appl
29	105	88.2	174	2	US-08-459-135A-13	Sequence 13, Appl
30	105	88.2	174	3	US-08-495-559-10	Sequence 10, Appl
31	105	88.2	174	3	US-08-495-559-13	Sequence 13, Appl
32	105	88.2	176	3	US-08-459-135A-6	Sequence 6, Appl
33	105	88.2	181	2	US-08-459-135A-6	Sequence 6, Appl
34	105	88.2	559	4	US-08-956-171E-5251	Sequence 5251, Ap
35	105	88.2	559	4	US-08-781-986A-5251	Sequence 5251, Ap
36	104	87.4	21	4	US-09-010-317-10	Sequence 10, Appl
37	104	87.4	21	4	US-09-010-317-20	Sequence 20, Appl
38	104	87.4	21	4	US-09-010-317-22	Sequence 22, Appl
39	104	87.4	21	4	US-09-010-317-32	Sequence 32, Appl
40	104	87.4	22	4	US-09-010-317-13	Sequence 13, Appl
41	102	85.7	21	4	US-09-010-317-17	Sequence 17, Appl
42	102	85.7	21	4	US-09-010-317-19	Sequence 19, Appl
43	102	85.7	21	4	US-09-010-317-21	Sequence 21, Appl
44	102	85.7	21	4	US-09-010-317-26	Sequence 26, Appl
45	96	80.7	19	1	US-08-234-622A-1	Sequence 1, Appl

ALIGNMENTS

RESULT 1
US-09-010-317-14
Sequence 14, Application US/09010317
Patent No. 6685943
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
APPLICANT: Patti, Joseph M.
APPLICANT: House-Pompeo, Karen L.
APPLICANT: Speziale, Pietro
APPLICANT: Joh, Danny
APPLICANT: McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
TITLE OF INVENTION: AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAMK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-09-010-317-14
Query Match 100.0%; Score 119; DB 4; Length 21;
Best Local Similarity 100.0%; Pred. No. 2.6e-12;

Matches	21, Conservative	0, Mismatches	0, Indels	0, Gaps
QY	1 PPSYQFGGHSNVDFEEDTLPK 21			
Db	1 PPSYQFGGHSNVDFEEDTLPK 21			

RESULT 2
US-09-010-317-9

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Sequence 9, Application US/09010317
Patent No. 6685943
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
APPLICANT: Patti, Joseph M.
APPLICANT: House-Pompeo, Karen L.
APPLICANT: Speziale, Pietro
APPLICANT: Joh, Danny
APPLICANT: McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
TITLE OF INVENTION: AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESSES:
ADDRESSER: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Releasee #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAMK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: amino acid
STRANDNESS:
TOPOLOGY: linear
US-09-010-317-9

Query Match          94.1%; Score 112; DB 4; Length 21;
Best Local Similarity 100.0%; Pred. No. 3,4e-11;
Matches    20; Conservative    0; Mismatches    0; Indels    0

QY      2 PSYRGGHNSVPEEPTLPK 21
       ||| ||||| ||||| |||
Db      2 PSYRGGHNSVDPEEDTLPK 21

RESULT 3
US-08-234-622A-4
; Sequence 4, Application US/08234622A
; Patent No. 5440014
; GENERAL INFORMATION:
; APPLICANT: HOOK, Magnus
; APPLICANT: MCGAVIN, Martin
; APPLICANT: RAUCCI, Giuseppe
; TITLE OF INVENTION: A FIBRONECTIN BINDING PEPTIDE

```

```

1  NUMBER OF SEQUENCES: 4
2  CORRESPONDENCE ADDRESS:
3  ADDRESSEE: Burns, Doane, Swecker & Mathis
4  STREET: P.O. Box 1404
5  CITY: Alexandria
6  STATE: Virginia
7  COUNTRY: United States
8  ZIP: 22313-1404
9
10 COMPUTER READABLE FORM:
11 MEDIUM TYPE: Floppy disk
12 COMPUTER: IBM PC compatible
13 OPERATING SYSTEM: PC-DOS/MS-DOS
14 SOFTWARE: PatentIn Release #1.0, Version #1.30
15 CURRENT APPLICATION DATA:
16 APPLICATION NUMBER: US/08/234,622A
17 FILING DATE: 28-APR-1994
18 CLASSIFICATION: 530
19 PRIOR APPLICATION DATA:
20 APPLICATION NUMBER: SE 9002617-0
21 FILING DATE: 10-AUG-1990
22 PRIOR APPLICATION DATA:
23 APPLICATION NUMBER: WO PCT/SB91/00534
24 FILING DATE: 09-AUG-1991
25 ATTORNEY/AGENT INFORMATION:
26 NAME: Neuth, Donna M
27 REGISTRATION NUMBER: 36,607
28 REFERENCE/DOCKET NUMBER: 012885-044
29 TELECOMMUNICATION INFORMATION:
30 TELEPHONE: (703) 836-6620
31 TELEFAX: (703) 836-2021
32 INFORMATION FOR SEQ ID NO: 4:
33 SEQUENCE CHARACTERISTICS:
34 LENGTH: 37 amino acids
35 TYPE: amino acid
36 STRANDEDNESS: single
37 TOPOLOGY: linear
38 MOLECULE TYPE: peptide
39
40 US-08-234-622A-4

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Query Match	94.1%	Score 112;	DB 1;	Length 37;
Best Local Similarity	100.0%	Pred. No. 6.5e-11;		
Matches 20; Conservative	0;	Mismatches 0;	Indels 0;	Gaps 0;

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1      RESULT 4
2      US-08-294-189-8
3      ; Sequence 8, Application US/08294189
4      ; Patent No. 5707822
5      ; GENERAL INFORMATION:
6      ; APPLICANT: Fischetti, Vincent A.
7      ; APPLICANT: Rakonjact, Jaana
8      ; APPLICANT: Robbins, John
9      ; TITLE OF INVENTION: GENE SERUM OPACITY FACTOR
10     ; NUMBER OF SEQUENCES: 23
11     ; CORRESPONDENCE ADDRESS:
12     ; ADDRESSEE: Klauber & Jackson
13     ; STREET: 411 Hackensack Avenue
14     ; CITY: Hackensack
15     ; STATE: New Jersey
16     ; COUNTRY: USA
17     ; ZIP: 07601
18     ; COMPUTER READABLE FORM:
19     ; MEDIUM TYPE: Floppy disk
20     ; COMPUTER: IBM PC compatible
21     ; OPERATING SYSTEM: PC-DOS/MS-DOS
22     ; SOFTWARE: Patentin Release #1.0, Version #1.25
23     ; CURRENT APPLICATION DATA:
24     ; APPLICATION NUMBER: US/08/294, 189
25     ; FILING DATE: 22-AUG-1994

```

CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-118
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 487-5800
TELEFAX: 201 343-1684
TELEX: 133521
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
ORGANISM: Streptococcus pyogenes
STRAIN: D734
INDIVIDUAL ISOLATE: 22
IMMEDIATE SOURCE:
CLONE: SAU3a
US-08-294-189-8

Query Match 94.1%; Score 112; DB 1; Length 38;
Best Local Similarity 100.0%; Pred. No. 6.7e-11;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PSYQFGHNSVDFEEDTLPK 21
DB 11 PSYQFGHNSVDFEEDTLPK 30

RESULT 5
US-08-729-767-5
Sequence 5, Application US/08729767
Patent No. 5770702
GENERAL INFORMATION:
APPLICANT: HOOK, Magnus
APPLICANT: LINDBERG, Martin Kjell
APPLICANT: SIGNAS, Lars Christer
APPLICANT: MADSTROM, Torkel Mikael
APPLICANT: FROMAN, Gunnar
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN AS WELL AS
TITLE OF INVENTION: ITS PREPARATION
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Burns, Doane, Swecker & Mathis, L.L.P.
STREET: P.O. Box 1404
CITY: Alexandria
STATE: Virginia
COUNTRY: United States
ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/729,767
FILING DATE: 07-OCT-1996
CLASSIFICATION: 435
TELECOMMUNICATION INFORMATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/259,000
FILING DATE: 13-JUN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/007,817
FILING DATE: 22-JAN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/201,028
FILING DATE: 01-JUN-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: SE 8702272-9

FILING DATE: 01-JUN-1987
ATTORNEY/AGENT INFORMATION:
NAME: McGowan, Malcolm K.
REGISTRATION NUMBER: 39,300
REFERENCE/DOCKET NUMBER: 012889-036
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-729-767-5

Query Match 94.1%; Score 112; DB 1; Length 38;
Best Local Similarity 100.0%; Pred. No. 6.7e-11;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PSYQFGHNSVDFEEDTLPK 21
DB 18 PSYQFGHNSVDFEEDTLPK 37

RESULT 6
US-08-259-000-3
Sequence 3, Application US/08259000
Patent No. 5571514
GENERAL INFORMATION:
APPLICANT: HOOK, Magnus
APPLICANT: LINDBERG, Martin Kjell
APPLICANT: SIGNAS, Lars Christer
APPLICANT: MADSTROM, Torkel Mikael
APPLICANT: FROMAN, Gunnar
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN AS WELL AS
TITLE OF INVENTION: ITS PREPARATION
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Burns, Doane, Swecker & Mathis
STREET: P.O. Box 1404
CITY: Alexandria
STATE: Virginia
COUNTRY: United States
ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/259,000
FILING DATE: 13-JUN-1994
CLASSIFICATION: 435
TELECOMMUNICATION INFORMATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: SE 8702272-9
FILING DATE: 01-JUN-1987
ATTORNEY/AGENT INFORMATION:
NAME: Meuth, Donna M
REGISTRATION NUMBER: 36,607
REFERENCE/DOCKET NUMBER: 012885-062
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 114 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-259-000-3

Query Match 94.1%; Score 112; DB 1; Length 114;
Best Local Similarity 100.0%; Pred. No. 2.3e-10;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 PSYQFGHNSVDFEEDTLPK 21
DB 94 PSYQFGHNSVDFEEDTLPK 113

RESULT 7
US-08-856-253-8
; Sequence 8, Application US/08856253
; Patent No. 6288214
; GENERAL INFORMATION:
; APPLICANT: Hook, Magnus
; APPLICANT: Patti, Joseph M.
; APPLICANT: House-Pompeo, Karen
; APPLICANT: Stenham, Narayana
; APPLICANT: Symersky, Jindrich
; TITLE OF INVENTION: COLLAGEN BINDING PROTEIN COMPOSITIONS
; TITLE OF INVENTION: AND METHODS OF USE
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: U.S.
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/856,253
; FILING DATE: Concurrently Herewith
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/017,678
; FILING DATE: 16-MAY-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Kitchell, Barbara S.
; REGISTRATION/DOCKET NUMBER: 33,928
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (512) 418-3000
; TELEFAX: (512) 474-7577
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 139 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
US-08-856-253-8

Query Match 94.1%; Score 112; DB 3; Length 139;
Best Local Similarity 100.0%; Pred. No. 2.9e-10;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 PSYQFGHNSVDFEEDTLPK 21
DB 108 PSYQFGHNSVDFEEDTLPK 127

RESULT 8
US-08-459-135A-12
; Sequence 12, Application US/08459135A
; Patent No. 5955078
; GENERAL INFORMATION:
; APPLICANT: BURHAM, Martin Karl Russel
; APPLICANT: CHOPRA, Ian

APPLICANT: CRITCHLEY, Ian Alfred
; APPLICANT: KNOWLES, David Justin Charles
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN: MONOCLONAL ANTIBODY AND THEIR US
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corporation
; STREET: 709 Swedeland Road
; CITY: King of Prussia
; STATE: PA
; COUNTRY: U.S.A.
; ZIP: 19406-0939
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: DOS
; SOFTWARE: Pastseq, Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/459,135A
; FILING DATE: 02-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB/94/00215
; FILING DATE: 04-Feb-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Gimm, Edward R.
; REGISTRATION NUMBER: 38,891
; REFERENCE/DOCKET NUMBER: P30591C2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-270-4478
; TELEFAX: 610-270-5090
; TELEX:
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 178 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Protein
US-08-459-135A-12

Query Match 94.1%; Score 112; DB 2; Length 178;
Best Local Similarity 100.0%; Pred. No. 3.8e-10;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 PSYQFGHNSVDFEEDTLPK 21
DB 94 PSYQFGHNSVDFEEDTLPK 113

RESULT 9
US-08-495-559-12
; Sequence 12, Application US/08495559A
; Patent No. 6054572
; GENERAL INFORMATION:
; APPLICANT: BURHAM, Martin Karl Russel
; APPLICANT: CHOPRA, Ian
; APPLICANT: CRITCHLEY, Ian Alfred
; APPLICANT: KNOWLES, David Justin Charles
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN: MONOCLONAL
; TITLE OF INVENTION: ANTIBODY AND THEIR USE IN PREVENTING BACTERIAL ADHESION
; FILE REFERENCE: P30591
; CURRENT APPLICATION NUMBER: US/08/495,559A
; CURRENT FILING DATE: 1995-08-03
; EARLIER APPLICATION NUMBER: GB 9302289.5
; EARLIER FILING DATE: 1993-02-05
; EARLIER APPLICATION NUMBER: GB 9321592.9
; EARLIER FILING DATE: 1993-10-20
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 12
; LENGTH: 178
; TYPE: PRT

ORGANISM: Staphylococcus aureus
US-08-495-559-12

Query Match 94.1%; Score 112; DB 3; Length 178;
Best Local Similarity 100.0%; Pred. No. 3.8e-10;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PSYQFGHNSVDFEEDTLPK 21
DB 94 PSYQFGHNSVDFEEDTLPK 113

RESULT 10
US-08-956-171E-5254

Sequence 5254, Application US/08956171E
Patent No. 6593114

GENERAL INFORMATION:

APPLICANT: Charles Kunsch

Gil H. Choi

Patrick S. Dillon

Craig A. Rosen

Steven C. Barash

Michael R. Fannon

TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences

NUMBER OF SEQUENCES: 5256

CORRESPONDENCE ADDRESS:

ADDRESSEE: Human Genome Sciences, Inc.

STREET: 9410 Key West Avenue

CITY: Rockville

STATE: Maryland

COUNTRY: USA

ZIP: 20850

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage

COMPUTER: HP Vectra 486/33

OPERATING SYSTEM: MSDOS version 6.2

SOFTWARE: ASCII Text

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/956,171E

FILING DATE: 20-Oct-1997

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 60/009,861

FILING DATE: January 5, 1996

APPLICATION NUMBER: 08/781,986

FILING DATE: January 3, 1997

ATTORNEY/AGENT INFORMATION:

NAME: Mark J. Hyman

REGISTRATION NUMBER: 46,789

REFERENCE/DOCKET NUMBER: PB248P1

TELECOMMUNICATION INFORMATION:

TELEPHONE: (240) 314-1224

TELEFAX: (301) 309-8439

INFORMATION FOR SEQ ID NO: 5254:

SEQUENCE CHARACTERISTICS:

LENGTH: 1027 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 5254:

US-08-956-171E-5254

Query Match 94.1%; Score 112; DB 4; Length 1027;

Best Local Similarity 100.0%; Pred. No. 2.8e-09;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PSYQFGHNSVDFEEDTLPK 21

DB 847 PSYQFGHNSVDFEEDTLPK 866

RESULT 11

US-08-781-986A-5254

Sequence 5254, Application US/08781986A

Patent No. 6737248

GENERAL INFORMATION:

APPLICANT: Charles Kunsch

TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences

NUMBER OF SEQUENCES: 5255

CORRESPONDENCE ADDRESS:

ADDRESSEE: Human Genome Sciences, Inc.

STREET: 9410 Key West Avenue

CITY: Rockville

STATE: Maryland

COUNTRY: USA

ZIP: 20850

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage

COMPUTER: HP Vectra 486/33

OPERATING SYSTEM: MSDOS version 6.2

SOFTWARE: ASCII Text

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/781,986A

FILING DATE:

PRIOR APPLICATION DATA:

APPLICATION NUMBER:

ATTORNEY/AGENT INFORMATION:

NAME: Benson, Bob

REGISTRATION NUMBER: 30,446

REFERENCE/DOCKET NUMBER: PB248PP

TELECOMMUNICATION INFORMATION:

TELEPHONE: (301) 309-8504

TELEFAX: (301) 309-8512

INFORMATION FOR SEQ ID NO: 5254:

SEQUENCE CHARACTERISTICS:

LENGTH: 1027 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-781-986A-5254

Query Match 94.1%; Score 112; DB 4; Length 1027;

Best Local Similarity 100.0%; Pred. No. 2.8e-09;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PSYQFGHNSVDFEEDTLPK 21

DB 847 PSYQFGHNSVDFEEDTLPK 866

RESULT 12

US-09-010-317-16

Sequence 16, Application US/09010317

Patent No. 6685943

GENERAL INFORMATION:

APPLICANT: Hook, Magnus

APPLICANT: Patti, Joseph M.

APPLICANT: House-Pompeo, Karen L.

APPLICANT: Speziale, Pietro

APPLICANT: Joh, Danny

APPLICANT: McGavin, Martin J.

TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS

NUMBER OF SEQUENCES: 105

CORRESPONDENCE ADDRESS:

ADDRESSEE: Arnold, White & Durkee

STREET: P.O. Box 4433

CITY: Houston

STATE: TX

COUNTRY: USA

ZIP: 77210-4433

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-09-010-317-16

Query Match 89.9%; Score 107; DB 4; Length 21;
Best Local Similarity 95.0%; Pred. No. 2.1e-10;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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DB 2 PSYQFGHNSVDFEETLPK 21

RESULT 13
US-09-010-317-23
Sequence 23, Application US/09010317
Patent No. 6685943
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
APPLICANT: Patti, Joseph M.
APPLICANT: House-Pompeo, Karen L.
APPLICANT: Speziale, Pietro
APPLICANT: Joh, Danny
APPLICANT: McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-09-010-317-33

TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-09-010-317-23

Query Match 89.9%; Score 107; DB 4; Length 21;
Best Local Similarity 95.0%; Pred. No. 2.1e-10;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 PSYQFGHNSVDFEETLPK 21
DB 2 PSYQFGHNSVDFEETLPK 21

RESULT 14
US-09-010-317-33
Sequence 33, Application US/09010317
Patent No. 6685943
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
APPLICANT: Patti, Joseph M.
APPLICANT: House-Pompeo, Karen L.
APPLICANT: Speziale, Pietro
APPLICANT: Joh, Danny
APPLICANT: McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-09-010-317-33

Query Match 89.9%; Score 107; DB 4; Length 21;
Best Local Similarity 100.0%; Pred. No. 2.1e-10;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PSYQFGHNSVDFEETLP 20
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Db 2 PSYQFGHNSVDFEEDTLP 20

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RESULT 15
US-09-010-317-18
; Sequence 18, Application US/09010317
; Patent No. 6685943
; GENERAL INFORMATION:
; APPLICANT: Hook, Magnus
; APPLICANT: Patti, Joseph M.
; APPLICANT: House-Pompeo, Karen L.
; APPLICANT: Speciale, Pietro
; APPLICANT: Joh, Danny
; APPLICANT: McGavin, Martin J.
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
; NUMBER OF INVENTIONS: 105
; NUMBER OF SEQUENCES: 105
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: TX
; COUNTRY: USA
; ZIP: 77210-4433
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/010,317
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/036,139
; FILING DATE: 21-JAN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Hibler, David W.
; REGISTRATION NUMBER: 41,071
; REFERENCE/DOCKET NUMBER: TAMK:189
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 512-418-3000
; TELEFAX: 512-474-7577
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
US-09-010-317-18

Query Match 89.1%; Score 106; DB 4; Length 21;
Best Local Similarity 95.0%; Pred. No. 3.1e-10;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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QY 2 PSYQFGHNSVDFEEDTLPK 21
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2 PSYQFGHNSVDFEEDTLPK 21

Search completed: October 22, 2005, 03:51:11
Job time : 16.9358 secs

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GenCore version 5.1.6
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OM protein - protein search, using SW model

Run on: October 22, 2005, 10:49:15 ; Search time 59.2367 Seconds
(without alignments)
148.005 Million cell updates/sec

Title: US-10-731-238-14

Perfect score: 119

Sequence: 1 PEPYQFGHNSVDFEEDLPK 21

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1862951 segs, 417491010 residues

Total number of hits satisfying chosen parameters: 1862951

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	119	100.0	21	18	US-10-731-238-14
2	112	94.1	21	18	US-10-731-238-9
3	112	94.1	37	20	US-11-066-697-1134
4	112	94.1	139	9	US-09-813-820-8
5	112	94.1	1018	9	US-09-815-242-5197
6	112	94.1	1018	9	US-09-815-242-12838
7	112	94.1	1018	17	US-10-470-0488-68
8	112	94.1	1027	8	US-08-781-986A-5254
9	112	94.1	1027	15	US-10-339-624-5254
10	109	91.6	961	15	US-10-282-122A-43778
11	109	91.6	978	9	US-09-815-242-5456

12	109	91.6	1001	9	US-09-815-242-12686	Sequence 12686, A
13	109	91.6	1038	15	US-10-282-122A-43827	Sequence 43827, A
14	107	89.9	21	18	US-10-731-238-16	Sequence 16, App1
15	107	89.9	21	18	US-10-731-238-23	Sequence 23, App1
16	107	89.9	21	18	US-10-731-238-33	Sequence 33, App1
17	106	89.1	21	18	US-10-731-238-18	Sequence 18, App1
18	106	89.1	21	18	US-10-731-238-24	Sequence 24, App1
19	106	89.1	21	18	US-10-731-238-27	Sequence 27, App1
20	106	89.1	21	18	US-10-731-238-28	Sequence 28, App1
21	106	89.1	21	18	US-10-731-238-30	Sequence 30, App1
22	105	88.2	21	18	US-10-731-238-15	Sequence 15, App1
23	105	88.2	21	18	US-10-731-238-25	Sequence 25, App1
24	105	88.2	21	18	US-10-731-238-29	Sequence 29, App1
25	105	88.2	21	18	US-10-731-238-31	Sequence 31, App1
26	105	88.2	388	8	US-08-901-062-1	Sequence 1, App1
27	105	88.2	559	8	US-08-781-986A-5251	Sequence 5251, Ap
28	105	88.2	559	15	US-10-329-624-5251	Sequence 5251, Ap
29	105	88.2	940	17	US-10-470-048B-424	Sequence 424, App
30	105	88.2	948	17	US-10-470-048B-69	Sequence 69, App1
31	104	87.4	21	18	US-10-731-238-10	Sequence 10, App1
32	104	87.4	21	18	US-10-731-238-20	Sequence 20, App1
33	104	87.4	21	18	US-10-731-238-22	Sequence 22, App1
34	104	87.4	21	18	US-10-731-238-32	Sequence 32, App1
35	104	87.4	22	18	US-10-731-238-13	Sequence 13, App1
36	102	85.7	21	18	US-10-731-238-17	Sequence 17, App1
37	102	85.7	21	18	US-10-731-238-19	Sequence 19, App1
38	102	85.7	21	18	US-10-731-238-21	Sequence 21, App1
39	102	85.7	21	18	US-10-731-238-26	Sequence 26, App1
40	95	79.8	21	18	US-10-731-238-34	Sequence 34, App1
41	78	65.5	14	18	US-10-731-238-61	Sequence 61, App1
42	59	49.6	10	18	US-10-731-238-96	Sequence 96, App1
43	58	48.7	10	18	US-10-731-238-97	Sequence 97, App1
44	57	47.9	10	18	US-10-731-238-98	Sequence 98, App1
45	56	47.1	10	18	US-10-731-238-99	Sequence 99, App1

ALIGNMENTS

RESULT 1
US-10-731-238-14
Sequence 14, Application US/10731238
Publication No. US20050123552A1
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
Patel, Joseph M.
House-Pompeo, Karen L.
Speziale, Pietro
Joh, Danny
McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/731,238
FILING DATE: 10-Dec-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE: 21-Jan-1998
APPLICATION NUMBER: US 60/036,139

FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAMK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 14:
US-10-731-238-14

Query Match 100.0%; Score 119; DB 18; Length 21;
Best Local Similarity 100.0%; Pred. No. 2, 2e-11;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PSYQFGHNSVDFEEDTLPK 21
Db 1 PSYQFGHNSVDFEEDTLPK 21

RESULT 2
US-10-731-238-9
Sequence 9, Application US/10731238
Publication No. US20050123552A1
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
Pacelli, Joseph M.
House-Pompeo, Karen L.
Speziale, Pietro
John, Danny
McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/731,238
FILING DATE: 10-Dec-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE: 21-Jan-1998
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAMK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>

TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 9:
US-10-731-238-9

Query Match 94.1%; Score 112; DB 18; Length 21;
Best Local Similarity 100.0%; Pred. No. 2, 8e-10;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PSYQFGHNSVDFEEDTLPK 21
Db 2 PSYQFGHNSVDFEEDTLPK 21

RESULT 3
US-11-066-697-1134
Sequence 1134, Application US/11066697
Publication No. US20050187159A1
GENERAL INFORMATION:
APPLICANT: Bridon, Dominique P.
APPLICANT: Ezrin, Alan M.
APPLICANT: Milner, Peter G.
APPLICANT: Holmes, Darren L.
APPLICANT: Thibaudau, Karen
TITLE OF INVENTION: PROTECTION OF ENDOGENOUS THERAPEUTIC PEPTIDES FROM
TITLE OF INVENTION: PEPTIDASE ACTIVITY THROUGH CONJUGATION TO BLOOD
TITLE OF INVENTION: COMPONENTS
FILE REFERENCE: 500862002301
CURRENT APPLICATION NUMBER: US/11/066,697
CURRENT FILING DATE: 2005-02-25
PRIOR APPLICATION NUMBER: 09/657,276
PRIOR FILING DATE: 2000-09-07
PRIOR APPLICATION NUMBER: 60/153,406
PRIOR FILING DATE: 1999-09-10
PRIOR APPLICATION NUMBER: 60/159,783
PRIOR FILING DATE: 1999-10-15
NUMBER OF SEQ ID NOS: 1617
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1134
LENGTH: 37
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-11-066-697-1134

Query Match 94.1%; Score 112; DB 20; Length 37;
Best Local Similarity 100.0%; Pred. No. 5, 1e-10;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PSYQFGHNSVDFEEDTLPK 21
Db 17 PSYQFGHNSVDFEEDTLPK 36

RESULT 4
US-09-813-820-8
Sequence 8, Application US/09813820
Patent No. US20020102262A1
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
Pacelli, Joseph M.
House-Pompeo, Karen
Sthanam, Narayana
Synerisky, Jindrich
TITLE OF INVENTION: COLLAGEN BINDING PROTEIN COMPOSITIONS
AND METHODS OF USE
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: Texas

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; COUNTRY: U.S.
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/813,820
; FILING DATE: 22-Mar-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/856,253
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Kitchell, Barbara S.
; REGISTRATION NUMBER: 33,928
; REFERENCE/DOCKET NUMBER: 7MMK:193
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (512) 418-3000
; TELEFAX: (512) 474-7577
; INFORMATION FOR SEQ ID NO: 8:
; LENGTH: 139 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-09-813-820-8

Query Match      94.1%; Score 112; DB 9; Length 139;
Best Local Similarity 100.0%; Pred. No. 2.2e-09;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 PSYFGGHSVDFEEDTLPK 21
Db      108 PSYFGGHSVDFEEDTLPK 127

RESULT 5
US-09-815-242-5797
; Sequence 5797, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Karl L.
; APPLICANT: Zyckind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; FILE REFERENCE: ELITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version 4.0

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; SEQ ID NO 5797
; LENGTH: 1018
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-09-815-242-5797

Query Match      94.1%; Score 112; DB 9; Length 1018;
Best Local Similarity 100.0%; Pred. No. 1.9e-08;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 PSYFGGHSVDFEEDTLPK 21
Db      838 PSYFGGHSVDFEEDTLPK 857

RESULT 6
US-09-815-242-12838
; Sequence 12838, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Karl L.
; APPLICANT: Zyckind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; FILE REFERENCE: ELITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12838
; LENGTH: 1018
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-09-815-242-12838

Query Match      94.1%; Score 112; DB 9; Length 1018;
Best Local Similarity 100.0%; Pred. No. 1.9e-08;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 PSYFGGHSVDFEEDTLPK 21
Db      838 PSYFGGHSVDFEEDTLPK 857

RESULT 7
US-10-470-048B-68
; Sequence 68, Application US/10470048B
; Publication No. US2005003744A1
; GENERAL INFORMATION:
; APPLICANT: MEINKE ET AL.
; TITLE OF INVENTION: A METHOD FOR IDENTIFICATION, ISOLATION AND PRODUCTION OF
; FILE REFERENCE: SONN.035US

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;; CURRENT APPLICATION NUMBER: US/10/470,048B
;; CURRENT FILING DATE: 2003-07-25
;; NUMBER OF SEQ ID NOS: 603
;; SOFTWARE: PatentIn version 3.1
;; SEQ ID NO 68
;; LENGTH: 1018
;; TYPE: PRF
;; ORGANISM: Staphylococcus aureus
US-10-470-048B-68

Query Match 94.1%; Score 112; DB 17; Length 1018;
Best Local Similarity 100.0%; Pred. No. 1.9e-08;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PSYQFGHNSVDFEEDTLPK 21
DB 838 PSYQFGHNSVDFEEDTLPK 857

RESULT 8
US-08-781-986A-5254
; Sequence 5254, Application US/08781986A
; Publication No. US2003005436A1
; GENERAL INFORMATION:
; APPLICANT: Charles Kunesch
; TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
; NUMBER OF SEQUENCES: 5255
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4MB storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/781,986A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Benson, Bob
; REGISTRATION NUMBER: 30,446
; REFERENCE/DOCKET NUMBER: PB248PP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 5254:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1027 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-781-986A-5254

Query Match 94.1%; Score 112; DB 8; Length 1027;
Best Local Similarity 100.0%; Pred. No. 2e-08;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PSYQFGHNSVDFEEDTLPK 21
DB 847 PSYQFGHNSVDFEEDTLPK 866

RESULT 9
US-10-329-624-5254

;; Sequence 5254, Application US/10329624
;; Publication No. US20040043037A1
;; GENERAL INFORMATION:
;; APPLICANT: Charles Kunesch
;; Gail H. Choi
;; Patrick S. Dillon
;; Craig A. Rosen
;; Steven C. Barash
;; Michael R. Fannon
;; TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
;; NUMBER OF SEQUENCES: 5256
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Human Genome Sciences, Inc.
;; STREET: 9410 Key West Avenue
;; CITY: Rockville
;; STATE: Maryland
;; COUNTRY: USA
;; ZIP: 20850
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Diskette, 3.50 inch, 1.4MB storage
;; COMPUTER: HP Vectra 486/33
;; OPERATING SYSTEM: MSDOS version 6.2
;; SOFTWARE: ASCII Text
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/10/329,624
;; FILING DATE: 27-Dec-2002
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 08/956,171
;; FILING DATE: October 20, 1997
;; APPLICATION NUMBER: 60/009,861
;; FILING DATE: January 5, 1996
;; APPLICATION NUMBER: 08/781,986
;; FILING DATE: January 3, 1997
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Mark J. Hyman
;; REGISTRATION NUMBER: 46,789
;; REFERENCE/DOCKET NUMBER: PB248P1D1
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (240) 314-1224
;; TELEFAX: (301) 309-8439
;; INFORMATION FOR SEQ ID NO: 5254:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 1027 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; SEQUENCE DESCRIPTION: SEQ ID NO: 5254:
US-10-329-624-5254

Query Match 94.1%; Score 112; DB 15; Length 1027;
Best Local Similarity 100.0%; Pred. No. 2e-08;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PSYQFGHNSVDFEEDTLPK 21
DB 847 PSYQFGHNSVDFEEDTLPK 866

RESULT 10
US-10-282-122A-43778
; Sequence 43778, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zykkind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant

```
APPLICANT: Yamamoto, Robert
APPLICANT: Foreyeh, R.
TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REFERENCE: ELITRA.034A
CURRENT FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/230,335
PRIOR FILING DATE: 2000-09-06
PRIOR APPLICATION NUMBER: 60/230,347
PRIOR FILING DATE: 2000-09-09
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/267,636
PRIOR FILING DATE: 2001-02-09
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 78614
SOFTWARE: PatentIn Version 3.1
SEQ ID NO 43778
LENGTH: 961
TYPE: PRT
ORGANISM: Staphylococcus aureus
US-10-282-122A-43778
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Query Match      91.6%; Score 109; DB 15; Length 961;
Best Local Similarity 95.0%; Pred. No. 5.4e-08;
Matches 19; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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OY      2 PSYFGGHSVDFEEDTLPK 21
Db      785 PNYQFGHSVDFEEDTLPK 804
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```
RESULT 11
US-09-815-242-5456
Sequence 5456, Application US/09815242
Patent No. US20020061569A1
GENERAL INFORMATION:
APPLICANT: Haeselbeck, Robert
APPLICANT: Ohlsen, Karl L.
APPLICANT: Zyekind, Judith W.
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John D.
APPLICANT: Carr, Grant J.
APPLICANT: Yamamoto, Robert T.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in
FILE REFERENCE: ELITRA.011A
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
```

```
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SOFTWARE: PatSeq for Windows Version 4.0
SEQ ID NO 5456
LENGTH: 578
TYPE: PRT
ORGANISM: Staphylococcus aureus
US-09-815-242-5456
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```
Query Match      91.6%; Score 109; DB 9; Length 978;
Best Local Similarity 95.0%; Pred. No. 5.5e-08;
Matches 19; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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OY      2 PSYFGGHSVDFEEDTLPK 21
Db      816 PNYQFGHSVDFEEDTLPK 835
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```
RESULT 12
US-09-815-242-12686
Sequence 12686, Application US/09815242
Patent No. US20020061569A1
GENERAL INFORMATION:
APPLICANT: Haeselbeck, Robert
APPLICANT: Ohlsen, Karl L.
APPLICANT: Zyekind, Judith W.
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John D.
APPLICANT: Carr, Grant J.
APPLICANT: Yamamoto, Robert T.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in
FILE REFERENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SOFTWARE: PatSeq for Windows Version 4.0
SEQ ID NO 12686
LENGTH: 1001
TYPE: PRT
ORGANISM: Staphylococcus aureus
US-09-815-242-12686
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Query Match      91.6%; Score 109; DB 9; Length 1001;
Best Local Similarity 95.0%; Pred. No. 5.6e-08;
Matches 19; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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OY      2 PSYFGGHSVDFEEDTLPK 21
Db      839 PNYQFGHSVDFEEDTLPK 858
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RESULT 13
US-10-282-122A-43827
Sequence 43827, Application US/10282122A
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Publication No. US20040029129A1
GENERAL INFORMATION:
APPLICANT: Wang, Liangou
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari
APPLICANT: Zyskind, Judith
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John
APPLICANT: Carr, Grant
APPLICANT: Yamamoto, Robert
APPLICANT: Forsyth, R.
APPLICANT: Xu, H.
TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REFERENCE: ELITRA 03A US/10/282,122A
CURRENT FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/230,335
PRIOR FILING DATE: 2000-09-06
PRIOR APPLICATION NUMBER: 60/230,347
PRIOR FILING DATE: 2000-09-09
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/267,636
PRIOR FILING DATE: 2001-02-09
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 78614
SOFTWARE: Patent version 3.1
SEQ ID NO 43827
LENGTH: 1038
TYPE: PRT
ORGANISM: Staphylococcus aureus
US-10-282-122A-43827
Query Match 91.6%; Score 109; DB 15; Length 1038;
Best Local Similarity 95.0%; Pred. No. 5,8e-08;
Matches 19; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 2 PSYQFGHNSVDFEEDTLPK 21
|:|||||||||||||||
Db 834 PNYQFGHNSVDFEEDTLPK 853
RESULT 14
US-10-731-238-16
Sequence 16, Application US/10731238
Publication No. US20050123552A1
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
Patli, Joseph M.
House-Pompeo, Karen L.
Speziale, Pietro
Joh, Danny
McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433

CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/731,238
FILING DATE: 10-Dec-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE: 21-Jan-1998
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TANK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 16:
US-10-731-238-16
Query Match 89.9%; Score 107; DB 18; Length 21;
Best Local Similarity 95.0%; Pred. No. 1.7e-09;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2 PSYQFGHNSVDFEEDTLPK 21
|:|||||||||||||||
Db 2 PNYQFGHNSVDFEEDTLPK 21
RESULT 15
US-10-731-238-23
Sequence 23, Application US/10731238
Publication No. US20050123552A1
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
Patli, Joseph M.
House-Pompeo, Karen L.
Speziale, Pietro
Joh, Danny
McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/731,238
FILING DATE: 10-Dec-2003
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE: 21-Jan-1998
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAMK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 23:
US-10-731-238-23

Query Match 89.9%; Score 107; DB 18; Length 21;
Best Local Similarity 95.0%; Pred. No. 1.7e-09;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2 PSYQFGGHSVDFEEDTLPK 21
DB 2 PSYQFGGHNPDVDFEEDTLPK 21

Search completed: October 22, 2005, 11:34:38
Job time : 59.2367 secs

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OM protein - protein search, using SW model

Run on: October 22, 2005, 02:23:36 ; Search time 10.5465 Seconds
(without alignments)
191.586 Million cell updates/sec

Title: US-10-731-238-14
Perfect score: 119
Sequence: 1 PPSYQFGHNSVDFEEDTLRK 21

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	112	94.1	1018	2 A32192	fibronectin-binding
2	109	91.6	961	2 G90053	hypothetical prote
3	109	91.6	1038	2 H90053	hypothetical prote
4	105	88.2	940	2 S19702	fibronectin-binding
5	54	45.4	387	2 I38449	extracellular prot
6	51	42.9	303	2 B75485	fructokinase - Del
7	49	41.3	474	2 B84357	serine-tRNA synthe
8	48	40.3	468	2 T26081	hypothetical prote
9	47	39.5	347	1 HPMS	haploglobin precu
10	47	38.7	574	2 T48113	inositol-1,4,5-tri
11	46	38.5	257	2 A36057	MHC class I histoc
12	46	38.7	453	2 G69494	DNA helicase homol
13	46	38.7	453	2 H70333	conserved hypochet
14	45.5	38.2	1038	2 T15098	hypothetical prote
15	45	37.8	216	2 A3926	hypothetical prote
16	45	37.8	462	1 A39356	3-oxoacyl-l-acyl-ca
17	45	37.8	469	2 T10061	myosin heavy chain
18	45	37.8	1322	2 A59288	related to gastric
19	45	37.8	1331	2 T49813	sp18 (Bacteriophag
20	44.5	37.4	345	2 AB1448	probable secreted
21	44.5	37.4	417	2 T34930	3-phosphoshikimate
22	44	37.0	427	2 D95159	3-phosphoshikimate
23	44	37.0	431	2 D98025	vesicle-associated
24	44	37.0	433	2 T01405	beta-amy-lase (EC 3
25	44	37.0	548	2 T52556	hypothetical prote
26	44	37.0	705	2 C84406	conserved hypochet
27	44	37.0	808	2 F81180	DNA-binding nuclea
28	44	37.0	1926	2 JC4842	probable receptor-
29	43.5	36.6	646	2 B84852	

30	43.5	36.6	1097	2 T31504	hypothetical prote
31	43	36.1	551	2 S57447	HPBRII-7 protein -
32	43	36.1	928	1 VGBEMC	glycoprotein B pre
33	42	35.3	157	2 AP2708	conserved hypochet
34	42	35.3	157	2 G97490	hypothetical prote
35	42	35.3	177	2 A86610	frame-shift with C
36	42	35.3	197	2 C69779	NAD(P)H oxidoreduc
37	42	35.3	222	2 S74066	hypothetical prote
38	42	35.3	282	2 G72369	hemk protein - The
39	42	35.3	322	2 D95078	transcription regu
40	42	35.3	329	2 H83099	probable oxidoredu
41	42	35.3	331	2 T51419	CARBONIC ANHYDRASE
42	42	35.3	336	1 S28412	carbonate dehydrat
43	42	35.3	348	2 A97946	regulatory functio
44	42	35.3	349	2 H82116	flagellar motor sw
45	42	35.3	371	2 A86520	41.8K hypothetical

ALIGNMENTS

RESULT 1

A32192
fibronectin-binding protein - Staphylococcus aureus
C/Species: Staphylococcus aureus
C/Date: 31-Jul-1989 #sequence_revision 31-Jul-1989 #ext_change 16-Feb-1997
C/Accession: A32192
R/Signaes, C.; Raucel, G.; Joensson, K.; Lindgren, P.E.; Anantharamiah, G.M.; Hoeck, M.
Proc. Natl. Acad. Sci. U.S.A. 86, 699-703, 1989
A/Title: Nucleotide sequence of the gene for a fibronectin-binding protein from Staphyloc
A/Reference number: A32192; PMID:8908998; PMID:2521391
A/Accession: A32192
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-1018 <SIG>
A/Cross-references: GB:J04151
C/Keywords: fibronectin binding

Query Match 94.1%; Score 112; DB 2; Length 1018;
Best Local Similarity 100.0%; Pred. No. 2.9e-09;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PPSYQFGHNSVDFEEDTLRK 21

DB 838 PPSYQFGHNSVDFEEDTLRK 857

RESULT 2

G90053
hypothetical protein fmb (imported) - Staphylococcus aureus (strain N315)
C/Species: Staphylococcus aureus
C/Date: 10-May-2001 #sequence_revision 10-May-2001 #ext_change 09-Jul-2004
C/Accession: G90053
R/Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguci
ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.; i
C.; Shibui, T.; Hattori, M.; Ogatawara, N.; Hayashi, H.; Hiratacshu, K.
Lancet 357, 1225-1240, 2001
A/Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.
A/Reference number: A89758; PMID:21311952; PMID:11418146
A/Accession: G90053
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-961 <KUR>
A/Cross-references: UNIPROT:Q99RD3; GB:BA000018; PID:G13702452; PIDN:BA843593.1; GSPDB:G
A/Experimental source: strain N315
C/Genetics:
A/Gene: fmb

Query Match 91.6%; Score 109; DB 2; Length 961;
Best Local Similarity 95.0%; Pred. No. 8.2e-09;
Matches 19; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 PPSYQFGHNSVDFEEDTLRK 21

Db 785 PNYQFGHNSVDFEEDTLRK 804

RESULT 3

H90053

C:Species: Staphylococcus aureus (strain N315)

C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004

C:Accession: H90053

R:Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Ogura, A.; Mizutani-Uji, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kato, C.; Sekimizu, K.; C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramoto, K. Lancet 357, 1225-1240, 2001

A:Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.

A:Reference number: A89758; UID:21311952; PMID:11418146

A:Accession: H90053

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-1038 <K1B>

A:Cross-references: UNIPROT:Q99RD2; GB:BA000018; PID:g13702453; PIDN:BA843594.1; GSPDB:C

A:Experimental source: strain N315

C:Genetics:

A:Gene: fnb

Query Match 91.6%; Score 109; DB 2; Length 1038;
Best Local Similarity 95.0%; Pred. No. 8.9e-09;
Matches 19; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 PSYQFGHNSVDFEEDTLRK 21

Db 834 PNYQFGHNSVDFEEDTLRK 853

RESULT 4

S19702

C:Species: Staphylococcus aureus

C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004

C:Accession: S19702

R:Joensson, K.; Signae, C.; Mueller, H.P.; Lindberg, M. Eur. J. Biochem. 202, 1041-1048, 1991

A:Title: Two different genes encode fibronectin binding proteins in Staphylococcus aureus

A:Reference number: S19702; UID:92111475; PMID:1837266

A:Accession: S19702

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-940 <JOE>

A:Cross-references: UNIPROT:Q53682; EMBL:X62992; NID:g49040; PIDN:CAA44726.1; PID:g58156

C:Keywords: fibronectin binding

Query Match 88.2%; Score 105; DB 2; Length 940;
Best Local Similarity 90.0%; Pred. No. 3.4e-08;
Matches 18; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 PSYQFGHNSVDFEEDTLRK 21

Db 774 PNYQFGHNSVDFEEDTLRK 793

RESULT 5

I38449

C:Species: Homo sapiens (man)

C:Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 21-Jul-2000

C:Accession: I38449

R:Lecka-Czerwik, B.; Lumpkin, C.K. Mol. Cell. Biol. 15, 120-128, 1995

A:Title: An overexpressed gene transcript in senescent and quiescent human fibroblasts

A:Reference number: I38449; UID:95087983; PMID:7799918

A:Accession: I38449

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-387 <RES>
A:Cross-references: EMBL:U03877; NID:g458227; PIDN:AAA65590.1; PID:g458228
C:Genetics:
A:Gene: SI-5

Query Match 45.4%; Score 54; DB 2; Length 387;
Best Local Similarity 50.0%; Pred. No. 1.3;
Matches 10; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

QY 1 PSYQFGHNSVDFEEDTLRK 20

Db 96 PBYQKRGQGVCDIDECTIP 115

RESULT 6

B75485

C:Species: Deinococcus radiodurans (strain R1)

C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004

C:Accession: B75485

R:White, O.; Eichen, J.A.; Heideberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.; Smith, H.O.; Venter, J.C.; Fraser, C.M. Science 286, 1571-1577, 1999

A:Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.

A:Reference number: A75250; UID:20036896; PMID:10567266

A:Accession: B75485

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-303 <WH1>

A:Cross-references: UNIPROT:Q9RWE1; GB:AE001928; GB:AE000513; NID:g6458421; PIDN:AAF10301

A:Experimental source: strain R1

C:Genetics:

A:Gene: DR0728

A:Map position: 1

A:Superfamily: ribokinase

Query Match 42.9%; Score 51; DB 2; Length 303;
Best Local Similarity 50.0%; Pred. No. 2.9;
Matches 11; Conservative 2; Mismatches 7; Indels 2; Gaps 1;

QY 1 PSYQFGHNSVD--FEEDTLRK 20

Db 93 PBYRFLGNSDLHFDPTLRP 114

RESULT 7

B84357

C:Species: Halobacterium sp. NRC-1

C:Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004

C:Accession: B84357

R:King, M.V.; Kennedy, S.P.; Mahairas, G.G.; Bergquist, B.; Pan, M.; Shukla, H.D.; Laaky, S.; Leithausen, B.; Keller, K.; Cruz, R.; Danon, M.J.; Hough, D.W.; Maddocks, D.G.; Jablor Jung, K.H.; Alam, M.; Freitas, T. Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000

A:Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ehardt, H.; Lowe, T.M.; Li

A:Title: Genome sequence of Halobacterium species NRC-1

A:Reference number: A84160; UID:20504483; PMID:11016950

A:Accession: B84357

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-474 <STO>

A:Cross-references: UNIPROT:Q9HNU8; GB:AE004437; NID:g10581491; PIDN:AA020222.1; GSPDB:G

C:Genetics:

A:Gene: sers

A:Superfamily: serine-tRNA ligase

Query Match 41.2%; Score 49; DB 2; Length 474;
Best Local Similarity 41.2%; Pred. No. 9.9;
Matches 7; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 3 SYQFGHNSVDFEEDTLRK 19

Db 22 GNDAMDFEDDSCPK 35

108 YCEGENDVAENSDTI. 123

A; Status: preliminary; nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA

A:Residues: 1-453 <KLE>
A:Cross-references: UNIPROT:Q28319; GB:AE000968; GB:AE000782; NID:G2689291; PIDN:AA8929

Query Match 38.7%; Score 46; DB 2; Length 453;
Best Local Similarity 50.0%; Pred. No. 28;
Matches 7; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 PSYFGHNSVDF 14
DB 230 PVEVGHKAKF 243

RESULT 13

H70333
conserved hypothetical protein aq_378 - Aquifex aeolicus

C:Species: Aquifex aeolicus
C:Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 09-Jul-2004
C:Accession: H70333

R:Decker, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.; Oy

V. Nature 392, 353-358, 1998

A:Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.

A:Reference number: A70300; WUID:98196666; PMID:9537320

A:Accession: H70333

A:Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-453 <NOF>

A:Cross-references: UNIPROT:Q66700; GB:AE000687; NID:G2983050; PIDN:AA06670.1; PID:G298

A:Experimental source: strain VFS

C:Genetics:

A:Gene: aq_378

Query Match 38.7%; Score 46; DB 2; Length 453;
Best Local Similarity 53.8%; Pred. No. 28;
Matches 7; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 3 SYFGHNSVDF 15
DB 114 SYFGSYNLEF 126

RESULT 14

T15098

hypothetical protein T22B11.5 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004

C:Accession: T15098

R:Rohlfing, T.; Wohldmann, P.

submitted to the EMBL Data Library, December 1997

A:Description: The sequence of C. elegans cosmid T22B11.

A:Reference number: Z18292

A:Accession: T15098

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-1038 <ROH>

A:Cross-references: UNIPROT:Q61199; EMBL:AF039040; NID:G2736374; PID:G2736379; PIDN:AA89

A:Experimental source: strain Bristol NZ; clone T22B11

C:Genetics:

A:Gene: CESP:T22B11.5

A:Map position: 4

A:introns: 45/3; 128/2; 225/3; 659/3; 707/3; 820/3; 969/3

C:Superfamily: oxoglutarate dehydrogenase (lipoamide); thiamin pyrophosphate-binding dom

F:420-465/Domain: thiamin pyrophosphate-binding domain homology <TPB>

Query Match 38.2%; Score 45.5; DB 2; Length 1038;
Best Local Similarity 37.0%; Pred. No. 83;
Matches 10; Conservative 3; Mismatches 5; Indels 9; Gaps 1;

QY 3 SYFGHNSVDF-----EDTLP 20
DB 156 SYTRGHNIADDPGINSADDDTIP 182

RESULT 15

A39926
hypothetical protein 1 - chicken anemia virus

C:Species: chicken anemia virus, CAV

C:Date: 17-Jan-1992 #sequence_revision 17-Jan-1992 #text_change 09-Jul-2004

C:Accession: A39926

R:Notborn, M.H.M.; de Boer, G.F.; van Roozelaar, D.J.; Karreman, C.; Kranenburg, O.; Vo

J. Virol. 65, 3131-3139, 1991

A:Title: Characterization of cloned chicken anemia virus DNA that contains all elements f

A:Reference number: A39926; WUID:91237831; PMID:1851873

A:Accession: A39926

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-216 <NOT>

A:Cross-references: UNIPROT:Q99151; GB:M55918; NID:G323250; PIDN:AAA91822.1; PID:G323251

C:Comment: This virus is unclassified.

Query Match 37.8%; Score 45; DB 2; Length 216;
Best Local Similarity 56.2%; Pred. No. 18;
Matches 9; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 2 PSYFGHNSVDFEED 17
DB 172 PSEEDGTTSSDFEDD 187

Search completed: October 22, 2005, 04:13:46
Job time : 13.5465 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 22, 2005, 02:23:35 ; Search time 51.4314 Seconds
(without alignments)
209.087 Million cell updates/sec

Title: US-10-731-238-14
Perfect score: 119
Sequence: 1 PPSYOGCHNSVDPEEDLPK 21

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database: UniProt_03:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	112	94.1	1018	1 FNBA STAU	P14738 staphylococ
2	109	91.6	961	2 Q99RD3	Q99RD3 staphylococ
3	109	91.6	961	2 Q7A318	Q7A318 staphylococ
4	109	91.6	965	2 Q6GDU5	Q6GDU5 staphylococ
5	109	91.6	1015	2 Q8NUU7	Q8NUU7 staphylococ
6	109	91.6	1015	2 Q6G6H3	Q6G6H3 staphylococ
7	109	91.6	1038	2 Q99RD2	Q99RD2 staphylococ
8	109	91.6	1038	2 Q7A317	Q7A317 staphylococ
9	105	88.2	940	2 Q51682	Q51682 staphylococ
10	105	88.2	943	2 Q8NUH8	Q8NUH8 staphylococ
11	105	88.2	957	2 Q6G6H4	Q6G6H4 staphylococ
12	100	84.0	152	2 Q9AEP9	Q9AEP9 staphylococ
13	54	45.4	493	1 FBL3 HUMAN	Q12805 homo sapien
14	54	45.4	493	2 Q7YOD7	Q7YOD7 macaca fasc
15	51	42.9	303	2 Q9RWE1	Q9RWE1 deinococcus
16	50	42.0	245	2 Q08866	Q08866 carassius a
17	50	42.0	305	2 Q7NY51	Q7NY51 chromobacte
18	49	41.2	302	2 Q62EN4	Q62EN4 butkholideri
19	49	41.2	302	2 Q63Y68	Q63Y68 butkholideri
20	49	41.2	307	2 Q8XOE7	Q8XOE7 ralsconia s
21	49	41.2	460	1 SYS HALNI	Q96cb9 halobacteri
22	49	41.2	469	2 Q6DCB9	Q6DCB9 xenopus lae
23	49	41.2	1726	2 Q6G4Z9	Q6G4Z9 bartonella
24	48	40.3	229	2 Q8HLQ8	Q8HLQ8 diretmoide
25	48	40.3	319	2 Q8SYW6	Q8SYW6 gossypium h
26	48	40.3	326	2 Q8LSC8	Q8LSC8 gossypium h
27	48	40.3	398	2 Q658L1	Q658L1 homo sapien
28	48	40.3	465	2 Q6PFM2	Q6PFM2 bartonella
29	48	40.3	468	2 Q9XUB2	Q9XUB2 caenorhabdi
30	48	40.3	772	2 Q9ADU3	Q9ADU3 streptomyce
31	47	39.5	296	2 Q6PBC9	Q6PBC9 xenopus tro

ALIGNMENTS

RESULT 1	FNBA STAU	STANDARD;	PRT;	1018 AA.
AC	P14738;			
DT	01-APR-1990 (Rel. 14, Created)			
DT	01-APR-1990 (Rel. 14, Last sequence update)			
DT	25-OCT-2004 (Rel. 45, Last annotation update)			
DE	Fibronectin-binding protein precursor (FNBP).			
GN	Name=fnbp;			
OS	Staphylococcus aureus.			
OC	Bacteria; Firmicutes; Bacillales; Staphylococcus.			
OX	NCBI_TaxID=1280;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=NCTC 8325-4;			
RX	MEDLINE=8908998; PubMed=2521391;			
RA	Signes C., Raucel G., Joensen K., Lindgren P.-E.,			
RA	Amantcharatmah G.M., Hoeck M., Lindberg M.,			
RT	Nucleotide sequence of the gene for a fibronectin-binding protein			
RT	from Staphylococcus aureus: use of this peptide sequence in the			
RT	synthesis of biologically active peptides."			
RL	Proc. Natl. Acad. Sci. U.S.A. 86:699-703(1989).			
CC	-1- FUNCTION: The ability of bacteria to bind fibronectin has been			
CC	proposed as a virulence factor enabling bacteria to colonize wound			
CC	tissues and blood clots. Binding of plasma fibronectin to the			
CC	bacterial surface might block adhesion receptors on S.aureus, thus			
CC	representing an important defense mechanism against tissue			
CC	invasion.			
CC	-1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by			
CC	an amide bond (Potential).			
CC	-----			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration			
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -			
CC	the European Bioinformatics Institute. There are no restrictions on its			
CC	use by non-profit institutions as long as its content is in no way			
CC	modified and this statement is not removed. Usage by and for commercial			
CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/			
CC	or send an email to license@isb-sib.ch).			
CC	-----			
DR	EMBL: J04151; AAA2632.1; -			
DR	InterPro: IPR004237; Fn_bind.			
DR	InterPro: IPR005877; Gpos_YsIRK.			
DR	InterPro: IPR001899; Gram_pos_anchor.			
DR	Pfam: PF02986; Fn_bind. 1.			
DR	Pfam: PF00746; Gram_pos_anchor. 1.			
DR	Pfam: PF04650; YsIRK_signal. 1.			
DR	TIGRFAMs: TIGR01167; LpxTG_anchor. 1.			
DR	TIGRFAMs: TIGR01168; YsIRK_signal. 1.			
DR	PROSITE: PS50847; GRAM_POS_ANCHORING. 1.			
KW	Cell adhesion; Cell wall; Peptidoglycan-anchor; Repeat; Signal;			
KW	Virulence.			
FT	SIGNAL	1	36	
FT	CHAIN	37	985	Fibronectin-binding protein.
FT	PROPEP	986	1018	Removed by sortase (Potential).

32	47	39.5	347	1	HPT MOUSE	Q61646 mus musculu
33	47	39.5	347	1	HPT_MUSCR	Q60574 mus caroli
34	47	39.5	347	1	HPT_MUOSA	Q62558 mus saxicol
35	47	39.5	347	2	Q63927	Q63927 mus sp. nap
36	47	39.5	392	2	Q64PS5	Q64PS5 bacterioides
37	47	39.5	394	2	Q8BOB6	Q8BOB6 mus musculu
38	47	39.5	482	2	Q76K22	Q76K22 streptococc
39	47	39.5	547	2	Q8GT50	Q8GT50 streptococc
40	47	39.5	574	2	Q9M1W5	Q9M1W5 arabidopsis
41	47	39.5	608	2	Q7QP79	Q7QP79 gliardia lam
42	46	38.7	58	2	Q8BAG9	Q8BAG9 chicken ane
43	46	38.7	118	2	Q91N88	Q91N88 chicken ane
44	46	38.7	118	2	Q91N94	Q91N94 chicken ane
45	46	38.7	118	2	Q91N96	Q91N96 chicken ane

```

FT REPEAT 545 574 B-1.
FT REPEAT 575 604 B-2.
FT DOMAIN 745 878 4 X approximate tandem repeats,
  fibronectin-binding domain.
FT REPEAT 745 782 D-1.
FT REPEAT 783 820 D-2.
FT REPEAT 821 859 D-3.
FT DOMAIN 860 878 D-4 (incomplete).
FT REPEAT 879 948 5 X tandem repeats, pro-rich (WR).
FT REPEAT 879 892 WR 1.
FT REPEAT 893 906 WR 2.
FT REPEAT 907 920 WR 3.
FT REPEAT 921 934 WR 4.
FT REPEAT 935 948 WR 5.
FT SITE 982 986 LpXTG sorting signal (potential).
FT MOD_RES 985 985 Pentaglycyl murein peptidoglycan amidated
  threonine (Potential).
SQ SEQUENCE 1018 AA; 111780 MM; 58175E020E81F1F CRC64;

Query Match 94.1%; Score 112; DB 1; Length 1018;
Best Local Similarity 100.0%; Pred. No. 2.5e-08;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 PSYQFGHNSVDFEEDTLPK 21
Db 838 PSYQFGHNSVDFEEDTLPK 857

RESULT 2
Q99RD3 PRELIMINARY; PRT; 961 AA.
ID Q99RD3;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 24, Last sequence update)
DE Fibronectin-binding protein homolog.
GN Name=fNB; Ordered locusNames=SAV2502;
OS Staphylococcus aureus (strain Mu50 / ATCC 700699).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=158878;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Mu50 / ATCC 700699;
RX MEDLINE=21111952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2;
  Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
  Cui L., Oguchi A., Aoki K.-I., Nagai Y., Lian J.-Q., Ito T.,
  Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hoshiyama A.,
  Mizutani-Ul Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
  Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
  Hatori M., Ogasawara N., Hayaishi H., Hiramatsu K.;
  "Whole genome sequencing of methicillin-resistant Staphylococcus
  aureus.";
  Lancet 357:1225-1240(2001).
  -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
    an amide bond (By similarity).
CC EMBL; AP003365; BAB58664.1; -.
CC PIR; G90053; G90053.
DR HSSP; O53653; IN67.
DR GO; GO:0009986; C:cell surface; IEA.
DR GO; GO:0005618; C:cell wall; IEA.
DR GO; GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:007155; P:cell adhesion; IEA.
DR InterPro; IPR008966; Adhes_Bact.
DR InterPro; IPR004237; Fn_bind.
DR InterPro; IPR005877; Gpos_YsIRK.
DR InterPro; IPR001899; Gram_pos_anchor.
DR Pfam; PF00746; Gram_pos_anchor; 1.
DR Pfam; PF04650; YsIRK_signal; 1.
DR TIGRfam; TIGR01167; LpXTG_anchor; 1.
DR TIGRfam; TIGR01168; YsIRK_signal; 1.

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DR PROSITE; PS50847; GRAM_POS_ANCHORING; 1.
KW Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ SEQUENCE 961 AA; 106010 MM; 364940F884EA4101 CRC64;

Query Match 91.6%; Score 109; DB 2; Length 961;
Best Local Similarity 95.0%; Pred. No. 6.7e-08;
Matches 19; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 PSYQFGHNSVDFEEDTLPK 21
Db 785 PSYQFGHNSVDFEEDTLPK 804

RESULT 3
Q7A3J8 PRELIMINARY; PRT; 961 AA.
ID Q7A3J8;
AC Q7A3J8;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE FNB protein.
GN Name=fNB; Ordered locusNames=SA2220;
OS Staphylococcus aureus (strain N315).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=158879;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21111952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2;
  Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
  Cui L., Oguchi A., Aoki K.-I., Nagai Y., Lian J.-Q., Ito T.,
  Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hoshiyama A.,
  Mizutani-Ul Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
  Kanemizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
  Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
  Hatori M., Ogasawara N., Hayaishi H., Hiramatsu K.;
  "Whole genome sequencing of methicillin-resistant Staphylococcus
  aureus.";
  Lancet 357:1225-1240(2001).
  -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
    an amide bond (By similarity).
CC EMBL; AP003137; BAB45593.1; -.
DR GO; GO:0009986; C:cell surface; IEA.
DR GO; GO:0005618; C:cell wall; IEA.
DR GO; GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:007155; P:cell adhesion; IEA.
DR InterPro; IPR008966; Adhes_Bact.
DR InterPro; IPR004237; Fn_bind.
DR InterPro; IPR005877; Gpos_YsIRK.
DR InterPro; IPR001899; Gram_pos_anchor.
DR Pfam; PF00746; Gram_pos_anchor; 1.
DR Pfam; PF04650; YsIRK_signal; 1.
DR TIGRfam; TIGR01167; LpXTG_anchor; 1.
DR TIGRfam; TIGR01168; YsIRK_signal; 1.
DR PROSITE; PS50847; GRAM_POS_ANCHORING; 1.
KW Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ SEQUENCE 961 AA; 106010 MM; 364940F884EA4101 CRC64;

Query Match 91.6%; Score 109; DB 2; Length 961;
Best Local Similarity 95.0%; Pred. No. 6.7e-08;
Matches 19; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 PSYQFGHNSVDFEEDTLPK 21
Db 785 PSYQFGHNSVDFEEDTLPK 804

RESULT 4
Q6GDU5 PRELIMINARY; PRT; 965 AA.
ID Q6GDU5;
AC Q6GDU5;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)

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DT 05-JUL-2004 (TrEMBLrel. 27, last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, last annotation update)
DE Fibronectin-binding protein.
GN Name=fndA; OrderedLocustNames=SA2580;
OS Staphylococcus aureus (strain MSSA52).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=282458;
[1]
SEQUENCE FROM N.A.
RX PubMed=15213324; DOI=10.1073/pnas.0402521101;
RA Holden M.T.G., Fell E.J., Lindsay J.A., Peacock S.J., Day N.P.J.,
RA Enright M.C., Foster T.J., Moore C.E., Hurst L., Atkin R., Barron A.,
RA Bason N., Bentley S.D., Chillingworth C., Chillingworth T.,
RA Churcher C., Clark L., Corton C., Cronin A., Doggett J., Dowd L.,
RA Felwell T., Hance Z., Harris B., Hauser H., Holtroyd S., Jagsels K.,
RA James K.D., Lennard N., Line A., Mayes R., Moule S., Mungall K.,
RA Ormond D., Quail M.A., Rabinowitsch E., Rutherford K.M., Sanders M.,
RA Sharp B.G., Simmonds M., Stevens K., Whitehead S., Barrett B.G.,
RA Spratt B.G., Parkhill J.;
RT "Complete genomes of two clinical Staphylococcus aureus strains:
RT evidence for the rapid evolution of virulence and drug resistance.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:9786-9791(2004).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
an amide bond (By similarity).
EMBL: BX571856; CAG41560.1; -.
DR GO: GO:0009986; C:cell surface; IEA.
DR GO: GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO: GO:0016020; C:membrane; IEA.
DR GO: GO:0007155; P:cell adhesion; IEA.
DR InterPro: IPR008966; Adhes. Bact.
DR InterPro: IPR004237; Fn_bind.
DR InterPro: IPR005877; Gpos_YsIRK.
DR InterPro: IPR001899; Gram_pos_anchor.
DR Pfam: PF02986; Fn_bind. 1.
DR Pfam: PF00746; Gram_pos_anchor. 1.
DR Pfam: PF04650; YsIRK_signal. 1.
DR TIGRPFAMs: TIGR01167; LPXTG_anchor. 1.
DR TIGRPFAMs: TIGR01168; YsIRK_signal. 1.
DR PROSITE: PS50847; GRAM_POS_ANCHORING. 1.
KW Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ
SEQUENCE 965 AA; 105691 MW; 2982E132164D0551 CRC64;

Query Match 91.6%; Score 109; DB 2; Length 965;
Best Local Similarity 95.0%; Pred. No. 6.8e-08;
Matches 19; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 PSYQFGHNSVDFEEDTLPK 21
Db 803 PNYQFGHNSVDFEEDTLPK 822

RESULT 5
Q8NUU7 PRELIMINARY; PRT; 1015 AA.
ID Q8NUU7;
AC Q8NUU7;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, last annotation update)
DE Fnb protein.
GN Name=fnb; OrderedLocustNames=NM2421;
OS Staphylococcus aureus (strain MW2).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=196620;
[1]
SEQUENCE FROM N.A.
RX STRAIN=NM2;
RX MEDLINE=22040717; PubMed=12044378; DOI=10.1016/S0140-6736(02)08713-5;
RA Baba T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Ogunuchi A.,
RA Nagai Y., Iwama N., Asano K., Naito T., Kuroda H., Cui L.,
RA Yamamoto K., Hiramatsu K.;
RT "Genome and virulence determinants of high virulence community-
RT acquired MRSA.";
RL Lancet 359:1819-1827(2002).
```

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CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
an amide bond (By similarity).
EMBL: AP004830; BAB96286.1; -.
DR GO: GO:0009986; C:cell surface; IEA.
DR GO: GO:0005618; C:cell wall; IEA.
DR GO: GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO: GO:0016020; C:membrane; IEA.
DR GO: GO:0007155; P:cell adhesion; IEA.
DR InterPro: IPR008966; Adhes. Bact.
DR InterPro: IPR004237; Fn_bind.
DR InterPro: IPR005877; Gpos_YsIRK.
DR InterPro: IPR001899; Gram_pos_anchor.
DR Pfam: PF02986; Fn_bind. 1.
DR Pfam: PF00746; Gram_pos_anchor. 1.
DR Pfam: PF04650; YsIRK_signal. 1.
DR TIGRPFAMs: TIGR01167; LPXTG_anchor. 1.
DR TIGRPFAMs: TIGR01168; YsIRK_signal. 1.
DR PROSITE: PS50847; GRAM_POS_ANCHORING. 1.
KW Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ
SEQUENCE 1015 AA; 111145 MW; D0F9281BB64D44D2 CRC64;

Query Match 91.6%; Score 109; DB 2; Length 1015;
Best Local Similarity 95.0%; Pred. No. 7.2e-08;
Matches 19; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 PSYQFGHNSVDFEEDTLPK 21
Db 839 PNYQFGHNSVDFEEDTLPK 858

RESULT 6
Q6G6H3 PRELIMINARY; PRT; 1015 AA.
ID Q6G6H3;
AC Q6G6H3;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, last annotation update)
DE Fibronectin-binding protein.
GN Name=fndA; OrderedLocustNames=SA2580;
OS Staphylococcus aureus (strain MSSA476).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=282459;
[1]
SEQUENCE FROM N.A.
RX PubMed=15213324; DOI=10.1073/pnas.0402521101;
RA Holden M.T.G., Fell E.J., Lindsay J.A., Peacock S.J., Day N.P.J.,
RA Enright M.C., Foster T.J., Moore C.E., Hurst L., Atkin R., Barron A.,
RA Bason N., Bentley S.D., Chillingworth C., Chillingworth T.,
RA Churcher C., Clark L., Corton C., Cronin A., Doggett J., Dowd L.,
RA Felwell T., Hance Z., Harris B., Hauser H., Holtroyd S., Jagsels K.,
RA James K.D., Lennard N., Line A., Mayes R., Moule S., Mungall K.,
RA Ormond D., Quail M.A., Rabinowitsch E., Rutherford K.M., Sanders M.,
RA Sharp B.G., Simmonds M., Stevens K., Whitehead S., Barrett B.G.,
RA Spratt B.G., Parkhill J.;
RT "Complete genomes of two clinical Staphylococcus aureus strains:
RT evidence for the rapid evolution of virulence and drug resistance.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:9786-9791(2004).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
an amide bond (By similarity).
EMBL: BX571857; CAG4202.1; -.
DR GO: GO:0009986; C:cell surface; IEA.
DR GO: GO:0005618; C:cell wall; IEA.
DR GO: GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO: GO:0016020; C:membrane; IEA.
DR GO: GO:0007155; P:cell adhesion; IEA.
DR InterPro: IPR008966; Adhes. Bact.
DR InterPro: IPR004237; Fn_bind.
DR InterPro: IPR005877; Gpos_YsIRK.
DR InterPro: IPR001899; Gram_pos_anchor.
DR Pfam: PF02986; Fn_bind. 1.
DR Pfam: PF00746; Gram_pos_anchor. 1.
DR Pfam: PF04650; YsIRK_signal. 1.
DR TIGRPFAMs: TIGR01167; LPXTG_anchor. 1.
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DR TIGRFAMS; TIGR01168; YSIK signal; 1.
DR PROSITE; PS50847; GRAM_POS_ANCHORING; 1.
KW Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ SEQUENCE 1015 AA; 11145 MW; D0F9281B64D44D2 CRC64;

Query Match

91.6%; Score 109; DB 2; Length 1015;

Best Local Similarity 95.0%; Pred. No. 7, 2e-08;
Matches 19; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 PSYQFGHNSVDFEEDTLRK 21

DB 839 PNYQFGHNSVDFEEDTLRK 858

RESULT 7

Q99RD2 PRELIMINARY; PRT; 1038 AA.

AC Q99RD2; 01-JUN-2001 (TREMblrel. 17, Created)
DT 01-JUN-2001 (TREMblrel. 17, Last sequence update)
DT 01-MAR-2004 (TREMblrel. 26, Last annotation update)
DE Fibronectin-binding protein homolog.
GN Name=fnb; OrderedLocustNames=SAV2503;
OS Staphylococcus aureus (strain Mu50 / ATCC 700699).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxId=158878;

RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Mu50 / ATCC 700699;
RX MEDLINE=21311952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2;
RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Iian J.-O., Ito T.,
RA Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,
RA Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
RA Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
RA Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
RA Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
RT "Whole genome sequencing of methicillin-resistant Staphylococcus
RT aureus";
RL Lancel 357,1225-1240(2001).

CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
an amide bond (By similarity).
CC EMBL, AP003137; BAB43594.1; -.

DR PIR; H90053; H90053.
DR GO; GO:0009986; C:cell surface; IEA.
DR GO; GO:0005618; C:cell wall; IEA.
DR GO; GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0007155; P:cell adhesion; IEA.
DR InterPro; IPR008966; Adhes_bact.
DR InterPro; IPR004237; Fn_bind.
DR InterPro; IPR005877; Gpos_YSIRK.
DR InterPro; IPR001899; Gram_pos_anchor.
DR Pfam; PF02986; Fn_bind. 1.
DR Pfam; PF00746; Gram_pos_anchor. 1.
DR Pfam; PF04650; YSIK signal. 1.
DR TIGRFAMS; TIGR01167; LpxTG anchor. 1.
DR TIGRFAMS; TIGR01168; YSIK signal. 1.
DR PROSITE; PS50847; GRAM_POS_ANCHORING; 1.
KW Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ SEQUENCE 1038 AA; 113618 MW; 666BF6BF2BFEB12 CRC64;

Query Match 91.6%; Score 109; DB 2; Length 1038;

Best Local Similarity 95.0%; Pred. No. 7, 3e-08;
Matches 19; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 PSYQFGHNSVDFEEDTLRK 21

DB 834 PNYQFGHNSVDFEEDTLRK 853

RESULT 8

Q7A3J7

ID Q7A3J7 PRELIMINARY; PRT; 1038 AA.

AC Q7A3J7; 05-JUL-2004 (TREMblrel. 27, Created)
DT 05-JUL-2004 (TREMblrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMblrel. 27, Last annotation update)
DE Fnb protein.
GN Name=fnb; OrderedLocustNames=SA2291;
OS Staphylococcus aureus (strain N315).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxId=158879;

RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=21311952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2;
RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Iian J.-O., Ito T.,
RA Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,
RA Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
RA Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
RA Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
RA Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
RT "Whole genome sequencing of methicillin-resistant Staphylococcus
RT aureus";
RL Lancel 357,1225-1240(2001).

CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
an amide bond (By similarity).
CC EMBL, AP003137; BAB43594.1; -.

DR GO; GO:0009986; C:cell surface; IEA.
DR GO; GO:0005618; C:cell wall; IEA.
DR GO; GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0007155; P:cell adhesion; IEA.
DR InterPro; IPR008966; Adhes_bact.
DR InterPro; IPR004237; Fn_bind.
DR InterPro; IPR005877; Gpos_YSIRK.
DR InterPro; IPR001899; Gram_pos_anchor.
DR Pfam; PF02986; Fn_bind. 1.
DR Pfam; PF00746; Gram_pos_anchor. 1.
DR Pfam; PF04650; YSIK signal. 1.
DR TIGRFAMS; TIGR01167; LpxTG anchor. 1.
DR TIGRFAMS; TIGR01168; YSIK signal. 1.
DR PROSITE; PS50847; GRAM_POS_ANCHORING; 1.
KW Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ SEQUENCE 1038 AA; 113618 MW; 666BF6BF2BFEB12 CRC64;

Query Match 91.6%; Score 109; DB 2; Length 1038;

Best Local Similarity 95.0%; Pred. No. 7, 3e-08;
Matches 19; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 PSYQFGHNSVDFEEDTLRK 21

DB 834 PNYQFGHNSVDFEEDTLRK 853

RESULT 9

ID Q53682 PRELIMINARY; PRT; 940 AA.

AC Q53682; 01-NOV-1996 (TREMblrel. 01, Created)
DT 01-NOV-1996 (TREMblrel. 01, Last sequence update)
DT 01-MAR-2004 (TREMblrel. 26, Last annotation update)
DE Fibronectin binding protein B.
GN Name=fnb;
OS Staphylococcus aureus.

OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxId=1280;

RN [1]
RP SEQUENCE FROM N.A.

RC STRAIN=8325-4;
RX MEDLINE=92111475; PubMed=1837266;

RA Jonsson K., Sigmas C., Muller H.P., Lindberg M.;
RT "Two different genes encode fibronectin binding proteins in
Staphylococcus aureus. The complete nucleotide sequence and
characterization of the second gene.";

```

RL Eur. J. Biochem. 202:1041-1048 (1991).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC an amide bond (By similarity).
DR EMBL: X62992; CAA44726.1; -.
DR PIR: S19702; S19702.
DR HSSP: Q53653; 1N67.
DR GO: GO:0009986; C:cell surface; IEA.
DR GO: GO:0005618; C:cell wall; IEA.
DR GO: GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO: GO:0016020; C:membrane; IEA.
DR GO: GO:0007155; P:cell adhesion; IEA.
DR InterPro: IPR008966; Adhes_bact.
DR InterPro: IPR004237; Fn_bind.
DR InterPro: IPR005877; Gpos_YsIRK.
DR Pfam: PF02986; Fn_bind; 2.
DR Pfam: PF02986; Gram_pos_anchor; 1.
DR Pfam: PF04650; YsIRK_signal; 1.
DR TIGRFAMs: TIGR01167; LPXTG_anchor; 1.
DR TIGRFAMs: TIGR01168; YsIRK_signal; 1.
DR PROSITE: PS50847; GRAM_POS_ANCHORING; 1.
KW Cell wall; Peptidoglycan-anchor.
SQ SEQUENCE 940 AA; 10355 MW; E35FBBQA907AE345 CRC64;

Query Match 88.2%; Score 105; DB 2; Length 940;
Best Local Similarity 90.0%; Pred. No. 2,7e-07;
Matches 18; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 PSYQFGHNSVDFEEDTLRK 21
DB 774 PNYQFGHNSVDFEEDTLRK 793

RESULT 10
ID Q8NUU8 PRELIMINARY; PRT; 943 AA.
AC Q8NUU8;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE FndB protein.
GN Name=fndB; OrderedLocustNames=MW2420;
OS Staphylococcus aureus (strain MW2).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
NC NCBITaxID=196620;
RX [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MW2;
RX MEDLINE=22040717; PubMed=12044378; DOI=10.1016/S0140-6736(02)08713-5;
RA Baba T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Oguchi A.,
RA Nagai Y., Iwano N., Amano K., Naito T., Kuroda H., Cui L.,
RA Yamamoto K., Hiramatsu K.;
RT "Genome and virulence determinants of high virulence community-
RT acquired MRSA."
RT Lancet 359:1819-1827(2002).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC an amide bond (By similarity).
DR EMBL: AP004830; BAB96285.1; -.
DR HSSP: Q53653; 1N67.
DR GO: GO:0009986; C:cell surface; IEA.
DR GO: GO:0005618; C:cell wall; IEA.
DR GO: GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO: GO:0016020; C:membrane; IEA.
DR GO: GO:0007155; P:cell adhesion; IEA.
DR InterPro: IPR008966; Adhes_bact.
DR InterPro: IPR004237; Fn_bind.
DR InterPro: IPR005877; Gpos_YsIRK.
DR Pfam: PF02986; Fn_bind; 1.
DR Pfam: PF02986; Gram_pos_anchor; 1.
DR TIGRFAMs: TIGR01167; LPXTG_anchor; 1.
DR TIGRFAMs: TIGR01168; YsIRK_signal; 1.

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DR PROSITE: PS50847; GRAM_POS_ANCHORING; 1.
KW Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ SEQUENCE 943 AA; 104537 MW; DABAF531947E1B6A CRC64;

Query Match 88.2%; Score 105; DB 2; Length 943;
Best Local Similarity 90.0%; Pred. No. 2,8e-07;
Matches 18; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 PSYQFGHNSVDFEEDTLRK 21
DB 781 PNYQFGHNSVDFEEDTLRK 800

RESULT 11
ID Q6G6H4 PRELIMINARY; PRT; 957 AA.
AC Q6G6H4;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Fibronectin-binding protein.
GN Name=fndB; OrderedLocustNames=SAS2387;
OS Staphylococcus aureus (strain MSSA476).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
NC NCBITaxID=282459;
RX [1]
RP SEQUENCE FROM N.A.
RC PubMed=15213324; DOI=10.1073/pnas.0402521101;
RA Holden M.T.G., Fell E.J., Lindsay J.A., Peacock S.J., Day N.P.J.,
RA Enright M.C., Foster T.J., Moore C.E., Hurst L., Atkin R., Barron A.,
RA Bason N., Bentley S.D., Chillingworth C., Chillingworth T.,
RA Churcher C., Clark L., Cotton C., Cronin A., Doggett J., Dowd L.,
RA Felwell T., Hance Z., Harris B., Hauser H., Holtroyd S., Jørgen K.,
RA James K.D., Lennard N., Line A., Mayes R., Mouton S., Mungall K.,
RA Ormond D., Quail M.A., Rabinowitsch B., Rutherford K.M., Sanders M.,
RA Sharp S., Simmonds M., Stevens K., Whitehead S., Barrett B.G.,
RA Spratt B.G., Parkhill J.;
RT "Complete genomes of two clinical Staphylococcus aureus strains:
RT evidence for the rapid evolution of virulence and drug resistance."
RT Proc. Natl. Acad. Sci. U.S.A. 101:9786-9791(2004).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC an amide bond (By similarity).
DR EMBL: BX571857; CAG44201.1; -.
DR GO: GO:0009986; C:cell surface; IEA.
DR GO: GO:0005618; C:cell wall; IEA.
DR GO: GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO: GO:0016020; C:membrane; IEA.
DR GO: GO:0007155; P:cell adhesion; IEA.
DR InterPro: IPR008966; Adhes_bact.
DR InterPro: IPR004237; Fn_bind.
DR InterPro: IPR005877; Gpos_YsIRK.
DR InterPro: IPR001899; Gram_pos_anchor.
DR Pfam: PF02986; Fn_bind; 1.
DR Pfam: PF02986; Gram_pos_anchor; 1.
DR Pfam: PF04650; YsIRK_signal; 1.
DR TIGRFAMs: TIGR01167; LPXTG_anchor; 1.
DR TIGRFAMs: TIGR01168; YsIRK_signal; 1.
DR PROSITE: PS50847; GRAM_POS_ANCHORING; 1.
KW Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ SEQUENCE 957 AA; 105980 MW; 28F8BA7FDFD3BAF CRC64;

Query Match 88.2%; Score 105; DB 2; Length 957;
Best Local Similarity 90.0%; Pred. No. 2,8e-07;
Matches 18; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 PSYQFGHNSVDFEEDTLRK 21
DB 781 PNYQFGHNSVDFEEDTLRK 800

RESULT 12
ID Q9AEP9 PRELIMINARY; PRT; 152 AA.

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AC Q9AEP9; 01-JUN-2001 (TrEMBLrel. 17, Created)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE Fibronectin-binding protein (Fragment).
 GN Name=fnb;
 OS Staphylococcus aureus.
 CC Staphylococcus aureus.
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 RX NCBI_TaxID=1280;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CMRSA-1;
 RX MEDLINE=21246681; PubMed=11349044;
 DOI=10.1128/IAI.69.6.3791-3799.2001;
 RA Rice K., Huesca M., Vaz D., McGavin M.J.;
 RT "Variation in fibronectin binding and fnb locus polymorphisms in
 RT Staphylococcus aureus: identification of antigenic variation in a
 RT fibronectin binding protein adhesin of the epidemic CMRSA-1 strain of
 RT methicillin-resistant *S. aureus*.";
 RL Infect. Immun. 69:3791-3799(2001).
 DR EMBL: AY029184; AAK31588.1; --
 FT NON_TER 1 152 1
 FT TER 152 152 1
 SQ SEQUENCE 152 AA; 17193 MW; CFA3913C2B11C025 CRC64;
 Query Match 84.0%; Score 100; DB 2; Length 152;
 BceI Local Similarity 85.0%; Pred No. 2.2e-07;
 Matches 17; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 QY 2 PSYQFGHNSVDFEEDTLPK 21
 DB 131 PSYQFGHNGIDFVDETLPK 150
 RESULT 13
 ID FBL3_HUMAN STANDARD; PRT; 493 AA.
 AC Q12805;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE EGF-containing fibulin-like extracellular matrix protein 1 precursor
 DE (Fibulin-3) (FBL-3) (Fibillin-like protein) (Extracellular protein
 DE S1-5).
 GN Name=EFGMP1; Synonyms=FBLN3, FBNL;
 OS Homo sapiens (Human);
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OC NCBI_TaxID=9606;
 RX [1]
 RP SEQUENCE FROM N.A., AND POSSIBLE ALTERNATIVE SPLICING.
 RC TISSUE=Skin;
 RX MEDLINE=95097983; PubMed=7799918;
 Leckla-Czerwik B., Lumpkin C.K. Jr., Goldstein S.;
 RT "An overexpressed gene transcript in senescent and quiescent human
 RT fibroblasts encoding a novel protein in the epidermal growth factor-
 RT like repeat family stimulates DNA synthesis.";
 RL Mol. Cell. Biol. 15:120-128(1995).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97001163; PubMed=8812496; DOI=10.1006/geno.1996.0402;
 RA Ikegawa S., Toda T., Okui K., Nakamura Y.;
 RT "Structure and chromosomal assignment of the human S1-5 gene (FBNL)
 RT that is highly homologous to fibillin.";
 RL Genomics 35:590-592(1996).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20068041; PubMed=10601734; DOI=10.1016/S0945-053X(99)00038-4;
 RA Gilray R., Timpl R., Koelke G.;
 RT "Sequence, recombinant expression and tissue localization of two novel
 RT extracellular matrix proteins, fibulin-3 and fibulin-4.";
 RL Matrix Biol. 18:469-480(1999).
 RN [4]

RP SEQUENCE FROM N.A. (ISOFORM 1).
 RC TISSUE=Lung;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strusberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shemen C.M., Schuler G.D.,
 RA Altshuler S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diachenko L., Marusha N., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Cantanti P., Prange C.,
 RA Rana S.S., Loggellano N.A., Peters G.J., Abramson R.D., Mullihy S.J.,
 RA Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Guneratne P.H.,
 RA Richards S., Worley K.C., Hale T., Garcia A.M., Gay L.J., Hulik S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettman M., Madan A., Rodriques S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butlerfield V.S.N., Krzywinski M.I., Skalska U., Smallus D.E.,
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [5]
 RP VARIANT DHRD TRP-345, AND VARIANT PHE-220.
 RX MEDLINE=99295941; PubMed=10369267; DOI=10.1038/9722;
 RA Stone R.M., Lotery A.J., Munier F.L., Heon E., Piguet B., Guymer R.H.,
 RA Vandenburgh K., Cousin P., Nishimura D., Swiderski R.E., Silvestri G.,
 RA Mackey D.A., Hagerman G.S., Bird A.C., Sheffield V.C.,
 RA Schorderet D.F.;
 RT "A single EFGMP1 mutation associated with both malactia Leventinese
 RT and Doyme honeycomb retinal dystrophy.";
 RL Nat. Genet. 22:199-202(1999).
 RN [6]
 RP VARIANT DHRD TRP-345.
 RX MEDLINE=21278111; PubMed=11384588; DOI=10.1016/S0002-9394(00)00926-0;
 RA Matsumoto M., Triboulet E.I.;
 RT "Dominant radial drusen and Arg345Trp EFGMP1 mutation.";
 RL Am. J. Ophthalmol. 131:810-812(2001).
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=4;
 CC Comment=Experimental confirmation may be lacking for some
 CC isoforms;
 CC Name=1;
 CC IsoId=Q12805-1; Sequence=Displayed;
 CC Name=2;
 CC IsoId=Q12805-2; Sequence=VSP_001392;
 CC Name=3;
 CC IsoId=Q12805-3; Sequence=VSP_001393;
 CC Name=4;
 CC IsoId=Q12805-4; Sequence=VSP_001394;
 CC -1- DISEASE: Defects in EFGMP1 are a cause of Doyme honeycomb retinal
 CC dystrophy (DHRD) [MIM:126600]; also known as malactia leventinese
 CC (MYLT OR ML). DHRD is an autosomal dominant disease characterized
 CC by yellow-white deposits known as drusen that accumulate beneath
 CC the retinal pigment epithelium.
 CC -1- SIMILARITY: Belongs to the fibulin family.
 CC -1- SIMILARITY: Contains 6 EGF-like domains.
 CC -1- DATABASE: NAME=Mutations of the EFGMP1 gene;
 CC NOTE=Retina International's Scientific Newsletter;
 CC WWW="http://www.retina-international.com/sci-news/efgmput.htm".
 CC -----
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 CC -----
 CC DR EMBL; U03877; AAA65590.1; --
 CC EMBL; BC014410; AAA14410.1; --

DR HSSP; P35555; 1EMN.
 DR Genew; HGNC:3218; EFEMP1.
 DR H-InVDB; HIX0002067; -.
 DR MIM; 126600; -.
 DR GO; GO:0005578; C:extracellular matrix; TMS.
 DR GO; GO:0007601; P:visual perception; TMS.
 DR InterPro; IPR000152; Asx hydroxyl_S.
 DR InterPro; IPR000742; EGF_2.
 DR InterPro; IPR001881; EGF_Ca.
 DR InterPro; IPR006209; EGF-like.
 DR InterPro; IPR009030; Grow_fac_recept.
 DR Pfam; PF00008; EGF_3.
 DR SMART; SM00179; EGF_CA; 4.
 DR PROSITE; PS00010; ASX_HYDROXYL; 4.
 DR PROSITE; PS00022; EGF_1; FALSE_NEG.
 DR PROSITE; PS01186; EGF_2; 4.
 DR PROSITE; PS00026; EGF_3; 4.
 DR PROSITE; PS01187; EGF_CA; 6.
 DR Alternative splicing; Calcium-binding; Disease mutation;
 KW EGF-like domain; Glycoprotein; Polymorphism; Repeat; Signal.
 FT SIGNAL 1 17 Potential
 FT CHAIN 18 493 EGF-containing fibulin-like extracellular
 FT DOMAIN 26 71 matrix protein 1
 FT DOMAIN 173 213 EGF-like 1 (atypical)
 FT DOMAIN 214 253 EGF-like 2, calcium-binding (Potential)
 FT DOMAIN 254 293 EGF-like 3, calcium-binding (Potential)
 FT DOMAIN 294 333 EGF-like 4, calcium-binding (Potential)
 FT DOMAIN 334 378 EGF-like 5, calcium-binding (Potential)
 FT DOMAIN 378 399 EGF-like 6, calcium-binding (Potential)
 FT DISULFID 177 190 By similarity.
 FT DISULFID 184 199 By similarity.
 FT DISULFID 201 212 By similarity.
 FT DISULFID 218 228 By similarity.
 FT DISULFID 224 237 By similarity.
 FT DISULFID 239 252 By similarity.
 FT DISULFID 258 268 By similarity.
 FT DISULFID 264 277 By similarity.
 FT DISULFID 279 292 By similarity.
 FT DISULFID 298 309 By similarity.
 FT DISULFID 305 318 By similarity.
 FT DISULFID 320 332 By similarity.
 FT DISULFID 338 350 By similarity.
 FT DISULFID 344 359 By similarity.
 FT DISULFID 365 377 By similarity.
 FT CARBOHYD 249 249 N-linked (GlcNAc...) (Potential).
 FT VARSPLIC 1 8 Missing (in isoform 2).
 FT VARSPLIC 58 58 /FtId=VSP_001392.
 FT VARSPLIC 106 106 Missing (in isoform 3).
 FT VARSPLIC 106 106 /FtId=VSP_001393.
 FT VARSPLIC 106 106 Missing (in isoform 4).
 FT VARIANT 220 220 /FtId=VSP_001394.
 FT VARIANT 220 220 I->F.
 FT VARIANT 345 345 /FtId=VAR_009512.
 FT VARIANT 345 345 R->W (in DHHD).
 FT SEQUENCE 493 AA; 54640 MW; 128CA5ED140DF414 CRC64;
 Query Match 45.4%; Score 54; DB 1; Length 493;
 Best Local Similarity 50.0%; Pred. No. 11;
 Matches 10; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

DT 05-JUL-2004 (TrEMBLrel. 27, last annotation update)
 DE EGF-containing fibulin-like extracellular matrix protein 1.
 GN Name=EFEMP1;
 OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
 OC Cercopithecoidea; Macaca.
 NC NCB1_TaxID=9541;
 RX (1)
 RP SEQUENCE FROM N.A.
 RA Umeda S., Suzuki M.T., Yoshikawa Y., Tanaka Y., Iwata T.;
 RL Submitted (JUN-2003) to the EMBL/Genbank/DBJ databases.
 DR EMBL; AY312414; AAP82236.1; -.
 DR EMBL; AY312408; AAP82236.1; JOINED.
 DR EMBL; AY312409; AAP82236.1; JOINED.
 DR EMBL; AY312410; AAP82236.1; JOINED.
 DR EMBL; AY312411; AAP82236.1; JOINED.
 DR EMBL; AY312412; AAP82236.1; JOINED.
 DR EMBL; AY312413; AAP82236.1; JOINED.
 DR EMBL; AY312415; AAP82238.1; -.
 DR HSSP; P35555; 1EMN.
 DR GO; GO:0005509; F:calcium ion binding; IEA.
 DR GO; GO:0005198; P:structural molecule activity; IEA.
 DR InterPro; IPR000152; Asx hydroxyl_S.
 DR InterPro; IPR000742; EGF_2.
 DR InterPro; IPR001881; EGF_Ca.
 DR InterPro; IPR006209; EGF-like.
 DR InterPro; IPR009030; Grow_fac_recept.
 DR Pfam; PF07645; EGF_CA; 6.
 DR SMART; SM00179; EGF_CA; 4.
 DR PROSITE; PS00010; ASX_HYDROXYL; 4.
 DR PROSITE; PS01186; EGF_2; 4.
 DR PROSITE; PS00026; EGF_3; 4.
 DR PROSITE; PS01187; EGF_CA; 6.
 KW EGF-like domain; Matrix protein.
 FT SEQUENCE 493 AA; 54547 MW; B3DAC01BC0FC1C7F CRC64;
 Query Match 45.4%; Score 54; DB 2; Length 493;
 Best Local Similarity 50.0%; Pred. No. 11;
 Matches 10; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

DT 01-MAY-2000 (TrEMBLrel. 13, last sequence update)
 DT 01-MAY-2000 (TrEMBLrel. 13, last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, last annotation update)
 DE Fructosekinase.
 GN OrderedListNames=DR0728;
 OS Deinococcus radiodurans.
 OC Bacteria; Deinococcus-Thermus; Deinococci; Deinococcales;
 OC Deinococcaceae; Deinococcus.
 NC NCB1_TaxID=1299;
 RX (1)
 RP SEQUENCE FROM N.A.
 RA STRAIN=RI / ATCC 13939 / DSM 20539 / NCIB 9279;
 RC MEDLINE=20036896; PubMed=10567266; DOI=10.1126/science.286.5444.1571;
 RA White O., Eisen J.A., Heidelberg J.F., Hickey E.K., Peterson J.D.,
 RA Dodson R.J., Haft D.H., Gwinn M.L., Nelson W.C., Richardson D.L.,
 RA Moffat K.S., Qin H., Jiang L., Pamphile W., Crosby M., Shen M.,
 RA Vamathevan J.J., Lam P., McDonald L.A., Uffnerback T.R., Zalewski C.,
 RA Makarova K.S., Aravind L., Daly M.U., Minton K.W., Fleischmann R.D.,
 RA Ketchum K.A., Nelson K.E., Salzberg S.L., Smith H.O., Venter J.C.,
 RA Fraser C.M.;
 RT "Genome sequence of the radioresistant bacterium Deinococcus
 RL radiodurans RI.";
 RT Science 286:1571-1577(1999).

DR EMBL; AE001928; AAP10301.1; -.
DR PIR; B75485; B75485.
DR TIGR; DR0728; -.
DR GO; GO:0016301; F:kinase activity; IEA.
DR InterPro; IPR002173; PfkB.
DR PROSITE; PS00583; PFKB_KINASES_1; UNKNOWN_1.
DR PROSITE; PS00584; PFKB_KINASES_2; 1.
KW Complete proteome; Kinase.
SQ SEQUENCE 303 AA; 3181 MW; 60BB688ABA446EC3 CRC64;

Query Match 42.9%; Score 51; DB 2; Length 303;
Best Local Similarity 50.0%; Pred. No. 19;
Matches 11; Conservative 2; Mismatches 7; Indels 2; Gaps 1;

QY 1 PPSYQFGHNSVD--FEEDTLP 20
|||:| | | | |:
Db 93 PPQYRFLGNSADLHFDPTRLP 114

Search completed: October 22, 2005, 04:09:53
Job time : 55.4314 secs

1	114	100.0	21	2	AAW65671	AAW65671 Fibronect
2	109	95.6	21	2	AAW65665	AAW65665 Fibronect
3	109	95.6	22	2	AAW21340	AAW21340 Fibronect
4	109	95.6	37	4	AAW91958	AAW91958 Fibronect
5	109	95.6	38	1	AAW60662	AAW60662 Protein v
6	109	95.6	134	2	AAW29087	AAW29087 S. aureus
7	109	95.6	139	2	AAW31556	AAW31556 Fibronect
8	109	95.6	1018	1	AAW82115	AAW82115 Fibronect
9	109	95.6	1018	4	AAW37245	AAW37245 Stephy1005
10	109	95.6	1018	4	AAW34301	AAW34301 Stephy1005
11	109	95.6	1018	6	ABU18922	ABU18922 Pathogen
12	109	95.6	1018	6	ABW72537	ABW72537 Stephy1005
13	109	95.6	1027	2	AAW89806	AAW89806 Stephy1005
14	106	93.0	961	6	ABU13854	ABU13854 Protein e
15	106	93.0	978	4	AAW33960	AAW33960 Stephy1005
16	106	93.0	1001	4	AAU37093	AAU37093 Stephy1005
17	106	93.0	1038	6	ABU15903	ABU15903 Protein e
18	105	92.1	21	2	AAW65670	AAW65670 Fibronect
19	104	91.2	21	2	AAW65689	AAW65689 Fibronect
20	104	91.2	21	2	AAW65679	AAW65679 Fibronect
21	104	91.2	21	2	AAW65672	AAW65672 Fibronect
22	103	90.4	21	2	AAW65680	AAW65680 Fibronect
23	103	90.4	21	2	AAW65683	AAW65683 Fibronect
24	103	90.4	21	2	AAW65684	AAW65684 Fibronect
25	103	90.4	21	2	AAW65686	AAW65686 Fibronect

26	103	90.4	21	2	AAW65674	AAW65674 Fibronect
27	102	89.5	21	2	AAW65685	AAW65685 Fibronect
28	102	89.5	21	2	AAW65687	AAW65687 Fibronect
29	102	89.5	21	2	AAW65681	AAW65681 Fibronect
30	102	89.5	77	2	AAW88749	AAW88749 S. aureus
31	102	89.5	101	2	AAW90939	AAW90939 D3D4 poly
32	102	89.5	113	2	AAW90937	AAW90937 D3D4 poly
33	102	89.5	124	2	AAW90940	AAW90940 D3D4 poly
34	102	89.5	128	2	AAW90941	AAW90941 D3D4 poly
35	102	89.5	130	2	AAW58806	AAW58806 Fibronect
36	102	89.5	130	2	AAW58807	AAW58807 Fibronect
37	102	89.5	130	2	AAW91202	AAW91202 DI-D4 fib
38	102	89.5	130	2	AAW91201	AAW91201 DI-D4 fib
39	102	89.5	134	2	AAW29068	AAW29068 S. aureus
40	102	89.5	132	2	AAW90942	AAW90942 D3D4 poly
41	102	89.5	164	2	AAW90938	AAW90938 D3D4 poly
42	102	89.5	174	2	AAW58808	AAW58808 FOP fibrtct
43	102	89.5	174	2	AAW91203	AAW91203 DI-D4 fib
44	102	89.5	181	2	AAW58805	AAW58805 Fibronect
45	102	89.5	181	2	AAW91200	AAW91200 DI-D4 fib

ALIGNMENTS

RESULT 1	
AAW65671	
ID	AAW65671 standard; peptide; 21 AA.

AC AAW65671;

DT 16-OCT-1998 (first entry)

Fibronectin binding protein-derived peptide #15.

microbial surface components recognising adhesive matrix molecule; MSCRAMM; fibronectin; fibronectin-binding protein; antibody; epitope
antibiotic; bacterial infection; antibiotic-resistant strain.

05 Synthetic.
05 *Staphylococcus aureus*.

PN W09831389-A2

PD 23-JUL-1998

PF 21-JAN-1998; 98WO-US001222.

PR 21-JAN-1997; 97US-0036139P

PA (TEKA) UNIV TEXAS A & M SYSTEM.

PI Hoebeek M, Patti JM, House-Pompeo KL, Speciale P, Joh D,

XX

XX

PT binding to fibronectin - used to treat or prevent bacterial infection,

XX

Example 8; Page 100; 201pp; English.

The invention relates to antibodies that bind to a fibronectin-binding domain of a fibronectin-binding protein, and inhibit binding of the protein to fibronectin. Also claimed are: (1) isolated peptides of a fibronectin-binding protein that do not bind to fibronectin; (2) fusion protein containing at least one peptide of a fibronectin-binding protein linked to a second amino acid sequence; (3) nucleic acid encoding the isolated peptide of (1). Antibodies, the isolated peptides of (1) and the nucleic acids are all useful for immunisation (active or passive) and (b) inhibiting binding of bacteria to fibronectin) for preventing or treating infection in humans or other animals, particularly by staphylococci or

CC streptococci, e.g. meningitis, otitis media, pneumonia, endocarditis,
 CC mastitis in cattle, abortion in horses and many others. Since the
 CC antibodies block binding of bacteria, they should be effective against
 CC antibiotic-resistant strains, and may replace antibiotic therapy or
 CC increase its effectiveness. Sequences AAW65670-90 represent a series of
 CC synthetic peptides based on the D3 repeat of *S. aureus* fibronectin
 CC binding protein A. They were synthesised to contain a proline residue at
 CC each position through the sequence (ie a proline scan)

XX
 SQ Sequence 21 AA;

QY Query Match 100.0%; Score 114; DB 2; Length 21;
 Best Local Similarity 100.0%; Pred. No. 6e-11;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 1 KASYQFGHNSVDFFEDTLPK 21
 1 KASYQFGHNSVDFFEDTLPK 21

RESULT 2
 AAW65665
 ID AAW65665 standard; peptide; 21 AA.
 XX
 AC AAW65665;
 XX
 DT 16-OCT-1998 (first entry)
 XX
 DE Fibronectin binding protein-derived peptide #9.
 XX
 KM microbial surface components recognising adhesive matrix molecule;
 KM MSCRAMM; fibronectin; fibronectin-binding protein; antibody; epitope;
 KM antibiotic; bacterial infection; antibiotic-resistant strain.
 XX
 OS Synthetic.
 OS Staphylococcus aureus.
 XX
 PN WO981389-A2.
 XX
 PD 23-JUL-1998.
 XX
 PF 21-JAN-1998; 98WO-US001222.
 XX
 PR 21-JAN-1997; 97US-0036139P.
 XX
 PA (TEXA) UNIV TEXAS A & M SYSTEM.
 XX
 PI Hoeoek M, Patli JM, House-Pompeo KL, Speziale P, Joh D;
 PI McGavin MJ;
 XX
 DR WPI; 1998-413816/35.
 XX
 XX
 PT Antibody that binds to fibronectin-binding protein, preventing its
 PT binding to fibronectin - used to treat or prevent bacterial infection,
 PT especially by Staphylococci and Streptococci.
 XX
 PS Example 2; Page 92; 201pp; English.

CC The invention relates to antibodies that bind to a fibronectin-binding
 CC domain of a fibronectin-binding protein, and inhibit binding of the
 CC protein to fibronectin. Also claimed are: (1) isolated peptides of a
 CC fibronectin-binding protein that do not bind to fibronectin; (2) fusion
 CC protein containing at least one peptide of a fibronectin-binding protein
 CC linked to a second amino acid sequence; (3) nucleic acid encoding the
 CC isolated peptide of (1). Antibodies, the isolated peptides of (1) and the
 CC nucleic acids are all useful for immunisation (active or passive) and (b)
 CC inhibiting binding of bacteria to fibronectin for preventing or treating
 CC infection in humans or other animals, particularly by staphylococci or
 CC streptococci, e.g. meningitis, otitis media, pneumonia, endocarditis,
 CC mastitis in cattle, abortion in horses and many others. Since the
 CC antibodies block binding of bacteria, they should be effective against
 CC antibiotic-resistant strains, and may replace antibiotic therapy or
 CC increase its effectiveness. Sequences AAW6559-68 represent synthetic

CC epitopes from the fibronectin binding domains DU and DI-D4 of the S.
 CC aureus fnba gene
 XX
 SQ Sequence 21 AA;

QY Query Match 95.6%; Score 109; DB 2; Length 21;
 Best Local Similarity 95.2%; Pred. No. 3.8e-10;
 Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

DB 1 KPSYQFGHNSVDFFEDTLPK 21
 1 KPSYQFGHNSVDFFEDTLPK 21

RESULT 3
 AAR21340
 ID AAR21340 standard; peptide; 22 AA.
 XX
 AC AAR21340;
 XX
 DT 25-MAR-2003 (revised)
 DT 15-JUN-1992 (first entry)
 XX
 DE Fibronectin binding protein.
 XX
 KM FBNP; wound infection reduction; vaccination; mastitis;
 KM Staphylococcal infections; D3.
 XX
 OS Synthetic.
 OS
 PN WO9202555-A.
 XX
 PD 20-FEB-1992.
 XX
 PF 10-AUG-1990; 90SE-00002617.
 XX
 PR 10-AUG-1990; 90SE-00002617.
 XX
 PA (ALFA) ALFA LAVAL AGRIC INT AB.
 XX
 PI Hook M, McGavin M, Raucel G;
 XX
 DR WPI; 1992-080035/10.
 XX
 XX
 PT New fibronectin binding peptide - combines with fusion peptide to form
 PT large antigen, used in immunisation, diagnosis and for treating wounds.
 XX
 PS Claim 1; Page 22; 33pp; English.
 XX
 XX
 CC The sequence comprises amino acids 17-33 of a tandem repeat, designated
 CC D3 of the fibronectin binding site of Staphylococcus aureus 8325-4 FBNP.
 CC The N-terminal DK may be replaced with H or K, and the C-terminal LKP may
 CC be replaced by either L, LP, or OH. The peptides were synthesised using
 CC standard methods and purified using reverse phase HPLC. The appropriate
 CC fractions were dialysed and lyophilised. Peptide sequencing was performed
 CC and the peptides digested and chemically modified by dihydroxypropylation
 CC of the amino side chain of lysine. The carboxylic side chains were
 CC converted to glycine methyl esters. The phenyl side chains of tyrosine
 CC residues were oxidised. Chemically modified peptide D3 was compared to
 CC unmodified D3. Lysine and tyrosine modifications only partially
 CC diminished its activity whereas modification of aspartic/glutamic
 CC residues resulted in complete loss of activity. The peptide can be used
 CC for the prevention or reduction of the risk of wound infection. The
 CC peptide can be used to create a large antigen for vaccinating ruminants
 CC against mastitis caused by Staphylococcal infections. It can also be used
 CC to diagnose Staphylococcal infections using ELISA or DNA probes. (Updated
 CC on 25-MAR-2003 to correct PA field.)
 XX
 SQ Sequence 22 AA;

QY Query Match 95.6%; Score 109; DB 2; Length 22;
 Best Local Similarity 95.2%; Pred. No. 4e-10;
 Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KASYOFGHNSVDFEEDTLPK 21
 ID AAB91958 standard; peptide; 37 AA.
 DB 2 KPSYQFGHNSVDFEEDTLPK 22

RESULT 4
 ID AAB91958 standard; peptide; 37 AA.
 AC AAB91958;
 XX
 DT 22-JUN-2001 (first entry)
 XX
 DE Fibronectin fragment and fibrin related peptide SEQ ID NO:1134.
 XX
 KW Protection; endogenous therapeutic peptide; peptidase; conjugation;
 KW blood component; modification; succinimide; maleimide group; amino;
 KW hydroxyl; thiol; hormone; growth factor; neurotransmitter.
 XX
 OS Homo sapiens.
 OS Synthetic.
 PA WO200069900-A2.
 PN 23-NOV-2000.
 PD 17-MAY-2000; 2000WO-US013576.
 PF 17-MAY-1999; 99US-0134406P.
 PR 10-SEP-1999; 99US-0153406P.
 PR 15-OCT-1999; 99US-0159783P.
 XX
 PA (CONU-) CONNUCHEM INC.
 PI Bridon DP, Ezrin AM, Milner PG, Holmes DL, Thibaudan K;
 DR WPI; 2001-112059/12.
 XX
 PT Modifying and attaching therapeutic peptides to albumin prevents
 PT peptidase degradation, useful for increasing length of in vivo activity.
 XX
 PS Disclosure; Page 566; 733pp; English.
 XX
 CC The present invention describes a modified therapeutic peptide (I)
 CC comprising a therapeutically active amino acid region (III) and a
 CC reactive group (II) (e.g. succinimide) and maleimide groups) attached to
 CC a less therapeutically active amino acid region (IV), which covalently
 CC bonds with amino/hydroxyl/thiol groups on blood components to form a
 CC peptidase stabilised therapeutic peptide composed of 3-50 amino acids.
 CC (I) are useful for modifying therapeutic peptides e.g. hormones, growth
 CC factors and neurotransmitters, to protect them from peptidase activity in
 CC vivo for the treatment of various disorders. Endogenous therapeutic
 CC peptides are not suitable as drug candidates as they require frequent
 CC administration due to rapid degradation by peptidases in the body.
 CC Modifying and attaching therapeutic peptides to albumin prevents or
 CC reduces the action of peptidases to increase length of activity (half
 CC life) and specificity as bonding to large molecules decreases
 CC intracellular uptake and interference with physiological processes.
 CC AAB90829 to AAB92441 represent peptides which can be used in the
 CC exemplification of the present invention
 XX
 SQ Sequence 37 AA;
 XX

Query Match 95.6%; Score 109; DB 4; Length 37;
 Best Local Similarity 95.2%; Pred. No. 7,1e-10;
 Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KASYOFGHNSVDFEEDTLPK 21
 ID AAB91958 standard; peptide; 37 AA.
 DB 16 KPSYQFGHNSVDFEEDTLPK 36

RESULT 5
 ID AAP80662 standard; protein; 38 AA.
 XX
 AC AAP80662;
 XX
 DT 25-MAR-2003 (revised)
 DT 07-OCT-1990 (first entry)
 XX
 DE Protein with fibronectin binding ability.
 XX
 KW Hybrid DNA molecule; fibronectin binding; mastitis; ruminants;
 KW wound infection.
 XX
 OS Staphylococcus aureus.
 XX
 PN EP294349-A.
 PN 07-DEC-1988.
 PD 30-MAY-1988; 88EP-00850188.
 PF 01-JUN-1987; 87SE-00002272.
 PR (ALFA) ALFA LAVAL AGRIC INT AB.
 PA Lindberg MK, Signas LC, Wadstrom TM, Froman G;
 DR WPI; 1988-347978/49.
 DR N-PSDB; AAN61099.
 XX
 PT Hybrid DNA encoding Staphylococcus aureus fibronectin binding protein -
 PT useful for immunisation and topical application to prevent staphylococcal
 PT infections.
 XX
 PS Claim 11; Page 12; 23pp; English.
 XX
 CC The peptide has fibronectin binding ability. It is useful for immunising
 CC ruminants against staphylococcal mastitis, pref. when used at 0.5-5
 CC micrograms/kg, using 3 doses given at 1-3 week intervals; for topical
 CC application to prevent wound infection, using an isotonic saline soln. of
 CC concn. 25-250 micrograms/ml; and, when immobilised on a carrier, for
 CC diagnosing staphylococcal infections. (Updated on 25-MAR-2003 to correct
 CC PF field.) (Updated on 25-MAR-2003 to correct PA field.)
 XX
 SQ Sequence 38 AA;
 XX

Query Match 95.6%; Score 109; DB 1; Length 38;
 Best Local Similarity 95.2%; Pred. No. 7,3e-10;
 Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KASYOFGHNSVDFEEDTLPK 21
 ID AAB91958 standard; peptide; 37 AA.
 DB 17 KPSYQFGHNSVDFEEDTLPK 37

RESULT 6
 ID AAY29087 standard; protein; 134 AA.
 AC AAY29087;
 XX
 DT 28-SEP-1999 (first entry)
 DE S. aureus fibronectin binding protein A (FnBA) binding domain.
 DE
 KW Bovine herpes virus-2; BHV-2; cytokine; immune response; immunogen; IL;
 KW interleukin; colony stimulating factor; CSF; interferon; IFN; TNF;
 KW tumour necrosis factor; recombinant virus; vaccine; mucosal disease;
 KW mastitis; breast cancer; stress-induced disease; binding domain; FnBA;
 KW fibronectin binding protein.
 XX
 OS Staphylococcus aureus.

XX WO9916892-A1.
XX 08-APR-1999.
XX 29-SEP-1998; 98WO-GB002927.
XX 29-SEP-1997; 97GB-00020633.
XX (UYBR-) UNIV BRISTOL.
XX Bradley AJ, Duffas WPH;
XX WPI; 1999-255101/21.
XX N-PSDB; AAX91504.
XX New bovine herpes virus-2 vectors.
XX
XX Example 2; Fig 8A-B; 130pp; English.
XX The invention provides bovine herpes virus-2 (BHV-2) based vectors that
XX comprise at least one cytokine-encoding DNA sequence. The expression of
XX cytokines in mammals can up-regulate immune responses to the immunogens.
XX The cytokine is selected from interleukins (IL), colony stimulating
XX factors (CSF), interferons (IFN) and tumour necrosis factors (TNF). The
XX BHV-2 based vector or recombinant virus can be used as vaccines. They can
XX be used for preventing or treating a mucosal disease in a subject, e.g.
XX ruminants, cattle, sheep, goats, dogs, cats, horses, or man, particularly
XX mastitis in cows or breast cancers in humans. They can also be used for
XX preventing or treating a stress-induced disease. The present sequence
XX represents the binding domain of a previously published S. aureus
XX fibronectin binding protein A (FnBA) sequence. The FnB binding domain
XX gene sequence FnBAB, cloned for use in this invention has 97.8 percent
XX identity when compared to the previously published FnBA and FnBB gene
XX sequences
SQ Sequence 134 AA;
Query Match 95.6%; Score 109; DB 2; Length 134;
Best Local Similarity 95.2%; Pred. No. 2.9e-09;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 KASYOFGHNSVDFEDTLPK 21
DB 93 KPSYOFGHNVSDFEDTLPK 113
RESULT 7
AAM31556
ID AAM31556 standard; protein; 139 AA.
AC AAM31556;
XX
DT 27-AUG-2003 (revised)
DT 25-MAR-2003 (revised)
DT 21-MAY-1998 (first entry)
XX
DE Fibronectin-binding MSCRAM derivative pQD.
XX
XX Fibronectin; pQD; collagen binding protein; sepsis; infection;
XX microbial surface component regioning adhesive matrix molecule; MSCRAM;
XX adhesin; vaccine; immunisation; diagnosis; therapy; mastitis.
XX
XX Staphylococcus aureus.
XX
XX Key Location/Qualifiers
XX FT 1..12
XX Peptide /note= "vector pQE30-derived peptide"
XX
XX WO9743314-A2.
XX
XX 20-NOV-1997.
XX

PF 14-MAY-1997; 97WO-US008210.
XX
XX 16-MAY-1996; 96US-0017678P.
XX
XX (TEXA) UNIV TEXAS A & M SYSTEM.
XX (UABR-) UAB RES FOUND.
XX
XX Hoeoek M, Patti JM, House-Pompeo K, Strhanam N, Symereky J;
XX WPI; 1998-008801/01.
XX
XX Antibody that interacts with collagen binding domain of Staphylococcal
XX cna gene product - useful to prevent bacterial sepsis in animal infected
XX with Staphylococcus aureus.
XX
XX Disclosure; Page 91; 143pp; English.
XX
XX This protein comprises Staphylococcus aureus fibronectin-binding
XX microbial surface component regionising adhesive matrix molecule (MSCRAM)
XX derivative pQD, plus a vector-derived N-terminal peptide. The invention
XX relates to claimed nucleic acid sequences (see AAT93436-38) encoding S.
XX aureus collagen binding protein (CBP) epitopes M17, M31 and M35 (see
XX AAM31552-54) that confer protection against S. aureus infection. CBP
XX protein and antigenic epitopes are contemplated for use in the treatment
XX of pathological infections, especially to prevent bacterial adhesion to
XX collagen. The epitopes are also contemplated for use in the preparation
XX of vaccines and as carrier proteins in vaccine formulations, as well as
XX in the formulation of compositions for the prevention of S. aureus
XX infection. pCF33 and pQD (see AAM31556) were used to raise anti-MSCRAM
XX polyclonal antibodies used in passive immunisation against bovine
XX mastitis. (Updated on 25-MAR-2003 to correct PI field.) (Updated on 27-
XX AUG-2003 to correct OS field.)
SQ Sequence 139 AA;
Query Match 95.6%; Score 109; DB 2; Length 139;
Best Local Similarity 95.2%; Pred. No. 3.1e-09;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 KASYOFGHNSVDFEDTLPK 21
DB 107 KPSYOFGHNVSDFEDTLPK 127
RESULT 8
AAP82115
ID AAP82115 standard; protein; 1018 AA.
AC AAP82115;
XX
DT 25-MAR-2003 (revised)
DT 05-JAN-1990 (first entry)
XX
DE Fibronectin binding protein.
XX
XX Fibronectin binding protein; S.aureus; immunisation; mastitis; ruminants;
XX wound infection; diagnosis.
XX
XX Staphylococcus aureus.
XX
XX EP294349-A.
XX
XX 07-DEC-1988.
XX
XX 30-MAY-1988; 88EP-00850188.
XX
XX 01-JUN-1987; 87SE-00002272.
XX
XX (ALFA) ALFA LAVAL AGRIC INT AB.
XX
XX Lindberg MK, Signas LC, Wadstrom TM, Froman G;
XX WPI; 1988-347978/49.
XX

DR P-PSDB; AAP82115.
XX
PT Hybrid DNA encoding *Staphylococcus aureus* fibronectin binding protein -
PT useful for immunisation and topical application to prevent staphylococcal
PT infections.
XX
PS Disclosure; Fig. 8A:1-8A:2; 23pp; English.
XX
CC The *S.aureus* fibronectin binding protein may be included in a hybrid
CC protein. The protein may be used to immunise ruminants against
CC staphylococcal mastitis, pref. when given at 0.5-5 microg/kg, using 3
CC doses at 1-3 week intervals; and for topical applicn. to prevent wound
CC infection, pref. using isotonic saline soln. of concn. 25-250 microg/mg.
CC The DNA encoding the binding protein and the hybrid protein may be
CC immobilised on a carrier and used to diagnose staphylococcal infections.
CC (Updated on 25-MAR-2003 to correct PA field.)
XX
SQ Sequence 1018 AA;
XX
Query Match 95.6%; Score 109; DB 1; Length 1018;
Best Local Similarity 95.2%; Pred. No. 2.8e-08;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 KASYQFGHNSVDFEEDTLPK 21
DB 837 KPSYQFGHNSVDFEEDTLPK 857
XX
RESULT 9
AAU37245
ID AAU37245 standard; protein; 1018 AA.
XX
AC AAU37245;
XX
DT 14-FEB-2002 (first entry)
XX
DE Staphylococcus aureus cellular proliferation protein #1415.
XX
KM Antisense; prokaryotic cellular proliferation protein; antibiotic;
KM antibacterial; drug design.
XX
OS Staphylococcus aureus.
XX
PN WO200170955-A2.
XX
PD 27-SEP-2001.
XX
PF 21-MAR-2001; 2001WO-US009180.
XX
PR 21-MAR-2000; 2000US-0191078P.
PR 23-MAY-2000; 2000US-0206848P.
PR 26-MAY-2000; 2000US-0207727P.
PR 23-OCT-2000; 2000US-0242578P.
PR 27-NOV-2000; 2000US-0253625P.
PR 22-DEC-2000; 2000US-0257931P.
PR 16-FEB-2001; 2001US-0269308P.
XX
PA (ELIT-) ELITRA PHARM INC.
XX
PI Haselbeck R, Ohlsen KL, Zyekind JW, Wall D, Trawick JD, Carr GJ;
PI Yamamoto RT, Xu HH;
XX
DR WPI; 2001-611495/70.
XX
DR N-PSDB; AAS55104.
XX
PT New polynucleotides for the identification and development of
PT antibiotics, comprise sequences of antisense nucleic acids.
XX
PS Example 3; SEQ ID NO 12838; 51pp; English.
XX
CC The invention relates to antisense inhibitors of genes essential to
CC prokaryotic cellular proliferation, their use in identifying the genes,
CC their use in the discovery of novel antibiotics, the essential genes

CC themselves and the encoded proteins. The prokaryotes used are *Escherichia*
CC coli, *Staphylococcus aureus*, *Salmonella typhi*, *Klebsiella pneumoniae*,
CC *Pseudomonas aeruginosa* and *Enterococcus faecalis*. The invention is also
CC useful for the identification of potential new targets for antibiotic
CC development. The antisense nucleic acids can also be used to identify
CC proteins used in proliferation, to express these proteins, and to obtain
CC antibodies capable of binding to the expressed proteins. The proteins can
CC be used to screen compounds in rational drug discovery programmes. The
CC antisense nucleic acid sequence is also useful to screen for homologous
CC nucleic acids which are required for cell proliferation in a wide variety
CC of organisms. The present sequence represents an essential prokaryotic
CC cellular proliferation protein. Note: The sequence data for this patent
CC did not form part of the printed specification, but was obtained in
CC electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 1018 AA;
XX
Query Match 95.6%; Score 109; DB 4; Length 1018;
Best Local Similarity 95.2%; Pred. No. 2.8e-08;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 KASYQFGHNSVDFEEDTLPK 21
DB 837 KPSYQFGHNSVDFEEDTLPK 857
XX
RESULT 10
AAU34301
ID AAU34301 standard; protein; 1018 AA.
XX
AC AAU34301;
XX
DT 14-FEB-2002 (first entry)
XX
DE Staphylococcus aureus cellular proliferation protein #577.
XX
KM Antisense; prokaryotic cellular proliferation protein; antibiotic;
KM antibacterial; drug design.
XX
OS Staphylococcus aureus.
XX
PN WO200170955-A2.
XX
PD 27-SEP-2001.
XX
PF 21-MAR-2001; 2001WO-US009180.
XX
PR 21-MAR-2000; 2000US-0191078P.
PR 23-MAY-2000; 2000US-0206848P.
PR 26-MAY-2000; 2000US-0207727P.
PR 23-OCT-2000; 2000US-0242578P.
PR 27-NOV-2000; 2000US-0253625P.
PR 22-DEC-2000; 2000US-0257931P.
PR 16-FEB-2001; 2001US-0269308P.
XX
PA (ELIT-) ELITRA PHARM INC.
XX
PI Haselbeck R, Ohlsen KL, Zyekind JW, Wall D, Trawick JD, Carr GJ;
PI Yamamoto RT, Xu HH;
XX
DR WPI; 2001-611495/70.
XX
DR N-PSDB; AAS52160.
XX
PT New polynucleotides for the identification and development of
PT antibiotics, comprise sequences of antisense nucleic acids.
XX
PS Example 3; SEQ ID NO 5797; 51pp; English.
XX
CC The invention relates to antisense inhibitors of genes essential to
CC prokaryotic cellular proliferation, their use in identifying the genes,
CC their use in the discovery of novel antibiotics, the essential genes
CC themselves and the encoded proteins. The prokaryotes used are *Escherichia*

CC coli, *Staphylococcus aureus*, *Salmonella typhi*, *Klebsiella pneumoniae*,
 CC *Pseudomonas aeruginosa* and *Enterococcus faecalis*. The invention is also
 CC useful for the identification of potential new targets for antibiotic
 CC development. The antisense nucleic acids can also be used to identify
 CC proteins used in proliferation, to express these proteins, and to obtain
 CC antibodies capable of binding to the expressed proteins. The proteins can
 CC be used to screen compounds in rational drug discovery programmes. The
 CC antisense nucleic acid sequence is also useful to screen for homologous
 CC nucleic acids which are required for cell proliferation in a wide variety
 CC of organisms. The present sequence represents an essential prokaryotic
 CC cellular proliferation protein. Note: The sequence data for this patent
 CC did not form part of the printed specification, but was obtained in
 CC electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences

XX Sequence 1018 AA;

Query Match 95.6%; Score 109; DB 4; Length 1018;

Best Local Similarity 95.2%; Pred. No. 2.8e-08; Mismatches 1; Indels 0; Gaps 0;

Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 KASYOFGHNSVDFEEDTLPK 21
 DB 837 KPSYQFGHNSVDFEEDTLPK 857

RESULT 11

ABJ18922
 ID ABJ18922 standard; protein; 1018 AA.

XX ABJ18922;

XX 06-MAR-2003 (first entry)

DE Pathogen specific antigen related staphylococcal protein SEQ ID No 68.

XX Antibacterial; virucide; fungicide; protozoacide; cytostatic; anti-HIV;

XX hyperimmune; serum-reactive; antigen; pathogen; tumour; allergen;

KW auto-immunity; vaccine; staphylococcal infection; antibody; cancer;

XX autotumour disease; HIV; hepatitis.

OS Staphylococcus sp.

XX WO200259148-A2.

XX 01-AUG-2002.

XX 21-JAN-2002; 2002WO-EP000546.

XX 26-JAN-2001; 2001AT-00000130.

XX (CIST-) CISTEM BIOTECHNOLOGIES GMBH.

XX Weinke A, Nagy E, Von Ahsen U, Klade C, Henics T, Zauner W;

XX Minh DB, Vytvytska O, Etcz H, Dryla A, Weichart T, Hafner M;

XX Tempelmeier B;

XX WPI; 2003-075410/07.

XX Identifying, isolating and producing hyperimmune serum-reactive antigens

XX from a pathogen, for preparing vaccine or medicament for treating or

XX preventing e.g. staphylococcal infections, comprises providing antibody

XX preparation.

XX Example 7; Page 157; 252pp; English.

XX The invention relates to a novel method for identifying, isolating and

XX producing hyperimmune serum-reactive antigens from a pathogen, tumour,

XX allergen, a tissue or host prone to auto-immunity, where the antigens are

XX used in a vaccine, comprises providing antibody preparation from a plasma

XX pool of a type of animal, or individual sera with antibodies against the

XX specific pathogen, tumour, allergen, tissue or host prone to auto-

XX immunity. The hyperimmune serum-reactive antigens comprising any of the

CC 62 sequences of 53-2261 amino acids fully defined in the specification,
 CC or their hyperimmune fragments are useful for the manufacture of a
 CC pharmaceutical preparation, particularly a vaccine against staphylococcal
 CC infections or colonisation against *S. aureus* or *S. epidermidis*. The
 CC preparation of antibodies is useful for the manufacture of a medicament
 CC for treating or preventing staphylococcal infections or colonisation
 CC against *S. aureus* or *S. epidermidis*. The antibody preparations may also
 CC be used for diagnostic and imaging purposes. Other conditions that can be
 CC treated include cancer, autoimmune diseases or infections caused by viral
 CC (e.g. HIV, hepatitis A, B or C), fungal or protozoan pathogens. This
 CC sequence represents a staphylococcal protein relating to the method for
 CC identifying and producing pathogen specific antigens of the invention

XX Sequence 1018 AA;

Query Match 95.6%; Score 109; DB 6; Length 1018;

Best Local Similarity 95.2%; Pred. No. 2.8e-08; Mismatches 1; Indels 0; Gaps 0;

Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 KASYOFGHNSVDFEEDTLPK 21
 DB 837 KPSYQFGHNSVDFEEDTLPK 857

RESULT 12

ABM72537
 ID ABM72537 standard; protein; 1018 AA.

XX ABM72537;

XX 20-NOV-2003 (first entry)

DE Staphylococcus aureus protein #1777.

XX Antibacterial; vaccine; gene therapy; infection; sepsis; diagnosis;

XX enzymatic assay; antibiotic target.

XX Staphylococcus aureus.

XX WO200294868-A2.

XX 28-NOV-2002.

XX 27-MAR-2002; 2002WO-IB002637.

XX 27-MAR-2001; 2001GB-00007661.

XX (CHIR-) CHIRON SPA.

XX Masignani V, Mora M, Scarselli M;

XX WPI; 2003-120786/11.

XX N-PSDB; ACF74097.

XX New Staphylococcus aureus protein, useful as a vaccine for treating or

XX preventing Staphylococcal infection, specifically an infection caused by

XX *S. aureus*, e.g. sepsis.

XX Claim 1; SEQ ID NO 3554; 49pp; English.

XX The invention relates to novel genes and encoded proteins from

XX *Staphylococcus aureus*. A composition comprising the *S. aureus* protein, a

XX nucleic acid encoding the protein, or an antibody to the protein, is

XX useful as a pharmaceutical, particularly as a vaccine for treating or

XX preventing infection due to *Staphylococcus bacterie*, specifically an

XX infection caused by *S. aureus*. The composition is particularly useful for

XX treating or preventing sepsis in a patient. The composition can also be

XX used for diagnostics. The protein is also used in an assay for enzymatic

XX studies and as a target for antibiotics. This sequence represents one of

XX the novel *S. aureus* proteins of the invention

XX Sequence 1018 AA;

Query Match 95.6%; Score 109; DB 6; Length 1018;
Best Local Similarity 95.2%; Pred. No. 2.8e-08;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KASYOFGHNSVDFEEDTLPK 21
ID |||||
DB 837 KPSYOFGCHNSVDFEEDTLPK 857

RESULT 13
ID AAM89806 standard; protein; 1027 AA.
XX AAM89806;
XX AAM89806;

DT 16-MAR-1999 (first entry)

XX Staphylococcus aureus protein SEQ ID #5254.

XX Computer readable medium; vaccine; S.aureus infection; immunodetection;
KW cellulitis; eyelid infection; food poisoning; osteomyelitis; therapy;
KW skin infection; surgical wound infection; scalded skin syndrome;
KW toxic shock syndrome.

XX Staphylococcus aureus.

PN EP786519-A2.

PD 30-JUL-1997.

PF 07-JAN-1997; 97BP-00100117.

PR 05-JAN-1996; 96US-0009861P.

PA (HUMA-) HUMAN GENOME SCT INC.

PI Kunesch CA, Choi GH, Barash SC, Dillon PJ, Fannon MR, Rosen CA;

XX WPI; 1997-374922/35.

PT Polynucleotide(s) and proteins derived from Staphylococcus aureus -
PT stored on computer readable medium and used in the production of anti-
PT S. aureus vaccines.

PS Claim 23; Page 3263-3267; 3271pp; English.

XX This sequence represents a Staphylococcus aureus protein sequence of the
CC invention. The DNA sequences encoding the S.aureus proteins are recorded
CC on a computer readable medium, preferably selected from a floppy or hard
CC disk, random access memory (RAM), read-only memory (ROM) or CD-ROM.
CC Homology searches using the S.aureus DNA sequences allows putative
CC functions to be assigned so that protein-encoding or regulatory regions
CC of commercial, therapeutic or industrial importance can be obtained.
CC Specifically, sequences which are likely to encode antigens have been
CC identified and these polypeptides can be used in a vaccine composition
CC against S.aureus infection. The polypeptides can also be used in a kit
CC for the immunodetection of S.aureus in a sample. S.aureus is implicated
CC in numerous human diseases, including cellulitis, eyelid infections, food
CC poisoning, osteomyelitis, skin and surgical wound infections, scalded
CC skin syndrome, toxic shock syndrome, etc. Organisms transformed with the
CC DNA sequences can be used for recombinant production of the polypeptides.
CC The new DNA sequences (and their fragments) are useful as primers or
CC probes for isolating homologues of any of the 5191 S.aureus DNA sequences
CC contained on the computer readable medium

XX Sequence 1027 AA;

Query Match 95.6%; Score 109; DB 2; Length 1027;
Best Local Similarity 95.2%; Pred. No. 2.8e-08;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KASYOFGHNSVDFEEDTLPK 21
ID |||||

DB 846 KPSYOFGCHNSVDFEEDTLPK 866

RESULT 14
ID ABU15854
ABU15854 standard; protein; 961 AA.
XX ABU15854;
XX ABU15854;

DT 19-JUN-2003 (first entry)

DE Protein encoded by prokaryotic essential gene #1381.

XX Antisense; prokaryotic essential gene; cell proliferation; drug design.

XX Staphylococcus aureus.

PN WO20027183-A2.

PD 03-OCT-2002.

PF 21-MAR-2002; 2002MO-US009107.

PR 21-MAR-2001; 2001US-00815242.

PR 06-SEP-2001; 2001US-00948993.

PR 25-OCT-2001; 2001US-0342323P.

PR 08-FEB-2002; 2002US-00072851.

PR 06-MAR-2002; 2002US-03626599P.

XX (ELIT-) ELITRA PHARM INC.

XX Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zykkind JW;

PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;

XX WPI; 2003-029926/02.

DR N-PSDB; ACA19724.

PT New antisense nucleic acids, useful for identifying proteins or screening

PT for homologous nucleic acids required for cellular proliferation to

PT isolate candidate molecules for rational drug discovery programs.

XX Claim 25; SEQ ID NO 43778; 1766pp; English.

XX The invention relates to an isolated nucleic acid comprising any one of
CC the 6213 antisense sequences given in the specification where expression
CC of the nucleic acid inhibits proliferation of a cell. Also included are:
CC (1) a vector comprising a promoter operably linked to the nucleic acid
CC encoding a polypeptide whose expression is inhibited by the antisense
CC nucleic acid; (2) a host cell containing the vector; (3) an isolated
CC polypeptide or its fragment whose expression is inhibited by the
CC antisense nucleic acid; (4) an antibody capable of specifically binding
CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular
CC proliferation or the activity of a gene in an operon required for
CC proliferation; (7) identifying a compound that influences the activity of
CC the gene product or that has an activity against a biological pathway
CC required for proliferation, or that inhibits cellular proliferation; (8)
CC identifying a gene required for cellular proliferation or the biological
CC pathway in which a proliferation-required gene or its gene product lies
CC or a gene on which the test compound that inhibits proliferation of an
CC organism acts; (9) manufacturing an antibiotic; (10) profiling a
CC compound's activity; (11) a culture comprising strains in which the gene
CC product is overexpressed or underexpressed; (12) determining the extent
CC to which each of the strains is present in a culture or collection of
CC strains; or (13) identifying the target of a compound that inhibits the
CC proliferation of an organism. The antisense nucleic acids are useful for
CC identifying proteins or screening for homologous nucleic acids required
CC for cellular proliferation to isolate candidate molecules for rational
CC drug discovery programs, or for screening homologous nucleic acids
CC required for proliferation in cells other than S. aureus, S. typhimurium,
CC K. pneumoniae or P. aeruginosa. The present sequence is encoded by one of
CC the target prokaryotic essential genes. Note: The sequence data for this
CC patent did not form part of the printed specification, but was obtained
CC in electronic format directly from WIPO at


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CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 961 AA;
Query Match 93.0%; Score 106; DB 6; Length 961;
Best Local Similarity 90.5%; Pred. No. 7.9e-08;
Matches 19; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 KASYOFGHNSVDFEEDTLPK 21
   |:|||||
DB 784 KPNYQFGHNSVDFEEDTLPK 804

RESULT 15
AAU33960
ID AAU33960 standard; protein; 978 AA.
XX
AC AAU33960;
XX
DT 14-FEB-2002 (first entry)
XX
DE Staphylococcus aureus cellular proliferation protein #236.
XX
KW Antisense; prokaryotic cellular proliferation protein; antibiotic;
XX antibacterial; drug design.
XX
OS Staphylococcus aureus.
XX
PN WO200170955-A2.
XX
PD 27-SEP-2001.
XX
PF 21-MAR-2001; 2001WO-US009180.
XX
PR 21-MAR-2000; 2000US-0191078P.
XX 23-MAY-2000; 2000US-0206848P.
PR 26-MAY-2000; 2000US-0207727P.
XX 23-OCT-2000; 2000US-0242578P.
PR 27-NOV-2000; 2000US-0253625P.
XX 22-DEC-2000; 2000US-0257931P.
PR 16-FEB-2001; 2001US-0269308P.
XX
PA (ELIT-) ELITRA PHARM INC.
XX
PI Haselbeck R, Ohlsen KL, Zyskind JW, Wall D, Trawick JD, Carr GJ,
PI Yamamoto RT, Xu HH;
XX WPI; 2001-611495/70.
XX N-PSDB; AAS51819.
XX
PT New polynucleotides for the identification and development of
XX antibiotics, comprise sequences of antisense nucleic acids.
XX
PS Example 3; SEQ ID NO 5456; 51pp; English.
XX
XX The invention relates to antisense inhibitors of genes essential to
XX prokaryotic cellular proliferation, their use in identifying the genes,
XX their use in the discovery of novel antibiotics, the essential genes
XX themselves and the encoded proteins. The prokaryotes used are Escherichia
XX coli, Staphylococcus aureus, Salmonella typhi, Klebsiella pneumoniae,
XX Pseudomonas aeruginosa and Enterococcus faecalis. The invention is also
XX useful for the identification of potential new targets for antibiotic
XX development. The antisense nucleic acids can also be used to identify
XX proteins used in proliferation, to express these proteins, and to obtain
XX antibodies capable of binding to the expressed proteins. The proteins can
XX be used to screen compounds in rational drug discovery programmes. The
XX antisense nucleic acid sequence is also useful to screen for homologous
XX nucleic acids which are required for cell proliferation in a wide variety
XX of organisms. The present sequence represents an essential prokaryotic
XX cellular proliferation protein. Note: The sequence data for this patent
XX did not form part of the printed specification, but was obtained in
XX electronic format directly from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX

```

```

XX
SQ Sequence 978 AA;
Query Match 93.0%; Score 106; DB 4; Length 978;
Best Local Similarity 90.5%; Pred. No. 8e-08;
Matches 19; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 KASYOFGHNSVDFEEDTLPK 21
   |:|||||
DB 815 KPNYQFGHNSVDFEEDTLPK 835

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Search completed: October 25, 2005, 19:38:27
Job time : 60.1473 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using SW model

Run on: October 22, 2005, 02:23:36 ; Search time 15.9358 Seconds
(without alignments)
98.371 Million cell updates/sec

Title: US-10-731-238-15

Perfect score: 114
Sequence: 1 KASYQFGHNSVDFEEDLPK 21

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
1: /cgn2_6/prodata/1/iaa/5A_COMB.pep:*
2: /cgn2_6/prodata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/prodata/1/iaa/5A_COMB.pep:*
4: /cgn2_6/prodata/1/iaa/5B_COMB.pep:*
5: /cgn2_6/prodata/1/iaa/PCITUS_COMB.pep:*
6: /cgn2_6/prodata/1/iaa/beckfile1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	114	100.0	21	4	US-09-010-317-15	Sequence 15, Appl
2	109	95.6	21	4	US-09-010-317-9	Sequence 9, Appl
3	109	95.6	37	1	US-08-234-622A-4	Sequence 4, Appl
4	109	95.6	38	1	US-08-294-189-8	Sequence 8, Appl
5	109	95.6	38	1	US-08-729-767-5	Sequence 5, Appl
6	109	95.6	114	1	US-08-259-000-3	Sequence 3, Appl
7	109	95.6	139	3	US-08-856-253-8	Sequence 8, Appl
8	109	95.6	178	2	US-08-459-135A-12	Sequence 12, Appl
9	109	95.6	178	3	US-08-495-559-12	Sequence 12, Appl
10	109	95.6	1027	4	US-08-956-171E-5254	Sequence 5254, Ap
11	109	95.6	1027	4	US-08-781-986A-5254	Sequence 5254, Ap
12	105	92.1	21	4	US-09-010-317-14	Sequence 14, Appl
13	104	91.2	21	4	US-09-010-317-16	Sequence 16, Appl
14	104	91.2	21	4	US-09-010-317-23	Sequence 23, Appl
15	104	91.2	21	4	US-09-010-317-33	Sequence 33, Appl
16	103	90.4	21	4	US-09-010-317-18	Sequence 18, Appl
17	103	90.4	21	4	US-09-010-317-24	Sequence 24, Appl
18	103	90.4	21	4	US-09-010-317-27	Sequence 27, Appl
19	103	90.4	21	4	US-09-010-317-28	Sequence 28, Appl
20	103	90.4	21	4	US-09-010-317-30	Sequence 30, Appl
21	103	89.5	21	4	US-09-010-317-25	Sequence 25, Appl
22	102	89.5	21	4	US-09-010-317-29	Sequence 29, Appl
23	102	89.5	21	4	US-09-010-317-31	Sequence 31, Appl
24	102	89.5	130	2	US-08-459-135A-7	Sequence 7, Appl
25	102	89.5	130	2	US-08-459-135A-8	Sequence 8, Appl
26	102	89.5	130	3	US-08-495-559-7	Sequence 7, Appl
27	102	89.5	130	3	US-08-495-559-8	Sequence 8, Appl

28	102	89.5	174	2	US-08-459-135A-10	Sequence 10, Appl
29	102	89.5	174	2	US-08-459-135A-13	Sequence 13, Appl
30	102	89.5	174	3	US-08-495-559-10	Sequence 10, Appl
31	102	89.5	174	3	US-08-495-559-13	Sequence 13, Appl
32	102	89.5	176	3	US-08-459-135A-6	Sequence 6, Appl
33	102	89.5	181	2	US-08-459-135A-6	Sequence 6, Appl
34	102	89.5	559	4	US-08-956-171E-5251	Sequence 5251, Ap
35	102	89.5	559	4	US-08-781-986A-5251	Sequence 5251, Ap
36	101	88.6	21	4	US-09-010-317-10	Sequence 10, Appl
37	101	88.6	21	4	US-09-010-317-20	Sequence 20, Appl
38	101	88.6	21	4	US-09-010-317-22	Sequence 22, Appl
39	101	88.6	22	4	US-09-010-317-32	Sequence 32, Appl
40	101	88.6	22	4	US-09-010-317-13	Sequence 13, Appl
41	99	86.8	21	4	US-09-010-317-17	Sequence 17, Appl
42	99	86.8	21	4	US-09-010-317-19	Sequence 19, Appl
43	99	86.8	21	4	US-09-010-317-21	Sequence 21, Appl
44	99	86.8	21	4	US-09-010-317-26	Sequence 26, Appl
45	93	81.6	21	4	US-09-010-317-34	Sequence 34, Appl

ALIGNMENTS

RESULT 1
US-09-010-317-15
Sequence 15, Application US/09010317
Patent No. 6685943
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
APPLICANT: Patti, Joseph M.
APPLICANT: House-Pompeo, Karen L.
APPLICANT: Speziale, Pietro
APPLICANT: John, Danny
APPLICANT: McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
TITLE OF INVENTION: AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAMK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-09-010-317-15
Query Match 100.0%; Score 114; DB 4; Length 21;
Best Local Similarity 100.0%; Pred. No. 3.9e-12;

Matches	21; Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0.
OY	1 KASYQFGGHSVDPEEDTLPK 21							
Dd	1 KASYQFGGHSVDPEEDTLPK 21							

RESULT 2
US-09-010-317-9

Sequence 9, Application US/09010317
Patent No. 6685943
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
APPLICANT: Patti, Joseph M.
APPLICANT: House-Pompeo, Karen L.
APPLICANT: Speziale, Pietro
APPLICANT: Joh, Danny
APPLICANT: McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
TITLE OF INVENTION: AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:

TOPOLGY;
US-09-010-317-9

RESULT 3
 US-08-234-622A-4
 ; Sequence 4, Application US/08234622A
 ; Patent No. 5440014
 ;
 ; GENERAL INFORMATION:
 ;
 ; APPLICANT: HOOK, Magnus
 ;
 ; APPLICANT: MCGAVIN, Martin
 ;
 ; APPLICANT: RAUCCI, Giuseppe
 ;
 ; TITLE OF INVENTION: A FIBROBLAST BINDING PEPTIDE

NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSSEE: Burns, Doane, Swecker & Mathis
STREET: P. O. Box 1404
CITY: Alexandria
STATE: Virginia
COUNTRY: United States
ZIP: 22313-1404

Query Match	95.6%	Score 109;	DB 1;	length 37;
Best Local Similarity	95.2%	Pred. No. 4.9e-11;		
Matches 20; Conservative	0;	Mismatches 1;	Indels 0;	Gaps 0.

US-08-294-189-8
Sequence 8, Application US/08294189
Patent No. 5707822
GENERAL INFORMATION:
APPLICANT: Fischetti, Vincent A.
APPLICANT: Rakontjac, Jaana
APPLICANT: Robbins, John
TITLE OF INVENTION: GENE SERUM OPACITY FACTOR
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack Avenue
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/294,189
FILING DATE: 22-AUG-1994

CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-118
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 487-5800
TELEFAX: 201 343-1684
TELEX: 133521
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
ORGANISM: Streptococcus pyogenes
STRAIN: D734
INDIVIDUAL ISOLATE: 22
IMMEDIATE SOURCE:
CLONE: SAU3a
US-08-294-183-8

Query Match 95.6%; Score 109; DB 1; Length 38;
Best Local Similarity 95.2%; Pred. No. 5e-11;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KASYQFGHNSVDFEETLPK 21
DB 10 KPSYQFGHNSVDFEETLPK 30

RESULT 5
US-08-729-767-5
Sequence 5, Application US/08729767
Patent No. 5770702
GENERAL INFORMATION:
APPLICANT: HOOK, Magnus
APPLICANT: LINDBERG, Martin Kjell
APPLICANT: SIGNAS, Lars Christer
APPLICANT: WADSTROM, Torkel Mikael
APPLICANT: FROMAN, Gunnar
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN AS WELL AS
TITLE OF INVENTION: ITS PREPARATION
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Burns, Doane, Swecker & Mathis, L.L.P.
STREET: P.O. Box 1404
CITY: Alexandria
STATE: Virginia
COUNTRY: United States
ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/729,767
FILING DATE: 07-OCT-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/259,000
FILING DATE: 13-JUN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/007,817
FILING DATE: 22-JAN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/201,028
FILING DATE: 01-JUN-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: SE 8702272-9

FILING DATE: 01-JUN-1987
ATTORNEY/AGENT INFORMATION:
NAME: McGowan, Malcolm K.
REGISTRATION NUMBER: 39,300
REFERENCE/DOCKET NUMBER: 012889-036
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-729-767-5

Query Match 95.6%; Score 109; DB 1; Length 38;
Best Local Similarity 95.2%; Pred. No. 5e-11;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KASYQFGHNSVDFEETLPK 21
DB 17 KPSYQFGHNSVDFEETLPK 37

RESULT 6
US-08-259-000-3
Sequence 3, Application US/08259000
Patent No. 5571514
GENERAL INFORMATION:
APPLICANT: HOOK, Magnus
APPLICANT: LINDBERG, Martin Kjell
APPLICANT: SIGNAS, Lars Christer
APPLICANT: WADSTROM, Torkel Mikael
APPLICANT: FROMAN, Gunnar
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN AS WELL AS
TITLE OF INVENTION: ITS PREPARATION
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Burns, Doane, Swecker & Mathis
STREET: P.O. Box 1404
CITY: Alexandria
STATE: Virginia
COUNTRY: United States
ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/259,000
FILING DATE: 13-JUN-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: SE 8702272-9
FILING DATE: 01-JUN-1987
ATTORNEY/AGENT INFORMATION:
NAME: Meuth, Donna M
REGISTRATION NUMBER: 36,607
REFERENCE/DOCKET NUMBER: 012885-062
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 114 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-259-000-3

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Query Match          95.6%: Score 109; DB 1; Length 114;
Best Local Similarity 95.2%: Pred. No. 1,7e-10;
Matches    20; Conservative   0; Mismatches    1; Indels      0; Gaps      0;

QY      1 KASYOFGGHSNVDFEEDTLTPK 21
|-----|
Db      93 KPSYOGGGHNSVDFEEDTLPK 113

RESULT 7
US-08-856-253-8
: Sequence 8, Application US/08856253
: Patent No. 6288214
: GENERAL INFORMATION:
: APPLICANT: Hook, Magnus
: APPLICANT: Patti, Joseph M.
: APPLICANT: House-Pompeo, Karen
: APPLICANT: Sthanam, Narayana
: APPLICANT: Symersky, Jindrich
: TITLE OF INVENTION: COLLAGEN BINDING PROTEIN COMPOSITIONS
: TITLE OF INVENTION: AND METHODS OF USE
: NUMBER OF SEQUENCES: 8
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Arnold, White & Durkee
: STREET: P.O. Box 4433
: CITY: Houston
: STATE: Texas
: COUNTRY: U.S.
: ZIP: 77210
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/856,253
: FILING DATE: Concurrently Herewith
: CLASSIFICATION: 514
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 60/017,678
: FILING DATE: 16-MAY-1996
: ATTORNEY/AGENT INFORMATION:
: NAME: Kitchell, Barbara S.
: REGISTRATION NUMBER: 33,928
: REFERENCE/DOCKET NUMBER: TMK:193
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (512) 418-3000
: TELEFAX: (512) 474-7577
: INFORMATION FOR SEQ ID NO.: 8:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 139 amino acids
: TYPE: amino acid
: STRANDEDNESS:
: TOPOLOGY: linear
: US-08-856-253-8

Query Match          95.6%: Score 109; DB 3; Length 139;
Best Local Similarity 95.2%: Pred. No. 2.2e-10;
Matches    20; Conservative   0; Mismatches    1; Indels      0; Gaps      0;

QY      1 KASYOFGGHSNVDFEEDTLTPK 21
|-----|
Db      107 KPSYOGGGHNSVDFEEDTLPK 127

RESULT 8
US-08-459-135A-12
: Sequence 12, Application US/08459135A
: Patent No. 5955078
: GENERAL INFORMATION:
: APPLICANT: BURNHAM, Martin Karl Russel
: APPLICANT: CHOPRA, Ian

```

```

APPLICANT: CRITCHLEY, Ian Alfred
APPLICANT: KNOWLES, David Justin Charles
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN: MONOCLONAL ANTIBODY AND THEIR USE
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSER: Smithkline Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
STATE: PA
COUNTRY: U.S.A.
ZIP: 19406-0939
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: Fastseq, Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/459,135A
FILING DATE: 02-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB/94/00215
FILING DATE: 04-Feb-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Gimmì, Edward R
REGISTRATION NUMBER: 38,891
REFERENCE/DOCKET NUMBER: PJ0591C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-4478
TELEFAX: 610-270-5090
TELEX:
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 178 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: Protein
US-08-459-135A-12

Query Match          95.6%; Score 109; DB 2; Length 178;
Best Local Similarity 95.2%; Pred. No. 2,8e-10;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 KASYQFGHNSVDFEEDTLPK 21
        |||
Db       93 KPSTYQFGHNSVDPEEDTLPK 113

RESULT 9
US-08-495-559-12
Sequence 12, Application US/08495559A
Patent No. 6054572
GENERAL INFORMATION:
APPLICANT: BURMAN, Martin Karl Russel
APPLICANT: CHOPIRA, Ian
APPLICANT: CRITCHLEY, Ian Alfred
APPLICANT: KNOWLES, David Justin Charles
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN: MONOCLONAL
TITLE OF INVENTION: ANTI-BODY AND THEIR USE IN PREVENTING BACTERIAL ADHESION
FILE REFERENCE: PJ0591
CURRENT APPLICATION NUMBER: US/08/495,559A
CURRENT FILING DATE: 1995-08-03
EARLIER APPLICATION NUMBER: GB 9302289.5
EARLIER FILING DATE: 1993-02-05
EARLIER APPLICATION NUMBER: GB 9321592.9
EARLIER FILING DATE: 1993-10-20
NUMBER OF SEQ ID NOS: 13
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 12
LENGTH: 178
TYPE: PRP

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ORGANISM: Staphylococcus aureus
US-08-495-559-12

Query Match 95.6%; Score 109; DB 3; Length 178;
Best Local Similarity 95.2%; Pred. No. 2.8e-10;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KASYFGGHSVDFEEDTLPK 21
DB 93 KPSYFGGHSVDFEEDTLPK 113

RESULT 10
US-08-956-171E-5254

Sequence 5254, Application US/08956171E
Patent No. 6593114
GENERAL INFORMATION:

APPLICANT: Charles Kunsch

Gil H. Choi

Patrick S. Dillon

Craig A. Rosen

Steven C. Barash

Michael R. Fannon

TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences

NUMBER OF SEQUENCES: 5256

CORRESPONDENCE ADDRESS:

ADDRESSEE: Human Genome Sciences, Inc.

STREET: 9410 Key West Avenue

CITY: Rockville

STATE: Maryland

COUNTRY: USA

ZIP: 20850

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.50 inch, 1.4MB storage

COMPUTER: HP Vectra 486/33

OPERATING SYSTEM: MSDOS version 6.2

SOFTWARE: ASCII Text

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/956.171E

FILING DATE: 20-Oct-1997

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 60/009,861

FILING DATE: January 5, 1996

APPLICATION NUMBER: 08/781,986

FILING DATE: January 3, 1997

ATTORNEY/AGENT INFORMATION:

NAME: Mark J. Hyman

REGISTRATION NUMBER: 46,789

REFERENCE/DOCKET NUMBER: PB248P1

TELECOMMUNICATION INFORMATION:

TELEPHONE: (240) 314-1224

TELEFAX: (301) 309-8439

INFORMATION FOR SEQ ID NO: 5254:

SEQUENCE CHARACTERISTICS:

LENGTH: 1027 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 5254:

US-08-956-171E-5254

Query Match 95.6%; Score 109; DB 4; Length 1027;
Best Local Similarity 95.2%; Pred. No. 2e-09;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KASYFGGHSVDFEEDTLPK 21
DB 846 KPSYFGGHSVDFEEDTLPK 866

RESULT 11

US-08-781-986A-5254
Sequence 5254, Application US/08781986A
Patent No. 6737248

GENERAL INFORMATION:

APPLICANT: Charles Kunsch

TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences

NUMBER OF SEQUENCES: 5255

CORRESPONDENCE ADDRESS:

ADDRESSEE: Human Genome Sciences, Inc.

STREET: 9410 Key West Avenue

CITY: Rockville

STATE: Maryland

COUNTRY: USA

ZIP: 20850

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.50 inch, 1.4MB storage

COMPUTER: HP Vectra 486/33

OPERATING SYSTEM: MSDOS version 6.2

SOFTWARE: ASCII Text

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/781,986A

FILING DATE:

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Benson, Bob

REGISTRATION NUMBER: 30,446

REFERENCE/DOCKET NUMBER: PB248PP

TELECOMMUNICATION INFORMATION:

TELEPHONE: (301) 309-8504

TELEFAX: (301) 309-8512

INFORMATION FOR SEQ ID NO: 5254:

SEQUENCE CHARACTERISTICS:

LENGTH: 1027 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-781-986A-5254

Query Match 95.6%; Score 109; DB 4; Length 1027;
Best Local Similarity 95.2%; Pred. No. 2e-09;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KASYFGGHSVDFEEDTLPK 21
DB 846 KPSYFGGHSVDFEEDTLPK 866

RESULT 12
US-09-010-317-14

Sequence 14, Application US/09010317

Patent No. 6685943

GENERAL INFORMATION:

APPLICANT: Hook, Magnus

APPLICANT: Patti, Joseph M.

APPLICANT: House-Pompeo, Karen L.

APPLICANT: Speziale, Pietro

APPLICANT: John, Danny

APPLICANT: McGavin, Martin J.

TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS

NUMBER OF SEQUENCES: 105

CORRESPONDENCE ADDRESS:

ADDRESSEE: Arnold, White & Durkee

STREET: P.O. Box 4433

CITY: Houston

STATE: TX

COUNTRY: USA

ZIP: 77210-4433

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-09-010-317-14

Query Match 92.1%; Score 105; DB 4; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.2e-10;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SYQFGGHSVDFEEDTLPK 21
DB 3 SYQFGGHSVDFEEDTLPK 21

RESULT 13
US-09-010-317-16
Sequence 16, Application US/09010317
Patent No. 6685943
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
APPLICANT: Patli, Joseph M.
APPLICANT: House-Pompeo, Karen L.
APPLICANT: Speziale, Pietro
APPLICANT: Uoh, Danny
APPLICANT: McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
NUMBER OF SEQUENCES: 105
CURRENT APPLICATION DATA:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-09-010-317-23

TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-09-010-317-16

Query Match 91.2%; Score 104; DB 4; Length 21;
Best Local Similarity 90.5%; Pred. No. 1.7e-10;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 KASYQFGGHSVDFEEDTLPK 21
DB 1 KPYQFGGHSVDFEEDTLPK 21

RESULT 14
US-09-010-317-23
Sequence 23, Application US/09010317
Patent No. 6685943
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
APPLICANT: Patli, Joseph M.
APPLICANT: House-Pompeo, Karen L.
APPLICANT: Speziale, Pietro
APPLICANT: Uoh, Danny
APPLICANT: McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
NUMBER OF SEQUENCES: 105
CURRENT APPLICATION DATA:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-09-010-317-23

Query Match 91.2%; Score 104; DB 4; Length 21;
Best Local Similarity 90.5%; Pred. No. 1.7e-10;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 KASYQFGGHSVDFEEDTLPK 21

Db 1 KPSYQFGHNPVDFEEDTLPK 21

RESULT 15

US-09-010-317-33
; Sequence 33, Application US/09010317
; Patent No. 6685943
; GENERAL INFORMATION:
; APPLICANT: Hook, Magnus
; APPLICANT: Patti, Joseph M.
; APPLICANT: House-Pompeo, Karen L.
; APPLICANT: Speziale, Pietro
; APPLICANT: John, Danny
; APPLICANT: McGavin, Martin J.
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
; NUMBER OF SEQUENCES: 105
; TITLE OF INVENTION: AND METHODS OF USE
; CORRESPONDENCE ADDRESSES:
; ADDRESSER: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: TX
; COUNTRY: USA
; ZIP: 77210-4433
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/010,317
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/036,139
; FILING DATE: 21-JAN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Hibler, David W.
; REGISTRATION NUMBER: 41,071
; REFERENCE/DOCKET NUMBER: TAMK:189
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 512-418-3000
; TELEFAX: 512-474-7577
; INFORMATION FOR SEQ ID NO: 33:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
US-09-010-317-33

Query Match 91.2%; Score 104; DB 4; Length 21;
Best Local Similarity 95.0%; Pred. No. 1.7e-10;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Db 1 KPSYQFGHNSVDFEEDTLP 20

Search completed: October 22, 2005, 03:51:11
Job time : 15.9356 secs

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GenCore version 5.1.6
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OW protein - protein search, using BW model

Run on: October 22, 2005, 10:49:15 ; Search time 59.2367 Seconds
(without alignments)
148.005 Million cell updates/sec

Title: US-10-731-238-15

Perfect score: 114

Sequence: 1 KASYQFGHNSVDFEEDTLPK 21

BLOSUM62

Gapop 10.0, Gapext 0.5

Scoring table: 1862951 segs, 417491010 residues

Searched: Total number of hits satisfying chosen parameters: 1862951

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database:

Published Applications AA:*

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11: /cgn2_6/prodata/2/pubppaa/US09C_PUBCOMB.pep:*

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16: /cgn2_6/prodata/2/pubppaa/US10D_PUBCOMB.pep:*

17: /cgn2_6/prodata/2/pubppaa/US10E_PUBCOMB.pep:*

18: /cgn2_6/prodata/2/pubppaa/US10_NEW_PUB.pep:*

19: /cgn2_6/prodata/2/pubppaa/US11A_PUBCOMB.pep:*

20: /cgn2_6/prodata/2/pubppaa/US11_NEW_PUB.pep:*

21: /cgn2_6/prodata/2/pubppaa/US60_NEW_PUB.pep:*

22: /cgn2_6/prodata/2/pubppaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	109	95.6	21	18	US-10-731-238-9
3	109	95.6	37	20	US-11-066-697-1134
4	109	95.6	139	9	US-09-813-820-8
5	109	95.6	1018	9	US-09-815-242-5797
6	109	95.6	1018	9	US-09-815-242-12838
7	109	95.6	1018	17	US-10-470-0488-68
8	109	95.6	1027	8	US-08-781-986A-5254
9	109	95.6	1027	15	US-10-339-624-5254
10	106	93.0	961	15	US-10-282-122A-43778
11	106	93.0	978	9	US-09-815-242-5456

12	106	93.0	1001	9	US-09-815-242-12686	Sequence 12686, A
13	106	93.0	1038	15	US-10-282-122A-43827	Sequence 43827, A
14	105	92.1	21	18	US-10-731-238-14	Sequence 14, Appl
15	104	91.2	21	18	US-10-731-238-16	Sequence 16, Appl
16	104	91.2	21	18	US-10-731-238-23	Sequence 23, Appl
17	104	91.2	21	18	US-10-731-238-33	Sequence 33, Appl
18	103	90.4	21	18	US-10-731-238-18	Sequence 18, Appl
19	103	90.4	21	18	US-10-731-238-24	Sequence 24, Appl
20	103	90.4	21	18	US-10-731-238-27	Sequence 27, Appl
21	103	90.4	21	18	US-10-731-238-28	Sequence 28, Appl
22	103	90.4	21	18	US-10-731-238-30	Sequence 30, Appl
23	102	89.5	21	18	US-10-731-238-25	Sequence 25, Appl
24	102	89.5	21	18	US-10-731-238-29	Sequence 29, Appl
25	102	89.5	21	18	US-10-731-238-31	Sequence 31, Appl
26	102	89.5	388	8	US-08-901-062-1	Sequence 1, Appl
27	102	89.5	559	8	US-08-781-986A-5251	Sequence 5251, Ap
28	102	89.5	559	15	US-10-329-624-5251	Sequence 5251, Ap
29	102	89.5	940	17	US-10-470-048B-424	Sequence 424, App
30	102	89.5	948	17	US-10-470-048B-69	Sequence 69, Appl
31	101	88.6	21	18	US-10-731-238-10	Sequence 10, Appl
32	101	88.6	21	18	US-10-731-238-20	Sequence 20, Appl
33	101	88.6	21	18	US-10-731-238-22	Sequence 22, Appl
34	101	88.6	21	18	US-10-731-238-32	Sequence 32, Appl
35	101	88.6	22	18	US-10-731-238-13	Sequence 13, Appl
36	99	86.8	21	18	US-10-731-238-17	Sequence 17, Appl
37	99	86.8	21	18	US-10-731-238-19	Sequence 19, Appl
38	99	86.8	21	18	US-10-731-238-21	Sequence 21, Appl
39	99	86.8	21	18	US-10-731-238-26	Sequence 26, Appl
40	93	81.6	21	18	US-10-731-238-34	Sequence 34, Appl
41	78	68.4	14	18	US-10-731-238-61	Sequence 61, Appl
42	58	50.9	10	18	US-10-731-238-97	Sequence 97, Appl
43	57	50.0	10	18	US-10-731-238-98	Sequence 98, Appl
44	56	49.1	10	18	US-10-731-238-99	Sequence 99, Appl
45	53	46.5	10	18	US-10-731-238-101	Sequence 101, App

ALIGNMENTS

RESULT 1

US-10-731-238-15

Sequence 15, Application US/10731238

Publication No. US20050123552A1

GENERAL INFORMATION:

APPLICANT: Hook, Magnus

Patli, Joseph M.

House-Pompeo, Karen L.

Speziale, Pietro

Joh, Danny

McGavin, Martin J.

TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS

AND METHODS OF USE

NUMBER OF SEQUENCES: 105

CORRESPONDENCE ADDRESS:

ADDRESSEE: Arnold, White & Durkee

STREET: P.O. Box 4433

CITY: Houston

STATE: TX

COUNTRY: USA

ZIP: 77210-4433

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/731,238

FILING DATE: 10-Dec-2003

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/010,317

FILING DATE: 21-Jan-1998

APPLICATION NUMBER: US 60/036,139

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: FILING DATE: 21-JAN-1997
: ATTORNEY/AGENT INFORMATION:
:   NAME: Hblier, David W.
:   REGISTRATION NUMBER: 41,071
:   REFERENCE/DOCKET NUMBER: TANK:189
: TELECOMMUNICATION INFORMATION:
:   TELEPHONE: 512-418-3000
:   TELEFAX: 512-474-7577
: INFORMATION FOR SEQ ID NO: 15:
:   SEQUENCE CHARACTERISTICS:
:     LENGTH: 21 amino acids
:     TYPE: amino acid
:     STRANDEDNESS: <Unknown>
:     TOPOLOGY: linear
:   SEQUENCE DESCRIPTION: SEQ ID NO: 15:
: US-10-731-238-15
:
: Query Match      100.0%; Score 114; DB 18; Length 21;
: Best Local Similarity 100.0%; Pred. No. 4,8e-11;
: Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0.
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: QY      1 KASYOFGGHSVDFEEDTLPK 21
:         |||||
: Db      1 KASYOFGGHSVDFEEDTLPK 21
:
: RESULT 2
: US-10-731-238-9
: Sequence 9, Application US/10731238
: Publication No. US20050123552A1
:
: GENERAL INFORMATION:
: APPLICANT: Hook, Magnus
:          Patti, Joseph M.
:          House-Pompeo, Karen L.
:          Speziale, Pietro
:          Joh, Danny
:          McGavin, Martin J.
:
: TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
:
: NUMBER OF SEQUENCES: 105
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Arnold, White & Durkee
: STREET: P. O. Box 4433
: CITY: Houston
: STATE: TX
: COUNTRY: USA
: ZIP: 77210-4433
:
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Releasee #1.0, Version #1.30
:
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/10/731,238
: FILING DATE: 10-Dec-2003
: CLASSIFICATION: <Unknown>
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US/09/010,317
: FILING DATE: 21-Jan-1998
: APPLICATION NUMBER: US 60/036,139
: FILING DATE: 21-JAN-1997
:
: ATTORNEY/AGENT INFORMATION:
: NAME: Hblier, David W.
: REGISTRATION NUMBER: 41,071
: REFERENCE/DOCKET NUMBER: TANK:189
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 512-418-3000
: TELEFAX: 512-474-7577
:
: INFORMATION FOR SEQ ID NO: 9:
: SEQUENCE CHARACTERISTICS:
:   LENGTH: 21 amino acids
:   TYPE: amino acid
:   STRANDEDNESS: <Unknown>

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:      TOPOLOGY: linear
:      SEQUENCE DESCRIPTION: SEQ ID NO: 9:
US-10-731-238-9

Query Match      95.6%; Score 109; DB 18; Length 21;
Best Local Similarity 95.2%; Pred. No. 3e-10;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY      1 KASYFGHNSVDFEEDTLPK 21
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Db      1 KPSTFGHNSVDFEEDTLPK 21

RESULT 3
US-11-066-697-1134
: Sequence 1134, Application US/11066697
: Publication No. US20050187159A1
: GENERAL INFORMATION:
: APPLICANT: Bridon, Dominique P.
: APPLICANT: Ezrin, Alan M.
: APPLICANT: Milner, Peter G.
: APPLICANT: Holmes, Darren L.
: APPLICANT: Thibaudau, Karen
: TITLE OF INVENTION: PROTECTION OF ENDOGENOUS THERAPEUTIC PEPTIDES FROM
: TITLE OF INVENTION: PEPTIDASE ACTIVITY THROUGH CONUGATION TO BLOOD
: TITLE OF INVENTION: COMPONENTS
: FILE REFERENCE: 500862002301
: CURRENT APPLICATION NUMBER: US/11/066,697
: PRIOR FILING DATE: 2005-02-25
: PRIOR APPLICATION NUMBER: 09/657,276
: PRIOR FILING DATE: 2000-09-07
: PRIOR APPLICATION NUMBER: 60/153,406
: PRIOR FILING DATE: 1999-09-10
: PRIOR APPLICATION NUMBER: 60/159,783
: PRIOR FILING DATE: 1999-10-15
: NUMBER OF SEQ ID NOS: 1617
: SOFTWARE: PatentIn Ver. 2.1
: SEQ ID NO 1134
: LENGTH: 37
: TYPE: PRT
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-11-066-697-1134

Query Match      95.6%; Score 109; DB 20; Length 37;
Best Local Similarity 95.2%; Pred. No. 5.7e-10;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY      1 KASYFGHNSVDFEEDTLPK 21
      |||||||
Db      1 KPSTFGHNSVDFEEDTLPK 36

RESULT 4
US-09-813-820-8
: Sequence 8, Application US/09813820
: Patent No. US20020102262A1
: GENERAL INFORMATION:
: APPLICANT: Hook, Magnus
: APPLICANT: Patil, Joseph M.
: APPLICANT: House-Pompeo, Karen
: APPLICANT: Sthanam, Narayana
: APPLICANT: Symersky, Jindrich
: TITLE OF INVENTION: COLLAGEN BINDING PROTEIN COMPOSITIONS
: TITLE OF INVENTION: AND METHODS OF USE
: NUMBER OF SEQUENCES: 8
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Arnold, White & Durkee
: STREET: P O. Box 4433
: CITY: Houston
: STATE: Texas
:

```

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COUNTRY: U.S.
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/813,820
FILING DATE: 22-Mar-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/856,253
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Kitchell, Barbara S.
REGISTRATION NUMBER: 33,928
REFERENCE/DOCKET NUMBER: TAMPK.193
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
TELEFAX: (512) 474-7577
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 139 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-09-813-820-8

Query Match      95.6%; Score 109; DB 9; Length 139;
Best Local Similarity 95.2%; Pred. No. 2.4e-09;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 KASYQFGHNSVDFEETLPK 21
DB      107 KPSYQFGHNSVDFEETLPK 127

RESULT 5
US-09-815-242-5797
Sequence 5797, Application US/09815242
Patent No. US20020061569A1
GENERAL INFORMATION:
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Karl L.
APPLICANT: Zyskind, Judith W.
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John D.
APPLICANT: Carr, Grant J.
APPLICANT: Yamamoto, Robert T.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in
FILE REFERENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FastSeq for Windows Version 4.0
FILE REFERENCE: SONN.03505
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SEQ ID NO 5797
LENGTH: 1018
TYPE: PRT
ORGANISM: Staphylococcus aureus
US-09-815-242-5797

Query Match      95.6%; Score 109; DB 9; Length 1018;
Best Local Similarity 95.2%; Pred. No. 2.1e-08;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 KASYQFGHNSVDFEETLPK 21
DB      837 KPSYQFGHNSVDFEETLPK 857

RESULT 6
US-09-815-242-12838
Sequence 12838, Application US/09815242
Patent No. US20020061569A1
GENERAL INFORMATION:
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Karl L.
APPLICANT: Zyskind, Judith W.
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John D.
APPLICANT: Carr, Grant J.
APPLICANT: Yamamoto, Robert T.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in
FILE REFERENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 12838
LENGTH: 1018
TYPE: PRT
ORGANISM: Staphylococcus aureus
US-09-815-242-12838

Query Match      95.6%; Score 109; DB 9; Length 1018;
Best Local Similarity 95.2%; Pred. No. 2.1e-08;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 KASYQFGHNSVDFEETLPK 21
DB      837 KPSYQFGHNSVDFEETLPK 857

RESULT 7
US-10-470-048B-68
Sequence 68, Application US/10470048B
Publication No. US2005003744A1
GENERAL INFORMATION:
APPLICANT: MEINKE ET AL.
TITLE OF INVENTION: A METHOD FOR IDENTIFICATION, ISOLATION AND PRODUCTION OF
FILE REFERENCE: SONN.03505
```

US-10-329-624-5254

! APPLICANT: Carr, Grant

```
APPLICANT: Yamamoto, Robert
APPLICANT: Foreyth, R.
APPLICANT: Xu, H.
TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REFERENCE: ELITRA.034A
CURRENT FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/230,335
PRIOR FILING DATE: 2000-09-06
PRIOR APPLICATION NUMBER: 60/230,347
PRIOR FILING DATE: 2000-09-09
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/267,636
PRIOR FILING DATE: 2001-02-09
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 78614
SOFTWARE: PatentIn Version 3.1
SEQ ID NO 43778
LENGTH: 961
TYPE: PR1
ORGANISM: Staphylococcus aureus
US-10-282-122A-43778
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Query Match      93.0%; Score 106; DB 15; Length 961;
Best Local Similarity 90.5%; Pred. No. 6,1e-08;
Matches 19; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
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QY      1 KASYQFGHNSVDFEEDTLPK 21
DB      784 KPNYQFGHNSVDFEEDTLPK 804
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RESULT 11
US-09-815-242-5456
Sequence 5456, Application US/09815242
Patent No. US20020061569A1
GENERAL INFORMATION:
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Karl L.
APPLICANT: Zykkind, Judith W.
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John D.
APPLICANT: Carr, Grant J.
APPLICANT: Yamamoto, Robert T.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in
FILE REFERENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
```

```
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 5456
LENGTH: 978
TYPE: PR1
ORGANISM: Staphylococcus aureus
US-09-815-242-5456
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```
Query Match      93.0%; Score 106; DB 9; Length 978;
Best Local Similarity 90.5%; Pred. No. 6,2e-08;
Matches 19; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
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QY      1 KASYQFGHNSVDFEEDTLPK 21
DB      815 KPNYQFGHNSVDFEEDTLPK 835
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```
RESULT 12
US-09-815-242-12686
Sequence 12686, Application US/09815242
Patent No. US20020061569A1
GENERAL INFORMATION:
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Karl L.
APPLICANT: Zykkind, Judith W.
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John D.
APPLICANT: Carr, Grant J.
APPLICANT: Yamamoto, Robert T.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in
FILE REFERENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 12686
LENGTH: 1001
TYPE: PR1
ORGANISM: Staphylococcus aureus
US-09-815-242-12686
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```
Query Match      93.0%; Score 106; DB 9; Length 1001;
Best Local Similarity 90.5%; Pred. No. 6,4e-08;
Matches 19; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
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QY      1 KASYQFGHNSVDFEEDTLPK 21
DB      838 KPNYQFGHNSVDFEEDTLPK 858
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RESULT 13
US-10-282-122A-43827
Sequence 43827, Application US/10282122A
```

Publication No. US20040029129A1
GENERAL INFORMATION:
APPLICANT: Wang, Liangu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Hasebeck, Robert
APPLICANT: Ohlsen, Karl
APPLICANT: Zvekand, Judith
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John
APPLICANT: Carr, Grant
APPLICANT: Yamamoto, Robert
APPLICANT: Foreyth, R.
APPLICANT: Xu, H.
TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REFERENCE: ELITRA.034A
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/230,335
PRIOR FILING DATE: 2000-09-06
PRIOR APPLICATION NUMBER: 60/230,347
PRIOR FILING DATE: 2000-09-09
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/267,636
PRIOR FILING DATE: 2001-02-09
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 78614
SOFTWARE: Patent version 3.1
SEQ ID NO: 43827
LENGTH: 1038
TYPE: PRT
ORGANISM: Staphylococcus aureus
US-10-282-122A-43827
Query Match 93.0%; Score 106; DB 15; Length 1038;
Best Local Similarity 90.5%; Pred. No. 6.6e-08;
Matches 19; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 KASYOFGHNSVDFEEDTLPK 21
DB 833 KENYOGGHNSVDFEEDTLPK 853
RESULT 14
US-10-731-238-14
Sequence 14, Application US/10731238
Publication No. US20050123552A1
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
Patti, Joseph M.
House-Pompeo, Karen L.
Speziale, Pietro
Joh, Danny
McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433

CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/731,238
FILING DATE: 10-Dec-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/010,117
FILING DATE: 21-Jan-1998
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TANK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 14:
US-10-731-238-14
Query Match 92.1%; Score 105; DB 18; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.3e-09;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3 SYOFGHNSVDFEEDTLPK 21
DB 3 SYOFGHNSVDFEEDTLPK 21
RESULT 15
US-10-731-238-16
Sequence 16, Application US/10731238
Publication No. US20050123552A1
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
Patti, Joseph M.
House-Pompeo, Karen L.
Speziale, Pietro
Joh, Danny
McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/731,238
FILING DATE: 10-Dec-2003
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/010,317
 FILING DATE: 21-Jan-1998
 APPLICATION NUMBER: US 60/036,139
 FILING DATE: 21-Jan-1997

ATTORNEY/AGENT INFORMATION:

NAME: Hibler, David W.
 REGISTRATION NUMBER: 41,071

REFERENCE/DOCKET NUMBER: TAMK:189
 TELECOMMUNICATION INFORMATION:

TELEPHONE: 512-418-3000
 TELEFAX: 512-474-7577

INFORMATION FOR SEQ ID NO: 16:

SEQUENCE CHARACTERISTICS:

LENGTH: 21 amino acids

TYPE: amino acid

STRANDEDNESS: <Unknown>

TOPOLOGY: linear

SEQUENCE DESCRIPTION: SEQ ID NO: 16:

US-10-731-238-16

Query Match 91.2%; Score 104; DB 18; Length 21;

Best Local Similarity 90.5%; Pred. No. 1.9e-09; Mismatches 2; Indels 0; Gaps 0;

Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 KASYQFGHNSVDFEEDTLPK 21

DB 1 KPPYQFGHNSVDFEEDTLPK 21

Search completed: October 22, 2005, 11:34:39
 Job time : 60.2367 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 22, 2005, 02:23:36 ; Search time 10.5465 Seconds
(without alignments)
191.586 Million cell updates/sec

Title: US-10-731-238-15

Sequence: 1 KASYQFGHNSVDFEEDLPK 21

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	109	95.6	1018	2 A32192	fibronectin-binding
2	106	93.0	961	2 G90053	hypothetical prote
3	106	93.0	1038	2 H90053	hypothetical prote
4	102	89.5	940	2 S19702	fibronectin-binding
5	49	43.0	474	2 B84357	serine-tRNA synthet
6	47	41.2	347	1 HPMS	haptoglobin precur
7	46	40.4	257	2 A36057	MHC class I histoc
8	46	40.4	453	2 H70333	conserved hypotet
9	45.5	39.9	1038	2 T15038	hypothetical prote
10	45	39.5	288	2 T37395	probable 33.6k pro
11	45	39.5	288	2 A42518	A8R protein - vacc
12	45	39.5	462	1 A39356	3-oxoacyl-[acyl-ca
13	45	39.5	469	2 T10061	3-oxoacyl-[acyl-ca
14	45	39.5	690	2 T33321	hypothetical prote
15	44	38.6	427	2 D5159	3-phosphoshikimate
16	44	38.6	431	2 D98025	3-phosphoshikimate
17	44	38.6	1926	2 JC4842	DNA-binding nuclea
18	43	37.7	188	2 E97318	transcription regu
19	43	37.7	327	1 D32550	phosphoprotein pho
20	43	37.7	327	1 S13829	phosphoprotein pho
21	43	37.7	327	1 S41052	phosphoprotein pho
22	43	37.7	327	2 I76330	phosphoprotein pho
23	43	37.7	327	2 I76330	phosphoprotein pho
24	43	37.7	350	2 A82299	outer membrane pro
25	43	37.7	551	2 S57447	HPHRII-7 protein -
26	43	37.7	928	1 VGBEMC	glycoprotein B pre
27	43	37.7	949	2 D90803	alpha-I adhesin-lik
28	43	37.7	987	2 A64474	hypothetical prote
29	43	37.7	1005	2 H85611	probable adhesin Z

30	43	37.7	1091	2 G64964	hypothetical prote
31	43	37.7	1544	2 T29482	hypothetical prote
32	42.5	37.3	899	2 S49634	hypothetical prote
33	42	36.8	168	2 AE0192	probable C4-dicard
34	42	36.8	197	2 C69779	NAD(P)H oxidoreduc
35	42	36.8	296	2 S38907	probable phosphati
36	42	36.8	322	2 D95078	transcription regu
37	42	36.8	331	2 T51419	CARBONIC ANHYDRASE
38	42	36.8	336	1 S28412	carbonate dehydrat
39	42	36.8	348	2 A97946	regulatory functio
40	42	36.8	349	2 H82116	flagellar motor sw
41	42	36.8	353	2 E64641	hypothetical prote
42	42	36.8	362	2 F71872	hypothetical prote
43	42	36.8	371	2 A88520	41.8k hypothetical
44	42	36.8	398	2 F75017	probable glycine C
45	42	36.8	398	2 E71454	probable glycine C

ALIGNMENTS

RESULT 1

A32192

C:Species: Staphylococcus aureus

C>Date: 31-Jul-1989 #sequence_revision 31-Jul-1989 #text_change 16-Feb-1997

C:Accession: A32192

R:Signaess, C.; Raucel, G.; Joensson, K.; Lindgren, P.E.; Anantharamaiah, G.M.; Hoeeck, M.
Proc. Natl. Acad. Sci. U.S.A. 86, 699-703, 1989

A:Title: Nucleotide sequence of the gene for a fibronectin-binding protein from Staphyloc
A:Reference number: A32192; MUID:8908998; PMID:2521391

A:Accession: A32192

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-1018 <SIG>

A:Cross-references: GB:J04151

C:Keywords: fibronectin binding

Query Match

Best Local Similarity 95.6%; Score 109, DB 2; Length 1018;
Pred. No. 3.4e-09;

Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KASYQFGHNSVDFEEDLPK 21

DB 837 KPSYQFGHNSVDFEEDLPK 857

RESULT 2

hypothetical protein fnbB [imported] - Staphylococcus aureus (strain N315)

C:Species: Staphylococcus aureus

C>Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004

R:Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguci
ma, A.; Mizutani, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.
C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001

A:Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.

A:Reference number: A89758; MUID:21311952; PMID:11418146

A:Accession: G90053

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-961 <KOR>

A:Cross-references: UNIPROT:Q99RD3; GB:BA000018; PID:g13702452; PIDN:BA843593.1; GSPDB:G

A:Experimental source: strain N315

C:Genetics:

A:Gene: fnbB

Query Match 93.0%; Score 106, DB 2; Length 961;
Best Local Similarity 90.5%; Pred. No. 9.6e-09;

Matches 19; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 KASYQFGHNSVDFEEDLPK 21

DB 784 KPNYQFGHNSVDFEEDTLPK 804

RESULT 3

hypothetical protein fnb [imported] - Staphylococcus aureus (strain N315)

C/Species: Staphylococcus aureus
C/Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004

C/Accession: H90053

R/Kuroda, M.; Ohba, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguc
ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.;
C.; Shiba, T.; Hatori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.

Lancet 357, 1225-1240, 2001

A/Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.

A/Reference number: A89758; PMID:21311952; PMID:11418146

A/Accession: H90053

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-1038 <KUP>

A/Cross-references: UNIPROT:Q99RD2; GB:BA000018; PID:g13702453; PIDN:BA843594.1; GSPDB:G

A/Experimental source: strain N315

C/Genetics:

A/Genes: fnb

Query Match 93.0%; Score 106; DB 2; Length 1038;
Best Local Similarity 90.5%; Pred. No. 1e-08; Indels 0; Gaps 0;
Matches 19; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 KASYQFGHNSVDFEEDTLPK 21

DB 833 KPNYQFGHNSVDFEEDTLPK 853

RESULT 4

fibronectin-binding protein B - Staphylococcus aureus

C/Species: Staphylococcus aureus
C/Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004

C/Accession: S19702

R/Joensson, K.; Signaes, C.; Mueller, H.P.; Lindberg, M.

Eur. J. Biochem. 202, 1041-1048, 1991

A/Title: Two different genes encode fibronectin binding proteins in Staphylococcus aureus

A/Reference number: S19702; PMID:92111475; PMID:1837266

A/Accession: S19702

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-940 <QOB>

A/Cross-references: UNIPROT:Q53682; EMBL:X62992; NID:g49040; PIDN:CAA44726.1; PID:G58156

C/Keywords: fibronectin binding

Query Match 89.5%; Score 102; DB 2; Length 940;
Best Local Similarity 85.7%; Pred. No. 4.1e-08;
Matches 18; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 KASYQFGHNSVDFEEDTLPK 21

DB 773 KPNYQFGHNSVDFEEDTLPK 793

RESULT 5

serine-tRNA synthetase [imported] - Halobacterium sp. NRC-1

C/Species: Halobacterium sp. NRC-1
C/Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004

C/Accession: B84357

R/Kg, M.V.; Kennedy, S.P.; Mahatras, G.G.; Benjuiet, B.; Pan, M.; Shukla, H.D.; Laeky, S
; Leichauer, B.; Kallier, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Jabid
Jung, K.H.; Alam, M.; Fretche, T.

Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000

A/Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ebhardt, H.; Lowe, T.M.; Li

A/Title: Genome sequence of Halobacterium species NRC-1.

A/Reference number: A84160; PMID:20504483; PMID:11016950

A/Accession: B84357
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-474 <STO>

A/Cross-references: UNIPROT:Q9HNU8; GB:AE004437; NID:g10581491; PIDN:AG30222.1; GSPDB:G

C/Genetics:

A/Genes: serS

C/Superfamily: serine-tRNA ligase

Query Match 43.0%; Score 49; DB 2; Length 474;
Best Local Similarity 41.2%; Pred. No. 6.6;
Matches 7; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 3 SYQFGHNSVDFEEDTL 19

DB 234 AVRIGENDADYDDDL 250

RESULT 6

hapoglobin precursor - mouse

N/Contains: hapoglobin alpha chain; hapoglobin beta chain
C/Species: Mus musculus (house mouse)

C/Date: 23-Mar-1995 #sequence_revision 31-May-1996 #text_change 18-Jun-1999

C/Accession: A48918

R/Yang, F.; Linhan, L.A.; Friedrichs, W.E.; Lalle, P.A.; Sakaguchi, A.Y.; Bowman, B.H.

Genomics 18, 374-380, 1993

A/Title: Characterization of the mouse hapoglobin gene.

A/Reference number: A48918; PMID:94117006; PMID:8288241

A/Accession: A48918

A/Molecule type: mRNA

A/Residues: 1-347 <YAN>

A/Cross-references: GB:S67972; NID:g461137; PIDN:AA829697.1; PID:g461138

A/Note: sequence extracted from NCBI backbone (NCBIN:142156, NCBI:142157); sequence inc

C/Comment: The mature hapoglobin molecule is a dimer of heterodimers, the two chains of

C/Comment: Hapoglobin is a plasma glycoprotein; hapoglobin forms a complex with hemogl

C/Genetics:

A/Genes: Hp

A/Map position: 8

C/Superfamily: hapoglobin; complement factor H repeat homology; trypsin homology

C/Keywords: acute phase; glycoprotein; hemoglobin binding; heterodimer; iron transport

F/1-18/Domain: signal sequence #status predicted <SIG>

F/19-101/Product: hapoglobin alpha chain #status predicted <ACH>

F/103-347/Product: complement factor H repeat homology <FH2>

F/103-347/Product: hapoglobin beta chain #status predicted <BCH>

F/103-340/Domain: trypsin homology <TRY>

F/33/Disulfide bonds: interchain #status predicted

F/32-86,90-207,250-281,292-322/Disulfide bonds: #status predicted

F/148,182,256,264/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 41.2%; Score 47; DB 1; Length 347;
Best Local Similarity 50.0%; Pred. No. 9.9;
Matches 7; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

QY 8 GHNSVDFEEDTLPK 21

DB 22 GNDAMDFEDSCPK 35

RESULT 7

MHC class I histocompatibility antigen alpha chain 1 (clone-lambdaTLAI-1) - common carp

C/Species: Cyprinus carpio (common carp)
C/Date: 18-Jan-1991 #sequence_revision 18-Jan-1991 #text_change 09-Jul-2004

C/Accession: A36057

R/Hashimoto, K.; Nakanishi, T.; Kurosawa, Y.

Proc. Natl. Acad. Sci. U.S.A. 87, 6863-6867, 1990

A/Title: Isolation of carp genes encoding major histocompatibility complex antigens.

A/Reference number: A36057; PMID:90370884; PMID:2395879

A/Accession: A36057

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-257 <HAS>

A; Cross-references: UNIPROT:Q95589; GB:M37106

Query Match	40.4%;	Score 46;	DB 2;	Length 257;
Best Local Similarity	56.2%;	Pred. No. 10;		
Matches	9;	Conservative	1;	Mismatches 6; Indels

```
Qy      4 YQFGHNSVDFEEDTL 19
         ||||:|||||
Db     108 YGFGGEDCVAFNSDL 123
```

RESULT 8
H70333

C/Species: *Aquilex aeolicus*
C/Date: 08-May-1998 #sequence_rev1sion 08-May-1998 #text_change 09-Jul-2004
C/Accession: H70333
C/Decker, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Gra

A:Title: The complete genome of the hyperthermophilic bacterium *Aquifex aeolicus*
A:Reference number: A70300; MUID:98196666; PMID:9537320

A:Accession: H/0333
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA

A:Accessions: 1-553 <A>
A:Cross-references: UNIPROT:O66700; GB:AE000687; NID:G2983050; PIDN:AA006670.1; PID:G2983050
A:Experimental source: strain VF5
C:Categories:

A;Gene: aq_378

Query Match	40.4%;	Score 46;	DB 2;	Length 453;
Best Local Similarity	53.8%;	Pred. No. 19;		
Matches	7;	Conservative	4;	Mismatches 2;
				Indels

```
QY      3 SYQFGGHSVDPE 15
          ||| :|||
Db     114 SYSPGSYNTLEFE 126
```

RESULT 9
T15098
hypothetical protein T22B1.5 - *Caenorhabditis elegans*

C:Species: *Caenorhabditis elegans*
C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C:Accession: T15098

A/Description: The sequence of *C. elegans* cosmid T22B11.
 A/Defining features: 710203
 R/Kohling, T.; Wohlmann, P.
 submitted to the EMBL Data Library, December 1997

A/Accession: T15098
A/Reference number: 484292
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA

A: nucleotide sequence
A: residues: 1-1038 <ROH>
A: cross-references: UNIPROT: O61199; EMBL: AF039040; NID: g2736374; PTD: g2736379; PIDN: AAB3
A: experimental source: strain Bristol N2; clone T2B11

A;Map position: 4
A;Gene: CESP:T22B1.5
C;Genetics:

A:introns: 45/3: 128/2; 225/3: 659/3: 707/3: 820/3: 966/3
C:superfamily: oxoglutarate dehydrogenase (lipoamide); thiamin pyrophosphate-binding domain
P:420-465/Domain: thiamin pyrophosphate-binding domain homology <RTB>

Query Match	39.9%	Score 45.5;	DB 2;	Length 1038;
Best Local Similarity	37.0%	Pred. No. 57;		
Matches 10;	Conservative 3;	Mismatches 5;	Indels 9;	Gaps 1;

```

Oy      3 SYQFGCHNSVDPE-----EDTLP 20
          ||| ||| | : |||
Db      156 SYQTRGHNIADLPKIGINSADDDTIP 182

```

RESULT 10

T37395
probable 33.6K protein - vaccinia virus (strain Ankara)

C:Species: vaccinia virus
A:Variety: strain Ankara
C:Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 09-Jul-2004
C:Accession: U37395
C:Antoine, G.; Scheiflinger, F.; Falkner, F.G.; Dörner, F.

A;Description: The complete genomic sequence of the Modified Vaccinia Ankara (MVA) strain submitted to the EMBL Data Library, March 1997

A:Accession: U31395
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Description: 1,288 bp

A/References: 1-208 (2012)
A/Cross-references: UNIPROT:O57221; EMBL:U94848; PIDN:AAB96520.1
A/Experimental source: strain Ankara
C/Genetics:

C/GeneCats:
A/Note: MVA119R
C/Superfamily: vaccinia virus probable 33.6K protein

Query Match	39.5%	Score 45	DB 2	Length 288
Best Local Similarity	53.3%	Pred. No. 17		
Matches 8	Conservative 2	Mismatches 5	Indels 0	Gaps 0

```
QY      1 KASYQFGHNSVDFE 15
        | |||| : : |||
Db      141 KLG YQFGNTHVYDFE 155
```

RESULI 11
A42518
A8R protein - vaccinia virus (strain Copenhagen)
C.Species: vaccinia virus

A:Note: host Homo sapiens (man)
C:Date: 09-Nov-1990 #sequence_revision 09-Nov-1990 #text_change 09-Jul-2004
C:Accession: A42518

R;Johnson, G.P.
submitted to GenBank, June 1990
A;Reference number: A33172

A;Accession: A42518
A;Status: preliminary
A;molecule type: DNA

A:Residues: 1-288 <JOH>
A:Cross-references: UNIPROT:P20986
C:Superfamily: vaccinia virus probable 33.6K protein

Query Match	39.5%;	Score 45;	DB 2;	Length 288;
Best Local Similarity	53.3%;	Pred. No. 17;		
Matches	8;	Conservative	2;	Mismatches 5;
				Indels 0;
				Gaps 0;

QY	1	KASYQFGCHNSVDFE	15
		:	
Db	141	KLGYQFGNHYHYDFE	155

RESULT 12
A29356
3-oxocetyl-[acyl-carrier-protein] synthase (EC 2.3.1.41) I beta chain precursor, chloroplast

N;Alternate names: beta-vetoxacyl-[acyl carrier protein] synthase 1
C;Species: Hordeum vulgare (barley)
C;Date: 06-Mar-1992 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004

C; Accession: A39356; A45129
R; Siggaard-Andersen, M.; Kauppinen, S.; von Wettstein-Knowles, P.
Proc. Natl. Acad. Sci. U.S.A. 88, 4114-4118, 1991
Title: Determination of the structure of a camellia-binding beta-ketoacyl-

A:Reference number: A39356; MID:91239517; PMID:2034657
A:Accession: A39356
A:Molecular type: mRNA

A:Residue: 1-462 <SIG>
A:Cross-references: UNIPROT:P23902; GB:M60410; NID:g167064; PIDN:AAA32968.1; PID:g167065
A:Experimental source: CV: Bonus, leaf

A; Note: parts of this sequence, including the amino end of the mature protein, were confirmed by R. Kauppinen, S.

J. Biol. Chem. 267, 23999-24006, 1992
 A:Title: Structure and expression of the KasII gene encoding a beta-ketoacyl-acyl carrier
 A:Reference number: A45129; M0ID:93054767; PMID:1429736
 A:Accession: A45129
 A:Molecule type: DNA
 A:Residues: 1-395,397-414, 'T', 415-462 <KAU>
 A:Cross-references: cv. Bonus
 A:Note: sequence inconsistent with the nucleotide translation; translation agrees with E
 A:Note: sequence extracted from NCBI backbone (NCBIP:118934)
 C:Genetics:
 A:Gene: KasII2
 A:Map position: 2
 A:introns: 144/3; 288/3; 346/3; 384/3; 418/3; 441/1
 C:Complex: homodimer or heterodimer with alpha chain
 C:Superfamily: 3-oxoacyl-[acyl-carrier-protein] synthase I; 3-oxoacyl-[acyl-carrier-prot
 C:Keywords: acyltransferase; chloroplast; fatty acid biosynthesis; heterodimer; homodime
 F:1-36/Domain: transit peptide (chloroplast) #status predicted <TNP>
 F:16-462/Product: 3-oxoacyl-[acyl-carrier-protein] synthase I beta chain #status experim
 F:68-457/Domain: 3-oxoacyl-[acyl-carrier-protein] synthase I homology <OAS>
 F:213/Active site: Cys #status experimental

Query Match 39.5%; Score 45; DB 1; Length 462;
 Best Local Similarity 80.0%; Pred. No. 28;
 Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 3 SYOFGHNSV 12
 | : ||||| |
 Db 445 SFOFGHNSV 454

RESULT 13
 T10061
 3-oxoacyl-[acyl-carrier-protein] synthase (EC 2.3.1.41) precursor, chloroplast - castor
 N:Alternate names: beta-ketoacyl-[acyl carrier protein] synthase
 C:Species: Ricinus communis (castor bean)
 C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004
 C:Accession: T10061
 R:Gene: A.L.
 Submitted to the EMBL Data Library, April 1993
 A:Description: Cloning and molecular characterization of B-ketoacyl-ACP synthases from er
 A:Reference number: Z16924
 A:Accession: T10061
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-469 <GEN>
 A:Cross-references: UNIPROT:Q41135; EMBL:LJ3242; NID:9294667; PID:9294668
 C:Genetics:
 A:Genome: nuclear
 C:Function:
 A:Pathway: fatty acid biosynthesis
 C:Superfamily: 3-oxoacyl-[acyl-carrier-protein] synthase I; 3-oxoacyl-[acyl-carrier-prot
 C:Keywords: acyltransferase; chloroplast; fatty acid biosynthesis
 F:1-42/Domain: transit peptide (chloroplast) #status predicted <TNP>
 F:43-469/Product: 3-oxoacyl-[acyl-carrier-protein] synthase #status predicted <MAT>
 F:77-464/Domain: 3-oxoacyl-[acyl-carrier-protein] synthase I homology <OAS>

Query Match 39.5%; Score 45; DB 2; Length 469;
 Best Local Similarity 80.0%; Pred. No. 29;
 Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 3 SYOFGHNSV 12
 | : ||||| |
 Db 452 SFOFGHNSV 461

RESULT 14
 T33321
 hypothetical protein C09E8.3 - Caenorhabditis elegans
 C:Species: Caenorhabditis elegans
 C:Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
 C:Accession: T33321
 R:Du, Z.; Graves, T.; Gibson, A.
 submitted to the EMBL Data Library, July 1998

A:Description: The sequence of Caenorhabditis elegans cosmid C09E8.
 A:Reference number: Z21322
 A:Accession: T33321
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-690 <DU2>
 A:Cross-references: UNIPROT:Q76555; EMBL:AF077529; PIDN:MAC26253.1; GSPDB:GN00020; CESP:
 A:Experimental source: strain Bristol N2; clone C09E8
 C:Genetics:
 A:Gene: CESP:C09E8.3
 A:Map position: 2
 A:introns: 14/1; 38/3; 262/3; 333/3; 381/1; 413/3; 492/2

Query Match 39.5%; Score 45; DB 2; Length 690;
 Best Local Similarity 42.1%; Pred. No. 44;
 Matches 8; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

OY 1 KASYOFGHNSVDFEEDTL 19
 | : ||||| |
 Db 296 KRALMGCGQNVDPQKTL 314

RESULT 15
 D95159
 3-phosphoshikimate 1-carboxyvinyltransferase [imported] - Streptococcus pneumoniae (stra
 C:Species: Streptococcus pneumoniae
 C:Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 09-Jul-2004
 C:Accession: D95159
 R:Teitelin, H.; Neilson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Heide
 on, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapfle, I
 neon, T.; Hickey, E.K.; Holt, I.E.
 Science 293, 498-506, 2001
 A:Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison,
 A:Title: Complete genome Sequence of a virulent isolate of Streptococcus pneumoniae.
 A:Reference number: A95000; M0ID:2157209; PMID:11463916
 A:Accession: D95159
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-427 <KUR>
 A:Cross-references: UNIPROT:Q9S400; GB:AE005672; PIDN:AAK75469.1; PID:gl4972856; GSPDB:IG
 A:Experimental source: strain TIGR4
 C:Genetics:
 A:Gene: SP1371
 C:Superfamily: 3-phosphoshikimate 1-carboxyvinyltransferase; 3-phosphoshikimate 1-carboxy

Query Match 38.6%; Score 44; DB 2; Length 427;
 Best Local Similarity 60.0%; Pred. No. 38;
 Matches 9; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

OY 5 OFGHNVSDFEEDTL 19
 ||||| ||||| :
 Db 202 OFGHNVSDFEEDTL 216

Search completed: October 22, 2005, 04:13:47
 Job time : 11.5465 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 22, 2005, 02:23:35 ; Search time 51.4314 Seconds
(without alignments)
209,087 Million cell updates/sec

Title: US-10-731-238-15
Perfect score: 114
Sequence: 1 KASYOGGHNSYDFEEDLPK 21

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues
Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: uniprot_03:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	109	95.6	1018	1 FNBA STAU	P14738 staphylococ
2	106	93.0	961	2 Q99RD3	Q99rd3 staphylococ
3	106	93.0	961	2 Q7A3J8	Q7a3j8 staphylococ
4	106	93.0	965	2 Q6GDU5	Q6gdu5 staphylococ
5	106	93.0	1015	2 Q8NUJ7	Q8nuj7 staphylococ
6	106	93.0	1015	2 Q6G6H3	Q6g6h3 staphylococ
7	106	93.0	1038	2 Q99RD2	Q99rd2 staphylococ
8	106	93.0	1038	2 Q7A3J7	Q7a3j7 staphylococ
9	102	89.5	940	2 Q516R2	Q516r2 staphylococ
10	102	89.5	943	2 Q8NUJ8	Q8nuj8 staphylococ
11	102	89.5	957	2 Q6G6H4	Q6g6h4 staphylococ
12	97	85.1	152	2 Q9AEP9	Q9aep9 staphylococ
13	52	45.6	772	2 Q9AD03	Q9ad03 streptomyce
14	50	43.9	245	2 Q08866	Q08866 carassius a
15	49	43.0	305	2 Q8DUZ9	Q8duz9 streptococc
16	49	43.0	460	1 SYS HALM1	Q9huj8 halobacteri
17	49	43.0	497	2 Q9FTU7	Q9ftu7 brassica na
18	49	43.0	1726	2 Q6G4Z9	Q6g4z9 bartonella
19	48	42.1	229	2 Q8HLQ8	Q8hlq8 dictyoides
20	48	42.1	311	2 Q938H3	Q938h3 haemophilus
21	48	42.1	316	2 Q938H2	Q938h2 haemophilus
22	48	42.1	319	2 Q9SYW6	Q9syw6 gossypium h
23	48	42.1	326	2 Q8LSC8	Q8lsc8 gossypium h
24	47	41.2	347	1 HPT MOUSE	Q61646 mus musculu
25	47	41.2	347	1 HPT MOUSE	Q60574 mus caroli
26	47	41.2	347	1 HPT MUSCR	Q65558 mus saxicol
27	47	41.2	347	1 HPT MUSSA	Q63927 mus sp. hap
28	47	41.2	353	1 Q8P8 HABIN	Q48221 haemophilus
29	47	41.2	392	2 Q64P55	Q64p55 bacteroides
30	47	41.2	482	2 Q76K22	Q76k22 streptococc
31	47	41.2	608	2 Q7Q7P9	Q7q7p9 giardia lam

32	46	40.4	225	2 Q6DH47	Q6dh47 brachydanio
33	46	40.4	255	2 Q7NNC7	Q7nncc gloeobacter
34	46	40.4	257	2 Q95589	Q95589 cyprinus ca
35	46	40.4	453	2 Q66700	Q66700 aquilex aeo
36	46	40.4	738	2 Q6FAM2	Q6fam2 acinetobact
37	46	40.4	1421	2 Q8FVU4	Q8fvu4 corynebacte
38	45.5	39.9	177	2 Q8VLA4	Q8vla4 actinobacil
39	45.5	39.9	177	2 Q8VLA4	Q8vla4 actinobacil
40	45.5	39.9	177	2 Q8VQ81	Q8vqb1 actinobacil
41	45.5	39.9	177	2 Q8VQ82	Q8vqb2 actinobacil
42	45.5	39.9	177	2 Q8VQ82	Q8vqb2 actinobacil
43	45.5	39.9	1029	2 Q61199	Q61199 caenorhabdi
44	45	39.5	229	2 Q8HLP5	Q8hlp5 dictyus ar
45	45	39.5	280	2 Q7S3M2	Q7s3m2 neurospora

ALIGNMENTS

RESULT 1
FNBA STAU STANDARD; PRT; 1018 AA.
ID FNBA STAU
AC P14738;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Fibronectin-binding protein precursor (FNBP).
GN Name=fnba;
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1280;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NCTC 8325-4;
RX MEDLINE=89098998; PubMed=2521391;
RA Signes C., Raucel G., Joensen K., Lindgren P.-E.,
R. Anantharamaiah G.M., Hoeck M., Lindberg M.;
RT "Nucleotide sequence of the gene for a fibronectin-binding protein
from Staphylococcus aureus: use of this peptide sequence in the
synthesis of biologically active peptides."
Proc. Natl. Acad. Sci. U.S.A. 86:699-703(1989).
RL
CC -!- FUNCTION: The ability of bacteria to bind fibronectin has been
proposed as a virulence factor enabling bacteria to colonize wound
tissues and blood clots. Binding of plasma fibronectin to the
bacterial surface might block adhesion receptors on S.aureus, thus
representing an important defense mechanism against tissue
invasion.
CC -!- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
an amide bond (Potential).
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
or send an email to license@isb-sib.ch).
CC
CC EMBL: J04151; AAA26632.1; -!
DR InterPro: IPR004237; Fn_bind.
DR InterPro: IPR005877; Gpob_YsIRK.
DR InterPro: IPR001899; Gram_pos_anchor.
DR Pfam: PF02986; Fn_bind; 1.
DR Pfam: PF00746; Gram_pos_anchor; 1.
DR Pfam: PF04650; YsIRK_signal; 1.
DR TIGRFAMs: TIGR01167; LpxNG_anchor; 1.
DR TIGRFAMs: TIGR01168; YsIRK_signal; 1.
DR TIGRFAMs: TIGR01168; YsIRK_signal; 1.
DR PROSITE: PS50847; GRAM_POS_ANCHORING; 1.
KW Cell adhesion; Cell wall; Peptidoglycan-anchor; Repeat; Signal;
KW Virulence.
FT SIGNAL 1 36
FT CHAIN 37 985
FT PROPEP 986 1018
Fibronectin-binding protein.
Removed by sortase (Potential).

```

FT REPEAT 545 574 B-1.
FT REPEAT 575 604 B-2.
FT DOMAIN 745 878 4 X approximate tandem repeats,
  fibronectin-binding domain.
FT REPEAT 745 782 D-1.
FT REPEAT 783 820 D-2.
FT REPEAT 821 859 D-3.
FT REPEAT 860 878 D-4 (incomplete).
FT DOMAIN 879 948 5 X tandem repeats, Pro-rich (WR).
FT REPEAT 879 892 WR 1.
FT REPEAT 893 906 WR 2.
FT REPEAT 907 920 WR 3.
FT REPEAT 921 934 WR 4.
FT REPEAT 935 948 WR 5.
FT SITE 982 986 LpXTG sorting signal (Potential).
FT MOD_RES 985 985 Pentaglycyl murein peptidoglycan amidated
  chreonine (Potential).
SQ SEQUENCE 1018 AA; 111780 MW; 58175E020E81F1F CRC64;

Query Match 95.6%; Score 109; DB 1; Length 1018;
Best Local Similarity 95.2%; Pred. No. 2.7e-08;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KASYOFGHNSVDFEEDTLPK 21
DB 837 KPSTYQFGHNSVDFEEDTLPK 857

RESULT 2
Q99RD3 PRELIMINARY; PRT; 961 AA.
ID Q99RD3;
AC Q99RD3;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Fibronectin-binding protein homolog.
GN Name=fnb3; OrderedLocustNames=SAV2502;
OS Staphylococcus aureus (strain Mu50 / ATCC 700699).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=158878;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=Mu50 / ATCC 700699;
RC MEDLINE=2111952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2;
RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
  Cui L., Oguchi A., Aoki K.-I., Nagai Y., Iian J.-Q., Ito T.,
  Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,
  Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
  Sekimizu K., Hirakawa H., Kohara S., Goto S., Yabuzaki J.,
  Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
  Hatori M., Ogasawara N., Hayashi H., Hiramatsu K.;
RA "Whole genome sequencing of methicillin-resistant Staphylococcus
  aureus."
RT Lancet 357:1225-1240(2001).
RL -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
  an amide bond (By similarity).
CC EMBL; AP003365; BAB58664.1; -.
DR HSP; G90053; G90053.
DR HSP; G90053; G90053.
DR HSP; G90053; G90053.
DR GO; GO:0009986; C:cell surface; IEA.
DR GO; GO:0005618; C:cell wall; IEA.
DR GO; GO:0093275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0007155; P:cell adhesion; IEA.
DR InterPro; IPR008966; Adhes_Bact.
DR InterPro; IPR004237; Fn_bind.
DR InterPro; IPR005877; Gpos_YsIRK.
DR InterPro; IPR001899; Gram_pos_anchor.
DR Pfam; PF02986; Fn_bind; 1.
DR Pfam; PF00746; Gram_pos_anchor; 1.
DR Pfam; PF04650; YsIRK_signal; 1.
DR TIGRfams; TIGR01167; LpXTG_anchor; 1.
DR TIGRfams; TIGR01168; YsIRK_signal; 1.

```

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DR PROSITE; PS50847; GRAM_POS_ANCHORING; 1.
KM Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ SEQUENCE 961 AA; 106010 MW; 364940F884EA4101 CRC64;

Query Match 93.0%; Score 106; DB 2; Length 961;
Best Local Similarity 90.5%; Pred. No. 7.7e-08;
Matches 19; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 KASYOFGHNSVDFEEDTLPK 21
DB 784 KPSTYQFGHNSVDFEEDTLPK 804

RESULT 3
Q7A3J8 PRELIMINARY; PRT; 961 AA.
ID Q7A3J8;
AC Q7A3J8;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Fnb3 protein.
GN Name=fnb3; OrderedLocustNames=SA2290;
OS Staphylococcus aureus (strain N315).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=158879;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=2111952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2;
RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
  Cui L., Oguchi A., Aoki K.-I., Nagai Y., Iian J.-Q., Ito T.,
  Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,
  Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
  Sekimizu K., Hirakawa H., Kohara S., Goto S., Yabuzaki J.,
  Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
  Hatori M., Ogasawara N., Hayashi H., Hiramatsu K.;
RA "Whole genome sequencing of methicillin-resistant Staphylococcus
  aureus."
RT Lancet 357:1225-1240(2001).
RL -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
  an amide bond (By similarity).
CC EMBL; AP003365; BAB58664.1; -.
DR GO; GO:0009986; C:cell surface; IEA.
DR GO; GO:0005618; C:cell wall; IEA.
DR GO; GO:0093275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0007155; P:cell adhesion; IEA.
DR InterPro; IPR008966; Adhes_Bact.
DR InterPro; IPR004237; Fn_bind.
DR InterPro; IPR005877; Gpos_YsIRK.
DR InterPro; IPR001899; Gram_pos_anchor.
DR Pfam; PF02986; Fn_bind; 1.
DR Pfam; PF00746; Gram_pos_anchor; 1.
DR Pfam; PF04650; YsIRK_signal; 1.
DR TIGRfams; TIGR01167; LpXTG_anchor; 1.
DR TIGRfams; TIGR01168; YsIRK_signal; 1.
DR PROSITE; PS50847; GRAM_POS_ANCHORING; 1.
KM Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ SEQUENCE 961 AA; 106010 MW; 364940F884EA4101 CRC64;

Query Match 93.0%; Score 106; DB 2; Length 961;
Best Local Similarity 90.5%; Pred. No. 7.7e-08;
Matches 19; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 KASYOFGHNSVDFEEDTLPK 21
DB 784 KPSTYQFGHNSVDFEEDTLPK 804

RESULT 4
Q6GDUS PRELIMINARY; PRT; 965 AA.
ID Q6GDUS;
AC Q6GDUS;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)

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DT 05-JUL-2004 (TReMBLrel. 27, last sequence update)
DT 05-JUL-2004 (TReMBLrel. 27, last annotation update)
DE Fibronectin-binding protein.
GN Name=fnbA, OrderedLocustNames=SA82580;
OS Staphylococcus aureus (strain MSSA252).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=282458;
[1]
RN SEQUENCE FROM N.A.
RX PubMed=15213324; DOI=10.1073/pnas.0402521101;
RA Holden M.T.G., Fell E.J., Lindsay J.A., Peacock S.J., Day N.P.J.,
RA Enright M.C., Foster T.J., Moore C.E., Hurst L., Atkin R., Barron A.,
RA Bason N., Bentley S.D., Chillingworth C., Chillingworth T.,
RA Churcher C., Clark L., Corton C., Cronin A., Doggett J., Dowd L.,
RA Felwell T., Hance Z., Harris B., Hauser H., Holtroyd S., Jørgensen K.,
RA James K.D., Lennard N., Line A., Mayes R., Moule S., Mungall K.,
RA Ormond D., Quail M.A., Rabinowitsch E., Rutherford K.M., Sanders M.,
RA Sharp S., Simmonds M., Stevens K., Whitehead S., Barrett B.G.,
RA Spratt B.G., Parkhill J.;
RT "Complete genomes of two clinical Staphylococcus aureus strains:
RT evidence for the rapid evolution of virulence and drug resistance.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:9786-9791(2004).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC an amide bond (By similarity).
DR EMBL: BX571856; CAC41560.1; -;
DR GO: GO:0009986; C:cell surface; IEA.
DR GO: GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO: GO:0016020; C:membrane; IEA.
DR GO: GO:0007155; P:cell adhesion; IEA.
DR InterPro: IPR004237; Fp_bind.
DR InterPro: IPR008966; Adhes_bact.
DR InterPro: IPR005877; Gpos_YsIRK.
DR InterPro: IPR001899; Gram_pos_anchor.
DR Pfam: PF02986; Fp_bind_1.
DR Pfam: PF00746; Gram_pos_anchor; 1.
DR Pfam: PF04650; YsIRK_signal; 1.
DR TIGRFAMs: TIGR01167; LPXTG_anchor; 1.
DR TIGRFAMs: TIGR01168; YsIRK_signal; 1.
DR PROSITE: PS50847; GRAM_POS_ANCHORING; 1.
KW Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ
SEQUENCE 965 AA; 105691 MW; 2982E132164D0551 CRC64;

Query Match 93.0%; Score 106; DB 2; Length 965;
Best Local Similarity 90.5%; Pred. No. 7.8e-08;
Matches 19; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 KASYQFGHNSVDFEEDTLPK 21
ID :|||||
DB 802 KPNYQFGHNSVDFEEDTLPK 822

RESULT 5
Q88NU7 PRELIMINARY; PRT; 1015 AA.
AC Q88NU7;
DT 01-OCT-2002 (TReMBLrel. 22, Created)
DT 01-OCT-2002 (TReMBLrel. 22, Last sequence update)
DT 01-OCT-2002 (TReMBLrel. 25, Last annotation update)
DE Fnb protein.
GN Name=fnb, OrderedLocustNames=MM2421;
OS Staphylococcus aureus (strain MW2).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=196620;
[1]
RN SEQUENCE FROM N.A.
RX STRAIN=MM2;
RX MEDLINE=22040717; PubMed=12044378; DOI=10.1016/S0140-6736(02)08713-5;
RA Baba T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Oguchi A.,
RA Nagai Y., Iwama N., Asano K., Naito T., Kuroda H., Cui L.,
RA Yamamoto K., Hiramatsu K.;
RT "Genome and virulence determinants of high virulence community-
RT acquired MRSA.";
RL Lancet 359:1819-1827(2002).
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CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC an amide bond (By similarity).
DR EMBL: AP004830; BAB96286.1; -;
DR GO: GO:0009986; C:cell surface; IEA.
DR GO: GO:0005618; C:cell wall; IEA.
DR GO: GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO: GO:0016020; C:membrane; IEA.
DR GO: GO:0007155; P:cell adhesion; IEA.
DR InterPro: IPR008966; Adhes_bact.
DR InterPro: IPR004237; Fp_bind.
DR InterPro: IPR005877; Gpos_YsIRK.
DR InterPro: IPR001899; Gram_pos_anchor.
DR Pfam: PF02986; Fp_bind_1.
DR Pfam: PF00746; Gram_pos_anchor; 1.
DR Pfam: PF04650; YsIRK_signal; 1.
DR TIGRFAMs: TIGR01167; LPXTG_anchor; 1.
DR TIGRFAMs: TIGR01168; YsIRK_signal; 1.
DR PROSITE: PS50847; GRAM_POS_ANCHORING; 1.
KW Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ
SEQUENCE 1015 AA; 111145 MW; D0F9281BB64D442 CRC64;

Query Match 93.0%; Score 106; DB 2; Length 1015;
Best Local Similarity 90.5%; Pred. No. 8.2e-08;
Matches 19; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 KASYQFGHNSVDFEEDTLPK 21
ID :|||||
DB 838 KPNYQFGHNSVDFEEDTLPK 858

RESULT 6
Q6G6H3 PRELIMINARY; PRT; 1015 AA.
AC Q6G6H3;
DT 05-JUL-2004 (TReMBLrel. 27, Created)
DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TReMBLrel. 27, Last annotation update)
DE Fibronectin-binding protein.
GN Name=fnbA, OrderedLocustNames=SA52388;
OS Staphylococcus aureus (strain MSSA476).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=282459;
[1]
RN SEQUENCE FROM N.A.
RX PubMed=15213324; DOI=10.1073/pnas.0402521101;
RA Holden M.T.G., Fell E.J., Lindsay J.A., Peacock S.J., Day N.P.J.,
RA Enright M.C., Foster T.J., Moore C.E., Hurst L., Atkin R., Barron A.,
RA Bason N., Bentley S.D., Chillingworth C., Chillingworth T.,
RA Churcher C., Clark L., Corton C., Cronin A., Doggett J., Dowd L.,
RA Felwell T., Hance Z., Harris B., Hauser H., Holtroyd S., Jørgensen K.,
RA James K.D., Lennard N., Line A., Mayes R., Moule S., Mungall K.,
RA Ormond D., Quail M.A., Rabinowitsch E., Rutherford K.M., Sanders M.,
RA Sharp S., Simmonds M., Stevens K., Whitehead S., Barrett B.G.,
RA Spratt B.G., Parkhill J.;
RT "Complete genomes of two clinical Staphylococcus aureus strains:
RT evidence for the rapid evolution of virulence and drug resistance.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:9786-9791(2004).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC an amide bond (By similarity).
DR EMBL: BX571857; CAC44202.1; -;
DR GO: GO:0009986; C:cell surface; IEA.
DR GO: GO:0005618; C:cell wall; IEA.
DR GO: GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO: GO:0016020; C:membrane; IEA.
DR GO: GO:0007155; P:cell adhesion; IEA.
DR InterPro: IPR008966; Adhes_bact.
DR InterPro: IPR004237; Fp_bind.
DR InterPro: IPR005877; Gpos_YsIRK.
DR InterPro: IPR001899; Gram_pos_anchor.
DR Pfam: PF02986; Fp_bind_1.
DR Pfam: PF00746; Gram_pos_anchor; 1.
DR Pfam: PF04650; YsIRK_signal; 1.
DR TIGRFAMs: TIGR01167; LPXTG_anchor; 1.
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DR TIGR01168; YSIRK signal; 1.
DR PROSITE; PSS0847; GRAM_POS_ANCHORING; 1.
SQ CELL wall; Complete proteome; Peptidoglycan-anchor.
SQ SEQUENCE 1015 AA; 11145 MW; D0F9281B564944D CRC64;

Query Match
Best Local Similarity 93.0%; Score 106; DB 2; Length 1015;
Matches 19; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 KASYOFGHNSVDFEEDTLPK 21
DB 838 KENYQFGHNSVDFEEDTLPK 858

RESULT 7
QY099RD2 PRELIMINARY; PRT; 1038 AA.
AC Q99RD2;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE Fibronectin-binding protein homolog.
GN Name=fnb; OrderedLocustNames=SAV2503;
OS Staphylococcus aureus (strain Mu50 / ATCC 700699).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=158878;

[1]
SEQUENCE FROM N.A.
RP STRAIN=Mu50 / ATCC 700699;
RX MEDLINE=21311952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2;
RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Iino J.-O., Ito T.,
RA Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,
RA Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
RA Kanehisa M., Yamashita A., Kuhara S., Goto S., Yabuzaki J.,
RA Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
RT "Whole genome sequencing of methicillin-resistant Staphylococcus
RT aureus."
RL Lancet 357:1225-1240(2001).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC an amide bond (By similarity).
EMBL; AP003137; BAB43594.1; -.
DR GO; GO:0009986; C:cell surface; IEA.
DR GO; GO:0005618; C:cell wall; IEA.
DR GO; GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0007155; P:cell adhesion; IEA.
DR InterPro; IPR008966; Adhes_bact.
DR InterPro; IPR004237; Fn_bind.
DR InterPro; IPR005877; Gpoe_YSIRK.
DR InterPro; IPR001899; Gram_pos_anchor.
DR Pfam; PF02986; Fn_bind.1.
DR Pfam; PF04650; YSIRK_signal.1.
DR TIGR01168; YSIRK signal; 1.
DR TIGR01168; YSIRK signal; 1.
DR TIGR01168; YSIRK signal; 1.
DR PROSITE; PSS0847; GRAM_POS_ANCHORING; 1.
DR CELL wall; Complete proteome; Peptidoglycan-anchor.
SQ SEQUENCE 1038 AA; 113618 MW; 666BF6BF2BFBEB12 CRC64;
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ID Q7A3J7 PRELIMINARY; PRT; 1038 AA.
AC Q7A3J7;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE Fnb protein.
GN Name=fnb; OrderedLocustNames=SA2291;
OS Staphylococcus aureus (strain N315).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=158879;

[1]
SEQUENCE FROM N.A.
RP MEDLINE=21311952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2;
RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Iino J.-O., Ito T.,
RA Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,
RA Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
RA Kanehisa M., Yamashita A., Kuhara S., Goto S., Yabuzaki J.,
RA Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
RT "Whole genome sequencing of methicillin-resistant Staphylococcus
RT aureus."
RL Lancet 357:1225-1240(2001).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC an amide bond (By similarity).
EMBL; AP003137; BAB43594.1; -.
DR GO; GO:0009986; C:cell surface; IEA.
DR GO; GO:0005618; C:cell wall; IEA.
DR GO; GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0007155; P:cell adhesion; IEA.
DR InterPro; IPR008966; Adhes_bact.
DR InterPro; IPR004237; Fn_bind.
DR InterPro; IPR005877; Gpoe_YSIRK.
DR InterPro; IPR001899; Gram_pos_anchor.
DR Pfam; PF02986; Fn_bind.1.
DR Pfam; PF04650; YSIRK_signal.1.
DR TIGR01168; YSIRK signal; 1.
DR TIGR01168; YSIRK signal; 1.
DR TIGR01168; YSIRK signal; 1.
DR PROSITE; PSS0847; GRAM_POS_ANCHORING; 1.
DR CELL wall; Complete proteome; Peptidoglycan-anchor.
SQ SEQUENCE 1038 AA; 113618 MW; 666BF6BF2BFBEB12 CRC64;

Query Match
Best Local Similarity 93.0%; Score 106; DB 2; Length 1038;
Matches 19; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 KASYOFGHNSVDFEEDTLPK 21
DB 833 KENYQFGHNSVDFEEDTLPK 853

RESULT 9
QY053682 PRELIMINARY; PRT; 940 AA.
ID Q53682;
AC Q53682;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE Fibronectin binding protein B.
GN Name=fnb;
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1280;

[1]
SEQUENCE FROM N.A.
RP STRAIN=8325-4;
RX MEDLINE=92111475; PubMed=1837266;
RA Jonsson K., Sigfus C., Muller H.P., Lindberg M.;
RT "Two different genes encode fibronectin binding proteins in
RT Staphylococcus aureus. The complete nucleotide sequence and
RT characterization of the second gene."
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RL  Eur. J. Biochem. 202:1041-1048(1991).
CC  -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
    an amide bond (By similarity).
DR  EMBL: X62992; CA944726.1; -.
DR  PIR: S19702; S19702.
DR  HSSP: O53653; 1N67.
DR  GO: GO:0009986; C:cell surface; IEA.
DR  GO: GO:0005618; C:cell wall; IEA.
DR  GO: GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR  GO: GO:0016020; C:membrane; IEA.
DR  GO: GO:0007155; P:cell adhesion; IEA.
DR  InterPro: IPR008966; Adhes_bact.
DR  InterPro: IPR004237; Fn_bind.
DR  InterPro: IPR001899; Gram_pos_anchor.
DR  InterPro: IPR001899; Gram_pos_anchor.
DR  Pfam: PF02986; Fn_bind_2.
DR  Pfam: PF00746; Gram_pos_anchor; 1.
DR  Pfam: PF04650; YSIRK_signal; 1.
DR  TIGRfams: TIGR01167; LPXTG_anchor; 1.
DR  TIGRfams: TIGR01168; YSIRK_signal; 1.
DR  PROSITE: PS50847; GRAM_POS_ANCHORING; 1.
KW  Cell wall; Peptidoglycan-anchor.
SQ  SEQUENCE 940 AA; 103555 MW; E35FBBCA907AE345 CRC64;

Query Match      89.5%; Score 102; DB 2; Length 940;
Best Local Similarity 85.7%; Pred. No. 3.3e-07;
Matches 18; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY  1 KASYOFGHNSVDFEEDLPK 21
    |:|||||
Db  773 KPNYFGGHNSVDFEEDLPQ 793

RESULT 10
Q8NU8      PRELIMINARY;      PRT;      943 AA.
AC  O8NU8;
DT  01-OCT-2002 (TrEMBLrel. 22, Created)
DT  01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT  01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE  FmbB protein.
GN  Name=fmbB; OrderedLocustNames=MM2420;
OS  Staphylococcus aureus (strain MM2).
OC  Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX  NCBI_TaxID=196620;
RN  [1]
RP  SEQUENCE FROM N.A.
RC  STRAIN=MM2;
RX  MEDLINE=22040717; PubMed=12044378; DOI=10.1016/S0140-6736(02)08713-5;
RA  Baba T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Oguchi A.,
RA  Nagai Y., Iwama N., Asano K., Naito T., Kuroda H., Cui L.,
RA  Yamamoto K., Hitamatsu K.,
RT  "Genome and virulence determinants of high virulence community-
RT  acquired MRSA.";
RT  Lancet 359:1819-1827(2002).
CC  -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
    an amide bond (By similarity).
DR  EMBL: AP004830; BAB96285.1; -.
DR  HSSP: O53653; 1N67.
DR  GO: GO:0009986; C:cell surface; IEA.
DR  GO: GO:0005618; C:cell wall; IEA.
DR  GO: GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR  GO: GO:0016020; C:membrane; IEA.
DR  GO: GO:0007155; P:cell adhesion; IEA.
DR  InterPro: IPR008966; Adhes_bact.
DR  InterPro: IPR004237; Fn_bind.
DR  InterPro: IPR005877; Gpos_YSIRK.
DR  InterPro: IPR001899; Gram_pos_anchor.
DR  Pfam: PF02986; Fn_bind_1.
DR  Pfam: PF00746; Gram_pos_anchor; 1.
DR  Pfam: PF04650; YSIRK_signal; 1.
DR  TIGRfams: TIGR01167; LPXTG_anchor; 1.
DR  TIGRfams: TIGR01168; YSIRK_signal; 1.
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DR  PROSITE: PS50847; GRAM_POS_ANCHORING; 1.
KW  Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ  SEQUENCE 943 AA; 104537 MW; DABAF531947E1B6A CRC64;

Query Match      89.5%; Score 102; DB 2; Length 943;
Best Local Similarity 85.7%; Pred. No. 3.3e-07;
Matches 18; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY  1 KASYOFGHNSVDFEEDLPK 21
    |:|||||
Db  780 KPNYFGGHNSVDFEEDLPQ 800

RESULT 11
Q6G6H4      PRELIMINARY;      PRT;      957 AA.
AC  Q6G6H4;
DT  05-JUL-2004 (TrEMBLrel. 27, Created)
DT  05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT  05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE  Fibronectin-binding protein.
GN  Name=fmbB; OrderedLocustNames=SA52387;
OS  Staphylococcus aureus (strain MSSA476).
OC  Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX  NCBI_TaxID=282459;
RN  [1]
RP  SEQUENCE FROM N.A.
RX  PubMed=15213324; DOI=10.1073/pnas.0402521101;
RA  Holden M.T.G., Fell E.J., Lindsay J.A., Peacock S.J., Day N.P.J.,
RA  Enright M.C., Foster T.J., Moore C.E., Hurst L., Atkin R., Barron A.,
RA  Bason N., Bentley S.D., Chillingworth C., Chillingworth T.,
RA  Churcher C., Clark L., Cotton C., Cronin A., Doggett J., Dowd L.,
RA  Felwell T., Hance Z., Harris B., Hauser H., Holtroyd S., Jędrals K.,
RA  James K.D., Leonard N., Line A., Mayes R., Moule S., Mungall K.,
RA  Ormond D., Quail M.A., Rabinowitsch B., Rutherford K.M., Sanders M.,
RA  Sharp S., Simmonds M., Stevens K., Whitehead S., Barrett B.G.,
RA  Spratt B.G., Parkhill J.,
RT  "Complete genomes of two clinical Staphylococcus aureus strains:
RT  evidence for the rapid evolution of virulence and drug resistance.";
RT  Proc. Natl. Acad. Sci. U.S.A. 101:9786-9791(2004).
CC  -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
    an amide bond (By similarity).
DR  EMBL: BX571857; CA944201.1; -.
DR  GO: GO:0009986; C:cell surface; IEA.
DR  GO: GO:0005618; C:cell wall; IEA.
DR  GO: GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR  GO: GO:0016020; C:membrane; IEA.
DR  GO: GO:0007155; P:cell adhesion; IEA.
DR  InterPro: IPR008966; Adhes_bact.
DR  InterPro: IPR004237; Fn_bind.
DR  InterPro: IPR005877; Gpos_YSIRK.
DR  InterPro: IPR001899; Gram_pos_anchor.
DR  Pfam: PF02986; Fn_bind_1.
DR  Pfam: PF00746; Gram_pos_anchor; 1.
DR  Pfam: PF04650; YSIRK_signal; 1.
DR  TIGRfams: TIGR01167; LPXTG_anchor; 1.
DR  TIGRfams: TIGR01168; YSIRK_signal; 1.
DR  PROSITE: PS50847; GRAM_POS_ANCHORING; 1.
KW  Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ  SEQUENCE 957 AA; 105980 MW; 28F8BA7FFDD3BAF CRC64;

Query Match      89.5%; Score 102; DB 2; Length 957;
Best Local Similarity 85.7%; Pred. No. 3.3e-07;
Matches 18; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY  1 KASYOFGHNSVDFEEDLPK 21
    |:|||||
Db  780 KPNYFGGHNSVDFEEDLPQ 800

RESULT 12
Q9AEP9      PRELIMINARY;      PRT;      152 AA.
ID  Q9AEP9
```

```

AC Q9AEP3; 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DE 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Fibronectin-binding protein (Fragment).
GN Name=fnb;
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1280;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CMRSA-1;
RX MEDLINE=21246681; Pubmed=11349044;
RA DOI=10.1128/IAI.69.6.3791-3799.2001;
RA Rice K., Huesca M., Vaz D., McCabe M.J.;
RT "Variation in fibronectin binding and fnb locus polymorphisms in a
RT Staphylococcus aureus: identification of antigenic variation in a
RT fibronectin binding protein adhesin of the epidemic CMRSA-1 strain of
RT methicillin-resistant S. aureus."
RL Infect. Immun. 69:3791-3799(2001).
DR EMBL; AY029184; AAK31588.1; -.
FT NON_TER
FT 1
SQ SEQUENCE 152 AA; 17193 MW; CFA3913CB2B11C025 CRC64;

Query Match
Best Local Similarity 85.1%; Score 97; DB 2; Length 152;
Matches 17; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 KASYOFGGHNVSDFEEDTLPK 21
| | | | | | | | | | | | | | | | | | | | | |
DB 130 KPSYOFGGHNGIDFVEDTLPK 150

RESULT 13
Q9AD03 PRELIMINARY; PRT; 772 AA.
AC Q9AD03;
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 24, Last annotation update)
DE Putative integral membrane protein.
GN OrderedLocusNames=SCPI.147;
OS Streptomyces coelicolor.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Streptomycinae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=1902;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=A3(2) / M145;
RX MEDLINE=21996410; Pubmed=12000953; DOI=10.1038/417141a;
RA Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,
RA Thomson N.R., James K.D., Harris D.E., Quail M.A., Kleiser H.,
RA Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
RA Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
RA Huang C.-H., Kleiser T., Larke L., Murphy L.D., Oliver K., O'Neill S.,
RA Rabinowitz E., Rajandream M.A., Rutherford K.M., Rutter S.,
RA Seeger K., Saunders D., Sharp S., Squares R., Squares R., Taylor K.,
RA Warren T., Wietzorrek A., Woodward J.R., Barrell B.G., Parkhill J.,
RA Hopwood D.A.;
RT "Complete genome sequence of the model actinomycete Streptomyces
RT coelicolor A3(2).";
RL Nature 417:141-147(2002).
DR EMBL; AL590463; CAC36668.1; -.
KW Complete proteome.
SQ SEQUENCE 772 AA; 82297 MW; AB501EED840DD91B CRC64;

Query Match
Best Local Similarity 45.6%; Score 52; DB 2; Length 772;
Matches 10; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 2 ASYOFGGHNVSDFEED 17
| | | | | | | | | | | | | | | | | | | | | |

```

DB	375	AAHQEGVPMWDFEKD	390
RESULT 14			
008866			
ID	008866	PRELIMINARY;	PRT; 245 AA.
AC	008866; Q31374;		
DT	01-NOV-1996 (TREMBLrel. 01, Created)		
DT	01-NOV-1996 (TREMBLrel. 01, Last sequence update)		
DT	01-MAR-2004 (TREMBLrel. 26, Last annotation update)		
DE	Carassius auratus langsdorffii MHC (Fragment).		
OS	Carassius auratus (Goldfish).		
CC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;		
CC	Cyprinidae; Carassius.		
OX	NCBI_TaxID=7957;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	TISSUE=Blood;		
RX	MEDLINE=93315835; PubMed=8326125;		
RA	Okamura K., Nakaiishi T., Kurosawa Y., Hashimoto K.;		
RT	"Expansion of genes that encode MHC class I molecules in cyprinid fishes.";		
RT	J. Immunol. 151:188-200(1993).		
RL	J. Immunol. 151:188-200(1993).		
DR	EMBL, L10418; AAA72345.1;		
DR	InterPro; IPR007110; IG-like.		
DR	InterPro; IPR003597; IG-cl.		
DR	InterPro; IPR003006; IG-MHC.		
DR	Pfam; PF07654; Cl-sec; 1.		
DR	SMART; SM00407; IGcl; 1.		
DR	PROSITE; PS50835; IG-LIKE; 1.		
DR	PROSITE; PS00290; IG-MHC; UNKNOWN 1.		
FT	NON TER		
FT	1		
SQ	SEQUENCE 245 AA; 28128 MW; C3E33032EA998A43 CRC64;		
Query Match	43.9%;	Score 50;	DB 2; Length 245;
Best local Similarity	60.0%;	Pred. NO. 14;	
Matches	9;	Conservative 1;	Mismatches 5; Indels 0; Gaps 0
QY	4	YQFGHNSVDFEEDT 18	
DB	102	YQFGGDCVDFSSDT 116	
RESULT 15			
08DUZ9			
ID	08DUZ9	PRELIMINARY;	PRT; 305 AA.
AC	08DUZ9;		
DT	01-MAR-2003 (TREMBLrel. 23, Created)		
DT	01-MAR-2003 (TREMBLrel. 23, Last sequence update)		
DT	01-JUN-2003 (TREMBLrel. 24, Last annotation update)		
DE	Hypothetical protein SMU.725c.		
GN	OrderedLocusNames=SMU.725c;		
OS	Streptococcus mutans.		
OC	Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;		
CC	Streptococcus.		
OX	NCBI_TaxID=1309;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=UA159 / ATCC 700610 / Serotype C;		
RX	MEDLINE=22295063; PubMed=12397186; DOI=10.1073/pnas.172501299;		
RA	Ajdacic D.J., McShan W.M., McLaughlin R.E., Savic G., Chang J.,		
RA	Carson M.B., Primeaux C., Tolan R., Kenton S., Jia H.G., Lin S.P.,		
RA	Qian Y., Li S., Zhu H., Najjar F.Z., Lai H., White J., Roe B.A.,		
RA	Ferretti J.J.;		
RT	"Genome sequence of Streptococcus mutans UA159, a cariogenic dental pathogen.";		
RL	Proc. Natl. Acad. Sci. U.S.A. 99:14434-14439(2002).		
DR	EMBL; AE014915; AAN58454.1;		
DR	GO; GO:0016787; F:hydrolase activity; IEA.		
DR	InterPro; IPR004843; M-pesterase.		
DR	Pfam; PF00149; Metallopro; 1.		
KW	Complete proteome.		

SQ SEQUENCE 305 AA; 36078 MW; FB8B2F8D54AF1A18 CRC64;

Query Match 43.0%; Score 49; DB 2; Length 305;

Best Local Similarity 36.8%; Pred. No. 26;

Matches 7; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

QY 1 KASYQFGHNSVDFEEDTL 19

DB 83 KVTYNLGNHMDLDEDAI 101

Search completed: October 22, 2005, 04:09:54
Job time : 52.4314 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 25, 2005, 18:43:07 ; Search time 59.0973 Seconds
(without alignments)
137.434 Million cell updates/sec

Title: US-10-731-238-16

Perfect score: 120

Sequence: 1 KPEYQFGHNSVDFEEDTLRK 21

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: Geneseq_16Dec04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	120	100.0	21	2	AAW65672
2	112	93.3	21	2	AAW65665
3	112	93.3	22	2	AAW65670
4	112	93.3	37	4	AAW65679
5	112	93.3	38	1	AAW65684
6	112	93.3	134	2	AAW65687
7	112	93.3	139	2	AAW65690
8	112	93.3	1018	1	AAW65692
9	112	93.3	1018	4	AAW65693
10	112	93.3	1018	4	AAW65694
11	112	93.3	1018	4	AAW65695
12	112	93.3	1018	6	AAW65696
13	112	93.3	1027	6	AAW65697
14	111	92.5	961	6	AAW65698
15	111	92.5	978	4	AAW65699
16	111	92.5	1001	4	AAW65700
17	111	92.5	1038	6	AAW65701
18	107	89.2	21	2	AAW65702
19	107	89.2	21	2	AAW65703
20	107	89.2	21	2	AAW65704
21	107	89.2	21	2	AAW65705
22	107	89.2	101	2	AAW65706
23	107	89.2	113	2	AAW65707
24	107	89.2	124	2	AAW65708
25	107	89.2	128	2	AAW65709

25	107	89.2	130	2	AAW65710
27	107	89.2	130	2	AAW65711
28	107	89.2	130	2	AAW65712
29	107	89.2	130	2	AAW65713
30	107	89.2	134	2	AAW65714
31	107	89.2	162	2	AAW65715
32	107	89.2	164	2	AAW65716
33	107	89.2	174	2	AAW65717
34	107	89.2	174	2	AAW65718
35	107	89.2	181	2	AAW65719
36	107	89.2	181	2	AAW65720
37	107	89.2	559	2	AAW65721
38	107	89.2	940	2	AAW65722
39	107	89.2	940	6	AAW65723
40	107	89.2	948	6	AAW65724
41	107	89.2	948	6	AAW65725
42	107	89.2	948	6	AAW65726
43	106	88.3	21	2	AAW65727
44	106	88.3	21	2	AAW65728
45	106	88.3	21	2	AAW65729

ALIGNMENTS

RESULT 1
AAW65672 standard; peptide; 21 AA.
XX
AC AAW65672;
XX
DT 16-OCT-1998 (first entry)
XX
DE Fibronectin binding protein-derived peptide #16.
XX
KW microRNA, fibronectin, fibronectin-binding protein; antibody; epitope;
KW MCRAMM; fibronectin; fibronectin-binding protein; antibody; epitope;
KW antibiotic; bacterial infection; antibiotic-resistant strain.
XX
OS Synthetic.
OS Staphylococcus aureus.
XX
PN W09831389-A2.
XX
PD 23-JUL-1998.
XX
PF 21-JAN-1998; 98MO-US001222.
XX
PR 21-JAN-1997; 97US-0036139P.
XX
PA (TEXA) UNIV TEXAS A & M SYSTEM.
XX
PI Hoosok M, Patil JM, House-Pompeo KL, Speziale P, Joh D;
PI Mogavvin MJ;
XX
XX WPI; 1998-413816/35.
XX
XX The invention relates to antibodies that bind to a fibronectin-binding
XX domain of a fibronectin-binding protein, and inhibit binding of a
XX protein to fibronectin. Also claimed are: (1) isolated peptides of a
XX fibronectin-binding protein that do not bind to fibronectin; (2) fusion
XX protein containing at least one peptide of a fibronectin-binding protein
XX linked to a second amino acid sequence; (3) nucleic acid encoding the
XX isolated peptide of (1). Antibodies, the isolated peptides of (1) and the
XX nucleic acids are all useful for immunisation (active or passive) and (by
XX inhibiting binding of bacteria to fibronectin) for preventing or treating
XX infection in humans or other animals, particularly by staphylococci or

CC epitopes from the fibronectin binding domains D1 and D1-D4 of the S.
CC aureus fmbA gene
XX
SQ Sequence 21 AA;
Query Match 93.3%; Score 112; DB 2; Length 21;
Best Local Similarity 95.2%; Pred. No. 5.5e-10;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 KPPYFGGHNVDPEEDTLRK 21
D1 |||||
D1 1 KPSYFGGHNVDPEEDTLRK 21
RESULT 3
ID AAR21340 standard; peptide; 22 AA.
XX AAR21340;
AC AAR21340;
XX 25-MAR-2003 (revised)
DT 15-JUN-1992 (first entry)
DE Fibronectin binding protein.
XX FMBP; wound infection reduction; vaccination; mastitis;
KW Staphylococcal infections; D3.
XX Synthetic.
XX MO9202555-A.
XX 20-FEB-1992.
PD 10-AUG-1990; 90SE-00002617.
PF 10-AUG-1990; 90SE-00002617.
PR 10-AUG-1990; 90SE-00002617.
XX (ALFA) ALFA LAVAL AGRIC INT AB.
PA Hook M, McGavin M, Raucel G;
PI WPI; 1992-080035/10.
DR New fibronectin binding peptide - combines with fusion peptide to form
PT large antigen, used in immunisation, diagnosis and for treating wounds.
XX
XX Claim 1; Page 22; 33pp; English.
XX The sequence comprises amino acids 17-33 of a tandem repeat, designated
CC D3 of the fibronectin binding site of *Staphylococcus aureus* 8325-4 FMBP.
CC The N-terminal DK may be replaced with H or K, and the C-terminal LKP may
CC be replaced by either L, LP, or OH. The peptides were synthesised using
CC standard methods and purified using reverse phase HPLC. The appropriate
CC fractions were dialysed and lyophilised. Peptide sequencing was performed
CC and the peptides digested and chemically modified by dinitroxypropylation
CC of the amino side chain of lysine. The carboxylic side chains were
CC converted to glycine methyl esters. The phenyl side chains of tyrosine
CC residues were oxidised. Chemically modified peptide D3 was compared to
CC unmodified D3. Lysine and tyrosine modifications only partially
CC diminished its activity whereas modification of aspartic/glutamic
CC residues resulted in complete loss of activity. The peptide can be used
CC for the prevention or reduction of the risk of wound infection. The
CC peptide can be used to create a large antigen for vaccinating ruminants
CC against mastitis caused by *Staphylococcal* infections. It can also be used
CC to diagnose *Staphylococcal* infections using ELISA or DNA probes. (Updated
CC on 25-MAR-2003 to correct PA field.)
XX
SQ Sequence 22 AA;
Query Match 93.3%; Score 112; DB 2; Length 22;
Best Local Similarity 95.2%; Pred. No. 5.5e-10;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 KPPYQFGHNSVDFEEDTLPK 21
|||
DB 2 KPSYQFGHNSVDFEEDTLPK 22

RESULT 4
AAB91958
ID AAB91958 standard; peptide; 37 AA.
XX

AC AAB91958;
XX

DT 22-JUN-2001 (first entry)
XX

DE Fibronectin fragment and fibrin related peptide SEQ ID NO:1134.
XX

KW Protection; endogenous therapeutic peptide; peptidase; conjugation;
KW blood component; modification; succinimide; maleimide group; amino;
KW hydroxyl; thiol; hormone; growth factor; neurotransmitter.
XX

OS Homo sapiens.
OS Synthetic.
XX

PN WO200069900-A2.
XX

PD 23-NOV-2000.
XX

PF 17-MAY-2000; 2000MO-US013576.
XX

PR 17-MAY-1999; 99US-0134406P.
XX

PR 10-SEP-1999; 99US-0153406P.
XX

PR 15-OCT-1999; 99US-0159783P.
XX

XX (CONJ-) CONJUCHEM INC.
XX

PI Bridon DP, Ezrin AM, Milner PG, Holmes DL, Thibaudau K;
XX

DR WPI; 2001-112059/12.
XX

PT Modifying and attaching therapeutic peptides to albumin prevents
PT peptidase degradation, useful for increasing length of in vivo activity.
XX

PS Disclosure; Page 566; 733pp; English.
XX

CC The present invention describes a modified therapeutic peptide (I)
CC comprising a therapeutically active amino acid region (III) and a
CC reactive group (II) (e.g. succinimide) and maleimide groups) attached to
CC a less therapeutically active amino acid region (IV), which covalently
CC bonds with amino/hydroxyl/thiol groups on blood components to form a
CC peptide stabilised therapeutic peptide composed of 3-50 amino acids.
CC (I) are useful for modifying therapeutic peptides e.g. hormones, growth
CC factors and neurotransmitters, to protect them from peptidase activity in
CC vivo for the treatment of various disorders. Endogenous therapeutic
CC peptides are not suitable as drug candidates as they require frequent
CC administration due to rapid degradation by peptidases in the body.
CC Modifying and attaching therapeutic peptides to albumin prevents or
CC reduces the action of peptidases to increase length of activity (half
CC life) and specificity as bonding to large molecules decreases
CC intracellular uptake and interference with physiological processes.
CC AAB90829 to AAB92441 represent peptides which can be used in the
CC exemplification of the present invention
XX

XX Sequence 37 AA;
SQ

Query Match 93.3%; Score 112; DB 4; Length 37;
Best Local Similarity 95.2%; Pred. No. 1e-09;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 KPPYQFGHNSVDFEEDTLPK 21
|||
DB 16 KPSYQFGHNSVDFEEDTLPK 36

RESULT 5
AAB80662
ID AAB80662 standard; protein; 38 AA.
XX

AC AAB80662;
XX

DT 25-MAR-2003 (revised)
DT 07-OCT-1990 (first entry)
XX

DE Protein with fibronectin binding ability.
XX

KW Hybrid DNA molecule; fibronectin binding; mastitis; ruminants;
KW wound infection.
XX

OS Staphylococcus aureus.
XX

PN EP294349-A.
XX

PD 07-DEC-1988.
XX

PF 30-MAY-1988; 88EP-00850188.
XX

PR 01-JUN-1987; 87SE-00002272.
XX

XX (ALFA) ALFA LAVAL AGRIC INT AB.
XX

PI Lindberg MK, Signas LC, Wadstrom TM, Froman G;
XX

DR WPI; 1988-347978/49.
XX

DR N-FSDB; AAN61099.
XX

PT Hybrid DNA encoding Staphylococcus aureus fibronectin binding protein -
PT useful for immunisation and topical application to prevent staphylococcal
PT infections.
XX

PS Claim 11; Page 12; 23pp; English.
XX

CC The peptide has fibronectin binding ability. It is useful for immunising
CC CC ruminants against staphylococcal mastitis, pref. when used at 0.5-5
CC micrograms/kg, using 3 doses given at 1-3 week intervals; for topical
CC application to prevent wound infection, using an isotonic saline soln. of
CC concn. 25-250 micrograms/ml; and, when immobilised on a carrier, for
CC diagnosing staphylococcal infections. (Updated on 25-MAR-2003 to correct
CC PF field.) (Updated on 25-MAR-2003 to correct PA field.)
XX

SQ Sequence 38 AA;
SQ

Query Match 93.3%; Score 112; DB 1; Length 38;
Best Local Similarity 95.2%; Pred. No. 1e-09;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 KPPYQFGHNSVDFEEDTLPK 21
|||
DB 17 KPSYQFGHNSVDFEEDTLPK 37

RESULT 6
AAV29087
ID AAV29087 standard; protein; 134 AA.
XX

AC AAV29087;
XX

DT 28-SEP-1999 (first entry)
XX

DE S. aureus fibronectin binding protein A (FnBA) binding domain.
XX

KW Bovine herpes virus-2; BHV-2; cytokine; immune response; immunogen; IL;
KW interleukin; colony stimulating factor; CSF; interferon; IFN; TNF;
KW tumour necrosis factor; recombinant virus; vaccine; mucosal disease;
KW mastitis; breast cancer; stress-induced disease; binding domain; FnBA;
KW fibronectin binding protein.
XX

OS Staphylococcus aureus.
XX

XX WO9916892-A1.
 XX 08-APR-1999.
 XX 29-SEP-1998; 98WO-GB002927.
 XX 29-SEP-1997; 97GB-00020633.
 XX (UYBR-) UNIV BRISTOL.
 XX Bradley AJ, Duffas WP;
 XX WPI: 1999-255101/21.
 XX N-PSDB; AAX91504.
 XX
 XX New bovine herpes virus-2 vectors.
 XX
 XX Example 2; Fig 8A-B; 130pp; English.
 XX
 XX The invention provides bovine herpes virus-2 (BHV-2) based vectors that
 XX comprise at least one cytokine-encoding DNA sequence. The expression of
 XX cytokines in mammals can up-regulate immune responses to the immunogens.
 XX The cytokine is selected from interleukins (IL), colony stimulating
 XX factors (CSF), interferons (IFN) and tumour necrosis factors (TNF). The
 XX BHV-2 based vector or recombinant virus can be used as vaccines. They can
 XX be used for preventing or treating a mucosal disease in a subject, e.g.
 XX ruminants, cattle, sheep, goats, dogs, cats, horses, or man, particularly
 XX mastitis in cows or breast cancers in humans. They can also be used for
 XX preventing or treating a stress-induced disease. The present sequence
 XX represents the binding domain of a previously published *S. aureus*
 XX fibronectin binding protein A (FnBA) sequence. The FnB binding domain
 XX gene sequence FnBAB, cloned for use in this invention has 97.8 percent
 XX identity when compared to the previously published FnBA and FnBB gene
 XX sequences
 XX
 XX Sequence 134 AA;
 XX
 XX Query Match 93.3%; Score 112; DB 2; Length 134;
 XX Best Local Similarity 95.2%; Pred. No. 4e-09;
 XX Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KPYPQFGHNSVDFEEDTLPK 21
 ||||||||||||||||
 DB 93 KPYPQFGHNSVDFEEDTLPK 113

RESULT 7
 AAW31556
 ID AAW31556 standard; protein; 139 AA.
 XX
 AC AAW31556;
 XX
 DT 27-AUG-2003 (revised)
 DT 25-MAR-2003 (revised)
 DT 21-MAY-1998 (first entry)
 XX
 XX Fibronectin-binding MSCRAMM derivative pOD.
 XX
 XX Fibronectin; pOD; collagen binding protein; sepsis; infection;
 XX microbial surface component recognising adhesive matrix molecule; MSCRAMM;
 XX adhesin; vaccine; immunisation; diagnosis; therapy; mastitis.
 XX
 OS Staphylococcus aureus.
 XX
 XX
 XX Key Location/Qualifiers
 FT 1..12
 FT Peptide /notes="vector pQE30-derived peptide"
 XX
 XX WO9743314-A2.
 XX
 XX 20-NOV-1997.
 XX

PF 14-MAY-1997; 97WO-US008210.
 XX
 XX 16-MAY-1996; 96US-0017678P.
 XX
 XX (TEXA) UNIV TEXAS A & M SYSTEM.
 XX (UABR-) UAB RES FOUND.
 XX
 XX Hoeek M, Patti JM, House-Pompeo K, Sthanam N, Symereky J;
 XX WPI: 1998-008801/01.
 XX
 XX Antibody that interacts with collagen binding domain of Staphylococcal
 XX cna gene product - useful to prevent bacterial sepsis in animal infected
 XX with Staphylococcus aureus.
 XX
 XX Disclosure; Page 91; 143pp; English.
 XX
 XX This protein comprises Staphylococcus aureus fibronectin-binding
 XX microbial surface component recognising adhesive matrix molecule (MSCRAMM)
 XX derivative pOD, plus a vector-derived N-terminal peptide. The invention
 XX relates to claimed nucleic acid sequences (see AAT93436-38) encoding *S.*
 XX aureus collagen binding protein (CBP) epitopes M17, M31 and M55 (see
 XX AAW1552-54) that confer protection against *S. aureus* infection. CBP
 XX protein and antigenic epitopes are contemplated for use in the treatment
 XX of pathological infections, especially to prevent bacterial adhesion to
 XX collagen. The epitopes are also contemplated for use in the preparation
 XX of vaccines and as carrier proteins in vaccine formulations, as well as
 XX in the formulation of compositions for the prevention of *S. aureus*
 XX infection. pCF33 and pOD (see AAW3156) were used to raise anti-MSCRAMM
 XX polyclonal antibodies used in passive immunisation against bovine
 XX mastitis. (Updated on 25-MAR-2003 to correct PI field.) (Updated on 27-
 XX AUG-2003 to correct OS field.)
 XX
 XX Sequence 139 AA;
 XX

Query Match 93.3%; Score 112; DB 2; Length 139;
 Best Local Similarity 95.2%; Pred. No. 4.1e-09;
 Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KPYPQFGHNSVDFEEDTLPK 21
 ||||||||||||||||
 DB 107 KPYPQFGHNSVDFEEDTLPK 127

RESULT 8
 AAP82115
 ID AAP82115 standard; protein; 1018 AA.
 XX
 AC AAP82115;
 XX
 DT 25-MAR-2003 (revised)
 DT 05-JAN-1990 (first entry)
 XX
 XX Fibronectin binding protein.
 XX
 XX Fibronectin binding protein; *S. aureus*; immunisation; mastitis; ruminants;
 XX wound infection; diagnosis.
 XX
 OS Staphylococcus aureus.
 XX
 XX
 XX EP294349-A.
 XX
 PD 07-DEC-1988.
 XX
 XX 30-MAY-1988; 88EP-00850188.
 XX
 XX 01-JUN-1987; 87SE-00002272.
 XX
 XX (ALFA) ALFA LAVAL AGRIC INT AB.
 XX
 XX Lindberg MK, Signas LC, Wadstrom TM, Froman G;
 XX WPI: 1988-347978/49.
 XX
 XX

DR P-PSDB; AAP82115.
XX Hybrid DNA encoding Staphylococcus aureus fibronectin binding protein -
PT useful for immunisation and topical application to prevent staphylococcal
PT infections.
XX
PS Disclosure; Fig. 8A:1-8A:2; 23pp; English.
CC The S.aureus fibronectin binding protein may be included in a hybrid
CC protein. The protein may be used to immunise ruminants against
CC staphylococcal mastitis, pref. when given at 0.5-5 microg/kg, using 3
CC doses at 1-3 week intervals; and for topical applicn. to prevent wound
CC infection, pref. using isotonic saline soln. of concn. 25-250 microg/mg.
CC The DNA encoding the binding protein and the hybrid protein may be
CC immobilised on a carrier and used to diagnose staphylococcal infections.
CC (updated on 25-MAR-2003 to correct PA field.)
XX
SQ Sequence 1018 AA;
Query Match 93.3%; Score 112; DB 1; Length 1018;
Best Local Similarity 95.2%; Pred. No. 3.4e-08;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 KPPYQFGHNSVDFEEDTLPK 21
DB 837 KPSYQFGHNSVDFEEDTLPK 857
RESULT 9
AAU37245
ID AAU37245 standard; protein; 1018 AA.
XX
AC AAU37245;
DT 14-FEB-2002 (first entry)
XX
DE Staphylococcus aureus cellular proliferation protein #1415.
XX
KM Antisense; prokaryotic cellular proliferation protein; antibiotic;
XX antibacterial; drug design.
XX
OS Staphylococcus aureus.
XX
PN WO200170955-A2.
PD 27-SEP-2001.
XX
PF 21-MAR-2001; 2001WO-US009180.
XX
PR 21-MAR-2000; 2000US-0191078P.
PR 23-MAY-2000; 2000US-0206848P.
PR 26-MAY-2000; 2000US-0207727P.
PR 23-OCT-2000; 2000US-0242578P.
PR 27-NOV-2000; 2000US-0253625P.
PR 22-DEC-2000; 2000US-0257931P.
PR 16-FEB-2001; 2001US-0269308P.
XX
PA (ELIT-) ELITRA PHARM INC.
XX
PI Haselbeck R, Ohlsen KL, Zyekind JW, Wall D, Trawick JD, Carr GJ;
PI Yamamoto RT, Xu HH;
XX
DR WPI; 2001-611495/70.
DR N-PSDB; AAS55104.
XX
PT New polynucleotides for the identification and development of
PT antibiotics, comprise sequences of antisense nucleic acids.
XX
PS Example 3; SEQ ID NO 12838; 511pp; English.
XX
CC The invention relates to antisense inhibitors of genes essential to
CC prokaryotic cellular proliferation, their use in identifying the genes,
CC their use in the discovery of novel antibiotics, the essential genes

CC themselves and the encoded proteins. The prokaryotes used are Escherichia
CC coli, Staphylococcus aureus, Salmonella typhi, Klebsiella pneumoniae.
CC Pseudomonas aeruginosa and Enterococcus faecalis. The invention is also
CC useful for the identification of potential new targets for antibiotic
CC development. The antisense nucleic acids can also be used to identify
CC proteins used in proliferation, to express these proteins, and to obtain
CC antibodies capable of binding to the expressed proteins. The proteins can
CC be used to screen compounds in rational drug discovery programmes. The
CC antisense nucleic acid sequence is also useful to screen for homologous
CC nucleic acids which are required for cell proliferation in a wide variety
CC of organisms. The present sequence represents an essential prokaryotic
CC cellular proliferation protein. Note: The sequence data for this patent
CC did not form part of the printed specification, but was obtained in
CC electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 1018 AA;
Query Match 93.3%; Score 112; DB 4; Length 1018;
Best Local Similarity 95.2%; Pred. No. 3.4e-08;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 KPPYQFGHNSVDFEEDTLPK 21
DB 837 KPSYQFGHNSVDFEEDTLPK 857
RESULT 10
AAU34301
ID AAU34301 standard; protein; 1018 AA.
XX
AC AAU34301;
DT 14-FEB-2002 (first entry)
XX
DE Staphylococcus aureus cellular proliferation protein #577.
XX
KM Antisense; prokaryotic cellular proliferation protein; antibiotic;
XX antibacterial; drug design.
XX
OS Staphylococcus aureus.
XX
PN WO200170955-A2.
PD 27-SEP-2001.
XX
PF 21-MAR-2001; 2001WO-US009180.
XX
PR 21-MAR-2000; 2000US-0191078P.
PR 23-MAY-2000; 2000US-0206848P.
PR 26-MAY-2000; 2000US-0207727P.
PR 23-OCT-2000; 2000US-0242578P.
PR 27-NOV-2000; 2000US-0253625P.
PR 22-DEC-2000; 2000US-0257931P.
PR 16-FEB-2001; 2001US-0269308P.
XX
PA (ELIT-) ELITRA PHARM INC.
XX
PI Haselbeck R, Ohlsen KL, Zyekind JW, Wall D, Trawick JD, Carr GJ;
PI Yamamoto RT, Xu HH;
XX
DR WPI; 2001-611495/70.
DR N-PSDB; AAS52160.
XX
PT New polynucleotides for the identification and development of
PT antibiotics, comprise sequences of antisense nucleic acids.
XX
PS Example 3; SEQ ID NO 5797; 511pp; English.
XX
CC The invention relates to antisense inhibitors of genes essential to
CC prokaryotic cellular proliferation, their use in identifying the genes,
CC their use in the discovery of novel antibiotics, the essential genes
CC themselves and the encoded proteins. The prokaryotes used are Escherichia

CC coli, *Staphylococcus aureus*, *Salmonella typhi*, *Klebsiella pneumoniae*,
 CC *Pseudomonas aeruginosa* and *Enterococcus faecalis*. The invention is also
 CC useful for the identification of potential new targets for antibiotic
 CC development. The antisense nucleic acids can also be used to identify
 CC proteins used in proliferation, to express these proteins, and to obtain
 CC antibodies capable of binding to the expressed proteins. The proteins can
 CC be used to screen compounds in rational drug discovery programmes. The
 CC antisense nucleic acid sequence is also useful to screen for homologous
 CC nucleic acids which are required for cell proliferation in a wide variety
 CC of organisms. The present sequence represents an essential prokaryotic
 CC cellular proliferation protein. Note: The sequence data for this patent
 CC did not form part of the printed specification, but was obtained in
 CC electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences

SO Sequence 1018 AA;

Query Match 93.3%; Score 112; DB 4; Length 1018;
 Best Local Similarity 95.2%; Pred. No. 3.4e-08;
 Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KPPYQFGHNSVDFEEDTLPK 21
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 DB 837 KPSYQFGHNSVDFEEDTLPK 857

RESULT 11

ABJ18922 standard; protein; 1018 AA.

AC ABJ18922;
 XX
 DT 06-MAR-2003 (first entry)

DE Pathogen specific antigen related staphylococcal protein SEQ ID No 68.

XX Antibacterial; virucide; fungicide; protozoacide; cytostatic; anti-HIV;
 XX hyperimmune; serum-reactive; antigen; pathogen; tumour; allergen;
 KW auto-immunity; vaccine; staphylococcal infection; antibody; cancer;
 KW autoimmune disease; HIV; hepatitis.

OS Staphylococcus sp.

PN WO200259148-A2.

PD 01-AUG-2002.

PF 21-JAN-2002; 2002WO-EP000546.

PR 26-JAN-2001; 2001AT-00000130.

PA (CIST-) CISTEM BIOTECHNOLOGIES GMBH.

PI Meinke A, Nagy E, Von Ahnen U, Klade C, Henics T, Zauner W;
 PI Minh DB, Vytvytska O, Etz H, Dryla A, Weichhart T, Hafner M;
 PI Tempelmeier B;

DR WPI; 2003-075410/07.

PT Identifying, isolating and producing hyperimmune serum-reactive antigens
 PT from a pathogen, for preparing vaccine or medicament for treating or
 PT preventing e.g. staphylococcal infections, comprises providing antibody
 PT preparation.

PS Example 7, Page 157; 252pp; English.

CC The invention relates to a novel method for identifying, isolating and
 CC producing hyperimmune serum-reactive antigens from a pathogen, tumour,
 CC allergen, a tissue or host prone to auto-immunity, where the antigens are
 CC used in a vaccine, comprises providing antibody preparation from a plasma
 CC pool of a type of animal, or individual sera with antibodies against the
 CC specific pathogen, tumour, allergen, tissue or host prone to auto-
 CC immunity. The hyperimmune serum-reactive antigens comprising any of the

CC 62 sequences of 53-2261 amino acids fully defined in the specification,
 CC or their hyperimmune fragments are useful for the manufacture of a
 CC pharmaceutical preparation, particularly a vaccine against staphylococcal
 CC infections or colonisation against *S. aureus* or *S. epidermidis*. The
 CC preparation of antibodies is useful for the manufacture of a medicament
 CC for treating or preventing staphylococcal infections or colonisation
 CC against *S. aureus* or *S. epidermidis*. The antibody preparations may also
 CC be used for diagnostic and imaging purposes. Other conditions that can be
 CC treated include cancer, autoimmune diseases or infections caused by viral
 CC (e.g. HIV, hepatitis A, B or C), fungal or protozoan pathogens. This
 CC sequence represents a staphylococcal protein relating to the method for
 CC identifying and producing pathogen specific antigens of the invention

SO Sequence 1018 AA;

Query Match 93.3%; Score 112; DB 6; Length 1018;
 Best Local Similarity 95.2%; Pred. No. 3.4e-08;
 Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KPPYQFGHNSVDFEEDTLPK 21
 ||||||||||||||||
 DB 837 KPSYQFGHNSVDFEEDTLPK 857

RESULT 12

ABM72537 standard; protein; 1018 AA.

AC ABM72537;

DT 20-NOV-2003 (first entry)

DE Staphylococcus aureus protein #1777.

KW Antibacterial; vaccine; gene therapy; infection; sepsis; diagnosis;
 KW enzymatic assay; antibiotic target.

OS Staphylococcus aureus.

PN WO200294868-A2.

PD 28-NOV-2002.

PF 27-MAR-2002; 2002WO-IB002637.

PR 27-MAR-2001; 2001GB-00007661.

PA (CHIR-) CHIRON SPA.

PI Masignani V, Mora M, Scarselli M;

DR WPI; 2003-120786/11.

DR N-PSDB; ACF74097.

PT New Staphylococcus aureus protein, useful as a vaccine for treating or
 PT preventing Staphylococcal infection, specifically an infection caused by
 PT *S. aureus*, e.g. sepsis.

PS Claim 1, SEQ ID NO 3554; 49pp; English.

CC The invention relates to novel genes and encoded proteins from
 CC *Staphylococcus aureus*. A composition comprising the *S. aureus* protein, a
 CC nucleic acid encoding the protein, or an antibody to the protein, is
 CC useful as a pharmaceutical, particularly as a vaccine for treating or
 CC preventing infection due to *Staphylococcus bacteris*, specifically an
 CC infection caused by *S. aureus*. The composition is particularly useful for
 CC treating or preventing sepsis in a patient. The composition can also be
 CC used for diagnostics. The protein is also used in an assay for enzymatic
 CC studies and as a target for antibiotics. This sequence represents one of
 CC the novel *S. aureus* proteins of the invention

SO Sequence 1018 AA;


```

CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 961 AA;
Query Match 92.5%; Score 111; DB 6; Length 961;
Best Local Similarity 95.2%; Pred. No. 4.6e-08;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 KPPYQFGHNSVDFEEDTLPK 21
DB 784 KPNYQFGHNSVDFEEDTLPK 804

RESULT 15
AAU33960
ID AAU33960 standard; protein; 978 AA.
AC AAU33960;
XX
XX
XX
DT 14-FEB-2002 (first entry)
XX
DE Staphylococcus aureus cellular proliferation protein #236.
XX
XX Antisense; prokaryotic cellular proliferation protein; antibiotic;
KW antibacterial; drug design.
XX
OS Staphylococcus aureus.
XX
XX WO200170955-A2.
XX
XX 27-SEP-2001.
XX
XX 21-MAR-2001; 2001WO-US009180.
XX
XX 21-MAR-2000; 2000US-0191078P.
XX
XX 23-MAY-2000; 2000US-0206848P.
XX
XX 26-MAY-2000; 2000US-0207727P.
XX
XX 23-OCT-2000; 2000US-0242578P.
XX
XX 27-NOV-2000; 2000US-0253625P.
XX
XX 22-DEC-2000; 2000US-0257931P.
XX
XX 16-FEB-2001; 2001US-0269308P.
XX
XX
XX (ELITR-) ELITRA PHARM INC.
XX
XX
XX Haselbeck R, Ohlsen KL, Zyskind JW, Wall D, Trawick JD, Carr GJ;
PI Yamamoto RT, Xu HH;
XX
XX WPI; 2001-611495/70.
XX
XX N-PSDB; AAS51819.
XX
XX
XX New polynucleotides for the identification and development of
PT antibiotics, comprise sequences of antisense nucleic acids.
XX
XX
XX Example 3; SEQ ID NO 5456; 511p; English.
XX
XX The invention relates to antisense inhibitors of genes essential to
CC prokaryotic cellular proliferation, their use in identifying the genes,
CC their use in the discovery of novel antibiotics, the essential genes,
CC themselves and the encoded proteins. The prokaryotes used are Escherichia
CC coli, Staphylococcus aureus, Salmonella typhi, Klebsiella pneumoniae,
CC Pseudomonas aeruginosa and Enterococcus faecalis. The invention is also
CC useful for the identification of potential new targets for antibiotic
CC development. The antisense nucleic acids can also be used to identify
CC proteins used in proliferation, to express these proteins, and to obtain
CC antibodies capable of binding to the expressed proteins. The proteins can
CC be used to screen compounds in rational drug discovery programmes. The
CC antisense nucleic acid sequence is also useful to screen for homologous
CC nucleic acids which are required for cell proliferation in a wide variety
CC of organisms. The present sequence represents an essential prokaryotic
CC cellular proliferation protein. Note: The sequence data for this patent
CC did not form part of the printed specification, but was obtained in
CC electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences

```

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XX
SQ Sequence 978 AA;
Query Match 92.5%; Score 111; DB 4; Length 978;
Best Local Similarity 95.2%; Pred. No. 4.7e-08;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 KPPYQFGHNSVDFEEDTLPK 21
DB 815 KPNYQFGHNSVDFEEDTLPK 835

Search completed: October 25, 2005, 19:38:27
Job time : 59.1473 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 22, 2005, 02:23:36 ; Search time 15.9358 Seconds
(without alignments)
98.371 Million cell updates/sec

Title: US-10-731-238-16
Perfect score: 120
Sequence: 1 KPYPQFGHNSVDFEEDLPK 21

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA: *
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	length	DB ID	Description
1	120	100.0	21	4	US-09-010-317-16
2	112	93.3	21	4	US-09-010-317-9
3	112	93.3	37	1	US-08-234-622A-4
4	112	93.3	38	1	US-08-294-189-8
5	112	93.3	38	1	US-08-729-767-5
6	112	93.3	114	1	US-08-259-000-3
7	112	93.3	139	1	US-08-836-253-8
8	112	93.3	178	2	US-08-459-135A-12
9	112	93.3	178	3	US-08-495-559-12
10	112	93.3	1027	4	US-08-956-171E-5254
11	112	93.3	1027	4	US-08-781-986A-5254
12	107	89.2	21	4	US-09-010-317-14
13	107	89.2	21	4	US-09-010-317-23
14	107	89.2	21	4	US-09-010-317-33
15	107	89.2	130	2	US-08-459-135A-7
16	107	89.2	130	2	US-08-459-135A-8
17	107	89.2	130	3	US-08-495-559-7
18	107	89.2	130	3	US-08-495-559-8
19	107	89.2	174	2	US-08-459-135A-10
20	107	89.2	174	2	US-08-459-135A-13
21	107	89.2	174	3	US-08-495-559-10
22	107	89.2	174	3	US-08-495-559-13
23	107	89.2	176	3	US-08-495-559-6
24	107	89.2	181	2	US-08-459-135A-6
25	107	89.2	559	4	US-08-956-171E-5251
26	107	89.2	559	4	US-08-781-986A-5251
27	106	88.3	21	4	US-09-010-317-18

28	106	88.3	21	4	US-09-010-317-24	Sequence 24, Appl
29	106	88.3	21	4	US-09-010-317-27	Sequence 27, Appl
30	106	88.3	21	4	US-09-010-317-28	Sequence 28, Appl
31	106	88.3	21	4	US-09-010-317-30	Sequence 30, Appl
32	105	87.5	21	4	US-09-010-317-25	Sequence 25, Appl
33	105	87.5	21	4	US-09-010-317-29	Sequence 29, Appl
34	105	87.5	21	4	US-09-010-317-31	Sequence 31, Appl
35	104	86.7	21	4	US-09-010-317-15	Sequence 15, Appl
36	104	86.7	21	4	US-09-010-317-16	Sequence 16, Appl
37	104	86.7	21	4	US-09-010-317-22	Sequence 22, Appl
38	104	86.7	21	4	US-09-010-317-23	Sequence 23, Appl
39	104	86.7	21	4	US-09-010-317-13	Sequence 13, Appl
40	104	86.7	21	4	US-09-010-317-17	Sequence 17, Appl
41	102	85.0	21	4	US-09-010-317-19	Sequence 19, Appl
42	102	85.0	21	4	US-09-010-317-21	Sequence 21, Appl
43	102	85.0	21	4	US-09-010-317-26	Sequence 26, Appl
44	102	85.0	21	4	US-09-010-317-26	Sequence 26, Appl
45	91	75.8	19	1	US-08-234-622A-1	Sequence 1, Appl

ALIGNMENTS

RESULT 1
US-09-010-317-16
Sequence 16, Application US/09010317
Patent No. 6685943
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
APPLICANT: Patti, Joseph M.
APPLICANT: House-Pompeo, Karen L.
APPLICANT: Speziale, Pietro
APPLICANT: Job, Danny
APPLICANT: McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
TITLE OF INVENTION: AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hilder, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAMK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-09-010-317-16
Query Match 100.0%; Score 120; DB 4; Length 21;
Best Local Similarity 100.0%; Pred. No. 3.6e-12;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KPYPQFGHNSVDFEEDTLPK 21

Db 1 KPYPQFGHNSVDFEEDTLPK 21

RESULT 2

US-09-010-317-9

; Sequence 9, Application US/09010317

; Patent No. 6685943

; GENERAL INFORMATION:

; APPLICANT: Hook, Magnus

; APPLICANT: Patti, Joseph M.

; APPLICANT: House-Pompeo, Karen L.

; APPLICANT: Speziale, Pietro

; APPLICANT: McGavin, Martin J.

; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS

; NUMBER OF SEQUENCES: 105

; CORRESPONDENCE ADDRESS:

; ADDRESSER: Arnold, White & Durkee

; STREET: P.O. Box 4433

; CITY: Houston

; STATE: TX

; COUNTRY: USA

; ZIP: 77210-4433

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Releasee #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/010,317

; FILING DATE:

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 60/036,139

; FILING DATE: 21-JAN-1997

; ATTORNEY/AGENT INFORMATION:

; NAME: Hibler, David W.

; REGISTRATION NUMBER: 41,071

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 512-418-3000

; TELEFAX: 512-474-7577

; INFORMATION FOR SEQ ID NO: 9:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 21 amino acids

; TYPE: amino acid

; STRANDEDNESS:

; TOPOLOGY: linear

US-09-010-317-9

Query Match 93.3%; Score 112; DB 4; Length 21;

Best Local Similarity 95.2%; Pred. No. 6.4e-11; Mismatches 1; Indels 0; Gaps 0;

Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KPYPQFGHNSVDFEEDTLPK 21

Db 1 KPYPQFGHNSVDFEEDTLPK 21

RESULT 3

US-08-234-622A-4

; Sequence 4, Application US/08234622A

; Patent No. 5440014

; GENERAL INFORMATION:

; APPLICANT: Hook, Magnus

; APPLICANT: MCGAVIN, Martin

; APPLICANT: RAUCCI, Giuseppe

; TITLE OF INVENTION: A FIBRONECTIN BINDING PEPTIDE

; NUMBER OF SEQUENCES: 4

; CORRESPONDENCE ADDRESS:

; ADDRESSER: Burns, Doane, Swecker & Machis

; STREET: P.O. Box 1404

; CITY: Alexandria

; STATE: Virginia

; COUNTRY: United States

; ZIP: 22313-1404

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Releasee #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/234,622A

; FILING DATE: 28-APR-1994

; CLASSIFICATION: 530

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: SE 9002617-0

; FILING DATE: 10-AUG-1990

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: WO PCT/SE91/00534

; FILING DATE: 09-AUG-1991

; ATTORNEY/AGENT INFORMATION:

; NAME: Neulth, Donna M

; REGISTRATION NUMBER: 36,607

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (703) 836-6620

; TELEFAX: (703) 836-6620

; INFORMATION FOR SEQ ID NO: 4:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 37 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

US-08-234-622A-4

Query Match 93.3%; Score 112; DB 1; Length 37;

Best Local Similarity 95.2%; Pred. No. 1.2e-10; Mismatches 1; Indels 0; Gaps 0;

Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KPYPQFGHNSVDFEEDTLPK 21

Db 16 KPYPQFGHNSVDFEEDTLPK 36

RESULT 4

US-08-294-189-8

; Sequence 8, Application US/08294189

; Patent No. 5707822

; GENERAL INFORMATION:

; APPLICANT: Fischetti, Vincent A.

; APPLICANT: Rakonjac, Jasna

; APPLICANT: Robbins, John

; TITLE OF INVENTION: GENE SERUM OPACITY FACTOR

; NUMBER OF SEQUENCES: 23

; CORRESPONDENCE ADDRESS:

; ADDRESSER: Klauber & Jackson

; STREET: 411 Hackensack Avenue

; CITY: Hackensack

; STATE: New Jersey

; COUNTRY: USA

; ZIP: 07601

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Releasee #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/294,189

; FILING DATE: 22-AUG-1994

CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Bag., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-118
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 487-5800
TELEFAX: 201 343-1684
TELEX: 133521
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
ORGANISM: Streptococcus pyogenes
STRAIN: D734
INDIVIDUAL ISOLATE: 22
IMMEDIATE SOURCE:
CLONE: SAU3a
US-08-294-189-8

Query Match 93.3%; Score 112; DB 1; Length 38;
Best Local Similarity 95.2%; Pred. No. 1,2e-10;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KPPYQFGHNSVDFEEDTLPK 21
Db 10 KPSYQFGHNSVDFEEDTLPK 30

RESULT 5
US-08-729-767-5
Sequence 5, Application US/08729767
Patent No. 5770702
GENERAL INFORMATION:
APPLICANT: HOOK, Magnus
APPLICANT: LINDBERG, Martin Kjell
APPLICANT: SIGNAS, Lars Christer
APPLICANT: WADSTROM, Torkel Mikael
APPLICANT: FROMAN, Gunnar
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN AS WELL AS
TITLE OF INVENTION: ITS PREPARATION
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Burns, Doane, Swecker & Mathis, L.L.P.
STREET: P.O. Box 1404
CITY: Alexandria
STATE: Virginia
COUNTRY: United States
ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/729,767
FILING DATE: 07-OCT-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/259,000
FILING DATE: 13-JUN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/007,817
FILING DATE: 22-JAN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/201,028
FILING DATE: 01-JUN-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: SE 8702272-9

FILING DATE: 01-JUN-1987
ATTORNEY/AGENT INFORMATION:
NAME: McGowan, Malcolm K.
REGISTRATION NUMBER: 39,300
REFERENCE/DOCKET NUMBER: 012889-036
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-729-767-5

Query Match 93.3%; Score 112; DB 1; Length 38;
Best Local Similarity 95.2%; Pred. No. 1,2e-10;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KPPYQFGHNSVDFEEDTLPK 21
Db 17 KPSYQFGHNSVDFEEDTLPK 37

RESULT 6
US-08-259-000-3
Sequence 3, Application US/08259000
Patent No. 5571514
GENERAL INFORMATION:
APPLICANT: HOOK, Magnus
APPLICANT: LINDBERG, Martin Kjell
APPLICANT: SIGNAS, Lars Christer
APPLICANT: WADSTROM, Torkel Mikael
APPLICANT: FROMAN, Gunnar
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN AS WELL AS
TITLE OF INVENTION: ITS PREPARATION
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Burns, Doane, Swecker & Mathis
STREET: P.O. Box 1404
CITY: Alexandria
STATE: Virginia
COUNTRY: United States
ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/259,000
FILING DATE: 13-JUN-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: SE 8702272-9
FILING DATE: 01-JUN-1987
ATTORNEY/AGENT INFORMATION:
NAME: Meuth, Donna M
REGISTRATION NUMBER: 36,607
REFERENCE/DOCKET NUMBER: 012885-062
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 114 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-259-000-3

ORGANISM: Staphylococcus aureus
US-08-495-559-12

Query Match 93.3%; Score 112; DB 3; Length 178;
Best Local Similarity 95.2%; Pred. No. 6.9e-10;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 KPPYQFGHNSVDFEEDTLPK 21
Db 93 KPSYQFGHNSVDFEEDTLPK 113

RESULT 10

US-08-956-171E-5254
Sequence 5254, Application US/08956171E
Patent No. 6593114
GENERAL INFORMATION:
APPLICANT: Charles Kunesh
Gil H. Choi
Patrick S. Dillon
Craig A. Rosen
Steven C. Barash
Michael R. Fannon
TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
NUMBER OF SEQUENCES: 5256
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COUNTRY: USA
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4MB storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/956,171E
FILING DATE: 20-Oct-1997
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/009,861
FILING DATE: January 5, 1996
APPLICATION NUMBER: 08/781,986
FILING DATE: January 3, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Mark J. Hyman
REGISTRATION/DOCKET NUMBER: 46,789
REFERENCE/DOCKET NUMBER: PB248P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (240) 314-1224
TELEFAX: (301) 309-8439
INFORMATION FOR SEQ ID NO: 5254:
SEQUENCE CHARACTERISTICS:
LENGTH: 1027 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 5254:
US-08-956-171E-5254

Query Match 93.3%; Score 112; DB 4; Length 1027;
Best Local Similarity 95.2%; Pred. No. 4.8e-09;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 KPPYQFGHNSVDFEEDTLPK 21
Db 846 KPSYQFGHNSVDFEEDTLPK 866

RESULT 11

US-08-781-986A-5254
Sequence 5254, Application US/08781986A
Patent No. 6737248

GENERAL INFORMATION:
APPLICANT: Charles Kunesh
TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
NUMBER OF SEQUENCES: 5255
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COUNTRY: USA
ZIP: 20850

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4MB storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/781,986A
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Benson, Bob
REGISTRATION/DOCKET NUMBER: 30,446
REFERENCE/DOCKET NUMBER: PB248PP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 5254:
SEQUENCE CHARACTERISTICS:
LENGTH: 1027 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-781-986A-5254

Query Match 93.3%; Score 112; DB 4; Length 1027;
Best Local Similarity 95.2%; Pred. No. 4.8e-09;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 KPPYQFGHNSVDFEEDTLPK 21
Db 846 KPSYQFGHNSVDFEEDTLPK 866

RESULT 12

US-09-010-317-14
Sequence 14, Application US/09010317
Patent No. 6685943
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
APPLICANT: Patti, Joseph M.
APPLICANT: House-Pompeo, Karen L.
APPLICANT: Speziale, Pietro
APPLICANT: Joh, Danny
APPLICANT: McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-09-010-317-14

Query Match 89.2%; Score 107; DB 4; Length 21;
Best Local Similarity 95.0%; Pred. No. 3.9e-10;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2 PPSYQFGHNSVDFEEDTLPK 21
DB 2 PPSYQFGHNSVDFEEDTLPK 21

RESULT 13
US-09-010-317-23
Sequence 23, Application US/09010317
Patent No. 6685943
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
APPLICANT: Patil, Joseph M.
APPLICANT: House-Pompeo, Karen L.
APPLICANT: Speziale, Pietro
APPLICANT: Joh, Danny
APPLICANT: McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
TITLE OF INVENTION: AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-09-010-317-33

TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-09-010-317-23

Query Match 89.2%; Score 107; DB 4; Length 21;
Best Local Similarity 90.5%; Pred. No. 3.9e-10;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 KPPYQFGHNSVDFEEDTLPK 21
DB 1 KPPYQFGHNSVDFEEDTLPK 21

RESULT 14
US-09-010-317-33
Sequence 33, Application US/09010317
Patent No. 6685943
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
APPLICANT: Patil, Joseph M.
APPLICANT: House-Pompeo, Karen L.
APPLICANT: Speziale, Pietro
APPLICANT: Joh, Danny
APPLICANT: McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
TITLE OF INVENTION: AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-09-010-317-33

Query Match 89.2%; Score 107; DB 4; Length 21;
Best Local Similarity 95.0%; Pred. No. 3.9e-10;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 KPPYQFGHNSVDFEEDTLPK 20
DB 1 KPPYQFGHNSVDFEEDTLPK 20

Db 1 KPSYQFGHNSVDFEEDLP 20

RESULT 15

US-08-459-135A-7
; Sequence 7, Application US/08459135A
; Patent No. 5955078
; GENERAL INFORMATION:
; APPLICANT: BURHAM, Martin Karl Russel
; APPLICANT: CHOPRA, Ian
; APPLICANT: CRITCHLEY, Ian Alfred
; APPLICANT: KNOWLES, David Justin Charles
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN: MONOCLONAL ANTIBODY AND THEIR US
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corporation
; STREET: 709 Swedeland Road
; CITY: King of Prussia
; STATE: PA
; COUNTRY: U.S.A.
; ZIP: 19406-0939
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: Fastseq, Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/459,135A
; FILING DATE: 02-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB/94/00215
; FILING DATE: 04-Feb-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Gilmel, Edward R
; REGISTRATION NUMBER: 38,891
; REFERENCE//DOCKET NUMBER: P30591C2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-270-4478
; TELEFAX: 610-270-5090
; TELEX:
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 130 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-459-135A-7

Query Match 89.2%; Score 107; DB 2; Length 130;
Best Local Similarity 90.5%; Pred. No. 3e-09; 1; Indels 0; Gaps 0;
Matches 19; Conservative 1; Mismatches 1;

QY 1 KPSYQFGHNSVDFEEDLPK 21
|||
Db 93 KPNYQFGHNSVDFEEDLPQ 113

Search completed: October 22, 2005, 03:51:11
Job time : 15.9358 secs

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OW protein - protein search, using sw model

Run on: October 22, 2005, 10:49:15 ; Search time 59.2367 Seconds
(without alignments)
148.005 Million cell updates/sec

Title: US-10-731-238-16
Perfect score: 120
Sequence: 1 KPPYQFGHNSVDFEEDLPK 21

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1862951 seqs, 417491010 residues
Total number of hits satisfying chosen parameters: 1862951

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: /cgns2_6/prodata/2/pubpaa/US07_PUBCOMB.pep.*
2: /cgns2_6/prodata/2/pubpaa/PCT_NEW_PUB.pep.*
3: /cgns2_6/prodata/2/pubpaa/US06_NEW_PUB.pep.*
4: /cgns2_6/prodata/2/pubpaa/US06_PUBCOMB.pep.*
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6: /cgns2_6/prodata/2/pubpaa/PCTUS_PUBCOMB.pep.*
7: /cgns2_6/prodata/2/pubpaa/US08_NEW_PUB.pep.*
8: /cgns2_6/prodata/2/pubpaa/US08_PUBCOMB.pep.*
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10: /cgns2_6/prodata/2/pubpaa/US09C_PUBCOMB.pep.*
11: /cgns2_6/prodata/2/pubpaa/US09_NEW_PUB.pep.*
12: /cgns2_6/prodata/2/pubpaa/US10_PUBCOMB.pep.*
13: /cgns2_6/prodata/2/pubpaa/US10C_PUBCOMB.pep.*
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16: /cgns2_6/prodata/2/pubpaa/US10E_PUBCOMB.pep.*
17: /cgns2_6/prodata/2/pubpaa/US10F_PUBCOMB.pep.*
18: /cgns2_6/prodata/2/pubpaa/US10_NEW_PUB.pep.*
19: /cgns2_6/prodata/2/pubpaa/US11A_PUBCOMB.pep.*
20: /cgns2_6/prodata/2/pubpaa/US11_NEW_PUB.pep.*
21: /cgns2_6/prodata/2/pubpaa/US60_NEW_PUB.pep.*
22: /cgns2_6/prodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	120	100.0	21	18	US-10-731-238-16
2	112	93.3	21	18	US-10-731-238-9
3	112	93.3	37	20	US-11-066-697-1134
4	112	93.3	139	9	US-09-813-820-8
5	112	93.3	1018	9	US-09-815-242-5797
6	112	93.3	1018	17	US-10-470-048B-68
7	112	93.3	1027	8	US-08-781-986A-5254
8	112	93.3	1027	15	US-10-329-624-5254
9	112	93.3	1027	15	US-10-329-624-5254
10	112	92.5	961	15	US-10-282-122A-43778
11	111	92.5	978	9	US-09-815-242-5456

12	111	92.5	1001	9	US-09-815-242-12686	Sequence 12686, A
13	111	92.5	1038	15	US-10-282-122A-43827	Sequence 43827, A
14	107	89.2	21	18	US-10-731-238-14	Sequence 14, Appl
15	107	89.2	21	18	US-10-731-238-23	Sequence 23, Appl
16	107	89.2	21	18	US-10-731-238-33	Sequence 33, Appl
17	107	89.2	388	8	US-08-901-062-1	Sequence 1, Appl1
18	107	89.2	559	8	US-08-781-986A-5251	Sequence 5251, Ap
19	107	89.2	559	15	US-10-329-624-5251	Sequence 5251, Ap
20	107	89.2	940	17	US-10-470-048B-63	Sequence 424, App
21	107	89.2	948	17	US-10-470-048B-63	Sequence 69, Appl
22	106	88.3	21	18	US-10-731-238-18	Sequence 18, Appl
23	106	88.3	21	18	US-10-731-238-24	Sequence 24, Appl
24	106	88.3	21	18	US-10-731-238-27	Sequence 27, Appl
25	106	88.3	21	18	US-10-731-238-28	Sequence 28, Appl
26	106	88.3	21	18	US-10-731-238-30	Sequence 30, Appl
27	105	87.5	21	18	US-10-731-238-25	Sequence 25, Appl
28	105	87.5	21	18	US-10-731-238-29	Sequence 29, Appl
29	105	87.5	21	18	US-10-731-238-31	Sequence 31, Appl
30	104	86.7	21	18	US-10-731-238-15	Sequence 15, Appl
31	104	86.7	21	18	US-10-731-238-19	Sequence 19, Appl
32	104	86.7	21	18	US-10-731-238-20	Sequence 20, Appl
33	104	86.7	21	18	US-10-731-238-22	Sequence 22, Appl
34	104	86.7	21	18	US-10-731-238-32	Sequence 32, Appl
35	104	86.7	22	18	US-10-731-238-13	Sequence 13, Appl
36	102	85.0	21	18	US-10-731-238-17	Sequence 17, Appl
37	102	85.0	21	18	US-10-731-238-21	Sequence 21, Appl
38	102	85.0	21	18	US-10-731-238-21	Sequence 26, Appl
39	102	85.0	21	18	US-10-731-238-26	Sequence 34, Appl
40	85	70.8	21	18	US-10-731-238-34	Sequence 61, Appl
41	78	65.0	14	18	US-10-731-238-61	Sequence 98, Appl
42	58	48.3	10	18	US-10-731-238-97	Sequence 99, Appl
43	57	47.5	10	18	US-10-731-238-99	Sequence 96, Appl
44	56	46.7	10	18	US-10-731-238-99	
45	54	45.0	10	18	US-10-731-238-96	

ALIGNMENTS

RESULT 1
US-10-731-238-16
Sequence 16, Application US//10731238
Publication No. US20050123552A1
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
Patel, Joseph M.
House-Pompeo, Karen L.
Speziale, Pietro
Joh, Danny
McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSER: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/731.238
FILING DATE: 10-Dec-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/010.317
FILING DATE: 21-Jan-1998
APPLICATION NUMBER: US 60/036,139

FILED DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAMK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 16:
US-10-731-238-16

Query Match 100.0%; Score 120; DB 18; Length 21;
Best Local Similarity 100.0%; Pred. No. 3, 9e-11;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KPYPQFGHNSVDFEEDTLPK 21
DB 1 KPYPQFGHNSVDFEEDTLPK 21

RESULT 2
US-10-731-238-9
Sequence 9, Application US/10731238
Publication No. US20050123552A1
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
Parti, Joseph M.
House-Pompeo, Karen L.
Speziale, Pietro
Joh, Danny
McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/731,238
FILING DATE: 10-Dec-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE: 21-Jan-1998
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAMK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>

TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 9:
US-10-731-238-9

Query Match 93.3%; Score 112; DB 18; Length 21;
Best Local Similarity 95.2%; Pred. No. 6, 5e-10;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KPYPQFGHNSVDFEEDTLPK 21
DB 1 KPYPQFGHNSVDFEEDTLPK 21

RESULT 3
US-11-066-697-1134
Sequence 1134, Application US/11066697
Publication No. US20050187159A1
GENERAL INFORMATION:
APPLICANT: Bridon, Dominique P.
APPLICANT: Ezrin, Alan M.
APPLICANT: Milner, Peter G.
APPLICANT: Holmes, Darren L.
APPLICANT: Thibaudau, Karen
TITLE OF INVENTION: PROTECTION OF ENDOGENOUS THERAPEUTIC PEPTIDES FROM
PEPTIDASE ACTIVITY THROUGH CONJUGATION TO BLOOD
COMPONENTS
FILE REFERENCE: 500862002301
CURRENT APPLICATION NUMBER: US/11/066,697
CURRENT FILING DATE: 2005-02-25
PRIOR APPLICATION NUMBER: 09/657,276
PRIOR FILING DATE: 2000-09-07
PRIOR APPLICATION NUMBER: 60/153,406
PRIOR FILING DATE: 1999-09-10
PRIOR APPLICATION NUMBER: 60/159,783
PRIOR FILING DATE: 1999-10-15
NUMBER OF SEQ ID NOS: 1617
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 1134
LENGTH: 37
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-11-066-697-1134

Query Match 93.3%; Score 112; DB 20; Length 37;
Best Local Similarity 95.2%; Pred. No. 1, 2e-09;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KPYPQFGHNSVDFEEDTLPK 21
DB 16 KPYPQFGHNSVDFEEDTLPK 36

RESULT 4
US-09-813-820-8
Sequence 8, Application US/09813820
Patent No. US20020102262A1
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
Parti, Joseph M.
House-Pompeo, Karen
Schanam, Narayana
Symersky, Jindrich
TITLE OF INVENTION: COLLAGEN BINDING PROTEIN COMPOSITIONS
AND METHODS OF USE
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: Texas

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; COUNTRY: U.S.
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/813,820
; FILING DATE: 22-Mar-2001
; CLASSIFICATION: <Unknown>
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: 08/856,253
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Kitchell, Barbara S.
; REGISTRATION NUMBER: 33,928
; REFERENCE/DOCKET NUMBER: TAMK.193
; TELEPHONE: (512) 418-3000
; TELEFAX: (512) 474-7577
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 139 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-09-813-820-8

Query Match      93.3%; Score 112; DB 9; Length 139;
Best Local Similarity 95.2%; Pred. No. 4.8e-09;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 KPPYQFGHNSVDFEEDTLPK 21
DB      107 KPSYQFGHNSVDFEEDTLPK 127

RESULT 5
US-09-815-242-5797
; Sequence 5797, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Karl L.
; APPLICANT: Zykkind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; FILE REFERENCE: ELITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; PRIORITY FILING DATE: 2001-03-21
; PRIORITY APPLICATION NUMBER: 60/191,078
; PRIORITY FILING DATE: 2000-03-21
; PRIORITY APPLICATION NUMBER: 60/206,848
; PRIORITY FILING DATE: 2000-05-23
; PRIORITY APPLICATION NUMBER: 60/207,727
; PRIORITY FILING DATE: 2000-05-26
; PRIORITY APPLICATION NUMBER: 60/242,578
; PRIORITY FILING DATE: 2000-10-23
; PRIORITY APPLICATION NUMBER: 60/253,625
; PRIORITY FILING DATE: 2000-11-27
; PRIORITY APPLICATION NUMBER: 60/257,931
; PRIORITY FILING DATE: 2000-12-22
; PRIORITY APPLICATION NUMBER: 60/269,308
; PRIORITY FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version 4.0
; FILE REFERENCE: SONN.03505
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; SEQ ID NO 5797
; LENGTH: 1018
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-09-815-242-5797

Query Match      93.3%; Score 112; DB 9; Length 1018;
Best Local Similarity 95.2%; Pred. No. 4e-08;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 KPPYQFGHNSVDFEEDTLPK 21
DB      837 KPSYQFGHNSVDFEEDTLPK 857

RESULT 6
US-09-815-242-12838
; Sequence 12838, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Karl L.
; APPLICANT: Zykkind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; FILE REFERENCE: ELITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; PRIORITY FILING DATE: 2001-03-21
; PRIORITY APPLICATION NUMBER: 60/191,078
; PRIORITY FILING DATE: 2000-03-21
; PRIORITY APPLICATION NUMBER: 60/206,848
; PRIORITY FILING DATE: 2000-05-23
; PRIORITY APPLICATION NUMBER: 60/207,727
; PRIORITY FILING DATE: 2000-05-26
; PRIORITY APPLICATION NUMBER: 60/242,578
; PRIORITY FILING DATE: 2000-10-23
; PRIORITY APPLICATION NUMBER: 60/253,625
; PRIORITY FILING DATE: 2000-11-27
; PRIORITY APPLICATION NUMBER: 60/257,931
; PRIORITY FILING DATE: 2000-12-22
; PRIORITY APPLICATION NUMBER: 60/269,308
; PRIORITY FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12838
; LENGTH: 1018
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-09-815-242-12838

Query Match      93.3%; Score 112; DB 9; Length 1018;
Best Local Similarity 95.2%; Pred. No. 4e-08;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 KPPYQFGHNSVDFEEDTLPK 21
DB      837 KPSYQFGHNSVDFEEDTLPK 857

RESULT 7
US-10-470-048B-68
; Sequence 68, Application US/10470048B
; Publication No. US2005003744A1
; GENERAL INFORMATION:
; APPLICANT: MEINKE ET AL.
; TITLE OF INVENTION: A METHOD FOR IDENTIFICATION, ISOLATION AND PRODUCTION OF
; FILE REFERENCE: SONN.03505
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/ CURRENT APPLICATION NUMBER: US/10/470,048B
/ CURRENT FILING DATE: 2003-07-25
/ NUMBER OF SEQ ID NOS: 603
/ SOFTWARE: Patentin version 3.1
/ SEQ ID NO 68
/ LENGTH: 1018
/ TYPE: PRF
/ ORGANISM: Staphylococcus aureus
US-10-470-048B-68

Query Match 93.3%; Score 112; DB 17; Length 1018;
Best Local Similarity 95.2%; Pred. No. 4e-08;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KPPYQFGHNSVDFEEDTLPK 21
DB 837 KPSYQFGHNSVDFEEDTLPK 857

RESULT 8
US-08-781-986A-5254
/ Sequence 5254, Application US/08781986A
/ Publication No. US20030054436A1
/ GENERAL INFORMATION:
/ APPLICANT: Charles Kunesh
/ TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
/ NUMBER OF SEQUENCES: 5255
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Human Genome Sciences, Inc.
/ STREET: 9410 Key West Avenue
/ CITY: Rockville
/ STATE: Maryland
/ COUNTRY: USA
/ ZIP: 20850
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
/ COMPUTER: HP Vectra 486/33
/ OPERATING SYSTEM: MSDOS version 6.2
/ SOFTWARE: ASCII Text
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/781,986A
/ FILING DATE:
/ CLASSIFICATION: 435
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER:
/ FILING DATE:
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Benson, Bob
/ REGISTRATION NUMBER: 30,446
/ REFERENCE/DOCKET NUMBER: PB248PP
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (301) 309-8504
/ TELEFAX: (301) 309-8512
/ INFORMATION FOR SEQ ID NO: 5254:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 1027 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
US-08-781-986A-5254

Query Match 93.3%; Score 112; DB 8; Length 1027;
Best Local Similarity 95.2%; Pred. No. 4.1e-08;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KPPYQFGHNSVDFEEDTLPK 21
DB 846 KPSYQFGHNSVDFEEDTLPK 866

RESULT 9
US-10-329-624-5254

/ Sequence 5254, Application US/10329624
/ Publication No. US20040043037A1
/ GENERAL INFORMATION:
/ APPLICANT: Charles Kunesh
/ Gail H. Choi
/ Patrick S. Dillon
/ Craig A. Rosen
/ Steven C. Barash
/ Michael R. Fannon
/ TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
/ NUMBER OF SEQUENCES: 5256
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Human Genome Sciences, Inc.
/ STREET: 9410 Key West Avenue
/ CITY: Rockville
/ STATE: Maryland
/ COUNTRY: USA
/ ZIP: 20850
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
/ COMPUTER: HP Vectra 486/33
/ OPERATING SYSTEM: MSDOS version 6.2
/ SOFTWARE: ASCII Text
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/10/329,624
/ FILING DATE: 27-Dec-2002
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/956,171
/ FILING DATE: October 20, 1997
/ APPLICATION NUMBER: 60/009,861
/ FILING DATE: January 5, 1996
/ APPLICATION NUMBER: 08/781,986
/ FILING DATE: January 3, 1997
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Mark J. Hyman
/ REGISTRATION NUMBER: 46,789
/ REFERENCE/DOCKET NUMBER: PB248P1D1
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (240) 314-1224
/ TELEFAX: (301) 309-8439
/ INFORMATION FOR SEQ ID NO: 5254:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 1027 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ SEQUENCE DESCRIPTION: SEQ ID NO: 5254:
US-10-329-624-5254

Query Match 93.3%; Score 112; DB 15; Length 1027;
Best Local Similarity 95.2%; Pred. No. 4.1e-08;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KPPYQFGHNSVDFEEDTLPK 21
DB 846 KPSYQFGHNSVDFEEDTLPK 866

RESULT 10
US-10-282-122A-43778
/ Sequence 43778, Application US/10282122A
/ Publication No. US20040029129A1
/ GENERAL INFORMATION:
/ APPLICANT: Wang, Liangou
/ APPLICANT: Zamudio, Carlos
/ APPLICANT: Malone, Cheryl
/ APPLICANT: Haselbeck, Robert
/ APPLICANT: Ohlsen, Kari
/ APPLICANT: Zykkind, Juddich
/ APPLICANT: Wall, Daniel
/ APPLICANT: Trawick, John
/ APPLICANT: Carr, Grant


```
/ Publication No. US20040029129A1
/ GENERAL INFORMATION:
/ APPLICANT: Wang, Liangsu
/ APPLICANT: Zamudio, Carlos
/ APPLICANT: Malone, Cheryl
/ APPLICANT: Haselbeck, Robert
/ APPLICANT: Ohlsen, Kari
/ APPLICANT: Zyskind, Judith
/ APPLICANT: Wall, Daniel
/ APPLICANT: Trawick, John
/ APPLICANT: Carr, Grant
/ APPLICANT: Yamamoto, Robert
/ APPLICANT: Foreyth, R.
/ APPLICANT: Xu, H.
/ TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
/ FILE REFERENCE: ELITRA.034A
/ CURRENT APPLICATION NUMBER: US/10/282,122A
/ PRIOR FILING DATE: 2003-02-20
/ PRIOR APPLICATION NUMBER: 60/191,078
/ PRIOR FILING DATE: 2000-03-21
/ PRIOR APPLICATION NUMBER: 60/206,848
/ PRIOR FILING DATE: 2000-05-23
/ PRIOR APPLICATION NUMBER: 60/207,727
/ PRIOR FILING DATE: 2000-05-26
/ PRIOR APPLICATION NUMBER: 60/230,335
/ PRIOR FILING DATE: 2000-09-06
/ PRIOR APPLICATION NUMBER: 60/230,347
/ PRIOR FILING DATE: 2000-09-09
/ PRIOR APPLICATION NUMBER: 60/242,578
/ PRIOR FILING DATE: 2000-10-23
/ PRIOR APPLICATION NUMBER: 60/253,625
/ PRIOR FILING DATE: 2000-11-27
/ PRIOR APPLICATION NUMBER: 60/257,931
/ PRIOR FILING DATE: 2000-12-22
/ PRIOR APPLICATION NUMBER: 60/267,636
/ PRIOR FILING DATE: 2001-02-09
/ PRIOR APPLICATION NUMBER: 60/269,308
/ PRIOR FILING DATE: 2001-02-16
/ Remaining Prior Application data removed - See file wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 78614
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 43827
/ LENGTH: 1038
/ TYPE: PRT
/ ORGANISM: Staphylococcus aureus
US-10-282-122A-43827

Query Match          92.5%; Score 111; DB 15; Length 1038;
Best Local Similarity 95.2%; Pred. No. 5.8e-08;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KPPYQFGHNSVDFEEDTLPK 21
DB 833 KPPYQFGHNSVDFEEDTLPK 853

RESULT 14
US-10-731-238-14
/ Sequence 14, Application US/10731238
/ Publication No. US20050123552A1
/ GENERAL INFORMATION:
/ APPLICANT: Hook, Magnus
/ APPLICANT: Patti, Joseph M.
/ APPLICANT: House-Pompeo, Karen L.
/ APPLICANT: Speziale, Pietro
/ APPLICANT: Joh, Danny
/ APPLICANT: McGavin, Martin J.
/ TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
/ AND METHODS OF USE
/ NUMBER OF SEQUENCES: 105
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Arnold, White & Durkee
/ STREET: P.O. Box 4433
```

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/ CITY: Houston
/ STATE: TX
/ COUNTRY: USA
/ ZIP: 77210-4433
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/10/731,238
/ FILING DATE: 10-Dec-2003
/ CLASSIFICATION: <Unknown>
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US/09/010,317
/ FILING DATE: 21-Jan-1998
/ APPLICATION NUMBER: US 60/036,139
/ FILING DATE: 21-Jan-1997
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Hibler, David W.
/ REGISTRATION NUMBER: 41,071
/ REFERENCE/DOCKET NUMBER: TANK:189
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 512-418-3000
/ TELEFAX: 512-474-7577
/ INFORMATION FOR SEQ ID NO: 14:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 21 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: <Unknown>
/ TOPOLOGY: linear
/ SEQUENCE DESCRIPTION: SEQ ID NO: 14:
US-10-731-238-14

Query Match          89.2%; Score 107; DB 18; Length 21;
Best Local Similarity 95.0%; Pred. No. 3.8e-09;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 PPYQFGHNSVDFEEDTLPK 21
DB 2 PPYQFGHNSVDFEEDTLPK 21

RESULT 15
US-10-731-238-23
/ Sequence 23, Application US/10731238
/ Publication No. US20050123552A1
/ GENERAL INFORMATION:
/ APPLICANT: Hook, Magnus
/ APPLICANT: Patti, Joseph M.
/ APPLICANT: House-Pompeo, Karen L.
/ APPLICANT: Speziale, Pietro
/ APPLICANT: Joh, Danny
/ APPLICANT: McGavin, Martin J.
/ TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
/ AND METHODS OF USE
/ NUMBER OF SEQUENCES: 105
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Arnold, White & Durkee
/ STREET: P.O. Box 4433
/ CITY: Houston
/ STATE: TX
/ COUNTRY: USA
/ ZIP: 77210-4433
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/10/731,238
/ FILING DATE: 10-Dec-2003
/ CLASSIFICATION: <Unknown>
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE: 21-Jan-1998
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-Jan-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAMK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 23:
US-10-731-238-23

Query Match 89.2%; Score 107; DB 18; Length 21;
Best Local Similarity 90.5%; Pred. No. 3.8e-09;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 KPPYQFGHNSVDFEEDTLPK 21
DB 1 KPSYQFGHNPVDFEEDTLPK 21

Search completed: October 22, 2005, 11:34:39
Job time : 59.2367 secs

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GenCore version 5.1.6
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OM protein - protein search, using 'sw model

Run on: October 22, 2005, 02:23:36 ; Search time 10.5465 Seconds
(without alignments)
191.586 Million cell updates/sec

Title: US-10-731-238-16
Perfect score: 120
Sequence: 1 KPYPQFGHNSVDFEEDTLRK 21

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Length	DB	ID	Description
1	112	93.3	1018	2	A32192 fibronectin-binding
2	111	92.5	961	2	G90053 hypothetical prote
3	111	92.5	1038	2	H90053 hypothetical prote
4	107	89.2	940	2	S19702 fibronectin-binding
5	56	46.7	468	2	T26081 hypothetical prote
6	52	43.3	808	2	F81180 conserved hypotet
7	48	40.0	474	2	H84357 serine-tRNA synth
8	47	39.2	347	1	HPMS7 haptoglobin precu
9	46	38.3	257	2	A36057 MHC class I histoc
10	46	38.3	445	2	F90562 hypothetical prote
11	46	38.3	467	2	S01943 hypothetical prote
12	45	37.5	387	2	I38449 extracellular prot
13	45	37.5	444	2	T01782 GDP dissociation i
14	45	37.5	808	2	DB1924 hypothetical prote
15	45	37.5	1271	2	T24008 hypothetical prote
16	44.5	37.1	386	2	T02409 ribose-phosphate d
17	44.5	37.1	928	1	VCBENC glycoprotein B pre
18	44	36.7	364	2	E71433 probable metallopr
19	44	36.7	427	2	D95159 3-phosphoshikimate
20	44	36.7	431	2	D98025 3-phosphoshikimate
21	44	36.7	1926	2	UC4842 DNA-binding nuclea
22	44	36.7	2332	1	GNNYF genome polyprotein
23	43.5	36.2	1091	2	S33850 fibronectin-binding
24	43	35.8	303	2	B75485 fructokinase - Del
25	43	35.8	405	2	T23321 hypothetical prote
26	43	35.8	432	2	T08771 hypothetical prote
27	43	35.8	448	2	E64407 hypothetical prote
28	43	35.8	471	2	S01937 hypothetical prote
29	43	35.8	551	2	SS7447 HPR11-7 protein -

30	43	35.8	585	2	T18885 hypothetical prote
31	43	35.8	811	2	T35581 probable transmemb
32	43	35.8	836	2	B96716 probable serine/th
33	43	35.8	846	2	T27282 hypothetical prote
34	43	35.8	1188	2	G72734 hypothetical prote
35	42.5	35.4	234	2	T30473 late expression fa
36	42.5	35.4	417	2	T34930 probable secreted
37	42.5	35.4	459	2	S59731 mRNA granuylitrans
38	42.5	35.4	168	2	B36502 insulin receptor-r
39	42	35.0	349	2	E97318 transcription regu
40	42	35.0	349	2	H82116 flagellar motor bw
41	42	35.0	371	2	A88520 41.8k hypothetical
42	42	35.0	374	2	A57583 histone acetyltran
43	42	35.0	398	2	F75017 probable glycine C
44	42	35.0	398	2	E71454 probable glycine C
45	42	35.0	433	2	T01405 vesicle-associated

ALIGNMENTS

RESULT 1
A32192
fibronectin-binding protein - Staphylococcus aureus
C/Species: Staphylococcus aureus
C/Date: 31-Jul-1989 #sequence_revision 31-Jul-1989 #text_change 16-Feb-1997
C/Accession: A32192
R/Signaes, C.; Raucel, G.; Joansson, K.; Lindgren, P.E.; Anantharamaiah, G.M.; Hoeck, M.
Proc. Natl. Acad. Sci. U.S.A. 86, 699-703, 1989
A/Title: Nucleotide sequence of the gene for a fibronectin-binding protein from Staphyloc
A/Reference number: A32192; PMID:8908998; PMID:2521391
A/Accession: A32192
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-1018 <SIG>
A/Cross-references: GB:J04151
C/Keywords: fibronectin binding

Query Match 93.3%; Score 112; DB 2; Length 1018;
Best Local Similarity 95.2%; Pred. No. 3.1e-09;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KPYPQFGHNSVDFEEDTLRK 21
DB 837 KPYPQFGHNSVDFEEDTLRK 857

RESULT 2
G90053
hypothetical protein fnb (imported) - Staphylococcus aureus (strain N315)
C/Species: Staphylococcus aureus
C/Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C/Accession: G90053
R/Kuroda, M.; Ohba, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguci
ma, A.; Mutsaers, U.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kato, C.; Sekimizu, K.; i
C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
A/Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.
A/Reference number: A89758; PMID:21311952; PMID:11418146
A/Accession: G90053
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-961 <KUR>
A/Cross-references: UNIPROT:Q99RD3; GB:BA000018; PID:913702452; PIDN:BB43593.1; GSPDB:GT
A/Experimental source: strain N315
C/Genetics:
A/Gene: fnbB

Query Match 92.5%; Score 111; DB 2; Length 961;
Best Local Similarity 95.2%; Pred. No. 4.1e-09;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KPYPQFGHNSVDFEEDTLRK 21

Db 784 KPNYOGGNSVDFFEDTLPK 804

RESULT 3

H90053
hypothetical protein fnb [imported] - Staphylococcus aureus (strain N315)

C:Species: Staphylococcus aureus
C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C:Accession: H90053
R:Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguc, M.; Mizutani-Uji, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.; C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
L: Lancer 357, 1225-1240, 2001
A:Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.
A:Reference number: A89758; MUID:21311952; PMID:11418146

A:Accession: H90053

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-1038 <KUR>

A:Cross-references: UNIPROT:Q99RD2; GB:BA000018; PID:g13702453; PIDN:BA843594.1; GSPDB:C

A:Experimental source: strain N315

C:Genetics:

A:Gene: fnb

Query Match 92.5%; Score 111; DB 2; Length 1038;

Best Local Similarity 95.2%; Pred. No. 4.5e-09;

Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

1 KPNYOGGNSVDFFEDTLPK 21

Db 833 KPNYOGGNSVDFFEDTLPK 853

RESULT 4

S19702
fibronectin-binding protein B - Staphylococcus aureus

C:Species: Staphylococcus aureus
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
C:Accession: S19702
R:Joensen, K.; Signaes, C.; Mueller, H.P.; Lindberg, M.
Eur. J. Biochem. 202, 1041-1048, 1991

A:Title: Two different genes encode fibronectin binding proteins in Staphylococcus aureus

A:Reference number: S19702; MUID:9211145; PMID:1837266

A:Accession: S19702

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-940 <JOE>

A:Cross-references: UNIPROT:Q53682; EMBL:X62992; NID:949040; PIDN:CAA44726.1; PID:958156

C:Keywords: fibronectin binding

Query Match 89.2%; Score 107; DB 2; Length 940;

Best Local Similarity 90.5%; Pred. No. 1.7e-08;

Matches 19; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

1 KPNYOGGNSVDFFEDTLPK 21

Db 773 KPNYOGGNSVDFFEDTLPK 793

RESULT 5

T26081
hypothetical protein W02A2.7 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T26081
R:Ainscough, R.
submitted to the EMBL Data Library, November 1996

A:Reference number: Z20148

A:Accession: T26081

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-468 <WIL>

A:Gene: sers

A:Superfamily: serine-tRNA ligase

C:Superfamily: serine-tRNA ligase

C:Superfamily: serine-tRNA ligase

C:Superfamily: serine-tRNA ligase

C:Superfamily: serine-tRNA ligase

C:Superfamily: serine-tRNA ligase

A:Cross-references: UNIPROT:Q9XUB2; EMBL:Z82286; PIDN:CAB05310.1; GSPDB:GN00022; CESP:W02A2

A:Experimental source: clone W02A2

C:Genetics:

A:Gene: CESP:W02A2.7

A:Map position: 4

A:Introns: 38/3; 212/2; 353/3; 403/2

Query Match 46.7%; Score 56; DB 2; Length 468;

Best Local Similarity 40.0%; Pred. No. 0.78;

Matches 8; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

2 PPNYOGGNSVDFFEDTLPK 21

Db 351 PPNYOGGNSVDFFEDTLPK 370

RESULT 6

F81180
conserved hypothetical protein NMB0593 [imported] - Neisseria meningitidis (strain MC58)

C:Species: Neisseria meningitidis
C:Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004
C:Accession: F81180
R:Teitelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.A.
Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.;
xi, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Maignani, V.; Pizzi, M.
Science 287, 1809-1815, 2000

A:Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; Ver

A:Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58.

A:Reference number: A81000; MUID:20175755; PMID:10710307

A:Accession: F81180

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-808 <TEF>

A:Cross-references: UNIPROT:Q9XOK2; GB:AE002415; GB:AE002098; NID:g7225816; PIDN:AAF1021

A:Experimental source: serogroup B, strain MC58

C:Genetics:

A:Gene: NMB0593

Query Match 43.3%; Score 52; DB 2; Length 808;

Best Local Similarity 47.4%; Pred. No. 6;

Matches 9; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

2 PPNYOGGNSVDFFEDTLPK 20

Db 453 PPNYOGGNSVDFFEDTLPK 471

RESULT 7

B84357
serine-tRNA synthetase [imported] - Halobacterium sp. NRC-1

C:Species: Halobacterium sp. NRC-1
C:Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
C:Accession: B84357
R:Ng, W.V.; Kennedy, S.P.; Mahairas, G.G.; Bergquist, B.; Pan, M.; Shukla, H.D.; Lasky, S.
; Leithausen, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Madocks, D.G.; Jablott
Jung, K.H.; Alam, Sci. U.S.A. 97, 12176-12181, 2000

A:Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Edhardt, H.; Lowe, T.M.; Lie

A:Title: Genome sequence of Halobacterium species NRC-1.

A:Reference number: A84160; MUID:20504483; PMID:11016950

A:Accession: B84357

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-474 <STO>

A:Cross-references: UNIPROT:Q9HNC8; GB:AE004437; NID:g10581491; PIDN:AA620222.1; GSPDB:G

C:Genetics:

A:Gene: sers

A:Superfamily: serine-tRNA ligase

C:Superfamily: serine-tRNA ligase

C:Superfamily: serine-tRNA ligase

C:Superfamily: serine-tRNA ligase

C:Superfamily: serine-tRNA ligase

C:Superfamily: serine-tRNA ligase

C:Superfamily: serine-tRNA ligase

C:Superfamily: serine-tRNA ligase

C:Superfamily: serine-tRNA ligase

C:Superfamily: serine-tRNA ligase

C:Superfamily: serine-tRNA ligase

C:Superfamily: serine-tRNA ligase

C:Superfamily: serine-tRNA ligase

RESULT 10
P90567

```

Best Local Similarity  47.44;  Pred. NO. 34;
Matches  9;  Conservative  2;  Mismatches  8;  Indels  0;  Gaps  0

```


QY 2 PPYQFGHNSVDFEEDTL 20
Db 97 PGYQKRGECCVDIDECTIP 115

RESULT 13

T01782
GDP dissociation inhibitor - common tobacco
C:Species: Nicotiana tabacum (common tobacco)
C>Date: 19-Feb-1999 #sequence_revision 19-Feb-1999 #text_change 09-Jul-2004
C:Accession: T01782
R:Szabo, B.; Koyanagi, M.; Gardner, R.C.; Matsumoto, H.
submitted to the EMBL Data Library, July 1997
A:Reference number: Z14424
A:Accession: T01782
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-444 <EZA>
A:Cross-references: UNIPROT:Q22402; EMBL:AF012823; NID:g2501849; PID:g2501850
A:Experimental source: cultivar Samsum
C:Genetics:
A:Gene: GDI
C:Function:
A:Description: Inhibits dissociation of GDP from GTP binding proteins
C:Superfamily: human GDP dissociation inhibitor XAP-4

Query Match 37.5%; Score 45; DB 2; Length 444;
Best Local Similarity 47.6%; Pred. No. 39;
Matches 10; Conservative 3; Mismatches 6; Indels 2; Gaps 1;
QY 1 KPPYQFGHNSVDFEEDTL 21
Db 60 KPPAEIG--SRDFNVDMIPK 78

RESULT 14

DB1924
hypothetical protein NMA0796 [imported] - Neisseria meningitidis (strain Z2491 serogroup
C:Species: Neisseria meningitidis
C>Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 09-Jul-2004
C:Accession: DB1924
R:Parthill, J.; Achtmann, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morel
S.; Holroyd, S.; Jagels, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandream,
Nature 404, 502-505, 2000
A:Title: Complete DNA sequence of a serogroup A strain of Neisseria meningitidis Z2491.
A:Reference number: AB1775; WUID:20222556; PMID:10761919
A:Accession: DB1924
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-808 <PAR>
A:Cross-references: UNIPROT:Q9UVK8; GB:AL162754; GB:AL157959; NID:g7379424; PIDN:CAB8407
A:Experimental source: serogroup A, strain Z2491
C:Genetics:
A:Gene: NMA0796

Query Match 37.5%; Score 45; DB 2; Length 808;
Best Local Similarity 42.1%; Pred. No. 76;
Matches 8; Conservative 4; Mismatches 7; Indels 0; Gaps 0;
QY 2 PPYQFGHNSVDFEEDTL 20
Db 453 PPYRHTTHNAVQFGSHR 471

RESULT 15

T24008
hypothetical protein R07B5.8 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T24008
R:Kelly, P.
submitted to the EMBL Data Library, May 1996

A:Reference number: Z19829
A:Accession: T24008
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-1271 <WIL>
A:Cross-references: UNIPROT:Q21789; EMBL:Z72512; PIDN:CAA96668.1; GSPDB:GN00023; CESP:R0;
A:Experimental source: clone R07B5
C:Genetics:
A:Gene: CESP:R07B5.8
A:Map position: 5
A:Introns: 34/1; 67/3; 129/3; 193/3; 313/2; 446/1; 479/2; 513/3; 571/3; 631/1; 845/3; 10;
Query Match 37.5%; Score 45; DB 2; Length 1271;
Best Local Similarity 42.1%; Pred. No. 1.2e+02;
Matches 8; Conservative 5; Mismatches 6; Indels 0; Gaps 0;
QY 1 KPPYQFGHNSVDFEEDTL 19
Db 1221 QPPYQNYPNQVDYQOPWL 1239

Search completed: October 22, 2005, 04:13:49
Job time : 12.5465 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 22, 2005, 02:23:35 (Search time 51.4314 Seconds
(without alignments)
209.087 Million cell updates/sec

Title: US-10-731-238-16
Perfect score: 120
Sequence: 1 KPPYQFGHNSVDFEEDLPK 21

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: UniProt_03:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	112	93.3	1018	1	FNBA STAU
2	111	92.5	961	2	Q99RD3
3	111	92.5	961	2	Q7A3J8
4	111	92.5	965	2	Q6GDU5
5	111	92.5	1015	2	Q8NUJ7
6	111	92.5	1015	2	Q6G6H3
7	111	92.5	1038	2	Q99RD2
8	111	92.5	1038	2	Q7A3J7
9	107	89.2	940	2	Q53682
10	107	89.2	943	2	Q8NUH4
11	107	89.2	957	2	Q6G6H4
12	100	83.3	152	2	Q9AEP9
13	56	46.7	468	2	Q9XUB2
14	52	43.3	808	2	Q9KOK2
15	51	42.5	985	2	Q7R5S5
16	50.5	42.1	463	1	MCBL ASHGO
17	50	41.7	245	2	Q08866
18	50	41.7	4189	2	Q7R1D9
19	49	40.8	188	2	Q9CPG0
20	49	40.8	190	2	Q7MHU1
21	48.5	40.4	330	2	Q9NKG1
22	48.5	40.4	340	2	Q6B097
23	48.5	40.4	418	2	Q6P653
24	48.5	40.4	434	2	Q9BR51
25	48.5	40.4	547	2	Q6R4Q4
26	48	40.0	333	2	Q86FC8
27	48	40.0	337	2	Q6FSI5
28	48	40.0	460	1	SYS HALNI
29	47	39.2	273	2	Q7NDT5
30	47	39.2	347	1	HPT_MOUSE
31	47	39.2	347	1	HPT_MOUSE

32	47	39.2	347	1	HPT MUSSA	Q62558 mus saxicol
33	47	39.2	347	2	Q63927	Q63927 mus sp. hap
34	47	39.2	392	2	Q64P55	Q64P55 muscoides
35	47	39.2	435	2	Q86788	Q86788 feline hepr
36	47	39.2	466	2	Q6GK22	Q6GK22 xenopus lae
37	47	39.2	477	2	Q642R1	Q642R1 xenopus lae
38	47	39.2	482	2	Q76K22	Q76K22 streptococ
39	47	39.2	772	2	Q9AD03	Q9AD03 streptomyce
40	46.5	38.8	1285	2	Q7SD24	Q7SD24 ashbya goss
41	46	38.3	255	2	Q7NNC7	Q7NNC7 glieobacter
42	46	38.3	257	2	Q95589	Q95589 cyprinus ca
43	46	38.3	314	2	Q9JKT6	Q9JKT6 rattus norv
44	46	38.3	445	2	Q98QG0	Q98QG0 mycoplasma
45	46	38.3	465	2	Q6FZM2	Q6FZM2 bartonella

ALIGNMENTS

```

RESULT 1
FNBA STAU          STANDARD;      PRT;  1018 AA.
ID FNBA STAU
AC P14738;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Fibronectin-binding protein precursor (FNBP).
GN Name=fnbp;
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1280;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NCTC 8325-4;
RX MEDLINE=8908998; Pubmed=2521391;
RA Signes C., Raucel G., Joensen K., Lindgren P.-E.,
  Mantharimath G.M., Hoeck M., Lindberg M.;
  "Nucleotide sequence of the gene for a fibronectin-binding protein
  from Staphylococcus aureus: use of this peptide sequence in the
  synthesis of biologically active peptides."
  Proc. Natl. Acad. Sci. U.S.A. 86:699-703(1989).
RL
CC -I- FUNCTION: The ability of bacteria to bind fibronectin has been
  proposed as a virulence factor enabling bacteria to colonize wound
  tissues and blood clots. Binding of plasma fibronectin to the
  bacterial surface might block adhesion receptors on S.aureus, thus
  representing an important defense mechanism against tissue
  invasion.
CC -I- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
  an amide bond (Potential).
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
  between the Swiss Institute of Bioinformatics and the EMBL outstation -
  the European Bioinformatics Institute. There are no restrictions on its
  use by non-profit institutions as long as its content is in no way
  modified and this statement is not removed. Usage by and for commercial
  entities requires a license agreement (See http://www.isb.ch/announce/
  or send an email to license@isb-sib.ch).
CC
CC EMBL: J04151; AAA26632.1; -.
  InterPro: IPR004237; Fn_bind.
  InterPro: IPR005877; Gpos_YsIRK.
  InterPro: IPR001899; Gram_pos_anchor.
  Pfam: PF02986; Fn_bind. 1.
  Pfam: PF00746; Gram_pos_anchor. 1.
  TIGRfam: TIGR01167; LpxNG_anchor. 1.
  TIGRfam: TIGR01168; YsIRK_signal. 1.
  PROSITE: PS50847; GRAM_POS_ANCHORING. 1.
  Cell adhesion; Cell wall; Peptidoglycan-anchor; Repeat; Signal;
  Virulence.
  SIGNAL
  CHAIN 1 36
  FT CHAIN 37 985
  PROPEP 986 1018
  Fibrinectin-binding protein.
  Removed by sortase (Potential).

```

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FT REPEAT 545 574 B-1.
FT REPEAT 575 604 B-2.
FT DOMAIN 745 878 4 X approximate tandem repeats,
  fibronectin-binding domain.
FT REPEAT 745 782 D-1.
FT REPEAT 783 820 D-2.
FT REPEAT 821 859 D-3.
FT REPEAT 860 878 D-4 (incomplete).
FT DOMAIN 879 948 5 X tandem repeats, Pro-rich (WR).
FT REPEAT 879 892 WR 1.
FT REPEAT 893 906 WR 2.
FT REPEAT 907 920 WR 3.
FT REPEAT 921 934 WR 4.
FT REPEAT 935 948 WR 5.
FT SITE 982 985 LPXTG sorting signal (potential).
FT MOD_RES 985 985 Pentaglycyl murein peptidoglycan amidated
  chreonine (potential).
SQ SEQUENCE 1018 AA; 111780 MW; 58175E020E81F1F CRC64;

Query Match 93.3%; Score 112; DB 1; Length 1018;
Best Local Similarity 95.2%; Pred. No. 2e-08;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KPPYFGGHNSVDFEEDTLPK 21
Db 837 KPPYFGGHNSVDFEEDTLPK 857

RESULT 2
Q99RD3 PRELIMINARY; PRT; 961 AA.
ID Q99RD3;
AC Q99RD3;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Fibronectin-binding protein homolog.
GN Name=fnb3; OrderedLocustNames=SAV2502;
OS Staphylococcus aureus (strain Mu50 / ATCC 700699).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_Taxid=158878;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=MU50 / ATCC 700699;
RC MEDLINE=21311952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2;
RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
  Cui L., Oguchi A., Aoki K.-I., Nagai Y., Iian J.-Q., Ito T.,
  Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,
  Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
  Sekimizu K., Hiramatsu H., Kohara S., Goto S., Yabuzaki J.,
  Kanahisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
  Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
RT "Whole genome sequencing of methicillin-resistant Staphylococcus
  aureus."
RL Lancet 357:1225-1240(2001).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
  an amide bond (By similarity).
EMBL: AP003365; BAB58664.1; -.
CC CC
DR PIR: G90053; G90053.
DR HSRP: Q53653; 1N67.
DR GO: GO:0009986; C:cell surface; IEA.
DR GO: GO:0005618; C:cell wall; IEA.
DR GO: GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO: GO:0016020; C:membrane; IEA.
DR GO: GO:0007155; P:cell adhesion; IEA.
DR InterPro: IPR008966; Adhes_Bact.
DR InterPro: IPR004237; Fn_bind.
DR InterPro: IPR005877; Gpos_YsIRK.
DR InterPro: IPR001899; Gram_pos_anchor.
DR Pfam: PF02986; Fn_bind. 1.
DR Pfam: PF00746; Gram_pos_anchor. 1.
DR Pfam: PF04650; YsIRK_signal. 1.
DR TIGRFAMs: TIGR0167; LPXTG_anchor. 1.
DR TIGRFAMs: TIGR0168; YsIRK_anchor. 1.
DR TIGRFAMs: TIGR0168; YsIRK_signal. 1.

```

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DR PROSITE; PSS0847; GRAM POS ANCHORING. 1.
KW Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ SEQUENCE 961 AA; 106010 MW; 364940F884EA4101 CRC64;

Query Match 92.5%; Score 111; DB 2; Length 961;
Best Local Similarity 95.2%; Pred. No. 2.7e-08;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KPPYFGGHNSVDFEEDTLPK 21
Db 784 KPPYFGGHNSVDFEEDTLPK 804

RESULT 3
Q7A3J8 PRELIMINARY; PRT; 961 AA.
ID Q7A3J8;
AC Q7A3J8;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE FnbB protein.
GN Name=fnb3; OrderedLocustNames=SA2290;
OS Staphylococcus aureus (strain N315).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_Taxid=158879;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21311952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2;
RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
  Cui L., Oguchi A., Aoki K.-I., Nagai Y., Iian J.-Q., Ito T.,
  Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,
  Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
  Sekimizu K., Hiramatsu H., Kohara S., Goto S., Yabuzaki J.,
  Kanahisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
  Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
RT "Whole genome sequencing of methicillin-resistant Staphylococcus
  aureus."
RL Lancet 357:1225-1240(2001).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
  an amide bond (By similarity).
EMBL: AP003137; BAB3593.1; -.
DR GO: GO:0009986; C:cell surface; IEA.
DR GO: GO:0005618; C:cell wall; IEA.
DR GO: GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO: GO:0016020; C:membrane; IEA.
DR GO: GO:0007155; P:cell adhesion; IEA.
DR InterPro: IPR008966; Adhes_Bact.
DR InterPro: IPR004237; Fn_bind.
DR InterPro: IPR005877; Gpos_YsIRK.
DR InterPro: IPR001899; Gram_pos_anchor.
DR Pfam: PF02986; Fn_bind. 1.
DR Pfam: PF00746; Gram_pos_anchor. 1.
DR Pfam: PF04650; YsIRK_signal. 1.
DR TIGRFAMs: TIGR0167; LPXTG_anchor. 1.
DR TIGRFAMs: TIGR0168; YsIRK_signal. 1.
DR PROSITE; PSS0847; GRAM POS ANCHORING. 1.
KW Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ SEQUENCE 961 AA; 106010 MW; 364940F884EA4101 CRC64;

Query Match 92.5%; Score 111; DB 2; Length 961;
Best Local Similarity 95.2%; Pred. No. 2.7e-08;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KPPYFGGHNSVDFEEDTLPK 21
Db 784 KPPYFGGHNSVDFEEDTLPK 804

RESULT 4
Q6GDUS PRELIMINARY; PRT; 965 AA.
ID Q6GDUS;
AC Q6GDUS;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)

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DT 05-JUL-2004 (TrEMBLrel. 27, last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, last annotation update)
DE Fibronectin-binding protein.
GN Name=fnbA; OrderedLocustNames=SA82580;
OS Staphylococcus aureus (strain MSSA252).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=282458;
[1]
RP SEQUENCE FROM N.A.
RX PubMed=15213324; DOI=10.1073/pnas.0402521101;
RA Holden M.T.G., Fell E.J., Lindsey J.A., Peacock S.J., Day N.P.J.,
RA Enright M.C., Foster T.J., Moore C.E., Hurst L., Atkin R., Barron A.,
RA Bason N., Bentley S.D., Chillingworth C., Chillingworth T.,
RA Churcher C., Clark L., Cotton C., Cronin A., Doggett J., Dowd L.,
RA Felwell T., Hance Z., Harris B., Hauser H., Holroyd S., Jagsels K.,
RA James K.D., Lennard N., Line A., Mayes R., Moule S., Mungall K.,
RA Ormond D., Quail M.A., Rabinowitch E., Rutherford K.M., Sanders M.,
RA Sharp S., Simmonds M., Stevens K., Whitehead S., Barrett B.G.,
RA Spratt B.G., Parkhill J.;
RT "Complete genomes of two clinical Staphylococcus aureus strains:
RT evidence for the rapid evolution of virulence and drug resistance.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:9786-9791(2004).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC an amide bond (By similarity).
DR EMBL: BX571856; CAC41560.1; -.
DR GO: GO:0009986; C:cell surface; IEA.
DR GO: GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO: GO:0016020; C:membrane; IEA.
DR GO: GO:0007155; P:cell adhesion; IEA.
DR InterPro: IPR008966; Adhes_bact.
DR InterPro: IPR004237; Fn_bind.
DR InterPro: IPR005877; Gpos_YsIRK.
DR InterPro: IPR001899; Gram_pos_anchor.
DR Pfam: PF02986; Fn_bind_1.
DR Pfam: PF00746; Gram_pos_anchor; 1.
DR Pfam: PF04650; YsIRK_signal; 1.
DR TIGRFAMs: TIGR01167; LPXTG_anchor; 1.
DR TIGRFAMs: TIGR01168; YsIRK_signal; 1.
DR PROSITE: PS50847; GRAM_POS_ANCHORING; 1.
KW Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ
SEQUENCE 965 AA; 105691 MW; 2982812164D0551 CRC64;

Query Match 92.5%; Score 111; DB 2; Length 965;
Best Local Similarity 95.2%; Pred. No. 2,7e-08;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KPPYQFGHNSVDFEEDTLRK 21
DB 802 KPPYQFGHNSVDFEEDTLRK 822

RESULT 5
Q8NUU7 PRELIMINARY; PRT; 1015 AA.
AC Q8NUU7;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Fnb protein.
GN Name=fnb; OrderedLocustNames=MW2421;
OS Staphylococcus aureus (strain MW2).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=196620;
[1]
RP SEQUENCE FROM N.A.
RX STRAIN=MW2;
RX MEDLINE=22040717; PubMed=12044378; DOI=10.1016/S0140-6736(02)08713-5;
RA Baba T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Ogunuchi A.,
RA Nagai Y., Iwama N., Asano K., Naito T., Kuroda H., Cui L.,
RA Yamamoto K., Hiramatsu K.;
RT "Genome and virulence determinants of high virulence community-
RT acquired MRSA.";
RL Lancet 359:1819-1827 (2002).

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CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC an amide bond (By similarity).
DR EMBL: AP004830; BAB96286.1; -.
DR GO: GO:0009986; C:cell surface; IEA.
DR GO: GO:0006618; C:cell wall; IEA.
DR GO: GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO: GO:0016020; C:membrane; IEA.
DR GO: GO:0007155; P:cell adhesion; IEA.
DR InterPro: IPR008966; Adhes_bact.
DR InterPro: IPR004237; Fn_bind.
DR InterPro: IPR005877; Gpos_YsIRK.
DR InterPro: IPR001899; Gram_pos_anchor.
DR Pfam: PF02986; Fn_bind_1.
DR Pfam: PF00746; Gram_pos_anchor; 1.
DR Pfam: PF04650; YsIRK_signal; 1.
DR TIGRFAMs: TIGR01167; LPXTG_anchor; 1.
DR TIGRFAMs: TIGR01168; YsIRK_signal; 1.
DR PROSITE: PS50847; GRAM_POS_ANCHORING; 1.
KW Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ
SEQUENCE 1015 AA; 111145 MW; D0F9281BB64D4D2 CRC64;

Query Match 92.5%; Score 111; DB 2; Length 1015;
Best Local Similarity 95.2%; Pred. No. 2,8e-08;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KPPYQFGHNSVDFEEDTLRK 21
DB 838 KPPYQFGHNSVDFEEDTLRK 858

RESULT 6
Q6G6H3 PRELIMINARY; PRT; 1015 AA.
AC Q6G6H3;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Fibronectin-binding protein.
GN OrderedLocustNames=SA52388;
OS Staphylococcus aureus (strain MSSA476).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=282459;
[1]
RP SEQUENCE FROM N.A.
RX PubMed=15213324; DOI=10.1073/pnas.0402521101;
RA Holden M.T.G., Fell E.J., Lindsey J.A., Peacock S.J., Day N.P.J.,
RA Enright M.C., Foster T.J., Moore C.E., Hurst L., Atkin R., Barron A.,
RA Bason N., Bentley S.D., Chillingworth C., Chillingworth T.,
RA Churcher C., Clark L., Cotton C., Cronin A., Doggett J., Dowd L.,
RA Felwell T., Hance Z., Harris B., Hauser H., Holroyd S., Jagsels K.,
RA James K.D., Lennard N., Line A., Mayes R., Moule S., Mungall K.,
RA Ormond D., Quail M.A., Rabinowitch E., Rutherford K.M., Sanders M.,
RA Sharp S., Simmonds M., Stevens K., Whitehead S., Barrett B.G.,
RA Spratt B.G., Parkhill J.;
RT "Complete genomes of two clinical Staphylococcus aureus strains:
RT evidence for the rapid evolution of virulence and drug resistance.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:9786-9791(2004).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC an amide bond (By similarity).
DR EMBL: BX571857; CAC44202.1; -.
DR GO: GO:0009986; C:cell surface; IEA.
DR GO: GO:0005518; C:cell wall; IEA.
DR GO: GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO: GO:0016020; C:membrane; IEA.
DR GO: GO:0007155; P:cell adhesion; IEA.
DR InterPro: IPR008966; Adhes_bact.
DR InterPro: IPR004237; Fn_bind.
DR InterPro: IPR005877; Gpos_YsIRK.
DR InterPro: IPR001899; Gram_pos_anchor.
DR Pfam: PF02986; Fn_bind_1.
DR Pfam: PF00746; Gram_pos_anchor; 1.
DR Pfam: PF04650; YsIRK_signal; 1.
DR TIGRFAMs: TIGR01167; LPXTG_anchor; 1.

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DR TIGR01168; YSIRK signal; 1.
 DR PROSITE; PS50847; GRAM_POS_ANCHORING; 1.
 KW Cell wall; Complete proteome; Peptidoglycan-anchor.
 SQ SEQUENCE 1015 AA; 11145 MW; D0F9281B64D44D2 CRC64;

Query Match 92.5%; Score 111; DB 2; Length 1015;
 Best Local Similarity 95.2%; Pred. No. 2.9e-08;
 Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KPPYOGGHN5VDFEEDTLPK 21
 |||
 DB 838 KPPYOGGHN5VDFEEDTLPK 858

RESULT 7
 ID Q99RD2 PRELIMINARY; PRT; 1038 AA.
 AC Q99RD2;
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Fibronectin-binding protein homolog.
 GN Name=fnb; OrderedlocusNames=SAV2503;
 OS Staphylococcus aureus (strain Mu50 / ATCC 700699).
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 OX NCBI_TaxID=158878;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Mu50 / ATCC 700699;
 RX MEDLINE=21311952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2;
 RA Kuroda M., Ohba T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
 Cui L., Oguchi A., Aoki K.-I., Nagai Y., Lian J.-Q., Ito T.,
 Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,
 Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
 Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
 Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
 Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
 RT "Whole genome sequencing of methicillin-resistant Staphylococcus
 aureus.";
 RL Lancet 357:1225-1240(2001).
 CC -i- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
 an amide bond (By similarity).
 DR EMBL; AP003365; BAB58665.1; -.
 DR PIR; H90053; H90053.
 DR GO; GO:0009986; C:cell surface; IEA.
 DR GO; GO:0005618; C:cell wall; IEA.
 DR GO; GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0007155; P:cell adhesion; IEA.
 DR InterPro; IPR008966; Adhes_bact.
 DR InterPro; IPR004237; Fn_bind.
 DR InterPro; IPR005877; Gpos_YSIRK.
 DR InterPro; IPR001899; Gram_pos_anchor.
 DR Pfam; PF02986; Fn_bind. 1.
 DR Pfam; PF00746; Gram_pos_anchor. 1.
 DR Pfam; PF04650; YSIRK_signal. 1.
 DR TIGR01167; LPRYG_anchor; 1.
 DR TIGR01168; YSIRK_signal; 1.
 DR PROSITE; PS50847; GRAM_POS_ANCHORING; 1.
 KW Cell wall; Complete proteome; Peptidoglycan-anchor.
 SQ SEQUENCE 1038 AA; 113618 MW; 666BF6BF2BFEBB12 CRC64;

Query Match 92.5%; Score 111; DB 2; Length 1038;
 Best Local Similarity 95.2%; Pred. No. 2.9e-08;
 Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KPPYOGGHN5VDFEEDTLPK 21
 |||
 DB 833 KPPYOGGHN5VDFEEDTLPK 853

RESULT 8
 Q7A3J7

ID Q7A3J7 PRELIMINARY; PRT; 1038 AA.
 AC Q7A3J7;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Fnb protein.
 GN Name=fnb; OrderedlocusNames=SA2291;
 OS Staphylococcus aureus (strain N315).
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 OX NCBI_TaxID=158879;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21311952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2;
 RA Kuroda M., Ohba T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
 Cui L., Oguchi A., Aoki K.-I., Nagai Y., Lian J.-Q., Ito T.,
 Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,
 Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
 Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
 Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
 Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
 RT "Whole genome sequencing of methicillin-resistant Staphylococcus
 aureus.";
 RL Lancet 357:1225-1240(2001).
 CC -i- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
 an amide bond (By similarity).
 DR EMBL; AP003365; BAB43594.1; -.
 DR GO; GO:0009986; C:cell surface; IEA.
 DR GO; GO:0005618; C:cell wall; IEA.
 DR GO; GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0007155; P:cell adhesion; IEA.
 DR InterPro; IPR008966; Adhes_bact.
 DR InterPro; IPR004237; Fn_bind.
 DR InterPro; IPR005877; Gpos_YSIRK.
 DR InterPro; IPR001899; Gram_pos_anchor.
 DR Pfam; PF02986; Fn_bind. 1.
 DR Pfam; PF00746; Gram_pos_anchor. 1.
 DR Pfam; PF04650; YSIRK_signal. 1.
 DR TIGR01167; LPRYG_anchor; 1.
 DR TIGR01168; YSIRK_signal; 1.
 DR PROSITE; PS50847; GRAM_POS_ANCHORING; 1.
 KW Cell wall; Complete proteome; Peptidoglycan-anchor.
 SQ SEQUENCE 1038 AA; 113618 MW; 666BF6BF2BFEBB12 CRC64;

Query Match 92.5%; Score 111; DB 2; Length 1038;
 Best Local Similarity 95.2%; Pred. No. 2.9e-08;
 Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KPPYOGGHN5VDFEEDTLPK 21
 |||
 DB 833 KPPYOGGHN5VDFEEDTLPK 853

RESULT 9
 ID Q53682 PRELIMINARY; PRT; 940 AA.
 AC Q53682;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Fibronectin binding protein B.
 GN Name=fnbB;
 OS Staphylococcus aureus.
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 OX NCBI_TaxID=1280;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=8325-4;
 RX MEDLINE=92111475; PubMed=1837266;
 RA Jonsson K., Signas C., Muller H.P., Lindberg M.;
 RT "Two different genes encode fibronectin binding proteins in
 Staphylococcus aureus. The complete nucleotide sequence and
 characterization of the second gene.";

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RL Eur. J. Biochem. 202;1041-1048(1991).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC an amide bond (By similarity).
DR EMBL: X62992; CAA44726.1; -.
DR PIR: S19702; S19702.
DR HSSP: Q53653; 1N67.
DR GO: GO:0009986; C:cell surface; IEA.
DR GO: GO:0005618; C:cell wall; IEA.
DR GO: GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO: GO:0016020; C:membrane; IEA.
DR GO: GO:0007155; P:cell adhesion; IEA.
DR InterPro: IPR008966; Adhes_bact.
DR InterPro: IPR004237; Fn_bind.
DR InterPro: IPR005877; Gpos_YsIRK.
DR InterPro: IPR01899; Gram_pos_anchor.
DR Pfam: PF02986; Fn_bind_2.
DR Pfam: PF00746; Gram_pos_anchor; 1.
DR Pfam: PF04650; YsIRK_signal; 1.
DR TIGRFAMs: TIGR01167; LpxTG_anchor; 1.
DR TIGRFAMs: TIGR01168; YsIRK_signal; 1.
DR PROSITE: PS50847; GRAM_POS_ANCHORING; 1.
DR Cell wall; Peptidoglycan-anchor.
KW SEQUENCE 940 AA; 103555 MW; E35FBBCA907AE345 CRC64;
SQ
Query Match 89.2%; Score 107; DB 2; Length 940;
Best Local Similarity 90.5%; Pred. No. 1.1e-07;
Matches 19; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KPPYQFGHNSVDFEEDTLPK 21
Db 773 KPNYQFGHNSVDFEEDTLPK 793

RESULT 10
ID Q8NU8 PRELIMINARY; PRT; 943 AA.
Q8NU8
AC Q8NU8;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE FndB protein.
DE Name=fndB; OrderedLocustNames=NM2420;
OS Staphylococcus aureus (strain MW2).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
CX NCBI_TaxID=196620;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NM2;
RX MEDLINE=22040717; PubMed=12044378; DOI=10.1016/S0140-6736(02)08713-5;
RA Baba T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Ogunchi A.,
RA Nagai Y., Iwama N., Asano K., Naimi T., Kuroda H., Cui L.,
RA Yamamoto K., Hiramatsu K.,
RT "Genome and virulence determinants of high virulence community-
RT acquired MRSA."
RL Lancet 359:1819-1827(2002).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC an amide bond (By similarity).
DR EMBL: AP004830; BAB96285.1; -.
DR HSSP: Q53653; 1N67.
DR GO: GO:0009986; C:cell surface; IEA.
DR GO: GO:0005618; C:cell wall; IEA.
DR GO: GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO: GO:0016020; C:membrane; IEA.
DR GO: GO:0007155; P:cell adhesion; IEA.
DR InterPro: IPR008966; Adhes_bact.
DR InterPro: IPR004237; Fn_bind.
DR InterPro: IPR005877; Gpos_YsIRK.
DR InterPro: IPR01899; Gram_pos_anchor.
DR Pfam: PF02986; Fn_bind; 1.
DR Pfam: PF00746; Gram_pos_anchor; 1.
DR Pfam: PF04650; YsIRK_signal; 1.
DR TIGRFAMs: TIGR01167; LpxTG_anchor; 1.
DR TIGRFAMs: TIGR01168; YsIRK_signal; 1.
DR PROSITE: PS50847; GRAM_POS_ANCHORING; 1.
KW Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ SEQUENCE 957 AA; 105980 MW; 28FBA7FFPDD3AF CRC64;

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DR PROSITE: PS50847; GRAM_POS_ANCHORING; 1.
KW Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ SEQUENCE 943 AA; 104537 MW; DABAS531947E1B6A CRC64;
SQ
Query Match 89.2%; Score 107; DB 2; Length 943;
Best Local Similarity 90.5%; Pred. No. 1.1e-07;
Matches 19; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KPPYQFGHNSVDFEEDTLPK 21
Db 780 KPNYQFGHNSVDFEEDTLPK 800

RESULT 11
ID Q6G6H4 PRELIMINARY; PRT; 957 AA.
Q6G6H4
AC Q6G6H4;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Fibronectin-binding protein.
DE Name=fnbB; OrderedLocustNames=SA52387;
OS Staphylococcus aureus (strain MSSA476).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
CX NCBI_TaxID=282459;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=15213324; DOI=10.1073/pnas.0402521101;
RA Holden M.T.G., Fell E.J., Lindsay J.A., Peacock S.J., Day N.P.J.,
RA Enright M.C., Foster T.J., Moore C.E., Hurst L., Atkin R., Barron A.,
RA Beeson N., Bentley S.D., Chillingworth C., Chillingworth T.,
RA Churcher C., Clark L., Cotton C., Cronin A., Doggett J., Dowd L.,
RA Feltham D., Hance Z., Harris B., Hauser H., Holtroyd S., Jorgensen K.,
RA James K.D., Leonard N., Line A., Mayes R., Moule S., Mungall K.,
RA Ormond D., Quail M.A., Rabinowitsch E., Rutherford K.M., Sanders M.,
RA Sharp S., Simmonds M., Stevens K., Whitehead S., Barrett B.G.,
RA Spratt B.G., Parkhill J.,
RT "Complete genomes of two clinical Staphylococcus aureus strains:
RT evidence for the rapid evolution of virulence and drug resistance."
RL Proc. Natl. Acad. Sci. U.S.A. 101:9786-9791(2004).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC an amide bond (By similarity).
DR EMBL: BX571857; CAG44201.1; -.
DR GO: GO:0009986; C:cell surface; IEA.
DR GO: GO:0005618; C:cell wall; IEA.
DR GO: GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO: GO:0016020; C:membrane; IEA.
DR GO: GO:0007155; P:cell adhesion; IEA.
DR InterPro: IPR008966; Adhes_bact.
DR InterPro: IPR004237; Fn_bind.
DR InterPro: IPR005877; Gpos_YsIRK.
DR InterPro: IPR01899; Gram_pos_anchor.
DR Pfam: PF02986; Fn_bind; 1.
DR Pfam: PF00746; Gram_pos_anchor; 1.
DR Pfam: PF04650; YsIRK_signal; 1.
DR TIGRFAMs: TIGR01167; LpxTG_anchor; 1.
DR TIGRFAMs: TIGR01168; YsIRK_signal; 1.
DR PROSITE: PS50847; GRAM_POS_ANCHORING; 1.
KW Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ SEQUENCE 957 AA; 105980 MW; 28FBA7FFPDD3AF CRC64;

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Query Match 89.2%; Score 107; DB 2; Length 957;
Best Local Similarity 90.5%; Pred. No. 1.1e-07;
Matches 19; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KPPYQFGHNSVDFEEDTLPK 21
Db 780 KPNYQFGHNSVDFEEDTLPK 800

RESULT 12
ID Q9AEP9 PRELIMINARY; PRT; 152 AA.
Q9AEP9

```

```
AC Q9AEP9;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Fibronectin-binding protein (Fragment).
GN Name=fnb;
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxId=1280;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CMRSA-1;
RX MEDLINE=2124684; PubMed=11349044;
RA DOI=10.1128/IAI.69.6.3791-3799.2001;
RA Rice K., Huesca M., Vaz D., McGavin M.J.;
RT "Variance in fibronectin binding and fnd locus polymorphisms in
RT Staphylococcus aureus: identification of antigenic variation in a
RT fibronectin binding protein adhesin of the epidemic CMRSA-1 strain of
RT methicillin-resistant S. aureus.";
RL Infect. Immun. 69:3791-3799(2001).
DR EMBL; AY029184; AK31568.1; -.
FT NON_TER
FT NON_TER
SQ SEQUENCE 152 AA; 17193 MW; CFA3913C2B11C025 CRC64;

Query Match
Best Local Similarity 83.3%; Score 100; DB 2; Length 152;
Matches 17; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy
1 KPYPQGHNSVDFEEDTLRK 21
|||
130 KPYPQGHNSVDFEEDTLRK 150

RESULT 13
Q9XUB2 PRELIMINARY; PRT; 468 AA.
ID Q9XUB2;
AC Q9XUB2;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein W02A2.7;
GN Name=mex-5; ORFNames=W02A2.7;
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditioidea;
OC Rhabditidae; Peloderae; Caenorhabditis.
OX NCBI_TaxId=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RX MEDLINE=99069613; PubMed=9851916;
RA none;
RT "Genome sequence of the nematode C. elegans: A platform for
RT investigating biology.";
RL Science 282:2012-2018(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Ainecough R.;
RN Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; Z82286; CAB05310.1; -.
DR PIR; T26081; T26081.
DR HSSP; P22893; 1M90.
DR WormBase; WBGene00003230; mex-5.
DR WormPeP; W02A2.7; CE21237.
DR GO; GO:0003676; F:nucleic acid binding; IEA.
DR InterPro; IPR000571; ZnF_CCHC.
DR Pfam; PF00642; zf-CCHC; 2.
DR SMART; SM00356; Znf_C3H1. 2.
KW Hypothetical protein.
SQ SEQUENCE 468 AA; 52820 MW; 6B086FC4971CF5CD CRC64;

Query Match 46.7%; Score 56; DB 2; Length 468;
```

```
Best Local Similarity 40.0%; Pred. No. 4.6;
Matches 8; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

Qy
2 PPYQFGHNSVDFEEDTLRK 21
|||
351 PPYQFGHNSVDFEEDTLRK 370

Db
351 PPYQFGHNSVDFEEDTLRK 370

RESULT 14
Q9KOK2 PRELIMINARY; PRT; 808 AA.
ID Q9KOK2;
AC Q9KOK2;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein NMB0593.
GN OrderedLocustNames=NMB0593;
OS Neisseria meningitidis (serogroup B).
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_TaxId=491;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MC58 / Serogroup B;
RX MEDLINE=2017575; PubMed=10710307; DOI=10.1126/science.287.5459.1809;
RA Tettelein H., Saunders N.J., Heidelberg J.F., Jeffries A.C.,
RA Nelson K.E., Eisen J.A., Ketchum K.A., Hood D.W., Peden J.F.,
RA Dodson R.J., Nelson W.C., Gwin M.L., DeBoy R.T., Peterson J.D.,
RA Hickey E.K., Haft D.H., Salzberg S.L., White O., Fleischmann R.D.,
RA Dougherty B.A., Mason T.M., Ciecko A., Parksey D.S., Blair B.,
RA Cifton E., Clark E.B., Cotton M.D., Ueberback T.R., Kouri H.M.,
RA Qin H., Vamathevan J.J., Gall J., Scarlato V., Maignani V., Piazza M.,
RA Grandi G., Sun L., Smith H.O., Fraser C.M., Moxon E.R., Rappaport R.,
RA Venter J.C.;
RT "Complete genome sequence of Neisseria meningitidis serogroup B strain
RT MC58.";
RL Science 287:1809-1815(2000).
DR EMBL; AE002415; AAFA1021.1; -.
DR PIR; F81180; F81180.
DR TIGR; NMB0593; -.
DR GO; GO:0008080; F:N-acetyltransferase activity; IEA.
DR InterPro; IPR003781; GCM5acetyl_trans.
DR InterPro; IPR000182; GCM5acetyl_trans.
DR Pfam; PF00583; Acetyltransf_1; 1.
DR Pfam; PF02629; CoA_binding_1.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 808 AA; 89114 MW; 6AE44801CC0F66A5 CRC64;

Query Match
Best Local Similarity 43.3%; Score 52; DB 2; Length 808;
Matches 9; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

Qy
2 PPYQFGHNSVDFEEDTLRK 20
|||
453 PPYQFGHNSVDFEEDTLRK 471

Db
453 PPYQFGHNSVDFEEDTLRK 471

RESULT 15
Q7RS55 PRELIMINARY; PRT; 985 AA.
ID Q7RS55;
AC Q7RS55;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE GLP_81_190882_193839.
OS Giardia lamblia ATCC 50803.
OC Eukaryota; Diplomonadida; Hexamitidae; Giardinales; Giardia.
OX NCBI_TaxId=184922;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=WB C6;
RA Morrison H.G., McArthur A.G., Adam R.D., Aley S.B., Gillin F.D.,
RA Olsen G.J., Sogin M.L.;
```

RT "Draft sequence of the Giardia lamblia genome."
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AACB01000003; EAA42779.1; -.
SQ SEQUENCE 985 AA; 106376 MW; A652EC8494FBCB99 CRC64;
Query Match 42.5%; Score 51; DB 2; Length 985;
Best Local Similarity 60.0%; Pred. No. 63;
Matches 9; Conservative 1; Mismatches 5; Indels 0; Gaps 0;
QY 3 PYQFGHNSVDFEED 17
|:||||| | | | | |
Db 133 PHQFGDHRHVSFGED 147

Search completed: October 22, 2005, 04:09:57
Job time : 54.4314 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 25, 2005, 18:43:07 ; Search time 59.0973 Seconds
(without alignments)
137.434 Million cell updates/sec

Title: US-10-731-238-21

Perfect score: 116
Sequence: 1 KPSYQFGSPNSVDFEEDTLRK 21

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760361 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :
1: Genesegp16Dec04:*
2: genesegp1980s:*
3: genesegp1990s:*
4: genesegp2000s:*
5: genesegp2001s:*
6: genesegp2002s:*
7: genesegp2003as:*
8: genesegp2003bs:*
9: genesegp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	116	100.0	21	AAW65677
2	107	92.2	21	AAW65677 Fibronect
3	107	92.2	22	AAW65665
4	107	92.2	37	AAW65665 Fibronect
5	107	92.2	37	AAW65665 Fibronect
6	107	92.2	38	AAW65665 Fibronect
7	107	92.2	134	AAW65665 Fibronect
8	107	92.2	139	AAW65665 Fibronect
9	107	92.2	1018	AAW65665 Fibronect
10	107	92.2	1018	AAW65665 Fibronect
11	107	92.2	1018	AAW65665 Fibronect
12	107	92.2	1018	AAW65665 Fibronect
13	107	92.2	1027	AAW65665 Fibronect
14	104	89.7	961	AAW65665 Fibronect
15	104	89.7	978	AAW65665 Fibronect
16	104	89.7	1001	AAW65665 Fibronect
17	104	89.7	1038	AAW65665 Fibronect
18	102	87.9	21	AAW65679
19	102	87.9	21	AAW65679 Fibronect
20	102	87.9	21	AAW65679 Fibronect
21	102	87.9	21	AAW65679 Fibronect
22	101	87.1	21	AAW65680
23	101	87.1	21	AAW65680 Fibronect
24	101	87.1	21	AAW65684
25	101	87.1	21	AAW65684 Fibronect

26	101	87.1	21	AAW65674	AAW65674 Fibronect
27	100	86.2	21	AAW65685	AAW65685 Fibronect
28	100	86.2	21	AAW65687	AAW65687 Fibronect
29	100	86.2	21	AAW65681	AAW65681 Fibronect
30	100	86.2	77	AAW65679	AAW65679 S. aureus
31	100	86.2	101	AAW65679	AAW65679 D3D4 poly
32	100	86.2	113	AAW65679	AAW65679 D3D4 poly
33	100	86.2	124	AAW65679	AAW65679 D3D4 poly
34	100	86.2	128	AAW65679	AAW65679 D3D4 poly
35	100	86.2	130	AAW65679	AAW65679 D3D4 poly
36	100	86.2	130	AAW65679	AAW65679 D3D4 poly
37	100	86.2	130	AAW65679	AAW65679 D3D4 poly
38	100	86.2	130	AAW65679	AAW65679 D3D4 poly
39	100	86.2	134	AAW65679	AAW65679 D3D4 poly
40	100	86.2	162	AAW65679	AAW65679 D3D4 poly
41	100	86.2	164	AAW65679	AAW65679 D3D4 poly
42	100	86.2	174	AAW65679	AAW65679 D3D4 poly
43	100	86.2	174	AAW65679	AAW65679 D3D4 poly
44	100	86.2	181	AAW65679	AAW65679 D3D4 poly
45	100	86.2	181	AAW65679	AAW65679 D3D4 poly

ALIGNMENTS

RESULT 1
ID AAW65677 standard; peptide; 21 AA.
XX
AC AAW65677;
XX
DT 16-OCT-1998 (first entry)
XX
DE Fibronectin binding protein-derived peptide #21.
XX
KW microbial surface components recognising adhesive matrix molecule;
KW MSCRAMM; fibronectin; fibronectin-binding protein; antibody; epitope;
KW antimicrobial; bacterial infection; antibiotic-resistant strain.
XX
OS Synthetic.
OS Staphylococcus aureus.
XX
FN W09831389-A2.
XX
PD 23-JUL-1998.
XX
PF 21-JAN-1998; 98WO-US001222.
XX
PR 21-JAN-1997; 97US-0036139P.
XX
(TEXA) UNIV TEXAS A & M SYSTEM.
XX
PI Hooeok M, Patti JM, House-Pompeo KL, Speziale P, Joh D;
PI McGavin MJ;
XX
DR WPI; 1998-413816/35.
XX
PT Antibody that binds to fibronectin-binding protein, preventing its
PT binding to fibronectin - used to treat or prevent bacterial infection,
PT especially by Staphylococci and Streptococci.
XX
PS Example 8; Page 100; 201pp; English.
XX
The invention relates to antibodies that bind to a fibronectin-binding
XX domain of a fibronectin-binding protein, and inhibit binding of the
XX protein to a fibronectin. Also claimed are: (1) isolated peptides of a
XX fibronectin-binding protein that do not bind to fibronectin; (2) fusion
XX protein containing at least one peptide of a fibronectin-binding protein
XX linked to a second amino acid sequence; (3) nucleic acid encoding the
XX isolated peptide of (1). Antibodies, the isolated peptides of (1) and the
XX nucleic acids are all useful for immunisation (active or passive) and (by
XX inhibiting binding of bacteria to fibronectin) for preventing or treating
XX infection in humans or other animals, particularly by staphylococci or

CC streptococci, e.g. meningitis, otitis media, pneumonia, endocarditis,
 CC mastitis in cattle, abortion in horses and many others. Since the
 CC antibodies block binding of bacteria, they should be effective against
 CC antibiotic-resistant strains, and may replace antibiotic therapy or
 CC increase its effectiveness. Sequences AAW65670-90 represent a series of
 CC synthetic peptides based on the D3 repeat of *S. aureus* fibronectin
 CC binding protein A. They were synthesised to contain a proline residue at
 CC each position through the sequence (ie a proline scan)

XX
 SQ Sequence 21 AA;

QY Query Match 100.0%; Score 116; DB 2; Length 21;
 Best Local Similarity 100.0%; Pred. No. 6.3e-11;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 1 KPSYQFGPNSVDFEDTLPK 21
 1 KPSYQFGPNSVDFEDTLPK 21

RESULT 2
 AAW65665
 ID AAW65665 standard; peptide; 21 AA.
 AC AAW65665;
 XX
 XX 16-OCT-1998 (first entry)
 DT
 DE Fibronectin binding protein-derived peptide #9.
 XX
 XX microbial surface components recognising adhesive matrix molecule;
 KM MSCRAMM; fibronectin; fibronectin-binding protein; antibody; epitope;
 KM antibiotic; bacterial infection; antibiotic-resistant strain.
 XX
 OS Synthetic.
 OS *Staphylococcus aureus*.
 XX
 PN MO9831389-A2.
 XX
 PD 23-UTL-1998.
 XX
 PF 21-JAN-1998; 98MO-US001222.
 XX
 PR 21-JAN-1997; 97US-0036139P.
 XX
 PA (TEXA) UNIV TEXAS A & M SYSTEM.
 XX
 PI Hoeoek M, Patli JM, House-Pompeo KL, Speciale P, Jch D;
 PI McGavin MJ;
 DR MPI; 1998-413816/35.
 XX
 PT Antibody that binds to fibronectin-binding protein, preventing its
 PT binding to fibronectin - used to treat or prevent bacterial infection,
 XX especially by *Staphylococci* and *Streptococci*.
 PS Example 2; Page 92; 201pp; English.

CC The invention relates to antibodies that bind to a fibronectin-binding
 CC domain of a fibronectin-binding protein, and inhibit binding of the
 CC protein to fibronectin. Also claimed are: (1) isolated peptides of a
 CC fibronectin-binding protein that do not bind to fibronectin; (2) fusion
 CC protein containing at least one peptide of a fibronectin-binding protein
 CC linked to a second amino acid sequence; (3) nucleic acid encoding the
 CC isolated peptide of (1). Antibodies, the isolated peptides of (1) and the
 CC nucleic acids are all useful for immunisation (active or passive) and (by
 CC inhibiting binding of bacteria to fibronectin) for preventing or treating
 CC infection in humans or other animals, particularly by *staphylococci* or
 CC streptococci, e.g. meningitis, otitis media, pneumonia, endocarditis,
 CC mastitis in cattle, abortion in horses and many others. Since the
 CC antibodies block binding of bacteria, they should be effective against
 CC antibiotic-resistant strains, and may replace antibiotic therapy or
 CC increase its effectiveness. Sequences AAW65659-68 represent synthetic

CC epitopes from the fibronectin binding domains DU and DI-D4 of the *S.*
 CC aureus fnba gene
 XX
 SQ Sequence 21 AA;

QY Query Match 92.2%; Score 107; DB 2; Length 21;
 Best Local Similarity 95.2%; Pred. No. 1.6e-09;
 Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

DB 1 KPSYQFGPNSVDFEDTLPK 21
 1 KPSYQFGPNSVDFEDTLPK 21

RESULT 3
 AAR21340
 ID AAR21340 standard; peptide; 22 AA.
 AC AAR21340;
 XX
 XX 25-MAR-2003 (revised)
 DT 15-UTN-1992 (first entry)
 XX
 DE Fibronectin binding protein.
 XX
 KM FbBP; wound infection reduction; vaccination; mastitis;
 KM *Staphylococcal* infections; D3.
 XX
 OS Synthetic.
 OS
 PN WO9202555-A.
 XX
 PD 20-FEB-1992.
 XX
 PF 10-AUG-1990; 90SE-00002617.
 XX
 PR 10-AUG-1990; 90SE-00002617.
 XX
 PA (ALFA) ALFA LAVAL AGRIC INT AB.
 XX
 PI Hook M, McGavin M, Raucchi G;
 PI
 DR MPI; 1992-080035/10.
 XX
 PT New fibronectin binding peptide - combines with fusion peptide to form
 PT large antigen, used in immunisation, diagnosis and for treating wounds.
 XX
 PS Claim 1; Page 22; 33pp; English.

CC The sequence comprises amino acids 17-33 of a tandem repeat, designated
 CC D3 of the fibronectin binding site of *Staphylococcus aureus* 8325-4 FnBP.
 CC The N-terminal DK may be replaced with H or K, and the C-terminal LKP may
 CC be replaced by either L, LP, or OH. The peptides were synthesised using
 CC standard methods and purified using reverse phase HPLC. The appropriate
 CC fractions were dialysed and lyophilised. Peptide sequencing was performed
 CC and the peptides digested and chemically modified by dihydroxypropylation
 CC of the amino side chain of lysine. The carboxylic side chains were
 CC converted to glycine methyl esters. The phenyl side chains of tyrosine
 CC residues were oxidised. Chemically modified peptide D3 was compared to
 CC unmodified D3. Lysine and tyrosine modifications only partially
 CC diminished its activity whereas modification of aspartic/glutamic
 CC residues resulted in complete loss of activity. The peptide can be used
 CC for the prevention or reduction of the risk of wound infection. The
 CC peptide can be used to create a large antigen for vaccinating ruminants
 CC against mastitis caused by *Staphylococcal* infections. It can also be used
 CC to diagnose *Staphylococcal* infections using ELISA or DNA probes. (Updated
 CC on 25-MAR-2003 to correct PA field.)
 XX
 SQ Sequence 22 AA;

QY Query Match 92.2%; Score 107; DB 2; Length 22;
 Best Local Similarity 95.2%; Pred. No. 1.7e-09;
 Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

XX MO9916892-A1.
XX 08-APR-1999.
XX 29-SEP-1998; 98WO-GB002927.
XX 29-SEP-1997; 97GB-00020633.
XX (UYBR-) UNIV BRISTOL.
XX Bradley AJ, Duffas WP;
XX MPI: 1999-255101/21.
XX N-PSDB; AAX91504.
XX New bovine herpes virus-2 vectors.
XX Example 2; Fig 8A-B; 130pp; English.
XX The invention provides bovine herpes virus-2 (BHV-2) based vectors that
XX comprise at least one cytokine-encoding DNA sequence. The expression of
XX cytokines in mammals can up-regulate immune responses to the immunogens.
XX The cytokine is selected from interleukins (IL), colony stimulating
XX factors (CSF), interferons (IFN) and tumour necrosis factors (TNF). The
XX BHV-2 based vector or recombinant virus can be used as vaccines. They can
XX be used for preventing or treating a mucosal disease in a subject, e.g.
XX ruminants, cattle, sheep, goats, dogs, cats, horses, or man, particularly
XX mastitis in cows or breast cancers in humans. They can also be used for
XX preventing or treating a stress-induced disease. The present sequence
XX represents the binding domain of a previously published S. aureus
XX fibronectin binding protein A (FnBA) sequence. The FnB binding domain
XX gene sequence FNBA8, cloned for use in this invention has 97.8 percent
XX identity when compared to the previously published FnBA and FnB gene
XX sequences
XX
XX Sequence 134 AA;
SQ

Query Match 92.2%; Score 107; DB 2; Length 134;
Best Local Similarity 95.2%; Pred. No. 1.2e-08;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KPSYQFGGNSVDFEEDTLPK 21
DB 93 KPSYQFGGNSVDFEEDTLPK 113

RESULT 7
AAM31556
ID AAM31556 standard; protein; 139 AA.
XX
AC AAM31556;
XX
XX 27-AUG-2003 (revised)
DT 25-MAR-2003 (revised)
DT 21-MAY-1998 (first entry)
XX
DE Fibronectin-binding MSCRAMM derivative pQD.
XX
XX Fibronectin; pQD; collagen binding protein; sepsis; infection;
XX microbial surface component regulating adhesive matrix molecule; MSCRAMM;
XX adhesin; vaccine; immunisation; diagnosis; therapy; mastitis.
XX
OS Staphylococcus aureus.
XX
XX
XX Key Location/Qualifiers
XX Peptide 1..12
XX /note= "vector pQE30-derived peptide"
XX
XX MO9743314-A2.
XX
XX 20-NOV-1997.
XX

PF 14-MAY-1997; 97WO-US008210.
XX
XX 16-MAY-1996; 96US-0017678P.
XX
XX (TEXA) UNIV TEXAS A & M SYSTEM.
XX (UABR-) UAB RES FOUND.
XX
XX Hoeoek M, Patti JM, House-Pompeo K, Schanam N, Symersky J;
XX MPI: 1998-008601/01.
XX
XX Antibody that interacts with collagen binding domain of Staphylococcal
XX cna gene product - useful to prevent bacterial sepsis in animal infected
XX with Staphylococcus aureus.
XX
XX
XX Disclosure; Page 91; 143pp; English.
XX

XX This protein comprises Staphylococcus aureus fibronectin-binding
XX microbial surface component regulating adhesive matrix molecule (MSCRAMM)
XX derivative pQD, plus a vector-derived N-terminal peptide. The invention
XX relates to claimed nucleic acid sequences (see AAT93436-38) encoding S.
XX aureus collagen binding protein (CBP) epitopes M17, M31 and M55 (see
XX AAM31552-54) that confer protection against S. aureus infection. CBP
XX protein and antigenic epitopes are contemplated for use in the treatment
XX of pathological infections, especially to prevent bacterial adhesion to
XX collagen. The epitopes are also contemplated for use in the preparation
XX of vaccines and as carrier proteins in vaccine formulations, as well as
XX in the formulation of compositions for the prevention of S. aureus
XX infection. PCR33 and pQD (see AAM31556) were used to raise anti-MSCRAMM
XX polyclonal antibodies used in passive immunisation against bovine
XX mastitis. (updated on 25-MAR-2003 to correct PI field.) (updated on 27-
XX AUG-2003 to correct OS field.)
XX

SQ Sequence 139 AA;
Query Match 92.2%; Score 107; DB 2; Length 139;
Best Local Similarity 95.2%; Pred. No. 1.3e-08;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KPSYQFGGNSVDFEEDTLPK 21
DB 107 KPSYQFGGNSVDFEEDTLPK 127

RESULT 8
AAP82115
ID AAP82115 standard; protein; 1018 AA.
XX
XX AAP82115;
XX
XX 25-MAR-2003 (revised)
DT 05-JAN-1990 (first entry)
XX
XX Fibronectin binding protein.
XX
XX Fibronectin binding protein; S. aureus; immunisation; mastitis; ruminants;
XX wound infection; diagnosis.
XX
XX Staphylococcus aureus.
XX
XX
XX EP294349-A.
XX
XX 07-DEC-1988.
XX
XX 30-MAY-1988; 88EP-00850188.
XX
XX 01-JUN-1987; 87SE-00002272.
XX
XX (ALFA) ALFA LAVAL AGRIC INT AB.
XX
XX Lindberg MK, Sigmas LC, Wadstrom TM, Froman G;
XX MPI: 1988-347978/49.
XX

DR P-PSDB; AAP82115.
XX
XX Hybrid DNA encoding Staphylococcus aureus fibronectin binding protein -
PT useful for immunisation and topical application to prevent staphylococcal
PT infections.
XX
XX Disclosure; Fig. 8A:1-8A:2; 23pp; English.
XX
XX The S. aureus fibronectin binding protein may be included in a hybrid
CC protein. The protein may be used to immunise ruminants against
CC staphylococcal mastitis, pref. when given at 0.5-5 microg/kg, using 3
CC doses at 1-3 week intervals; and for topical applicn. to prevent wound
CC infection, pref. using isotonic saline soln. of concn. 25-250 microg/mg.
CC The DNA encoding the binding protein and the hybrid protein may be
CC immobilised on a carrier and used to diagnose staphylococcal infections.
CC (Updated on 25-MAR-2003 to correct PA field.)
XX
XX
SQ Sequence 1018 AA;
Query Match 92.2%; Score 107; DB 1; Length 1018;
Best Local Similarity 95.2%; Pred. No. 1.1e-07;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 KPSYQFGGNSVDFEDTLPK 21
DB 837 KPSYQFGGNSVDFEDTLPK 857
RESULT 9
AAU37245
ID AAU37245 standard; protein; 1018 AA.
XX
XX AAU37245;
AC
XX 14-FEB-2002 (first entry)
DT
XX Staphylococcus aureus cellular proliferation protein #1415.
DE
XX Antisense; prokaryotic cellular proliferation protein; antibiotic;
KM antibacterial; drug design.
XX
XX Staphylococcus aureus.
OS
XX WO200170955-A2.
PN
XX 27-SEP-2001.
PD
XX
XX 21-MAR-2001; 2001WO-US009180.
PF
XX
XX 21-MAR-2000; 2000US-0191078P.
PR 23-MAY-2000; 2000US-0206848P.
PR 26-MAY-2000; 2000US-0207727P.
PR 23-OCT-2000; 2000US-0242578P.
PR 27-NOV-2000; 2000US-0253625P.
PR 22-DEC-2000; 2000US-0257931P.
PR 16-FEB-2001; 2001US-0269308P.
XX
XX (ELIT-) ELITRA PHARM INC.
PA
XX Haselbeck R, Ohlsen KL, Zyekind JW, Wall D, Trawick JD, Carr GJ;
PI Yamamoto RT, Xu HH;
PI WPI; 2001-611495/70.
DR N-PSDB; AAS55104.
XX
XX New polynucleotides for the identification and development of
PT antibiotics, comprise sequences of antisense nucleic acids.
XX
XX Example 3; SEQ ID NO 12638; 511pp; English.
PS
XX The invention relates to antisense inhibitors of genes essential to
CC prokaryotic cellular proliferation, their use in identifying the genes,
CC their use in the discovery of novel antibiotics, the essential genes

CC themselves and the encoded proteins. The prokaryotes used are Escherichia
CC coli, Staphylococcus aureus, Salmonella typhi, Klebsiella pneumoniae,
CC Pseudomonas aeruginosa and Enterococcus faecalis. The invention is also
CC useful for the identification of potential new targets for antibiotic
CC development. The antisense nucleic acids can also be used to identify
CC proteins used in proliferation, to express these proteins, and to obtain
CC antibodies capable of binding to the expressed proteins. The proteins can
CC be used to screen compounds in rational drug discovery programmes. The
CC antisense nucleic acid sequence is also useful to screen for homologous
CC nucleic acids which are required for cell proliferation in a wide variety
CC of organisms. The present sequence represents an essential prokaryotic
CC cellular proliferation protein. Note: The sequence data for this patent
CC did not form part of the printed specification, but was obtained in
CC electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX
SQ Sequence 1018 AA;
Query Match 92.2%; Score 107; DB 4; Length 1018;
Best Local Similarity 95.2%; Pred. No. 1.1e-07;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 KPSYQFGGNSVDFEDTLPK 21
DB 837 KPSYQFGGNSVDFEDTLPK 857
RESULT 10
AAU34301
ID AAU34301 standard; protein; 1018 AA.
XX
XX AAU34301;
AC
XX 14-FEB-2002 (first entry)
DT
XX Staphylococcus aureus cellular proliferation protein #577.
DE
XX Antisense; prokaryotic cellular proliferation protein; antibiotic;
KM antibacterial; drug design.
XX
XX Staphylococcus aureus.
OS
XX WO200170955-A2.
PN
XX 27-SEP-2001.
PD
XX
XX 21-MAR-2001; 2001WO-US009180.
PF
XX
XX 21-MAR-2000; 2000US-0191078P.
PR 23-MAY-2000; 2000US-0206848P.
PR 26-MAY-2000; 2000US-0207727P.
PR 23-OCT-2000; 2000US-0242578P.
PR 27-NOV-2000; 2000US-0253625P.
PR 22-DEC-2000; 2000US-0257931P.
PR 16-FEB-2001; 2001US-0269308P.
XX
XX (ELIT-) ELITRA PHARM INC.
PA
XX Haselbeck R, Ohlsen KL, Zyekind JW, Wall D, Trawick JD, Carr GJ;
PI Yamamoto RT, Xu HH;
PI WPI; 2001-611495/70.
DR N-PSDB; AAS52160.
XX
XX New polynucleotides for the identification and development of
PT antibiotics, comprise sequences of antisense nucleic acids.
XX
XX Example 3; SEQ ID NO 5797; 511pp; English.
PS
XX The invention relates to antisense inhibitors of genes essential to
CC prokaryotic cellular proliferation, their use in identifying the genes,
CC their use in the discovery of novel antibiotics, the essential genes
CC themselves and the encoded proteins. The prokaryotes used are Escherichia

CC coli, *Staphylococcus aureus*, *Salmonella typhi*, *Klebsiella pneumoniae*,
 CC *Pseudomonas aeruginosa* and *Enterococcus faecalis*. The invention is also
 CC useful for the identification of potential new targets for antibiotic
 CC development. The antisense nucleic acids can also be used to identify
 CC proteins used in proliferation, to express these proteins, and to obtain
 CC antibodies capable of binding to the expressed proteins. The proteins can
 CC be used to screen compounds in rational drug discovery programmes. The
 CC antisense nucleic acid sequence is also useful to screen for homologous
 CC nucleic acids which are required for cell proliferation in a wide variety
 CC of organisms. The present sequence represents an essential prokaryotic
 CC cellular proliferation protein. Note: The sequence data for this patent
 CC did not form part of the printed specification, but was obtained in
 CC electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences

XX Sequence 1018 AA;

Query Match 92.2%; Score 107; DB 4; Length 1018;

Best Local Similarity 95.2%; Pred. No. 1.1e-07; Mismatches 1; Indels 0; Gaps 0;

Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 KPSYQFGGNSVDFFEDTLPK 21
 DB 837 KPSYQFGGNSVDFFEDTLPK 857

RESULT 11

ABJ18922 standard; protein; 1018 AA.

ABJ18922;

06-MAR-2003 (first entry)

Pathogen specific antigen related staphylococcal protein SEQ ID No 68.

Antibacterial; virucide; fungicide; protozoacide; cytostatic; anti-HIV;
 hyperimmune; serum-reactive; antigen; pathogen; tumour; allergen;
 auto-immunity; vaccine; staphylococcal infection; antibody; cancer;
 autoimmune disease; HIV; hepatitis.

Staphylococcus sp.

MO200259148-A2.

01-AUG-2002.

21-JAN-2002; 2002WO-EP000546.

26-JAN-2001; 2001AT-00000130.

(CIST-) CISTEM BIOTECHNOLOGIES GMBH.

Weinke A, Nagy E, Von Ahsen U, Klade C, Henics T, Zauner W;
 Minh DB, Vytvytska O, Etz H, Dryla A, Weichart T, Hafner M;
 Tempelmeier B;

WPI; 2003-075410/07.

Identifying, isolating and producing hyperimmune serum-reactive antigens
 from a pathogen, for preparing vaccine or medicament for treating or
 preventing e.g. staphylococcal infections, comprises providing antibody
 preparation.

Example 7; Page 157; 252pp; English.

The invention relates to a novel method for identifying, isolating and
 producing hyperimmune serum-reactive antigens from a pathogen, tumour,
 allergen, a tissue or host prone to auto-immunity, where the antigens are
 used in a vaccine, comprises providing antibody preparation from a plasma
 pool of a type of animal, or individual sera with antibodies against the
 specific pathogen, tumour, allergen, tissue or host prone to auto-
 immunity. The hyperimmune serum-reactive antigens comprising any of the

CC 62 sequences of 53-2261 amino acids fully defined in the specification,
 CC or their hyperimmune fragments are useful for the manufacture of a
 CC pharmaceutical preparation, particularly a vaccine against staphylococcal
 CC infections or colonisation against *S. aureus* or *S. epidermidis*. The
 CC preparation of antibodies is useful for the manufacture of a medicament
 CC for treating or preventing staphylococcal infections or colonisation
 CC against *S. aureus* or *S. epidermidis*. The antibody preparations may also
 CC be used for diagnostic and imaging purposes. Other conditions that can be
 CC treated include cancer, autoimmune diseases or infections caused by viral
 CC (e.g. HIV, hepatitis A, B or C), fungal or protozoan pathogens. This
 CC sequence represents a staphylococcal protein relating to the method for
 CC identifying and producing pathogen specific antigens of the invention

XX Sequence 1018 AA;

Query Match 92.2%; Score 107; DB 6; Length 1018;

Best Local Similarity 95.2%; Pred. No. 1.1e-07; Mismatches 1; Indels 0; Gaps 0;

Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 KPSYQFGGNSVDFFEDTLPK 21
 DB 837 KPSYQFGGNSVDFFEDTLPK 857

RESULT 12

ABM72537 standard; protein; 1018 AA.

ABM72537;

20-NOV-2003 (first entry)

Staphylococcus aureus protein #1777.

Antibacterial; vaccine; gene therapy; infection; sepsis; diagnosis;
 enzymatic assay; antibiotic target.

Staphylococcus aureus.

MO200294868-A2.

28-NOV-2002.

27-MAR-2002; 2002WO-IB002637.

27-MAR-2001; 2001GB-00007661.

(CHIR-) CHIRON SPA.

Maignani V, Mora M, Scarselli M;

WPI; 2003-120786/11.

New *Staphylococcus aureus* protein, useful as a vaccine for treating or
 preventing *Staphylococcal* infection, specifically an infection caused by
S. aureus, e.g. sepsis.

Claim 1; SEQ ID NO 3554; 49pp; English.

The invention relates to novel genes and encoded proteins from
Staphylococcus aureus. A composition comprising the *S. aureus* protein, a
 nucleic acid encoding the protein, or an antibody to the protein, is
 useful as a pharmaceutical, particularly as a vaccine for treating or
 preventing infection due to *Staphylococcus* bacteria, specifically an
 infection caused by *S. aureus*. The composition is particularly useful for
 treating or preventing sepsis in a patient. The composition can also be
 used for diagnostics. The protein is also used in an assay for enzymatic
 studies and as a target for antibiotics. This sequence represents one of
 the novel *S. aureus* proteins of the invention

XX Sequence 1018 AA;

Query Match 92.2%; Score 107; DB 6; Length 1018;
Best Local Similarity 95.2%; Pred. No. 1.1e-07;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KPSYQFGGPNVSDFEEDTLPK 21
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DB 837 KPSYQFGGHNVSDFEEDTLPK 857

RESULT 13
AAW89806 standard; protein; 1027 AA.
XX AAW89806;
XX
XX 16-MAR-1999 (first entry)
XX
XX Staphylococcus aureus protein SEQ ID #5254.
XX
XX Computer readable medium; vaccine; S.aureus infection; immunodetection;
XX cellulitis; eyelid infection; food poisoning; osteomyelitis; therapy;
XX skin infection; surgical wound infection; scalded skin syndrome;
XX toxic shock syndrome.
XX
XX Staphylococcus aureus.
XX
XX EP786519-A2.
XX
XX 30-JUL-1997.
XX
XX 07-JAN-1997; 97EP-00100117.
XX
XX 05-JAN-1996; 96US-0009661P.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Kunsch CA, Choi GH, Barash SC, Dillon PJ, Fannon MR, Rosen CA;
XX WPI; 1997-374922/35.
XX
XX Polynucleotide(s) and proteins derived from Staphylococcus aureus -
XX stored on computer readable medium and used in the production of anti-
XX S.aureus vaccines.
XX
XX Claim 23; Page 3263-3267; 3271pp; English.

XX This sequence represents a Staphylococcus aureus protein sequence of the
XX invention. The DNA sequences encoding the S.aureus proteins are recorded
XX on a computer readable medium, preferably selected from a floppy or hard
XX disk, random access memory (RAM), read-only memory (ROM) or CD-ROM.
XX Homology searches using the S.aureus DNA sequences allows putative
XX functions to be assigned so that protein-encoding or regulatory regions
XX of commercial, therapeutic or industrial importance can be obtained.
XX Specifically, sequences which are likely to encode antigens have been
XX identified and these polypeptides can be used in a vaccine composition
XX against S.aureus infection. The polypeptides can also be used in a kit
XX for the immunodetection of S.aureus in a sample. S.aureus is implicated
XX in numerous human diseases, including cellulitis, eyelid infections, food
XX poisoning, osteomyelitis, skin and surgical wound infections, scalded
XX skin syndrome, toxic shock syndrome, etc. Organisms transformed with the
XX DNA sequences can be used for recombinant production of the polypeptides.
XX The new DNA sequences (and their fragments) are useful as primers or
XX probes for isolating homologues of any of the 5191 S.aureus DNA sequences
XX contained on the computer readable medium

XX Sequence 1027 AA;
XX
XX Query Match 92.2%; Score 107; DB 2; Length 1027;
XX Best Local Similarity 95.2%; Pred. No. 1.2e-07;
XX Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KPSYQFGGPNVSDFEEDTLPK 21
|||||

DB 846 KPSYQFGGHNVSDFEEDTLPK 866

RESULT 14
ABU15854
ID ABU15854 standard; protein; 961 AA.
XX
XX ABU15854;
XX
XX 19-JUN-2003 (first entry)
XX
XX Protein encoded by prokaryotic essential gene #1381.
XX
XX Antisense, prokaryotic essential gene; cell proliferation; drug design.
XX
XX Staphylococcus aureus.
XX
XX WO200277183-A2.
XX
XX 03-OCT-2002.
XX
XX 21-MAR-2002; 2002WO-US009107.
XX
XX 21-MAR-2001; 2001US-00815242.
XX
XX 06-SEP-2001; 2001US-00948993.
XX
XX 25-OCT-2001; 2001US-0342323P.
XX
XX 08-FEB-2002; 2002US-00072851.
XX
XX 06-MAR-2002; 2002US-0362699P.
XX
XX (ELIT-) ELITRA PHARM INC.
XX
XX Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zykkind JW;
XX Pi Wall D, Trawick JD, Carr GU, Yamamoto R, Foreyn RA, Xu HH;
XX WPI; 2003-029926/02.
XX
XX N-PSDB; ACA19724.
XX
XX DR
XX
XX Claim 25; SEQ ID NO 43778; 1766pp; English.

XX The invention relates to an isolated nucleic acid comprising any one of
XX the 6213 antisense sequences given in the specification where expression
XX of the nucleic acid inhibits proliferation of a cell. Also included are:
XX (1) a vector comprising a promoter operably linked to the nucleic acid
XX encoding a polypeptide whose expression is inhibited by the antisense
XX nucleic acid; (2) a host cell containing the vector; (3) an isolated
XX polypeptide or its fragment whose expression is inhibited by the
XX antisense nucleic acid; (4) an antibody capable of specifically binding
XX the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular
XX proliferation or the activity of a gene in an operon required for
XX proliferation; (7) identifying a compound that influences the activity of
XX the gene product or that has an activity against a biological pathway
XX required for proliferation, or that inhibits cellular proliferation; (8)
XX identifying a gene required for cellular proliferation or the biological
XX pathway in which a proliferation-required gene or its gene product lies
XX or a gene on which the test compound that inhibits proliferation of an
XX organism acts; (9) manufacturing an antibiotic; (10) profiling a
XX compound's activity; (11) a culture comprising strains in which the gene
XX product is overexpressed or underexpressed; (12) determining the extent
XX to which each of the strains is present in a culture or collection of
XX strains; or (13) identifying the target of a compound that inhibits the
XX proliferation of an organism. The antisense nucleic acids are useful for
XX identifying proteins or screening for homologous nucleic acids required
XX for cellular proliferation to isolate candidate molecules for rational
XX drug discovery programs, or for screening homologous nucleic acids
XX required for proliferation in cells other than S. aureus, S. typhimurium,
XX K. pneumoniae or P. aeruginosa. The present sequence is encoded by one of
XX the target prokaryotic essential genes. Note: The sequence data for this
XX patent did not form part of the printed specification, but was obtained
XX in electronic format directly from WIPO at


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CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 961 AA;
Query Match 89.7%; Score 104; DB 6; Length 961;
Best Local Similarity 90.5%; Pred. No. 3.2e-07;
Matches 19; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 KPSYQFGGPNVSVPFEDTLPK 21
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DB 784 KPNYQFGGHNSVDFEDTLPK 804

RESULT 15
AAU33960
ID AAU33960 standard; protein, 978 AA.
XX
AC AAU33960;
XX
DT 14-FEB-2002 (first entry)
XX
DE Staphylococcus aureus cellular proliferation protein #236.
XX
KW Antisense; prokaryotic cellular proliferation protein; antibiotic;
XX antibacterial; drug design.
OS Staphylococcus aureus.
XX
PN WO200170955-A2.
XX
PD 27-SEP-2001.
XX
PF 21-MAR-2001; 2001WO-US009180.
XX
PR 21-MAR-2000; 2000US-0191078P.
XX PR 23-MAY-2000; 2000US-0206848P.
XX PR 26-MAY-2000; 2000US-0207727P.
XX PR 23-OCT-2000; 2000US-0242578P.
XX PR 27-NOV-2000; 2000US-0253625P.
XX PR 22-DEC-2000; 2000US-0257931P.
XX PR 16-FEB-2001; 2001US-0269308P.
XX
PA (ELIT-) ELITRA PHARM INC.
XX
PI Haeselbeck R, Ohlsen KL, Zyskind JW, Wall D, Trawick JD, Carr GJ;
PI Yamamoto RT, Xu HH;
XX
DR N-PSDB; AAS51819.
XX
WPI; 2001-611495/70.
XX
DR N-PSDB; AAS51819.
XX
PT New polynucleotides for the identification and development of
PT antibiotics, comprise sequences of antisense nucleic acids.
XX
XX
XX Example 3; SEQ ID NO 5456; 511pp; English.
XX
XX The invention relates to antisense inhibitors of genes essential to
XX prokaryotic cellular proliferation, their use in identifying the genes,
XX their use in the discovery of novel antibiotics, the essential genes
XX themselves and the encoded proteins. The prokaryotes used are Escherichia
XX coli, Staphylococcus aureus, Salmonella typhi, Klebsiella pneumoniae,
XX Pseudomonas aeruginosa and Enterococcus faecalis. The invention is also
XX useful for the identification of potential new targets for antibiotic
XX development. The antisense nucleic acids can also be used to identify
XX proteins used in proliferation, to express these proteins, and to obtain
XX antibodies capable of binding to the expressed proteins. The proteins can
XX be used to screen compounds in rational drug discovery programmes. The
XX antisense nucleic acid sequence is also useful to screen for homologous
XX nucleic acids which are required for cell proliferation in a wide variety
XX of organisms. The present sequence represents an essential prokaryotic
XX cellular proliferation protein. Note: The sequence data for this patent
XX did not form part of the printed specification, but was obtained in
XX electronic format directly from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
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XX
SQ Sequence 978 AA;
Query Match 89.7%; Score 104; DB 4; Length 978;
Best Local Similarity 90.5%; Pred. No. 3.2e-07;
Matches 19; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 KPSYQFGGPNVSVPFEDTLPK 21
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DB 815 KPNYQFGGHNSVDFEDTLPK 835
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Job time : 59.1473 secs

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Run on: October 22, 2005, 02:23:36 ; Search time 15.9358 Seconds
(Without alignments)
98.371 Million cell updates/sec

Title: US-10-731-238-21

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Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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- 4: /cgn2_6/ptodata/1/1aa/6B COMB pep:*
- 5: /cgn2_6/ptodata/1/1aa/PTUS COMB pep:*
- 6: /cgn2_6/ptodata/1/1aa/backfile1 pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	107	92.2	21	4	US-09-010-317-9
3	107	92.2	37	1	US-08-234-622A-4
4	107	92.2	38	1	US-08-294-189-8
5	107	92.2	38	1	US-08-729-767-5
6	107	92.2	114	1	US-08-259-000-3
7	107	92.2	139	1	US-08-856-253-8
8	107	92.2	178	2	US-08-459-135A-12
9	107	92.2	178	3	US-08-495-559-12
10	107	92.2	1027	4	US-08-956-171B-5254
11	107	92.2	1027	4	US-08-781-986A-5254
12	102	87.9	21	4	US-09-010-317-14
13	102	87.9	21	4	US-09-010-317-16
14	102	87.9	21	4	US-09-010-317-13
15	102	87.9	21	4	US-09-010-317-33
16	101	87.1	21	4	US-09-010-317-18
17	101	87.1	21	4	US-09-010-317-24
18	101	87.1	21	4	US-09-010-317-27
19	101	87.1	21	4	US-09-010-317-28
20	101	87.1	21	4	US-09-010-317-30
21	100	86.2	21	4	US-09-010-317-25
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23	100	86.2	21	4	US-09-010-317-31
24	100	86.2	130	2	US-08-459-135A-7
25	100	86.2	130	2	US-08-459-135A-8
26	100	86.2	130	3	US-08-495-559-7
27	100	86.2	130	3	US-08-495-559-8

28	100	86.2	174	2	US-08-459-135A-10	Sequence 10, Appl
29	100	86.2	174	2	US-08-459-135A-13	Sequence 13, Appl
30	100	86.2	174	3	US-08-495-559-10	Sequence 10, Appl
31	100	86.2	174	3	US-08-495-559-13	Sequence 13, Appl
32	100	86.2	176	3	US-08-459-135A-6	Sequence 6, Appl
33	100	86.2	181	2	US-08-459-135A-6	Sequence 6, Appl
34	100	86.2	559	4	US-08-956-171B-5251	Sequence 5251, Ap
35	100	86.2	559	4	US-08-781-986A-5251	Sequence 5251, Ap
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37	99	85.3	21	4	US-09-010-317-15	Sequence 15, Appl
38	99	85.3	21	4	US-09-010-317-20	Sequence 20, Appl
39	99	85.3	21	4	US-09-010-317-32	Sequence 32, Appl
40	99	85.3	22	4	US-09-010-317-13	Sequence 13, Appl
41	99	85.3	22	4	US-09-010-317-17	Sequence 17, Appl
42	97	83.6	21	4	US-09-010-317-19	Sequence 19, Appl
43	97	83.6	21	4	US-09-010-317-26	Sequence 26, Appl
44	97	83.6	21	4	US-09-010-317-26	Sequence 26, Appl
45	86	74.1	19	1	US-08-234-622A-1	Sequence 1, Appl

ALIGNMENTS

RESULT 1
US-09-010-317-21
Sequence 21, Application US/09010317
Patent No. 6685943
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
APPLICANT: Patti, Joseph M.
APPLICANT: House-Pompeo, Karen L.
APPLICANT: Speziale, Pietro
APPLICANT: Jon, Danny
APPLICANT: McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
TITLE OF INVENTION: AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/010.317
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/036.139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-09-010-317-21
Query Match 100.0%; Score 116; DB 4; Length 21;
Best Local Similarity 100.0%; Pred. No. 2.3e-11;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KPSYOGGPNVDFEEDTLPK 21
|||||
Db 1 KPSYOGGPNVDFEEDTLPK 21

RESULT 2
US-09-010-317-9
; Sequence 9, Application US/09010317
; Patent No. 6685943
; GENERAL INFORMATION:
; APPLICANT: Hook, Magnus
; APPLICANT: Patti, Joseph M.
; APPLICANT: House-Pompeo, Karen L.
; APPLICANT: Speziale, Pietro
; APPLICANT: McGavin, Martin J.
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
; TITLE OF INVENTION: AND METHODS OF USE
; NUMBER OF SEQUENCES: 105
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: TX
; COUNTRY: USA
; ZIP: 77210-4433
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Releasee #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/010,317
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/036,139
; FILING DATE: 21-JAN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Hibler, David W.
; REGISTRATION NUMBER: 41,071
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 512-418-3000
; TELEFAX: 512-474-7577
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; US-09-010-317-9

Query Match 92.2%; Score 107; DB 4; Length 21;
Best Local Similarity 95.2%; Pred. No. 5.6e-10;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KPSYOGGPNVDFEEDTLPK 21
|||||
Db 1 KPSYOGGPNVDFEEDTLPK 21

RESULT 3
US-08-234-622A-4
; Sequence 4, Application US/08234622A
; Patent No. 5440014
; GENERAL INFORMATION:
; APPLICANT: Hook, Magnus
; APPLICANT: McGavin, Martin
; APPLICANT: RAUCCI, Giuseppe
; TITLE OF INVENTION: A FIBRONECTIN BINDING PEPTIDE

NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Burns, Doane, Swecker & Mathis
STREET: P.O. Box 1404
CITY: Alexandria
STATE: Virginia
COUNTRY: United States
ZIP: 22313-1404

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Releasee #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/234,622A
FILING DATE: 28-APR-1994
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: SE 9002617-0
FILING DATE: 10-AUG-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/SE91/00534
FILING DATE: 09-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: Neuth, Donna M
REGISTRATION NUMBER: 36,607
REFERENCE/DOCKET NUMBER: 012885-044
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 37 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-234-622A-4

Query Match 92.2%; Score 107; DB 1; Length 37;
Best Local Similarity 95.2%; Pred. No. 1e-09;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KPSYOGGPNVDFEEDTLPK 21
|||||
Db 16 KPSYOGGPNVDFEEDTLPK 36

RESULT 4
US-08-294-189-8
; Sequence 8, Application US/08294189
; Patent No. 5707822
; GENERAL INFORMATION:
; APPLICANT: Fischetti, Vincent A.
; APPLICANT: Rakonjac, Jasna
; APPLICANT: Robbins, John
; TITLE OF INVENTION: GENE SERUM OPACITY FACTOR
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack Avenue
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Releasee #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/294,189
FILING DATE: 22-AUG-1994

CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Reg., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-118
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 487-5800
TELEFAX: 201 343-1684
TELEX: 133521
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
ORGANISM: Streptococcus pyogenes
STRAIN: D734
INDIVIDUAL ISOLATE: 22
IMMEDIATE SOURCE:
CLONE: SAU3a
US-08-294-189-8
Query Match 92.2%; Score 107; DB 1; Length 38;
Best Local Similarity 95.2%; Pred. No. 1.1e-09;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 KPSYQFGGNSVDFEEDTLPK 21
Db 10 KPSYQFGGHSVDFEEDTLPK 30
RESULT 5
US-08-729-767-5.
Sequence 5, Application US/08729767
Patent No. 5770702
GENERAL INFORMATION:
APPLICANT: HOOK, Magnus
APPLICANT: LINDBERG, Martin Kjell
APPLICANT: SIGNAS, Lars Christer
APPLICANT: WADSTROM, Torkel Mikael
APPLICANT: FROMAN, Gunnar
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN AS WELL AS
TITLE OF INVENTION: ITS PREPARATION
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Burns, Doane, Swecker & Mathis, L.L.P.
STREET: P.O. Box 1404
CITY: Alexandria
STATE: Virginia
COUNTRY: United States
ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/729,767
FILING DATE: 07-OCT-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/259,000
FILING DATE: 13-JUN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/007,817
FILING DATE: 22-JAN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/201,028
FILING DATE: 01-JUN-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: SE 8702272-9

FILING DATE: 01-JUN-1987
ATTORNEY/AGENT INFORMATION:
NAME: McGowan, Malcolm K.
REGISTRATION NUMBER: 39,300
REFERENCE/DOCKET NUMBER: 012889-036
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-729-767-5
Query Match 92.2%; Score 107; DB 1; Length 38;
Best Local Similarity 95.2%; Pred. No. 1.1e-09;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 KPSYQFGGNSVDFEEDTLPK 21
Db 17 KPSYQFGGHSVDFEEDTLPK 37
RESULT 6
US-08-259-000-3
Sequence 3, Application US/08259000
Patent No. 5571514
GENERAL INFORMATION:
APPLICANT: HOOK, Magnus
APPLICANT: LINDBERG, Martin Kjell
APPLICANT: SIGNAS, Lars Christer
APPLICANT: WADSTROM, Torkel Mikael
APPLICANT: FROMAN, Gunnar
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN AS WELL AS
TITLE OF INVENTION: ITS PREPARATION
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Burns, Doane, Swecker & Mathis
STREET: P.O. Box 1404
CITY: Alexandria
STATE: Virginia
COUNTRY: United States
ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/259,000
FILING DATE: 13-JUN-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: SE 8702272-9
FILING DATE: 01-JUN-1987
ATTORNEY/AGENT INFORMATION:
NAME: Meuth, Donna M
REGISTRATION NUMBER: 36,607
REFERENCE/DOCKET NUMBER: 012885-062
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 114 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-259-000-3

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Query Match      92.2%; Score 107; DB 1; Length 114;
Best Local Similarity 95.2%; Pred. No. 3.7e-09;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 KPSYQFGHNSVDFEDTLPK 21
      ||||| ||||| ||||| |||||
Db      93 KPSYQFGHNSVDFEDTLPK 113

RESULT 7
US-08-856-253-8
; Sequence 8, Application US/08856253
; Patent No. 6238214
; GENERAL INFORMATION:
; APPLICANT: Hook, Magnus
; APPLICANT: Patti, Joseph M.
; APPLICANT: House-Pompeo, Karen
; APPLICANT: Sthanam, Narayana
; APPLICANT: Symersky, Jindrich
; TITLE OF INVENTION: COLLAGEN BINDING PROTEIN COMPOSITIONS
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: U.S.
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/856,253
; FILING DATE: Concurrently Herewith
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/017,678
; FILING DATE: 16-MAY-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Kitchell, Barbara S.
; REGISTRATION NUMBER: 33,928
; REFERENCE/DOCKET NUMBER: TAMK:193
; TELEPHONE: (512) 418-3000
; TELEFAX: (512) 474-7577
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 139 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
US-08-856-253-8

Query Match      92.2%; Score 107; DB 3; Length 139;
Best Local Similarity 95.2%; Pred. No. 4.6e-09;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 KPSYQFGHNSVDFEDTLPK 21
      ||||| ||||| ||||| |||||
Db      107 KPSYQFGHNSVDFEDTLPK 127

RESULT 8
US-08-459-135A-12
; Sequence 12, Application US/08459135A
; Patent No. 5955078
; GENERAL INFORMATION:
; APPLICANT: BURHAM, Martin Karl Russel
; APPLICANT: CHOPRA, Ian
US-08-459-135A-12

APPLICANT: CRITCHLEY, Ian Alfred
; APPLICANT: KNOWLES, David Justin Charles
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN: MONOCLONAL ANTIBODY AND THEIR US
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corporation
; STREET: 709 Swedeland Road
; CITY: King of Prussia
; STATE: PA
; COUNTRY: U.S.A.
; ZIP: 19406-0939
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: DOS
; SOFTWARE: Fastseq, Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/459,135A
; FILING DATE: 02-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB/94/00215
; FILING DATE: 04-Feb-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Gimm, Edward R.
; REGISTRATION NUMBER: 38,891
; REFERENCE/DOCKET NUMBER: P30591C2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-270-4478
; TELEFAX: 610-270-5090
; TELEX:
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 178 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Protein
US-08-459-135A-12

Query Match      92.2%; Score 107; DB 2; Length 178;
Best Local Similarity 95.2%; Pred. No. 6.1e-09;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 KPSYQFGHNSVDFEDTLPK 21
      ||||| ||||| ||||| |||||
Db      93 KPSYQFGHNSVDFEDTLPK 113

RESULT 9
US-08-495-559-12
; Sequence 12, Application US/08495559A
; Patent No. 6054572
; GENERAL INFORMATION:
; APPLICANT: BURHAM, Martin Karl Russel
; APPLICANT: CHOPRA, Ian
; APPLICANT: CRITCHLEY, Ian Alfred
; APPLICANT: KNOWLES, David Justin Charles
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN: MONOCLONAL
; TITLE OF INVENTION: ANTIBODY AND THEIR USE IN PREVENTING BACTERIAL ADHESION
; FILE REFERENCE: P30591
; CURRENT APPLICATION NUMBER: US/08/495,559A
; CURRENT FILING DATE: 1995-08-03
; EARLIER APPLICATION NUMBER: GB 9302289.5
; EARLIER FILING DATE: 1993-02-05
; EARLIER APPLICATION NUMBER: GB 9321592.9
; EARLIER FILING DATE: 1993-10-20
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: Fastseq for windows Version 3.0
; SEQ ID NO 12
; LENGTH: 178
; TYPE: PRT
```

ORGANISM: Staphylococcus aureus
US-08-495-559-12

Query Match 92.2% Score 107, DB 3; Length 178;
Best Local Similarity 95.2% Pred. No. 6.1e-09;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KPSYFGGPNVDFEEDTLPK 21
|||||
DB 93 KPSYFGGPNVDFEEDTLPK 113

RESULT 10

US-08-956-171E-5254
Sequence 5254, Application US/08956171E
Patent No. 6593114
GENERAL INFORMATION:
APPLICANT: Charles Kunsch
Gil H. Choi
Patrick S. Dillon
Craig A. Rosen
Steven C. Barash
Michael R. Fannon
TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
NUMBER OF SEQUENCES: 5256
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COUNTRY: USA
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/956,171E
FILING DATE: 20-Oct-1997
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/009,861
FILING DATE: January 5, 1996
APPLICATION NUMBER: 08/781,986
FILING DATE: January 3, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Mark J. Hyman
REGISTRATION/DOCKET NUMBER: 46,789
TELEPHONE: (240) 314-1224
TELEFAX: (301) 309-8439
INFORMATION FOR SEQ ID NO: 5254:
SEQUENCE CHARACTERISTICS:
LENGTH: 1027 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 5254:
US-08-956-171E-5254

Query Match 92.2% Score 107, DB 4; Length 1027;
Best Local Similarity 95.2% Pred. No. 4.3e-08;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KPSYFGGPNVDFEEDTLPK 21
|||||
DB 846 KPSYFGGPNVDFEEDTLPK 866

RESULT 11

US-08-781-986A-5254
Sequence 5254, Application US/08781986A
Patent No. 6737248
GENERAL INFORMATION:

APPLICANT: Charles Kunsch
TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
NUMBER OF SEQUENCES: 5255
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COUNTRY: USA
ZIP: 20850

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage

COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/781,986A

FILING DATE:
CLASSIFICATION: 435

PRIOR APPLICATION DATA:
APPLICATION NUMBER:

FILING DATE:
ATTORNEY/AGENT INFORMATION:

NAME: Benson, Bob

REGISTRATION/DOCKET NUMBER: 30,446

TELEPHONE: (301) 309-8504

TELEFAX: (301) 309-8512

INFORMATION FOR SEQ ID NO: 5254:

SEQUENCE CHARACTERISTICS:

LENGTH: 1027 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-781-986A-5254

QY 1 KPSYFGGPNVDFEEDTLPK 21
|||||
DB 846 KPSYFGGPNVDFEEDTLPK 866

RESULT 12

US-09-010-317-14
Sequence 14, Application US/09010317
Patent No. 6685943
GENERAL INFORMATION:

APPLICANT: Hook, Magnus

APPLICANT: Patti, Joseph M.

APPLICANT: House-Pompeo, Karen L.

APPLICANT: Speziale, Pietro

APPLICANT: John, Danny

APPLICANT: McGavin, Martin J.

TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS

NUMBER OF SEQUENCES: 105

CORRESPONDENCE ADDRESS:

ADDRESSEE: Arnold, White & Durkee

STREET: P.O. Box 4433

CITY: Houston

STATE: TX

COUNTRY: USA

ZIP: 77210-4433

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAMK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-09-010-317-14

Query Match 87.9%; Score 102; DB 4; Length 21;
Best Local Similarity 95.0%; Pred. No. 3.3e-09;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 PSYOGFGNSVDFEEDTLPK 21
DB 2 PSYOGFGNSVDFEEDTLPK 21

RESULT 13
US-09-010-317-16
Sequence 16, Application US/09010317
Patent No. 6685943
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
APPLICANT: Patti, Joseph M.
APPLICANT: House-Pompeo, Karen L.
APPLICANT: Speziale, Pietro
APPLICANT: Job, Danny
APPLICANT: McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
TITLE OF INVENTION: AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAMK:189
TELECOMMUNICATION INFORMATION:

TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-09-010-317-16

Query Match 87.9%; Score 102; DB 4; Length 21;
Best Local Similarity 90.5%; Pred. No. 3.3e-09;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 KPSYOGFGNSVDFEEDTLPK 21
DB 1 KPSYOGFGNSVDFEEDTLPK 21

RESULT 14
US-09-010-317-23
Sequence 23, Application US/09010317
Patent No. 6685943
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
APPLICANT: Patti, Joseph M.
APPLICANT: House-Pompeo, Karen L.
APPLICANT: Speziale, Pietro
APPLICANT: Job, Danny
APPLICANT: McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
TITLE OF INVENTION: AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAMK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-09-010-317-23

Query Match 87.9%; Score 102; DB 4; Length 21;
Best Local Similarity 90.5%; Pred. No. 3.3e-09;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 KPSYOGFGNSVDFEEDTLPK 21

Db 1 KPSYQFGHNPVDFEEDTLPK 21

RESULT 15

US-09-010-317-33

; Sequence 33, Application US/09010317
; Patent No. 6685943

GENERAL INFORMATION:

APPLICANT: Hook, Magnus

APPLICANT: Patti, Joseph M.

APPLICANT: House-Pompeo, Karen L.

APPLICANT: Speciale, Pietro

APPLICANT: McGavin, Martin J.

TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS

TITLE OF INVENTION: AND METHODS OF USE

NUMBER OF SEQUENCES: 105

CORRESPONDENCE ADDRESS:

ADDRESSEE: Arnold, White & Durkee

STREET: P.O. Box 4433

CITY: Houston

STATE: TX

COUNTRY: USA

ZIP: 77210-4433

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: IBM PC compatible

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/010,317

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 60/036,139

FILING DATE: 21-JAN-1997

ATTORNEY/AGENT INFORMATION:

NAME: Hibler, David W.

REGISTRATION NUMBER: 41,071

REFERENCE/DOCKET NUMBER: TAMK.189

TELECOMMUNICATION INFORMATION:

TELEPHONE: 512-418-3000

TELEFAX: 512-474-7577

INFORMATION FOR SEQ ID NO: 33:

SEQUENCE CHARACTERISTICS:

LENGTH: 21 amino acids

TYPE: amino acid

STRANDEDNESS:

TOPOLOGY: linear

US-09-010-317-33

Query Match 87.9%; Score 102; DB 4; Length 21;
Best Local Similarity 95.0%; Pred. No. 3.3e-09;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KPSYQFGHNPVDFEEDTLPK 20
1 KPSYQFGHNPVDFEEDTLPK 20

Db 1 KPSYQFGHNPVDFEEDTLPK 20

Search completed: October 22, 2005, 03:51:11

Job time : 15.9358 secs

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OM protein - protein search, using sw model

Run on: October 22, 2005, 10:49:15 ; Search time 59.2367 Seconds
(without alignments)
148.005 Million cell updates/sec

Title: US-10-731-238-21

Sequence: 1 KPSYQFGPNVDFEEDLPK 21

Scoring table: BLOSUM62
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Searched: 1862951 seqs, 417491010 residues

Total number of hits satisfying chosen parameters: 1862951

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database:

Published Applications AA:
1: /cgn2_6/prodata/2/pubppa/US07_PUBCOMB.pep:*
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3: /cgn2_6/prodata/2/pubppa/US06_NEW_PUB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	116	100.0	21	US-10-731-238-21	Sequence 21, Appl1
2	107	92.2	21	US-10-731-238-9	Sequence 9, Appl1
3	107	92.2	37	US-11-066-697-1134	Sequence 1134, Ap
4	107	92.2	139	US-09-813-820-8	Sequence 8, Appl1
5	107	92.2	1018	US-09-815-242-5797	Sequence 5797, Ap
6	107	92.2	1018	US-09-815-242-12838	Sequence 12838, A
7	107	92.2	1018	US-10-470-048B-68	Sequence 68, Appl
8	107	92.2	1027	US-08-781-986A-5254	Sequence 5254, Ap
9	107	92.2	1027	US-10-329-624-5254	Sequence 5254, Ap
10	104	89.7	961	US-10-282-122A-43778	Sequence 43778, A
11	104	89.7	978	US-09-815-242-5456	Sequence 5456, Ap

12	104	89.7	1001	US-09-815-242-12686	Sequence 12686, A
13	104	89.7	1038	US-10-282-122A-43827	Sequence 43827, A
14	102	87.9	21	US-10-731-238-14	Sequence 14, Appl
15	102	87.9	21	US-10-731-238-16	Sequence 16, Appl
16	102	87.9	21	US-10-731-238-23	Sequence 23, Appl
17	102	87.9	21	US-10-731-238-33	Sequence 33, Appl
18	101	87.1	21	US-10-731-238-18	Sequence 18, Appl
19	101	87.1	21	US-10-731-238-24	Sequence 24, Appl
20	101	87.1	21	US-10-731-238-27	Sequence 27, Appl
21	101	87.1	21	US-10-731-238-28	Sequence 28, Appl
22	101	87.1	21	US-10-731-238-30	Sequence 30, Appl
23	100	86.2	21	US-10-731-238-25	Sequence 25, Appl
24	100	86.2	21	US-10-731-238-29	Sequence 29, Appl
25	100	86.2	21	US-10-731-238-31	Sequence 31, Appl
26	100	86.2	8	US-08-901-062-1	Sequence 1, Appl
27	100	86.2	559	US-08-781-986A-5251	Sequence 5251, Ap
28	100	86.2	559	US-10-329-624-5251	Sequence 5251, Ap
29	100	86.2	940	US-10-470-048B-424	Sequence 424, Ap
30	100	86.2	948	US-10-470-048B-69	Sequence 69, Appl
31	99	85.3	21	US-10-731-238-10	Sequence 10, Appl
32	99	85.3	21	US-10-731-238-15	Sequence 15, Appl
33	99	85.3	21	US-10-731-238-19	Sequence 19, Appl
34	99	85.3	21	US-10-731-238-20	Sequence 20, Appl
35	99	85.3	21	US-10-731-238-22	Sequence 22, Appl
36	99	85.3	21	US-10-731-238-32	Sequence 32, Appl
37	97	83.6	21	US-10-731-238-13	Sequence 13, Appl
38	97	83.6	21	US-10-731-238-17	Sequence 17, Appl
39	97	83.6	21	US-10-731-238-19	Sequence 19, Appl
40	97	83.6	21	US-10-731-238-26	Sequence 26, Appl
41	68	58.6	14	US-10-731-238-61	Sequence 34, Appl
42	54.5	47.0	781	US-10-437-963-204716	Sequence 61, Appl
43	54.5	47.0	969	US-10-437-963-204719	Sequence 204719, Sequence 67597, A
44	54	46.6	30	US-10-282-122A-67597	Sequence 101, App
45	53	45.7	10	US-10-731-238-101	

ALIGNMENTS

RESULT 1
US-10-731-238-21
Sequence 21, Application US/1071238
Publication No. US20050123552A1
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
Patel, Joseph M.
House-Pompeo, Karen L.
Speziale, Pietro
Joh, Danny
McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/731,238
FILING DATE: 10-Dec-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE: 21-Jan-1998
APPLICATION NUMBER: US 60/036,139

FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAMK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 21:
US-10-731-238-21

Query Match 100.0%; Score 116; DB 18; Length 21;
Best Local Similarity 100.0%; Pred. No. 6, 2e-11;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 KPSYQFGGNSVDPEDTLPK 21

RESULT 2
US-10-731-238-9
Sequence 9, Application US/10731238
Publication No. US20050123552A1
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
Patti, Joseph M.
House-Pompeo, Karen L.
Speziale, Pietro
John, Danny
McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/731,238
FILING DATE: 10-Dec-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE: 21-Jan-1998
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAMK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>

TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 9:
US-10-731-238-9

Query Match 92.2%; Score 107; DB 18; Length 21;
Best Local Similarity 95.2%; Pred. No. 1, 6e-09;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KPSYQFGGNSVDPEDTLPK 21
DB 1 KPSYQFGGNSVDPEDTLPK 21

RESULT 3
US-11-066-697-1134
Sequence 1134, Application US/11066697
Publication No. US20050187159A1
GENERAL INFORMATION:
APPLICANT: Bridon, Dominique P.
APPLICANT: Ezrin, Alan M.
APPLICANT: Milner, Peter G.
APPLICANT: Holmes, Darren L.
APPLICANT: Thibaudau, Karen
TITLE OF INVENTION: PROTECTION OF ENDOGENOUS THERAPEUTIC PEPTIDES FROM
PEPTIDASE ACTIVITY THROUGH CONJUGATION TO BLOOD
FILE REFERENCE: 500862002301
CURRENT APPLICATION NUMBER: US/11/066,697
CURRENT FILING DATE: 2005-02-25
PRIOR APPLICATION NUMBER: 09/657,276
PRIOR FILING DATE: 2000-09-07
PRIOR APPLICATION NUMBER: 60/153,406
PRIOR FILING DATE: 1999-09-10
PRIOR APPLICATION NUMBER: 60/159,783
PRIOR FILING DATE: 1999-10-15
NUMBER OF SEQ ID NOS: 1617
SOFTWARE: Patent In Ver. 2.1
SEQ ID NO 1134
LENGTH: 37
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-11-066-697-1134

Query Match 92.2%; Score 107; DB 20; Length 37;
Best Local Similarity 95.2%; Pred. No. 3e-09;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KPSYQFGGNSVDPEDTLPK 21
DB 16 KPSYQFGGNSVDPEDTLPK 36

RESULT 4
US-09-813-820-8
Sequence 8, Application US/09813820
Patent No. US20020102262A1
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
Patti, Joseph M.
House-Pompeo, Karen
Schanam, Narayana
Symersky, Jindrich
TITLE OF INVENTION: COLLAGEN BINDING PROTEIN COMPOSITIONS
AND METHODS OF USE
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: Texas

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; COUNTRY: U.S.
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/813,820
; FILING DATE: 22-Mar-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/856,253
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Kitchell, Barbara S.
; REGISTRATION NUMBER: 33,928
; REFERENCE/DOCKET NUMBER: TANK:193
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (512) 418-3000
; TELEFAX: (512) 474-7577
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 139 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-09-813-820-8

Query Match      92.2%; Score 107; DB 9; Length 139;
Best Local Similarity 95.2%; Pred. No. 1.3e-08;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1 KPSYQFGGNSVDPEEDTLPK 21
Db      107 KPSYQFGGNSVDPEEDTLPK 127

RESULT 5
US-09-815-242-5797
; Sequence 5797, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; FILE REFERENCE: ELITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version 4.0

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; SEQ ID NO 5797
; LENGTH: 1018
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-09-815-242-5797

Query Match      92.2%; Score 107; DB 9; Length 1018;
Best Local Similarity 95.2%; Pred. No. 1.2e-07;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1 KPSYQFGGNSVDPEEDTLPK 21
Db      837 KPSYQFGGNSVDPEEDTLPK 857

RESULT 6
US-09-815-242-12838
; Sequence 12838, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; FILE REFERENCE: ELITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12838
; LENGTH: 1018
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-09-815-242-12838

Query Match      92.2%; Score 107; DB 9; Length 1018;
Best Local Similarity 95.2%; Pred. No. 1.2e-07;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1 KPSYQFGGNSVDPEEDTLPK 21
Db      837 KPSYQFGGNSVDPEEDTLPK 857

RESULT 7
US-10-470-048B-68
; Sequence 68, Application US/10470048B
; Publication No. US2005003744A1
; GENERAL INFORMATION:
; APPLICANT: MEINKE ET AL.
; TITLE OF INVENTION: A METHOD FOR IDENTIFICATION, ISOLATION AND PRODUCTION OF
; FILE REFERENCE: SONN.03505

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;; CURRENT APPLICATION NUMBER: US/10/470,048B
;; CURRENT FILING DATE: 2003-07-25
;; NUMBER OF SEQ ID NOS: 603
;; SOFTWARE: PatentIn version 3.1
;; SEQ ID NO: 68
;; LENGTH: 1018
;; TYPE: PRF
;; ORGANISM: Staphylococcus aureus
US-10-470-048B-68

Query Match 92.2%; Score 107; DB 17; Length 1018;
Best Local Similarity 95.2%; Pred. No. 1.2e-07;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KPSYQFGGNSVDPEEDTLPK 21
DB 837 KPSYQFGGNSVDPEEDTLPK 857

RESULT 8
US-08-781-986A-5254
; Sequence 5254, Application US/08781986A
; Publication No. US20030054436A1
; GENERAL INFORMATION:
; APPLICANT: Charles Kunsch
; TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
; NUMBER OF SEQUENCES: 5255
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4MB storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/781,986A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Benson, Bob
; REGISTRATION NUMBER: 30,446
; REFERENCE/DOCKET NUMBER: PB248PP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 5254:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1027 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-781-986A-5254

Query Match 92.2%; Score 107; DB 8; Length 1027;
Best Local Similarity 95.2%; Pred. No. 1.2e-07;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KPSYQFGGNSVDPEEDTLPK 21
DB 846 KPSYQFGGNSVDPEEDTLPK 866

RESULT 9
US-10-329-624-5254

;; Sequence 5254, Application US/10329624
;; Publication No. US20040043037A1
;; GENERAL INFORMATION:
;; APPLICANT: Charles Kunsch
;; Gail H. Choi
;; Patrick S. Dillon
;; Craig A. Rosen
;; Steven C. Barash
;; Michael R. Fannon
; TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
; NUMBER OF SEQUENCES: 5256
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4MB storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/329,624
; FILING DATE: 27-Dec-2002
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/956,171
; FILING DATE: October 20, 1997
; APPLICATION NUMBER: 60/009,861
; FILING DATE: January 5, 1996
; APPLICATION NUMBER: 08/781,986
; FILING DATE: January 3, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Mark J. Hyman
; REGISTRATION NUMBER: 46,789
; REFERENCE/DOCKET NUMBER: PB248P1D1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (240) 314-1224
; TELEFAX: (301) 309-8439
; INFORMATION FOR SEQ ID NO: 5254:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1027 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 5254:
US-10-329-624-5254

Query Match 92.2%; Score 107; DB 15; Length 1027;
Best Local Similarity 95.2%; Pred. No. 1.2e-07;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KPSYQFGGNSVDPEEDTLPK 21
DB 846 KPSYQFGGNSVDPEEDTLPK 866

RESULT 10
US-10-282-122A-43778
; Sequence 43778, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zykkind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant

```
APPLICANT: Yamamoto, Robert
APPLICANT: Foreyth, R.
APPLICANT: Xu, H.
TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REFERENCE: ELITRA.034A
CURRENT FILING DATE: 2003-02-20
PRIORITY APPLICATION NUMBER: US/10/282.122A
PRIORITY FILING DATE: 2000-03-21
PRIORITY APPLICATION NUMBER: 60/191,078
PRIORITY FILING DATE: 2000-05-23
PRIORITY APPLICATION NUMBER: 60/207,727
PRIORITY FILING DATE: 2000-05-26
PRIORITY APPLICATION NUMBER: 60/230,335
PRIORITY FILING DATE: 2000-09-06
PRIORITY APPLICATION NUMBER: 60/230,347
PRIORITY FILING DATE: 2000-09-09
PRIORITY APPLICATION NUMBER: 60/242,578
PRIORITY FILING DATE: 2000-10-23
PRIORITY APPLICATION NUMBER: 60/253,625
PRIORITY FILING DATE: 2000-11-27
PRIORITY APPLICATION NUMBER: 60/257,931
PRIORITY FILING DATE: 2000-12-22
PRIORITY APPLICATION NUMBER: 60/267,636
PRIORITY FILING DATE: 2001-02-09
PRIORITY APPLICATION NUMBER: 60/269,308
PRIORITY FILING DATE: 2001-02-16
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 78614
SOFTWARE: PatentIn version 3.1
SEQ ID NO 43778
LENGTH: 961
TYPE: PRT
ORGANISM: Staphylococcus aureus
US-10-282-122A-43778

Query Match      89.7%; Score 104; DB 15; Length 961;
Best Local Similarity 90.5%; Pred. No. 3.3e-07;
Matches 19; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1 KPSYFGGPNVDFEEDTLPK 21
Db      784 KPNYFGGHNVSDFEEDTLPK 804

RESULT 11
US-09-815-242-5456
Sequence 5456, Application US/09815242
Patent No. US20020061569A1
GENERAL INFORMATION:
APPLICANT: Haeselbeck, Robert
APPLICANT: Ohlsen, Karl L.
APPLICANT: Zykkind, Judith W.
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John D.
APPLICANT: Carr, Grant J.
APPLICANT: Yamamoto, Robert T.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in
FILE REFERENCE: ELITRA.011A
CURRENT FILING DATE: 2001-03-21
PRIORITY APPLICATION NUMBER: US/09/815,242
PRIORITY FILING DATE: 2000-03-21
PRIORITY APPLICATION NUMBER: 60/191,078
PRIORITY FILING DATE: 2000-03-21
PRIORITY APPLICATION NUMBER: 60/206,848
PRIORITY FILING DATE: 2000-05-23
PRIORITY APPLICATION NUMBER: 60/207,727
PRIORITY FILING DATE: 2000-05-26
PRIORITY APPLICATION NUMBER: 60/242,578
PRIORITY FILING DATE: 2000-10-23
PRIORITY APPLICATION NUMBER: 60/253,625
PRIORITY FILING DATE: 2000-11-27
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PRIORITY APPLICATION NUMBER: 60/257,931
PRIORITY FILING DATE: 2000-12-22
PRIORITY APPLICATION NUMBER: 60/269,308
PRIORITY FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 5456
LENGTH: 978
TYPE: PRT
ORGANISM: Staphylococcus aureus
US-09-815-242-5456

Query Match      89.7%; Score 104; DB 9; Length 978;
Best Local Similarity 90.5%; Pred. No. 3.3e-07;
Matches 19; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1 KPSYFGGPNVDFEEDTLPK 21
Db      815 KPNYFGGHNVSDFEEDTLPK 835

RESULT 12
US-09-815-242-12686
Sequence 12686, Application US/09815242
Patent No. US20020061569A1
GENERAL INFORMATION:
APPLICANT: Haeselbeck, Robert
APPLICANT: Ohlsen, Karl L.
APPLICANT: Zykkind, Judith W.
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John D.
APPLICANT: Carr, Grant J.
APPLICANT: Yamamoto, Robert T.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in
FILE REFERENCE: ELITRA.011A
CURRENT FILING DATE: 2001-03-21
PRIORITY APPLICATION NUMBER: 60/191,078
PRIORITY FILING DATE: 2000-03-21
PRIORITY APPLICATION NUMBER: 60/206,848
PRIORITY FILING DATE: 2000-05-23
PRIORITY APPLICATION NUMBER: 60/207,727
PRIORITY FILING DATE: 2000-05-26
PRIORITY APPLICATION NUMBER: 60/242,578
PRIORITY FILING DATE: 2000-10-23
PRIORITY APPLICATION NUMBER: 60/253,625
PRIORITY FILING DATE: 2000-11-27
PRIORITY APPLICATION NUMBER: 60/257,931
PRIORITY FILING DATE: 2000-12-22
PRIORITY APPLICATION NUMBER: 60/269,308
PRIORITY FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 12686
LENGTH: 1001
TYPE: PRT
ORGANISM: Staphylococcus aureus
US-09-815-242-12686

Query Match      89.7%; Score 104; DB 9; Length 1001;
Best Local Similarity 90.5%; Pred. No. 3.4e-07;
Matches 19; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1 KPSYFGGPNVDFEEDTLPK 21
Db      838 KPNYFGGHNVSDFEEDTLPK 858

RESULT 13
US-10-282-122A-43827
Sequence 43827, Application US/10282122A
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; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haseibeck, Robert
; APPLICANT: Ohlsen, Karl
; APPLICANT: Zvekind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 43827
; LENGTH: 1038
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
; US-10-282-122A-43827

Query Match      89.7%; Score 104; DB 15; Length 1038;
Best Local Similarity 90.5%; Pred. No. 3.5e-07;
Matches 19; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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      833 KPNYFGGHNVDFFEDTLPK 853

RESULT 14
US-10-731-238-14
; Sequence 14, Application US/10731238
; Publication No. US20050123552A1
; GENERAL INFORMATION:
; APPLICANT: Hook, Magnus
; APPLICANT: Patti, Joseph M.
; APPLICANT: House-Pompeo, Karen L.
; APPLICANT: Speziale, Pietro
; APPLICANT: Joh, Danny
; APPLICANT: McGavin, Martin J.
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
; AND METHODS OF USE
; NUMBER OF SEQUENCES: 105
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Arnold, White & Durkee
; STREET: P.O. Box 4433
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; CITY: Houston
; STATE: TX
; COUNTRY: USA
; ZIP: 77210-4433
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/731,238
; FILING DATE: 10-Dec-2003
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/010,317
; FILING DATE: 21-Jan-1998
; APPLICATION NUMBER: US 60/036,139
; FILING DATE: 21-Jan-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Hibler, David W.
; REGISTRATION NUMBER: 41,071
; REFERENCE/DOCKET NUMBER: TANK:189
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 512-418-3000
; TELEFAX: 512-474-7577
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 14:
US-10-731-238-14

Query Match      87.9%; Score 102; DB 18; Length 21;
Best Local Similarity 95.0%; Pred. No. 9.5e-09;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      2 PSYFGGPNVDFEEDTLPK 21
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RESULT 15
US-10-731-238-15
; Sequence 16, Application US/10731238
; Publication No. US20050123552A1
; GENERAL INFORMATION:
; APPLICANT: Hook, Magnus
; APPLICANT: Patti, Joseph M.
; APPLICANT: House-Pompeo, Karen L.
; APPLICANT: Speziale, Pietro
; APPLICANT: Joh, Danny
; APPLICANT: McGavin, Martin J.
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
; AND METHODS OF USE
; NUMBER OF SEQUENCES: 105
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: TX
; COUNTRY: USA
; ZIP: 77210-4433
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/731,238
; FILING DATE: 10-Dec-2003
; CLASSIFICATION: <Unknown>
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PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/09/010.317
 FILING DATE: 21-Jan-1998
 APPLICATION NUMBER: US 60/036.139
 FILING DATE: 21-JAN-1997
 ATTORNEY/AGENT INFORMATION:
 NAME: Hibler, David W.
 REGISTRATION NUMBER: 41,071
 REFERENCE/DOCKET NUMBER: TAMK:189
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 512-418-3000
 TELEFAX: 512-474-7577
 INFORMATION FOR SEQ ID NO: 16:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 21 amino acids
 TYPE: amino acid
 STRANDEDNESS: <Unknown>
 TOPOLOGY: linear
 SEQUENCE DESCRIPTION: SEQ ID NO: 16:
 US-10-731-238-16

Query March 87.9%; Score 102; DB 18; Length 21;
 Best Local Similarity 90.5%; Pred. No. 9.5e-09;
 Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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 Db 1 KPYQFGGPNVDFEEDTLPK 21

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GenCore version 5.1.6
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Title: US-10-731-238-21

Sequence: 1 KPSYQPGGNSVDFEEDLPK 21

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	107	92.2	37	20	US-09-623-548A-1134	Sequence 1134, Ap
2	107	92.2	37	20	US-09-657-276-1134	Sequence 1134, Ap
3	107	92.2	139	23	US-09-813-820-8	Sequence 8, Appl
4	107	92.2	178	13	US-08-970-963A-12	Sequence 12, Appl
5	107	92.2	1018	13	PCT-US02-03981-5797	Sequence 5797, Ap
6	107	92.2	1018	1	PCT-US02-03981-15838	Sequence 12838, A
7	107	92.2	1018	23	US-09-815-244-5797	Sequence 5797, Ap
8	107	92.2	1018	23	US-09-815-244-12838	Sequence 12838, A
9	107	92.2	1018	26	US-10-072-851-5797	Sequence 5797, Ap
10	107	92.2	1018	26	US-10-072-851-12838	Sequence 12838, A
11	107	92.2	1018	30	US-10-470-046B-68	Sequence 68, Appl
12	107	92.2	1018	37	US-09-242-578-1037	Sequence 1037, Ap
13	107	92.2	1018	37	US-09-253-625-2381	Sequence 2381, Ap
14	107	92.2	1018	37	US-09-257-931-3375	Sequence 3375, Ap
15	107	92.2	1018	37	US-09-329-624-5254	Sequence 5254, Ap
16	107	92.2	1027	29	US-10-807-556-5254	Sequence 5254, Ap
17	107	92.2	1027	34	US-10-807-556-5254	Sequence 5254, Ap
18	104	89.7	428	20	US-09-611-529-7150	Sequence 7150, Ap
19	104	89.7	428	25	US-09-950-084-7150	Sequence 7150, Ap
20	104	89.7	883	12	US-08-827-356-5488	Sequence 5488, Ap
21	104	89.7	961	1	PCT-US02-09107B-43778	Sequence 43778, A
22	104	89.7	961	28	US-10-282-122A-43778	Sequence 43778, A
23	104	89.7	978	1	PCT-US02-03987-5456	Sequence 5456, Ap
24	104	89.7	978	23	US-09-815-242-5456	Sequence 5456, Ap
25	104	89.7	978	26	US-10-072-851-5456	Sequence 824, App
26	104	89.7	978	37	US-09-242-578-824	Sequence 2168, Ap
27	104	89.7	978	37	US-09-253-625-2168	Sequence 3000, Ap
28	104	89.7	978	37	US-09-257-931-3000	Sequence 4021, Ap
29	104	89.7	978	37	US-09-269-308-4021	Sequence 12686, A
30	104	89.7	1001	1	PCT-US02-03987-12686	Sequence 12686, A
31	104	89.7	1001	23	US-09-815-242-12686	Sequence 12686, A
32	104	89.7	1001	26	US-10-072-851-12686	Sequence 42827, A
33	104	89.7	1038	1	PCT-US02-09107B-43827	Sequence 43827, A
34	104	89.7	1038	28	US-10-282-122A-43827	Sequence 43827, A
35	104	89.7	1047	20	US-09-611-529-6425	Sequence 6425, Ap
36	104	89.7	1047	25	US-09-950-084-6425	Sequence 6425, Ap
37	100	86.2	130	8	US-08-458-947-7	Sequence 7, Appl
38	100	86.2	130	8	US-08-458-947-8	Sequence 8, Appl
39	100	86.2	130	8	US-08-459-135-7	Sequence 7, Appl
40	100	86.2	130	8	US-08-459-135-8	Sequence 8, Appl
41	100	86.2	130	8	US-08-495-559-7	Sequence 7, Appl
42	100	86.2	130	8	US-08-495-559-8	Sequence 8, Appl
43	100	86.2	130	13	US-08-970-963-7	Sequence 7, Appl
44	100	86.2	130	13	US-08-970-963-8	Sequence 8, Appl
45	100	86.2	130	13	US-08-970-963A-7	Sequence 7, Appl

ALIGNMENTS

RESULT 1
US-09-623-548A-1134
Sequence 1134, Application US/09623548A
GENERAL INFORMATION:
APPLICANT: ConjuChem, Inc.
APPLICANT: Bridon, Dominique
APPLICANT: Ezrin, Alan
APPLICANT: Milner, Peter
APPLICANT: Holmes, Darren
TITLE OF INVENTION: THABAIDEAU, Karen
TITLE OF INVENTION: PROTECTION OF ENDOGENOUS THERAPEUTIC PEPTIDES FROM
TITLE OF INVENTION: PEPTIDASE ACTIVITY THROUGH COMMUNICATION TO BLOOD
TITLE OF INVENTION: COMPONENTS
FILE REFERENCE: 2110
CURRENT APPLICATION NUMBER: US/09/623, 548A
CURRENT FILING DATE: 2000-09-05
PRIOR APPLICATION NUMBER: 60/134,406
PRIOR FILING DATE: 1999-05-17
PRIOR APPLICATION NUMBER: 60/153,406

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; PRIOR FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: 60/159,783
; PRIOR FILING DATE: 1999-10-18
; NUMBER OF SEQ ID NOS: 1617
; SOFTWARE: Patentln Ver. 2.1
; SEQ ID NO 1134
; LENGTH: 37
; TYPE: PRF
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-623-548A-1134

Query Match          92.2%; Score 107; DB 20; Length 37;
Best Local Similarity 95.2%; Pred. No. 3.2e-09;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KPSYOGGNSVDFFEDTLPK 21
DB 16 KPSYOGGNSVDFFEDTLPK 36

RESULT 2
US-09-657-276-1134
; Sequence 1134, Application US/09657276
; GENERAL INFORMATION:
; APPLICANT: Conjuchem, Inc.
; APPLICANT: Bridon, Dominique
; APPLICANT: Ezrin, Alan
; APPLICANT: Milner, Peter
; APPLICANT: Holmes, Darren
; APPLICANT: Thibudeau, Karen
; TITLE OF INVENTION: PROTECTION OF ENDOGENOUS THERAPEUTIC PEPTIDES FROM
; TITLE OF INVENTION: PEPTIDASE ACTIVITY THROUGH CONJUGATION TO BLOOD
; FILE REFERENCE: 2110
; CURRENT APPLICATION NUMBER: US/09/657,276
; CURRENT FILING DATE: 2000-09-07
; PRIOR APPLICATION NUMBER: 60/134,406
; PRIOR FILING DATE: 1999-05-17
; PRIOR APPLICATION NUMBER: 60/153,406
; PRIOR FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: 60/159,783
; PRIOR FILING DATE: 1999-10-18
; NUMBER OF SEQ ID NOS: 1617
; SOFTWARE: Patentln Ver. 2.1
; SEQ ID NO 1134
; LENGTH: 37
; TYPE: PRF
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-657-276-1134

Query Match          92.2%; Score 107; DB 20; Length 37;
Best Local Similarity 95.2%; Pred. No. 3.2e-09;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KPSYOGGNSVDFFEDTLPK 21
DB 16 KPSYOGGNSVDFFEDTLPK 36

RESULT 3
US-09-813-820-8
; Sequence 8, Application US/09813820
; GENERAL INFORMATION:
; APPLICANT: Hook, Magnus
; APPLICANT: Patti, Joseph M.
; APPLICANT: House-Pompeo, Karen
; APPLICANT: Sthanam, Narayana
```

```

; Symersky, Jindrich
; TITLE OF INVENTION: COLLAGEN BINDING PROTEIN COMPOSITIONS
; AND METHODS OF USE
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: U.S.
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentln Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE: 22-Mar-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/856,253
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Kitchell, Barbara S.
; REGISTRATION NUMBER: 33,928
; REFERENCE/DOCKET NUMBER: TANK:193
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (512) 418-5000
; TELEFAX: (512) 474-7577
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 139 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 8:

US-09-813-820-8

Query Match          92.2%; Score 107; DB 23; Length 139;
Best Local Similarity 95.2%; Pred. No. 1.7e-08;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KPSYOGGNSVDFFEDTLPK 21
DB 107 KPSYOGGNSVDFFEDTLPK 127

RESULT 4
US-08-970-963A-12
; Sequence 12, Application US/08970963A
; GENERAL INFORMATION:
; APPLICANT: BURNHAM, Martin Karl Russel
; APPLICANT: CHOPRA, Ian
; APPLICANT: CRITCHLEY, Ian Alfred
; APPLICANT: KNOWLES, David Justen Charles
; TITLE OF INVENTION: MONOCLONAL ANTIBODY AND THEIR USE IN PREVENTING
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corporation
; STREET: 709 Swedeland Road
; CITY: King of Prussia
; STATE: PA
; COUNTRY: U.S.A.
; ZIP: 19406-0939
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: Fastseq, Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/970,963A
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/ FILING DATE: 14-NOV-1997
/ CLASSIFICATION: 530
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/458,947
/ FILING DATE: 2-JUN-1995
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Glamm, Edward R
/ REGISTRATION NUMBER: 38,891
/ REFERENCE/DOCKET NUMBER: P30591C1FWC
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 610-270-4478
/ TELEFAX: 610-270-5090
/ TELEX:
/ INFORMATION FOR SEQ ID NO: 12:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 178 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: Protein
/ US-08-970-963A-12

Query Match          92.2%; Score 107; DB 13; Length 178;
Best Local Similarity 95.2%; Pred. No. 2.3e-08;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Db 93 KPSYQFGGNSVDFEEDTLRK 113

RESULT 5
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/ Sequence 5797, Application PC/TUS0203987
/ GENERAL INFORMATION:
/ APPLICANT: Elittra Pharmaceuticals, Inc.
/ TITLE OF INVENTION: Methods for identifying the Target of a Compound which Inhibits C
/ TITLE OF INVENTION: Proliferation
/ FILE REFERENCE: ELITRA.028VPC
/ CURRENT APPLICATION NUMBER: PCT/US02/03987
/ CURRENT FILING DATE: 2002-02-02
/ PRIOR APPLICATION NUMBER: 60/267,636
/ PRIOR FILING DATE: 2001-02-09
/ NUMBER OF SEQ ID NOS: 15811
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 5797
/ LENGTH: 1018
/ TYPE: PRT
/ ORGANISM: Staphylococcus aureus
/ PCT-US02-03987-5797

Query Match          92.2%; Score 107; DB 1; Length 1018;
Best Local Similarity 95.2%; Pred. No. 2e-07;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KPSYQFGGNSVDFEEDTLRK 21
Db 837 KPSYQFGGNSVDFEEDTLRK 857

RESULT 6
PCT-US02-03987-12838
/ Sequence 12838, Application PC/TUS0203987
/ GENERAL INFORMATION:
/ APPLICANT: Elittra Pharmaceuticals, Inc.
/ TITLE OF INVENTION: Methods for identifying the Target of a Compound which Inhibits C
/ TITLE OF INVENTION: Proliferation
/ FILE REFERENCE: ELITRA.028VPC
/ CURRENT APPLICATION NUMBER: PCT/US02/03987
/ CURRENT FILING DATE: 2002-02-02
/ PRIOR APPLICATION NUMBER: 60/267,636
/ PRIOR FILING DATE: 2001-02-09
/ NUMBER OF SEQ ID NOS: 15811
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/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 12838
/ LENGTH: 1018
/ TYPE: PRT
/ ORGANISM: Staphylococcus aureus
/ PCT-US02-03987-12838

Query Match          92.2%; Score 107; DB 1; Length 1018;
Best Local Similarity 95.2%; Pred. No. 2e-07;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KPSYQFGGNSVDFEEDTLRK 21
Db 837 KPSYQFGGNSVDFEEDTLRK 857

RESULT 7
US-09-815-242-5797
/ Sequence 5797, Application US/09815242
/ GENERAL INFORMATION:
/ APPLICANT: Haselbeck, Robert
/ APPLICANT: Ohlsen, Kari L.
/ APPLICANT: Zyskind, Judith W.
/ APPLICANT: Wall, Daniel
/ APPLICANT: Trawick, John D.
/ APPLICANT: Carr, Grant J.
/ APPLICANT: Yamamoto, Robert T.
/ TITLE OF INVENTION: Identification of Essential Genes in
/ TITLE OF INVENTION: Prokaryotes
/ FILE REFERENCE: ELITRA.011A
/ CURRENT APPLICATION NUMBER: US/09/815,242
/ CURRENT FILING DATE: 2001-03-21
/ PRIOR APPLICATION NUMBER: 60/191,078
/ PRIOR FILING DATE: 2000-03-21
/ PRIOR APPLICATION NUMBER: 60/206,848
/ PRIOR FILING DATE: 2000-05-23
/ PRIOR APPLICATION NUMBER: 60/207,727
/ PRIOR FILING DATE: 2000-05-26
/ PRIOR APPLICATION NUMBER: 60/242,578
/ PRIOR FILING DATE: 2000-10-23
/ PRIOR APPLICATION NUMBER: 60/253,625
/ PRIOR FILING DATE: 2000-11-27
/ PRIOR APPLICATION NUMBER: 60/257,931
/ PRIOR FILING DATE: 2000-12-22
/ PRIOR APPLICATION NUMBER: 60/269,308
/ PRIOR FILING DATE: 2001-02-16
/ NUMBER OF SEQ ID NOS: 14110
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 5797
/ LENGTH: 1018
/ TYPE: PRT
/ ORGANISM: Staphylococcus aureus
/ US-09-815-242-5797

Query Match          92.2%; Score 107; DB 23; Length 1018;
Best Local Similarity 95.2%; Pred. No. 2e-07;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KPSYQFGGNSVDFEEDTLRK 21
Db 837 KPSYQFGGNSVDFEEDTLRK 857

RESULT 8
US-09-815-242-12838
/ Sequence 12838, Application US/09815242
/ GENERAL INFORMATION:
/ APPLICANT: Haselbeck, Robert
/ APPLICANT: Ohlsen, Kari L.
/ APPLICANT: Zyskind, Judith W.
/ APPLICANT: Wall, Daniel
/ APPLICANT: Trawick, John D.
```

```

; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; FILE REFERENCE: ELITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 12838
; LENGTH: 1018
; TYPE: PRF
; ORGANISM: Staphylococcus aureus
US-09-815-242-12838
```

```

Query Match          92.2%; Score 107; DB 23; Length 1018;
Best Local Similarity 95.2%; Pred. No. 2e-07;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
Qy      1 KPSYQFGPNSVDFEEDTLPK 21
         ||||| ||||| ||||| |||||
Db      837 KPSYQFGHNSVDFEEDTLPK 857
```

```

RESULT 9
US-10-072-851-5797
; Sequence 5797, Application US/10072851
; GENERAL INFORMATION:
; APPLICANT: Carr, Grant J.
; APPLICANT: Xu, H. Howard
; APPLICANT: Foulkes, J. Gordon
; APPLICANT: Zamudio, Carlos
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Karl L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Roemer, Terry
; APPLICANT: Jiang, Bo
; APPLICANT: Boone, Charles
; APPLICANT: Bussey, Howard
; TITLE OF INVENTION: Methods for Identifying the Target of a Compound which Inhibits C
; FILE REFERENCE: ELITRA.028A
; CURRENT APPLICATION NUMBER: US/10/072,851
; CURRENT FILING DATE: 2002-02-08
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; NUMBER OF SEQ ID NOS: 15811
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 5797
; LENGTH: 1018
; TYPE: PRF
; ORGANISM: Staphylococcus aureus
US-10-072-851-5797
```

```
Query Match          92.2%; Score 107; DB 26; Length 1018;
```

```

Best Local Similarity 95.2%; Pred. No. 2e-07;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
Qy      1 KPSYQFGPNSVDFEEDTLPK 21
         ||||| ||||| ||||| |||||
Db      837 KPSYQFGHNSVDFEEDTLPK 857
```

```

RESULT 10
US-10-072-851-12838
; Sequence 12838, Application US/10072851
; GENERAL INFORMATION:
; APPLICANT: Carr, Grant J.
; APPLICANT: Xu, H. Howard
; APPLICANT: Foulkes, J. Gordon
; APPLICANT: Zamudio, Carlos
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Karl L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Roemer, Terry
; APPLICANT: Jiang, Bo
; APPLICANT: Boone, Charles
; APPLICANT: Bussey, Howard
; TITLE OF INVENTION: Methods for Identifying the Target of a Compound which Inhibits C
; FILE REFERENCE: ELITRA.028A
; CURRENT APPLICATION NUMBER: US/10/072,851
; CURRENT FILING DATE: 2002-02-08
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; NUMBER OF SEQ ID NOS: 15811
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 12838
; LENGTH: 1018
; TYPE: PRF
; ORGANISM: Staphylococcus aureus
US-10-072-851-12838
```

```

Query Match          92.2%; Score 107; DB 26; Length 1018;
Best Local Similarity 95.2%; Pred. No. 2e-07;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
Qy      1 KPSYQFGPNSVDFEEDTLPK 21
         ||||| ||||| ||||| |||||
Db      837 KPSYQFGHNSVDFEEDTLPK 857
```

```

RESULT 11
US-10-470-048B-68
; Sequence 68, Application US/10470048B
; GENERAL INFORMATION:
; APPLICANT: MEINKE ET AL.
; TITLE OF INVENTION: A METHOD FOR IDENTIFICATION, ISOLATION AND PRODUCTION OF
; FILE REFERENCE: SONN.035US
; CURRENT APPLICATION NUMBER: US/10/470,048B
; CURRENT FILING DATE: 2003-07-25
; NUMBER OF SEQ ID NOS: 603
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 68
; LENGTH: 1018
; TYPE: PRF
; ORGANISM: Staphylococcus aureus
US-10-470-048B-68
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```

Query Match          92.2%; Score 107; DB 30; Length 1018;
Best Local Similarity 95.2%; Pred. No. 2e-07;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
Qy      1 KPSYQFGPNSVDFEEDTLPK 21
```

Db 837 KPSYQFGHNSVDFEEDTLPK 857

RESULT 12

US-60-242-578-1037
; Sequence 1037, Application US/60242578
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, R
; APPLICANT: Ohlsen, K. L.
; APPLICANT: Zysek, J. W.
; TITLE OF INVENTION: Genes identified as essential in
; FILE REFERENCE: ELITRA.017PR2
; CURRENT APPLICATION NUMBER: US/60/242,578
; CURRENT FILING DATE: 2000-10-23
; NUMBER OF SEQ ID NOS: 1057
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1037
; LENGTH: 1018
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-60-242-578-1037

Query Match 92.2%; Score 107; DB 37; Length 1018;
Best Local Similarity 95.2%; Pred. No. 2e-07;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KPSYQFGHNSVDFEEDTLPK 21
Db 837 KPSYQFGHNSVDFEEDTLPK 857

RESULT 13

US-60-253-625-2381
; Sequence 2381, Application US/60253625
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, RH
; APPLICANT: Ohlsen, KL
; APPLICANT: Zysek, JW
; APPLICANT: Trawick, JD
; APPLICANT: Wall, D
; TITLE OF INVENTION: Identification of essential genes in
; TITLE OF INVENTION: Staphylococcus aureus, Pseudomonas aeruginosa, Klebsiella
; TITLE OF INVENTION: pneumoniae and Salmonella typhimurium
; FILE REFERENCE: ELITRA.017PR3
; CURRENT APPLICATION NUMBER: US/60/253,625
; CURRENT FILING DATE: 2000-11-27
; NUMBER OF SEQ ID NOS: 2768
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2381
; LENGTH: 1018
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-60-253-625-2381

Query Match 92.2%; Score 107; DB 37; Length 1018;
Best Local Similarity 95.2%; Pred. No. 2e-07;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KPSYQFGHNSVDFEEDTLPK 21
Db 837 KPSYQFGHNSVDFEEDTLPK 857

RESULT 14

US-60-257-931-3375
; Sequence 3375, Application US/60257931
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, R
; APPLICANT: Ohlsen, KL
; APPLICANT: Zysek, JW
; APPLICANT: Trawick, JD

; APPLICANT: Wall, D
; TITLE OF INVENTION: Genes identified as essential in Staphylococcus aureus, Salmonella
; TITLE OF INVENTION: typhimurium, Klebsiella pneumoniae and Pseudomonas aeruginosa
; FILE REFERENCE: ELITRA.017PR4
; CURRENT APPLICATION NUMBER: US/60/257,931
; CURRENT FILING DATE: 2000-12-22
; NUMBER OF SEQ ID NOS: 3592
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3375
; LENGTH: 1018
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-60-257-931-3375

Query Match 92.2%; Score 107; DB 37; Length 1018;
Best Local Similarity 95.2%; Pred. No. 2e-07;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KPSYQFGHNSVDFEEDTLPK 21
Db 837 KPSYQFGHNSVDFEEDTLPK 857

RESULT 15

US-60-269-308-4397
; Sequence 4397, Application US/60269308
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, RW
; APPLICANT: Ohlsen, KL
; APPLICANT: Zysek, JW
; APPLICANT: Trawick, JD
; APPLICANT: Wall, D
; TITLE OF INVENTION: Identification of Essential Genes in Staphylococcus aureus, Pseud
; TITLE OF INVENTION: aeruginosa, Klebsiella pneumoniae, Salmonella typhimurium, and E
; FILE REFERENCE: ELITRA.017PR5
; CURRENT APPLICATION NUMBER: US/60/269,308
; CURRENT FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 4774
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4397
; LENGTH: 1018
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-60-269-308-4397

Query Match 92.2%; Score 107; DB 37; Length 1018;
Best Local Similarity 95.2%; Pred. No. 2e-07;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KPSYQFGHNSVDFEEDTLPK 21
Db 837 KPSYQFGHNSVDFEEDTLPK 857

Search completed: October 22, 2005, 05:29:06
Job time : 209.721 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 22, 2005, 02:23:48 ; Search time 32.5221 Seconds
(without alignments)
144.114 Million cell updates/sec

Title: US-10-731-238-21
Perfect score: 116
Sequence: 1 KPSPQFGPNSVDFEEDLPK 21

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 958983 seqs, 223185384 residues
Total number of hits satisfying chosen parameters: 958983

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Pending Patents_AA_New:*
1: /cgn2_6/ptodata/2/paa/PCT_NEW_COMB.pep:*
2: /cgn2_6/ptodata/2/paa/US06_NEW_COMB.pep:*
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8: /cgn2_6/ptodata/2/paa/US60_NEW_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	116	100.0	21	6	US-10-731-238-21
2	107	92.2	21	6	US-10-731-238-9
3	107	92.2	37	7	US-11-066-697-1134
4	107	92.2	1018	6	US-10-471-571A-1354
5	104	89.7	428	6	US-10-914-020-7150
6	104	89.7	1047	6	US-10-914-020-6425
7	102	87.9	21	6	US-10-731-238-14
8	102	87.9	21	6	US-10-731-238-16
9	102	87.9	21	6	US-10-731-238-23
10	102	87.9	21	6	US-10-731-238-33
11	101	87.1	21	6	US-10-731-238-18
12	101	87.1	21	6	US-10-731-238-24
13	101	87.1	21	6	US-10-731-238-27
14	101	87.1	21	6	US-10-731-238-28
15	101	87.1	21	6	US-10-731-238-30
16	100	86.2	21	6	US-10-731-238-25
17	100	86.2	21	6	US-10-731-238-29
18	100	86.2	21	6	US-10-731-238-31
19	100	86.2	21	6	US-10-471-571A-3552
20	99	85.3	21	6	US-10-731-238-10
21	99	85.3	21	6	US-10-731-238-15
22	99	85.3	21	6	US-10-731-238-20
23	99	85.3	21	6	US-10-731-238-22
24	99	85.3	21	6	US-10-731-238-32
25	99	85.3	22	6	US-10-731-238-13

26	97	83.6	21	6	US-10-731-238-17	Sequence 17, Appl
27	97	83.6	21	6	US-10-731-238-19	Sequence 19, Appl
28	97	83.6	21	6	US-10-731-238-26	Sequence 26, Appl
29	79	68.1	21	6	US-10-731-238-34	Sequence 34, Appl
30	68	58.6	14	6	US-10-731-238-61	Sequence 61, Appl
31	53	45.7	10	6	US-10-731-238-101	Sequence 101, Appl
32	53	45.7	11	6	US-10-731-238-86	Sequence 86, Appl
33	51	44.0	10	6	US-10-731-238-100	Sequence 100, Appl
34	50.5	43.5	38	6	US-10-731-238-43	Sequence 43, Appl
35	50	43.1	204	7	US-11-216-782-10261	Sequence 10261, A
36	50	43.1	233	7	US-11-097-143-41724	Sequence 41724, A
37	49.5	42.7	38	6	US-10-731-238-49	Sequence 49, Appl
38	49.5	42.7	191	7	US-11-150-804-8997	Sequence 8997, Ap
39	49.5	42.7	191	7	US-11-216-782-11554	Sequence 11554, A
40	49.5	42.7	191	8	US-60-579-902A-8897	Sequence 8897, Ap
41	49	42.2	10	6	US-10-731-238-96	Sequence 96, Appl
42	49	42.2	10	6	US-10-731-238-102	Sequence 102, App
43	48.5	41.8	38	6	US-10-731-238-5	Sequence 5, Appl1
44	48.5	41.8	38	6	US-10-731-238-7	Sequence 7, Appl1
45	48.5	41.8	38	6	US-10-731-238-35	Sequence 35, Appl1

ALIGNMENTS

RESULT 1
US-10-731-238-21
Sequence 21, Application US/10731238
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
Patci, Joseph M.
House-Pompeo, Karen L.
Speziale, Pietro
Joh, Danny
McGavin, Martin J.

TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433

COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10731,238
FILING DATE: 10-Dec-2003
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE: 21-Jan-1998

APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.

REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TMMK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577

INFORMATION FOR SEQ ID NO: 21:

SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 21:

US-10-731-238-21

Query Match 100.0%; Score 116; DB 6; Length 21;
Best Local Similarity 100.0%; Pred. No. 9, 6e-12;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KPSYQFGGNSVDPEEDTLPK 21
| | | | | | | | | | | | | | | | | | | | | |
Db 1 KPSYQFGGNSVDPEEDTLPK 21

RESULT 2
US-10-731-238-9
Sequence 9, Application US/10731238
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
Patti, Joseph M.
House-Pompeo, Karen L.
Speziale, Pietro
Joh, Danny
McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSES: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/731,238
FILING DATE: 10-Dec-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE: 21-Jan-1998
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-Jan-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAMK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 9:
US-10-731-238-9

Query Match 92.2%; Score 107; DB 6; Length 21;
Best Local Similarity 95.2%; Pred. No. 2, 7e-10;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KPSYQFGGNSVDPEEDTLPK 21
| | | | | | | | | | | | | | | | | | | | | |
Db 1 KPSYQFGGNSVDPEEDTLPK 21

RESULT 3
US-11-066-697-1134
Sequence 1134, Application US/11066697

GENERAL INFORMATION:
APPLICANT: Bridon, Dominique P.
APPLICANT: Ezrin, Alan M.
APPLICANT: Milner, Peter G.
APPLICANT: Holmes, Darren L.
APPLICANT: Thibaudau, Karen
TITLE OF INVENTION: PROTECTION OF ENDOGENOUS THERAPEUTIC PEPTIDES FROM
PEPTIDASE ACTIVITY THROUGH CONJUGATION TO BLOOD
TITLE OF INVENTION: COMPONENTS
FILE REFERENCE: 50062002301
CURRENT APPLICATION NUMBER: US/11/066,697
CURRENT FILING DATE: 2005-02-25
PRIOR APPLICATION NUMBER: 09/657,276
PRIOR FILING DATE: 2000-09-07
PRIOR APPLICATION NUMBER: 60/153,406
PRIOR FILING DATE: 1999-09-10
PRIOR APPLICATION NUMBER: 60/159,783
PRIOR FILING DATE: 1999-10-15
NUMBER OF SEQ ID NOS: 1617
SOFTWARE: Patent in Ver. 2.1
SEQ ID NO 1134
LENGTH: 37
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-11-066-697-1134

Query Match 92.2%; Score 107; DB 7; Length 37;
Best Local Similarity 95.2%; Pred. No. 5, 1e-10;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KPSYQFGGNSVDPEEDTLPK 21
| | | | | | | | | | | | | | | | | | | | | |
Db 16 KPSYQFGGNSVDPEEDTLPK 36

RESULT 4
US-10-471-571A-3554
Sequence 3554, Application US/10471571A
GENERAL INFORMATION:
APPLICANT: CHIRON SpA
TITLE OF INVENTION: STAPHYLOCOCCUS AUREUS PROTEINS AND NUCLEIC ACIDS
FILE REFERENCE: P0269270
CURRENT APPLICATION NUMBER: US/10/471,571A
CURRENT FILING DATE: 2003-09-12
PRIOR APPLICATION NUMBER: GB-0107661.1
PRIOR FILING DATE: 2001-03-27
NUMBER OF SEQ ID NOS: 5642
SOFTWARE: SeqWin99, version 1.03
SEQ ID NO 3554
LENGTH: 1018
TYPE: PRT
ORGANISM: Staphylococcus aureus
FEATURE:
NAME/KEY: MISC FEATURE
LOCATION: (1)-(1018)
OTHER INFORMATION: Fibronectin-binding protein
US-10-471-571A-3554

Query Match 92.2%; Score 107; DB 6; Length 1018;
Best Local Similarity 95.2%; Pred. No. 2e-08;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KPSYQFGGNSVDPEEDTLPK 21
| | | | | | | | | | | | | | | | | | | | | |
Db 837 KPSYQFGGNSVDPEEDTLPK 857

RESULT 5
US-10-914-020-7150
Sequence 7150, Application US/10914020

GENERAL INFORMATION:
APPLICANT: George H. Shimer, Jr. et al.
TITLE OF INVENTION: Staphylococcus aureus Related Compositions and Methods
FILE REFERENCE: 1034/1C9630S1
CURRENT FILING DATE: 2004-08-06
PRIOR APPLICATION NUMBER: US 09/417,811
PRIOR FILING DATE: 1999-10-14
PRIOR APPLICATION NUMBER: US 09/353,718
PRIOR FILING DATE: 1999-07-14
PRIOR APPLICATION NUMBER: US 09/266,557
PRIOR FILING DATE: 1999-03-11
PRIOR APPLICATION NUMBER: US 09/266,556
PRIOR FILING DATE: 1999-03-11
PRIOR APPLICATION NUMBER: US 09/266,555
PRIOR FILING DATE: 1999-03-11
PRIOR APPLICATION NUMBER: US 09/266,542
PRIOR FILING DATE: 1999-03-11
PRIOR APPLICATION NUMBER: US 09/266,541
PRIOR FILING DATE: 1999-03-11
PRIOR APPLICATION NUMBER: US 09/266,541
PRIOR FILING DATE: 1999-03-11
PRIOR APPLICATION NUMBER: US 09/037,934
PRIOR FILING DATE: 1998-03-10
PRIOR APPLICATION NUMBER: US 09/036,720
PRIOR FILING DATE: 1998-03-06
PRIOR APPLICATION NUMBER: US 09/036,338
PRIOR FILING DATE: 1998-03-06
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 7451
SEQ ID NO 7150
LENGTH: 428
TYPE: PRT
ORGANISM: Staphylococcus aureus
US-10-914-020-7150

Query Match 89.7%; Score 104; DB 6; Length 428;
Best Local Similarity 90.5%; Pred. No. 2.4e-08;
Matches 19; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KPSYFGGNSVDFEEDTLPK 21
||:|||||
Db 251 KPNYFGGNSVDFEEDTLPK 271

RESULT 6
US-10-914-020-6425
Sequence 6425, Application US/10914020
GENERAL INFORMATION:
APPLICANT: George H. Shimer, Jr. et al.
TITLE OF INVENTION: Staphylococcus aureus Related Compositions and Methods
FILE REFERENCE: 1034/1C9630S1
CURRENT FILING DATE: 2004-08-06
PRIOR APPLICATION NUMBER: US/10/914,020
CURRENT FILING DATE: 2004-08-06
PRIOR APPLICATION NUMBER: US 09/417,811
PRIOR FILING DATE: 1999-10-14
PRIOR APPLICATION NUMBER: US 09/353,718
PRIOR FILING DATE: 1999-07-14
PRIOR APPLICATION NUMBER: US 09/266,557
PRIOR FILING DATE: 1999-03-11
PRIOR APPLICATION NUMBER: US 09/266,556
PRIOR FILING DATE: 1999-03-11
PRIOR APPLICATION NUMBER: US 09/266,555
PRIOR FILING DATE: 1999-03-11
PRIOR APPLICATION NUMBER: US 09/266,542
PRIOR FILING DATE: 1999-03-11
PRIOR APPLICATION NUMBER: US 09/266,541
PRIOR FILING DATE: 1999-03-11
PRIOR APPLICATION NUMBER: US 09/037,934
PRIOR FILING DATE: 1998-03-10
PRIOR APPLICATION NUMBER: US 09/036,720
PRIOR FILING DATE: 1998-03-06
PRIOR APPLICATION NUMBER: US 09/036,338
PRIOR FILING DATE: 1998-03-06
Remaining Prior Application data removed - See File Wrapper or PALM.

NUMBER OF SEQ ID NOS: 7451
SEQ ID NO 6425
LENGTH: 1047
TYPE: PRT
ORGANISM: Staphylococcus aureus
US-10-914-020-6425

Query Match 89.7%; Score 104; DB 6; Length 1047;
Best Local Similarity 90.5%; Pred. No. 6.4e-08;
Matches 19; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KPSYFGGNSVDFEEDTLPK 21
||:|||||
Db 842 KPNYFGGNSVDFEEDTLPK 862

RESULT 7
US-10-731-238-14
Sequence 14, Application US/10731238
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
Pattl, Joseph M.
House-Pompeo, Karen L.
Speziale, Pietro
Joh, Danny
McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/731,238
FILING DATE: 10-Dec-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE: 21-Jan-1998
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAMK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-474-7577
TELEFAX: 512-474-3000
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 14:
US-10-731-238-14

Query Match 87.9%; Score 102; DB 6; Length 21;
Best Local Similarity 95.0%; Pred. No. 1.8e-09;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 PSYFGGNSVDFEEDTLPK 21
||:|||||
Db 2 PSYFGGNSVDFEEDTLPK 21

RESULT 8
US-10-731-238-16
Sequence 16, Application US/10731238
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
Pacti, Joseph M.
House-Pompeo, Karen L.
Speziale, Pietro
John, Danny
McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/731,238
FILING DATE: 10-Dec-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE: 21-Jan-1998
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAMK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 16:
US-10-731-238-16
Query Match 87.9%; Score 102; DB 6; Length 21;
Best Local Similarity 90.5%; Pred. No. 1.8e-09;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 KPSYQFGHNSVDFEEDTLPK 21
Db 1 KPSYQFGHNSVDFEEDTLPK 21
RESULT 9
US-10-731-238-23
Sequence 23, Application US/10731238
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
Pacti, Joseph M.
House-Pompeo, Karen L.
Speziale, Pietro
John, Danny
McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
AND METHODS OF USE

NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/731,238
FILING DATE: 10-Dec-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE: 21-Jan-1998
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAMK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 23:
US-10-731-238-23
Query Match 87.9%; Score 102; DB 6; Length 21;
Best Local Similarity 90.5%; Pred. No. 1.8e-09;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 KPSYQFGHNSVDFEEDTLPK 21
Db 1 KPSYQFGHNSVDFEEDTLPK 21
RESULT 10
US-10-731-238-33
Sequence 33, Application US/10731238
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
Pacti, Joseph M.
House-Pompeo, Karen L.
Speziale, Pietro
John, Danny
McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/731,238
FILING DATE: 10-Dec-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE: 21-Jan-1998
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TMMK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 33:
US-10-731-238-33

Query Match 87.9%; Score 102; DB 6; Length 21;
Best Local Similarity 95.0%; Pred. No. 1,8e-09;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KPSYQFGHNSVDFEEDTLK 20
Db 1 KPSYQFGHNSVDFEEDTLK 20

RESULT 11
US-10-731-238-18
Sequence 18, Application US/10731238
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
Patti, Joseph M.
House-Pompeo, Karen L.
Speziale, Pietro
John, Danny
McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/731,238
FILING DATE: 10-Dec-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE: 21-Jan-1998
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TMMK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000

TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 18:
US-10-731-238-18

Query Match 87.1%; Score 101; DB 6; Length 21;
Best Local Similarity 90.5%; Pred. No. 2,5e-09;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 KPSYQFGHNSVDFEEDTLK 21
Db 1 KPSYQFGHNSVDFEEDTLK 21

RESULT 12
US-10-731-238-24
Sequence 24, Application US/10731238
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
Patti, Joseph M.
House-Pompeo, Karen L.
Speziale, Pietro
John, Danny
McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/731,238
FILING DATE: 10-Dec-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE: 21-Jan-1998
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TMMK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 24:
US-10-731-238-24

Query Match 87.1%; Score 101; DB 6; Length 21;
Best Local Similarity 90.5%; Pred. No. 2,5e-09;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 KPSYOGFGHNSVDFEEDTLPK 21
| | | | | | | | | | | | | | | | | | | | | |
Db 1 KPSYOGFGHNSVDFEEDTLPK 21

RESULT 13
US-10-731-238-27
; Sequence 27, Application US/10731238
; GENERAL INFORMATION:
; APPLICANT: Hook, Magnus
; Patti, Joseph M.
; House-Pompeo, Karen L.
; Speziale, Pietro
; John, Danny
; McGavin, Martin J.
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
; AND METHODS OF USE
; NUMBER OF SEQUENCES: 105
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: TX
; COUNTRY: USA
; ZIP: 77210-4433
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/731,238
; FILING DATE: 10-Dec-2003
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/010,317
; FILING DATE: 21-Jan-1998
; APPLICATION NUMBER: US 60/036,139
; FILING DATE: 21-JAN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Hibler, David W.
; REGISTRATION NUMBER: 41,071
; REFERENCE/DOCKET NUMBER: TAMK:189
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 512-418-3000
; TELEFAX: 512-474-7577
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 27:
US-10-731-238-27

Query Match 87.1%; Score 101; DB 6; Length 21;
Best Local Similarity 90.5%; Pred. No. 2.5e-09;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 KPSYOGFGHNSVDFEEDTLPK 21
| | | | | | | | | | | | | | | | | | | | | |
Db 1 KPSYOGFGHNSVDFEEDTLPK 21

RESULT 14
US-10-731-238-28
; Sequence 28, Application US/10731238
; GENERAL INFORMATION:
; APPLICANT: Hook, Magnus
; Patti, Joseph M.
; House-Pompeo, Karen L.
; Speziale, Pietro
; John, Danny

McGavin, Martin J.
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
; AND METHODS OF USE
; NUMBER OF SEQUENCES: 105
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: TX
; COUNTRY: USA
; ZIP: 77210-4433
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/731,238
; FILING DATE: 10-Dec-2003
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/010,317
; FILING DATE: 21-Jan-1998
; APPLICATION NUMBER: US 60/036,139
; FILING DATE: 21-JAN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Hibler, David W.
; REGISTRATION NUMBER: 41,071
; REFERENCE/DOCKET NUMBER: TAMK:189
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 512-418-3000
; TELEFAX: 512-474-7577
; INFORMATION FOR SEQ ID NO: 28:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 28:
US-10-731-238-28

Query Match 87.1%; Score 101; DB 6; Length 21;
Best Local Similarity 90.5%; Pred. No. 2.5e-09;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 KPSYOGFGHNSVDFEEDTLPK 21
| | | | | | | | | | | | | | | | | | | | | |
Db 1 KPSYOGFGHNSVDFEEDTLPK 21

RESULT 15
US-10-731-238-30
; Sequence 30, Application US/10731238
; GENERAL INFORMATION:
; APPLICANT: Hook, Magnus
; Patti, Joseph M.
; House-Pompeo, Karen L.
; Speziale, Pietro
; John, Danny
; McGavin, Martin J.
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
; AND METHODS OF USE
; NUMBER OF SEQUENCES: 105
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: TX
; COUNTRY: USA
; ZIP: 77210-4433
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/731,238
FILING DATE: 10-Dec-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE: 21-Jan-1998
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-Jan-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAMK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 30:
US-10-731-238-30

Query Match 87.1%; Score 101; DB 6; Length 21;
Best Local Similarity 90.5%; Pred. No. 2.5e-09;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 KPSYQFGGPNVDFEEDLPK 21
DB 1 KPSYQFGGPNVDFEEDLPK 21

Search completed: October 22, 2005, 05:40:53
Job time : 32.5221 secs

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OM protein - protein search, using sw model

Run on: October 22, 2005, 02:23:36 ; Search time 10.5465 Seconds
(without alignments)
191.586 Million cell updates/sec

Title: US-10-731-238-21

Sequence: 1 KPSYQFGPNSVDFEEDLPK 21

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	107	92.2	1018	2	A32192	fibronectin-binding
2	104	89.7	961	2	G90053	hypothetical prote
3	104	89.7	1038	2	H90053	hypothetical prote
4	100	86.2	940	2	S19702	fibronectin-bindin
5	48	41.4	474	2	B84357	serine-trna synth
6	48	41.4	483	2	A55033	keratin 12 - mouse
7	47	40.5	206	2	AH0259	probable phage tai
8	47	40.5	277	2	A64404	hypothetical prote
9	46	39.7	216	2	A59926	hypothetical prote
10	46	39.7	387	2	I38449	extracellular prote
11	45	38.8	218	2	AH2149	hypothetical prote
12	45	38.8	257	2	A36057	MHC class I histoc
13	45	38.8	515	2	T21107	hypothetical prote
14	45	38.8	555	2	T21110	hypothetical prote
15	45	38.8	581	2	I45971	prolactin receptor
16	45	38.8	616	2	A30304	nucleoporin NUP2
17	45	38.8	720	2	S51340	conserved hypotet
18	44	37.9	65	2	H95280	hypothetical prote
19	44	37.9	149	2	B64447	glycoprotein VP7 p
20	44	37.9	326	1	VGXKRS	glycoprotein VP7 p
21	44	37.9	326	1	VGXKRS	glycoprotein VP7 p
22	44	37.9	326	1	VGXKRS	glycoprotein VP7 p
23	44	37.9	326	1	VGXKRS	glycoprotein VP7 p
24	44	37.9	326	1	VGXKRS	glycoprotein VP7 p
25	44	37.9	326	1	VGXKRS	glycoprotein VP7 p
26	44	37.9	405	2	T23321	hypothetical prote
27	44	37.9	405	2	T23321	hypothetical prote
28	44	37.9	617	2	T15408	detritin matrix acid
29	43.5	37.5	1091	2	S33850	fibronectin-binding

30	43	37.1	303	2	B75485	fructokinase - Det
31	43	37.1	349	2	H82116	flagellar motor sw
32	43	37.1	353	2	AF3199	zinc-binding oxid
33	43	37.1	376	2	S45763	hypothetical prote
34	43	37.1	397	2	AC2110	hypothetical prote
35	43	37.1	465	2	D69785	beta-glucosidase h
36	43	37.1	466	2	P84139	beta-glucosidase B
37	43	37.1	477	2	A24115	transcription init
38	43	37.1	670	2	S67383	probable signal tr
39	43	37.1	690	2	T33321	hypothetical prote
40	43	37.1	806	2	D87627	xylosidase/arabino
41	43	37.1	1076	1	A35622	nuclear pore prote
42	43	37.1	1506	2	T51900	related to PAN2 pr
43	42.5	36.6	521	2	D81026	GMP synthase NM19
44	42.5	36.6	521	2	G81971	probable GMP synth
45	42	36.2	188	2	E97318	transcription regu

ALIGNMENTS

RESULT 1

A32192
fibronectin-binding protein - Staphylococcus aureus

C/Species: Staphylococcus aureus

C/Date: 31-Jul-1989 #sequence_revision 31-Jul-1989 #text_change 16-Feb-1997

C/Accession: A32192

R/Signaes, C.; Raucet, G.; Joensson, K.; Lindgren, P.E.; Anantharamaiah, G.M.; Hoeoek, M

Proc. Natl. Acad. Sci. U.S.A. 86, 699-703, 1989

A/Title: Nucleotide sequence of the gene for a fibronectin-binding protein from Staphyloc

A/Reference number: A32192; PMID:8908998; PMID:2521391

A/Accession: A32192

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-1018 <SIG>

A/Cross-references: GB:J04151

C/Keywords: fibronectin binding

Query Match 92.2% ; Score 107, DB 2; Length 1018;
Best Local Similarity 95.2% ; Pred. No. 1.6e-08;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KPSYQFGPNSVDFEEDLPK 21

DB 837 KPSYQFGPNSVDFEEDLPK 857

RESULT 2

G90053
hypothetical protein fnbB [imported] - Staphylococcus aureus (strain N315)

C/Species: Staphylococcus aureus

C/Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004

C/Accession: G90053

R/Kuroda, M.; Ohba, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Ogi

ma, A.; Mizutani, U.; Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kato, C.; Sekimizu, K.

C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hitamatsu, K.

Lancet 357, 1225-1240, 2001

A/Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.

A/Reference number: A89758; PMID:11418146

A/Accession: G90053

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-961 <KUR>

A/Cross-references: UNIPROT:Q99RD3; GB:BA000018; PTD:G13702452; PIDN:BBB43593.1; GSP

A/Experimental source: strain N315

C/Genetics:

A/Genes: fnbB

Query Match 89.7% ; Score 104, DB 2; Length 961;
Best Local Similarity 90.5% ; Pred. No. 4.5e-08;
Matches 19; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 KPSYQFGPNSVDFEEDLPK 21

Db 784 KENYQFGCHNSVDPEEDTLPK 804

RESULT 3

H90053

hypothetical protein fnb [imported] - Staphylococcus aureus (strain N315)

C:Species: Staphylococcus aureus

C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004

C:Accession: H90053

R:Kuroda, M.; Onaka, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguc

ma, A.; Mizutani-Uji, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.;

C.; Shiba, T.; Hatcori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.

Lancet 357, 1225-1240, 2001

A:Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.

A:Reference number: A89758; PMID:21311952; PMID:11418146

A:Accession: H90053

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-1038 <KUR>

A:Cross-references: UNIPROT:Q99RD2; GB:BA000018; PID:g13702453; PIDN:BA843594.1; GSPDB:G

C:Genetics: A:Experimental source: strain N315

A:Gene: fnb

Query Match 89.7%; Score 104; DB 2; Length 1038;

Best Local Similarity 90.5%; Pred. No. 4,9e-08;

Matches 19; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 KPSYQFGCHNSVDPEEDTLPK 21

Db 833 KENYQFGCHNSVDPEEDTLPK 853

RESULT 4

S19702

fibronectin-binding protein B - Staphylococcus aureus

C:Species: Staphylococcus aureus

C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004

C:Accession: S19702

R:Joensen, K.; Signaen, C.; Mueller, H.P.; Lindberg, M.

Eur. J. Biochem. 202, 1041-1048, 1991

A:Title: Two different genes encode fibronectin binding proteins in Staphylococcus aureu

A:Reference number: S19702; PMID:92111475; PMID:1837266

A:Accession: S19702

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-940 <OES>

A:Cross-references: UNIPROT:Q53682; EMBL:X62992; NID:g49040; PIDN:CAA44726.1; PID:G58156

C:Keywords: fibronectin binding

Query Match 86.2%; Score 100; DB 2; Length 940;

Best Local Similarity 85.7%; Pred. No. 1.9e-07;

Matches 18; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 KPSYQFGCHNSVDPEEDTLPK 21

Db 773 KENYQFGCHNSVDPEEDTLPK 793

RESULT 5

B84357

serine-tRNA synthetase [imported] - Halobacterium sp. NRC-1

C:Species: Halobacterium sp. NRC-1

C:Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004

C:Accession: B84357

R:Ng, W.V.; Kennedy, S.P.; Mahapatra, G.G.; Berquiste, B.; Pan, M.; Shukla, H.D.; Laeky, S

Jung, K.H.; Alam, M.; Fretz, R.; Danon, M.J.; Hough, D.W.; Maddocks, D.G.; Jablo

Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000

A:Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ehardt, H.; Lowe, T.M.; Li

A:Title: Genome sequence of Halobacterium species NRC-1.

A:Reference number: A84160; PMID:2050483; PMID:11016950

A:Accession: B84357

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-474 <STO>

A:Cross-references: UNIPROT:Q9HNU8; GB:AE004437; NID:g10581491; PIDN:AG20222.1; GSPD

C:Genetics: A:Gene: serS

C:Superfamily: serine-tRNA ligase

Query Match 41.4%; Score 48; DB 2; Length 474;

Best Local Similarity 41.2%; Pred. No. 13;

Matches 7; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 3 SYQFGCHNSVDPEEDTL 19

Db 234 AYRIGENDADYDDDL 250

RESULT 6

A55033

keratin 12 - mouse

C:Species: Mus musculus (house mouse)

C:Date: 18-Nov-1994 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004

C:Accession: A55033

R:Li, C.Y.; Zhu, G.; Converse, R.; Kao, C.W.C.; Nakamura, H.; Tseng, S.C.G.; Mui, M.M.

J. Biol. Chem. 269, 24627-24636, 1994

A:Title: Characterization and chromosomal localization of the cornea-specific murine ker

A:Reference number: A55033; PMID:95014223; PMID:7523376

A:Accession: A55033

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-483 <LIU>

A:Cross-references: UNIPROT:Q64291; GB:U08095; NID:9565659; PIDN:AA52359.1; PID:G565660

A:Note: authors translated the codon ATC for residue 225 as Thr, and GCG for residue 388

C:Superfamily: cytoskeletal keratin

Query Match 41.4%; Score 48; DB 2; Length 483;

Best Local Similarity 50.0%; Pred. No. 14;

Matches 9; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

QY 3 SYQFGCHNSVDPEEDTL 20

Db 266 SFQAGFGCHNSVDPEEDTL 283

RESULT 7

AH0259

probable phage tail assembly protein YPO2129 [imported] - Yersinia pestis (strain CO92)

C:Species: Yersinia pestis

C:Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Jul-2004

C:Accession: AH0259

R:Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titchall, R.W.; Holden, M.T.G.; Prentice, M.B.

deno-Farraga, A.M.; Chillingworth, T.; Cronin, A.; Davis, R.M.; Davis, P.; Dougan, G.;

H. M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrett, T.

Nature 413, 523-527, 2001

A:Title: Genome sequence of Yersinia pestis, the causative agent of plague.

A:Reference number: AB0001; PMID:21470413; PMID:1156360

A:Accession: AH0259

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-206 <KUR>

A:Cross-references: UNIPROT:Q8Z8N2; GB:AL590842; PIDN:CAC90940.1; PID:g15980136; GSPDB:G

C:Genetics: A:Gene: YPO2129

C:Superfamily: phage lambda tail assembly protein I

Query Match 40.5%; Score 47; DB 2; Length 206;

Best Local Similarity 88.9%; Pred. No. 7.5;

Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KPSYQFGCP 9

Db 164 KPSYAFGCP 172

```
RESULT 8
A:Accession: A64404
A:Title: Hypothetical protein M00833 - Methanococcus jannaschii
C:Species: Methanococcus jannaschii
C>Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 04-Mar-2000
C:Accession: A64404
R:Rult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blake,
; Reich, C.I.; Overbeek, R.; Kirsch, E.F.; Weissbrock, K.G.; Merrick, J.M.; Glodok, A.;
; reon, J.D.; Sadow, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurec, M.A.
Science 273, 1058-1073, 1996
A:Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese, C
A:Title: Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschii
A:Reference number: A64300; MUID:96337999; PMID:868087
A:Accession: A64404
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-277 <BUL>
A:Cross-references: GB:U67527; GB:L77117; NID:G1591519; PID:G1591521; TIGR:M00833; PID:G
C:Genetics:
A:Map position: REV759071-758228
A:Start codon: TTG
C:Superfamily: Methanococcus jannaschii hypothetical protein M00833

Query Match 40.5%; Score 47; DB 2; Length 277;
Best Local Similarity 61.5%; Pred. No. 10;
Matches 8; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 9 PMSVDFEEDTLPK 21
|:|:|:|:|:|:|
DB 55 PMSVDFEEDTLPK 67

RESULT 9
A:Accession: A39926
A:Title: Hypothetical protein 1 - chicken anemia virus
C:Species: chicken anemia virus, CAV
C>Date: 17-Jan-1992 #sequence_revision 17-Jan-1992 #text_change 09-Jul-2004
C:Accession: A39926
R:Notoborn, M.H.M.; de Boer, G.F.; van Roozelaar, D.J.; Karreman, C.; Kranenburg, O.; VC
J. Virol. 65, 3131-3139, 1991
A:Title: Characterization of cloned chicken anemia virus DNA that contains all elements
A:Reference number: A39926; MUID:91237831; PMID:1851873
A:Accession: A39926
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-216 <NOT>
A:Cross-references: UNIPROT:Q99151; GB:M55918; NID:G323250; PID:AAA91822.1; PID:G323251
C:Comment: This virus is unclassified.

Query Match 39.7%; Score 46; DB 2; Length 216;
Best Local Similarity 56.2%; Pred. No. 11;
Matches 9; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 2 PSYQFGPNSVDFEED 17
|:|:|:|:|:|:|
DB 172 PSYQFGPNSVDFEED 187

RESULT 10
A:Accession: I38449
A:Title: extracellular protein - human
C:Species: Homo sapiens (man)
C>Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 21-Jul-2000
C:Accession: I38449
R:Lecka-Czernik, B.; Lumpkin, C.K.
Mol. Cell. Biol. 15, 120-128, 1995
A:Title: An overexpressed gene transcript in senescent and quiescent human fibroblasts
A:Reference number: I38449; MUID:95097983; PMID:7799918
A:Accession: I38449
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
```

```
A:Residues: 1-387 <RES>
A:Cross-references: EMBL:U03877; NID:G458227; PID:AAA65590.1; PID:G458228
C:Genetics:
A:Gene: S1-5

Query Match 39.7%; Score 46; DB 2; Length 387;
Best Local Similarity 47.4%; Pred. No. 22;
Matches 9; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

QY 2 PSYQFGPNSVDFEEDTL 20
|:|:|:|:|:|:|
DB 97 PSYQFGPNSVDFEEDTL 115

RESULT 11
A:Accession: AH2149
A:Title: hypothetical protein alr2751 [imported] - Nostoc sp. (strain PCC 7120)
C:Species: Nostoc sp. PCC 7120
A:Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C>Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004
C:Accession: AH2149
R:Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kurlitz, T.; Sasamoto, S.; Watanabe, A.; Iriuchi,
; Nakazaki, N.; Shimo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S.
DNA Res. 8, 205-213, 2001
A:Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Anat
A:Reference number: AB1807; MUID:21595285; PMID:11759840
A:Accession: AH2149
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-218 <KUR>
A:Cross-references: UNIPROT:Q8YTG6; GB:BA000019; PID:BA074450.1; PID:G1731844; GSPDB:G
A:Experimental source: strain PCC 7120
C:Genetics:
A:Gene: alr2751
C:Superfamily: hypothetical protein YMR090W

Query Match 38.8%; Score 45; DB 2; Length 218;
Best Local Similarity 60.0%; Pred. No. 16;
Matches 9; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 KPSYQFGPNSVDFE 15
|:|:|:|:|:|
DB 75 KPSYQFGPNSVDFE 89

RESULT 12
A:Accession: A36057
A:Title: MHC class I histocompatibility antigen alpha chain 1 (clone-lambdaALAI-1) - common carp
C:Species: Cyprinus carpio (common carp)
C>Date: 18-Jan-1991 #sequence_revision 18-Jan-1991 #text_change 09-Jul-2004
C:Accession: A36057
R:Hashimoto, K.; Nakanishi, T.; Kurowsawa, Y.
Proc. Natl. Acad. Sci. U.S.A. 87, 6863-6867, 1990
A:Title: Isolation of carp genes encoding major histocompatibility complex antigens.
A:Reference number: A36057; MUID:90370884; PMID:2355879
A:Accession: A36057
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-257 <HAS>
A:Cross-references: UNIPROT:Q95589; GB:M37106

Query Match 38.8%; Score 45; DB 2; Length 257;
Best Local Similarity 56.2%; Pred. No. 20;
Matches 9; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 4 YQFGPNSVDFEEDTL 19
|:|:|:|:|:|:|
DB 108 YQFGPNSVDFEEDTL 123

RESULT 13
A:Accession: T21107
A:Title: hypothetical protein F19B6.1a - Caenorhabditis elegans
```


GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 22, 2005, 02:23:35 ; Search time 51.4314 Seconds
(without alignments)
209.087 Million cell updates/sec

Title: US-10-731-238-21
Perfect score: 116
Sequence: 1 KPSYQFGPNVDFEEDLPK 21

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues
Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: 1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	107	92.2	1018	1	FNBA STAU
2	104	89.7	961	2	Q99RD3
3	104	89.7	961	2	Q7A3J8
4	104	89.7	965	2	Q6GDU5
5	104	89.7	1015	2	Q8NUJ7
6	104	89.7	1015	2	Q8G6H3
7	104	89.7	1038	2	Q99RD2
8	104	89.7	1038	2	Q7A3J7
9	100	86.2	940	2	Q53682
10	100	86.2	943	2	Q8NUH8
11	100	86.2	957	2	Q6G6H4
12	95	81.9	152	2	Q9AEP9
13	54	46.6	330	2	Q88PD2
14	51.5	44.4	372	2	Q6CII4
15	50.5	43.5	237	2	Q7F0T3
16	50	43.1	233	2	Q9VPY6
17	50	43.1	599	2	Q8AER9
18	49	42.2	245	2	Q08866
19	49	42.2	772	2	Q9AD03
20	48.5	41.8	336	2	Q72P06
21	48.5	41.8	336	2	Q8F7F3
22	48	41.4	419	2	Q9BMX4
23	48	41.4	456	2	Q6TFM5
24	48	41.4	457	2	Q6S4W5
25	48	41.4	460	1	SYS_HALNT1
26	48	41.4	476	2	Q97044
27	48	41.4	483	1	K1CL_MOUSE
28	48	41.4	668	2	Q75C56
29	48	41.4	819	2	Q616P7
30	47.5	40.9	1112	1	RFOB_GLOVI
31	47	40.5	58	2	Q8BAG9

32	47	40.5	118	2	Q91N88	Q91n88 chicken ane
33	47	40.5	118	2	Q91N94	Q91n94 chicken ane
34	47	40.5	118	2	Q91N96	Q91n96 chicken ane
35	47	40.5	118	2	Q91NB5	Q91nb5 chicken ane
36	47	40.5	118	2	Q91NC1	Q91nc1 chicken ane
37	47	40.5	206	2	Q8ZEN2	Q8zen2 yersinia pe
38	47	40.5	216	2	Q91N82	Q91n82 chicken ane
39	47	40.5	277	1	Y833_METUA	Y8333 methanococc
40	47	40.5	608	2	Q7QP79	Q7qp79 giardia lam
41	46	39.7	118	2	Q91N85	Q91n85 chicken ane
42	46	39.7	118	2	Q91N91	Q91n91 chicken ane
43	46	39.7	118	2	Q91NA0	Q91na0 chicken ane
44	46	39.7	118	2	Q91NA9	Q91na9 chicken ane
45	46	39.7	118	2	Q91NB2	Q91nb2 chicken ane

ALIGNMENTS

RESULT 1
FNBA STAU STANDARD; PRT; 1018 AA.
ID FNBA STAU
AC P14738;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Fibronectin-binding protein precursor (FBNP).
GN Name=fndb;
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1280;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NCTC 8325-4;
RX MEDLINE=8908998; PubMed=2521391;
RA Signes C., Raucel G., Joensen K., Lindgren P.-E.,
Ramantharaman G.M., Hoeck M., Lindberg M.,
RT "Nucleotide sequence of the gene for a fibronectin-binding protein
from Staphylococcus aureus: use of this peptide sequence in the
synthesis of biologically active peptides."
RL Proc. Natl. Acad. Sci. U.S.A. 86:699-703(1989).
CC -!- FUNCTION: The ability of bacteria to bind fibronectin has been
proposed as a virulence factor enabling bacteria to colonize wound
tissues and blood clots. Binding of plasma fibronectin to the
bacterial surface might block adhesion receptors on S.aureus, thus
representing an important defense mechanism against tissue
invasion.
CC -!- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
an amide bond (Potential).
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL Outstation -
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See <http://www.ebi.ac.uk/announcements>)
or send an email to license@ebi.ac.uk.
CC EMBL: J04151; AAA26532.1; -;
DR InterPro: IPR004237; Fb_bind.
DR InterPro: IPR005877; GPOB_XSIRK.
DR InterPro: IPR001899; Gram_pos_anchor.
DR Pfam: PF02986; Fb_bind; 1.
DR Pfam: PF00746; Gram_pos_anchor; 1.
DR Pfam: PF04650; XSIRK_signal; 1.
DR TIGRfams: TIGR01167; LPTXG_anchor; 1.
DR TIGRfams: TIGR01168; XSIRK_signal; 1.
DR PROSITE: PS50847; GRAM_POS_ANCHORING; 1.
KW Cell adhesion; Cell wall; Peptidoglycan-anchor; Repeat; Signal;
KW Virulence.
FT SIGNAL 1 36
FT CHAIN 37 985 Fibronectin-binding protein.
FT PROPEP 986 1018 Removed by sortase (Potential).
FT


```
RT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Fibronectin-binding protein.
GN Name=fibnA; OrderedLocustNames=SAB2580;
OS Staphylococcus aureus (strain MSSA252).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=282458;
RN [1]
RS SEQUENCE FROM N.A.
RX PubMed=15213324; DOI=10.1073/pnas.0402521101;
RA Holden M.T.G., Fell E.J., Lindsay J.A., Peacock S.J., Day N.P.J.,
RA Enright M.C., Foster T.J., Moore C.E., Hurst L., Atkin R., Barron A.,
RA Bason N., Bentley S.D., Chillingworth C., Chillingworth T.,
RA Churcher C., Clark L., Corton C., Cronin A., Doggett J., Dowd L.,
RA Felwell T., Hance Z., Harris B., Hauser H., Holroyd S., Jagsels K.,
RA James K.D., Lennard N., Line A., Mayes R., Moule S., Mungall K.,
RA Ormond D., Quail M.A., Rabinowitsch E., Rutherford K.M., Sanders M.,
RA Spratt B.G., Parkhill J.;
RT "Complete genomes of two clinical Staphylococcus aureus strains:
RT evidence for the rapid evolution of virulence and drug resistance.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:9786-9791(2004).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC an amide bond (By similarity).
EMBL: BK571856; CAG41560.1; -
DR GO: GO:0009986; C:cell surface; IEA.
DR GO: GO:0009375; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO: GO:0016020; C:membrane; IEA.
DR GO: GO:0007155; P:cell adhesion; IEA.
DR InterPro: IPR008966; Adhes_bact.
DR InterPro: IPR004237; Fn_bind.
DR InterPro: IPR005877; Gpos_YsIRK.
DR InterPro: IPR001899; Gram_pos_anchor.
DR Pfam: PF02986; Fn_bind. 1.
DR Pfam: PF00746; Gram_pos_anchor. 1.
DR Pfam: PF04650; YsIRK_signal. 1.
DR TIGRFAMs: TIGR01167; LPXTG_anchor. 1.
DR TIGRFAMs: TIGR01168; YsIRK_signal. 1.
DR PROSITE: PSS0847; GRAM_POS_ANCHORING. 1.
KW Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ SEQUENCE 965 AA; 105691 MW; 2982813164D0551 CRC64;

Query Match 89.7%; Score 104; DB 2; Length 965;
Best Local Similarity 90.5%; Pred. No. 2.5e-07;
Matches 19; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 KPSYQFGGPNVDPEDTLPK 21
Db 802 KPNYQFGGHNVDPEEDTLPK 822

RESULT 5
Q8NUU7 PRELIMINARY; PRT; 1015 AA.
ID Q8NUU7;
AC Q8NUU7;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Fmb protein.
GN Name=fmb; OrderedLocustNames=MMW2421;
OS Staphylococcus aureus (strain MM2).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=196620;
RN [1]
RS SEQUENCE FROM N.A.
RX STRAIN=MM2;
RC MEDLINE=22040717; PubMed=12044378; DOI=10.1016/S0140-6736(02)08713-5;
RA Baba T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Oguchi A.,
RA Nagai Y., Ikawa N., Asano K., Naito T., Kuroda H., Cui L.,
RA Yamamoto K., Hirumatsu K.;
RT "Genome and virulence determinants of high virulence community-
RT acquired MRSA.";
RL Lancet 359:1819-1827(2002).
```

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CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC an amide bond (By similarity).
EMBL: AP004830; BAB96286.1; -
DR GO: GO:0009986; C:cell surface; IEA.
DR GO: GO:0005618; C:cell wall; IEA.
DR GO: GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO: GO:0016020; C:membrane; IEA.
DR GO: GO:0007155; P:cell adhesion; IEA.
DR GO: GO:0004237; Fn_bind.
DR InterPro: IPR008966; Adhes_bact.
DR InterPro: IPR004237; Fn_bind.
DR InterPro: IPR005877; Gpos_YsIRK.
DR InterPro: IPR001899; Gram_pos_anchor.
DR Pfam: PF02986; Fn_bind. 1.
DR Pfam: PF00746; Gram_pos_anchor. 1.
DR Pfam: PF04650; YsIRK_signal. 1.
DR TIGRFAMs: TIGR01167; LPXTG_anchor. 1.
DR TIGRFAMs: TIGR01168; YsIRK_signal. 1.
DR PROSITE: PSS0847; GRAM_POS_ANCHORING. 1.
KW Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ SEQUENCE 1015 AA; 111145 MW; D0F9281BB64D44D2 CRC64;

Query Match 89.7%; Score 104; DB 2; Length 1015;
Best Local Similarity 90.5%; Pred. No. 2.6e-07;
Matches 19; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 KPSYQFGGPNVDPEDTLPK 21
Db 838 KPNYQFGGHNVDPEEDTLPK 858

RESULT 6
Q6G6H3 PRELIMINARY; PRT; 1015 AA.
ID Q6G6H3;
AC Q6G6H3;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Fibronectin-binding protein.
GN OrderedLocustNames=SAS2388;
OS Staphylococcus aureus (strain MSSA476).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=282459;
RN [1]
RS SEQUENCE FROM N.A.
RX PubMed=15213324; DOI=10.1073/pnas.0402521101;
RA Holden M.T.G., Fell E.J., Lindsay J.A., Peacock S.J., Day N.P.J.,
RA Enright M.C., Foster T.J., Moore C.E., Hurst L., Atkin R., Barron A.,
RA Bason N., Bentley S.D., Chillingworth C., Chillingworth T.,
RA Churcher C., Clark L., Corton C., Cronin A., Doggett J., Dowd L.,
RA Felwell T., Hance Z., Harris B., Hauser H., Holroyd S., Jagsels K.,
RA James K.D., Lennard N., Line A., Mayes R., Moule S., Mungall K.,
RA Ormond D., Quail M.A., Rabinowitsch E., Rutherford K.M., Sanders M.,
RA Sharp S., Simmonds M., Stevens K., Whitehead S., Barrell B.G.,
RA Spratt B.G., Parkhill J.;
RT "Complete genomes of two clinical Staphylococcus aureus strains:
RT evidence for the rapid evolution of virulence and drug resistance.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:9786-9791(2004).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC an amide bond (By similarity).
EMBL: BK571857; CAG44202.1; -
DR GO: GO:0009986; C:cell surface; IEA.
DR GO: GO:0005618; C:cell wall; IEA.
DR GO: GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO: GO:0016020; C:membrane; IEA.
DR GO: GO:0007155; P:cell adhesion; IEA.
DR InterPro: IPR008966; Adhes_bact.
DR InterPro: IPR004237; Fn_bind.
DR InterPro: IPR005877; Gpos_YsIRK.
DR InterPro: IPR001899; Gram_pos_anchor.
DR Pfam: PF02986; Fn_bind. 1.
DR Pfam: PF00746; Gram_pos_anchor. 1.
DR Pfam: PF04650; YsIRK_signal. 1.
DR TIGRFAMs: TIGR01167; LPXTG_anchor. 1.
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DR TIGR01168: YSIRK signal; 1.
KW PROSITE: PS50847; GRAM_POS_ANCHORING: 1.
DR Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ SEQUENCE 1015 AA; 11145 MW; D0F9281B864D4D2 CRC64;

Query Match 89.7%; Score 104; DB 2; Length 1015;
Best Local Similarity 90.5%; Pred. No. 2.6e-07;
Matches 19; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 KPSYQFGHNSVDFEEDTLPK 21
DB 838 KPNYQFGHNSVDFEEDTLPK 858

RESULT 7
ID 099RD2 PRELIMINARY; PRT; 1038 AA.
AC 099RD2;
DT 01-JUN-2001 (TReMBLrel. 17, Created)
DT 01-JUN-2001 (TReMBLrel. 17, Last sequence update)
DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)
DE Fibronectin-binding protein homolog.
GN Name=fnb; OrderedLocustNames=SAV2503;
OS Staphylococcus aureus (strain Mu50 / ATCC 700699).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=158878;

RP SEQUENCE FROM N.A.
RX STRAIN=Mu50 / ATCC 700699;
RC MEDLINE=21311952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2;
RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Lian J.-Q., Ito T.,
RA Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,
RA Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
RA Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
RA Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
RA Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
RT "Whole genome sequencing of methicillin-resistant Staphylococcus
RT aureus.";

RL Lancel 357.1225-1240(2001).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC an amide bond (By similarity).

DR EMBL; AP003137; BAB3594.1; -.

DR PIR; H90053; H90053.

DR GO; GO:0009986; C:cell surface; IEA.

DR GO; GO:0005618; C:cell wall; IEA.

DR GO; GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.

DR GO; GO:0016020; C:membrane; IEA.

DR GO; GO:0007155; P:cell adhesion; IEA.

DR InterPro; IPR008966; Adhes Bact.

DR InterPro; IPR004237; Fn bind.

DR InterPro; IPR005877; Gpox_YsIRK.

DR InterPro; IPR001899; Gram_pos_anchor.

DR Pfam; PF02986; Fn_bind; 1.

DR Pfam; PF00746; Gram_pos_anchor; 1.

DR TIGR01167; LPTG anchor; 1.

DR TIGR01168; YSIRK signal; 1.

DR PROSITE; PS50847; GRAM_POS_ANCHORING; 1.

DR Cell wall; Complete proteome; Peptidoglycan-anchor.

SQ SEQUENCE 1038 AA; 113618 MW; 666BF6BF2BFBEB12 CRC64;

Query Match 89.7%; Score 104; DB 2; Length 1038;
Best Local Similarity 90.5%; Pred. No. 2.7e-07;
Matches 19; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 KPSYQFGHNSVDFEEDTLPK 21
DB 833 KPNYQFGHNSVDFEEDTLPK 853

RESULT 8
Q7A3J7

ID 07A3J7 PRELIMINARY; PRT; 1038 AA.
AC 07A3J7;
DT 05-JUL-2004 (TReMBLrel. 27, Created)
DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TReMBLrel. 27, Last annotation update)
DE Fnb protein.
GN Name=fnb; OrderedLocustNames=SA2291;
OS Staphylococcus aureus (strain N315).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=158879;

RP SEQUENCE FROM N.A.
RX MEDLINE=21311952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2;
RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Lian J.-Q., Ito T.,
RA Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,
RA Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
RA Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
RA Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
RA Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
RT "Whole genome sequencing of methicillin-resistant Staphylococcus
RT aureus.";

RL Lancel 357.1225-1240(2001).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC an amide bond (By similarity).

DR EMBL; AP003137; BAB43594.1; -.

DR GO; GO:0009986; C:cell surface; IEA.

DR GO; GO:0005618; C:cell wall; IEA.

DR GO; GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.

DR GO; GO:0016020; C:membrane; IEA.

DR GO; GO:0007155; P:cell adhesion; IEA.

DR InterPro; IPR008966; Adhes Bact.

DR InterPro; IPR004237; Fn bind.

DR InterPro; IPR005877; Gpox_YsIRK.

DR InterPro; IPR001899; Gram_pos_anchor.

DR Pfam; PF02986; Fn_bind; 1.

DR Pfam; PF00746; Gram_pos_anchor; 1.

DR TIGR01167; LPTG anchor; 1.

DR TIGR01168; YSIRK signal; 1.

DR PROSITE; PS50847; GRAM_POS_ANCHORING; 1.

DR Cell wall; Complete proteome; Peptidoglycan-anchor.

SQ SEQUENCE 1038 AA; 113618 MW; 666BF6BF2BFBEB12 CRC64;

Query Match 89.7%; Score 104; DB 2; Length 1038;
Best Local Similarity 90.5%; Pred. No. 2.7e-07;
Matches 19; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 KPSYQFGHNSVDFEEDTLPK 21
DB 833 KPNYQFGHNSVDFEEDTLPK 853

RESULT 9

Q53682 ID 053682 PRELIMINARY; PRT; 940 AA.

AC 053682;

DT 01-NOV-1996 (TReMBLrel. 01, Created)

DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)

DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)

DE Fibronectin binding protein B.

GN Name=fnbB;

OS Staphylococcus aureus.

OC Bacteria; Firmicutes; Bacillales; Staphylococcus.

OX NCBI_TaxID=1280;

RN 11

RP SEQUENCE FROM N.A.

RC STRAIN=8325-4;

RX MEDLINE=92111475; PubMed=1837266;

RA Jonsson K., Sigfus C., Muller H.P., Lindberg M.;

RT "Two different genes encode fibronectin binding proteins in
RT Staphylococcus aureus. The complete nucleotide sequence and
RT characterization of the second gene."/;

```
RL Eur. J. Biochem. 202;1041-1048(1991).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC an amide bond (By similarity).
DR EMBL: X62992; CAA44726.1; -.
DR PIR: S19702; S19702.
DR HSSP: Q53653; 1N67.
DR GO: GO:0009986; C:cell surface; IEA.
DR GO: GO:0005618; C:cell wall; IEA.
DR GO: GO:0009275; C:cell wall (senu Gram-positive Bacteria); IEA.
DR GO: GO:0016020; C:membrane; IEA.
DR GO: GO:0007155; P:cell adhesion; IEA.
DR InterPro: IPR008966; Adhes_bact.
DR InterPro: IPR004237; Fn_bind.
DR InterPro: IPR005877; Gpos_YsIRK.
DR InterPro: IPR01899; Gram_pos_anchor.
DR Pfam: PF02986; Fn_bind_2.
DR Pfam: PF00746; Gram_pos_anchor; 1.
DR Pfam: PF04650; YsIRK_signal; 1.
DR TIGRFAMs: TIGR01167; LPTXG_anchor; 1.
DR TIGRFAMs: TIGR01168; YsIRK_signal; 1.
DR PROSITE: PS50847; GRAM_POS_ANCHORING; 1.
KM Cell wall, peptidoglycan-anchor.
SQ SEQUENCE 940 AA; 10355 MW; E35FBBCA907AE345 CRC64;

Query Match 86.2%; Score 100; DB 2; Length 940;
Best Local Similarity 85.7%; Pred. No. 1e-06;
Matches 18; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KPSYQFGGPNVDFEEDTLPK 21
Db 773 KPNYQFGHNSVDFEEDTLPO 793

RESULT 10
ID Q8NU08 PRELIMINARY; PRT; 943 AA.
AC Q8NU08;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE FndB protein.
OS Name=fndB; OrderedLocustNames=NM2420;
OS Staphylococcus aureus (strain MW2).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
CX NCBI_TaxID=196620;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NM2;
RX MEDLINE=22040717; PubMed=12044378; DOI=10.1016/S0140-6736(02)08713-5;
RA Baba T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Ogunchi A.,
RA Nagai Y., Iwama N., Asano K., Naimi T., Kuroda H., Cui L.,
RA Yamamoto K., Hiramatsu K.,
RA "Genome and virulence determinants of high virulence community-
RT acquired MRSA."
RT Lancet 359:1819-1827(2002).
RL -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC an amide bond (By similarity).
CC EMBL: AP004830; BAB96285.1; -.
DR HSSP: Q53653; 1N67.
DR GO: GO:0009986; C:cell surface; IEA.
DR GO: GO:0005618; C:cell wall; IEA.
DR GO: GO:0009275; C:cell wall (senu Gram-positive Bacteria); IEA.
DR GO: GO:0016020; C:membrane; IEA.
DR GO: GO:0007155; P:cell adhesion; IEA.
DR InterPro: IPR008966; Adhes_bact.
DR InterPro: IPR004237; Fn_bind.
DR InterPro: IPR005877; Gpos_YsIRK.
DR InterPro: IPR01899; Gram_pos_anchor.
DR Pfam: PF02986; Fn_bind_1.
DR Pfam: PF04650; YsIRK_signal; 1.
DR TIGRFAMs: TIGR01167; LPTXG_anchor; 1.
DR TIGRFAMs: TIGR01168; YsIRK_signal; 1.
DR PROSITE: PS50847; GRAM_POS_ANCHORING; 1.
KM Cell wall, Complete proteome; Peptidoglycan-anchor.
SQ SEQUENCE 957 AA; 105980 MW; 28F8BA7FFDFD3EAF CRC64;
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DR PROSITE: PS50847; GRAM_POS_ANCHORING; 1.
KM Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ SEQUENCE 943 AA; 104537 MW; DA6A5F31947E1B6A CRC64;

Query Match 86.2%; Score 100; DB 2; Length 943;
Best Local Similarity 85.7%; Pred. No. 1e-06;
Matches 18; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KPSYQFGGPNVDFEEDTLPK 21
Db 780 KPNYQFGHNSVDFEEDTLPO 800

RESULT 11
ID Q6G6H4 PRELIMINARY; PRT; 957 AA.
AC Q6G6H4;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Fibrinectin-binding protein.
OS Name=fndB; OrderedLocustNames=SA52387;
OS Staphylococcus aureus (strain MSSA476).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
CX NCBI_TaxID=282459;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=15213324; DOI=10.1073/pnas.0402521101;
RA Holden M.T.G., Fell E.J., Lindsay J.A., Peacock S.J., Day N.P.J.,
RA Enright M.C., Foster T.J., Moore C.E., Hurst L., Atkin R., Barron A.,
RA Baeson N., Bentley S.D., Chillingworth C., Chillingworth T.,
RA Churcher C., Clark L., Corton C., Cronin A., Doggett J., Dowd L.,
RA James K.D., Lennard N., Hance Z., Harris B., Hauser H., Holtroyd S., Jørgen K.,
RA Ommond D., Quail M.A., Rabinowitsch E., Rutherford K.M., Sanders M.,
RA Sharp S., Simmonds M., Stevens K., Whitehead S., Barrett B.G.,
RA Spratt B.G., Parkhill J.,
RT "Complete genomes of two clinical Staphylococcus aureus strains:
RT evidence for the rapid evolution of virulence and drug resistance."
RT Proc. Natl. Acad. Sci. U.S.A. 101:9786-9791(2004).
RL -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC an amide bond (By similarity).
CC EMBL: BX571857; CAC44201.1; -.
DR GO: GO:0009986; C:cell surface; IEA.
DR GO: GO:0005618; C:cell wall; IEA.
DR GO: GO:0009275; C:cell wall (senu Gram-positive Bacteria); IEA.
DR GO: GO:0016020; C:membrane; IEA.
DR GO: GO:0007155; P:cell adhesion; IEA.
DR InterPro: IPR008966; Adhes_bact.
DR InterPro: IPR004237; Fn_bind.
DR InterPro: IPR005877; Gpos_YsIRK.
DR InterPro: IPR01899; Gram_pos_anchor.
DR Pfam: PF02986; Fn_bind_1.
DR Pfam: PF00746; Gram_pos_anchor; 1.
DR Pfam: PF04650; YsIRK_signal; 1.
DR TIGRFAMs: TIGR01167; LPTXG_anchor; 1.
DR TIGRFAMs: TIGR01168; YsIRK_signal; 1.
DR PROSITE: PS50847; GRAM_POS_ANCHORING; 1.
KM Cell wall, Complete proteome; Peptidoglycan-anchor.
SQ SEQUENCE 957 AA; 105980 MW; 28F8BA7FFDFD3EAF CRC64;

Query Match 86.2%; Score 100; DB 2; Length 957;
Best Local Similarity 85.7%; Pred. No. 1e-06;
Matches 18; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KPSYQFGGPNVDFEEDTLPK 21
Db 780 KPNYQFGHNSVDFEEDTLPO 800

RESULT 12
ID Q9AEP9 PRELIMINARY; PRT; 152 AA.
```


AC 09AEP9;
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE Fibronectin-binding protein (Fragment).
 GN Name=fnb;
 OS Staphylococcus aureus.
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 OX NCBI_TaxID=1280;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CMRSA-1;
 RX MEDLINE=21246681; PubMed=11349044;
 RX DOI=10.1128/IAI.69.6.3791-3799.2001;
 RX Rice K., Huesca M., Vaz D., McGavin M.J.,
 "Variance in fibronectin binding and fnb locus polymorphisms in
 RT Staphylococcus aureus: identification of antigenic variation in a
 RT fibronectin binding protein adhesin of the epidemic CMRSA-1 strain of
 RT methicillin-resistant S. aureus."
 RL Infect. Immun. 69:3791-3799(2001).
 DR EMBL: AY029184; MAK31588.1; -.
 FT NON_TER
 FT 152 152
 SQ SEQUENCE 152 AA; 17193 MW; CFA3913C2B11C025 CRC64;

Query Match 81.9%; Score 95; DB 2; Length 152;
 Best Local Similarity 81.0%; Pred. No. 7.8e-07;
 Matches 17; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 KPSYQFGPNSVDFEEDTLPK 21
 |||||
 Db 130 KPSYQFGHNGIDFVEDTLPK 150

RESULT 13
 Q88PD2 PRELIMINARY; PRT; 330 AA.
 AC Q88PD2;
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE 3-beta hydroxysteroid dehydrogenase/isomerase family protein,
 DE putative.
 GN OrderedLocuNames=PP0918;
 OS Pseudomonas putida (strain KT2440).
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
 OC Pseudomonadaceae; Pseudomonas.
 OX NCBI_TaxID=160488;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22423060; PubMed=12534463;
 RA Nelson K.E., Weinel C., Paulsen I.T., Dodson R.J., Hilbert H.,
 RA Martins dos Santos V.A.P., Fouts D.E., Gill S.R., Pop M., Holmes M.,
 RA Brinkac L.M., Beaman M.J., DeBoy R.T., Daugherty S.C., Kolonay J.F.,
 RA Madupu R., Nelson W.C., White O., Peterson J.D., Khouri H.M.,
 RA Hance I., Chris Lee P., Holtzapfel E.K., Scanlan D., Tran K.,
 RA Moazzez A., Uterback T.R., Rizzo M., Lee K., Kosack D., Moestl D.,
 RA Medler H., Lauber J., Stegandic D., Hohnsbeil U., Straetz M., Helm S.,
 RA Kiewitz C., Eisen J.A., Timmis K.N., Duesterhoeft A., Thummler B.,
 RA Frazer C.M.;
 RT "Complete genome sequence and comparative analysis of the
 RT metabolically versatile Pseudomonas putida KT2440."
 RL Environ. Microbiol. 4:799-808(2002).
 DR EMBL: AA016777; AAN6543.1; -.
 DR TIGR: PP0918; -.
 GO GO:0016853; F:isomerase activity; IEA.
 KW Complete proteome; Isomerase.
 SQ SEQUENCE 330 AA; 37056 MW; A60498E263091AC5 CRC64;

Query Match 46.6%; Score 54; DB 2; Length 330;
 Best Local Similarity 45.0%; Pred. No. 5.8;
 Matches 9; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

QY 2 PSYQFGPNSVDFEEDTLPK 21
 |||||
 Db 113 PSYFNGPSRLVDREDOVR 132

RESULT 14
 O6CII4 PRELIMINARY; PRT; 372 AA.
 ID O6CII4
 AC O6CII4;
 DT 25-OCT-2004 (TrEMBLrel. 28, Created)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
 DE Similar to sp|P36083 Saccharomyces cerevisiae YKL075C hypothetical
 DE protein singleton.
 GN ORFNames=K11A0F26378g;
 OS Kluyveromyces fragilis NRRL Y-1140.
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Saccharomycetaceae; Kluyveromyces.
 OX NCBI_TaxID=284590;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=NRRL Y-1140;
 RG Genolevures;
 RA Dujon B., Sherman D., Fischer G., Durrens P., Casaregola S.,
 RA Lafontaine I., de Montigny J., Marcq C., Neveglisse C., Talla E.,
 RA Goffard N., Frangeul L., Aigle M., Anthonard V., Babour A., Barbe V.,
 RA Barnay S., Blanchin S., Beckerich J.M., Beyne E., Bleykassen C.,
 RA Boistrame A., Boyer J., Catolico L., Confanioli F., de Darvar A.,
 RA Despons L., Fabre E., Fairhead C., Ferry-Dunazet H., Groppi A.,
 RA Hanttraye F., Hennequin C., Jauniaux N., Joyet P., Kachouri R.,
 RA Kerrest A., Koszul R., Lemaire M., Lesur I., Ma L., Muller H.,
 RA Nicaud J.M., Nikolski M., Oztas S., Ozier-Kalogeropoulos O.,
 RA Pellenz S., Pottier S., Richard G.F., Straub M.L., Suleau A.,
 RA Swennens D., Tekala F., Wesolowski-Louvel M., Westhof E., Wirth B.,
 RA Zenou-Meyer M., Zivanovic I., Botocin-Fukuhara M., Thierry A.,
 RA Bouchier C., Caudron B., Scarpelli C., Galliard C., Weissbach J.,
 RA Wincker P., Souciet J.L.;
 RL "Genome evolution in yeasts."
 RN Nature 430:35-44(2004).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=NRRL Y-1140;
 RA GenomeScope;
 RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL: CR382126; CAG98963.1; -.
 KW Hypothetical protein.
 SQ SEQUENCE 372 AA; 43695 MW; A657AD038AE45169 CRC64;

Query Match 44.4%; Score 51.5; DB 2; Length 372;
 Best Local Similarity 47.8%; Pred. No. 16;
 Matches 11; Conservative 3; Mismatches 6; Indels 3; Gaps 1;

QY 2 PSY---QFGPNSVDFEEDTLPK 21
 |||||
 Db 104 PDYWDKMGKPNSSDYEEVEPK 126

RESULT 15
 Q7F0T3 PRELIMINARY; PRT; 237 AA.
 ID Q7F0T3;
 DT 25-OCT-2004 (TrEMBLrel. 28, Created)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
 DE O2116_C07.12 protein.
 GN Name=O2116_C07.12;
 OS Oryza sativa (japonica cultivar-group).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Ehrhartoideae; Oryzaceae; Oryza.
 OX NCBI_TaxID=39947;
 RN [1]
 RP SEQUENCE FROM N.A.

PubMed=12447438; DOI=10.1038/nature01184;
RA Sasaki T., Matsumoto T., Yamamoto K., Sakata K., Baba T., Katayose Y.,
Wu J., Nimura Y., Cheng Z., Nagamura Y., Antonio B.A., Kanamori H.,
Hosokawa S., Masukawa M., Arikawa K., Chiden Y., Hayashi M.,
Okamoto M., Ando T., Aoki H., Arita K., Hamada M., Harada C.,
Hijishita S., Honda M., Ichikawa Y., Ikonuma A., Iijima M., Ikeda M.,
Ikono M., Itoh S., Itoh T., Itoh Y., Itoh Y., Iwabuchi A., Kamiya K.,
Karasawa W., Katagiri S., Kikuta A., Kobayashi N., Kono I.,
Machita K., Maehara T., Mizuno H., Mizubayashi T., Mukai Y.,
Nagasaki H., Nakashima M., Nakama Y., Nakamichi Y., Nakamura M.,
Namiiki N., Negishi M., Ohta I., Ono N., Saji S., Sakai K., Shibata M.,
Shimokawa T., Shomura A., Song J., Takazaki Y., Teraawa K., Tsuji K.,
Waki K., Yamagata H., Yamane H., Yoshiki S., Yoshihara R., Yukawa K.,
Zhong H., Iwama H., Endo T., Ito H., Hahn J.H., Kim H.I., Eun M.Y.,
Yano M., Jiang J., Gojobori T.;
RT "the genome sequence and structure of rice chromosome 1.";
RL Nature 420:312-316(2002).
DR EMBL; AP004253; BAC00695.1; -.
DR Gramene; Q8L409; -.
SQ SEQUENCE 237 AA; 26918 MW; C90425B72826585A CRC64;

Query Match 43.5%; Score 50.5; DB 2; Length 237;
Best Local Similarity 73.3%; Pred. No. 14;
Matches 11; Conservative 1; Mismatches 2; Indels 1; Gaps 1;
QY 1 KPSTYQFGSPNSVDPE 15
DB 122 RPS-QGGGPNKVDPE 135

Search completed: October 22, 2005, 04:09:59
Job time : 53.4314 secs

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CC streptococci, e.g. meningitis, otitis media, pneumonia, endocarditis,
 CC mastitis in cattle, abortion in horses and many others. Since the
 CC antibodies block binding of bacteria, they should be effective against
 CC antibiotic-resistant strains, and may replace antibiotic therapy or
 CC increase its effectiveness. Sequences AAW65670-90 represent a series of
 CC synthetic peptides based on the D3 repeat of *S. aureus* fibronectin
 CC binding protein A. They were synthesised to contain a proline residue at
 CC each position through the sequence (ie a proline scan)
 XX
 SQ Sequence 21 AA;
 Query Match 100.0%; Score 118; DB 2; Length 21;
 Best Local Similarity 100.0%; Pred. No. 6.9e-12;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KPSYQFGHPSVDFEEDTLPK 21
 DB 1 KPSYQFGHPSVDFEEDTLPK 21
 RESULT 2
 ID AAW65665 standard; peptide; 21 AA.
 XX AAW65665;
 AC
 XX 16-OCT-1998 (first entry)
 DT
 XX Fibronectin binding protein-derived peptide #9.
 DE
 XX microbial surface components recognising adhesive matrix molecule;
 KM MSCRAMM; fibronectin; fibronectin-binding protein; antibody; epitope;
 KW antibiotic; bacterial infection; antibiotic-resistant strain.
 XX
 XX Synthetic.
 OS Staphylococcus aureus.
 OS
 XX WO9831389-A2.
 PN
 XX 23-JUL-1998.
 PD
 XX 21-JAN-1998; 98WO-US001222.
 PF
 XX 21-JAN-1997; 97US-0036139P.
 PR
 XX (TEXA) UNIV TEXAS A & M SYSTEM.
 PA
 XX Hoeoek M, Patci JM, House-Pompeo KL, Speziale P, Joh D;
 PI Mcgavin MJ;
 PI
 XX WPI; 1998-413816/35.
 DR
 XX
 XX Antibody that binds to fibronectin-binding protein, preventing its
 PT binding to fibronectin - used to treat or prevent bacterial infection,
 PR especially by Staphylococci and Streptococci.
 PT
 PS Example 2; Page 92; 201pp; English.
 XX
 CC The invention relates to antibodies that bind to a fibronectin-binding
 CC domain of a fibronectin-binding protein, and inhibit binding of the
 CC protein to fibronectin. Also claimed are: (1) isolated peptides of a
 CC fibronectin-binding protein that do not bind to fibronectin; (2) fusion
 CC protein containing at least one peptide of a fibronectin-binding protein
 CC linked to a second amino acid sequence; (3) nucleic acid encoding the
 CC isolated peptide of (1). Antibodies, the isolated peptides of (1) and the
 CC nucleic acids are all useful for immunisation (active or passive) and (by
 CC inhibiting binding of bacteria to fibronectin) for preventing or treating
 CC infection in humans or other animals, particularly by staphylococci or
 CC streptococci, e.g. meningitis, otitis media, pneumonia, endocarditis,
 CC mastitis in cattle, abortion in horses and many others. Since the
 CC antibodies block binding of bacteria, they should be effective against
 CC antibiotic-resistant strains, and may replace antibiotic therapy or
 CC increase its effectiveness. Sequences AAW65659-68 represent synthetic

CC epitopes from the fibronectin binding domains DU and D1-D4 of the *S.*
 CC aureus fnbA gene
 CC
 XX
 SQ Sequence 21 AA;
 Query Match 92.4%; Score 109; DB 2; Length 21;
 Best Local Similarity 95.2%; Pred. No. 2e-10;
 Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 KPSYQFGHPSVDFEEDTLPK 21
 DB 1 KPSYQFGHNSVDFEEDTLPK 21
 RESULT 3
 ID AAR21340 standard; peptide; 22 AA.
 XX AAR21340;
 AC
 XX 25-MAR-2003 (revised)
 DT 15-JUN-1992 (first entry)
 XX
 DE Fibronectin binding protein.
 XX
 KM FbBP; wound infection reduction; vaccination; mastitis;
 KW Staphylococcal infections; D3.
 XX
 XX Synthetic.
 OS
 XX WO9202555-A.
 PN
 XX 20-FEB-1992.
 PD
 XX 10-AUG-1990; 90SE-00002617.
 PF
 XX 10-AUG-1990; 90SE-00002617.
 PR
 XX (ALFA) ALFA LAVIL AGRIC INT AB.
 PA
 XX Hook M, McGavin M, Raucchi G;
 PI
 XX WPI; 1992-080035/10.
 DR
 XX
 XX New fibronectin binding peptide - combines with fusion peptide to form
 PT large antigen, used in immunisation, diagnosis and for treating wounds.
 PT
 XX Claim 1; Page 22; 33pp; English.
 PS
 XX
 CC The sequence comprises amino acids 17-33 of a tandem repeat, designated
 CC D3 of the fibronectin binding site of Staphylococcus aureus 8325-4 FbBP.
 CC The N-terminal DK may be replaced with H or K, and the C-terminal LKP may
 CC be replaced by either L, LP, or OH. The peptides were synthesised using
 CC standard methods and purified using reverse phase HPLC. The appropriate
 CC fractions were dialysed and lyophilised. Peptide sequencing was performed
 CC and the peptides digested and chemically modified by dihydroxypropylation
 CC of the amino side chain of lysine. The carboxylic side chains were
 CC converted to glycine methyl esters. The phenyl side chains of tyrosine
 CC residues were oxidised. Chemically modified peptide D3 was compared to
 CC unmodified D3. Lysine and tyrosine modifications only partially
 CC diminished its activity whereas modification of aspartic/glutamic
 CC residues resulted in complete loss of activity. The peptide can be used
 CC for the prevention or reduction of the risk of wound infection. The
 CC peptide can be used to create a large antigen for vaccinating ruminants
 CC against mastitis caused by Staphylococcal infections. It can also be used
 CC to diagnose Staphylococcal infections using ELISA or DNA probes. (Updated
 CC on 25-MAR-2003 to correct PA field.)
 CC
 XX
 SQ Sequence 22 AA;
 Query Match 92.4%; Score 109; DB 2; Length 22;
 Best Local Similarity 95.2%; Pred. No. 2.1e-10;
 Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KPSYQFGHPSVDFEEDTLPK 21
ID |||||
DB 2 KPSYQFGHNSVDFEEDTLPK 22

RESULT 4
AAB91958
ID AAB91958 standard; peptide; 37 AA.

AC AAB91958;

DT 22-JUN-2001 (first entry)

XX Fibrinectin fragment and fibrin related peptide SEQ ID NO:1134.

XX Protection; endogenous therapeutic peptide; peptidase; conjugation;
KW blood component; modification; succinimidy; maleimido group; amino;
KW hydroxyl; thiol; hormone; growth factor; neurotransmitter.

XX Homo sapiens.

OS Synthetic.

XX WO200069900-A2.

XX 23-NOV-2000.

XX 17-MAY-2000; 2000MO-US013576.

XX 17-MAY-1999; 99US-0134406P.

XX 10-SEP-1999; 99US-0153406P.

XX 15-OCT-1999; 99US-0159783P.

XX (CONT-) CONJUCHEM INC.

XX Bridon DP, Ezrin AM, Milner PG, Holmes DL, Thibaudau K;

XX WPI; 2001-112059/12.

XX The present invention describes a modified therapeutic peptide (I)
CC comprising a therapeutically active amino acid region (III) and a
CC reactive group (II) (e.g. succinimidy and maleimido groups) attached to
CC a less therapeutically active amino acid region (IV), which covalently
CC bonds with amino/hydroxyl/thiol groups on blood components to form a
CC peptidase stabilised therapeutic peptide composed of 3-50 amino acids.
CC (I) are useful for modifying therapeutic peptides e.g. hormones, growth
CC factors and neurotransmitters, to protect them from peptidase activity in
CC vivo for the treatment of various disorders. Endogenous therapeutic
CC peptides are not suitable as drug candidates as they require frequent
CC administration due to rapid degradation by peptidases in the body.
CC Modifying and attaching therapeutic peptides to albumin prevents or
CC reduces the action of peptidases to increase length of activity (half
CC life) and specificity as bonding to large molecules decreases.
CC intracellular uptake and interference with physiological processes.
CC AAB90829 to AAB92441 represent peptides which can be used in the
CC exemplification of the present invention

XX Sequence 37 AA;

XX

Query Match 92.4%; Score 109; DB 4; Length 37;
Best Local Similarity 95.2%; Pred. No. 3.9e-10;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KPSYQFGHPSVDFEEDTLPK 21
ID |||||
DB 16 KPSYQFGHNSVDFEEDTLPK 36

RESULT 5
AAP80662
ID AAP80662 standard; protein; 38 AA.

XX AAP80662;

XX 25-MAR-2003 (revised)

XX 07-OCT-1990 (first entry)

XX Protein with fibronectin binding ability.

XX Hybrid DNA molecule; fibronectin binding; mastitis; ruminants;
KW wound infection.

XX Staphylococcus aureus.

XX EP294349-A.

XX 07-DEC-1988.

XX 30-MAY-1988; 88EP-00850188.

XX 01-JUN-1987; 87SE-00002272.

XX (ALFA) ALFA LAVAL AGRIC INT AB.

XX Lindberg MK, Signas LC, Wadstrom TM, Froman G;

XX WPI; 1988-347978/49.

XX N-PSDB; AAN61099.

XX Hybrid DNA encoding Staphylococcus aureus fibronectin binding protein -
PT useful for immunisation and topical application to prevent staphylococcal
PT infections.

XX Claim 11; Page 12; 23pp; English.

XX The peptide has fibronectin binding ability. It is useful for immunising
CC ruminants against staphylococcal mastitis, pref. when used at 0.5-5
CC micrograms/kg, using 3 doses given at 1-3 week intervals; for topical
CC application to prevent wound infection, using an isotonic saline soln. of
CC concn. 25-250 micrograms/ml; and, when immobilised on a carrier, for
CC diagnosing staphylococcal infections. (Updated on 25-MAR-2003 to correct
CC PF field.) (Updated on 25-MAR-2003 to correct PA field.)

XX Sequence 38 AA;

QY 1 KPSYQFGHPSVDFEEDTLPK 21
ID |||||
DB 17 KPSYQFGHNSVDFEEDTLPK 37

RESULT 6
AAY29087
ID AAY29087 standard; protein; 134 AA.

XX AAY29087;

XX 28-SEP-1999 (first entry)

XX S. aureus fibronectin binding protein A (FnBA) binding domain.

XX Bovine herpes virus-2; BHV-2; cytokine; immune response; immunogen; IL;
KW interleukin; colony stimulating factor; CSF; interferon; IFN; TNF;
KW tumour necrosis factor; recombinant virus; vaccine; mucosal disease;
KW mastitis; breast cancer; stress-induced disease; binding domain; FnBA;
KW fibronectin binding protein.

XX Staphylococcus aureus.

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XX  MO9916892-A1.
PN  08-APR-1999.
XX  29-SEP-1998; 98WO-GB002927.
XX  29-SEP-1997; 97GB-00020633.
XX  (UYBR-) UNIV BRISTOL.
XX  Bradley AJ, Duffas WP;
XX  WPI; 1999-255101/21.
XX  N-PSDB; AAX91504.
XX  New bovine herpes virus-2 vectors.
XX  Example 2; Fig 8A-B; 130pp; English.
XX  The invention provides bovine herpes virus-2 (BHV-2) based vectors that
XX  comprise at least one cytokine-encoding DNA sequence. The expression of
XX  cytokines in mammals can up-regulate immune responses to the immunogens.
XX  The cytokine is selected from interleukins (IL), colony stimulating
XX  factors (CSF), interferons (IFN) and tumour necrosis factors (TNF). The
XX  BHV-2 based vector or recombinant virus can be used as vaccines. They can
XX  be used for preventing or treating a mucosal disease in a subject, e.g.
XX  ruminants, cattle, sheep, goats, dogs, cats, horses, or man, particularly
XX  mastitis in cows or breast cancers in humans. They can also be used for
XX  preventing or treating a stress-induced disease. The present sequence
XX  represents the binding domain of a previously published S. aureus
XX  fibronectin binding protein A (FnBA) sequence. The FnB binding domain
XX  gene sequence FNBA, cloned for use in this invention has 97.8 percent
XX  identity when compared to the previously published FnBA and FnB gene
XX  sequences
XX  Sequence 134 AA;
SO

Query Match          92.4%; Score 109; DB 2; Length 134;
Best Local Similarity 95.2%; Pred. No. 1.7e-09;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY  1 KPSYQFGHPSVDFEEDTLPK 21
    ||||| ||||| ||||| |||||
DB  93 KPSYQFGHNSVDFEEDTLPK 113

RESULT 7
AAW31556
ID  AAW31556 standard; protein; 139 AA.
XX  AAW31556;
AC
XX  27-AUG-2003 (revised)
DT  25-MAR-2003 (revised)
DT  21-MAY-1998 (first entry)
XX
DE  Fibronectin-binding MSCRAMM derivative pOD.
XX
XX  Fibronectin; pOD; collagen binding protein; sepsis; infection;
XX  microbial surface component recognising adhesive matrix molecule; MSCRAMM;
XX  adhesin; vaccine; immunisation; diagnosis; therapy; mastitis.
XX
XX  Staphylococcus aureus.
XX
XX  Key Location/Qualifiers
XX  Peptide 1..12
XX  /note= "vector pQE30-derived peptide"
XX
XX  MO9743314-A2.
XX
XX  20-NOV-1997.
XX

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PF  14-MAY-1997; 97WO-US008210.
XX
XX  16-MAY-1996; 96US-0017678P.
XX
XX  (TEXA ) UNIV TEXAS A & M SYSTEM.
XX  (UABR-) UAB RES FOUND.
XX
XX  Hoeoek M, Patti JM, House-Pompeo K, Schanam N, Symersky J;
XX  WPI; 1998-008601/01.
XX
XX  Antibody that interacts with collagen binding domain of Staphylococcal
XX  cna gene product - useful to prevent bacterial sepsis in animal infected
XX  with Staphylococcus aureus.
XX
XX  Disclosure; Page 91; 143pp; English.
XX
XX  This protein comprises Staphylococcus aureus fibronectin-binding
XX  microbial surface component recognising adhesive matrix molecule (MSCRAMM)
XX  derivative pOD, plus a vector-derived N-terminal peptide. The invention
XX  relates to claimed nucleic acid sequences (see AAT93436-38) encoding S.
XX  aureus collagen binding protein (CBP) epitopes M17, M31 and M55 (see
XX  AAW31552-54) that confer protection against S. aureus infection. CBP
XX  protein and antigenic epitopes are contemplated for use in the treatment
XX  of pathological infections, especially to prevent bacterial adhesion to
XX  collagen. The epitopes are also contemplated for use in the preparation
XX  of vaccines and as carrier proteins in vaccine formulations, as well as
XX  in the formulation of compositions for the prevention of S. aureus
XX  infection. PCR3 and pOD (see AAW31556) were used to raise anti-MSCRAMM
XX  polyclonal antibodies used in passive immunisation against bovine
XX  mastitis. (Updated on 25-MAR-2003 to correct PI field.) (Updated on 27-
XX  AUG-2003 to correct OS field.)
XX
XX  Sequence 139 AA;
SO

Query Match          92.4%; Score 109; DB 2; Length 139;
Best Local Similarity 95.2%; Pred. No. 1.7e-09;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY  1 KPSYQFGHPSVDFEEDTLPK 21
    ||||| ||||| ||||| |||||
DB  107 KPSYQFGHNSVDFEEDTLPK 127

RESULT 8
AAP82115
ID  AAP82115 standard; protein; 1018 AA.
XX  AAP82115;
AC
XX  25-MAR-2003 (revised)
DT  05-JAN-1990 (first entry)
XX
XX  Fibronectin binding protein.
DE  Fibronectin binding protein.
XX
XX  Fibronectin binding protein; S. aureus; immunisation; mastitis; ruminants;
XX  wound infection; diagnosis.
XX
XX  Staphylococcus aureus.
XX
XX  EP294349-A.
XX
XX  07-DEC-1988.
XX
XX  30-MAY-1988; 88EP-00850188.
XX
XX  01-JUN-1987; 87SE-00002272.
XX
XX  (ALFA ) ALFA LAVAL AGRIC INT AB.
XX
XX  Lindberg MK, Sigmas LC, Wadstrom TM, Froman G;
XX  WPI; 1988-347978/49.
XX

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CC P-PSDB; AAP82115.
XX Hybrid DNA encoding Staphylococcus aureus fibronectin binding protein -
PT useful for immunisation and topical application to prevent staphylococcal
PT infections.
XX Disclosure; Fig. 8A:1-8A:2; 23pp; English.
XX
XX The S.aureus fibronectin binding protein may be included in a hybrid
CC protein. The protein may be used to immunise ruminants against
CC staphylococcal mastitis, pref. when given at 0.5-5 microg/kg, using 3
CC doses at 1-3 week intervals; and for topical applicn. to prevent wound
CC infection, pref. using isotonic saline soln. of concn. 25-250 microg/mg.
CC The DNA encoding the binding protein and the hybrid protein may be
CC immobilised on a carrier and used to diagnose staphylococcal infections.
CC (updated on 25-MAR-2003 to correct PA field.)
XX
SQ Sequence 1018 AA;
Query Match 92.4%; Score 109; DB 1; Length 1018;
Best Local Similarity 95.2%; Pred. No. 1.7e-08;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 1 KPSYQFGHPSVDFEEDTLPK 21
DB 837 KPSYQFGHNSVDFEEDTLPK 857
RESULT 9
AAU37245
ID AAU37245 standard; protein; 1018 AA.
XX
XX AAU37245;
AC
XX
DT 14-FEB-2002 (first entry)
XX
DE Staphylococcus aureus cellular proliferation protein #1415.
XX
XX Antisense; prokaryotic cellular proliferation protein; antibiotic;
KM antibacterial; drug design.
XX
XX Staphylococcus aureus.
OS
XX MO200170955-A2.
PN
XX 27-SEP-2001.
PD
XX
PF 21-MAR-2001; 2001MO-US009180.
XX
XX 21-MAR-2000; 2000US-0191078P.
PR 23-MAY-2000; 2000US-0206848P.
PR 26-MAY-2000; 2000US-0207727P.
PR 23-OCT-2000; 2000US-0242578P.
PR 27-NOV-2000; 2000US-0253625P.
PR 22-DEC-2000; 2000US-0257931P.
PR 16-FEB-2001; 2001US-0269308P.
XX
XX (ELIT-) ELITRA PHARM INC.
PA
XX
XX Haselbeck R, Ohlsen KL, Zykkind JW, Wall D, Trawick JD, Carr GJ;
PI Yamamoto RT, Xu HH;
PI WPI; 2001-611495/70.
DR N-PSDB; AAS55104.
XX
XX New polynucleotides for the identification and development of
PT antibiotics, comprise sequences of antisense nucleic acids.
XX
XX Example 3; SEQ ID NO 12638; 51pp; English.
PS
XX The invention relates to antisense inhibitors of genes essential to
CC prokaryotic cellular proliferation, their use in identifying the genes,
CC their use in the discovery of novel antibiotics, the essential genes

CC themselves and the encoded proteins. The prokaryotes used are Escherichia
CC coli, Staphylococcus aureus, Salmonella typhi, Klebsiella pneumoniae,
CC Pseudomonas aeruginosa and Enterococcus faecalis. The invention is also
CC useful for the identification of potential new targets for antibiotic
CC development. The antisense nucleic acids can also be used to identify
CC proteins used in proliferation, to express these proteins, and to obtain
CC antibodies capable of binding to the expressed proteins. The proteins can
CC be used to screen compounds in rational drug discovery programmes. The
CC antisense nucleic acid sequence is also useful to screen for homologous
CC nucleic acids which are required for cell proliferation in a wide variety
CC of organisms. The present sequence represents an essential prokaryotic
CC cellular proliferation protein. Note: The sequence data for this patent
CC did not form part of the printed specification, but was obtained in
CC electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 1018 AA;
Query Match 92.4%; Score 109; DB 4; Length 1018;
Best Local Similarity 95.2%; Pred. No. 1.7e-08;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 1 KPSYQFGHPSVDFEEDTLPK 21
DB 837 KPSYQFGHNSVDFEEDTLPK 857
RESULT 10
AAU34301
ID AAU34301 standard; protein; 1018 AA.
XX
XX AAU34301;
AC
XX
DT 14-FEB-2002 (first entry)
XX
DE Staphylococcus aureus cellular proliferation protein #577.
XX
XX Antisense; prokaryotic cellular proliferation protein; antibiotic;
KM antibacterial; drug design.
XX
XX Staphylococcus aureus.
OS
XX MO200170955-A2.
PN
XX 27-SEP-2001.
PD
XX
PF 21-MAR-2001; 2001MO-US009180.
XX
XX 21-MAR-2000; 2000US-0191078P.
PR 23-MAY-2000; 2000US-0206848P.
PR 26-MAY-2000; 2000US-0207727P.
PR 23-OCT-2000; 2000US-0242578P.
PR 27-NOV-2000; 2000US-0253625P.
PR 22-DEC-2000; 2000US-0257931P.
PR 16-FEB-2001; 2001US-0269308P.
XX
XX (ELIT-) ELITRA PHARM INC.
PA
XX
XX Haselbeck R, Ohlsen KL, Zykkind JW, Wall D, Trawick JD, Carr GJ;
PI Yamamoto RT, Xu HH;
PI WPI; 2001-611495/70.
DR N-PSDB; AAS52160.
XX
XX New polynucleotides for the identification and development of
PT antibiotics, comprise sequences of antisense nucleic acids.
XX
XX Example 3; SEQ ID NO 5797; 51pp; English.
PS
XX The invention relates to antisense inhibitors of genes essential to
CC prokaryotic cellular proliferation, their use in identifying the genes,
CC their use in the discovery of novel antibiotics, the essential genes
CC themselves and the encoded proteins. The prokaryotes used are Escherichia

Query Match 92.4%; Score 109; DB 6; Length 1018;
Best Local Similarity 95.2%; Pred. No. 1.7e-08;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KPSYQFGHNSVDPEEDTLPK 21
ID AAM89806
AAW89806 standard; protein; 1027 AA.

DB 837 KPSYQFGHNSVDPEEDTLPK 857

RESULT 13

AAW89806
AAW89806;
16-MAR-1999 (first entry)

Staphylococcus aureus protein SEQ ID #5254.

Computer readable medium; vaccine; S.aureus infection; immunodetection;
cellulitis; eyelid infection; food poisoning; osteomyelitis; therapy;
skin infection; surgical wound infection; scalded skin syndrome;
toxic shock syndrome.

Staphylococcus aureus.

EP786519-A2.

30-JUL-1997.

07-JAN-1997; 97BP-00100117.

05-JAN-1996; 96US-0009861P.

(HUMA-) HUMAN GENOME SCI INC.

Kunsch CA, Choi GH, Barash SC, Dillon PJ, Fannon MR, Rosen CA;
WPI; 1997-374922/35.

Polynucleotide(s) and proteins derived from Staphylococcus aureus -
stored on computer readable medium and used in the production of anti-
S.aureus vaccines.

Claim 23; Page 3263-3267; 3271pp; English.

This sequence represents a Staphylococcus aureus protein sequence of the
invention. The DNA sequences encoding the S.aureus proteins are recorded
on a computer readable medium, preferably selected from a floppy or hard
disk, random access memory (RAM), read-only memory (ROM) or CD-ROM.
Homology searches using the S.aureus DNA sequences allows putative
functions to be assigned so that protein-encoding or regulatory regions
of commercial, therapeutic or industrial importance can be obtained.
Specifically, sequences which are likely to encode antigens have been
identified and these polypeptides can be used in a vaccine composition
against S.aureus infection. The polypeptides can also be used in a kit
for the immunodetection of S.aureus in a sample. S.aureus is implicated
in numerous human diseases, including cellulitis, eyelid infections, food
poisoning, osteomyelitis, skin and surgical wound infections, scalded
skin syndrome, toxic shock syndrome, etc. Organisms transformed with the
CC DNA sequences can be used for recombinant production of the polypeptides.
The new DNA sequences (and their fragments) are useful as primers or
probes for isolating homologues of any of the 5191 S.aureus DNA sequences
contained on the computer readable medium

Sequence 1027 AA;

Query Match 92.4%; Score 109; DB 2; Length 1027;
Best Local Similarity 95.2%; Pred. No. 1.7e-08;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KPSYQFGHNSVDPEEDTLPK 21
ID AAM89806
AAW89806 standard; protein; 1027 AA.

DB 846 KPSYQFGHNSVDPEEDTLPK 866

RESULT 14

ABU15854
ABU15854 standard; protein; 961 AA.

ABU15854;
19-JUN-2003 (first entry)

Protein encoded by prokaryotic essential gene #1381.

Antisense; prokaryotic essential gene; cell proliferation; drug design.

Staphylococcus aureus.

MO200277183-A2.

03-OCT-2002.

21-MAR-2002; 2002MO-US009107.

21-MAR-2001; 2001US-00815242.

06-SEP-2001; 2001US-00948993.

25-OCT-2001; 2001US-0342923P.

08-FEB-2002; 2002US-00072851.

06-MAR-2002; 2002US-0362699P.

(ELIT-) ELITRA PHARM INC.

Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;
Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;
WPI; 2003-029926/02.

N-PSDB; ACA19724.

New antisense nucleic acids, useful for identifying proteins or screening
for homologous nucleic acids, required for cellular proliferation to
isolate candidate molecules for rational drug discovery programs.

Claim 25; SEQ ID NO 43778; 1766pp; English.

The invention relates to an isolated nucleic acid comprising any one of
the 6213 antisense sequences given in the specification where expression
of the nucleic acid inhibits proliferation of a cell. Also included are:
(1) a vector comprising a promoter operably linked to the nucleic acid
encoding a polypeptide whose expression is inhibited by the antisense
nucleic acid; (2) a host cell containing the vector; (3) an isolated
polypeptide or its fragment whose expression is inhibited by the
antisense nucleic acid; (4) an antibody capable of specifically binding
the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular
proliferation or the activity of a gene in an operon required for
proliferation; (7) identifying a compound that influences the activity of
the gene product or that has an activity against a biological pathway
required for proliferation, or that inhibits cellular proliferation; (8)
identifying a gene required for cellular proliferation or the biological
pathway in which a proliferation-required gene or its gene product lies
or a gene on which the test compound that inhibits proliferation of an
organism acts; (9) manufacturing an antibiotic; (10) profiling a
compound's activity; (11) a culture comprising strains in which the gene
product is overexpressed or underexpressed; (12) determining the extent
to which each of the strains is present in a culture or collection of
strains; or (13) identifying the target of a compound that inhibits the
proliferation of an organism. The antisense nucleic acids are useful for
identifying proteins or screening for homologous nucleic acids required
for cellular proliferation to isolate candidate molecules for rational
drug discovery programs, or for screening homologous nucleic acids
K. pneumoniae or P. aeruginosa. The present sequence is encoded by one of
the target prokaryotic essential genes. Note: The sequence data for this
patent did not form part of the printed specification, but was obtained
in electronic format directly from WIPO at

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CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 961 AA;
Query Match 89.8%; Score 106; DB 6; Length 961;
Best Local Similarity 90.5%; Pred. No. 4.8e-08;
Matches 19; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 KPSYQFGHPSVDFEEDTLPK 21
   ||:|||||
DB 784 KPNYQFGHNSVDFEEDTLPK 804

RESULT 15
AUU33960
ID AUU33960 standard; protein; 978 AA.
XX
AC AUU33960;
XX
DT 14-FEB-2002 (first entry)
XX
DE Staphylococcus aureus cellular proliferation protein #236.
XX
KW Antisense; prokaryotic cellular proliferation protein; antibiotic;
XX antibacterial; drug design.
OS Staphylococcus aureus.
XX
PN WO200170955-A2.
XX
PD 27-SEP-2001.
XX
PF 21-MAR-2001; 2001WO-US009180.
XX
PR 21-MAR-2000; 2000US-0191078P.
XX PR 23-MAY-2000; 2000US-0206848P.
XX PR 26-MAY-2000; 2000US-0207727P.
XX PR 23-OCT-2000; 2000US-0242578P.
XX PR 27-NOV-2000; 2000US-0253625P.
XX PR 22-DEC-2000; 2000US-0257931P.
XX PR 16-FEB-2001; 2001US-0269308P.
XX
PA (ELIT-) ELITRA PHARM INC.
XX
PI Haeselbeck R, Ohlsen KL, Zyskind JW, Wall D, Trawick JD, Carr GJ;
PI Yamamoto RT, Xu HH;
XX
DR N-PSDB; AAS51819.
XX
PT MPI; 2001-611495/70.
XX
PT New polynucleotides for the identification and development of
XX antibiotics, comprise sequences of antisense nucleic acids.
XX
XX Example 3; SEQ ID NO 5456; 511pp; English.
XX
XX The invention relates to antisense inhibitors of genes essential to
XX prokaryotic cellular proliferation, their use in identifying the genes,
XX their use in the discovery of novel antibiotics, the essential genes
XX themselves and the encoded proteins. The prokaryotes used are Escherichia
XX coli, Staphylococcus aureus, Salmonella typhi, Klebsiella pneumoniae,
XX Pseudomonas aeruginosa and Enterococcus faecalis. The invention is also
XX useful for the identification of potential new targets for antibiotic
XX development. The antisense nucleic acids can also be used to identify
XX proteins used in proliferation, to express these proteins, and to obtain
XX antibodies capable of binding to the expressed proteins. The proteins can
XX be used to screen compounds in rational drug discovery programmes. The
XX antisense nucleic acid sequence is also useful to screen for homologous
XX nucleic acids which are required for cell proliferation in a wide variety
XX of organisms. The present sequence represents an essential prokaryotic
XX cellular proliferation protein. Note: The sequence data for this patent
XX did not form part of the printed specification, but was obtained in
XX electronic format directly from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
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XX
SQ Sequence 978 AA;
Query Match 89.8%; Score 106; DB 4; Length 978;
Best Local Similarity 90.5%; Pred. No. 4.9e-08;
Matches 19; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 KPSYQFGHPSVDFEEDTLPK 21
   ||:|||||
DB 815 KPNYQFGHNSVDFEEDTLPK 835

Search completed: October 25, 2005, 19:38:28
Job time : 60.1473 secs
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GenCore version 5.1.6
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OM protein - protein search, using SW model

Run on: October 22, 2005, 02:23:36 ; Search time 15.9358 Seconds
(without alignments)
98.371 Million cell updates/sec

Title: US-10-731-238-22

Sequence: 1 KPSYQFGHPYDFEEDLPK 21

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*

1: /cgn2_6/ptodata/1/1aa/5A.COMB.pep:*

2: /cgn2_6/ptodata/1/1aa/5B.COMB.pep:*

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4: /cgn2_6/ptodata/1/1aa/6B.COMB.pep:*

5: /cgn2_6/ptodata/1/1aa/PCTUS.COMB.pep:*

6: /cgn2_6/ptodata/1/1aa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	118	100.0	21	4	US-09-010-317-22
2	109	92.4	21	4	US-09-010-317-9
3	109	92.4	37	1	US-08-234-622A-4
4	109	92.4	38	1	US-08-294-189-8
5	109	92.4	38	1	US-08-729-767-5
6	109	92.4	114	1	US-08-259-000-3
7	109	92.4	139	3	US-08-856-253-8
8	109	92.4	178	3	US-08-459-135A-12
9	109	92.4	178	3	US-08-495-559-12
10	109	92.4	1027	4	US-08-956-171E-5254
11	109	92.4	1027	4	US-08-781-986A-5254
12	104	88.1	21	4	US-09-010-317-14
13	104	88.1	21	4	US-09-010-317-16
14	104	88.1	21	4	US-09-010-317-23
15	104	88.1	21	4	US-09-010-317-33
16	103	87.3	21	4	US-09-010-317-18
17	103	87.3	21	4	US-09-010-317-24
18	103	87.3	21	4	US-09-010-317-27
19	103	87.3	21	4	US-09-010-317-28
20	103	87.3	21	4	US-09-010-317-30
21	102	86.4	21	4	US-09-010-317-25
22	102	86.4	21	4	US-09-010-317-29
23	102	86.4	21	4	US-09-010-317-31
24	102	86.4	130	2	US-08-459-135A-7
25	102	86.4	130	2	US-08-459-135A-8
26	102	86.4	130	3	US-08-495-559-7
27	102	86.4	130	3	US-08-495-559-8

28	102	86.4	174	2	US-08-459-135A-10	Sequence 10, Appl
29	102	86.4	174	2	US-08-459-135A-13	Sequence 13, Appl
30	102	86.4	174	3	US-08-495-559-10	Sequence 10, Appl
31	102	86.4	174	3	US-08-495-559-13	Sequence 13, Appl
32	102	86.4	176	3	US-08-495-559-6	Sequence 6, Appl
33	102	86.4	181	2	US-08-459-135A-6	Sequence 6, Appl
34	102	86.4	559	4	US-08-956-171E-5251	Sequence 5251, Ap
35	102	86.4	559	4	US-08-781-986A-5251	Sequence 5251, Ap
36	101	85.6	21	4	US-09-010-317-10	Sequence 10, Appl
37	101	85.6	21	4	US-09-010-317-15	Sequence 15, Appl
38	101	85.6	21	4	US-09-010-317-20	Sequence 20, Appl
39	101	85.6	22	4	US-09-010-317-32	Sequence 32, Appl
40	101	85.6	22	4	US-09-010-317-13	Sequence 13, Appl
41	99	83.9	21	4	US-09-010-317-17	Sequence 17, Appl
42	99	83.9	21	4	US-09-010-317-19	Sequence 19, Appl
43	99	83.9	21	4	US-09-010-317-21	Sequence 21, Appl
44	99	83.9	21	4	US-09-010-317-26	Sequence 26, Appl
45	88	74.6	19	1	US-08-234-622A-1	Sequence 1, Appl

ALIGNMENTS

RESULT 1
US-09-010-317-22
Sequence 22, Application US/09010317
Patent No. 6685943
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
APPLICANT: Patti, Joseph M.
APPLICANT: House-Pompeo, Karen L.
APPLICANT: Speziale, Pietro
APPLICANT: Jon, Danny
APPLICANT: Mcgavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
TITLE OF INVENTION: AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAMK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-09-010-317-22
Query Match 100.0%; Score 118; DB 4; Length 21;
Best Local Similarity 100.0%; Pred. No. 2.1e-12;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KPSYQFGHPSVDFEEDTLPK 21
Db 1 KPSYQFGHPSVDFEEDTLPK 21

RESULT 2
US-09-010-317-9
Sequence 9, Application US/09010317
Patent No. 6685943
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
APPLICANT: Patti, Joseph M.
APPLICANT: House-Pompeo, Karen L.
APPLICANT: Speziale, Pietro
APPLICANT: McGavin, Martin J.
APPLICANT: John, Danny
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
TITLE OF INVENTION: AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hbldler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAMK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-09-010-317-9

Query Match 92.4%; Score 109; DB 4; Length 21;
Best Local Similarity 95.2%; Pred. No. 6e-11; 1; Indels 0; Gaps 0;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KPSYQFGHPSVDFEEDTLPK 21
Db 1 KPSYQFGHNSVDFEEDTLPK 21

RESULT 3
US-08-234-622A-4
Sequence 4, Application US/08234622A
Patent No. 5440014
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
APPLICANT: McGavin, Martin
APPLICANT: RAUCCI, Giuseppe
TITLE OF INVENTION: A FIBRONECTIN BINDING PEPTIDE

NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Burns, Doane, Swecker & Mathis
STREET: P.O. Box 1404
CITY: Alexandria
STATE: Virginia
COUNTRY: United States
ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/234,622A
FILING DATE: 28-APR-1994
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: SE 9002617-0
FILING DATE: 10-AUG-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/SE91/00534
FILING DATE: 09-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: Meuth, Donna M
REGISTRATION NUMBER: 36,607
REFERENCE/DOCKET NUMBER: 01885-044
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-6620
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 37 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-234-622A-4

Query Match 92.4%; Score 109; DB 1; Length 37;
Best Local Similarity 95.2%; Pred. No. 1.1e-10;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KPSYQFGHPSVDFEEDTLPK 21
Db 16 KPSYQFGHNSVDFEEDTLPK 36

RESULT 4
US-08-294-189-8
Sequence 8, Application US/08294189
Patent No. 5707822
GENERAL INFORMATION:
APPLICANT: Fischetti, Vincent A.
APPLICANT: Rakonjac, Jasna
APPLICANT: Robbins, John
TITLE OF INVENTION: GENE SERUM OPACITY FACTOR
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack Avenue
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/294,189
FILING DATE: 22-AUG-1994

CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Bag., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-118
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 487-5800
TELEFAX: 201 343-1684
TELEX: 133521
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
ORGANISM: Streptococcus pyogenes
STRAIN: D734
INDIVIDUAL ISOLATE: 22
IMMEDIATE SOURCE:
CLONE: 8AU3a
US-08-294-189-8
Query Match 92.4%; Score 109; DB 1; Length 38;
Best Local Similarity 95.2%; Pred. No. 1,2e-10;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 KPSYFGHPSVDFEETLPK 21
Db 10 KPSYFGHNSVDFEETLPK 30
RESULT 5
US-08-729-767-5
Sequence 5, Application US/08729767
Patent No. 5770702
GENERAL INFORMATION:
APPLICANT: HOOK, Magnus
APPLICANT: LINDBERG, Martin Kjell
APPLICANT: SIGNAS, Lars Christer
APPLICANT: WADSTROM, Torkel Mikael
APPLICANT: FROMAN, Gunnar
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN AS WELL AS
TITLE OF INVENTION: ITS PREPARATION
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Burns, Doane, Swecker & Mathis, L.L.P.
STREET: P.O. Box 1404
CITY: Alexandria
STATE: Virginia
COUNTRY: United States
ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/729,767
FILING DATE: 07-OCT-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/259,000
FILING DATE: 13-JUN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/007,817
FILING DATE: 22-JAN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/201,028
FILING DATE: 01-JUN-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: SE 8702272-9

FILING DATE: 01-JUN-1987
ATTORNEY/AGENT INFORMATION:
NAME: McGowan, Malcolm K.
REGISTRATION NUMBER: 39,300
REFERENCE/DOCKET NUMBER: 012889-036
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-729-767-5
Query Match 92.4%; Score 109; DB 1; Length 38;
Best Local Similarity 95.2%; Pred. No. 1,2e-10;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 KPSYFGHPSVDFEETLPK 21
Db 17 KPSYFGHNSVDFEETLPK 37
RESULT 6
US-08-259-000-3
Sequence 3, Application US/08259000
Patent No. 5571514
GENERAL INFORMATION:
APPLICANT: HOOK, Magnus
APPLICANT: LINDBERG, Martin Kjell
APPLICANT: SIGNAS, Lars Christer
APPLICANT: WADSTROM, Torkel Mikael
APPLICANT: FROMAN, Gunnar
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN AS WELL AS
TITLE OF INVENTION: ITS PREPARATION
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Burns, Doane, Swecker & Mathis
STREET: P.O. Box 1404
CITY: Alexandria
STATE: Virginia
COUNTRY: United States
ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/259,000
FILING DATE: 13-JUN-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: SE 8702272-9
FILING DATE: 01-JUN-1987
ATTORNEY/AGENT INFORMATION:
NAME: Meuth, Donna M
REGISTRATION NUMBER: 36,607
REFERENCE/DOCKET NUMBER: 012885-062
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 114 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-259-000-3

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Query Match      92.4% Score 109; DB 1; Length 114;
Best Local Similarity 95.2%; Pred. No. 4.2e-10;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY          1 KPSYQFGHSPSVDFEEDTLPK 21
            |||||
Db           93 KPSYQFGGHNSVDFEEDTLPK 113

RESULT 7
US-08-856-253-8
Sequence 8, Application US/08856253
Patent No. 6288214
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
APPLICANT: Patil, Joseph M.
APPLICANT: House-Pompeo, Karen
APPLICANT: Schanah, Narayana
APPLICANT: Symersky, Jindrich
TITLE OF INVENTION: COLLAGEN BINDING PROTEIN COMPOSITIONS
TITLE OF INVENTION: AND METHODS OF USE
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: Texas
COUNTRY: U.S.
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/856,253
FILING DATE: Concurrently Herewith
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/017,678
FILING DATE: 16-MAY-1996
ATTORNEY/AGENT INFORMATION:
NAME: Kitchell, Barbara S.
REGISTRATION NUMBER: 33,928
REFERENCE/DOCKET NUMBER: TMK-193
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
TELEFAX: (512) 474-7577
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-08-856-253-8

Query Match      92.4% Score 109; DB 3; Length 139;
Best Local Similarity 95.2%; Pred. No. 5.3e-10;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY          1 KPSYQFGHSPSVDFEEDTLPK 21
            |||||
Db           107 KPSYQFGGHNSVDFEEDTLPK 127

RESULT 8
US-08-459-135A-12
Sequence 12, Application US/08459135A
Patent No. 5955078
GENERAL INFORMATION:
APPLICANT: BURHAM, Martin Karl Russel
APPLICANT: CHOPRA, Ian
```

```

APPLICANT: CRITCHLEY, Ian Alfred
APPLICANT: KNOWLES, David Justin Charles
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN: MONOCLONAL ANTIBODY AND THEIR USE
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESSES:
ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
STATE: PA
COUNTRY: U.S.A.
ZIP: 19406-0939
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq, Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/459,135A
FILING DATE: 02-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB/94/00215
FILING DATE: 04-Feb-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Gimmì, Edward R
REGISTRATION NUMBER: 38,891
REFERENCE/DOCKET NUMBER: PJ0591C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-4478
TELEFAX: 610-270-5090
TELEX:
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 178 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: Protein
US-08-459-135A-12

Query March          92.4%; Score 109; DB 2; Length 178;
Best Local Similarity 95.2%; Pred. No. 7e-10;
Matches   20; Conservative    0; Mismatches    1; Indels      0; Gaps      0;

QY       1 KPSYFGSHPSVDFEEDTLPR 21
         |||||
Db        93 KPSYFGSHNSVDPEEDTLPR 113

RESULT 9
US-08-495-559-12
Sequence 12, Application US/08495559A
Patent No. 6054572
GENERAL INFORMATION:
APPLICANT: BURMAN, Martin Karl Russel
APPLICANT: CHOERA, Ian
APPLICANT: CRITCHLEY, Ian Alfred
APPLICANT: KNOWLES, David Justin Charles
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN: MONOCLONAL
TITLE OF INVENTION: ANTIBODY AND THEIR USE IN PREVENTING BACTERIAL ADHESION
FILE REFERENCE: PJ0591
CURRENT APPLICATION NUMBER: US/08/495,559A
CURRENT FILING DATE: 1995-08-03
EARLIER APPLICATION NUMBER: GB 9302289.5
EARLIER FILING DATE: 1993-02-05
EARLIER APPLICATION NUMBER: GB 9321592.9
EARLIER FILING DATE: 1993-10-20
NUMBER OF SEQ ID NOS: 13
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 12
LENGTH: 178
TYPE: PRP

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ORGANISM: Staphylococcus aureus
US-08-495-559-12

Query Match 92.4%; Score 109; DB 3; Length 178;
Best Local Similarity 95.2%; Pred. No. 7e-10; 1; Indels 0; Gaps 0;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KPSYFGHPSVDFEEDTLPK 21
Db 93 KPSYFGHNSVDFEEDTLPK 113

RESULT 10

US-08-956-171E-5254
Sequence 5254, Application US/08956171E
Patent No. 6593114
GENERAL INFORMATION:
APPLICANT: Charles Kunesh
Gil H. Choi
Patrick S. Dillon
Craig A. Rosen
Steven C. Barash
Michael R. Fannon
TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
NUMBER OF SEQUENCES: 5256
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COUNTRY: USA
ZIP: 20850

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/956.171E
FILING DATE: 20-Oct-1997
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 60/009,861
FILING DATE: January 5, 1996
APPLICATION NUMBER: 08/781,986
FILING DATE: January 3, 1997

ATTORNEY/AGENT INFORMATION:

NAME: Mark J. Hyman
REGISTRATION/DOCKET NUMBER: 46,789
REFERENCE/DOCKET NUMBER: PB248P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (240) 314-1224
TELEFAX: (301) 309-8439

INFORMATION FOR SEQ ID NO: 5254:

SEQUENCE CHARACTERISTICS:
LENGTH: 1027 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 5254:
US-08-956-171E-5254

Query Match 92.4%; Score 109; DB 4; Length 1027;
Best Local Similarity 95.2%; Pred. No. 5.3e-09;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KPSYFGHPSVDFEEDTLPK 21
Db 846 KPSYFGHNSVDFEEDTLPK 866

RESULT 11

US-08-781-986A-5254
Sequence 5254, Application US/08781986A
Patent No. 6737248

GENERAL INFORMATION:
APPLICANT: Charles Kunesh
TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
NUMBER OF SEQUENCES: 5255

CORRESPONDENCE ADDRESS:

ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COUNTRY: USA
ZIP: 20850

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/781,986A
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:

ATTORNEY/AGENT INFORMATION:

NAME: Benson, Bob
REGISTRATION/DOCKET NUMBER: 30,446
REFERENCE/DOCKET NUMBER: PB248PP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
TELEFAX: (301) 309-8512

INFORMATION FOR SEQ ID NO: 5254:

SEQUENCE CHARACTERISTICS:
LENGTH: 1027 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-781-986A-5254

Query Match 92.4%; Score 109; DB 4; Length 1027;
Best Local Similarity 95.2%; Pred. No. 5.3e-09;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KPSYFGHPSVDFEEDTLPK 21
Db 846 KPSYFGHNSVDFEEDTLPK 866

RESULT 12

US-09-010-317-14
Sequence 14, Application US/09010317
Patent No. 6685943

GENERAL INFORMATION:

APPLICANT: Hook, Magnus
APPLICANT: Patli, Joseph M.
APPLICANT: House-Pompeo, Karen L.
APPLICANT: Speziale, Pietro

APPLICANT: McGavin, Martin J.

TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS

NUMBER OF SEQUENCES: 105

CORRESPONDENCE ADDRESS:

ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-09-010-317-14

Query Match 88.1%; Score 104; DB 4; Length 21;
Best Local Similarity 95.0%; Pred. No. 3.8e-10;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 2 PSYQFGHPSVDFEEDTLPK 21
Db 2 PSYQFGHNSVDFEEDTLPK 21

RESULT 13
US-09-010-317-16
Sequence 16, Application US/09010317
Patent No. 6685943
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
APPLICANT: Patil, Joseph M.
APPLICANT: House-Pompeo, Karen L.
APPLICANT: Speziale, Pietro
APPLICANT: Joh, Danny
APPLICANT: McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
NUMBER OF SEQUENCES: 105
TITLE OF INVENTION: AND METHODS OF USE
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-09-010-317-23

TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-09-010-317-16

Query Match 88.1%; Score 104; DB 4; Length 21;
Best Local Similarity 90.5%; Pred. No. 3.8e-10;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 KPSYQFGHPSVDFEEDTLPK 21
Db 1 KPSYQFGHNSVDFEEDTLPK 21

RESULT 14
US-09-010-317-23
Sequence 23, Application US/09010317
Patent No. 6685943
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
APPLICANT: Patil, Joseph M.
APPLICANT: House-Pompeo, Karen L.
APPLICANT: Speziale, Pietro
APPLICANT: Joh, Danny
APPLICANT: McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
NUMBER OF SEQUENCES: 105
TITLE OF INVENTION: AND METHODS OF USE
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-09-010-317-23

Query Match 88.1%; Score 104; DB 4; Length 21;
Best Local Similarity 90.5%; Pred. No. 3.8e-10;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 KPSYQFGHPSVDFEEDTLPK 21
Db 1 KPSYQFGHNSVDFEEDTLPK 21

Db 1 KPSYQFGGHNVPDEEDTLRK 21

RESULT 15

US-09-010-317-33
 ; Sequence 33, Application US/09010317
 ; Patent No. 6685943
 ; GENERAL INFORMATION:
 ; APPLICANT: Hook, Magnus
 ; APPLICANT: Patti, Joseph M.
 ; APPLICANT: House-Pompeo, Karen L.
 ; APPLICANT: Speziale, Pietro
 ; APPLICANT: Jon, Danny
 ; APPLICANT: McGavin, Martin J.
 ; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
 ; TITLE OF INVENTION: AND METHODS OF USE
 ; NUMBER OF SEQUENCES: 105
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Arnold, White & Durkee
 ; STREET: P.O. Box 4433
 ; CITY: Houston
 ; STATE: TX
 ; COUNTRY: USA
 ; ZIP: 77210-4433
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patentin Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/010.317
 ; FILING DATE:
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 60/036,139
 ; FILING DATE: 21-JAN-1997
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Hibler, David W.
 ; REGISTRATION NUMBER: 41,071
 ; REFERENCE/DOCKET NUMBER: TMRK:189
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 512-418-3000
 ; TELEFAX: 512-474-7577
 ; INFORMATION FOR SEQ ID NO: 33:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 21 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS:
 ; TOPOLOGY: linear
 ; US-09-010-317-33

Query Match 88.1%; Score 104; DB 4; Length 21;
 Best Local Similarity 95.0%; Pred. No. 3.8e-10;
 Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KPSYQFGGHNVPDEEDTLRP 20
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 Db 1 KPSYQFGGHNVPDEEDTLRP 20

Search completed: October 22, 2005, 03:51:12
 Job time : 16.9358 secs

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GenCore version 5.1.6
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OM protein - protein search, using SW model

Run on: October 22, 2005, 10:49:15 ; Search time 59.2367 Seconds
(without alignments)
148.005 Million cell updates/sec

Title: US-10-731-238-22
Perfect score: 118
Sequence: 1 KPSYQFGHPSVDFEEDLPK 21

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 1862951 seqs, 417491010 residues
Total number of hits satisfying chosen parameters: 1862951

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

Published Applications AA:
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2: /cgn2_6/prodata/2/pubpaa/PCR_NEW_PUB.pep:*
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19: /cgn2_6/prodata/2/pubpaa/US11A_PUBCOMB.pep:*
20: /cgn2_6/prodata/2/pubpaa/US11_NEW_PUB.pep:*
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22: /cgn2_6/prodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	118	100.0	21	18	US-10-731-238-22
2	109	92.4	21	18	US-10-731-238-9
3	109	92.4	37	20	US-11-066-697-1134
4	109	92.4	139	9	US-09-813-820-8
5	109	92.4	1018	9	US-09-815-242-5797
6	109	92.4	1018	9	US-09-815-242-12838
7	109	92.4	1018	17	US-10-470-048B-68
8	109	92.4	1027	8	US-08-781-986A-5254
9	109	92.4	1027	15	US-10-329-624-5254
10	106	89.8	961	15	US-10-282-122A-43778
11	106	89.8	978	9	US-09-815-242-5456

12	106	89.8	1001	9	US-09-815-242-12686	Sequence 12686, A
13	106	89.8	1038	15	US-10-282-122A-43827	Sequence 43827, A
14	104	88.1	21	18	US-10-731-238-14	Sequence 14, Appl
15	104	88.1	21	18	US-10-731-238-16	Sequence 16, Appl
16	104	88.1	21	18	US-10-731-238-23	Sequence 23, Appl
17	104	88.1	21	18	US-10-731-238-33	Sequence 33, Appl
18	103	87.3	21	18	US-10-731-238-18	Sequence 18, Appl
19	103	87.3	21	18	US-10-731-238-24	Sequence 24, Appl
20	103	87.3	21	18	US-10-731-238-27	Sequence 27, Appl
21	103	87.3	21	18	US-10-731-238-28	Sequence 28, Appl
22	103	87.3	21	18	US-10-731-238-30	Sequence 30, Appl
23	102	86.4	21	18	US-10-731-238-25	Sequence 25, Appl
24	102	86.4	21	18	US-10-731-238-29	Sequence 29, Appl
25	102	86.4	21	18	US-10-731-238-31	Sequence 31, Appl
26	102	86.4	388	8	US-08-901-062-1	Sequence 1, Appl
27	102	86.4	559	8	US-08-781-986A-5251	Sequence 5251, Ap
28	102	86.4	559	15	US-10-329-624-5251	Sequence 5251, Ap
29	102	86.4	940	17	US-10-470-048B-424	Sequence 424, Ap
30	102	86.4	948	17	US-10-470-048B-69	Sequence 69, Appl
31	101	85.6	21	18	US-10-731-238-10	Sequence 10, Appl
32	101	85.6	21	18	US-10-731-238-15	Sequence 15, Appl
33	101	85.6	21	18	US-10-731-238-20	Sequence 20, Appl
34	101	85.6	21	18	US-10-731-238-32	Sequence 32, Appl
35	101	85.6	22	18	US-10-731-238-13	Sequence 13, Appl
36	99	83.9	21	18	US-10-731-238-17	Sequence 17, Appl
37	99	83.9	21	18	US-10-731-238-19	Sequence 19, Appl
38	99	83.9	21	18	US-10-731-238-21	Sequence 21, Appl
39	99	83.9	21	18	US-10-731-238-26	Sequence 26, Appl
40	81	68.6	21	18	US-10-731-238-34	Sequence 34, Appl
41	70	59.3	10	18	US-10-731-238-61	Sequence 61, Appl
42	54	45.8	10	18	US-10-731-238-95	Sequence 95, Appl
43	53	44.9	10	18	US-10-731-238-101	Sequence 101, Ap
44	53	44.9	11	18	US-10-731-238-86	Sequence 86, Appl
45	51	43.2	10	18	US-10-731-238-96	Sequence 96, Appl

ALIGNMENTS

RESULT 1
US-10-731-238-22
; Sequence 22, Application US/10731238
; Publication No. US20050123552A1
; GENERAL INFORMATION:
; APPLICANT: Hook, Magnus
; Partl, Joseph M.
; House-Pompeo, Karen L.
; Speziale, Pietro
; John, Danny
; McGavin, Martin J.
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
; AND METHODS OF USE
; NUMBER OF SEQUENCES: 105
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: TX
; COUNTRY: USA
; ZIP: 77210-4433
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/731,238
; FILING DATE: 10-Dec-2003
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/010,317
; FILING DATE: 21-Jan-1998
; APPLICATION NUMBER: US 60/036,139

FILED DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAMK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 22:
US-10-731-238-22

Query Match 100.0%; Score 118; DB 18; Length 21;
Best Local Similarity 100.0%; Pred. No. 3, 4e-11;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KPSYQFGHPSVDFEEDTLPK 21
|||||
1 KPSYQFGHPSVDFEEDTLPK 21

RESULT 2
US-10-731-238-9
Sequence 9, Application US/10731238
Publication No. US20050123552A1
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
Patel, Joseph M.
House-Pompeo, Karen L.
Speziale, Pietro
Joh, Danny
McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/731,238
FILING DATE: 10-Dec-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE: 21-Jan-1998
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAMK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>

TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 9:
US-10-731-238-9

Query Match 92.4%; Score 109; DB 18; Length 21;
Best Local Similarity 95.2%; Pred. No. 8, 7e-10;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KPSYQFGHPSVDFEEDTLPK 21
|||||
1 KPSYQFGHNSVDFEEDTLPK 21

RESULT 3
US-11-066-697-1134
Sequence 1134, Application US/11066697
Publication No. US20050187159A1
GENERAL INFORMATION:
APPLICANT: Bridon, Dominique P.
APPLICANT: Ezrin, Alan M.
APPLICANT: Milner, Peter G.
APPLICANT: Holmes, Darren L.
APPLICANT: Thibaudau, Karen
TITLE OF INVENTION: PROTECTION OF ENDOGENOUS THERAPEUTIC PEPTIDES FROM
TITLE OF INVENTION: PEPTIDASE ACTIVITY THROUGH CONJUGATION TO BLOOD
FILE REFERENCE: 500862002301
CURRENT APPLICATION NUMBER: US/11/066,697
CURRENT FILING DATE: 2005-02-25
PRIOR APPLICATION NUMBER: 09/657,276
PRIOR FILING DATE: 2000-09-07
PRIOR APPLICATION NUMBER: 60/153,406
PRIOR FILING DATE: 1998-09-10
PRIOR APPLICATION NUMBER: 60/159,783
PRIOR FILING DATE: 1999-10-15
NUMBER OF SEQ ID NOS: 1617
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 1134
LENGTH: 37
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-11-066-697-1134

Query Match 92.4%; Score 109; DB 20; Length 37;
Best Local Similarity 95.2%; Pred. No. 1, 6e-09;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KPSYQFGHPSVDFEEDTLPK 21
|||||
16 KPSYQFGHNSVDFEEDTLPK 36

RESULT 4
US-09-813-820-8
Sequence 8, Application US/09813820
Patent No. US2002010262A1
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
Patel, Joseph M.
House-Pompeo, Karen
Shanham, Narayana
Sywetsky, Jindrich
TITLE OF INVENTION: COLLAGEN BINDING PROTEIN COMPOSITIONS
AND METHODS OF USE
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: Texas

```

; COUNTRY: U.S.
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/813,820
; FILING DATE: 22-Mar-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/856,253
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Kitchell, Barbara S.
; REGISTRATION NUMBER: 33,928
; REFERENCE/DOCKET NUMBER: TAMK.193
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (512) 418-3000
; TELEFAX: (512) 474-7577
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 139 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-09-813-820-8

Query Match          92.4%; Score 109; DB 9; Length 139;
Best Local Similarity 95.2%; Pred. No. 7,1e-09;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 KPSYQFGHNSVDFEEDTLRK 21
Db      107 KPSYQFGHNSVDFEEDTLRK 127

RESULT 5
US-09-815-242-5797
; Sequence 5797, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Karl L.
; APPLICANT: Zykkind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; FILE REFERENCE: ELITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version 4.0
; FILE REFERENCE: SONN.03505
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; SEQ ID NO 5797
; LENGTH: 1018
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-09-815-242-5797

Query Match          92.4%; Score 109; DB 9; Length 1018;
Best Local Similarity 95.2%; Pred. No. 6,6e-08;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 KPSYQFGHNSVDFEEDTLRK 21
Db      837 KPSYQFGHNSVDFEEDTLRK 857

RESULT 6
US-09-815-242-12838
; Sequence 12838, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Karl L.
; APPLICANT: Zykkind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; FILE REFERENCE: ELITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12838
; LENGTH: 1018
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-09-815-242-12838

Query Match          92.4%; Score 109; DB 9; Length 1018;
Best Local Similarity 95.2%; Pred. No. 6,6e-08;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 KPSYQFGHNSVDFEEDTLRK 21
Db      837 KPSYQFGHNSVDFEEDTLRK 857

RESULT 7
US-10-470-048B-68
; Sequence 68, Application US/10470048B
; Publication No. US2005003744A1
; GENERAL INFORMATION:
; APPLICANT: MEINKE ET AL.
; TITLE OF INVENTION: A METHOD FOR IDENTIFICATION, ISOLATION AND PRODUCTION OF
; FILE REFERENCE: SONN.03505
```

;; CURRENT APPLICATION NUMBER: US/10/470,048B
;; CURRENT FILING DATE: 2003-07-25
;; NUMBER OF SEQ ID NOS: 603
;; SOFTWARE: PatentIn version 3.1
;; SEQ ID NO 68
;; LENGTH: 1018
;; TYPE: PRF
;; ORGANISM: Staphylococcus aureus
US-10-470-048B-68

Query Match 92.4%; Score 109; DB 17; Length 1018;
Best Local Similarity 95.2%; Pred. No. 6.6e-08;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KPSYQFGHPSYDFEEDTLPK 21
DB 837 KPSYQFGHNSYDFEEDTLPK 857

RESULT 8
US-08-781-986A-5254
; Sequence 5254, Application US/08781986A
; Publication No. US20030054436A1
; GENERAL INFORMATION:
; APPLICANT: Charles Kunsch
; TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
; NUMBER OF SEQUENCES: 5255
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/781,986A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Benson, Bob
; REGISTRATION NUMBER: 30,446
; REFERENCE/DOCKET NUMBER: PB248PP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 5254:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1027 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-781-986A-5254

Query Match 92.4%; Score 109; DB 8; Length 1027;
Best Local Similarity 95.2%; Pred. No. 6.6e-08;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KPSYQFGHPSYDFEEDTLPK 21
DB 846 KPSYQFGHNSYDFEEDTLPK 866

RESULT 9
US-10-329-624-5254

;; Sequence 5254, Application US/10329624
;; Publication No. US20040043037A1
;; GENERAL INFORMATION:
;; APPLICANT: Charles Kunsch
;; Gail H. Choi
;; Patrick S. Dillon
;; Craig A. Rosen
;; Steven C. Barash
;; Michael R. Fannon
;; TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
;; NUMBER OF SEQUENCES: 5256
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Human Genome Sciences, Inc.
;; STREET: 9410 Key West Avenue
;; CITY: Rockville
;; STATE: Maryland
;; COUNTRY: USA
;; ZIP: 20850
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
;; COMPUTER: HP Vectra 486/33
;; OPERATING SYSTEM: MSDOS version 6.2
;; SOFTWARE: ASCII Text
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/10/329,624
;; FILING DATE: 27-Dec-2002
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 08/956,171
;; FILING DATE: October 20, 1997
;; APPLICATION NUMBER: 60/009,861
;; FILING DATE: January 5, 1996
;; APPLICATION NUMBER: 08/781,986
;; FILING DATE: January 3, 1997
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Mark J. Hyman
;; REGISTRATION NUMBER: 46,789
;; REFERENCE/DOCKET NUMBER: PB248P1D1
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (240) 314-1224
;; TELEFAX: (301) 309-8439
;; INFORMATION FOR SEQ ID NO: 5254:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 1027 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; SEQUENCE DESCRIPTION: SEQ ID NO: 5254:
US-10-329-624-5254

Query Match 92.4%; Score 109; DB 15; Length 1027;
Best Local Similarity 95.2%; Pred. No. 6.6e-08;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KPSYQFGHPSYDFEEDTLPK 21
DB 846 KPSYQFGHNSYDFEEDTLPK 866

RESULT 10
US-10-282-122A-43778
; Sequence 43778, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant

```

; APPLICANT: Yamamoto, Robert
; APPLICANT: Foreyth, R.
; APPLICANT: Xu, H.
; FILE REFERENCE: ELITRA.034A
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; CURRENT APPLICATION NUMBER: US/10/282.122A
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 43778
; LENGTH: 961
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
; US-10-282-122A-43778

Query Match      89.8%; Score 106; DB 15; Length 961;
Best Local Similarity 90.5%; Pred. No. 1.8e-07;
Matches 19; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1 KPSYFGGHPDVDFEEDTLPK 21
Db      784 KPNYFGGHNVDVEEDTLPK 804

RESULT 11
US-09-815-242-5456
; Sequence 5456, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Karl L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; FILE REFERENCE: ELITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: PatsSeq for Windows Version 4.0
; SEQ ID NO 12686
; LENGTH: 1001
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
; US-09-815-242-12686

Query Match      89.8%; Score 106; DB 15; Length 1001;
Best Local Similarity 90.5%; Pred. No. 1.8e-07;
Matches 19; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
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; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: PatsSeq for Windows Version 4.0
; SEQ ID NO 5456
; LENGTH: 978
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
; US-09-815-242-5456

Query Match      89.8%; Score 106; DB 9; Length 978;
Best Local Similarity 90.5%; Pred. No. 1.8e-07;
Matches 19; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1 KPSYFGGHPDVDFEEDTLPK 21
Db      815 KPNYFGGHNVDVEEDTLPK 835

RESULT 12
US-09-815-242-12686
; Sequence 12686, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Karl L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; FILE REFERENCE: ELITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: PatsSeq for Windows Version 4.0
; SEQ ID NO 12686
; LENGTH: 1001
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
; US-09-815-242-12686

Query Match      89.8%; Score 106; DB 9; Length 1001;
Best Local Similarity 90.5%; Pred. No. 1.9e-07;
Matches 19; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1 KPSYFGGHPDVDFEEDTLPK 21
Db      838 KPNYFGGHNVDVEEDTLPK 858

RESULT 13
US-10-282-122A-43827
; Sequence 43827, Application US/10282122A
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Publication No. US20040029129A1
GENERAL INFORMATION:
APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Hasebeck, Robert
APPLICANT: Ohlsen, Kari
APPLICANT: Zyskind, Judith
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John
APPLICANT: Carr, Grant
APPLICANT: Yamamoto, Robert
APPLICANT: Foreyeth, R.
APPLICANT: Xu, H.
TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REFERENCE: ELITPA.034A
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/230,335
PRIOR FILING DATE: 2000-09-06
PRIOR APPLICATION NUMBER: 60/230,347
PRIOR FILING DATE: 2000-09-09
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/267,636
PRIOR FILING DATE: 2001-02-09
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 78614
SOFTWARE: PatentIn version 3.1
SEQ ID NO 43827
LENGTH: 1038
TYPE: PRT
ORGANISM: Staphylococcus aureus
US-10-282-122A-43827
Query Match 89.8%; Score 106; DB 15; Length 1038;
Best Local Similarity 90.5%; Pred. No. 2e-07;
Matches 19; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 KPSYQFGHPSVDFEEDTLPK 21
DB 833 KPMYQFGHNSVDFEEDTLPK 853
RESULT 14
US-10-731-238-14
Sequence 14, Application US/10731238
Publication No. US20050123552A1
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
Patli, Joseph M.
House-Pompeo, Karen L.
Speziale, Pietro
John, Danny
McGavin, Martin J.
TITLE OF INVENTION: AND METHODS OF USE
FIBRONECTIN BINDING PROTEIN COMPOSITIONS
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433

CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/731,238
FILING DATE: 10-Dec-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE: 21-Jan-1998
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TANK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 14:
US-10-731-238-14
Query Match 88.1%; Score 104; DB 18; Length 21;
Best Local Similarity 95.0%; Pred. No. 5.2e-09;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2 PSYQFGHNSVDFEEDTLPK 21
DB 2 PSYQFGHNSVDFEEDTLPK 21
RESULT 15
US-10-731-238-16
Sequence 16, Application US/10731238
Publication No. US20050123552A1
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
Patli, Joseph M.
House-Pompeo, Karen L.
Speziale, Pietro
John, Danny
McGavin, Martin J.
TITLE OF INVENTION: AND METHODS OF USE
FIBRONECTIN BINDING PROTEIN COMPOSITIONS
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/731,238
FILING DATE: 10-Dec-2003
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE: 21-Jan-1998
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAMK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 16:
US-10-731-238-16

Query Match 88.1%; Score 104; DB 18; Length 21;
Best Local Similarity 90.5%; Pred. No. 5.2e-09;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 KPSYQFGHPSVDFFEDTLRK 21
DB 1 KPPYQFGHNSVDFFEDTLRK 21

Search completed: October 22, 2005, 11:34:40
Job time : 60.2367 secs

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OM protein - protein search, using sw model

Run on: October 22, 2005, 02:23:36 ; Search time 10.5465 Seconds
(without alignments)
191.586 Million cell updates/sec

Title: US-10-731-238-22
Perfect score: 118
Sequence: 1 KPSYQFGHPSVDFEEDLPK 21

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_79:.*
1: p1r1:.*
2: p1r2:.*
3: p1r3:.*
4: p1r4:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	109	92.4	1018	2 A32192	fibronectin-binding
2	106	89.8	961	2 G90053	hypothetical prote
3	106	89.8	1038	2 H90053	hypothetical prote
4	102	86.4	940	2 S19702	fibronectin-bindin
5	46	39.0	241	1 RRMZPP	phosphoprotein p -
6	46	39.0	387	2 T38449	extracellular prot
7	46	39.0	468	2 T26081	hypothetical prote
8	46	39.0	548	2 T23436	hypothetical prote
9	46	39.0	867	2 DB6393	hypothetical prote
10	46	39.0	1025	2 T45647	receptor protein k
11	45	38.1	347	1 HPMS	haptoglobin precu
12	45	38.1	350	2 S70135	hypothetical prote
13	45	38.1	1047	2 B71402	hypothetical prote
14	44	37.3	95	2 T18730	hypothetical prote
15	44	37.3	175	2 S42095	capsid protein - o
16	44	37.3	216	2 A39926	hypothetical prote
17	44	37.3	226	2 T30478	hypothetical prote
18	44	37.3	257	2 A36057	MHC class I histoc
19	44	37.3	277	2 AD3256	aminocyclase (EC 3
20	44	37.3	396	2 A61800	peptidase homolog
21	44	37.3	427	2 D95159	3-phosphoshikimate
22	44	37.3	431	2 D98025	3-phosphoshikimate
23	44	37.3	1322	2 A59288	myosin heavy chain
24	43.5	36.9	558	2 S32914	type IV pilus asse
25	43.5	36.9	558	2 C81213	hypothetical prote
26	43.5	36.9	561	2 H64238	hypothetical prote
27	43	36.4	241	1 RRMZ	phosphoprotein p -
28	43	36.4	270	2 P84255	hypothetical prote
29	43	36.4	323	2 T52297	squamosa promoter

30	43	36.4	457	2 D69059	glycinamide ribonu
31	43	36.4	705	2 C84406	hypothetical prote
32	43	36.4	733	2 S44254	alpha-galactosidas
33	43	36.4	1926	2 JC4842	DNA-binding nuclea
34	43	36.4	3137	2 A37797	collagen alpha 3(V
35	42.5	36.0	234	2 T30473	late expression fa
36	42.5	36.0	284	2 B69945	phage-related prot
37	42.5	36.0	417	2 T34930	probable secreted
38	42.5	36.0	487	2 T21645	hypothetical prote
39	42.5	36.0	492	2 T43346	nuclear receptor N
40	42.5	36.0	1091	2 S33850	fibronectin-binding
41	42	35.6	115	2 D89103	protein C18B10.5 l
42	42	35.6	188	2 B97318	transcription regu
43	42	35.6	253	2 S73563	hypothetical prote
44	42	35.6	283	2 S61156	hypothetical prote
45	42	35.6	399	1 D69056	conserved hypochet

ALIGNMENTS

RESULT 1
A32192
fibronectin-binding protein - Staphylococcus aureus
C/Species: Staphylococcus aureus
C/Date: 31-Jul-1989 #sequence_revision 31-Jul-1989 #text_change 16-Feb-1997
C/Accession: A32192
R/Signaes, C.; Raucel, G.; Joensen, K.; Lindgren, P.E.; Anantharamaiah, G.M.; Hoeoek, M.
Proc. Natl. Acad. Sci. U.S.A. 86, 699-703, 1989
A/Title: Nucleotide sequence of the gene for a fibronectin-binding protein from Staphyloc
A/Reference number: A32192; PMID:8908998; PMID:2521391
A/Accession: A32192
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-1018 <SIG>
A/Cross-references: GB:U04151
C/Keywords: fibronectin binding

Query Match 92.4%; Score 109; DB 2; Length 1018;
Best Local Similarity 95.2%; Pred. No. 6.1e-09;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KPSYQFGHPSVDFEEDLPK 21
DB 837 KPSYQFGHNSVDFEEDLPK 857

RESULT 2

hypothetical protein fnbB [imported] - Staphylococcus aureus (strain N315)
C/Species: Staphylococcus aureus
C/Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C/Accession: G90053
R/Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Gai, L.; Oguci
ma, A.; Mizutani-Ti, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.; I
c., Shiba, T.; Hattori, W.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
A/Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.
A/Reference number: A89758; PMID:21311952; PMID:11418146
A/Accession: G90053
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-961 <KUR>
A/Cross-references: UNIPROT:Q99RD3; GB:BA000018; PID:g13702452; PID:BA043593.1; GSPDB:G
A/Experimental source: strain N315
C/Genetics:
A/Genes: fnbB

Query Match 89.8%; Score 106; DB 2; Length 961;
Best Local Similarity 90.5%; Pred. No. 1.7e-08;
Matches 19; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 KPSYQFGHPSVDFEEDLPK 21

Db 784 KPNYQFGHNSVDFEEDTLPK 804

RESULT 3

H90053

hypothetical protein fnb [imported] - Staphylococcus aureus (strain N315)

C:Species: Staphylococcus aureus

C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004

C:Accession: H90053

R:Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguc

ma, A.; Mizutani-Uji, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kato, C.; Sekimizu, K.;

C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramoto, K.

Lancet 357, 1225-1240, 2001

A:Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.

A:Reference number: A89736; PMID:21311952; PMID:11418146

A:Accession: H90053

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-1038 <KUN>

A:Cross-references: UNIPROT:Q99RP2; GB:BA000018; PDB:1G13702453; PDB:1BAB43594.1; GSPDB:C

A:Experimental source: strain N315

C:Genetics:

A:Gene: fnb

Query Match 89.8%; Score 106; DB 2; Length 1038;

Best Local Similarity 90.5%; Pred. No. 1.9e-08; Indels 0; Gaps 0;

Matches 19; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 KPSYQFGHPSVDFEEDTLPK 21

Db 833 KPNYQFGHNSVDFEEDTLPK 853

RESULT 4

S19702

fibronecin-binding protein B - Staphylococcus aureus

C:Species: Staphylococcus aureus

C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004

C:Accession: S19702

R:Joensen, K.; Signaes, C.; Mueller, H.P.; Lindberg, M.

Eur. J. Biochem. 202, 1041-1048, 1991

A:Title: Two different genes encode fibronecin binding proteins in Staphylococcus aureus

A:Reference number: S19702; PMID:92111475; PMID:1837266

A:Accession: S19702

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-940 <JOE>

A:Cross-references: UNIPROT:Q53682; EMBL:X62992; NID:G49040; PDB:1CAA44726.1; PDB:1G58156

C:Keywords: fibronecin binding

Query Match 86.4%; Score 102; DB 2; Length 940;

Best Local Similarity 85.7%; Pred. No. 7.2e-08; Indels 0; Gaps 0;

Matches 18; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 KPSYQFGHPSVDFEEDTLPK 21

Db 773 KPNYQFGHNSVDFEEDTLPK 793

RESULT 5

RRNZPP

phosphoprotein P - human respiratory syncytial virus (strain Long)

C:Species: human respiratory syncytial virus

C:Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 09-Jul-2004

C:Accession: S07428

R:Lopez, J.A.; Villanueva, N.; Melero, J.A.; Portela, A.

Virus Res. 10, 249-262, 1988

A:Title: Nucleotide sequence of the fusion and phosphoprotein genes of human respiratory

A:Reference number: S07428; PMID:88323192; PMID:3414184

A:Accession: S07428

A:Molecule type: mRNA

A:Residues: 1-241 <LOP>

A:Cross-references: UNIPROT:P12579; EMBL:M2644; NID:G333949; PDB:AAA47415.1; PDB:G33399;
C:Genetics:
A:Gene: P
C:Superfamily: respiratory syncytial virus phosphoprotein P
C:Keywords: phosphoprotein

Query Match 39.0%; Score 46; DB 1; Length 241;
Best Local Similarity 50.0%; Pred. No. 12;
Matches 10; Conservative 3; Mismatches 5; Indels 2; Gaps 1;

QY 1 KPSYQFGHPSVDFEEDTLPK 20

Db 76 KPNYQ--RKPLVFKEDP 93

RESULT 6

I38449

extracellular protein - human

C:Species: Homo sapiens (man)

C:Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 21-Jul-2000

C:Accession: I38449

R:Jleicka-Czernik, B.; Lumpkin, C.K.

Mol. Cell. Biol. 15, 120-128, 1995

A:Title: An overexpressed gene transcript in senescent and quiescent human fibroblasts er

A:Reference number: I38449; PMID:95097983; PMID:7799918

A:Accession: I38449

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-387 <RES>

A:Cross-references: EMBL:U03877; NID:G458227; PDB:AAA65590.1; PDB:G458228

C:Genetics:

A:Gene: SI-5

Query Match 39.0%; Score 46; DB 2; Length 387;
Best Local Similarity 47.4%; Pred. No. 21;
Matches 9; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

QY 2 PSYQFGHPSVDFEEDTLPK 20

Db 97 PSYQFGHPSVDFEEDTLPK 115

RESULT 7

T26081

hypothetical protein W02A2.7 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004

C:Accession: T26081

R:Ainscough, R.

submitted to the EMBL Data Library, November 1996

A:Reference number: Z20148

A:Accession: T26081

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-468 <WIL>

A:Cross-references: UNIPROT:Q9XUB2; EMBL:Z82286; PDB:1CAB05310.1; GSPDB:GN00022; CESP:W02

A:Experimental source: clone W02A2

C:Genetics:

A:Gene: CESP:W02A2.7

A:Map position: 4

A:introns: 38/3; 212/2; 353/3; 403/2

Query Match 39.0%; Score 46; DB 2; Length 468;
Best Local Similarity 35.0%; Pred. No. 25;
Matches 7; Conservative 5; Mismatches 8; Indels 0; Gaps 0;

QY 2 PSYQFGHPSVDFEEDTLPK 21

Db 351 PSYQFGHPSVDFEEDTLPK 370

RESULT 8

T23436

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hypothetical protein K08C7.2 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T23436
R:Berks, M.
submitted to the EMBL Data Library, March 1996
A:Reference number: Z19740
A:Accession: T23436
A:Status: preliminary; translated from GB/EMBL/DBD
A:Molecule type: DNA
A:Residues: 1-548 <WIL>
A:Cross-references: UNIPROT:Q21311; EMBL:Z70286; PDB:CAA94291.1; GSPDB:GN00022; CESP:K0
A:Experimental source: clone K08C7
C:Genetics:
A:Gene: CESP:K08C7.2
A:Map position: 4
A:Introns: 53/1; 134/2; 179/3; 326/3; 466/3
C:Superfamily: dimethylalanine monooxygenase (N-oxide-forming)

Query Match          39.0%; Score 46; DB 2; Length 548;
Best Local Similarity 52.4%; Pred. No. 31;
Matches 11; Conservative 4; Mismatches 2; Indels 4; Gaps 2;

Cy      1 KPSYO-FGGHPSYDVEDTLR 20
      |||::|||::|::|
Db      274 KPSHRVFGAHPVTVN--DELP 291

RESULT 9
D86393
hypothetical protein TIK7.1 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C:Accession: D86393
R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federpiel, N.A.; Kaul, S.; White, O.; Alonso,
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;
ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Lueros, J.S.; Maiti, R.; Marziani,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A:Reference number: A86141; MUID:21016719; PMID:11130712
A:Accession: D86393
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-867 <STO>
A:Cross-references: UNIPROT:Q9FZE6; GB:AE005172; NID:g9797740; PDB:AAF98558.1; GSPDB:GN
C:Genetics:
A:Map position: 1

Query Match          39.0%; Score 46; DB 2; Length 867;
Best Local Similarity 61.5%; Pred. No. 52;
Matches 8; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Cy      8 GHSPVDVEDTLR 20
      |||::|||::|
Db      753 GRPKRDFQRDTLR 765

RESULT 10
T45647
receptor protein kinase-like protein - Arabidopsis thaliana
N:Alternate names: Protein F13112.160
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 09-Jul-2004
C:Accession: T45647
R:Cholant, N.; Robert, C.; Brothier, P.; Wincker, P.; Catolico, L.; Artiguenave, F.; Se
submitted to the Protein Sequence Database, November 1999
A:Reference number: Z23010
A:Accession: T45647

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A:Status: Preliminary
A:Molecule type: DNA
A:Residues: 1-1025 <CHO>
A:Cross-references: UNIPROT:O9SD62; EMBL:AL133292
A:Experimental source: cultivar Columbia; BAC clone F13112
C:Genetics:
A:Map position: 3
A:introns: 908/1
A:Note: F13112.160
C:Superfamily: protein kinase Xa21; leucine-rich alpha-2-glycoprotein repeat homology; p1

Query Match      39.0%; Score 46; DB 2; Length 1025;
Best local Similarity 63.6%; Pred. No. 62;
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY      2 PSYQCGHPSV 12
      |||
Db      907 PEYMGCHPSI 917

RESULT 11
HPMS
hapctoglobin precursor - mouse
N:Contains: hapctoglobin alpha chain; hapctoglobin beta chain
C:Species: Mus musculus (house mouse)
C:Date: 23-Mar-1995 #sequence_revision 31-May-1996 #text_change 18-Jun-1999
C:Accession: A48918
R:Yang, F.; Linahan, L.A.; Friedrichs, W.E.; Lalley, P.A.; Sakaguchi, A.Y.; Bowman, B.H.
Genomics 18, 374-380, 1993
A:Title: Characterization of the mouse hapctoglobin gene.
A:Reference number: A48918; MUID:94117006; PMID:8288241
A:Accession: A48918
A:Molecule type: mRNA
A:Residues: 1-347 <YAN>
A:Cross-references: GB:S67972; NID:g461137; PTDN:AA829697.1; PID:g461138
A:Note: sequence extracted from NCBI backbone (NCBIN:142156, NCBIRP:142157); sequence incor-
C:Comment: The mature hapctoglobin molecule is a dimer of heterodimers, the two chains of
C:Genetics:
A:Gene: Hp
A:Map position: 8
C:Superfamily: hapctoglobin; complement factor H repeat homology; trypsin homology
C:Keywords: acute phase; glycoprotein; hemoglobin binding; heterotetramer; iron transport
F:1-18/Domain: signal sequence #status predicted <SIG>
F:19-101/Product: hapctoglobin alpha chain #status predicted <ACH>
F:33-86/Domain: complement factor H repeat homology <FH2>
F:103-347/Product: trypsin homology <TRY>
F:103-340/Domain: trypsin homology beta chain #status predicted <BCH>
F:33-86/Product: complement factor H repeat homology <TRY>
F:33-86/Domain: trypsin homology beta chain #status predicted <BCH>
F:52-86,90-207,250-281,292-332/Disulfide bonds: #status predicted
F:148,182,256,264/Binding site: carbohydrate (Asn) (covalent) #status predicted
F:148,182,256,264/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match      38.1%; Score 45; DB 1; Length 347;
Best local Similarity 50.0%; Pred. No. 26;
Matches 7; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY      8 GHPVDFEEDTLPK 21
      |||
Db      22 GNDAMDFEDDSCPK 35

RESULT 12
S70135
hypothetical protein YDR279W - yeast (Saccharomyces cerevisiae)
N:Alternate names: hypothetical protein D9954.2
C:Species: Saccharomyces cerevisiae
C:Date: 24-Aug-1996 #sequence_revision 06-Sep-1996 #text_change 09-Jul-2004
C:Accession: S70135
R:Le, T.
submitted to the EMBL Data Library, May 1996
A:Description: The sequence of S. cerevisiae cosmid 9954.
A:Reference number: S70124
A:Accession: S70135

```


GenCore version 5.1.6
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OM protein - protein search, using SW model

Run on: October 22, 2005, 02:23:35 ; Search time 51.4314 Seconds
(without alignments)
209.087 Million cell updates/sec

Title: US-10-731-238-22
Perfect score: 118
Sequence: 1 KPSYQFGHPHYDFEEDLPK 21

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: UniProt_03.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	109	92.4	1018	1	FNBA_STAU
2	106	89.8	961	2	Q99RD3
3	106	89.8	961	2	Q7A3J8
4	106	89.8	965	2	O6GDU5
5	106	89.8	1015	2	O8NUU7
6	106	89.8	1015	2	O6G6H3
7	106	89.8	1038	2	O99RD2
8	106	89.8	1038	2	O7A3J7
9	102	86.4	940	2	O53682
10	102	86.4	943	2	O8NUU8
11	102	86.4	957	2	O6G6H4
12	97	88.2	152	2	O9AEP9
13	57	48.3	772	2	O9AD03
14	51	43.2	232	1	V4IK_RHISN
15	50	42.4	410	2	P72454
16	50	42.4	436	2	O8ENM4
17	49	41.5	840	2	O6ME76
18	49	41.5	1146	2	O8AEM0
19	48	40.7	245	2	O08866
20	48	40.7	475	2	O74C32
21	48	40.7	744	2	O8RYF9
22	47.5	40.3	45	2	O855T1
23	47.5	40.3	46	2	O855T0
24	47.5	40.3	403	2	O9SE39
25	47.5	40.3	1057	2	O6PEY30
26	47	39.8	229	2	O8HLO8
27	47	39.8	317	2	O7MR14
28	47	39.8	466	2	O6GN22
29	47	39.8	1726	2	O6G4Z9
30	46	39.0	234	2	O8PW99
31	46	39.0	241	1	R8PP_HRSVL

ALIGNMENTS

32	46	39.0	241	2	O8UYD5	O8uyd5 human resp1
33	46	39.0	377	2	O8SV75	O8sv75 encephalitc
34	46	39.0	465	2	O6F2M2	O6f2m2 bartonella
35	46	39.0	466	2	O6P319	O6p319 xenopus tro
36	46	39.0	468	2	O9XUB2	O9xub2 caenorhabd1
37	46	39.0	493	1	FBL3_HUMAN	012805 homo sapien
38	46	39.0	493	2	O7YOD7	O7yod7 macaca fasc
39	46	39.0	533	2	O213D1	O213d1 caenorhabd1
40	46	39.0	608	2	O7OP79	O7op79 giardia lam
41	46	39.0	831	2	O7UR31	O7ur31 rhodospirell
42	46	39.0	867	2	O9FZE6	O9fze6 arabidopsis
43	46	39.0	1025	2	O9SDP2	O9sdp2 arabidopsis
44	46	39.0	3298	2	O9VB11	O9vb11 drosophila
45	45.5	38.6	377	2	O74MK6	O74mk6 nanorarchaeu

RESULT 1
FNBA_STAU STANDARD; PRT; 1018 AA.
ID FNBA_STAU
AC P14738;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Fibronectin-binding protein precursor (FNBP).
GN Name=fnba;
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1280;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NCTC 8325-4;
RX MEDLINE=9008998; PubMed=2521391;
RA Signes C., Raucel G., Joensen K., Lindgren P.-E.,
R Mantharajah G.M., Hoeck M., Lindberg M.;
RT "Nucleotide sequence of the gene for a fibronectin-binding protein
from Staphylococcus aureus: use of this peptide sequence in the
synthesis of biologically active peptides."
RL Proc. Natl. Acad. Sci. U.S.A. 86:699-703(1989).
CC -1- FUNCTION: The ability of bacteria to bind fibronectin has been
proposed as a virulence factor enabling bacteria to colonize wound
tissues and blood clots. Binding of plasma fibronectin to the
bacterial surface might block adhesion receptors on S.aureus, thus
representing an important defense mechanism against tissue
invasion.
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
an amide bond (Potential).
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
or send an email to license@isb-sib.ch).
CC
CC EMBL: J04151; AAA2632.1; -;
DR InterPro: IPR004237; Fn_bind.
DR InterPro: IPR005877; Gpos_YsIRK.
DR InterPro: IPR001899; Gram_pos_anchor.
DR Pfam: PF02986; Fn_bind; 1.
DR Pfam: PF00746; Gram_pos_anchor; 1.
DR Pfam: PF04650; YsIRK_signal; 1.
DR TIGRfams: TIGR01167; LpxTG_anchor; 1.
DR TIGRfams: TIGR01168; YsIRK_signal; 1.
DR PROSITE: PS50847; GRAM_POS_ANCHORING; 1.
KW Cell adhesion; Cell wall; Peptidoglycan-anchor; Repeat; Signal;
KW Virulence.
FT SIGNAL 1 36
FT CHAIN 37 985
FT PROPEP 986 1018
FT Fibrinectin-binding protein.
FT Removed by sortase (Potential).


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FT REPEAT 545 574 B-1.
FT REPEAT 575 604 B-2.
FT DOMAIN 745 878 4 X approximate tandem repeats,
  fibronectin-binding domain.
FT REPEAT 745 782 D-1.
FT REPEAT 821 820 D-2.
FT REPEAT 860 878 D-3.
FT DOMAIN 879 948 D-4 (incomplete).
FT REPEAT 879 892 5 X tandem repeats, Pro-rich (WR).
FT REPEAT 893 906 WR 1.
FT REPEAT 907 920 WR 2.
FT REPEAT 921 934 WR 3.
FT REPEAT 935 948 WR 4.
FT SITE 982 986 WR 5.
FT MOD_RES 985 985 LpxTG sorting signal (Potential).
SQ SEQUENCE 1018 AA; 111780 MW; 58175E020E81F1F CRC64;
  chreonine (Potential).
Query Match 92.4%; Score 109; DB 1; Length 1018;
Best Local Similarity 95.2%; Pred. No. 5.9e-08;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KPSYFGGHPSPVDFEEDTLPK 21
DB 837 KPSYFGGHPSPVDFEEDTLPK 857

RESULT 2
Q99RD3 PRELIMINARY; PRT; 961 AA.
AC Q99RD3;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2003 (TrEMBLrel. 17, Last sequence update)
DE Fibronectin-binding protein homolog.
GN Name=fnbB; OrderedLocustNames=SAV2502;
OS Staphylococcus aureus (strain Mu50 / ATCC 700699).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=158878;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=Mu50 / ATCC 700699;
RC MEDLINE=21311952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2;
RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
  Cui L., Oguchi A., Aoki K.-I., Nagai Y., Iian J.-Q., Ito T.,
  Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosooyama A.,
  Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
  Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
  Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
  Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
RT "Whole genome sequencing of methicillin-resistant Staphylococcus
  aureus";
RL Lancel 357.1225-1240(2001).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
  an amide bond (By similarity).
EMBL, AF003365; BAB58664.1; -.
DR PIR; G90053; G90053.
DR HSSP; Q53653; 1N67.
DR GO; GO:0009986; C:cell surface; IEA.
DR GO; GO:0005618; C:cell wall; IEA.
DR GO; GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR InterPro; IPR008966; Adhes_bact.
DR InterPro; IPR004237; Fn_bind.
DR InterPro; IPR005877; Gpos_YsIRK.
DR Pfam; PF02986; Fn_bind; 1.
DR Pfam; PF00746; Gram_pos_anchor; 1.
DR Pfam; PF04650; YsIRK_signal; 1.
DR TIGRFAMs; TIGR01167; LpxTG_anchor; 1.
DR TIGRFAMs; TIGR01168; YsIRK_signal; 1.
DR TIGRFAMs; TIGR01169; YsIRK_signal; 1.

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DR PROSITE; PSS0847; GRAM_POS_ANCHORING; 1.
KW Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ SEQUENCE 961 AA; 106010 MW; 364940F884E4101 CRC64;

Query Match 89.8%; Score 106; DB 2; Length 961;
Best Local Similarity 90.5%; Pred. No. 1.6e-07;
Matches 19; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 KPSYFGGHPSPVDFEEDTLPK 21
DB 784 KPSYFGGHPSPVDFEEDTLPK 804

RESULT 3
Q7A3J8 PRELIMINARY; PRT; 961 AA.
AC Q7A3J8;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE FnbB protein.
GN Name=fnbB; OrderedLocustNames=SA2290;
OS Staphylococcus aureus (strain N315).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=158879;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21311952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2;
RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
  Cui L., Oguchi A., Aoki K.-I., Nagai Y., Iian J.-Q., Ito T.,
  Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosooyama A.,
  Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
  Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
  Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
  Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
RT "Whole genome sequencing of methicillin-resistant Staphylococcus
  aureus";
RL Lancel 357.1225-1240(2001).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
  an amide bond (By similarity).
EMBL, AF003137; BAB43593.1; -.
DR GO; GO:0009986; C:cell surface; IEA.
DR GO; GO:0005618; C:cell wall; IEA.
DR GO; GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0007155; P:cell adhesion; IEA.
DR InterPro; IPR008966; Adhes_bact.
DR InterPro; IPR004237; Fn_bind.
DR InterPro; IPR005877; Gpos_YsIRK.
DR Pfam; PF02986; Fn_bind; 1.
DR Pfam; PF00746; Gram_pos_anchor; 1.
DR Pfam; PF04650; YsIRK_signal; 1.
DR TIGRFAMs; TIGR01167; LpxTG_anchor; 1.
DR TIGRFAMs; TIGR01168; YsIRK_signal; 1.
DR PROSITE; PSS0847; GRAM_POS_ANCHORING; 1.
KW Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ SEQUENCE 961 AA; 106010 MW; 364940F884E4101 CRC64;

Query Match 89.8%; Score 106; DB 2; Length 961;
Best Local Similarity 90.5%; Pred. No. 1.6e-07;
Matches 19; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 KPSYFGGHPSPVDFEEDTLPK 21
DB 784 KPSYFGGHPSPVDFEEDTLPK 804

RESULT 4
Q6GDUS PRELIMINARY; PRT; 965 AA.
AC Q6GDUS;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)

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DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update)
DE Fibronectin-binding protein.
GN Name=fnbA; OrderedLocustNames=SA82580;
OS Staphylococcus aureus (strain MRSA252).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=282458;
[1]
RP SEQUENCE FROM N.A.
RX PubMed=15213324; DOI=10.1073/pnas.0402521101;
RA Holden M.T.G., Fell E.J., Lindsay J.A., Peacock S.J., Day N.P.J.,
RA Enright M.C., Foster T.J., Moore C.E., Hurst L., Atkin R., Barron A.,
RA Bason N., Bentley S.D., Chillingworth C., Chillingworth T.,
RA Churcher C., Clark L., Corton C., Cronin A., Doggett J., Dowd L.,
RA Feltwell T., Harris B., Hauser H., Holtroyd S., Jørgensen K.,
RA James K.D., Lennard N., Line A., Mayes R., Mould S., Mungall K.,
RA James K.D., Quail M.A., Rabinowitch E., Rutherford K.M., Sanders M.,
RA Sharp S., Simmonds M., Stevens K., Whitehead S., Barrett B.G.,
RA Spratt B.G., Parkhill J.;
RT "Complete genomes of two clinical Staphylococcus aureus strains:
RT evidence for the rapid evolution of virulence and drug resistance.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:9786-9791 (2004).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
an amide bond (By similarity).
DR EMBL; BX571856; CAG41560.1; -
DR GO; GO:0009986; C:cell surface; IEA.
DR GO; GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0007155; P:cell adhesion; IEA.
DR InterPro; IPR008966; Adhes_bact.
DR InterPro; IPR004237; Fn_bind.
DR InterPro; IPR001899; Gram_pos_anchor.
DR InterPro; IPR001899; Gram_pos_anchor.
DR Pfam; PF02986; Fn_bind; 1.
DR Pfam; PF00746; Gram_pos_anchor; 1.
DR TIGRFAMs; TIGR01167; LPXTG_anchor; 1.
DR TIGRFAMs; TIGR01167; LPXTG_anchor; 1.
DR PROSITE; PS50847; GRAM_POS_ANCHORING; 1.
KM Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ SEQUENCE 965 AA; 105691 MW; 2982132164D0551 CRC64;

Query Match 89.8%; Score 106; DB 2; Length 965;
Best Local Similarity 90.5%; Pred. No. 1.7e-07;
Matches 19; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 KPSYQFGHPSVDFEEDTLPK 21
Db 802 KPNYQFGHNSVDFEEDTLPK 822

RESULT 5
Q8NUU7 PRELIMINARY; PRT; 1015 AA.
AC Q8NUU7;
DT 01-OCT-2002 (TReMBLrel. 22, Created)
DT 01-OCT-2002 (TReMBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE Fnb protein.
GN Name=fnb; OrderedLocustNames=MM2421;
OS Staphylococcus aureus (strain MM2).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=196620;
[1]
RP SEQUENCE FROM N.A.
RX STRAIN=MM2;
RX MEDLINE=22040717; PubMed=12044378; DOI=10.1016/S0140-6736(02)08713-5;
RA Baba T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Oguchi A.,
RA Nagai Y., Iwana N., Asano K., Naito T., Kuroda H., Cui L.,
RA Yamamoto K., Hiramatsu K.;
RT "Genome and virulence determinants of high virulence community-
RT acquired MRSA.";
RL Lancet 359:1819-1827 (2002).
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CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC an amide bond (By similarity).
DR EMBL; AP004830; BAB96286.1; -
DR GO; GO:0009986; C:cell surface; IEA.
DR GO; GO:0005618; C:cell wall; IEA.
DR GO; GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0007155; P:cell adhesion; IEA.
DR InterPro; IPR008966; Adhes_bact.
DR InterPro; IPR004237; Fn_bind.
DR InterPro; IPR005877; Gpos_YsIRK.
DR InterPro; IPR001899; Gram_pos_anchor.
DR Pfam; PF02986; Fn_bind; 1.
DR Pfam; PF00746; Gram_pos_anchor; 1.
DR TIGRFAMs; TIGR01167; LPXTG_anchor; 1.
DR TIGRFAMs; TIGR01167; LPXTG_anchor; 1.
DR PROSITE; PS50847; GRAM_POS_ANCHORING; 1.
KM Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ SEQUENCE 1015 AA; 111145 MW; D0F9281BB64D44D2 CRC64;

Query Match 89.8%; Score 106; DB 2; Length 1015;
Best Local Similarity 90.5%; Pred. No. 1.7e-07;
Matches 19; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 KPSYQFGHPSVDFEEDTLPK 21
Db 838 KPNYQFGHNSVDFEEDTLPK 858

RESULT 6
Q6G6H3 PRELIMINARY; PRT; 1015 AA.
AC Q6G6H3;
DT 05-JUL-2004 (TReMBLrel. 27, Created)
DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TReMBLrel. 27, Last annotation update)
DE Fibronectin-binding protein.
GN Name=fnbA; OrderedLocustNames=SA82580;
OS Staphylococcus aureus (strain MRSA476).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=282459;
[1]
RP SEQUENCE FROM N.A.
RX PubMed=15213324; DOI=10.1073/pnas.0402521101;
RA Holden M.T.G., Fell E.J., Lindsay J.A., Peacock S.J., Day N.P.J.,
RA Enright M.C., Foster T.J., Moore C.E., Hurst L., Atkin R., Barron A.,
RA Bason N., Bentley S.D., Chillingworth C., Chillingworth T.,
RA Churcher C., Clark L., Corton C., Cronin A., Doggett J., Dowd L.,
RA Feltwell T., Harris B., Hauser H., Holtroyd S., Jørgensen K.,
RA James K.D., Lennard N., Line A., Mayes R., Mould S., Mungall K.,
RA James K.D., Quail M.A., Rabinowitch E., Rutherford K.M., Sanders M.,
RA Sharp S., Simmonds M., Stevens K., Whitehead S., Barrett B.G.,
RA Spratt B.G., Parkhill J.;
RT "Complete genomes of two clinical Staphylococcus aureus strains:
RT evidence for the rapid evolution of virulence and drug resistance.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:9786-9791 (2004).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
an amide bond (By similarity).
DR EMBL; BX571857; CAG44202.1; -
DR GO; GO:0009986; C:cell surface; IEA.
DR GO; GO:0005618; C:cell wall; IEA.
DR GO; GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0007155; P:cell adhesion; IEA.
DR InterPro; IPR008966; Adhes_bact.
DR InterPro; IPR004237; Fn_bind.
DR InterPro; IPR005877; Gpos_YsIRK.
DR InterPro; IPR001899; Gram_pos_anchor.
DR Pfam; PF02986; Fn_bind; 1.
DR Pfam; PF00746; Gram_pos_anchor; 1.
DR TIGRFAMs; TIGR01167; LPXTG_anchor; 1.
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DR TIGR01168; YSIRK signal; 1.
DR PROSITE; PSS0847; GRAM_POS_ANCHORING; 1.
DR Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ SEQUENCE 1015 AA; 11145 MW; D0F9281B64D44D2 CRC64;

Query Match
Best Local Similarity 90.5%; Pred. No. 1,7e-07;
Matches 19; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 KPSYQFGHPSVDFEEDTLPK 21
   ||:|||||
DB 833 KENYQFGHNSVDFEEDTLPK 858

RESULT 7
QY99RD2 PRELIMINARY; PRT; 1038 AA.
ID Q99RD2;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Fibronectin-binding protein homolog.
DE Name=fnb; OrderedlocusNames=SAV2503;
OS Staphylococcus aureus (strain Mu50 / ATCC 700699).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxId=158878;

SEQUENCE FROM N.A.
RP STRAIN=Mu50 / ATCC 700699;
RX MEDLINE=2111952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2;
RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Iian J.-O., Ito T.,
RA Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,
RA Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
RA Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
RA Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
RA Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
RT "Whole genome sequencing of methicillin-resistant Staphylococcus
RT aureus."
RL Lancet 357;1225-1240(2001).
CC -1 SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC an amide bond (By similarity).
EMBL; AP003137; BAB43594.1; -.
DR GO; GO:0009986; C:cell surface; IEA.
DR GO; GO:0005618; C:cell wall; IEA.
DR GO; GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:007155; P:cell adhesion; IEA.
DR InterPro; IPR008966; Adhes_bact.
DR InterPro; IPR004237; Fn_bind.
DR InterPro; IPR005877; Gpos_YSIRK.
DR InterPro; IPR001899; Gram_pos_anchor.
DR Pfam; PF02986; Fn_bind; 1.
DR Pfam; PF00746; Gram_pos_anchor; 1.
DR TIGR01167; LpxTG_anchor; 1.
DR TIGR01168; YSIRK_signal; 1.
DR PROSITE; PSS0847; GRAM_POS_ANCHORING; 1.
DR Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ SEQUENCE 1038 AA; 113618 MW; 666BF6BF2BFEBB12 CRC64;
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ID 07A3J7 PRELIMINARY; PRT; 1038 AA.
AC 07A3J7;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Fnb protein.
DE Name=fnb; OrderedlocusNames=SA2291;
OS Staphylococcus aureus (strain N315).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxId=158879;

SEQUENCE FROM N.A.
RP MEDLINE=2111952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2;
RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Iian J.-O., Ito T.,
RA Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,
RA Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
RA Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
RA Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
RA Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
RT "Whole genome sequencing of methicillin-resistant Staphylococcus
RT aureus."
RL Lancet 357;1225-1240(2001).
CC -1 SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC an amide bond (By similarity).
EMBL; AP003137; BAB43594.1; -.
DR GO; GO:0009986; C:cell surface; IEA.
DR GO; GO:0005618; C:cell wall; IEA.
DR GO; GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:007155; P:cell adhesion; IEA.
DR InterPro; IPR008966; Adhes_bact.
DR InterPro; IPR004237; Fn_bind.
DR InterPro; IPR005877; Gpos_YSIRK.
DR InterPro; IPR001899; Gram_pos_anchor.
DR Pfam; PF02986; Fn_bind; 1.
DR Pfam; PF00746; Gram_pos_anchor; 1.
DR TIGR01167; LpxTG_anchor; 1.
DR TIGR01168; YSIRK_signal; 1.
DR PROSITE; PSS0847; GRAM_POS_ANCHORING; 1.
DR Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ SEQUENCE 1038 AA; 113618 MW; 666BF6BF2BFEBB12 CRC64;

Query Match
Best Local Similarity 90.5%; Pred. No. 1,8e-07;
Matches 19; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 KPSYQFGHPSVDFEEDTLPK 21
   ||:|||||
DB 833 KENYQFGHNSVDFEEDTLPK 853

RESULT 9
QY93682 PRELIMINARY; PRT; 940 AA.
ID 053682;
AC 053682;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Fibronectin binding protein B.
DE Name=fnbB;
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxId=1280;

SEQUENCE FROM N.A.
RP STRAIN=8325-4;
RX MEDLINE=92111475; PubMed=1837266;
RA Jonsson K., Signae C., Muller H.P., Lindberg M.;
RT "Two different genes encode fibronectin binding proteins in
RT Staphylococcus aureus. The complete nucleotide sequence and
RT characterization of the second gene."
```

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RL Eur. J. Biochem. 202:1041-1048 (1991).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
an amide bond (By similarity).
DR EMBL: X62992; CAA44726.1; -.
DR PIR: S19702; S19702.
DR HSSP: Q53653; 1N67.
DR GO: GO:0009986; C:cell surface; IEA.
DR GO: GO:0005618; C:cell wall; IEA.
DR GO: GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO: GO:0016020; C:membrane; IEA.
DR GO: GO:0007155; P:cell adhesion; IEA.
DR InterPro: IPR008966; Adhes_bact.
DR InterPro: IPR004237; Fn_bind.
DR InterPro: IPR001899; Gram_pos_anchor.
DR Pfam: PF02986; Fn_bind_2.
DR Pfam: PF00746; Gram_pos_anchor; 1.
DR TIGRFAMs: TIGR01167; LpxTG_anchor; 1.
DR PROSITE: PS50847; GRAM_POS_ANCHORING; 1.
KW Cell wall; Peptidoglycan-anchor.
SQ SEQUENCE 940 AA; 103555 MW; E35FBBCA907AE345 CRC64;

Query Match 86.4%; Score 102; DB 2; Length 940;
Best Local Similarity 85.7%; Pred. No. 6,7e-07;
Matches 18; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 KPSYQFGHPSVDFEEDTLPK 21
DB 773 KPNYQFGHNSVDFEEDTLQ 793

RESULT 10
ID Q8NU8 PRELIMINARY; PRT; 943 AA.
AC Q8NU8;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE FndB protein.
GN Name=fndB; OrderedLocustNames=MW2420;
OS Staphylococcus aureus (strain MW2).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=196620;
RX [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MW2;
RX MEDLINE=22040717; PubMed=12044378; DOI=10.1016/S0140-6736(02)08713-5;
RA Baba T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Ogunchi A.,
Yanagita Y., Iwano N., Asano K., Naito T., Kuroda H., Cui L.,
Yamamoto K., Hiramatsu K.;
RT "genome and virulence determinants of high virulence community-
acquired MRSA.";
RL Lancet 359:1819-1827 (2002).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
an amide bond (By similarity).
DR EMBL: AP004830; BAB96285.1; -.
DR HSSP: Q53653; 1N67.
DR GO: GO:0009986; C:cell surface; IEA.
DR GO: GO:0005618; C:cell wall; IEA.
DR GO: GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO: GO:0016020; C:membrane; IEA.
DR GO: GO:0007155; P:cell adhesion; IEA.
DR InterPro: IPR008966; Adhes_bact.
DR InterPro: IPR004237; Fn_bind.
DR InterPro: IPR005877; Gpos_YsIRK.
DR InterPro: IPR001899; Gram_pos_anchor.
DR Pfam: PF02986; Fn_bind_1.
DR Pfam: PF00746; Gram_pos_anchor; 1.
DR TIGRFAMs: TIGR01167; LpxTG_anchor; 1.
DR TIGRFAMs: TIGR01168; YsIRK_signal; 1.
DR TIGRFAMs: TIGR01168; YsIRK_signal; 1.

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DR PROSITE: PS50847; GRAM_POS_ANCHORING; 1.
KW Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ SEQUENCE 943 AA; 104537 MW; DA6A5F31947E1B6A CRC64;

Query Match 86.4%; Score 102; DB 2; Length 943;
Best Local Similarity 85.7%; Pred. No. 6,7e-07;
Matches 18; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 KPSYQFGHPSVDFEEDTLPK 21
DB 780 KPNYQFGHNSVDFEEDTLQ 800

RESULT 11
ID Q6G6H4 PRELIMINARY; PRT; 957 AA.
AC Q6G6H4;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Fibronectin-binding protein.
GN Name=fndB; OrderedLocustNames=SAS2387;
OS Staphylococcus aureus (strain MSSA476).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=282459;
RX [1]
RP SEQUENCE FROM N.A.
RC PubMed=15213324; DOI=10.1073/pnas.0402521101;
RX Holden M.T.G., Fell E.J., Lindsay J.A., Peacock S.J., Day N.P.J.,
Enright M.C., Foster T.J., Moore C.E., Hurst L., Atkin R., Barron A.,
Bason N., Bentley S.D., Chillingworth C., Chillingworth T.,
Churcher C., Clark L., Cotton C., Cronin A., Doggett J., Dowd L.,
Feltwell T., Hance Z., Harris B., Hauser H., Holtroyd S., Jags K.,
James K.D., Leonard N., Line A., Mayes R., Moll S., Murgall K.,
Ormond D., Quail M.A., Rabinowitsch B., Rutherford K.M., Sanders M.,
Sharp S., Simmonds M., Stevens K., Whitehead S., Barrall B.G.,
Spratt B.G., Parkhill J.;
RT "Complete genomes of two clinical Staphylococcus aureus strains:
evidence for the rapid evolution of virulence and drug resistance.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:9786-9791 (2004).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
an amide bond (By similarity).
DR EMBL: BX571857; CAG44201.1; -.
DR GO: GO:0009986; C:cell surface; IEA.
DR GO: GO:0005618; C:cell wall; IEA.
DR GO: GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO: GO:0016020; C:membrane; IEA.
DR GO: GO:0007155; P:cell adhesion; IEA.
DR InterPro: IPR008966; Adhes_bact.
DR InterPro: IPR004237; Fn_bind.
DR InterPro: IPR005877; Gpos_YsIRK.
DR InterPro: IPR001899; Gram_pos_anchor.
DR Pfam: PF02986; Fn_bind_1.
DR Pfam: PF00746; Gram_pos_anchor; 1.
DR Pfam: PF04650; YsIRK_signal; 1.
DR TIGRFAMs: TIGR01167; LpxTG_anchor; 1.
DR TIGRFAMs: TIGR01168; YsIRK_signal; 1.
DR PROSITE: PS50847; GRAM_POS_ANCHORING; 1.
KW Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ SEQUENCE 957 AA; 105980 MW; 28F8BA7FFD3EAF CRC64;

Query Match 86.4%; Score 102; DB 2; Length 957;
Best Local Similarity 85.7%; Pred. No. 6,8e-07;
Matches 18; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 KPSYQFGHPSVDFEEDTLPK 21
DB 780 KPNYQFGHNSVDFEEDTLQ 800

RESULT 12
Q9AEP9 PRELIMINARY; PRT; 152 AA.
ID Q9AEP9

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AC 09AEP9;
DT 01-JUN-2001 (T-EMBLrel. 17, Created)
DT 01-JUN-2001 (T-EMBLrel. 17, Last sequence update)
DE 01-DEC-2001 (T-EMBLrel. 19, Last annotation update)
DE Fibronectin-binding protein (fragment).
GN Name=fnb;
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxId=1280;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CMRSA-1;
RX MEDLINE=21246681; PubMed=11349044;
RA DOI=10.1128/IAI.69.6.3791-3799.2001;
RA Rice K., Huesca M., Vaz D., McGavin M.J.;
RT "Variance in fibronectin binding and fnb locus polymorphisms in
RT Staphylococcus aureus: identification of antigenic variation in a
RT fibronectin binding protein adhesin of the epidemic CMRSA-1 strain of
RT methicillin-resistant S. aureus.";
RL Infect. Immun. 69:3791-3799(2001).
DR EMBL; AY029184; AK31588.1; -.
FT NON_TER
FT TER 152 152
SQ SEQUENCE 152 AA; 17193 MW; CFA3913C2B11C025 CRC64;

Query Match 82.2%; Score 97; DB 2; Length 152;
Best Local Similarity 81.0%; Pred. No. 5.4e-07;
Matches 17; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 KPSYQFGHPSVDFEEDLPK 21
Db 130 KPSYQFGHNGIDFVEDTLPK 150

RESULT 13
Q9AD03 PRELIMINARY; PRT; 772 AA.
ID Q9AD03;
AC Q9AD03;
DT 01-JUN-2001 (T-EMBLrel. 17, Created)
DT 01-JUN-2001 (T-EMBLrel. 17, Last sequence update)
DE 01-JUN-2003 (T-EMBLrel. 24, Last annotation update)
DE Putative integral membrane protein.
GN OrderedLocNames=SCPI.147;
OS Streptomyces coelicolor.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Streptomycinae; Streptomycetaceae; Streptomycetes.
OX NCBI_TaxId=1902;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=A3(2) / M145;
RX MEDLINE=21966410; PubMed=12000953; DOI=10.1038/417141a;
RA Bentley S.D., Chater K.F., Cerdano-Tarraga A.-M., Challis G.L.,
RA Thomson N.R., James K.D., Harris D.E., Quail M.A., Kießer H.,
RA Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
RA Cronin A., Fraser A., Goble A., Hidalgo J., Hornaby T., Howarth S.,
RA Huang C.-H., Kießer T., Larke L., Murphy L.D., Oliver K., O'Neill S.,
RA Rabinowitch E., Rajandream M.A., Rutherford K.M., Rutter S.,
RA Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,
RA Warren T., Wietzorrek A., Woodward J.R., Barrell B.G., Parkhill J.,
RA Hopwood D.A.;
RT "Complete genome sequence of the model actinomycete Streptomyces
RT coelicolor A3(2)";
RL Nature 417:141-147(2002).
DR EMBL; AL590463; CAC36668.1; -.
KW Complete proteome.
SQ SEQUENCE 772 AA; 82297 MW; AB5016BD840DD91B CRC64;

Query Match 48.3%; Score 57; DB 2; Length 772;
Best Local Similarity 66.7%; Pred. No. 5.7;
Matches 10; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 3 SYQFGHPSVDFEED 17
:::|||||:||||:|

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Db 376 AHQFGVPMVDFEED 390

RESULT 14
Y4IK_RHISN STANDARD; PRT; 232 AA.
ID Y4IK_RHISN
AC P55494;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DE 05-UTL-2004 (Rel. 44, Last annotation update)
DE Hypothetical 26.8 kDa protein Y4IK.
GN ORFNames=Y4IK;
OS Rhizobium sp. (strain NGR234).
OG Plasmid sym pNGR234a.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Rhizobiaceae; Rhizobium/Agrobacterium group; Rhizobium.
OX NCBI_TaxId=394;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97305956; PubMed=9163424;
RA Freilberg C.A., Fellay R., Bairoch A., Broughton W.J., Rosenthal A.,
RA Perret X.;
RT "Molecular basis of symbiosis between Rhizobium and legumes.";
RL Nature 387:394-401(1997).
CC -1- SIMILARITY: None obvious.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
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CC or send an email to license@sib-sib.ch).
CC -----
DR EMBL; AE000078; AAB91706.1; -.
DR InterPro; IPR002226; Catalase.
KW Hypothetical protein; Plasmid.
SQ SEQUENCE 232 AA; 26804 MW; BDAF9BCE74816C67 CRC64;

Query Match 43.2%; Score 51; DB 1; Length 232;
Best Local Similarity 47.1%; Pred. No. 13;
Matches 8; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

Qy 1 KPSYQFGHPSVDFEED 17
Db 90 RPEFRKNGHPSMDAEND 106

RESULT 15
P72454 PRELIMINARY; PRT; 410 AA.
ID P72454;
AC P72454;
DT 01-FEB-1997 (T-EMBLrel. 02, Created)
DT 01-FEB-1997 (T-EMBLrel. 02, Last sequence update)
DE 01-JUN-2003 (T-EMBLrel. 24, Last annotation update)
DE L-alanine:N-amidino-3-keto-scyllo-inosamine aminotransferase.
GN Name=staA;
OS Streptomyces griseus.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Streptomycinae; Streptomycetaceae; Streptomycetes.
OX NCBI_TaxId=1911;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=N2-3-11;
RX MEDLINE=97385085; PubMed=9238101;
RA Ahlert J., Distler J., Mansouri K., Piepersberg W.;
RT "Identification of stcC, the gene encoding the L-glutamine:scyllo-
RT inosose aminotransferase from streptomycin-producing Streptomyces";
RL Arch. Microbiol. 168:102-113(1997).
DR EMBL; Y08763; CAA70010.1; -.
DR HSSP; Q8ZNF3; IMDO.
DR GO; GO:0008483; P:transaminase activity; IEA.
DR GO; GO:0016740; P:transferase activity; IEA.

```

DR InterPro: IPR000653; Degt DnrJ_EryC1.
DR Pfam: PF01041; Degt DnrJ_EryC1; 1.
KW Aminotransferase; Transferase.
SQ SEQUENCE 410 AA; 43473 MW; DB7F4B797C328CD7 CRC64;

Query Match 42.4%; Score 50; DB 2; Length 410;
Best Local Similarity 60.0%; Pred. No. 35;
Matches 9; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 7 GGHPSVDFEEDTLPK 21
DB 344 GGRPSASFEPGTLPR 358

Search completed: October 22, 2005, 04:10:01
Job time : 53.4314 secs

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CC streptococci, e.g. meningitis, otitis media, pneumonia, endocarditis,
 CC mastitis in cattle, abortion in horses and many others. Since the
 CC antibodies block binding of bacteria, they should be effective against
 CC antibiotic-resistant strains, and may replace antibiotic therapy or
 CC increase its effectiveness. Sequences AAW65670-90 represent a series of
 CC synthetic peptides based on the D3 repeat of *S. aureus* fibronectin
 CC binding protein A. They were synthesised to contain a proline residue at
 CC each position through the sequence (ie a proline scan)
 XX
 SQ Sequence 21 AA;
 QY
 Query Match 100.0%; Score 120; DB 2; Length 21;
 Best Local Similarity 100.0%; Pred. No. 6.1e-12;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Db 1 KPSYQFGHNHPVDFEDTLPK 21
 1 KPSYQFGHNHPVDFEDTLPK 21
 RESULT 2
 AAW65665
 ID AAW65665 standard; peptide; 21 AA.
 XX
 XX AAW65665;
 AC
 XX 16-OCT-1998 (first entry)
 DT
 XX Fibronectin binding protein-derived peptide #9.
 DE
 XX
 XX
 XX microbial surface components recognising adhesive matrix molecule;
 KM MSCRAMM; fibronectin; fibronectin-binding protein; antibody; epitope;
 KW antibiotic; bacterial infection; antibiotic-resistant strain.
 XX
 XX Synthetic.
 OS
 OS Staphylococcus aureus.
 XX
 PN MO981389-A2.
 XX
 XX 23-JUL-1998.
 PD
 XX 21-JAN-1998; 98WO-US001222.
 PF
 XX 21-JAN-1997; 97US-0036139P.
 PR
 XX (TEXA) UNIV TEXAS A & M SYSTEM.
 XX
 PA Hoecek M, Patti JM, House-Pompeo KL, Speziale P, Jch D;
 PI McGavin MJ;
 XX MPI; 1998-413816/35.
 DR
 XX
 XX Antibody that binds to fibronectin-binding protein, preventing its
 PT binding to fibronectin - used to treat or prevent bacterial infection,
 PT especially by Staphylococci and Streptococci.
 XX
 PS Example 2; Page 92; 201pp; English.
 CC The invention relates to antibodies that bind to a fibronectin-binding
 CC domain of a fibronectin-binding protein, and inhibit binding of the
 CC protein to fibronectin. Also claimed are: (1) isolated peptides of a
 CC fibronectin-binding protein that do not bind to fibronectin; (2) fusion
 CC protein containing at least one peptide of a fibronectin-binding protein
 CC linked to a second amino acid sequence; (3) nucleic acid encoding the
 CC isolated peptide of (1). Antibodies, the isolated peptides of (1) and the
 CC nucleic acids are all useful for immunisation (active or passive) and (by
 CC inhibiting binding of bacteria to fibronectin) for preventing or treating
 CC infection in humans or other animals, particularly by staphylococci or
 CC streptococci, e.g. meningitis, otitis media, pneumonia, endocarditis,
 CC mastitis in cattle, abortion in horses and many others. Since the
 CC antibodies block binding of bacteria, they should be effective against
 CC antibiotic-resistant strains, and may replace antibiotic therapy or
 CC increase its effectiveness. Sequences AAW65659-68 represent synthetic

CC epitopes from the fibronectin binding domains DU and DI-D4 of the S.
 CC aureus fnbA gene
 XX
 SQ Sequence 21 AA;
 QY
 Query Match 93.3%; Score 112; DB 2; Length 21;
 Best Local Similarity 95.2%; Pred. No. 1.2e-10;
 Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Db 1 KPSYQFGHNHPVDFEDTLPK 21
 1 KPSYQFGHNHPVDFEDTLPK 21
 RESULT 3
 AAR21340
 ID AAR21340 standard; peptide; 22 AA.
 XX
 XX AAR21340;
 AC
 XX 25-MAR-2003 (revised)
 DT 15-JUN-1992 (first entry)
 XX
 XX Fibronectin binding protein.
 DE
 XX FNBp; wound infection reduction; vaccination; mastitis;
 KM Staphylococcal infections; D3.
 KW
 XX Synthetic.
 OS
 OS WO9202555-A.
 PN
 XX 20-FEB-1992.
 PD
 XX 10-AUG-1990; 90SE-00002617.
 PF
 XX 10-AUG-1990; 90SE-00002617.
 PR
 XX 10-AUG-1990; 90SE-00002617.
 XX
 PA (ALFA) ALFA LAVAL AGRIC INT AB.
 XX
 PI Hook M, McGavin M, Raucel G;
 XX MPI; 1992-080035/10.
 DR
 XX
 XX New fibronectin binding peptide - combines with fusion peptide to form
 PT large antigen, used in immunisation, diagnosis and for treating wounds.
 PT
 XX Claim 1; Page 22; 33pp; English.
 PS
 XX The sequence comprises amino acids 17-33 of a tandem repeat, designated
 CC D3 of the fibronectin binding site of Staphylococcus aureus 8325-4 FNBp.
 CC The N-terminal DK may be replaced with H or K, and the C-terminal LKP may
 CC be replaced by either L, LP, or OH. The peptides were synthesised using
 CC standard methods and purified using reverse phase HPLC. The appropriate
 CC fractions were dialysed and lyophilised. Peptide sequencing was performed
 CC and the peptides digested and chemically modified by dihydroxypropylation
 CC of the amino side chain of lysine. The carboxylic side chains were
 CC converted to glycine methyl esters. The phenyl side chains of tyrosine
 CC residues were oxidised. Chemically modified peptide D3 was compared to
 CC unmodified D3. Lysine and tyrosine modifications only partially
 CC diminished its activity whereas modification of aspartic/glutamic
 CC residues resulted in complete loss of activity. The peptide can be used
 CC for the prevention or reduction of the risk of wound infection. The
 CC peptide can be used to create a large antigen for vaccinating ruminants
 CC against mastitis caused by Staphylococcal infections. It can also be used
 CC to diagnose Staphylococcal infections using ELISA or DNA probes. (Updated
 CC on 25-MAR-2003 to correct PA field.)
 XX
 SQ Sequence 22 AA;
 QY
 Query Match 93.3%; Score 112; DB 2; Length 22;
 Best Local Similarity 95.2%; Pred. No. 1.2e-10;
 Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KPSYQFGHNVPDFEEDTLPK 21
 |||||
 DB 2 KPSYQFGHNVPDFEEDTLPK 22

RESULT 4
 ID AAB91958 standard; peptide; 37 AA.
 XX AAB91958;

DT 22-JUN-2001 (first entry)

DE Fibronectin fragment and fibrin related peptide SEQ ID NO:1134.

XX Protection; endogenous therapeutic peptide; peptidase; conjugation;
 KW blood component; modification; succinimide; maleimide group; amino;
 KM hydroxyl; thiol; hormone; growth factor; neurotransmitter.

XX Homo sapiens.
 OS Synthetic.

PN WO200069900-A2.

PD 23-NOV-2000.

PF 17-MAY-2000; 2000MO-US013576.

PR 17-MAY-1999; 99US-0134406P.

PR 10-SEP-1999; 99US-0153406P.

PR 15-OCT-1999; 99US-0159783P.

XX (CONJ-) CONJUCHEM INC.

PI Bridon DP, Ezrin AM, Milner PG, Holmes DL, Thibaudau K;

DR WPI; 2001-112059/12.

PT Modifying and attaching therapeutic peptides to albumin prevents
 PT peptidase degradation, useful for increasing length of in vivo activity.

PS Disclosure; Page 566; 733pp; English.

XX The present invention describes a modified therapeutic peptide (I)
 CC comprising a therapeutically active amino acid region (III) and a
 CC reactive group (II) (e.g. succinimide) and maleimide groups) attached to
 CC a less therapeutically active amino acid region (IV), which covalently
 CC bonds with amino/hydroxyl/thiol groups on blood components to form a
 CC peptidase stabilised therapeutic peptide composed of 3-50 amino acids.
 CC (I) are useful for modifying therapeutic peptides e.g. hormones, growth
 CC factors and neurotransmitters, to protect them from peptidase activity in
 CC vivo for the treatment of various disorders. Endogenous therapeutic
 CC peptides are not suitable as drug candidates as they require frequent
 CC administration due to rapid degradation by peptidases in the body.
 CC Modifying and attaching therapeutic peptides to albumin prevents or
 CC reduces the action of peptidases to increase length of activity (half
 CC life) and specificity as bonding to large molecules decreases
 CC intracellular uptake and interference with physiological processes.
 CC AAB90829 to AAB92441 represent peptides which can be used in the
 CC exemplification of the present invention

XX Sequence 37 AA;

Query Match 93.3%; Score 112; DB 4; Length 37;

Best Local Similarity 95.2%; Pred. No. 2.2e-10; Mismatches 1; Indels 0; Gaps 0;

Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KPSYQFGHNVPDFEEDTLPK 21
 |||||
 DB 16 KPSYQFGHNVPDFEEDTLPK 36

RESULT 5
 ID AAB80662 standard; protein; 38 AA.
 XX AAB80662;

AC AAB80662;

DT 25-MAR-2003 (revised)

DT 07-OCT-1990 (first entry)

DE Protein with fibronectin binding ability.

XX Hybrid DNA molecule; fibronectin binding; mastitis; ruminants;
 KW wound infection.

XX Staphylococcus aureus.

OS Staphylococcus aureus.

PN EP294349-A.

PD 07-DEC-1988.

PF 30-MAY-1988; 88EP-00850188.

PR 01-JUN-1987; 87SE-00022272.

PR (ALFA) ALFA LAVAL AGRIC. INT AB.

PI Lindberg MK, Signas LC, Wadstrom TM, Froman G;

DR WPI; 1988-347978/49.

DR N-PSDB; AAN01099.

PT Hybrid DNA encoding Staphylococcus aureus fibronectin binding protein -

PT useful for immunisation and topical application to prevent staphylococcal

PT infections.

PS Claim 11; Page 12; 23pp; English.

XX The peptide has fibronectin binding ability. It is useful for immunising

XX CC ruminants against staphylococcal mastitis, pref. when used at 0.5-5

XX CC micrograms/kg, using 3 doses given at 1-3 week intervals; for topical

XX CC application to prevent wound infection, using an isotonic saline soln. of

XX CC concn. 25-250 micrograms/ml; and, when immobilised on a carrier, for

XX CC diagnosing staphylococcal infections. (Updated on 25-MAR-2003 to correct

XX CC PF field.) (Updated on 25-MAR-2003 to correct PA field.)

XX Sequence 38 AA;

Query Match 93.3%; Score 112; DB 1; Length 38;

Best Local Similarity 95.2%; Pred. No. 2.3e-10; Mismatches 1; Indels 0; Gaps 0;

Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KPSYQFGHNVPDFEEDTLPK 21
 |||||
 DB 17 KPSYQFGHNVPDFEEDTLPK 37

RESULT 6
 ID AAY29087 standard; protein; 134 AA.

AC AAY29087;

DT 28-SEP-1999 (first entry)

DE S. aureus fibronectin binding protein A (FnBA) binding domain.

XX Bovine herpes virus-2; BHV-2; cytokine; immune response; immunogen; IL;

XX KW interleukin; colony stimulating factor; CSF; interferon; IFN; TNF;

XX KW tumour necrosis factor; recombinant virus; vaccine; mucosal disease;

XX KW mastitis; breast cancer; stress-induced disease; binding domain; FnBA;

XX KW fibronectin binding protein.

OS Staphylococcus aureus.

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XX PN WO9916892-A1.
XX PD 08-APR-1999.
XX PF 29-SEP-1998; 98WO-GB002927.
XX PR 29-SEP-1997; 97GB-00020633.
XX PA (UYBR-) UNIV BRISTOL.
XX PI Bradley AJ, Duffas WPJ;
XX WPI: 1999-255101/21.
XX DR N-PSDB; AAX91504.
XX PT New bovine herpes virus-2 vectors.
XX PS Example 2; Fig 8A-B; 130pp; English.
XX CC The invention provides bovine herpes virus-2 (BHV-2) based vectors that
XX CC comprise at least one cytokine-encoding DNA sequence. The expression of
XX CC cytokines in mammals can up-regulate immune responses to the immunogens.
XX CC The cytokine is selected from interleukins (IL), colony stimulating
XX CC factors (CSF), interferons (IFN) and tumour necrosis factors (TNF). The
XX CC BHV-2 based vector or recombinant virus can be used as vaccines. They can
XX CC be used for preventing or treating a mucosal disease in a subject, e.g.
XX CC ruminants, cattle, sheep, goats, dogs, cats, horses, or man, particularly
XX CC mastitis in cows or breast cancers in humans. They can also be used for
XX CC preventing or treating a stress-induced disease. The present sequence
XX CC represents the binding domain of a previously published S. aureus
XX CC fibronectin binding protein A (FnBA) sequence. The FnB binding domain
XX CC gene sequence FnBAB, cloned for use in this invention has 97.8 percent
XX CC identity when compared to the previously published FnBA and FnBB gene
XX CC sequences
XX SQ Sequence 134 AA;

Query Match          93.3%; Score 112; DB 2; Length 134;
Best Local Similarity 95.2%; Pred. No. 9.4e-10;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KPSYQFGHNVPYDFEDTLPK 21
   |||||
Db 93 KPSYQFGHNSYDFEDTLPK 113

RESULT 7
AAW31556
ID AAW31556 standard; protein; 139 AA.
XX
AC AAW31556;
XX
DT 27-AUG-2003 (revised)
DT 25-MAR-2003 (revised)
DT 21-MAY-1998 (first entry)
XX
DE Fibronectin-binding MSCRAMM derivative pOD.
XX
KW Fibronectin; pOD; collagen binding protein; sepsis; infection;
KW microbial surface component regaining adhesive matrix molecule; MSCRAMM;
KW adhesin; vaccine; immunisation; diagnosis; therapy; mastitis.
XX
OS Staphylococcus aureus.
XX
XX Key Location/Qualifiers
XX Peptide 1..12
XX /note= "vector pQE30-derived peptide"
XX
XX WO9743314-A2.
XX PN
XX PD 20-NOV-1997.
XX

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PF 14-MAY-1997; 97WO-US008210.
XX
XX PR 16-MAY-1996; 96US-0017678P.
XX
XX PA (TEXA) UNIV TEXAS A & M SYSTEM.
XX PA (UYBR-) UAB RES FOUND.
XX
XX PI Hoeek M, Patti JM, House-Pompeo K, Sthanam N, Symereky J;
XX WPI: 1998-008601/01.
XX DR
XX PT Antibody that interacts with collagen binding domain of Staphylococcal
XX PT cna gene product - useful to prevent bacterial sepsis in animal infected
XX PT with Staphylococcus aureus.
XX
XX PS Disclosure, Page 91; 143pp; English.
XX
XX CC This protein comprises Staphylococcus aureus fibronectin-binding
XX CC microbial surface component regaining adhesive matrix molecule (MSCRAMM)
XX CC derivative pOD, plus a vector-derived N-terminal peptide. The invention
XX CC relates to claimed nucleic acid sequences (see AAT93436-38) encoding S.
XX CC aureus collagen binding protein (CBP) epitopes M17, M31 and M55 (see
XX CC AAW31552-54) that confer protection against S. aureus infection. CBP
XX CC protein and antigenic epitopes are contemplated for use in the treatment
XX CC of pathological infections, especially to prevent bacterial adhesion to
XX CC collagen. The epitopes are also contemplated for use in the preparation
XX CC of vaccines and as carrier proteins in vaccine formulations, as well as
XX CC in the formulation of compositions for the prevention of S. aureus
XX CC infection. pCF3 and pOD (see AAW31556) were used to raise anti-MSCRAMM
XX CC polyclonal antibodies used in passive immunisation against bovine
XX CC mastitis. (Updated on 25-MAR-2003 to correct PI field.) (Updated on 27-
XX CC AUG-2003 to correct OS field.)
XX SQ Sequence 139 AA;

Query Match          93.3%; Score 112; DB 2; Length 139;
Best Local Similarity 95.2%; Pred. No. 9.8e-10;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KPSYQFGHNVPYDFEDTLPK 21
   |||||
Db 107 KPSYQFGHNSYDFEDTLPK 127

RESULT 8
AAP82115
ID AAP82115 standard; protein; 1018 AA.
XX
AC AAP82115;
XX
DT 25-MAR-2003 (revised)
DT 05-JAN-1990 (first entry)
XX
DE Fibronectin binding protein.
XX
KW Fibronectin binding protein; S. aureus; immunisation; mastitis; ruminants;
KW wound infection; diagnosis.
XX
OS Staphylococcus aureus.
XX
XX EP294349-A.
XX PN
XX PD 07-DEC-1988.
XX
XX PF 30-MAY-1988; 88EP-00850188.
XX
XX PR 01-JUN-1987; 87SE-00002272.
XX
XX PA (ALFA ) ALFA LAVAL AGRIC INT AB.
XX
XX Lindberg MK, Signas LC, Wadstrom TM, Froman G;
XX WPI: 1988-347978/49.
XX

```

DR P-PSDB; AAP82115.
XX Hybrid DNA encoding Staphylococcus aureus fibronectin binding protein -
PT useful for immunisation and topical application to prevent staphylococcal
PT infections.
XX disclosare; Fig. 8A:1-8A:2; 23pp; English.
XX The S.aureus fibronectin binding protein may be included in a hybrid
CC protein. The protein may be used to immunise ruminants against
CC staphylococcal mastitis, pref. when given at 0.5-5 microg/kg, using 3
CC doses at 1-3 week intervals; and for topical applicn. to prevent wound
CC infection, pref. using isotonic saline soln. of concn. 25-250 microg/mg.
CC The DNA encoding the binding protein and the hybrid protein may be
CC immobilised on a carrier and used to diagnose staphylococcal infections.
CC (updated on 25-MAR-2003 to correct PA field.)
SQ Sequence 1018 AA;
Query Match 93.3%; Score 112; DB 1; Length 1018;
Best Local Similarity 95.2%; Pred. No. 9.2e-09;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 KPSYQFGCHNPVDFEEDTLPK 21
Db 837 KPSYQFGCHNSVDFEEDTLPK 857
RESULT 9
AAU37245
ID AAU37245 standard; protein; 1018 AA.
AC AAU37245;
AC AAU37245;
DT 14-FEB-2002 (first entry)
XX Staphylococcus aureus cellular proliferation protein #1415.
XX Antisense; prokaryotic cellular proliferation protein; antibiotic;
KM antibacterial; drug design.
XX Staphylococcus aureus.
OS WO200170955-A2.
PN WO200170955-A2.
PD 27-SEP-2001.
XX 21-MAR-2001; 2001WO-US009180.
PF 21-MAR-2000; 2000US-0191078P.
PR 23-MAY-2000; 2000US-0206848P.
PR 26-MAY-2000; 2000US-0207727P.
PR 23-OCT-2000; 2000US-0242578P.
PR 27-NOV-2000; 2000US-0253625P.
PR 22-DEC-2000; 2000US-0257931P.
PR 16-FEB-2001; 2001US-0269308P.
XX (ELIT-) ELITRA PHARM INC.
XX Haselbeck R, Ohlsen KL, Zyekind JW, Wall D, Trawick JD, Carr GJ;
PI Yamamoto RT, Xu HH;
PI WPI; 2001-611495/70.
DR N-PSDB; AAS55104.
XX New polynucleotides for the identification and development of
PT antibiotics, comprise sequences of antisense nucleic acids.
XX Example 3; SEQ ID NO 12838; 511pp; English.
XX The invention relates to antisense inhibitors of genes essential to
CC prokaryotic cellular proliferation, their use in identifying the genes,
CC their use in the discovery of novel antibiotics, the essential genes

CC themselves and the encoded proteins. The prokaryotes used are Escherichia
CC coli, Staphylococcus aureus, Salmonella typhi, Klebsiella pneumoniae,
CC Pseudomonas aeruginosa and Enterococcus faecalis. The invention is also
CC useful for the identification of potential new targets for antibiotic
CC development. The antisense nucleic acids can also be used to identify
CC proteins used in proliferation, to express these proteins, and to obtain
CC antibodies capable of binding to the expressed proteins. The proteins can
CC be used to screen compounds in rational drug discovery programmes. The
CC antisense nucleic acid sequence is also useful to screen for homologous
CC nucleic acids which are required for cell proliferation in a wide variety
CC of organisms. The present sequence represents an essential prokaryotic
CC cellular proliferation protein. Note: The sequence data for this patent
CC did not form part of the printed specification, but was obtained in
CC electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
SQ Sequence 1018 AA;
Query Match 93.3%; Score 112; DB 4; Length 1018;
Best Local Similarity 95.2%; Pred. No. 9.2e-09;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 KPSYQFGCHNPVDFEEDTLPK 21
Db 837 KPSYQFGCHNSVDFEEDTLPK 857
RESULT 10
AAU34301
ID AAU34301 standard; protein; 1018 AA.
AC AAU34301;
AC AAU34301;
DT 14-FEB-2002 (first entry)
XX Staphylococcus aureus cellular proliferation protein #577.
XX Antisense; prokaryotic cellular proliferation protein; antibiotic;
KM antibacterial; drug design.
XX Staphylococcus aureus.
OS WO200170955-A2.
PN WO200170955-A2.
PD 27-SEP-2001.
XX 21-MAR-2001; 2001WO-US009180.
PF 21-MAR-2000; 2000US-0191078P.
PR 23-MAY-2000; 2000US-0206848P.
PR 26-MAY-2000; 2000US-0207727P.
PR 23-OCT-2000; 2000US-0242578P.
PR 27-NOV-2000; 2000US-0253625P.
PR 22-DEC-2000; 2000US-0257931P.
PR 16-FEB-2001; 2001US-0269308P.
XX (ELIT-) ELITRA PHARM INC.
XX Haselbeck R, Ohlsen KL, Zyekind JW, Wall D, Trawick JD, Carr GJ;
PI Yamamoto RT, Xu HH;
PI WPI; 2001-611495/70.
DR N-PSDB; AAS52160.
XX New polynucleotides for the identification and development of
PT antibiotics, comprise sequences of antisense nucleic acids.
XX Example 3; SEQ ID NO 5797; 511pp; English.
XX The invention relates to antisense inhibitors of genes essential to
CC prokaryotic cellular proliferation, their use in identifying the genes,
CC their use in the discovery of novel antibiotics, the essential genes
CC themselves and the encoded proteins. The prokaryotes used are Escherichia

CC coli, *Staphylococcus aureus*, *Salmonella typhi*, *Klebsiella pneumoniae*,
 CC *Pseudomonas aeruginosa* and *Enterococcus faecalis*. The invention is also
 CC useful for the identification of potential new targets for antibiotic
 CC development. The antisense nucleic acids can also be used to identify
 CC proteins used in proliferation, to express these proteins, and to obtain
 CC antibodies capable of binding to the expressed proteins. The proteins can
 CC be used to screen compounds in rational drug discovery programmes. The
 CC antisense nucleic acid sequence is also useful to screen for homologous
 CC nucleic acids which are required for cell proliferation in a wide variety
 CC of organisms. The present sequence represents an essential prokaryotic
 CC cellular proliferation protein. Note: The sequence data for this patent
 CC did not form part of the printed specification, but was obtained in
 CC electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences

XX Sequence 1018 AA;
 SQ
 Query Match 93.3%; Score 112; DB 4; Length 1018;
 Best Local Similarity 95.2%; Pred. No. 9.2e-09;
 Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KPSYQFGHNVPDFEEDTLPK 21
 |||||
 Db 837 KPSYQFGHNSVDFEEDTLPK 857

RESULT 11

ABJ18922
 ID ABJ18922 standard; protein; 1018 AA.

XX
 AC ABJ18922;

XX
 DT 06-MAR-2003 (first entry)

DE Pathogen specific antigen related staphylococcal protein SEQ ID No 68.

XX Antibacterial; virucide; fungicide; protozoacide; cytostatic; anti-HIV;

XX hyperimmune; serum-reactive; antigen; pathogen; tumour; allergen;

KW auto-immunity; vaccine; staphylococcal infection; antibody; cancer;

KM autoimmune disease; HIV; hepatitis.

OS *Staphylococcus* sp.

XX
 PN WO200259148-A2.

XX
 PD 01-AUG-2002.

XX
 PF 21-JAN-2002; 2002WO-BP000546.

XX
 PR 26-JAN-2001; 2001AT-00000130.

XX
 PA (CIST-) CISTEM BIOTECHNOLOGIES GMBH.

XX
 PI Meinke A, Nagy E, Von Ahnen U, Klade C, Henics T, Zauner W;
 PT Minh DB, Vytvytska O, Etz H, Dryla A, Weichart T, Hafner M;
 PI Tempelmeier B;

XX
 DR WPI, 2003-075410/07.

XX
 PS Identifying, isolating and producing hyperimmune serum-reactive antigens
 PT from a pathogen, for preparing vaccine or medicament for treating or
 PT preventing e.g. staphylococcal infections, comprises providing antibody
 PT preparation.

XX
 PS Example 7; Page 157; 252pp; English.

XX The invention relates to a novel method for identifying, isolating and
 CC producing hyperimmune serum-reactive antigens from a pathogen, tumour,
 CC allergen, a tissue or host prone to auto-immunity, where the antigens are
 CC used in a vaccine, comprises providing antibody preparation from a plasma
 CC pool of a type of animal, or individual sera with antibodies against the
 CC specific pathogen, tumour, allergen, tissue or host prone to auto-
 CC immunity. The hyperimmune serum-reactive antigens comprising any of the

CC 62 sequences of 53-2261 amino acids fully defined in the specification,
 CC or their hyperimmune fragments are useful for the manufacture of a
 CC pharmaceutical preparation, particularly a vaccine against staphylococcal
 CC infections or colonisation against *S. aureus* or *S. epidermidis*. The
 CC preparation of antibodies is useful for the manufacture of a medicament
 CC for treating or preventing staphylococcal infections or colonisation
 CC against *S. aureus* or *S. epidermidis*. The antibody preparations may also
 CC be used for diagnostic and imaging purposes. Other conditions that can be
 CC treated include cancer, autoimmune diseases or infections caused by viral
 CC (e.g. HIV, hepatitis A, B or C), fungal or protozoan pathogens. This
 CC sequence represents a staphylococcal protein relating to the method for
 CC identifying and producing pathogen specific antigens of the invention

XX Sequence 1018 AA;
 SQ
 Query Match 93.3%; Score 112; DB 6; Length 1018;
 Best Local Similarity 95.2%; Pred. No. 9.2e-09;
 Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KPSYQFGHNVPDFEEDTLPK 21
 |||||
 Db 837 KPSYQFGHNSVDFEEDTLPK 857

RESULT 12

ABM72537
 ID ABM72537 standard; protein; 1018 AA.

XX
 AC ABM72537;

XX
 DT 20-NOV-2003 (first entry)

DE *Staphylococcus aureus* protein #1777.

XX Antibacterial; vaccine; gene therapy; infection; sepsis; diagnosis;

KW enzymatic assay; antibiotic target.

XX
 OS *Staphylococcus aureus*.

XX
 PN WO200294868-A2.

XX
 PD 28-NOV-2002.

XX
 PF 27-MAR-2002; 2002WO-IB002637.

XX
 PR 27-MAR-2001; 2001GB-00007661.

XX
 PA (CHIR-) CHIRON SPA.

XX
 PI Masignani V, Mora M, Scarselli M;

XX
 DR WPI, 2003-120786/11.

XX
 DR N-PSDB; ACF74097.

XX
 PT New *Staphylococcus aureus* protein, useful as a vaccine for treating or
 PT preventing *Staphylococcal* infection, specifically an infection caused by
 PT *S. aureus*, e.g. sepsis.

XX
 PS Claim 1; SEQ ID NO 3554; 49pp; English.

XX The invention relates to novel genes and encoded proteins from
 CC *Staphylococcus aureus*. A composition comprising the *S. aureus* protein, a
 CC nucleic acid encoding the protein, or an antibody to the protein, is
 CC useful as a pharmaceutical, particularly as a vaccine for treating or
 CC preventing infection due to *Staphylococcus* bacteria, specifically an
 CC infection caused by *S. aureus*. The composition is particularly useful for
 CC treating or preventing sepsis in a patient. The composition can also be
 CC used for diagnostics. The protein is also used in an assay for enzymatic
 CC studies and as a target for antibiotics. This sequence represents one of
 CC the novel *S. aureus* proteins of the invention

XX
 SQ Sequence 1018 AA;

Query Match 93.3%; Score 112; DB 6; Length 1018;
Best Local Similarity 95.2%; Pred. No. 9.2e-09;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KPSYQFGHNSVDFEEDTLPK 21
|||||
Db 837 KPSYQFGHNSVDFEEDTLPK 857

RESULT 13
AAW89806
ID AAW89806 standard; protein: 1027 AA.

XX AAW89806;
XX 16-MAR-1999 (first entry)
XX Staphylococcus aureus protein SEQ ID #5254.

XX Computer readable medium; vaccine; S.aureus infection; immunodetection;
XX cellulitis; eyelid infection; food poisoning; osteomyelitis; therapy;
XX skin infection; surgical wound infection; scalded skin syndrome;
XX toxic shock syndrome.

XX Staphylococcus aureus.

XX EP786519-A2.

XX 30-JUL-1997.

XX 07-JAN-1997; 97EP-00100117.

XX 05-JAN-1996; 96US-0009861P.

XX (HUMA-) HUMAN GENOME SCI INC.

XX Kunsch CA, Choi GH, Barash SC, Dillon PJ, Fannon MR, Rosen CA;

XX WPI; 1997-374922/35.

PT Polynucleotide(s) and proteins derived from Staphylococcus aureus -
PT stored on computer readable medium and used in the production of anti-
PT S.aureus vaccines.

PS Claim 23; Page 3263-3267; 3271pp; English.

XX This sequence represents a Staphylococcus aureus protein sequence of the
CC invention. The DNA sequences encoding the S.aureus proteins are recorded
CC on a computer readable medium, preferably selected from a floppy or hard
CC disk, random access memory (RAM), read-only memory (ROM) or CD-ROM.
CC Homology searches using the S.aureus DNA sequences allows putative
CC functions to be assigned so that protein-encoding or regulatory regions
CC of commercial, therapeutic or industrial importance can be obtained.
CC Specifically, sequences which are likely to encode antigens have been
CC identified and these polypeptides can be used in a vaccine composition
CC against S.aureus infection. The polypeptides can also be used in a kit
CC for the immunodetection of S.aureus in a sample. S.aureus is implicated
CC in numerous human diseases, including cellulitis, eyelid infections, food
CC poisoning, osteomyelitis, skin and surgical wound infections, scalded
CC skin syndrome, toxic shock syndrome, etc. Organisms transformed with the
CC DNA sequences can be used for recombinant production of the polypeptides.
CC The new DNA sequences (and their fragments) are useful as primers or
CC probes for isolating homologues of any of the 5191 S.aureus DNA sequences
CC contained on the computer readable medium

XX Sequence 1027 AA;

Query Match 93.3%; Score 112; DB 2; Length 1027;
Best Local Similarity 95.2%; Pred. No. 9.3e-09;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KPSYQFGHNSVDFEEDTLPK 21
|||||

Db 846 KPSYQFGHNSVDFEEDTLPK 866

RESULT 14
ABU15854
ID ABU15854 standard; protein: 961 AA.

XX ABU15854;

XX 19-JUN-2003 (first entry)

XX Protein encoded by prokaryotic essential gene #1381.

XX Antisense; prokaryotic essential gene; cell proliferation; drug design.

XX Staphylococcus aureus.

XX WO20027183-A2.

XX 03-OCT-2002.

XX 21-MAR-2002; 2002WO-US009107.

XX 21-MAR-2001; 2001US-00815242.

XX 06-SEP-2001; 2001US-00948993.

XX 25-OCT-2001; 2001US-0342923P.

XX 08-FEB-2002; 2002US-00072851.

XX 06-MAR-2002; 2002US-0362699P.

XX (ELIT-) ELITRA PHARM INC.

XX Wang L, Zamudio C, Malone C, Haeselbeck R, Ohlsen KU, Zyckind JW;

XX Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;

XX WPI; 2003-029926/02.

XX N-PSDB; ACA19724.

XX New antisense nucleic acids, useful for identifying proteins or screening
XX for homologous nucleic acids, required for cellular proliferation to
XX isolate candidate molecules for rational drug discovery programs.

XX Claim 25; SEQ ID NO 43778; 1766pp; English.

XX The invention relates to an isolated nucleic acid comprising any one of
CC the 6213 antisense sequences given in the specification where expression
CC of the nucleic acid inhibits proliferation of a cell. Also included are:
CC (1) a vector comprising a promoter operably linked to the nucleic acid
CC encoding a polypeptide whose expression is inhibited by the antisense
CC nucleic acid; (2) a host cell containing the vector; (3) an isolated
CC polypeptide or its fragment whose expression is inhibited by the
CC antisense nucleic acid; (4) an antibody capable of specifically binding
CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular
CC proliferation or the activity of a gene in an operon required for
CC proliferation; (7) identifying a compound that influences the activity of
CC the gene product or that has an activity against a biological pathway
CC required for proliferation, or that inhibits cellular proliferation; (8)
CC identifying a gene required for cellular proliferation or the biological
CC pathway in which a proliferation-required gene or its gene product lies
CC or a gene on which the test compound that inhibits proliferation of an
CC organism acts; (9) manufacturing an antibiotic; (10) profiling a
CC compound's activity; (11) a culture comprising strains in which the gene
CC product is overexpressed or underexpressed; (12) determining the extent
CC to which each of the strains is present in a culture or collection of
CC strains; or (13) identifying the target of a compound that inhibits the
CC proliferation of an organism. The antisense nucleic acids are useful for
CC identifying proteins or screening for homologous nucleic acids required
CC for cellular proliferation to isolate candidate molecules for rational
CC drug discovery programs, or for screening homologous nucleic acids
CC required for proliferation in cells other than S. aureus, S. typhimurium,
CC K. pneumoniae or P. aeruginosa. The present sequence is encoded by one of
CC the target prokaryotic essential genes. Note: The sequence data for this
CC patent did not form part of the printed specification, but was obtained
CC in electronic format directly from WIPO at

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CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 961 AA;
Query Match          90.8%; Score 109; DB 6; Length 961;
Best Local Similarity 90.5%; Pred. No. 2.6e-08;
Matches 19; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1 KPSTQFGHNPPVDFEEDTLPK 21
        ||:|||||
DB      784 KPNYQFGHNSYDFEEDTLPK 804

RESULT 15
AAU33960
ID AAU33960 standard; protein; 978 AA.
XX
AC AAU33960;
XX
DT 14-FEB-2002 (first entry)
XX
DE Staphylococcus aureus cellular proliferation protein #236.
XX
KM Antisense; prokaryotic cellular proliferation protein; antibiotic;
XX antibacterial; drug design.
XX
OS Staphylococcus aureus.
XX
PN W0200170955-A2.
XX
PD 27-SEP-2001.
XX
PI 21-MAR-2001; 2001MO-US009180.
XX
PR 21-MAR-2000; 2000US-0191078P.
XX
PR 23-MAY-2000; 2000US-0206848P.
XX
PR 26-MAY-2000; 2000US-0207727P.
XX
PR 23-OCT-2000; 2000US-0242578P.
XX
PR 27-NOV-2000; 2000US-0253625P.
XX
PR 22-DEC-2000; 2000US-0257931P.
XX
PR 16-FEB-2001; 2001US-0269308P.
XX
PA (ELIT-) ELITRA PHARM INC.
PI Haselbeck R, Ohlsen KL, Zykkind JW, Wall D, Trawick JD, Carr GJ,
PI Yamamoto RT, Xu HH;
XX
DR N-PSDB; AASS1819.
XX
WPI; 2001-611495/70.
XX
N-PSDB; AASS1819.
XX
PT New polynucleotides for the identification and development of
XX antibiotics, comprise sequences of antisense nucleic acids.
XX
PS Example 3; SEQ ID NO 5456; 51pp; English.
XX
XX The invention relates to antisense inhibitors of genes essential to
XX prokaryotic cellular proliferation, their use in identifying the genes,
XX their use in the discovery of novel antibiotics, the essential genes
XX themselves and the encoded proteins. The prokaryotes used are Escherichia
XX coli, Staphylococcus aureus, Salmonella typhi, Klebsiella pneumoniae,
XX Pseudomonas aeruginosa and Enterococcus faecalis. The invention is also
XX useful for the identification of potential new targets for antibiotic
XX development. The antisense nucleic acids can also be used to identify
XX antibodies used in proliferation, to express these proteins, and to obtain
XX proteins capable of binding to the expressed proteins. The proteins can
XX be used to screen compounds in rational drug discovery programmes. The
XX antisense nucleic acid sequence is also useful to screen for homologous
XX nucleic acids which are required for cell proliferation in a wide variety
XX of organisms. The present sequence represents an essential prokaryotic
XX cellular proliferation protein. Note: The sequence data for this patent
XX did not form part of the printed specification, but was obtained in
XX electronic format directly from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences

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XX
SQ Sequence 978 AA;
Query Match          90.8%; Score 109; DB 4; Length 978;
Best Local Similarity 90.5%; Pred. No. 2.7e-08;
Matches 19; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1 KPSTQFGHNPPVDFEEDTLPK 21
        ||:|||||
DB      815 KPNYQFGHNSYDFEEDTLPK 835

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Job time : 59.1473 secs

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OM protein - protein search, using SW model

Run on: October 22, 2005, 02:23:36 ; Search time 15.9358 Seconds
(without alignments)
98.371 Million cell updates/sec

Title: US-10-731-238-23

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Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	120	100.0	21	4	US-09-010-317-23 Sequence 23, Appl
2	112	93.3	21	4	US-09-010-317-9 Sequence 9, Appl
3	112	93.3	37	1	US-08-234-622A-4 Sequence 4, Appl
4	112	93.3	38	1	US-08-294-189-8 Sequence 8, Appl
5	112	93.3	38	1	US-08-729-767-5 Sequence 5, Appl
6	112	93.3	114	1	US-08-259-000-3 Sequence 3, Appl
7	112	93.3	139	3	US-08-856-253-8 Sequence 8, Appl
8	112	93.3	178	2	US-08-459-135A-12 Sequence 12, Appl
9	112	93.3	178	3	US-08-495-559-12 Sequence 12, Appl
10	112	93.3	1027	4	US-08-956-171B-5254 Sequence 5254, Ap
11	112	93.3	1027	4	US-08-781-986A-5254 Sequence 5254, Ap
12	107	89.2	21	4	US-09-010-317-14 Sequence 14, Appl
13	107	89.2	21	4	US-09-010-317-16 Sequence 16, Appl
14	107	89.2	21	4	US-09-010-317-33 Sequence 33, Appl
15	106	88.3	21	4	US-09-010-317-18 Sequence 18, Appl
16	106	88.3	21	4	US-09-010-317-24 Sequence 24, Appl
17	106	88.3	21	4	US-09-010-317-27 Sequence 27, Appl
18	106	88.3	21	4	US-09-010-317-28 Sequence 28, Appl
19	106	88.3	21	4	US-09-010-317-30 Sequence 30, Appl
20	105	87.5	21	4	US-09-010-317-25 Sequence 25, Appl
21	105	87.5	21	4	US-09-010-317-29 Sequence 29, Appl
22	105	87.5	21	4	US-09-010-317-31 Sequence 31, Appl
23	105	87.5	130	2	US-08-459-135A-7 Sequence 7, Appl
24	105	87.5	130	2	US-08-459-135A-8 Sequence 8, Appl
25	105	87.5	130	3	US-08-495-559-7 Sequence 7, Appl
26	105	87.5	130	3	US-08-495-559-8 Sequence 8, Appl
27	105	87.5	174	2	US-08-459-135A-10 Sequence 10, Appl

28	105	87.5	174	2	US-08-459-135A-13 Sequence 13, Appl
29	105	87.5	174	3	US-08-495-559-10 Sequence 10, Appl
30	105	87.5	174	3	US-08-495-559-13 Sequence 13, Appl
31	105	87.5	176	3	US-08-495-559-6 Sequence 6, Appl
32	105	87.5	181	2	US-08-459-135A-6 Sequence 6, Appl
33	105	87.5	559	4	US-08-956-171B-5251 Sequence 5251, Ap
34	105	87.5	559	4	US-08-781-986A-5251 Sequence 5251, Ap
35	104	86.7	21	4	US-09-010-317-10 Sequence 10, Appl
36	104	86.7	21	4	US-09-010-317-15 Sequence 15, Appl
37	104	86.7	21	4	US-09-010-317-20 Sequence 20, Appl
38	104	86.7	21	4	US-09-010-317-22 Sequence 22, Appl
39	104	86.7	21	4	US-09-010-317-32 Sequence 32, Appl
40	104	86.7	22	4	US-09-010-317-13 Sequence 13, Appl
41	102	85.0	21	4	US-09-010-317-17 Sequence 17, Appl
42	102	85.0	21	4	US-09-010-317-19 Sequence 19, Appl
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44	102	85.0	21	4	US-09-010-317-26 Sequence 26, Appl
45	91	75.8	19	1	US-08-234-622A-1 Sequence 1, Appl

ALIGNMENTS

RESULT 1
US-09-010-317-23
Sequence 23, Application US/09010317
Patent No. 6685943
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
APPLICANT: Patti, Joseph M.
APPLICANT: House-Pompeo, Karen L.
APPLICANT: Speciale, Pietro
APPLICANT: McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
TITLE OF INVENTION: AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/010.317
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAMK.189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-09-010-317-23
Query Match 100.0%; Score 120; DB 4; Length 21;
Best Local Similarity 100.0%; Pred. No. 8.5e-13;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KPSYQFGHNPVDFEEDTLPK 21
|||||

DB 1 KPSYQFGHNPVDFEEDTLPK 21

RESULT 2
US-09-010-317-9
Sequence 9, Application US/09010317
Patent No. 6685943
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
APPLICANT: Patti, Joseph M.
APPLICANT: House-Pompeo, Karen L.
APPLICANT: Speziale, Pietro
APPLICANT: McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
TITLE OF INVENTION: AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSER: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hblber, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TANK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-09-010-317-9

Query Match 93.3%; Score 112; DB 4; Length 21;
Best Local Similarity 95.2%; Pred. No. 1.7e-11;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KPSYQFGHNPVDFEEDTLPK 21
|||||

DB 1 KPSYQFGHNSVDFEEDTLPK 21

RESULT 3
US-08-234-622A-4
Sequence 4, Application US/08234622A
Patent No. 5440014
GENERAL INFORMATION:
APPLICANT: HOOK, Magnus
APPLICANT: MCGAVIN, Martin
APPLICANT: RAUCCI, Giuseppe
TITLE OF INVENTION: A FIBRONECTIN BINDING PEPTIDE

NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSER: Burns, Doane, Swecker & Machis
STREET: P.O. Box 1404
CITY: Alexandria
STATE: Virginia
COUNTRY: United States
ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/234,622A
FILING DATE: 28-APR-1994
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: SE 9002617-0
FILING DATE: 10-AUG-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/SE91/00534
FILING DATE: 09-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: Neuth, Donna M
REGISTRATION NUMBER: 36,607
REFERENCE/DOCKET NUMBER: 012885-044
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 37 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-234-622A-4

Query Match 93.3%; Score 112; DB 1; Length 37;
Best Local Similarity 95.2%; Pred. No. 3.2e-11;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KPSYQFGHNPVDFEEDTLPK 21
|||||

DB 16 KPSYQFGHNSVDFEEDTLPK 36

RESULT 4
US-08-294-189-8
Sequence 8, Application US/08294189
Patent No. 5707822
GENERAL INFORMATION:
APPLICANT: Fischetti, Vincent A.
APPLICANT: Rakonjac, Jasna
APPLICANT: Robbins, John
TITLE OF INVENTION: GENE SERUM OPACITY FACTOR
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSER: Klauber & Jackson
STREET: 411 Hackensack Avenue
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/294,189
FILING DATE: 22-AUG-1994

CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-118
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 487-5800
TELEFAX: 201 343-1684
TELEX: 133521
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
ORGANISM: Streptococcus pyogenes
STRAIN: D734
INDIVIDUAL ISOLATE: 22
IMMEDIATE SOURCE:
CLONE: SAU3a
US-08-294-189-8

Query Match 93.3%; Score 112; DB 1; Length 38;
Best Local Similarity 95.2%; Pred. No. 3.3e-11;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KPSYQFGHNVPVDEDTLPK 21
Db 10 KPSYQFGHNSVDFEEDTLPK 30

RESULT 5
US-08-729-767-5
Sequence 5, Application US/08729767
Patent No. 5770702
GENERAL INFORMATION:
APPLICANT: HOOK, Magnus
APPLICANT: LINDBERG, Martin Kjell
APPLICANT: SIGNAS, Lars Christer
APPLICANT: WADSTROM, Torkel Mikael
APPLICANT: FROMAN, Gunnar
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN AS WELL AS
TITLE OF INVENTION: ITS PREPARATION
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Burns, Doane, Swecker & Mathis, L.L.P.
STREET: P.O. Box 1404
CITY: Alexandria
STATE: Virginia
COUNTRY: United States
ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/729,767
FILING DATE: 07-OCT-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/259,000
FILING DATE: 13-JUN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/007,817
FILING DATE: 22-JAN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/201,028
FILING DATE: 01-JUN-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: SE 8702272-9

FILING DATE: 01-JUN-1987
ATTORNEY/AGENT INFORMATION:
NAME: McGowan, Malcolm K.
REGISTRATION NUMBER: 39,300
REFERENCE/DOCKET NUMBER: 012889-036
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-729-767-5

Query Match 93.3%; Score 112; DB 1; Length 38;
Best Local Similarity 95.2%; Pred. No. 3.3e-11;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KPSYQFGHNVPVDEDTLPK 21
Db 17 KPSYQFGHNSVDFEEDTLPK 37

RESULT 6
US-08-259-000-3
Sequence 3, Application US/08259000
Patent No. 5571514
GENERAL INFORMATION:
APPLICANT: HOOK, Magnus
APPLICANT: LINDBERG, Martin Kjell
APPLICANT: SIGNAS, Lars Christer
APPLICANT: WADSTROM, Torkel Mikael
APPLICANT: FROMAN, Gunnar
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN AS WELL AS
TITLE OF INVENTION: ITS PREPARATION
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Burns, Doane, Swecker & Mathis
STREET: P.O. Box 1404
CITY: Alexandria
STATE: Virginia
COUNTRY: United States
ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/259,000
FILING DATE: 13-JUN-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: SE 8702272-9
FILING DATE: 01-JUN-1987
ATTORNEY/AGENT INFORMATION:
NAME: Meuth, Donna M
REGISTRATION NUMBER: 36,607
REFERENCE/DOCKET NUMBER: 012885-062
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 114 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-259-000-3

Query Match 93.3%; Score 112; DB 1; Length 114;
Best Local Similarity 95.2%; Pred. No. 1.2e-10;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KPSYFGGHNVPDEFDTLPK 21
Db 93 KPSYFGGHNVPDEFDTLPK 113

RESULT 7
US-08-856-253-8
; Sequence 8, Application US/08856253
; Patent No. 6288214
; GENERAL INFORMATION:
; APPLICANT: Hook, Magnus
; APPLICANT: Patti, Joseph M.
; APPLICANT: House-Pompeo, Karen
; APPLICANT: Stahanam, Narayana
; APPLICANT: Symesky, Jindrich
; TITLE OF INVENTION: COLLAGEN BINDING PROTEIN COMPOSITIONS
; TITLE OF INVENTION: AND METHODS OF USE
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: U.S.
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/856,253
; FILING DATE: Concurrently Herewith
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/017,678
; FILING DATE: 16-MAY-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Kitchell, Barbara S.
; REGISTRATION NUMBER: 33,928
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (512) 474-7577
; TELEFAX: (512) 418-3000
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 139 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
US-08-856-253-8

Query Match 93.3%; Score 112; DB 3; Length 139;
Best Local Similarity 95.2%; Pred. No. 1.5e-10;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KPSYFGGHNVPDEFDTLPK 21
Db 107 KPSYFGGHNVPDEFDTLPK 127

RESULT 8
US-08-459-135A-12
; Sequence 12, Application US/08459135A
; Patent No. 5955078
; GENERAL INFORMATION:
; APPLICANT: BURHAM, Martin Karl Russel
; APPLICANT: CHOPRA, Ian

APPLICANT: CRITCHLEY, Ian Alfred
; APPLICANT: KNOWLES, David Justin Charles
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN: MONOCLONAL ANTIBODY AND THEIR US
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corporation
; STREET: 709 Swedeland Road
; CITY: King of Prussia
; STATE: PA
; COUNTRY: U.S.A.
; ZIP: 19406-0939
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: DOS
; SOFTWARE: Fastseq, Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/459,135A
; FILING DATE: 02-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB/94/00215
; FILING DATE: 04-Feb-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Gimm, Edward R.
; REGISTRATION NUMBER: 38,891
; REFERENCE/DOCKET NUMBER: P30591C2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-270-4478
; TELEFAX: 610-270-5090
; TELEX:
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 178 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Protein
US-08-459-135A-12

Query Match 93.3%; Score 112; DB 2; Length 178;
Best Local Similarity 95.2%; Pred. No. 2e-10;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KPSYFGGHNVPDEFDTLPK 21
Db 93 KPSYFGGHNVPDEFDTLPK 113

RESULT 9
US-08-495-559-12
; Sequence 12, Application US/08495559A
; Patent No. 6054572
; GENERAL INFORMATION:
; APPLICANT: BURHAM, Martin Karl Russel
; APPLICANT: CHOPRA, Ian
; APPLICANT: CRITCHLEY, Ian Alfred
; APPLICANT: KNOWLES, David Justin Charles
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN: MONOCLONAL
; TITLE OF INVENTION: ANTIBODY AND THEIR USE IN PREVENTING BACTERIAL ADHESION
; FILE REFERENCE: P30591
; CURRENT APPLICATION NUMBER: US/08/495,559A
; CURRENT FILING DATE: 1995-08-03
; EARLIER APPLICATION NUMBER: GB 9302289.5
; EARLIER FILING DATE: 1993-02-05
; EARLIER APPLICATION NUMBER: GB 9321592.9
; EARLIER FILING DATE: 1993-10-20
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: Fastseq for Windows Version 3.0
; SEQ ID NO 12
; LENGTH: 178
; TYPE: PRT

ORGANISM: Staphylococcus aureus
US-08-495-559-12

Query Match 93.3%; Score 112; DB 3; Length 178;
Best Local Similarity 95.2%; Pred. No. 2e-10;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KPSYOGGHNVPDPEEDTLPK 21
DB 93 KPSYOGGHNVPDPEEDTLPK 113

RESULT 10
US-08-956-171E-5254

Sequence 5254, Application US/08956171E
Patent No. 6593114
GENERAL INFORMATION:

APPLICANT: Charles Kunsch

Gil H. Choi

Patrick S. Dillon

Craig A. Rosen

Steven C. Barash

Michael R. Fannon

TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences

NUMBER OF SEQUENCES: 5256

CORRESPONDENCE ADDRESS:

ADDRESSEE: Human Genome Sciences, Inc.

STREET: 9410 Key West Avenue

CITY: Rockville

STATE: Maryland

COUNTRY: USA

ZIP: 20850

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.50 inch, 1.4mb storage

COMPUTER: HP Vectra 486/33

OPERATING SYSTEM: MSDOS version 6.2

SOFTWARE: ASCII Text

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/956,171E

FILING DATE: 20-Oct-1997

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 60/009,861

FILING DATE: January 5, 1996

APPLICATION NUMBER: 08/781,986

FILING DATE: January 3, 1997

ATTORNEY/AGENT INFORMATION:

NAME: Mark J. Hyman

REGISTRATION NUMBER: 46,789

REFERENCE/DOCKET NUMBER: PB248P1

TELEPHONE: (240) 314-1224

TELEFAX: (301) 309-8439

INFORMATION FOR SEQ ID NO: 5254:

SEQUENCE CHARACTERISTICS:

LENGTH: 1027 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 5254:

US-08-956-171E-5254

Query Match 93.3%; Score 112; DB 4; Length 1027;
Best Local Similarity 95.2%; Pred. No. 1.5e-09;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KPSYOGGHNVPDPEEDTLPK 21
DB 846 KPSYOGGHNVPDPEEDTLPK 866

RESULT 11

US-08-781-986A-5254
Sequence 5254, Application US/08781986A

Patent No. 6737248

GENERAL INFORMATION:

APPLICANT: Charles Kunsch

TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences

NUMBER OF SEQUENCES: 5255

CORRESPONDENCE ADDRESS:

ADDRESSEE: Human Genome Sciences, Inc.

STREET: 9410 Key West Avenue

CITY: Rockville

STATE: Maryland

COUNTRY: USA

ZIP: 20850

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.50 inch, 1.4mb storage

COMPUTER: HP Vectra 486/33

OPERATING SYSTEM: MSDOS version 6.2

SOFTWARE: ASCII Text

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/781,986A

FILING DATE:

PRIOR APPLICATION DATA:

ATTORNEY/AGENT INFORMATION:

NAME: Benson, Bob

REGISTRATION NUMBER: 30,446

REFERENCE/DOCKET NUMBER: PB248PP

TELEPHONE: (301) 309-8504

TELEFAX: (301) 309-8512

INFORMATION FOR SEQ ID NO: 5254:

SEQUENCE CHARACTERISTICS:

LENGTH: 1027 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-781-986A-5254

Query Match 93.3%; Score 112; DB 4; Length 1027;
Best Local Similarity 95.2%; Pred. No. 1.5e-09;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KPSYOGGHNVPDPEEDTLPK 21
DB 846 KPSYOGGHNVPDPEEDTLPK 866

RESULT 12
US-09-010-317-14

Sequence 14, Application US/09010317

Patent No. 6685943

GENERAL INFORMATION:

APPLICANT: Hook, Magnus

APPLICANT: Patti, Joseph M.

APPLICANT: House-Pompeo, Karen L.

APPLICANT: Speziale, Pietro

APPLICANT: John, Danny

APPLICANT: McGavin, Martin J

TITLE OF INVENTION: FIBROECTIN BINDING PROTEIN COMPOSITIONS

NUMBER OF SEQUENCES: 105

CORRESPONDENCE ADDRESS:

ADDRESSEE: Arnold, White & Durkee

STREET: P.O. Box 4433

CITY: Houston

STATE: TX

COUNTRY: USA

ZIP: 77210-4433

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TANK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-09-010-317-14

Query Match 89.2%; Score 107; DB 4; Length 21;
Best Local Similarity 95.0%; Pred. No. 1.1e-10;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 PSYQFGHNPVDFEEDTLPK 21
Db 2 PSYQFGHNSVDFEEDTLPK 21

RESULT 13
US-09-010-317-16
Sequence 16, Application US/09010317
Patent No. 6685943
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
APPLICANT: Patti, Joseph M.
APPLICANT: House-Pompeo, Karen L.
APPLICANT: Speziale, Pietro
APPLICANT: Joh, Danny
APPLICANT: McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
TITLE OF INVENTION: AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TANK:189
TELECOMMUNICATION INFORMATION:

TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-09-010-317-16

Query Match 89.2%; Score 107; DB 4; Length 21;
Best Local Similarity 90.5%; Pred. No. 1.1e-10;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 KPSYQFGHNPVDFEEDTLPK 21
Db 1 KPSYQFGHNSVDFEEDTLPK 21

RESULT 14
US-09-010-317-33
Sequence 33, Application US/09010317
Patent No. 6685943
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
APPLICANT: Patti, Joseph M.
APPLICANT: House-Pompeo, Karen L.
APPLICANT: Speziale, Pietro
APPLICANT: Joh, Danny
APPLICANT: McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
TITLE OF INVENTION: AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TANK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-09-010-317-33

Query Match 89.2%; Score 107; DB 4; Length 21;
Best Local Similarity 95.0%; Pred. No. 1.1e-10;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KPSYQFGHNPVDFEEDTLPK 20
|||||

Db 1 KPSYQFGGHNVSDFEEDTLP 20

RESULT 15

US-09-010-317-18

/ Sequence 18, Application US/09010317
/ Patent No. 6685943

GENERAL INFORMATION:

APPLICANT: Hook, Magnus

APPLICANT: Patti, Joseph M.

APPLICANT: House-Pompeo, Karen L.

APPLICANT: Speciale, Pietro

APPLICANT: McGavin, Martin J.

TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS

TITLE OF INVENTION: AND METHODS OF USE

NUMBER OF SEQUENCES: 105

CORRESPONDENCE ADDRESS:

ADDRESSEE: Arnold, White & Durkee

STREET: P.O. Box 4433

CITY: Houston

STATE: TX

COUNTRY: USA

ZIP: 77210-4433

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: IBM PC compatible

SOFTWARE: Patentln Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/010,317

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 60/036,139

FILING DATE: 21-JAN-1997

ATTORNEY/AGENT INFORMATION:

NAME: Hibler, David W.

REGISTRATION NUMBER: 41,071

REFERENCE/DOCKET NUMBER: TAMK:189

TELECOMMUNICATION INFORMATION:

TELEPHONE: 512-418-5000

TELEFAX: 512-474-7577

INFORMATION FOR SEQ ID NO: 18:

SEQUENCE CHARACTERISTICS:

LENGTH: 21 amino acids

TYPE: amino acid

STRANDEDNESS:

TOPOLOGY: linear

US-09-010-317-18

Query Match 88.3%; Score 106; DB 4; Length 21;

Best Local Similarity 90.5%; Pred.No.1.6e-10;

Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 KPSYQFGGHNVSDFEEDTLPK 21

1 KPSYQFGGHNVSDFEEDTLPK 21

Db 1 KPSYQFGGHNVSDFEEDTLPK 21

Search completed: October 22, 2005, 03:51:12
Job time : 15.9358 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 22, 2005, 10:49:15 ; Search time 59.2367 Seconds
(without alignments)
148.005 Million cell updates/sec

Title: US-10-731-238-23

Perfect score: 120

Sequence: 1 KESYQFGCHNPVDFEEDLPK 21

Scoring table: BLASTSUM62
Gapop 10.0, Gapext 0.5

Searched: 1862951 seqs, 417491010 residues

Total number of hits satisfying chosen parameters: 1862951

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

Published Applications AA:*

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- 22: /cgn2_6/ptodata/2/pubppaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	120	100.0	21	18	US-10-731-238-23
2	112	93.3	21	18	US-10-731-238-9
3	112	93.3	37	20	US-11-066-697-1134
4	112	93.3	139	9	US-09-813-820-8
5	112	93.3	1018	9	US-09-815-242-5797
6	112	93.3	1018	9	US-09-815-242-12838
7	112	93.3	1018	17	US-10-470-0488-68
8	112	93.3	1027	8	US-08-781-986A-5254
9	112	93.3	1027	15	US-10-339-624-2254
10	109	90.8	961	15	US-10-282-122A-43778
11	109	90.8	978	9	US-09-815-242-5456

12	109	90.8	1001	9	US-09-815-242-12686	Sequence 12686, A
13	109	90.8	1038	15	US-10-282-122A-43827	Sequence 43827, A
14	107	89.2	21	18	US-10-731-238-14	Sequence 14, App1
15	107	89.2	21	18	US-10-731-238-16	Sequence 16, App1
16	107	89.2	21	18	US-10-731-238-33	Sequence 33, App1
17	106	88.3	21	18	US-10-731-238-18	Sequence 18, App1
18	106	88.3	21	18	US-10-731-238-24	Sequence 24, App1
19	106	88.3	21	18	US-10-731-238-27	Sequence 27, App1
20	106	88.3	21	18	US-10-731-238-28	Sequence 28, App1
21	106	88.3	21	18	US-10-731-238-30	Sequence 30, App1
22	105	87.5	21	18	US-10-731-238-25	Sequence 25, App1
23	105	87.5	21	18	US-10-731-238-29	Sequence 29, App1
24	105	87.5	21	18	US-10-731-238-31	Sequence 31, App1
25	105	87.5	388	8	US-08-901-062-1	Sequence 1, App1
26	105	87.5	559	8	US-08-781-986A-5251	Sequence 5251, Ap
27	105	87.5	559	15	US-10-329-624-5251	Sequence 5251, Ap
28	105	87.5	940	17	US-10-470-048B-424	Sequence 424, App
29	105	87.5	948	17	US-10-470-048B-69	Sequence 69, App1
30	104	86.7	21	18	US-10-731-238-10	Sequence 10, App1
31	104	86.7	21	18	US-10-731-238-15	Sequence 15, App1
32	104	86.7	21	18	US-10-731-238-20	Sequence 20, App1
33	104	86.7	21	18	US-10-731-238-22	Sequence 22, App1
34	104	86.7	21	18	US-10-731-238-32	Sequence 32, App1
35	104	86.7	22	18	US-10-731-238-13	Sequence 13, App1
36	102	85.0	21	18	US-10-731-238-17	Sequence 17, App1
37	102	85.0	21	18	US-10-731-238-19	Sequence 19, App1
38	102	85.0	21	18	US-10-731-238-21	Sequence 21, App1
39	102	85.0	21	18	US-10-731-238-26	Sequence 26, App1
40	84	70.0	21	18	US-10-731-238-34	Sequence 34, App1
41	73	60.8	14	18	US-10-731-238-61	Sequence 61, App1
42	55	45.8	10	18	US-10-731-238-96	Sequence 96, App1
43	54	45.0	10	18	US-10-731-238-95	Sequence 95, App1
44	53	44.2	10	18	US-10-731-238-97	Sequence 97, App1
45	53	44.2	10	18	US-10-731-238-101	Sequence 101, App

ALIGNMENTS

RESULT 1
US-10-731-238-23
Sequence 23, Application US/10731238
Publication No. US20050123552A1
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
Patel, Joseph M.
House-Pompeo, Karen L.
Speziale, Pietro
Joh, Danny
McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/731,238
FILING DATE: 10-Dec-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE: 21-Jan-1998
APPLICATION NUMBER: US 60/036,139

FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAMK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 23:
US-10-731-238-23

Query Match 100.0%; Score 120; DB 18; Length 21;
Best Local Similarity 100.0%; Pred. No. 4e-11;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KPSYQFGHNVPVDFEDTLPK 21
Db 1 KPSYQFGHNVPVDFEDTLPK 21

RESULT 2
US-10-731-238-9
Sequence 9, Application US/10731238
Publication No. US20050123552A1
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
Patti, Joseph M.
House-Pompeo, Karen L.
Speziale, Pietro
McGavin, Martin J.
John, Danny
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/731,238
FILING DATE: 10-Dec-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE: 21-Jan-1998
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAMK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>

TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 9:
US-10-731-238-9

Query Match 93.3%; Score 112; DB 18; Length 21;
Best Local Similarity 95.2%; Pred. No. 6.6e-10;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KPSYQFGHNVPVDFEDTLPK 21
Db 1 KPSYQFGHNVPVDFEDTLPK 21

RESULT 3
US-11-066-697-1134
Sequence 1134, Application US/11066697
Publication No. US20050187159A1
GENERAL INFORMATION:
APPLICANT: Bridon, Dominique P.
APPLICANT: Ezrin, Alan M.
APPLICANT: Milner, Peter G.
APPLICANT: Holmes, Darren L.
APPLICANT: Thibaudau, Karen
TITLE OF INVENTION: PROTECTION OF ENDOGENOUS THERAPEUTIC PEPTIDES FROM
PEPTIDASE ACTIVITY THROUGH CONJUGATION TO BLOOD
TITLE OF INVENTION: COMPONENTS
FILE REFERENCE: 500862002301
CURRENT APPLICATION NUMBER: US/11/066,697
CURRENT FILING DATE: 2005-02-25
PRIOR APPLICATION NUMBER: 09/657,276
PRIOR FILING DATE: 2000-09-07
PRIOR APPLICATION NUMBER: 60/153,406
PRIOR FILING DATE: 1999-09-10
PRIOR APPLICATION NUMBER: 60/159,783
PRIOR FILING DATE: 1999-10-15
NUMBER OF SEQ ID NOS: 1617
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 1134
LENGTH: 37
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-11-066-697-1134

Query Match 93.3%; Score 112; DB 20; Length 37;
Best Local Similarity 95.2%; Pred. No. 1.2e-09;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KPSYQFGHNVPVDFEDTLPK 21
Db 16 KPSYQFGHNVPVDFEDTLPK 36

RESULT 4
US-09-813-820-8
Sequence 8, Application US/09813820
Patent No. US20020102262A1
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
Patti, Joseph M.
House-Pompeo, Karen
Scham, Narayana
Synerky, Jindrich
TITLE OF INVENTION: COLLAGEN BINDING PROTEIN COMPOSITIONS
AND METHODS OF USE
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: Texas

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1 COUNTRY: U.S.
2 ZIP: 77210
3 COMPUTER READABLE FORM:
4 MEDIUM TYPE: Floppy disk
5 COMPUTER: IBM PC Compatible
6 OPERATING SYSTEM: PC-DOS/MS-DOS
7 SOFTWARE: Patentin Release #1.0, Version #1.30
8 CURRENT APPLICATION DATA:
9 APPLICATION NUMBER: US/09/813,820
10 FILING DATE: 22-Mar-2001
11 CLASSIFICATION: <Unknown>
12 PRIOR APPLICATION DATA:
13 APPLICATION NUMBER: 08/856,253
14 FILING DATE: <Unknown>
15 ATTORNEY/AGENT INFORMATION:
16 NAME: Kirchell, Barbara S.
17 REGISTRATION NUMBER: 33,928
18 REFERENCE/DOCKET NUMBER: TMK:193
19 TELECOMMUNICATION INFORMATION:
20 TELEPHONE: (512) 418-3000
21 TELEFAX: (512) 474-7577
22 INFORMATION FOR SEQ ID NO: 8:
23 SEQUENCE CHARACTERISTICS:
24 LENGTH: 139 amino acids
25 TYPE: amino acid
26 STRANDEDNESS: <Unknown>
27 TOPOLOGY: linear
28 SEQUENCE DESCRIPTION: SEQ ID NO: 8:
29 US-09-813-820-8
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31 Query Match 93.3%; Score 112; DB 9; Length 139;
32 Best Local Similarity 95.2%; Pred. No. 5e-09; 1; Indels 0; Gaps 0;
33 Matches 20; Conservative 0; Mismatches 1;
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35 QY 1 KPSTGFGHNVPDEEDTLPK 21
36 DB 107 KPSTGFGHNVPDEEDTLPK 127
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38 RESULT 5
39 US-09-815-242-5797
40 Sequence 5797, Application US/09815242
41 Patent No. US20020061569A1
42 GENERAL INFORMATION:
43 APPLICANT: Haeselbeck, Robert
44 APPLICANT: Ohlsen, Kari L.
45 APPLICANT: Zykkind, Judith W.
46 APPLICANT: Wall, Daniel
47 APPLICANT: Trawick, John D.
48 APPLICANT: Carr, Grant J.
49 APPLICANT: Yamamoto, Robert T.
50 APPLICANT: Xu, H. Howard
51 TITLE OF INVENTION: Identification of Essential Genes in
52 FILE REFERENCE: ELITRA.011A
53 CURRENT APPLICATION NUMBER: US/09/815,242
54 CURRENT FILING DATE: 2001-03-21
55 PRIOR APPLICATION NUMBER: 60/191,078
56 PRIOR FILING DATE: 2000-03-21
57 PRIOR APPLICATION NUMBER: 60/206,848
58 PRIOR FILING DATE: 2000-05-23
59 PRIOR APPLICATION NUMBER: 60/207,727
60 PRIOR FILING DATE: 2000-05-26
61 PRIOR APPLICATION NUMBER: 60/242,578
62 PRIOR FILING DATE: 2000-10-23
63 PRIOR APPLICATION NUMBER: 60/253,625
64 PRIOR FILING DATE: 2000-11-27
65 PRIOR APPLICATION NUMBER: 60/257,931
66 PRIOR FILING DATE: 2000-12-22
67 PRIOR APPLICATION NUMBER: 60/269,308
68 PRIOR FILING DATE: 2001-02-16
69 NUMBER OF SEQ ID NOS: 14110
70 SOFTWARE: FastSeq for Windows Version 4.0

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; SEQ ID NO 5797
; LENGTH: 1018
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-09-815-242-5797

Query Match          93.3%; Score 112; DB 9; Length 1018;
Best Local Similarity 95.2%; Pred. No. 4.3e-08;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 KPSYQFGHNPVDFEEDTLPK 21
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Db       837 KPSYQFGHNSVDPEEDTLPK 857

RESULT 6
US-09-815-242-12838
; Sequence 12838, Application US/09815242
; Patent No. US20020061569A1
GENERAL INFORMATION:
APPLICANT: Haegelbeck, Robert
APPLICANT: Ohlsen, Karl L.
APPLICANT: Zyskind, Judith W.
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John D.
APPLICANT: Carr, Grant J.
APPLICANT: Yamamoto, Robert T.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in
FILE REFERENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SOFTWARE: PasteSeq for Windows Version 4.0
SEQ ID NO 12838
LENGTH: 1018
TYPE: PRT
ORGANISM: Staphylococcus aureus
US-09-815-242-12838

Query Match          93.3%; Score 112; DB 9; Length 1018;
Best Local Similarity 95.2%; Pred. No. 4.3e-08;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 KPSYQFGHNPVDFEEDTLPK 21
        |||||
Db       837 KPSYQFGHNSVDPEEDTLPK 857

RESULT 7
US-10-470-048B-68
; Sequence 68, Application US/10470048B
; Publication No. US2005003744A1
GENERAL INFORMATION:
APPLICANT: MEINKE ET AL.
TITLE OF INVENTION: A METHOD FOR IDENTIFICATION, ISOLATION AND PRODUCTION OF
FILE REFERENCE: SONN.0350S

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;; CURRENT APPLICATION NUMBER: US/10/470,048B
;; CURRENT FILING DATE: 2003-07-25
;; NUMBER OF SEQ ID NOS: 603
;; SOFTWARE: PatentIn version 3.1
;; SEQ ID NO 68
;; LENGTH: 1018
;; TYPE: PRF
;; ORGANISM: Staphylococcus aureus
US-10-470-048B-68

Query Match 93.3%; Score 112; DB 17; Length 1018;
Best Local Similarity 95.2%; Pred. No. 4.3e-08;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KPSYQFGHNVPDFEEDTLPK 21
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Db 837 KPSYQFGHNVPDFEEDTLPK 857

RESULT 8
US-08-781-986A-5254
; Sequence 5254, Application US/08781986A
; Publication No. US20030054436A1
; GENERAL INFORMATION:
; APPLICANT: Charles Kunach
; TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
; NUMBER OF SEQUENCES: 5255
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4MB storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/781,986A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Benson, Bob
; REGISTRATION NUMBER: 30,446
; REFERENCE/DOCKET NUMBER: PB248PP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 5254:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1027 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-781-986A-5254

Query Match 93.3%; Score 112; DB 8; Length 1027;
Best Local Similarity 95.2%; Pred. No. 4.3e-08;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KPSYQFGHNVPDFEEDTLPK 21
|||
Db 846 KPSYQFGHNVPDFEEDTLPK 866

RESULT 9
US-10-329-624-5254

;; Sequence 5254, Application US/10329624
;; Publication No. US20040043037A1
;; GENERAL INFORMATION:
;; APPLICANT: Charles Kunach
;; Gail H. Choi
;; Patrick S. Dillon
;; Craig A. Rosen
;; Steven C. Barash
;; Michael R. Fannon
;; TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
;; NUMBER OF SEQUENCES: 5256
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Human Genome Sciences, Inc.
;; STREET: 9410 Key West Avenue
;; CITY: Rockville
;; STATE: Maryland
;; COUNTRY: USA
;; ZIP: 20850
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Diskette, 3.50 inch, 1.4MB storage
;; COMPUTER: HP Vectra 486/33
;; OPERATING SYSTEM: MSDOS version 6.2
;; SOFTWARE: ASCII Text
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/10/329,624
;; FILING DATE: 27-Dec-2002
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 08/956,171
;; FILING DATE: October 20, 1997
;; APPLICATION NUMBER: 60/009,861
;; FILING DATE: January 5, 1996
;; APPLICATION NUMBER: 08/781,986
;; FILING DATE: January 3, 1997
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Mark J. Hyman
;; REGISTRATION NUMBER: 46,789
;; REFERENCE/DOCKET NUMBER: PB248P1D1
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (240) 314-1224
;; TELEFAX: (301) 309-8439
;; INFORMATION FOR SEQ ID NO: 5254:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 1027 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; SEQUENCE DESCRIPTION: SEQ ID NO: 5254:
US-10-329-624-5254

Query Match 93.3%; Score 112; DB 15; Length 1027;
Best Local Similarity 95.2%; Pred. No. 4.3e-08;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KPSYQFGHNVPDFEEDTLPK 21
|||
Db 846 KPSYQFGHNVPDFEEDTLPK 866

RESULT 10
US-10-282-122A-43778
; Sequence 43778, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant

```

APPLICANT: Yamamoto, Robert
APPLICANT: Forsyth, R.
APPLICANT: Xu, H.
TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REFERENCE: ELITRA.034A
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
PRIORITY APPLICATION NUMBER: 60/191,078
PRIORITY FILING DATE: 2000-03-21
PRIORITY APPLICATION NUMBER: 60/206,848
PRIORITY FILING DATE: 2000-05-23
PRIORITY APPLICATION NUMBER: 60/207,727
PRIORITY FILING DATE: 2000-05-26
PRIORITY APPLICATION NUMBER: 60/230,335
PRIORITY FILING DATE: 2000-09-06
PRIORITY APPLICATION NUMBER: 60/230,347
PRIORITY FILING DATE: 2000-09-09
PRIORITY APPLICATION NUMBER: 60/242,578
PRIORITY FILING DATE: 2000-10-23
PRIORITY APPLICATION NUMBER: 60/253,625
PRIORITY FILING DATE: 2000-11-27
PRIORITY APPLICATION NUMBER: 60/257,931
PRIORITY FILING DATE: 2000-12-22
PRIORITY APPLICATION NUMBER: 60/267,636
PRIORITY FILING DATE: 2001-02-09
PRIORITY APPLICATION NUMBER: 60/269,308
PRIORITY FILING DATE: 2001-02-16
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 78614
SOFTWARE: PatentIn version 3.1
SEQ ID NO 43778
LENGTH: 961
TYPE: PRT
ORGANISM: Staphylococcus aureus
US-10-282-122A-43778

Query Match          90.8%  Score 109;  DB 15;  Length 961;
Best Local Similarity 90.5%  Pred. No. 1,1e-07;
Matches 19;  Conservative 1;  Mismatches 1;  Indels 0;  Gaps 0

OY      1  KPSYOPGSHNPVDFEEDTLPK 21
Db      784  KPNYOPGSHNSVDFEEDTLPK 804

RESULT 11
US-09-815-242-5456
Sequence 5456, Application US/09815242
Patent No. US20020061569A1
GENERAL INFORMATION:
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari L.
APPLICANT: Wall, Daniel
APPLICANT: Zyckind, Judith W.
APPLICANT: Trawick, John D.
APPLICANT: Carr, Grant J.
APPLICANT: Yamamoto, Robert T.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in
FILE REFERENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
PRIORITY APPLICATION NUMBER: 60/191,078
PRIORITY FILING DATE: 2000-03-21
PRIORITY APPLICATION NUMBER: 60/206,848
PRIORITY FILING DATE: 2000-05-23
PRIORITY APPLICATION NUMBER: 60/207,727
PRIORITY FILING DATE: 2000-05-26
PRIORITY APPLICATION NUMBER: 60/242,578
PRIORITY FILING DATE: 2000-10-23
PRIORITY APPLICATION NUMBER: 60/253,625
PRIORITY FILING DATE: 2000-11-27

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; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5456
; LENGTH: 978
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-09-815-242-5456

Query Match      90.8%; Score 109; DB 9; Length 978;
Best Local Similarity 90.5%; Pred. No. 1,2e-07;
Matches 19; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1 KPSYFGGHNVPDFFEDTLPK 21
      ||:|||||:|||||:|||||
Db      815 KPNYFGGHNVSVPEDTLPK 835

RESULT 12
US-09-815-242-12686
; Sequence 12686, Application US/09815242
; Patent No. US20020061569A1
GENERAL INFORMATION:
; APPLICANT: Haeselbeck, Robert
; APPLICANT: Ohlsen, Karl L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12686
; LENGTH: 1001
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-09-815-242-12686

Query Match      90.8%; Score 109; DB 9; Length 1001;
Best Local Similarity 90.5%; Pred. No. 1,2e-07;
Matches 19; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1 KPSYFGGHNVPDFFEDTLPK 21
      ||:|||||:|||||:|||||
Db      838 KPNYFGGHNVSVPEDTLPK 858

RESULT 13
US-10-282-122A-43827
; Sequence 43827, Application US/10282122A

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/ Publication No. US20040029129A1
/ GENERAL INFORMATION:
/ APPLICANT: Wang, Liangsu
/ APPLICANT: Zamudio, Carlos
/ APPLICANT: Malone, Cheryl
/ APPLICANT: Haselbeck, Robert
/ APPLICANT: Ohlsen, Karl
/ APPLICANT: Zyskind, Judith
/ APPLICANT: Wall, Daniel
/ APPLICANT: Trawick, John
/ APPLICANT: Carr, Grant
/ APPLICANT: Yamamoto, Robert
/ APPLICANT: Foreyth, R.
/ APPLICANT: Xu, H.
/ TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
/ FILE REFERENCE: ELITRA.034A
/ CURRENT FILING DATE: 2003-02-20
/ PRIOR APPLICATION NUMBER: 60/191,078
/ PRIOR FILING DATE: 2000-03-21
/ PRIOR APPLICATION NUMBER: 60/206,848
/ PRIOR FILING DATE: 2000-05-23
/ PRIOR APPLICATION NUMBER: 60/207,727
/ PRIOR FILING DATE: 2000-05-26
/ PRIOR APPLICATION NUMBER: 60/230,335
/ PRIOR FILING DATE: 2000-09-06
/ PRIOR APPLICATION NUMBER: 60/230,347
/ PRIOR FILING DATE: 2000-09-09
/ PRIOR APPLICATION NUMBER: 60/242,578
/ PRIOR FILING DATE: 2000-10-23
/ PRIOR APPLICATION NUMBER: 60/253,625
/ PRIOR FILING DATE: 2000-11-27
/ PRIOR APPLICATION NUMBER: 60/257,931
/ PRIOR FILING DATE: 2000-12-22
/ PRIOR APPLICATION NUMBER: 60/267,636
/ PRIOR FILING DATE: 2001-02-09
/ PRIOR APPLICATION NUMBER: 60/269,308
/ PRIOR FILING DATE: 2001-02-16
/ Remaining Prior Application data removed - See file wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 78614
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 43827
/ LENGTH: 1038
/ TYPE: PRT
/ ORGANISM: Staphylococcus aureus
/ US-10-282-122A-43827

Query Match          90.8%; Score 109; DB 15; Length 1038;
Best Local Similarity 90.5%; Pred. No. 1.2e-07;
Matches 19; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 KPSYFGGHNPVDFEEDTLPK 21
DB 833 KPNYQFGHNSVDFEEDTLPK 853

RESULT 14
US-10-731-238-14
/ Sequence 14, Application US/10731238
/ Publication No. US20050123552A1
/ GENERAL INFORMATION:
/ APPLICANT: Hook, Magnus
/ APPLICANT: Patti, Joseph M.
/ APPLICANT: House-Pompeo, Karen L.
/ APPLICANT: Speziale, Pietro
/ APPLICANT: Jon, Danny
/ APPLICANT: McGavin, Martin J.
/ TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
/ AND METHODS OF USE
/ NUMBER OF SEQUENCES: 105
/ CORRESPONDENCE ADDRESS:
/ ADDRESSER: Arnold, White & Durkee
/ STREET: P.O. Box 4433
```

```
/ CITY: Houston
/ STATE: TX
/ COUNTRY: USA
/ ZIP: 77210-4433
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/10/731,238
/ FILING DATE: 10-Dec-2003
/ CLASSIFICATION: <Unknown>
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US/09/010,317
/ FILING DATE: 21-Jan-1998
/ APPLICATION NUMBER: US 60/036,139
/ FILING DATE: 21-Jan-1997
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Hibler, David W.
/ REGISTRATION NUMBER: 41,071
/ REFERENCE/DOCKET NUMBER: TAMK:189
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 512-418-3000
/ TELEFAX: 512-474-7577
/ INFORMATION FOR SEQ ID NO: 14:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 21 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: <Unknown>
/ TOPOLOGY: linear
/ SEQUENCE DESCRIPTION: SEQ ID NO: 14:
US-10-731-238-14

Query Match          89.2%; Score 107; DB 18; Length 21;
Best Local Similarity 95.0%; Pred. No. 3.8e-09;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 PSYQFGGHNPVDFEEDTLPK 21
DB 2 PSYQFGHNSVDFEEDTLPK 21

RESULT 15
US-10-731-238-15
/ Sequence 16, Application US/10731238
/ Publication No. US20050123552A1
/ GENERAL INFORMATION:
/ APPLICANT: Hook, Magnus
/ APPLICANT: Patti, Joseph M.
/ APPLICANT: House-Pompeo, Karen L.
/ APPLICANT: Speziale, Pietro
/ APPLICANT: Jon, Danny
/ APPLICANT: McGavin, Martin J.
/ TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
/ AND METHODS OF USE
/ NUMBER OF SEQUENCES: 105
/ CORRESPONDENCE ADDRESS:
/ ADDRESSER: Arnold, White & Durkee
/ STREET: P.O. Box 4433
/ CITY: Houston
/ STATE: TX
/ COUNTRY: USA
/ ZIP: 77210-4433
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/10/731,238
/ FILING DATE: 10-Dec-2003
/ CLASSIFICATION: <Unknown>
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE: 21-Jan-1998
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAMK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 16:
US-10-731-238-16

Query Match 89.2%; Score 107; DB 18; Length 21;
Best Local Similarity 90.5%; Pred. No. 3.8e-09;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 KPSYQFGHNVPDPEEDTLPK 21
DB 1 KPPYQFGHNSVDFEEDTLPK 21

Search completed: October 22, 2005, 11:34:40
Job time : 59.2367 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 22, 2005, 02:23:36 ; Search time 10.5465 Seconds
(without alignments)
191.586 Million cell updates/sec

Title: US-10-731-238-23

Sequence: 1 KPSYQFGGHNVPFEDTLRK 21

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database:

1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	112	93.3	1018	2	A32192 fibronectin-binding
2	109	90.8	961	2	G90053 hypothetical prote
3	109	90.8	1038	2	H90053 hypothetical prote
4	105	87.5	940	2	S19702 fibronectin-bindin
5	51.5	42.9	1091	2	S33850 fibronectin-binding
6	48	40.0	84	2	T17676 hypothetical prote
7	48	40.0	156	2	B98046 single stranded bi
8	48	40.0	156	2	C95179 serine-trna synth
9	48	40.0	474	2	B84357 protein R19.7 (im
10	48	40.0	583	2	G87719 conserved hypothet
11	47	39.2	373	1	D69027 hypothetical prote
12	47	39.2	468	2	T26081 hypothetical prote
13	45.5	37.9	973	2	T21463 haptoglobin precu
14	45	37.5	347	1	HPMS extracellular prot
15	45	37.5	387	2	I18449 hypothetical prote
16	45	37.5	445	2	F90562 probable ATP-depen
17	45	37.5	607	2	T40906 pilf protein - Nei
18	44.5	37.1	558	2	S32914 type IV pilus asse
19	44.5	37.1	558	2	C32123 phosphoenolpyruvat
20	44.5	37.1	755	2	A93059 enzyme I-nter prote
21	44.5	37.1	755	2	C98217 hypothetical prote
22	44.5	37.1	1038	2	A36057 MHC class I histoc
23	44	36.7	257	2	T15098 conserved hypothet
24	44	36.7	437	2	H96504 conserved hypothet
25	44	36.7	453	2	H70333 conserved hypothet
26	44	36.7	690	2	T33321 hypothetical prote
27	44	36.7	975	2	T26737 phage-related prot
28	43.5	36.2	284	2	B69945 gp18 (Bacteriophag
29	43.5	36.2	345	2	AB1448

30	43.5	36.2	692	2	T21722 hypothetical prote
31	43.5	36.2	1025	2	S69790 fibronectin-bindin
32	43	35.8	122	2	S34566 hypothetical 13.7k
33	43	35.8	229	2	AG0698 probable patchenl
34	43	35.8	253	2	S76336 hypothetical prote
35	43	35.8	288	2	T37395 probable 33.6k pro
36	43	35.8	288	2	A42518 ABR protein - vacc
37	43	35.8	330	2	S55733 uroporphyrinogen d
38	43	35.8	370	2	E69754 nifs protein homol
39	43	35.8	391	2	S55732 uroporphyrinogen d
40	43	35.8	394	2	B84830 probable uroporphyr
41	43	35.8	433	2	T01405 vesicle-associated
42	43	35.8	687	2	A41905 ferric vibriobacti
43	43	35.8	705	2	C84406 hypothetical prote
44	43	35.8	1041	2	A81960 probable DNA helic
45	42.5	35.4	234	2	T30473 late expression fa

ALIGNMENTS

RESULT 1

A32192 fibronectin-binding protein - Staphylococcus aureus

C:Species: Staphylococcus aureus
C:Date: 31-Jul-1989 #sequence_revision 31-Jul-1989 #text_change 16-Feb-1997

C:Accession: A32192
R:Signaes, C.; Raucet, G.; Joensen, K.; Lindgren, P.E.; Anantharamaiah, G.M.; Heoek, M.

Proc. Natl. Acad. Sci. U.S.A. 86, 699-703, 1989
A:Title: Nucleotide sequence of the gene for a fibronectin-binding protein from Staphyloc

A:Reference number: A32192; MUID:8908998; PMID:2521391
A:Accession: A32192
A:Status: preliminary

A:Molecule type: DNA
A:Residues: 1-1018 <SIG>

A:Cross-references: GB:J04151
C:Keywords: fibronectin binding

Query Match 93.3%; Score 112, DB 2; Length 1018;
Best Local Similarity 95.2%; Pred. No. 3.3e-09;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KPSYQFGGHNVPFEDTLRK 21
|||||

DB 837 KPSYQFGGHNVPFEDTLRK 857
|||||

RESULT 2

G90053 hypothetical protein fnbB [imported] - Staphylococcus aureus (strain N315)

C:Species: Staphylococcus aureus
C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004

C:Accession: G90053
R:Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguci

ma, A.; Mitsunari, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.; i
C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.

Lancet 357, 1225-1240, 2001
A:Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.

A:Reference number: A89758; MUID:21311952; PMID:11418146
A:Accession: G90053

A:Status: preliminary
A:Molecule type: DNA

A:Residues: 1-961 <KUR>
A:Cross-references: UNIPROT:Q99RD3; GB:BA000018; PID:q13702452; PIDN:BBB43593.1; GSPDB:GT

A:Experimental source: strain N315
A:Gene: fnbB

Query Match 90.8%; Score 109, DB 2; Length 961;
Best Local Similarity 90.5%; Pred. No. 9.1e-09;
Matches 19; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 KPSYQFGGHNVPFEDTLRK 21

Db 784 KPNYQFGHNSVDFEEDTLPK 804

RESULT 3
H90053
hypothetical protein fnb [imported] - Staphylococcus aureus (strain N315)

C/Species: Staphylococcus aureus
C/Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C/Accession: H90053
R/Kuroda, M.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguc
ma, A.; Mizutani-U, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kato, C.; Sekimizu, K.;
C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001

A/Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.
A/Reference number: A89758; MUID:21311952; PMID:11418146
A/Accession: H90053
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-1038 <KUR>
A/Cross-references: UNIPROT:Q99RD2; GB:BA000018; PID:g13702453; PIDN:BA843594.1; GSPDB:C
A/Experimental source: strain N315
C/Genetics:
A/Note: fnb

Query Match 90.8%; Score 109; DB 2; Length 1038;
Best Local Similarity 90.5%; Pred. No. 9.9e-09;
Matches 19; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 KPSYQFGHNPVDFEEDTLPK 21
Db 833 KPNYQFGHNSVDFEEDTLPK 853

RESULT 4
S19702
fibronectin-binding protein B - Staphylococcus aureus

C/Species: Staphylococcus aureus
C/Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
C/Accession: S19702
R./Joensson, K.; Signaes, C.; Mueller, H.P.; Lindberg, M.
Eur. J. Biochem. 202, 1041-1048, 1991
A/Title: Two different genes encode fibronectin binding proteins in Staphylococcus aureus
A/Reference number: S19702; MUID:92111475; PMID:18377266
A/Accession: S19702
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-940 <QOE>
A/Cross-references: UNIPROT:Q53682; EMBL:X62992; NID:g49040; PIDN:CAA44726.1; PID:G58156
C/Keyword: fibronectin binding

Query Match 87.5%; Score 105; DB 2; Length 940;
Best Local Similarity 85.7%; Pred. No. 3.7e-08;
Matches 18; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 KPSYQFGHNPVDFEEDTLPK 21
Db 773 KPNYQFGHNSVDFEEDTLPK 793

RESULT 5

S33850
fibronectin-binding protein - Streptococcus dysgalactiae

C/Species: Streptococcus dysgalactiae
C/Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Jul-2004
C/Accession: S33850; S32632
R./Lindgren, P.B.; McGavin, M.J.; Signaes, C.; Guse, B.; Gurusiddappa, S.; Hoesek, M.; Li
Eur. J. Biochem. 214, 819-827, 1993
A/Title: Two different genes coding for fibronectin-binding proteins from Streptococcus
A/Reference number: S33850; MUID:93307299; PMID:8319691
A/Status: preliminary
A/Molecule type: DNA

A/Residues: 1-1091 <LIN>
A/Cross-references: UNIPROT:Q06556; EMBL:Z22150; NID:g288966; PIDN:CAA80121.1; PID:g28896

Query Match 42.9%; Score 51.5; DB 2; Length 1091;
Best Local Similarity 52.4%; Pred. No. 10;
Matches 11; Conservative 2; Mismatches 7; Indels 1; Gaps 1;

QY 1 KPSYQFGHNPVDFEEDTLPK 20
Db 977 KPEIIMGQSDPIDVEDTLPK 997

RESULT 6
T17676
hypothetical protein a186L - Chlorella virus PBCV-1

C/Species: Chlorella virus PBCV-1
C/Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C/Accession: T17676
R./Graves, M.V.; Van Etten, J.L.
submitted to the EMBL Data Library, May 1999
A/Reference number: Z18806
A/Accession: T17676
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-84 <GRA>
A/Cross-references: UNIPROT:Q84506; EMBL:U42580; NID:g4028896; PIDN:AAC96554.1
A/Experimental source: specific host Chlorella strain NC64A
C/Genetics:
A/Note: a186L

Query Match 40.0%; Score 48; DB 2; Length 84;
Best Local Similarity 57.1%; Pred. No. 2.2;
Matches 8; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 3 SYQFGHNPVDFEEDTLPK 16
Db 11 SLQFGYNNPLDFEQ 24

RESULT 7

B98046
single stranded binding protein [imported] - Streptococcus pneumoniae (strain R6)

C/Species: Streptococcus pneumoniae
C/Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 09-Jul-2004
C/Accession: B98046
R./Hoskins, J.A.; Alborn Jr., W.; Arnold, J.; Blaszczak, L.; Burgett, S.; Dehoff, B.S.; Et
e, R.; LeBlanc, D.J.; Lee, L.N.; Letkowitz, E.C.; Lu, J.; Matsushima, P.; Mathren, S.; Mc
Y, P.; Sun, P.M.; Winkler, M.B.
J. Bacteriol. 183, 5709-5717, 2001
A/Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaakkus, S.R.;
A/Title: Genome of the Bacterium Streptococcus pneumoniae Strain R6.
A/Reference number: A97872; MUID:21429245; PMID:11544234
A/Accession: B98046
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-156 <KUR>

A/Cross-references: UNIPROT:Q97PR2; GB:AE007317; PIDN:AAL00199.1; PID:g15459046; GSPDB:GT
A/Genetics: sbda
C/Superfamily: single-strand binding protein; single-stranded DNA-binding protein homolog

Query Match 40.0%; Score 48; DB 2; Length 156;
Best Local Similarity 53.3%; Pred. No. 4.3;
Matches 8; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 6 FGSHNPVDFEEDTLPK 20
Db 141 FGATNPIDISDDLP 155

RESULT 8

C95179
single-strand binding protein [imported] - Streptococcus pneumoniae (strain TIGR4)

C/Species: Streptococcus pneumoniae
C/Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 09-Jul-2004
C/Accession: C95179
R/Retellin, H.; Nelson, K.R.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Heid
on, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapple,
neon, T.; Hickey, E.K.; Holt, I.E.
Science 293, 498-506, 2001
A/Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison,
A./Title: Complete Genome Sequence of a Virulent Isolate of Streptococcus pneumoniae.
A/Reference number: A95000; MUID:21357209; PMID:11463916
A/Accession: C95179
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-156 <KUR>
A/Cross-references: UNIPROT:Q97PR2; GB:AE005672; PIDN:AAK75628.1; PID:G14973030; GSPDB:G
A/Experimental source: strain TIGR4
A/Genetics:
A/Gene: SP1540
C/Superfamily: single-strand binding protein; single-stranded DNA-binding protein homolo

Query Match 40.0%; Score 48; DB 2; Length 156;
Best Local Similarity 53.3%; Pred. No. 4.3;
Matches 8; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 6 FCGHNPVDFEEDLP 20
DB 141 FCGATNPDIIDDDLP 155

RESULT 9
B84357
serine-tRNA synthetase [imported] - Halobacterium sp. NRC-1
C/Species: Halobacterium sp. NRC-1
C/Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
C/Accession: B84357
R/Ng, W.V.; Kennedy, S.P.; Mahirae, G.G.; Bergquist, B.; Pan, M.; Shukla, H.D.; Lasky, S
; Leithauer, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Jaidic
Jung, K.H.; Alam, M.; Preltas, T.
Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000
A/Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ebhardt, H.; Lowe, T.M.; Li
A./Title: Genome sequence of Halobacterium species NRC-1.
A/Reference number: A84160; MUID:20504483; PMID:11016950
A/Accession: B84357
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-474 <STO>
A/Cross-references: UNIPROT:Q9HNU8; GB:AE004437; NID:G10581491; PIDN:AAJ20222.1; GSPDB:G
C/Genetics:
A/Gene: serS
C/Superfamily: serine-tRNA ligase

Query Match 40.0%; Score 48; DB 2; Length 474;
Best Local Similarity 41.2%; Pred. No. 15;
Matches 7; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 3 SYOGGHNVPDFEEDLP 19
DB 234 AYRIGENDADYDDDL 250

RESULT 10
G87719
protein R119.7 [imported] - Caenorhabditis elegans
C/Species: Caenorhabditis elegans
C/Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C/Accession: G87719
R/anonymus, The C. elegans Sequencing Consortium.
Science 282, 2012-2018, 1998
A/Title: Genome sequence of the nematode C. elegans: a platform for investigating biolog
A/Reference number: A75000; MUID:99069613; PMID:9851916
A/Note: see websites genome.wustl.edu/gsc/C_elegans/ and www.sanger.ac.uk/Projects/C_ele
A/Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and
A/Accession: G87719

A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-583 <STO>
A/Cross-references: UNIPROT:O61711; GB:chr_1; PIDN:AAAC16433.1; PID:G3133013; GSPDB:GN0001
C/Genetics:
A/Gene: R119.7
A/Map position: 1

Query Match 40.0%; Score 48; DB 2; Length 583;
Best Local Similarity 50.0%; Pred. No. 18;
Matches 8; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 2 PSYOGGHNVPDFEED 17
DB 183 PVOQSGFNIDFRFD 198

RESULT 11
D69027
conserved hypothetical protein MTH1201 - Methanobacterium thermoautotrophicum (strain DeJ
C/Species: Methanobacterium thermoautotrophicum
C/Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 09-Jul-2004
C/Accession: D69027
R/Smith, D.R.; Doucette-Stamm, L.A.; DeLoughery, C.; Lee, H.; Dubois, J.; Aldredge, T.; I
; Qui, D.; Spatafora, R.; Vicalire, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiwani, N.;
ki, S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N.
J. Bacteriol. 179, 7135-7155, 1997
A/Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: functi
A/Reference number: A69000; MUID:98037514; PMID:9371463
A/Accession: D69027
A/Status: nucleic acid sequence not shown; translation not shown
A/Molecule type: DNA
A/Residues: 1-377 <MTH>
A/Cross-references: UNIPROT:O27269; GB:AE000888; GB:AE000666; NID:G2622304; PIDN:AA85690
A/Experimental source: strain Delta H
C/Genetics:
A/Gene: MTH1201
C/Superfamily: conserved hypothetical protein M0136

Query Match 39.2%; Score 47; DB 1; Length 377;
Best Local Similarity 45.0%; Pred. No. 16;
Matches 9; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

QY 2 PSYOGGHNVPDFEEDLPK 21
DB 267 PSYVTGNHPVAMRESLLPQ 286

RESULT 12
T26081
hypothetical protein W02A2.7 - Caenorhabditis elegans
C/Species: Caenorhabditis elegans
C/Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C/Accession: T26081
R/Alincougn, R.
submitted to the EMBL Data Library, November 1996
A/Reference number: Z20148
A/Accession: T26081
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-468 <WIL>
A/Cross-references: UNIPROT:Q9XUB2; EMBL:Z82286; PIDN:CAB05310.1; GSPDB:GN00022; CESP:W0;
A/Experimental source: clone W02A2
C/Genetics:
A/Gene: CESP:W02A2.7
A/Map position: 4
A/Introns: 38/3; 212/2; 353/3; 403/2

Query Match 39.2%; Score 47; DB 2; Length 468;
Best Local Similarity 35.0%; Pred. No. 21;
Matches 7; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

QY 2 PSYOGGHNVPDFEEDLPK 21

Db 351 PBYQRMSHDDQDYDQVIFPS 370

RESULT 13

T21463

hypotheical protein F28B1.2 - Caenorhabditis elegans

C/Species: Caenorhabditis elegans

C/Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004

C/Accession: T21463

R/Matchews, L.

submitted to the EMBL Data Library, November 1996

A/Reference number: Z19426

A/Accession: T21463

A/Status: preliminary; translated from GB/EMBL/DBD

A/Molecule type: DNA

A/Residues: 1-973 <MIL>

A/Cross-references: UNIPROT:O45412; EMBL:Z81517; PIDN:CAB04209.1; GSPDB:GN00023; CESP:F2

A/Experimental source: clone F28B1

C/Genetics:

A/Map position: 5

A/Intons: 70/3; 234/1; 267/3; 380/3; 600/3; 711/3; 926/3

Query Match 37.5%; Score 45.5; DB 2; Length 973;

Best Local Similarity 41.7%; Pred. No. 79;

Matches 10; Conservative 3; Mismatches 6; Indels 5; Gaps 1;

QY 2 PSYQF-----GHNVPVFEEDTLP 20

Db 242 PSWEFFMFCEDGHKPVFSENNPP 265

RESULT 14

HENS

haptoglobin precursor - mouse

N:Contains: haptoglobin alpha chain; haptoglobin beta chain

C/Species: Mus musculus (house mouse)

C/Date: 23-Mar-1995 #sequence_revision 31-May-1996 #text_change 18-Jun-1999

C/Accession: A48918

R/Yang, F.; Linenhan, L.A.; Friedrichs, W.E.; Talley, P.A.; Sakaguchi, A.Y.; Bowman, B.H.

Genomics 18, 374-380, 1993

A/Title: Characterization of the mouse haptoglobin gene.

A/Reference number: A48918; MUID:94117006; PMID:8288241

A/Accession: A48918

A/Molecule type: mRNA

A/Residues: 1-347 <YAN>

A/Cross-references: GB:S67972; NID:9461137; PIDN:AAB29697.1; PID:9461138

A/Note: sequence extracted from NCBI backbone (NCBIN:142156, NCBI:P.142157); sequence ind

C/Comment: The mature haptoglobin molecule is a dimer of heterodimers, the two chains of

C/Comment: Haptoglobin is a plasma glycoprotein; haptoglobin forms a complex with hemogl

C/Genetics:

A/Map position: 8

A/Suprafamily: haptoglobin; complement factor H repeat homology; trypsin homology

C/Keywords: acute phase; glycoprotein; hemoglobin binding; heterotetramer; iron transpor

F:1-18/Domain: signal sequence #status predicted <SIG>

F:19-101/Product: haptoglobin alpha chain #status predicted <ACH>

F:33-86/Domain: complement factor H repeat homology <PH2>

F:103-347/Product: haptoglobin beta chain #status predicted <BCH>

F:103-340/Domain: trypsin homology <TRY>

F:33/Disulfide bonds: interchain #status predicted

F:52-86, 90-207, 250-281, 292-322/Disulfide bonds: #status predicted

F:148, 182, 256, 264/Binding site: carbohydrate (asn) (covalent) #status predicted

Query Match 37.5%; Score 45; DB 1; Length 347;

Best Local Similarity 50.0%; Pred. No. 31;

Matches 7; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 8 GHNVPVFEEDTLPK 21

Db 22 GNDAMDFEDDSCPK 35

RESULT 15

I38449

extracellular protein - human

C/Species: Homo sapiens (man)

C/Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 21-Jul-2000

C/Accession: I38449

R/Lecka-Czernik, B.; Lampkin, C.K.

Mol. Cell. Biol. 15, 120-128, 1995

A/Title: An overexpressed gene transcript in senescent and quiescent human fibroblasts er

A/Reference number: I38449; MUID:95097983; PMID:779918

A/Accession: I38449

A/Status: preliminary; translated from GB/EMBL/DBD

A/Molecule type: mRNA

A/Residues: 1-387 <RES>

A/Cross-references: EMBL:U03877; NID:9458227; PIDN:AAA65590.1; PID:9458228

C/Genetics:

A/Map position: 5

Query Match 37.5%; Score 45; DB 2; Length 387;

Best Local Similarity 47.4%; Pred. No. 35;

Matches 9; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

QY 2 PSYQFGHNVPVFEEDTLP 20

Db 97 PGYQKRGECVDIDECTIP 115

Search completed: October 22, 2005, 04:13:52
Job time : 11.5465 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using SW model

Run on: October 22, 2005, 02:23:35 ; Search time 51.4314 Seconds
(without alignments)
209.087 Million cell updates/sec

Title: US-10-731-238-23
Perfect score: 120
Sequence: 1 KPSYQFGGNPVPFEDTLRK 21

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : UniProt_03.*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	112	93.3	1018 1 FNBA_STAU	P14738 staphylococ
2	109	90.8	099R3 staphylococ	Q99R3 staphylococ
3	109	90.8	07A3J8 staphylococ	Q7A3J8 staphylococ
4	109	90.8	06GDU5 staphylococ	Q6GDU5 staphylococ
5	109	90.8	08NUU7 staphylococ	Q8NUU7 staphylococ
6	109	90.8	01015 2 Q6G6H3 staphylococ	Q6G6H3 staphylococ
7	109	90.8	099R2 staphylococ	Q99R2 staphylococ
8	109	90.8	07A3J7 staphylococ	Q7A3J7 staphylococ
9	105	87.5	053682 staphylococ	Q53682 staphylococ
10	105	87.5	08NUU8 staphylococ	Q8NUU8 staphylococ
11	105	87.5	06G6H4 staphylococ	Q6G6H4 staphylococ
12	103	85.8	09AEP9 staphylococ	Q9AEP9 staphylococ
13	103	85.8	08VLA5 actinobacil	Q8VLA5 actinobacil
14	53.5	44.6	177 2 Q8VLA2 actinobacil	Q8VLA2 actinobacil
15	53.5	44.6	177 2 Q8VLA4 actinobacil	Q8VLA4 actinobacil
16	53.5	44.6	177 2 Q8VQ81 actinobacil	Q8VQ81 actinobacil
17	53.5	44.6	177 2 Q8VQ82 actinobacil	Q8VQ82 actinobacil
18	51.5	42.9	178 2 Q7VND4 haemophilus	Q7VND4 haemophilus
19	51.5	42.9	1091 2 Q06556 streptococ	Q06556 streptococ
20	51	42.5	139 2 Q0938M7 temperate p	Q0938M7 temperate p
21	51	42.5	139 2 Q79XV9 streptococ	Q79XV9 streptococ
22	51	42.5	139 2 Q8NZO2 streptococ	Q8NZO2 streptococ
23	51	42.5	150 2 Q7NRP3 streptococ	Q7NRP3 streptococ
24	51	42.5	150 2 Q8VPP4 micrococci	Q8VPP4 micrococci
25	50	41.7	444 2 Q7TTZ8 streptococ	Q7TTZ8 streptococ
26	49	40.8	123 2 Q38257 lactococci	Q38257 lactococci
27	49	40.8	163 1 SSB1_STRA3 streptococ	SSB1_STRA3 streptococ
28	49	40.8	163 1 SSB2_STRA5 streptococ	SSB2_STRA5 streptococ
29	49	40.8	163 1 SSB_STRP3 streptococ	SSB_STRP3 streptococ
30	49	40.8	163 1 SSB_STRP3 streptococ	SSB_STRP3 streptococ
31	49	40.8	163 1 SSB_STRP3 streptococ	SSB_STRP3 streptococ

ALIGNMENTS

RESULT 1	FNBA_STAU	STANDARD;	PRT;	1018 AA.	
AC P14738;					Q94F5 streptococ
DT 01-APR-1990 (Rel. 14, Created)					Q84506 parametium
DT 01-APR-1990 (Rel. 14, Last sequence update)					P66554 streptococ
DT 25-OCT-2004 (Rel. 45, Last annotation update)					P6655 streptococ
DE Fibronectin-binding protein precursor (FNBP).					Q8488 streptococ
GN Name=fnba;					Q0866 carassius a
OS Staphylococcus aureus.					Q9HJ8 halobacteri
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.					Q61711 caenorhabdi
OX NCBI_TaxID=1280;					Q9486 m mus muscu
RN [1]					Q7VU4 bordetella
RP SEQUENCE FROM N.A.					Q7VU4 bordetella
RC STRAIN=NCCTC 8325-4;					Q7W37 bordetella
RX MEDLINE=89098998; PubMed=2521391;					Q7W37 bordetella
RA Sjoganes C., Raucsi G., Joensson K., Lindgren P.-E.,					Q27269 methanobact
RA Mantharimath G.M., Hoeck M., Lindberg M.;					Q93VB5 oryza sativ
RT "Nucleotide sequence of the gene for a fibronectin-binding protein					
RT from Staphylococcus aureus: use of this peptide sequence in the					
RT synthesis of biologically active peptides."					
RL Proc. Natl. Acad. Sci. U.S.A. 86:699-703(1989).					
CC -I- FUNCTION: The ability of bacteria to bind fibronectin has been					
CC proposed as a virulence factor enabling bacteria to colonize wound					
CC tissues and blood clots. Binding of plasma fibronectin to the					
CC bacterial surface might block adhesion receptors on S.aureus, thus					
CC representing an important defense mechanism against tissue					
CC invasion.					
CC -I- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by					
CC an amide bond (potential).					
CC -----					
CC This SWISS-PROT entry is copyright. It is produced through a collaboration					
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -					
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CC use by non-profit institutions as long as its content is in no way					
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CC or send an email to license@ebi.ac.uk .					
CC -----					
CC EMBL: J04151; AAA26632.1; -					
DR InterPro: IPR004237; Fn_bind.					
DR InterPro: IPR005877; Gpos_YSTRK.					
DR InterPro: IPR001899; Gram_pos_anchor.					
DR Pfam: PF00796; Fn_bind; 1.					
DR Pfam: PF04650; YSTRK_signal; 1.					
DR TIGRPFAMs: TIGR01167; LPXTG_anchor; 1.					
DR TIGRPFAMs: TIGR01169; YSTRK_signal; 1.					
DR PROSITE: PS50847; GRAM_POS_ANCHORING; 1.					
KW Cell adhesion; Cell wall; Peptidoglycan-anchor; Repeat; Signal;					
FT SIGNAL	1	36			
FT CHAIN	37	985			
FT PROPEP	986	1018			
					Fibronectin-binding protein.
					Removed by sortase (potential).

```
FT REPEAT 545 574 B-1.
FT REPEAT 575 604 B-2.
FT DOMAIN 745 878 4 X approximate tandem repeats,
  fibronectin-binding domain.
FT REPEAT 745 782 D-1.
FT REPEAT 783 820 D-2.
FT REPEAT 821 859 D-3.
FT REPEAT 860 878 D-4 (incomplete).
FT DOMAIN 879 948 5 X tandem repeats, pro-rich (WR).
FT REPEAT 879 892 WR 1.
FT REPEAT 893 906 WR 2.
FT REPEAT 907 920 WR 3.
FT REPEAT 921 934 WR 4.
FT REPEAT 935 948 WR 5.
FT SITE 982 986 LpXTG sorting signal (potential).
FT MOD_RES 985 985 Pentaglycyl murein peptidoglycan amidated
  threonine (Potential).
SQ SEQUENCE 1018 AA; 111780 MW; 58175E020E81F1F CRC64;

Query Match 93.3%; Score 112; DB 1; Length 1018;
Best Local Similarity 95.2%; Pred. No. 7.1e-08;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KPSYQFGHNVPDFEDTLPK 21
Db 837 KPSYQFGHNVPDFEDTLPK 857
```

```
RESULT 2
Q99RD3 PRELIMINARY; PRT; 961 AA.
ID Q99RD3;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Fibronectin-binding protein homolog.
GN Name=fnbB; OrderedLocustNames=SAV2502;
OS Staphylococcus aureus (strain Mu50 / ATCC 700699).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
NCBI_TaxID=158878;
RN [1]
  SEQUENCE FROM N.A.
  RX STRAIN=Mu50 / ATCC 700699;
  RC MEDLINE=21311952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2;
  RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
  RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Lian J.-Q., Ito T.,
  RA Kanamori M., Matsumaru H., Maruyama A., Murakami H., HosoYama A.,
  RA Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
  RA Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
  RA Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
  RA Hattori M., Ogasawara N., Hayashi H., Hiratacu K.;
  RT "Whole genome sequencing of methicillin-resistant Staphylococcus
  aureus."
  RL Lancet 357:1225-1240(2001).
  CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
  an amide bond (By similarity).
  EMBL; AP003137; BAB43593.1; -.
  DR HSSP; G90053; G90053.
  DR HSSP; Q53653; IN67.
  DR GO; GO:0009986; C:cell surface; IEA.
  DR GO; GO:0005618; C:cell wall; IEA.
  DR GO; GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
  DR GO; GO:0016020; C:membrane; IEA.
  DR GO; GO:0007155; P:cell adhesion; IEA.
  DR InterPro; IPR008966; Adhes_bact.
  DR InterPro; IPR004237; Fn_bind.
  DR InterPro; IPR005877; Gpos_YsIRK.
  DR InterPro; IPR001899; Gram_pos_anchor.
  DR Pfam; PF02986; Fn_bind; 1.
  DR Pfam; PF00746; Gram_pos_anchor; 1.
  DR Pfam; PF04650; YsIRK_signal; 1.
  DR TIGRfams; TIGR01167; LpXTG_anchor; 1.
  DR TIGRfams; TIGR01168; YsIRK_signal; 1.
```

```
DR PROSITE; PSS0847; GRAM_POS_ANCHORING; 1.
KW Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ SEQUENCE 961 AA; 106010 MW; 364940F884EA4101 CRC64;
```

```
Query Match 90.8%; Score 109; DB 2; Length 961;
Best Local Similarity 90.5%; Pred. No. 1.9e-07;
Matches 19; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 1 KPSYQFGHNVPDFEDTLPK 21
Db 784 KPSYQFGHNVPDFEDTLPK 804
```

```
RESULT 3
Q7A3J8 PRELIMINARY; PRT; 961 AA.
ID Q7A3J8;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE FnbB protein.
GN Name=fnbB; OrderedLocustNames=SA2290;
OS Staphylococcus aureus (strain N315).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
NCBI_TaxID=158879;
RN [1]
  SEQUENCE FROM N.A.
  RX MEDLINE=21311952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2;
  RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
  RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Lian J.-Q., Ito T.,
  RA Kanamori M., Matsumaru H., Maruyama A., Murakami H., HosoYama A.,
  RA Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
  RA Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
  RA Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
  RA Hattori M., Ogasawara N., Hayashi H., Hiratacu K.;
  RT "Whole genome sequencing of methicillin-resistant Staphylococcus
  aureus."
  RL Lancet 357:1225-1240(2001).
  CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
  an amide bond (By similarity).
  EMBL; AP003137; BAB43593.1; -.
  DR GO; GO:0009986; C:cell surface; IEA.
  DR GO; GO:0005618; C:cell wall; IEA.
  DR GO; GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
  DR GO; GO:0016020; C:membrane; IEA.
  DR GO; GO:0007155; P:cell adhesion; IEA.
  DR InterPro; IPR008966; Adhes_bact.
  DR InterPro; IPR004237; Fn_bind.
  DR InterPro; IPR005877; Gpos_YsIRK.
  DR InterPro; IPR001899; Gram_pos_anchor.
  DR Pfam; PF02986; Fn_bind; 1.
  DR Pfam; PF00746; Gram_pos_anchor; 1.
  DR Pfam; PF04650; YsIRK_signal; 1.
  DR TIGRfams; TIGR01167; LpXTG_anchor; 1.
  DR TIGRfams; TIGR01168; YsIRK_signal; 1.
  DR PROSITE; PSS0847; GRAM_POS_ANCHORING; 1.
  KW Cell wall; Complete proteome; Peptidoglycan-anchor.
  SQ SEQUENCE 961 AA; 106010 MW; 364940F884EA4101 CRC64;

Query Match 90.8%; Score 109; DB 2; Length 961;
Best Local Similarity 90.5%; Pred. No. 1.9e-07;
Matches 19; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 KPSYQFGHNVPDFEDTLPK 21
Db 784 KPSYQFGHNVPDFEDTLPK 804
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RESULT 4
Q6GDU5 PRELIMINARY; PRT; 965 AA.
ID Q6GDU5;
AC Q6GDU5;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
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DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TReMBLrel. 27, Last annotation update)
 DE Fibronectin-binding protein.
 GN Name=fnba; OrderedLocustNames=SAR2580;
 OS Staphylococcus aureus (strain MRSA252).
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 CX NCBI_TaxID=282458;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX PubMed=15213324; DOI=10.1073/pnas.0402521101;
 RA Holden M.T.G., Feil E.J., Lindsay J.A., Peacock S.J., Day N.P.J.,
 RA Enright M.C., Foster T.J., Moore C.E., Hurst L., Atkin R., Barron A.,
 RA Bason N., Bentley S.D., Chillingworth C., Chillingworth T.,
 RA Churcher C., Clark L., Corton C., Cronin A., Doggett J., Dowd L.,
 RA Felwell T., Hance Z., Harris B., Hauser H., Holtroyd S., Jørgels K.,
 RA James K.D., Lennard N., Line A., Mayes R., Moulé S., Mungall K.,
 RA Ormond D., Quail M.A., Rabinowitsch E., Rutherford K.M., Sanders M.,
 RA Sharp S., Simmonds M., Stevens K., Whitehead S., Barrell B.G.,
 RA Spratt B.G., Parkhill J.;
 RT "Complete genomes of two clinical Staphylococcus aureus strains:
 RT evidence for the rapid evolution of virulence and drug resistance.";
 RL Proc. Natl. Acad. Sci. U.S.A. 101:9786-9791(2004).
 CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
 an amide bond (By similarity).
 CC EMBL: BX571856; CAG41560.1; -;
 DR GO: GO:0009986; C:cell surface; IEA.
 DR GO: GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
 DR GO: GO:0016020; C:membrane; IEA.
 DR GO: GO:0007155; P:cell adhesion; IEA.
 DR InterPro: IPR008966; Adhes_bact.
 DR InterPro: IPR004237; Fn_bind.
 DR InterPro: IPR005877; Gpos_YsIRK.
 DR InterPro: IPR001899; Gram_pos_anchor.
 DR Pfam: PF00746; Gram_pos_anchor; 1.
 DR Pfam: PF04650; YsIRK_signal; 1.
 DR TIGRFAMs: TIGR01167; LpxTG_anchor; 1.
 DR TIGRFAMs: TIGR01168; YsIRK_signal; 1.
 DR PROSITE: PS50847; GRAM_POS_ANCHORING; 1.
 KM Cell wall, Complete proteome; Peptidoglycan-anchor.
 SQ SEQUENCE 965 AA; 105691 MW; 298213164D0551 CRC64;
 Query Match 90.8%; Score 109; DB 2; Length 965;
 Best Local Similarity 90.5%; Pred. No. 1.9e-07;
 Matches 19; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 1 KPSTQFGGHNVPDEEDTLPK 21
 DB 802 KPSTQFGGHNVPDEEDTLPK 822
 RESULT 5
 ID Q8NUU7 PRELIMINARY; PRT; 1015 AA.
 AC Q8NUU7;
 DT 01-OCT-2002 (TReMBLrel. 22, Created)
 DT 01-OCT-2002 (TReMBLrel. 22, Last sequence update)
 DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
 DE Fnb protein.
 GN Name=fnb; OrderedLocustNames=MM2421;
 OS Staphylococcus aureus (strain MM2).
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 CX NCBI_TaxID=196620;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=MM2;
 RX MEDLINE=22040717; PubMed=12044378; DOI=10.1016/S0140-6736(02)08713-5;
 RA Baba T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Oguchi A.,
 RA Nagai Y., Iwano N., Asano K., Naito T., Kuroda H., Cui L.,
 RA Yamamoto K., Hizmatou K.;
 RT "Genome and virulence determinants of high virulence community-
 RT acquired MRSA.";
 RL Lancet 359:1819-1827(2002).

CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
 an amide bond (By similarity).
 CC EMBL: AP004830; BAB96286.1; -;
 DR GO: GO:0009986; C:cell surface; IEA.
 DR GO: GO:0005618; C:cell wall; IEA.
 DR GO: GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
 DR GO: GO:0016020; C:membrane; IEA.
 DR GO: GO:0007155; P:cell adhesion; IEA.
 DR InterPro: IPR008966; Adhes_bact.
 DR InterPro: IPR004237; Fn_bind.
 DR InterPro: IPR005877; Gpos_YsIRK.
 DR InterPro: IPR001899; Gram_pos_anchor.
 DR Pfam: PF00746; Gram_pos_anchor; 1.
 DR Pfam: PF04650; YsIRK_signal; 1.
 DR TIGRFAMs: TIGR01167; LpxTG_anchor; 1.
 DR TIGRFAMs: TIGR01168; YsIRK_signal; 1.
 DR PROSITE: PS50847; GRAM_POS_ANCHORING; 1.
 KM Cell wall, Complete proteome; Peptidoglycan-anchor.
 SQ SEQUENCE 1015 AA; 111145 MW; D0F9201BB64D44D2 CRC64;
 Query Match 90.8%; Score 109; DB 2; Length 1015;
 Best Local Similarity 90.5%; Pred. No. 2e-07;
 Matches 19; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 1 KPSTQFGGHNVPDEEDTLPK 21
 DB 838 KPSTQFGGHNVPDEEDTLPK 858
 RESULT 6
 ID Q6G6H3 PRELIMINARY; PRT; 1015 AA.
 AC Q6G6H3;
 DT 05-JUL-2004 (TReMBLrel. 27, Created)
 DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TReMBLrel. 27, Last annotation update)
 DE Fibronectin-binding protein.
 GN OrderedLocustNames=SAS2388;
 OS Staphylococcus aureus (strain MSSA476).
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 CX NCBI_TaxID=282459;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX PubMed=15213324; DOI=10.1073/pnas.0402521101;
 RA Holden M.T.G., Feil E.J., Lindsay J.A., Peacock S.J., Day N.P.J.,
 RA Enright M.C., Foster T.J., Moore C.E., Hurst L., Atkin R., Barron A.,
 RA Bason N., Bentley S.D., Chillingworth C., Chillingworth T.,
 RA Churcher C., Clark L., Corton C., Cronin A., Doggett J., Dowd L.,
 RA Felwell T., Hance Z., Harris B., Hauser H., Holtroyd S., Jørgels K.,
 RA James K.D., Lennard N., Line A., Mayes R., Moulé S., Mungall K.,
 RA Ormond D., Quail M.A., Rabinowitsch E., Rutherford K.M., Sanders M.,
 RA Sharp S., Simmonds M., Stevens K., Whitehead S., Barrell B.G.,
 RA Spratt B.G., Parkhill J.;
 RT "Complete genomes of two clinical Staphylococcus aureus strains:
 RT evidence for the rapid evolution of virulence and drug resistance.";
 RL Proc. Natl. Acad. Sci. U.S.A. 101:9786-9791(2004).
 CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
 an amide bond (By similarity).
 CC EMBL: BX571857; CAG44202.1; -;
 DR GO: GO:0009986; C:cell surface; IEA.
 DR GO: GO:0005618; C:cell wall; IEA.
 DR GO: GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
 DR GO: GO:0016020; C:membrane; IEA.
 DR GO: GO:0007155; P:cell adhesion; IEA.
 DR InterPro: IPR008966; Adhes_bact.
 DR InterPro: IPR004237; Fn_bind.
 DR InterPro: IPR005877; Gpos_YsIRK.
 DR InterPro: IPR001899; Gram_pos_anchor.
 DR Pfam: PF00746; Gram_pos_anchor; 1.
 DR Pfam: PF04650; YsIRK_signal; 1.
 DR TIGRFAMs: TIGR01167; LpxTG_anchor; 1.

DR TIGR01168; YSIRK signal; 1.
 DR PROSITE; PSS0847; GRAM_POS_ANCHORING; 1.
 DR Cell wall; Complete proteome; Peptidoglycan-anchor.
 SQ SEQUENCE 1015 AA; 11145 MW; D0F9281BB64D4D2 CRC64;

Query Match 90.8%; Score 109; DB 2; Length 1015;
 Best Local Similarity 90.5%; Pred. No. 2e-07;
 Matches 19; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 KPSYQFGHNVPDFEDTLPK 21
 ||:|||||
 DB 838 KPNYQFGHNSVDFEDTLPK 858

RESULT 7
 OY99RD2 PRELIMINARY; PRT; 1038 AA.

AC OY99RD2; (T-EMBLrel. 17, Created)
 DT 01-JUN-2001 (T-EMBLrel. 17, Last sequence update)
 DT 01-JUN-2001 (T-EMBLrel. 26, Last annotation update)
 DT 01-MAR-2004 (T-EMBLrel. 26, Last annotation update)
 DE Fibronectin-binding protein homolog.
 DE Name=fnd; OrderedlocusNames=SAV503;
 OS Staphylococcus aureus (strain Mu50 / ATCC 700699).
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 OX NCBI_TaxID=158878;

RP SEQUENCE FROM N.A.
 RC STRAIN=Mu50 / ATCC 700699;
 RX MEDLINE=21311952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2;
 RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
 RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Lian J.-O., Ito T.,
 RA Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,
 RA Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
 RA Sekizima K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
 RA Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
 RA Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
 RT "Whole genome sequencing of methicillin-resistant Staphylococcus
 aureus.";
 RL Lancet 357:1225-1240(2001).
 CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
 an amide bond (By similarity).
 DR EMBL; AP003365; BAB58665.1; -;
 DR PIR; H90053; H90053.

DR GO; GO:0009986; C:cell surface; IEA.
 DR GO; GO:0005618; C:cell wall; IEA.
 DR GO; GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0007155; P:cell adhesion; IEA.
 DR InterPro; IPR008966; Adhes_bact.
 DR InterPro; IPR004237; Fn_bind.
 DR InterPro; IPR005877; Gpob_YSIRK.
 DR InterPro; IPR001899; Gram_pos_anchor.
 DR Pfam; PF02986; Fn_bind. 1.
 DR Pfam; PF00746; Gram_pos_anchor; 1.
 DR Pfam; PF04650; YSIRK signal; 1.
 DR TIGR01167; LPTXG_anchor; 1.
 DR TIGR01168; YSIRK signal; 1.
 DR PROSITE; PSS0847; GRAM_POS_ANCHORING; 1.
 DR Cell wall; Complete proteome; Peptidoglycan-anchor.
 SQ SEQUENCE 1038 AA; 113618 MW; 666BF6BF2BFEBB12 CRC64;

Query Match 90.8%; Score 109; DB 2; Length 1038;
 Best Local Similarity 90.5%; Pred. No. 2e-07;
 Matches 19; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 KPSYQFGHNVPDFEDTLPK 21
 ||:|||||
 DB 833 KPNYQFGHNSVDFEDTLPK 853

RESULT 8
 OY7A3J7

ID 07A3J7 PRELIMINARY; PRT; 1038 AA.

AC OY7A3J7; (T-EMBLrel. 27, Created)
 DT 05-JUL-2004 (T-EMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (T-EMBLrel. 27, Last annotation update)
 DE Fnb protein.
 DE Name=fnd; OrderedlocusNames=SA2291;
 OS Staphylococcus aureus (strain N315).
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 OX NCBI_TaxID=158879;

RP SEQUENCE FROM N.A.
 RX MEDLINE=21311952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2;
 RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
 RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Lian J.-O., Ito T.,
 RA Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,
 RA Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
 RA Sekizima K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
 RA Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
 RA Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
 RT "Whole genome sequencing of methicillin-resistant Staphylococcus
 aureus.";
 RL Lancet 357:1225-1240(2001).
 CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
 an amide bond (By similarity).
 DR EMBL; AP003337; BAB43594.1; -;
 DR GO; GO:0009986; C:cell surface; IEA.
 DR GO; GO:0005618; C:cell wall; IEA.
 DR GO; GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0007155; P:cell adhesion; IEA.
 DR InterPro; IPR008966; Adhes_bact.
 DR InterPro; IPR004237; Fn_bind.
 DR InterPro; IPR005877; Gpob_YSIRK.
 DR InterPro; IPR001899; Gram_pos_anchor.
 DR Pfam; PF02986; Fn_bind. 1.
 DR Pfam; PF00746; Gram_pos_anchor; 1.
 DR Pfam; PF04650; YSIRK signal; 1.
 DR TIGR01167; LPTXG_anchor; 1.
 DR TIGR01168; YSIRK signal; 1.
 DR PROSITE; PSS0847; GRAM_POS_ANCHORING; 1.
 DR Cell wall; Complete proteome; Peptidoglycan-anchor.
 SQ SEQUENCE 1038 AA; 113618 MW; 666BF6BF2BFEBB12 CRC64;

Query Match 90.8%; Score 109; DB 2; Length 1038;
 Best Local Similarity 90.5%; Pred. No. 2e-07;
 Matches 19; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 KPSYQFGHNVPDFEDTLPK 21
 ||:|||||
 DB 833 KPNYQFGHNSVDFEDTLPK 853

RESULT 9
 OY53682 PRELIMINARY; PRT; 940 AA.

AC OY53682; (T-EMBLrel. 01, Created)
 DT 01-NOV-1996 (T-EMBLrel. 01, Last sequence update)
 DT 01-NOV-1996 (T-EMBLrel. 01, Last sequence update)
 DT 01-MAR-2004 (T-EMBLrel. 26, Last annotation update)
 DE Fibronectin binding protein B.
 DE Name=fnd;
 OS Staphylococcus aureus.
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 OX NCBI_TaxID=1280;
 RN [1]

RP SEQUENCE FROM N.A.
 RC STRAIN=8325-4;
 RX MEDLINE=92111475; PubMed=1837266;
 RA Jonsson K., Signas C., Muller H.P., Lindberg M.;
 RT "Two different genes encode fibronectin binding proteins in
 Staphylococcus aureus. The complete nucleotide sequence and
 characterization of the second gene.";

RL Eur. J. Biochem. 202;1041-1048(1991).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
an amide bond (By similarity).
DR EMBL: X62992; CAA44726.1; -.
DR PIR: S19702; S19702.
DR HSSP: Q53653; 1N67.
DR GO: GO:0009986; C:cell surface; IEA.
DR GO: GO:0005618; C:cell wall; IEA.
DR GO: GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO: GO:0016020; C:membrane; IEA.
DR GO: GO:0007155; P:cell adhesion; IEA.
DR InterPro: IPR008966; Adhes_bact.
DR InterPro: IPR004237; Fn_bind.
DR InterPro: IPR005877; Gpos_YsIRK.
DR InterPro: IPR001899; Gram_pos_anchor.
DR Pfam: PF02986; Fn_bind_2.
DR Pfam: PF00746; Gram_pos_anchor; 1.
DR Pfam: PF04650; YsIRK_signal; 1.
DR TIGRFAMs: TIGR01167; LPXTG_anchor; 1.
DR TIGRFAMs: TIGR01168; YsIRK_signal; 1.
DR PROSITE: PSS0847; GRAM_POS_ANCHORING; 1.
KW Cell wall; Peptidoglycan-anchor.
SQ SEQUENCE 940 AA; 10355 MW; E35FBBCA907AE345 CRC64;
Query Match 87.5%; Score 105; DB 2; Length 940;
Best Local Similarity 85.7%; Pred. No. 7.3e-07;
Matches 18; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 1 KPSYQFGHNVPDEEDTLPK 21
Db 773 KPNYQFGHNSVDFEEDLPQ 793
RESULT 10
ID Q8NU8 PRELIMINARY; PRT; 943 AA.
AC Q8NU8;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE FnbB protein.
GN Name=fnbB; OrderedLocustNames=MW2420;
OS Staphylococcus aureus (strain MW2).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=196620;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MW2;
RX MEDLINE=22040717; PubMed=12044378; DOI=10.1016/S0140-6736(02)08713-5;
RA Baba T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Ogunchi A.,
RA Nagao Y., Iwano N., Asano K., Naito T., Kuroda H., Cui L.,
RA Yamamoto K., Hiramatsu K.,
RT "genome and virulence determinants of high virulence community-
acquired MRSA.";
RT Lancer 359:1819-1827(2002).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
an amide bond (By similarity).
DR EMBL: AP004830; BAB96285.1; -.
DR HSSP: Q53653; 1N67.
DR GO: GO:0009986; C:cell surface; IEA.
DR GO: GO:0005618; C:cell wall; IEA.
DR GO: GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO: GO:0016020; C:membrane; IEA.
DR GO: GO:0007155; P:cell adhesion; IEA.
DR InterPro: IPR008966; Adhes_bact.
DR InterPro: IPR004237; Fn_bind.
DR InterPro: IPR005877; Gpos_YsIRK.
DR InterPro: IPR001899; Gram_pos_anchor.
DR Pfam: PF02986; Fn_bind_1.
DR Pfam: PF00746; Gram_pos_anchor; 1.
DR Pfam: PF04650; YsIRK_signal; 1.
DR TIGRFAMs: TIGR01167; LPXTG_anchor; 1.
DR TIGRFAMs: TIGR01168; YsIRK_signal; 1.

DR PROSITE: PSS0847; GRAM_POS_ANCHORING; 1.
KW Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ SEQUENCE 943 AA; 10457 MW; D8A5F31947EB6A CRC64;
Query Match 87.5%; Score 105; DB 2; Length 943;
Best Local Similarity 85.7%; Pred. No. 7.3e-07;
Matches 18; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 1 KPSYQFGHNVPDEEDTLPK 21
Db 780 KPNYQFGHNSVDFEEDLPQ 800
RESULT 11
ID Q6G6H4 PRELIMINARY; PRT; 957 AA.
AC Q6G6H4;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Fibronectin-binding protein.
GN Name=fnbB; OrderedLocustNames=SAS2387;
OS Staphylococcus aureus (strain MSSA476).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=282459;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=15213324; DOI=10.1073/pnas.0402521101;
RA Holden M.T.G., Fell E.J., Lindsay J.A., Peacock S.J., Day N.P.J.,
RA Enright M.C., Foster T.J., Moore C.E., Hurst L., Atkin R., Barron A.,
RA Bason N., Bentley S.D., Chillingworth C., Chillingworth T.,
RA Churcher C., Clark L., Cotton C., Cronin A., Doggett J., Dowd L.,
RA Felwell T., Hance Z., Harris B., Hauser H., Holtroyd S., Jagsels K.,
RA James K.D., Leonard N., Line A., Mayes R., Moule S., Mungall K.,
RA Ormond D., Quail M.A., Rabinowitsch E., Rutherford K.M., Sanders M.,
RA Sparr S., Simmonds M., Stevens K., Whitehead S., Barrett B.G.,
RA Spratt B.G., Parkhill J.;
RT "Complete genomes of two clinical Staphylococcus aureus strains:
evidence for the rapid evolution of virulence and drug resistance.";
RT Proc. Natl. Acad. Sci. U.S.A. 101:9786-9791(2004).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
an amide bond (By similarity).
DR EMBL: BX571857; CAG44201.1; -.
DR GO: GO:0009986; C:cell surface; IEA.
DR GO: GO:0005618; C:cell wall; IEA.
DR GO: GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO: GO:0016020; C:membrane; IEA.
DR GO: GO:0007155; P:cell adhesion; IEA.
DR InterPro: IPR008966; Adhes_bact.
DR InterPro: IPR004237; Fn_bind.
DR InterPro: IPR005877; Gpos_YsIRK.
DR InterPro: IPR001899; Gram_pos_anchor.
DR Pfam: PF02986; Fn_bind_1.
DR Pfam: PF00746; Gram_pos_anchor; 1.
DR Pfam: PF04650; YsIRK_signal; 1.
DR TIGRFAMs: TIGR01167; LPXTG_anchor; 1.
DR TIGRFAMs: TIGR01168; YsIRK_signal; 1.
DR PROSITE: PSS0847; GRAM_POS_ANCHORING; 1.
KW Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ SEQUENCE 957 AA; 105980 MW; 28F8BA7FFDFD3EAF CRC64;
Query Match 87.5%; Score 105; DB 2; Length 957;
Best Local Similarity 85.7%; Pred. No. 7.4e-07;
Matches 18; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 1 KPSYQFGHNVPDEEDTLPK 21
Db 780 KPNYQFGHNSVDFEEDLPQ 800
RESULT 12
ID Q9AEP9 PRELIMINARY; PRT; 152 AA.


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RT sequence of a dsbE-like gene.;
RL Vet. Microbiol. 83:147-159(2001).
RN [2]
RP SEQUENCE FROM N.A.
RA Chierts K., Van Overbeke I., Ducatelle R., Haesebrouck F.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF458429; AAL67746.1; -.
DR EMBL; AF458418; AAL67744.1; -.
DR EMBL; AF458419; AAL67746.1; -.
DR EMBL; AF458420; AAL67748.1; -.
DR EMBL; AF458421; AAL67750.1; -.
DR EMBL; AF458425; AAL67758.1; -.
DR EMBL; AF458426; AAL67760.1; -.
DR EMBL; AF458427; AAL67762.1; -.
DR EMBL; AF458428; AAL67764.1; -.
DR GO; GO:0005489; F:electron transporter activity; IEA.
DR GO; GO:0006118; P:electron transport; IEA.
DR PRINTS; PR00421; THIOREDOXIN.
DR ProDom; PD003679; Thioredoxin-like; 1.
DR PROSITE; PS00194; THIOREDOXIN; UNKNOWN_1.
KW Redox-active center.
SQ SEQUENCE 177 AA; 20433 MW; A2D5560933BF753C CRC64;

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Search completed: October 22, 2005, 04:10:08
 Job time : 58.4314 secs

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Query Match      44.6%; Score 53.5; DB 2; Length 177;
Best Local Similarity 61.1%; Pred. No. 6.6;
Matches 11; Conservative 3; Mismatches 3; Indels 1; Gaps 1;

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QY 4 YQGGHNPVDFFEDTLPK 21
DB 153 YQKGYNP-DFFQDFLPR 169

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OM protein - protein search, using SW model

Run on: October 25, 2005, 18:43:07 ; Search time 59.0973 Seconds
(without alignments)
137.434 Million cell updates/sec

Title: US-10-731-238-24

Perfect score: 120
Sequence: 1 KPSYQFGHNSPDFFEDTLRK 21

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: geneseq_16Dec04:*
2: geneseqp1980s:*
3: geneseqp1990s:*
4: geneseqp2000s:*
5: geneseqp2001s:*
6: geneseqp2002s:*
7: geneseqp2003as:*
8: geneseqp2003bs:*
9: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	120	100.0	21 2	AAW65680
2	111	92.5	21 2	AAW65685
3	111	92.5	22 2	AAW65665
4	111	92.5	37 4	AAW65670
5	111	92.5	37 4	AAW65679
6	111	92.5	38 1	AAW65683
7	111	92.5	134 2	AAW65686
8	111	92.5	139 2	AAW65687
9	111	92.5	1018 1	AAW65688
10	111	92.5	1018 4	AAW65689
11	111	92.5	1018 6	AAW65690
12	111	92.5	1018 6	AAW65691
13	111	92.5	1027 2	AAW65692
14	108	90.0	961 6	AAW65693
15	108	90.0	978 4	AAW65694
16	108	90.0	1001 4	AAW65695
17	108	90.0	1038 6	AAW65696
18	106	88.3	21 2	AAW65697
19	106	88.3	21 2	AAW65698
20	106	88.3	21 2	AAW65699
21	106	88.3	21 2	AAW65700
22	105	87.5	21 2	AAW65701
23	105	87.5	21 2	AAW65702
24	105	87.5	21 2	AAW65703
25	105	87.5	21 2	AAW65704

26	104	86.7	21 2	AAW65685	AAW65685 Fibronect
27	104	86.7	21 2	AAW65687	AAW65687 Fibronect
28	104	86.7	21 2	AAW65681	AAW65681 Fibronect
29	104	86.7	77 2	AAW65679	AAW65679 S. aureus
30	104	86.7	101 2	AAW65693	AAW65693 D3D4 poly
31	104	86.7	113 2	AAW65697	AAW65697 D3D4 poly
32	104	86.7	124 2	AAW65690	AAW65690 D3D4 poly
33	104	86.7	128 2	AAW65694	AAW65694 D3D4 poly
34	104	86.7	130 2	AAW65686	AAW65686 Fibronect
35	104	86.7	130 2	AAW65687	AAW65687 Fibronect
36	104	86.7	130 2	AAW65680	AAW65680 D1-D4 fib
37	104	86.7	130 2	AAW65681	AAW65681 D1-D4 fib
38	104	86.7	134 2	AAW65688	AAW65688 S. aureus
39	104	86.7	132 2	AAW65692	AAW65692 D3D4 poly
40	104	86.7	164 2	AAW65693	AAW65693 FBP fibro
41	104	86.7	174 2	AAW65680	AAW65680 FBP fibro
42	104	86.7	174 2	AAW65681	AAW65681 D1-D4 fib
43	104	86.7	181 2	AAW65685	AAW65685 Fibronect
44	104	86.7	181 2	AAW65686	AAW65686 D1-D4 fib
45	104	86.7	559 2	AAW65683	AAW65683 Staphyloc

ALIGNMENTS

RESULT 1
AAW65680 standard; peptide; 21 AA.

AAW65680:

16-OCT-1998 (first entry)

Fibronectin binding protein-derived peptide #24.

microbial surface components recognising adhesive matrix molecule;
MSRAMM; fibronectin; fibronectin-binding protein; antibody; epitope;
antibiotic; bacterial infection; antibiotic-resistant strain.

Synthetic.

Staphylococcus aureus.

W09831389-A2.

23-JUL-1998.

21-JAN-1998; 98WO-US001222.

21-JAN-1997; 97US-0036139P.

(TEXA) UNIV TEXAS A & M SYSTEM.

Hosoeck M, Patti JM, House-Pompeo KL, Speziale P, Joh D;
McGavin MJ;

WPI; 1998-413816/35.

Antibody that binds to fibronectin-binding protein, preventing its
binding to fibronectin - used to treat or prevent bacterial infection,
especially by Staphylococci and Streptococci.

Example 8; Page 100; 201p; English.

The invention relates to antibodies that bind to a fibronectin-binding
domain of a fibronectin-binding protein, and inhibit binding of the
protein to fibronectin. Also claimed are: (1) isolated peptides of a
fibronectin-binding protein that do not bind to fibronectin; (2) fusion
protein containing at least one peptide of a fibronectin-binding protein
linked to a second amino acid sequence; (3) nucleic acid encoding the
isolated peptide of (1). Antibodies, the isolated peptides of (1) and the
nucleic acids are all useful for immunisation (active or passive) and (by
inhibiting binding of bacteria to fibronectin) for preventing or treating
infection in humans or other animals, particularly by staphylococci or

```

CC streptococci, e.g. meningitis, otitis media, pneumonia, endocarditis,
CC mastitis in cattle, abortion in horses and many others. Since the
CC antibodies block binding of bacteria, they should be effective against
CC antibiotic-resistant strains, and may replace antibiotic therapy or
CC increase its effectiveness. Sequences AAW65670-90 represent a series of
CC synthetic peptides based on the D3 repeat of S. aureus fibronectin
CC binding protein A. They were synthesised to contain a proline residue at
CC each position through the sequence (1e a proline scan)
XX
SQ Sequence 21 AA;
Query March 100.0%; Score 120; DB 2; Length 21;
Best Local Similarity 100.0%; Pred. NO. 1.1e-11;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0.
QY 1 KPSTYFGSHNSPDEEDTLPK 21
Db 1 KPSTYFGSHNSPDEEDTLPK 21
RESULT 2
AAW65665
ID AAW65665 standard; peptide; 21 AA.
AC AAW65665;
XX
XX 16-OCT-1998 (first entry)
XX
XX Fibronectin binding protein-derived peptide #9.
XX
XX microbial surface components recognising adhesive matrix molecule;
KM MSCRAM; fibronectin; fibronectin-binding protein; antibody; epitope;
XX antibiotic; bacterial infection; antibiotic-resistant strain.
XX
XX Synthetic.
OS Staphylococcus aureus.
XX
XX WO9831389-A2.
XX
XX 23-JUL-1998.
PD
PF 21-JAN-1998; 98WO-US001222.
XX
XX 21-JAN-1997; 97US-0036139P.
PR
PA (TEXA ) UNIV TEXAS A & M SYSTEM.
XX
XX Hoeoek M, Patti JM, House-Pompeo KL, Speziale P, Joh D;
PI Mcgavin MJ;
PI
XX
XX WPI; 1998-413816/35.
DR
PT Antibody that binds to fibronectin-binding protein, preventing its
PT binding to fibronectin - used to treat or prevent bacterial infection,
PT especially by Staphylococci and Streptococci.
PS
PS Example 2; Page 92; 201pp; English.
XX
CC The invention relates to antibodies that bind to a fibronectin-binding
CC domain of a fibronectin-binding protein, and inhibit binding of the
CC protein to fibronectin. Also claimed are: (1) isolated peptides of a
CC fibronectin-binding protein that do not bind to fibronectin; (2) fusion
CC protein containing at least one peptide of a fibronectin-binding protein
CC linked to a second amino acid sequence; (3) nucleic acid encoding the
CC isolated peptide of (1). Antibodies, the isolated peptides of (1) and the
CC nucleic acids are all useful for immunisation (active or passive) and (by
CC inhibiting binding of bacteria to fibronectin) for preventing or treating
CC infection in humans or other animals, particularly by staphylococci or
CC streptococci, e.g. meningitis, otitis media, pneumonia, endocarditis,
CC mastitis in cattle, abortion in horses and many others. Since the
CC antibodies block binding of bacteria, they should be effective against
CC antibiotic-resistant strains, and may replace antibiotic therapy or
CC increase its effectiveness. Sequences AAW65659-68 represent synthetic
CC

```

CC epitopes from the fibronectin binding domains DU and DI-D4 of the S.
XX aureus fmbA gene

SQ Sequence 21 AA;

OY Query March 92.5%; Score 111; DB 2; Length 21;
Best Local Similarity 95.2%; Pred. No. 2, 9e-10;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Dy 1 KPSYFGGHNSPDEEDTLRK 21
| | | | |
Dd 1 KPSTVGGHNSVDPEEDTLRK 21
| | | | |

RESULT 3
AAK21340 AAK21340 standard; peptide; 22 AA.

AC AAR21340;
DT 25-MAR-2003 (revised)
DT 15-JUN-1992 (first entry)

XX Fibronection binding protein.
DE FMBP; wound infection reduction; vaccination; mastitis;
KW Staphylococcal infections; D3.
OS Synthetic.
SS W09202555-A.
PN 20-FEB-1992.
PD 10-AUG-1990; 90SE-00002617.
PF 10-AUG-1990; 90SE-00002617.
PR 10-AUG-1990; 90SE-00002617.
XA (ALFA) ALFA LAVAL AGRIC INT AB.
XN Hook M., Mcgavin M., Raucel G;
PI WPJ; 1992-080035/10.

XZ New fibronection binding peptide - combines with fusion peptide to form large antigen, used in immunisation, diagnosis and for treating wounds.

Pt Claim 1; Page 22; 33pp; English.

XX The sequence comprises amino acids 17-33 of a tandem repeat, designated CC D3 of the fibronection binding site of *Staphylococcus aureus* 8325-4 FMBP. CC The N-terminal DK may be replaced with H or R, and the C-terminal LKP may CC be replaced by either L, LP, or OH. The peptides were synthesised using CC standard methods and purified using reverse phase HPLC. The appropriate CC fractions were dialysed and lyophilised. Peptide sequencing was performed CC and the peptides digested and chemically modified by dihydroxypropylation CC of the amino side chain of lysine. The carboxylic acid chains were CC converted to glycyl methyl esters. The phenyl side chains of tyrosine CC residues were oxidised. Chemically modified peptide D3 was compared to CC unmodified D3. Lysine and tyrosine modifications only partially CC diminished its activity whereas modification of aspartic/glutamic CC residues resulted in complete loss of activity. The peptide can be used CC for the prevention or reduction of the risk of wound infection. The CC peptide can be used to create a large antigen for vaccinating ruminants CC against mastitis caused by staphylococcal infections. It can also be used CC to diagnose staphylococcal infections using ELISA or DNA probes. (Updated CC on 25-MAR-2003 to correct PA field.) XX

SQ Sequence 22 AA;

Query Match 92.5%; Score 111; DB 2; Length 22;
Best Local Similarity 95.2%; Pred. No. 3e-10;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 KPSYOGGHNSPDFEDTLPK 21
 ID |||||
 DB 2 KPSYOGGHNSPDFEDTLPK 22

RESULT 4
 AAB91958
 ID AAB91958 standard; peptide; 37 AA.
 AC AAB91958;
 XX
 DT 22-JUN-2001 (first entry)
 XX
 XX

XX Fibrinectin fragment and fibrin related peptide SEQ ID NO:1134.
 DE

XX Protection; endogenous therapeutic peptide; peptidase; conjugation;
 KW blood component; modification; succinimidyl; maleimido group; amino;
 KW hydroxyl; thiol; hormone; growth factor; neurotransmitter.
 XX

XX Homo sapiens.
 OS Synthetic.
 OS

XX MO200069900-A2.
 PN

XX 23-NOV-2000.
 PD

XX 17-MAY-2000; 2000MO-US013576.
 PF

XX 17-MAY-1999; 99US-0134406P.
 PR

XX 10-SEP-1999; 99US-0153406P.
 PR

XX 15-OCT-1999; 99US-0159783P.
 PR

XX (CONT-) CONUTCHEM INC.
 PA

XX Bridon DP, Ezrin AM, Milner PG, Holmes DL, Thibaudau K;
 PI

XX WPI; 2001-112059/12.
 DR

XX Modifying and attaching therapeutic peptides to albumin prevents
 PT peptidase degradation, useful for increasing length of in vivo activity.
 PT

XX Disclosure; Page 566; 733pp; English.
 PS

XX The present invention describes a modified therapeutic peptide (I)
 CC comprising a therapeutically active amino acid region (III) and a
 CC reactive group (II) (e.g. succinimidyl and maleimido groups) attached to
 CC a less therapeutically active amino acid region (IV), which covalently
 CC bonds with amino/hydroxyl/thiol groups on blood components to form a
 CC peptidase stabilised therapeutic peptide composed of 3-50 amino acids.
 CC (I) are useful for modifying therapeutic peptides e.g. hormones, growth
 CC factors and neurotransmitters, to protect them from peptidase activity in
 CC vivo for the treatment of various disorders. Endogenous therapeutic
 CC peptides are not suitable as drug candidates as they require frequent
 CC administration due to rapid degradation by peptidases in the body.
 CC Modifying and attaching therapeutic peptides to albumin prevents or
 CC reduces the action of peptidases to increase length of activity (half
 CC life) and specificity as bonding to large molecules decreases
 CC intracellular uptake and interference with physiological processes.
 CC AAB90829 to AAB92441 represent peptides which can be used in the
 CC exemplification of the present invention
 CC

XX Sequence 37 AA;
 SQ

Query Match 92.5%; Score 111; DB 4; Length 37;
 Best Local Similarity 95.2%; Pred. No. 5,4e-10;
 Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 KPSYOGGHNSPDFEDTLPK 21
 ID |||||
 DB 16 KPSYOGGHNSPDFEDTLPK 36

RESULT 5
 AAP80662
 ID AAP80662 standard; protein; 38 AA.
 XX
 AC AAP80662;
 XX

XX 25-MAR-2003 (revised).
 DT
 DT 07-OCT-1990 (first entry)
 XX

XX Protein with fibrinectin binding ability.
 DE

XX Hybrid DNA molecule; fibrinectin binding; mastitis; ruminants;
 KW wound infection.
 KW

XX Staphylococcus aureus.
 OS

XX EP294349-A.
 PN

XX 07-DEC-1988.
 PD

XX 30-MAY-1988; 88EP-00850188.
 PF

XX 01-JUN-1987; 87SE-00002272.
 PR

XX (ALFA) ALFA LAVAL AGRIC INT AB.
 PA

XX Lindberg MK, Signas LC, Wadstrom TM, Froman G;
 PI

XX WPI; 1988-347978/49.
 DR

XX N-PSDB; AAN61099.
 DR

XX Hybrid DNA encoding Staphylococcus aureus fibrinectin binding protein -
 PT useful for immunisation and topical application to prevent staphylococcal
 PT infections.
 PT

XX Claim 11; Page 12; 23pp; English.
 PS

XX The peptide has fibrinectin binding ability. It is useful for immunising
 CC ruminants against staphylococcal mastitis, pref. when used at 0.5-5
 CC micrograms/kg, using 3 doses given at 1-3 week intervals; for topical
 CC application to prevent wound infection, using an isotonic saline soln. of
 CC concn. 25-250 micrograms/ml; and, when immobilised on a carrier, for
 CC diagnosing staphylococcal infections. (Updated on 25-MAR-2003 to correct
 CC PF field.) (Updated on 25-MAR-2003 to correct PA field.)
 CC

XX Sequence 38 AA;
 SQ

Query Match 92.5%; Score 111; DB 1; Length 38;
 Best Local Similarity 95.2%; Pred. No. 5,6e-10;
 Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 KPSYOGGHNSPDFEDTLPK 21
 ID |||||
 DB 17 KPSYOGGHNSPDFEDTLPK 37

RESULT 6
 AAY29087
 ID AAY29087 standard; protein; 134 AA.
 AC AAY29087;
 XX

XX 28-SEP-1999 (first entry)
 DT
 DT
 XX

XX S. aureus fibrinectin binding protein A (FnBA) binding domain.
 DE

XX Bovine herpes virus-2; BHV-2; cytokine; immune response; immunogen; IL;
 KW interleukin; colony stimulating factor; CSF; interferon; IFN; TNF;
 KW tumour necrosis factor; recombinant virus; vaccine; mucosal disease;
 KW mastitis; breast cancer; stress-induced disease; binding domain; FnBA;
 KW fibrinectin binding protein.
 KW

OS Staphylococcus aureus.
 OS

```

XX  MO9916892-A1.
XX
XX  08-APR-1999.
XX
XX  29-SEP-1998; 98MO-GB002927.
XX
XX  29-SEP-1997; 97GB-00020633.
XX
XX  (UYBR-) UNIV BRISTOL.
XX
XX  Bradley AJ, Duffas WPJ;
XX
XX  WPI; 1999-255101/21.
XX
XX  N-PSDB; AAX91504.
XX
XX  New bovine herpes virus-2 vectors.
XX
XX  Example 2; Fig 8A-B; 130pp; English.
XX
XX  The invention provides bovine herpes virus-2 (BHV-2) based vectors that
XX  comprise at least one cytokine-encoding DNA sequence. The expression of
XX  cytokines in mammals can up-regulate immune responses to the immunogens.
XX  The cytokine is selected from interleukins (IL), colony stimulating
XX  factors (CSF), interferons (IFN) and tumour necrosis factors (TNF). The
XX  BHV-2 based vector or recombinant virus can be used as vaccines. They can
XX  be used for preventing or treating a mucosal disease in a subject, e.g.
XX  ruminants, cattle, sheep, goats, dogs, cats, horses, or man, particularly
XX  mastitis in cows or breast cancers in humans. They can also be used for
XX  preventing or treating a stress-induced disease. The present sequence
XX  represents the binding domain of a previously published S. aureus
XX  fibronectin binding protein A (FnBA) sequence. The FnB binding domain
XX  gene sequence FnBAB, cloned for use in this invention has 97.8 percent
XX  identity when compared to the previously published FnBA and FnBB gene
XX  sequences
XX
XX  Sequence 134 AA:
XX
XX  Query Match          92.5%; Score 111; DB 2; Length 134;
XX  Best Local Similarity 95.2%; Pred. No. 2.3e-09;
XX  Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX  1 KPSYQFGHNSVPDEFDTLPK 21
XX  . ||||| ||||| ||||| |||||
XX  93 KPSYQFGHNSVPDEFDTLPK 113
XX
XX  RESULT 7
XX  AAW31556
XX  ID AAW31556 standard; protein; 139 AA.
XX
XX  AAW31556;
XX
XX  27-AUG-2003 (revised)
XX  25-MAR-2003 (revised)
XX  21-MAY-1998 (first entry)
XX
XX  Fibronectin-binding MSCRAMM derivative pQD.
XX
XX  Fibronectin; pQD; collagen binding protein; sepsis; infection;
XX  microbial surface component regioning adhesive matrix molecule; MSCRAMM;
XX  adhesin; vaccine; immunisation; diagnosis; therapy; mastitis.
XX
XX  Staphylococcus aureus.
XX
XX  Key Location/Qualifiers
XX  Peptide 1..12
XX  /note= "vector pQE30-derived peptide"
XX
XX  MO9743314-A2.
XX
XX  20-NOV-1997.
XX

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PF  14-MAY-1997; 97MO-US008210.
XX
XX  16-MAY-1996; 96US-0017678P.
XX
XX  (TEXA ) UNIV TEXAS A & M SYSTEM.
XX
XX  (UABR-) UAB RES FOUND.
XX
XX  Hoeoek M, Patti JM, House-Pompeo K, Stahanam N, Symersky J;
XX
XX  WPI; 1998-008801/01.
XX
XX  Antibody that interacts with collagen binding domain of Staphylococcal
XX  ptna gene product - useful to prevent bacterial sepsis in animal infected
XX  with Staphylococcus aureus.
XX
XX  Disclosure; Page 91; 143pp; English.
XX
XX  This protein comprises Staphylococcus aureus fibronectin-binding
XX  microbial surface component regioning adhesive matrix molecule (MSCRAMM)
XX  derivative pQD, plus a vector-derived N-terminal peptide. The invention
XX  relates to claimed nucleic acid sequences (see AAT93436-38) encoding S.
XX  aureus collagen binding protein (CBP) epitopes M17, M31 and M55 (see
XX  AAW31552-54) that confer protection against S. aureus infection. CBP
XX  protein and antigenic epitopes are contemplated for use in the treatment
XX  of pathological infections, especially to prevent bacterial adhesion to
XX  collagen. The epitopes are also contemplated for use in the preparation
XX  of vaccines and as carrier proteins in vaccine formulations, as well as
XX  in the formulation of compositions for the prevention of S. aureus
XX  infection. pCR33 and pQD (see AAW31556) were used to raise anti-MSCRAMM
XX  polyclonal antibodies used in passive immunisation against bovine
XX  mastitis. (Updated on 25-MAR-2003 to correct PI field.) (Updated on 27-
XX  AUG-2003 to correct OS field.)
XX
XX  Sequence 139 AA:
XX
XX  Query Match          92.5%; Score 111; DB 2; Length 139;
XX  Best Local Similarity 95.2%; Pred. No. 2.4e-09;
XX  Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX  1 KPSYQFGHNSVPDEFDTLPK 21
XX  ||||| ||||| ||||| |||||
XX  107 KPSYQFGHNSVPDEFDTLPK 127
XX
XX  RESULT 8
XX  AAP82115
XX  ID AAP82115 standard; protein; 1018 AA.
XX
XX  AAP82115;
XX
XX  25-MAR-2003 (revised)
XX  05-JAN-1990 (first entry)
XX
XX  Fibronectin binding protein.
XX
XX  Fibronectin binding protein; S. aureus; immunisation; mastitis; ruminants;
XX  wound infection; diagnosis.
XX
XX  Staphylococcus aureus.
XX
XX  BP294349-A.
XX
XX  07-DEC-1988.
XX
XX  30-MAY-1988; 88EP-00850188.
XX
XX  PF
XX  PR 01-JUN-1987; 87SE-00002272.
XX
XX  (ALFA ) ALFA LAVAL AGRIC INT AB.
XX
XX  Lindberg MK, Signas LC, Wadstrom TM, Froman G;
XX
XX  WPI; 1988-347978/49.
XX

```

DR P-PSDB; AAP82115.
 XX Hybrid DNA encoding Staphylococcus aureus fibronectin binding protein -
 PT useful for immunisation and topical application to prevent staphylococcal
 PT infections.
 PS
 XX Disclosure; Fig. 8A:1-8A:2; 23pp; English.
 CC
 CC The S aureus fibronectin binding protein may be included in a hybrid
 CC protein. The protein may be used to immunise ruminants against
 CC staphylococcal mastitis, pref. when given at 0.5-5 microg/kg, using 3
 CC doses at 1-3 week intervals; and for topical applicn. to prevent wound
 CC infection, pref. using isotonic saline soln. of concn. 25-250 microg/mg.
 CC The DNA encoding the binding protein and the hybrid protein may be
 CC immobilised on a carrier and used to diagnose staphylococcal infections.
 CC (updated on 25-MAR-2003 to correct PA field.)
 CC
 XX
 SQ Sequence 1018 AA;
 Query Match 92.5%; Score 111; DB 1; Length 1018;
 Best Local Similarity 95.2%; Pred. No. 2.2e-08;
 Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 KPSTQFGGHNSDPDEFDTLPK 21
 |||||
 Db 837 KPSTQFGGHNSVDPDEFDTLPK 857
 |||||
 RESULT 9
 AAU37245
 ID AAU37245 standard; protein, 1018 AA.
 XX
 AC AAU37245;
 XX
 DT 14-FEB-2002 (first entry)
 XX
 DE Staphylococcus aureus cellular proliferation protein #1415.
 XX
 KW Antisense; prokaryotic cellular proliferation protein; antibiotic;
 RM antibacterial; drug design.
 XX
 OS Staphylococcus aureus.
 XX
 WO200170955-A2.
 XX
 PD 27-SEP-2001.
 XX
 XX 21-MAR-2001; 2001WO-US009180.
 PF
 XX 21-MAR-2000; 2000US-0191078P.
 FR 23-MAY-2000; 2000US-0206848P.
 PR 26-MAY-2000; 2000US-0207727P.
 PR 23-OCT-2000; 2000US-0242578P.
 PR 27-NOV-2000; 2000US-0253625P.
 PR 22-DEC-2000; 2000US-0257931P.
 PR 16-FEB-2001; 2001US-0269308P.
 XX
 PA (ELIT-) ELITRA PHARM INC.
 XX
 PI Haeselbeck R, Ohlsen KL, Zyskind JW, Wall D, Trawick JD, Carr GJ;
 PI Yamamoto RT, Xu HH;
 DR WPI: 2001-611495/70.
 DR N-PSDB; AAS55104.
 XX
 PT New polynucleotides for the identification and development of
 PT antibiotics, comprise sequences of antisense nucleic acids.
 XX
 PS Example 3; SEQ ID NO 12838; 511pp; English.
 CC The invention relates to antisense inhibitors of genes essential to
 CC prokaryotic cellular proliferation, their use in identifying the genes,
 CC their use in the discovery of novel antibiotics, the essential genes

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CC themselves and the encoded proteins. The prokaryotes used are Escherichia
CC coli, Staphylococcus aureus, Salmonella typhi, Klebsiella pneumoniae,
CC Pseudomonas aeruginosa and Enterococcus faecalis. The invention is also
CC useful for the identification of potential new targets for antibiotic
CC development. The antisense nucleic acids can also be used to identify
CC proteins used in proliferation, to express these proteins, and to obtain
CC antibodies capable of binding to the expressed proteins. The proteins can
CC be used to screen compounds in rational drug discovery programmes. The
CC antisense nucleic acid sequence is also useful to screen for homologous
CC nucleic acids which are required for cell proliferation in a wide variety
CC of organisms. The present sequence represents an essential prokaryotic
CC cellular proliferation protein. Note: The sequence data for this patent
CC did not form part of the printed specification, but was obtained in
CC electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_ptc_sequences
XX
XX
XX Sequence 1018 AA:
XX
XX
XX
XX Query Match 92.5%; Score 111; DB 4; Length 1018;
XX Best Local Similarity 95.2%; Pred. No. 2.2e-08;
XX Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0
XX
XX 1 KPSTYFGGHNSPDPEEDTLPK 21
XX |||||
XX 837 KPSTYFGGHNSPDPEEDTLPK 857
XX
XX
XX RESULT 10
XX AAU34301
XX ID AAU34301 standard; protein, 1018 AA.
XX
XX AAU34301;
XX
XX 14-FEB-2002 (first entry)
XX
XX Staphylococcus aureus cellular proliferation protein #577.
XX
XX Antisense: prokaryotic cellular proliferation protein; antibiotic;
XX antibacterial; drug design.
XX
XX Staphylococcus aureus.
XX
XX WO200170955-A2.
XX
XX 27-SEP-2001.
XX
XX 21-MAR-2001; 2001WO-US009180.
XX
XX 21-MAR-2000; 2000US-0191078P.
XX
XX 23-MAY-2000; 2000US-0206848P.
XX
XX 26-MAY-2000; 2000US-0207727P.
XX
XX 23-OCT-2000; 2000US-0245278P.
XX
XX 27-NOV-2000; 2000US-0253625P.
XX
XX 22-DEC-2000; 2000US-0257931P.
XX
XX 16-FEB-2001; 2001US-0263308P.
XX
XX
XX (ELITRA PHARM INC.
XX
XX Haselbeck R, Ohlsen KU, Zyskind JW, Wall D, Trawick JD, Carr GU;
XX Yamamoto RT, Xu HH;
XX WPI; 2001-611495/70.
XX
XX N-PSDB; AAS52160.
XX
XX New polynucleotides for the identification and development of
XX antibiotics, comprise sequences of antisense nucleic acids.
XX
XX Example 3; SEQ ID NO 5797; 511pp; English.
XX
XX The invention relates to antisense inhibitors of genes essential to
XX prokaryotic cellular proliferation, their use in identifying the genes,
XX their use in the discovery of novel antibiotics, the essential genes
XX themselves and the encoded proteins. The prokaryotes used are Escherichia

```


CC coli. *Staphylococcus aureus*, *Salmonella typhi*, *Klebsiella pneumoniae*,
 CC *Pseudomonas aeruginosa* and *Enterococcus faecalis*. The invention is also
 CC useful for the identification of potential new targets for antibiotic
 CC development. The antisense nucleic acids can also be used to identify
 CC proteins used in proliferation, to express these proteins, and to obtain
 CC antibodies capable of binding to the expressed proteins. The proteins can
 CC be used to screen compounds in rational drug discovery programmes. The
 CC antisense nucleic acid sequence is also useful to screen for homologous
 CC nucleic acids which are required for cell proliferation in a wide variety
 CC of organisms. The present sequence represents an essential prokaryotic
 CC cellular proliferation protein. Note: The sequence data for this patent
 CC did not form part of the printed specification, but was obtained in
 CC electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences

XX Sequence 1018 AA;

Query Match 92.5%; Score 111; DB 4; Length 1018;
 Best Local Similarity 95.2%; Pred. No. 2.2e-08;
 Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 KPSYQFGHNSPDEDTLPK 21
 |||||
 Db 837 KPSYQFGHNSVDPEDTLPK 857

RESULT 11

ABJ18922
 ID ABJ18922 standard; protein; 1018 AA.

XX
 AC ABJ18922;

XX
 DT 06-MAR-2003 (first entry)

DE Pathogen specific antigen related staphylococcal protein SEQ ID No 68.

XX Antibacterial; virucide; fungicide; protozoacide; cytosstatic; anti-HIV;
 XX hyperimmune; serum-reactive; antigen; pathogen; tumour; allergen;
 KM auto-immunity; vaccine; staphylococcal infection; antibody; cancer;
 KM autoimmune disease; HIV; hepatitis.

XX *Staphylococcus* sp.

XX WO200259148-A2.

XX 01-AUG-2002.

XX 21-JAN-2002; 2002WO-EP000546.

XX 26-JAN-2001; 2001AT-00000130.

XX (CISTEM) BIOTECHNOLOGIES GMBH.

XX Meinke A, Nagy E, Von Ahnen U, Klade C, Henies T, Zauner W;
 PI Minh DB, Vytvytska O, Bez H, Dryla A, Welchart T, Hatner M;
 PI Tempelmeier B;

XX WPI; 2003-075410/07.

XX Identifying, isolating and producing hyperimmune serum-reactive antigens
 PT from a pathogen, for preparing vaccine or medicament for treating or
 PT preventing e.g. staphylococcal infections, comprises providing antibody
 PT preparation.

XX Example 7; Page 157; 252pp; English.

XX The invention relates to a novel method for identifying, isolating and
 CC producing hyperimmune serum-reactive antigens from a pathogen, tumour,
 CC allergen, a tissue or host prone to auto-immunity, where the antigens are
 CC used in a vaccine, comprises providing antibody preparation from a plasma
 CC pool of a type of animal, or individual sera with antibodies against the
 CC specific pathogen, tumour, allergen, tissue or host prone to auto-
 CC immunity. The hyperimmune serum-reactive antigens comprising any of the

CC 62 sequences of 53-2261 amino acids fully defined in the specification,
 CC or their hyperimmune fragments are useful for the manufacture of a
 CC pharmaceutical preparation, particularly a vaccine against staphylococcal
 CC infections or colonisation against *S. aureus* or *S. epidermidis*. The
 CC preparation of antibodies is useful for the manufacture of a medicament
 CC for treating or preventing staphylococcal infections or colonisation
 CC against *S. aureus* or *S. epidermidis*. The antibody preparations may also
 CC be used for diagnostic and imaging purposes. Other conditions that can be
 CC treated include cancer, autoimmune diseases or infections caused by viral
 CC (e.g. HIV, hepatitis A, B or C), fungal or protozoan pathogens. This
 CC sequence represents a staphylococcal protein relating to the method for
 CC identifying and producing pathogen specific antigens of the invention

XX Sequence 1018 AA;

Query Match 92.5%; Score 111; DB 6; Length 1018;
 Best Local Similarity 95.2%; Pred. No. 2.2e-08;
 Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 KPSYQFGHNSPDEDTLPK 21
 |||||
 Db 837 KPSYQFGHNSVDPEDTLPK 857

RESULT 12

ABM72537
 ID ABM72537 standard; protein; 1018 AA.

XX
 AC ABM72537;

XX
 DT 20-NOV-2003 (first entry)

DE *Staphylococcus aureus* protein #1777.

KM Antibacterial; vaccine; gene therapy; infection; sepsis; diagnosis;
 KM enzymatic assay; antibiotic target.

XX *Staphylococcus aureus*.

XX WO200294868-A2.

XX 28-NOV-2002.

XX 27-MAR-2002; 2002WO-IB002637.

XX 27-MAR-2001; 2001GB-00007661.

XX (CHIR-) CHIRON SPA.

XX Masignani V, Mora M, Scarselli M;

XX WPI; 2003-120786/11.

XX N-PDB; ACF74097.

XX New *Staphylococcus aureus* protein, useful as a vaccine for treating or
 PT preventing staphylococcal infection, specifically an infection caused by
 PT *S. aureus*, e.g. sepsis.

XX Claim 1; SEQ ID NO 3554; 49pp; English.

XX The invention relates to novel genes and encoded proteins from
 CC *Staphylococcus aureus*. A composition comprising the *S. aureus* protein, a
 CC nucleic acid encoding the protein, or an antibody to the protein, is
 CC useful as a pharmaceutical, particularly as a vaccine for treating or
 CC preventing infection due to *Staphylococcus bacteria*, specifically an
 CC infection caused by *S. aureus*. The composition is particularly useful for
 CC treating or preventing sepsis in a patient. The composition can also be
 CC used for diagnostics. The protein is also used in an assay for enzymatic
 CC studies and as a target for antibiotics. This sequence represents one of
 CC the novel *S. aureus* proteins of the invention

XX Sequence 1018 AA;

Query Match 92.5%; Score 111; DB 6; Length 1018;
Best Local Similarity 95.2%; Pred. No. 2.2e-08;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 KPSYFGHNSVDFEEDTLPK 21
DB 837 KPSYFGHNSVDFEEDTLPK 857

RESULT 13

AAW89806 ID AAW89806 standard; procein; 1027 AA.
AC AAW89806;
XX 16-MAR-1999 (first entry)
DT Staphylococcus aureus protein SEQ ID #5254.
XX
XX Computer readable medium; vaccine; S.aureus infection; immunodetection;
KM cellulitis; eyelid infection; food poisoning; osteomyelitis; therapy;
KM skin infection; surgical wound infection; scalded skin syndrome;
KM toxic shock syndrome.
XX Staphylococcus aureus.
OS EP786519-A2.
XX 30-JUL-1997.
PD 07-JAN-1997; 97EP-00100117.
PF 05-JAN-1996; 96US-0009861P.
PR (HUMA-) HUMAN GENOME SCL INC.
XX
XX Kunsch CA, Choi GH, Barash SC, Dillon PJ, Fannon MR, Rosen CA;
PI WPI; 1997-374922/35.
DR Polynucleotide(s) and proteins derived from Staphylococcus aureus -
XX stored on computer readable medium and used in the production of anti-
PT S.aureus vaccines.
XX
XX Claim 23; Page 3263-3267; 3271pp; English.
XX
XX This sequence represents a Staphylococcus aureus protein sequence of the
CC invention. The DNA sequences encoding the S.aureus proteins are recorded
CC on a computer readable medium, preferably selected from a floppy or hard
CC disk, random access memory (RAM), read-only memory (ROM) or CD-ROM.
XX Homology searches using the S.aureus DNA sequences allows putative
CC functions to be assigned so that protein-encoding or regulatory regions
CC of commercial, therapeutic or industrial importance can be obtained.
XX Specifically, sequences which are likely to encode antigens have been
CC identified and these polypeptides can be used in a vaccine composition
CC against S.aureus infection. The polypeptides can also be used in a kit
CC for the immunodetection of S.aureus in a sample. S.aureus is implicated
CC in numerous human diseases, including cellulitis, eyelid infections, food
CC poisoning, osteomyelitis, skin and surgical wound infections, scalded
CC skin syndrome, toxic shock syndrome, etc. Organisms transformed with the
CC DNA sequences can be used for recombinant production of the polypeptides.
CC The new DNA sequences (and their fragments) are useful as primers or
CC probes for isolating homologues of any of the 5191 S.aureus DNA sequences
CC contained on the computer readable medium
XX
XX Sequence 1027 AA;

Query Match 92.5%; Score 111; DB 2; Length 1027;
Best Local Similarity 95.2%; Pred. No. 2.2e-08;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Oy 1 KPSYFGHNSVDFEEDTLPK 21
|||||

DB 846 KPSYFGHNSVDFEEDTLPK 866

RESULT 14

ABU15854 ID ABU15854 standard; protein; 961 AA.
XX
XX ABU15854;
AC
XX 19-JUN-2003 (first entry)
DT
XX Protein encoded by Prokaryotic essential gene #1381.
DE
XX Antisense; prokaryotic essential gene; cell proliferation; drug design.
XX
XX Staphylococcus aureus.
OS WO200277183-A2.
XX 03-OCT-2002.
PD 21-MAR-2002; 2002WO-US009107.
PF 21-MAR-2001; 2001US-00815242.
XX 06-SEP-2001; 2001US-00948993.
PR 25-OCT-2001; 2001US-0342923P.
PR 08-FEB-2002; 2002US-00072851.
PR 06-MAR-2002; 2002US-0362699P.
XX
XX (ELIT-) ELITRA PHARM INC.
XX Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;
PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Foreyeh RA, Xu HH;
XX WPI; 2003-029926/02.
DR N-PsDB; ACA19724.
XX
XX New antisense nucleic acids, useful for identifying proteins or screening
PT for homologous nucleic acids required for cellular proliferation to
XX isolate candidate molecules for rational drug discovery programs.
XX
XX Claim 25; SEQ ID NO 43778; 1766pp; English.

XX
XX The invention relates to an isolated nucleic acid comprising any one of
CC the 6213 antisense sequences given in the specification where expression
CC of the nucleic acid inhibits proliferation of a cell. Also included are:
CC (1) a vector comprising a promoter operably linked to the nucleic acid
CC encoding a polypeptide whose expression is inhibited by the antisense
CC nucleic acid; (2) a host cell containing the vector; (3) an isolated
CC polypeptide or its fragment whose expression is inhibited by the
CC antisense nucleic acid; (4) an antibody capable of specifically binding
CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular
CC proliferation or the activity of a gene in an operon required for
CC proliferation; (7) identifying a compound that influences the activity of
CC the gene product or that has an activity against a biological pathway
CC required for proliferation, or that inhibits cellular proliferation; (8)
CC identifying a gene required for cellular proliferation or the biological
CC pathway in which a proliferation-regulated gene or its gene product lies
CC or a gene on which the test compound that inhibits proliferation of an
CC organism acts; (9) manufacturing an antibiotic; (10) profiling a
CC compound's activity; (11) a culture comprising strains in which the gene
CC product is overexpressed or underexpressed; (12) determining the extent
CC to which each of the strains is present in a culture or collection of
CC strains; or (13) identifying the target of a compound that inhibits the
CC proliferation of an organism. The antisense nucleic acids are useful for
CC identifying proteins or screening for homologous nucleic acids required
CC for cellular proliferation to isolate candidate molecules for rational
CC drug discovery programs, or for screening homologous nucleic acids
CC required for proliferation in cells other than S. aureus, S. typhimurium,
CC K. pneumoniae or P. aeruginosa. The present sequence is encoded by one of
CC the target prokaryotic essential genes. Note: The sequence data for this
CC patent did not form part of the printed specification, but was obtained
CC in electronic format directly from WIPO at

```

CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 961 AA:
Query Match          90.0%; Score 108; DB 6; Length 961;
Best Local Similarity 90.5%; Pred. No. 6.1e-08;
Matches 19; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1 KPSYQFGHNSPDPEDTLPK 21
      ||:|||||
DB      784 KPNYQFGHNSVDFEDTLPK 804

RESULT 15
AAU33960
ID AAU33960 standard; protein; 978 AA.
XX
AC AAU33960;
XX
DT 14-FEB-2002 (first entry)
XX
DE Staphylococcus aureus cellular proliferation protein #236.
XX
KW Antisense; prokaryotic cellular proliferation protein; antibiotic;
XX antibacterial; drug design.
XX
OS Staphylococcus aureus.
XX
PN WO200170955-A2.
XX
PD 27-SEP-2001.
XX
PF 21-MAR-2001; 2001WO-US009180.
XX
PR 21-MAR-2000; 2000US-0191078P.
XX 23-MAY-2000; 2000US-0206848P.
XX 26-MAY-2000; 2000US-0207727P.
XX 23-OCT-2000; 2000US-0242578P.
XX 27-NOV-2000; 2000US-0253625P.
XX 22-DEC-2000; 2000US-0257931P.
XX 16-FEB-2001; 2001US-0269308P.
XX
PA (ELIT-) ELITRA PHARM INC.
XX
PI Haselbeck R, Ohlsen KL, Zyekind JW, Wall D, Trawick JD, Carr GJ;
PI Yamamoto RT, Xu HH;
XX
DR N-PSDB; AAS51819.
XX
PS MPI; 2001-611495/70.
XX
PT New polynucleotides for the identification and development of
XX antibiotics, comprise sequences of antisense nucleic acids.
XX
PS Example 3; SEQ ID NO 5456; 511pp; English.
XX
CC The invention relates to antisense inhibitors of genes essential to
CC prokaryotic cellular proliferation, their use in identifying the genes,
CC their use in the discovery of novel antibiotics, the essential genes,
CC themselves and the encoded proteins. The prokaryotes used are Escherichia
CC coli, Staphylococcus aureus, Salmonella typhi, Klebsiella pneumoniae,
CC Pseudomonas aeruginosa and Enterococcus faecalis. The invention is also
CC useful for the identification of potential new targets for antibiotic
CC development. The antisense nucleic acids can also be used to identify
CC proteins used in proliferation, to express these proteins, and to obtain
CC antibodies capable of binding to the expressed proteins. The proteins can
CC be used to screen compounds in rational drug discovery programmes. The
CC antisense nucleic acid sequence is also useful to screen for homologous
CC nucleic acids which are required for cell proliferation in a wide variety
CC of organisms. The present sequence represents an essential prokaryotic
CC cellular proliferation protein. Note: The sequence data for this patent
CC did not form part of the printed specification, but was obtained in
CC electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences

```

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XX
SQ Sequence 978 AA:
Query Match          90.0%; Score 108; DB 4; Length 978;
Best Local Similarity 90.5%; Pred. No. 6.3e-08;
Matches 19; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1 KPSYQFGHNSPDPEDTLPK 21
      ||:|||||
DB      815 KPNYQFGHNSVDFEDTLPK 835

Search completed: October 25, 2005, 19:38:29
Job time : 60.1473 secs

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GenCore version 5.1.6
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OM protein - protein search, using SW model

Run on: October 22, 2005, 02:23:36 ; Search time 15.9358 Seconds
(without alignments)
98.371 Million cell updates/sec

Title: US-10-731-238-24

Sequence: 1 KPSYQFGHNSPDFEDTLPEK 21

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

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- 6: /cgn2_6/ptodata/1/iaa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	120	100.0	21	4	US-09-010-317-24
2	111	92.5	21	4	US-09-010-317-9
3	111	92.5	37	1	US-08-234-622A-4
4	111	92.5	38	1	US-08-294-189-8
5	111	92.5	38	1	US-08-729-767-5
6	111	92.5	114	1	US-08-259-000-3
7	111	92.5	139	3	US-08-856-253-8
8	111	92.5	178	3	US-08-459-135A-12
9	111	92.5	178	3	US-08-495-559-12
10	111	92.5	1027	4	US-08-956-171E-5254
11	111	92.5	1027	4	US-08-781-986A-5254
12	106	88.3	21	4	US-09-010-317-14
13	106	88.3	21	4	US-09-010-317-16
14	106	88.3	21	4	US-09-010-317-23
15	106	88.3	21	4	US-09-010-317-33
16	105	87.5	21	4	US-09-010-317-18
17	105	87.5	21	4	US-09-010-317-27
18	105	87.5	21	4	US-09-010-317-28
19	105	87.5	21	4	US-09-010-317-30
20	104	86.7	21	4	US-09-010-317-25
21	104	86.7	21	4	US-09-010-317-29
22	104	86.7	21	4	US-09-010-317-31
23	104	86.7	130	2	US-08-459-135A-7
24	104	86.7	130	2	US-08-459-135A-8
25	104	86.7	130	3	US-08-495-559-7
26	104	86.7	130	3	US-08-495-559-8
27	104	86.7	174	2	US-08-459-135A-10

28	104	86.7	174	2	US-08-459-135A-13	Sequence 13, Appl
29	104	86.7	174	3	US-08-495-559-10	Sequence 10, Appl
30	104	86.7	174	3	US-08-495-559-13	Sequence 13, Appl
31	104	86.7	176	3	US-08-495-559-6	Sequence 6, Appl
32	104	86.7	181	2	US-08-459-135A-6	Sequence 6, Appl
33	104	86.7	559	4	US-08-956-171B-5251	Sequence 5251, Ap
34	104	86.7	559	4	US-08-781-986A-5251	Sequence 5251, Ap
35	103	85.8	21	4	US-09-010-317-10	Sequence 10, Appl
36	103	85.8	21	4	US-09-010-317-15	Sequence 15, Appl
37	103	85.8	21	4	US-09-010-317-20	Sequence 20, Appl
38	103	85.8	21	4	US-09-010-317-22	Sequence 22, Appl
39	103	85.8	21	4	US-09-010-317-32	Sequence 32, Appl
40	103	85.8	22	4	US-09-010-317-13	Sequence 13, Appl
41	101	84.2	21	4	US-09-010-317-17	Sequence 17, Appl
42	101	84.2	21	4	US-09-010-317-19	Sequence 19, Appl
43	101	84.2	21	4	US-09-010-317-21	Sequence 21, Appl
44	101	84.2	21	4	US-09-010-317-26	Sequence 26, Appl
45	90	75.0	19	1	US-08-234-622A-1	Sequence 1, Appl

ALIGNMENTS

RESULT 1
US-09-010-317-24
Sequence 24, Application US/09010317
Patent No. 6685943
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
APPLICANT: Patti, Joseph M.
APPLICANT: House-Pompeo, Karen L.
APPLICANT: Speziale, Pietro
APPLICANT: Job, Danny
APPLICANT: McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
TITLE OF INVENTION: AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/010.317
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-09-010-317-24
Query Match 100.0%; Score 120; DB 4; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.7e-12;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KPSYQFGHNSPDFFEDTLPK 21
|||||
Db 1 KPSYQFGHNSPDFFEDTLPK 21

RESULT 2

US-09-010-317-9
; Sequence 9, Application US/09010317
; Patent No. 6685943
; GENERAL INFORMATION:
; APPLICANT: Hook, Magnus
; APPLICANT: Patti, Joseph M.
; APPLICANT: House-Pompeo, Karen L.
; APPLICANT: Speziale, Pietro
; APPLICANT: McGavin, Martin J.
; APPLICANT: John, Danny
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
; TITLE OF INVENTION: AND METHODS OF USE
; NUMBER OF SEQUENCES: 105
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: TX
; COUNTRY: USA
; ZIP: 77210-4433
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/010,317
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/036,139
; FILING DATE: 21-JAN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Habler, David W.
; REGISTRATION NUMBER: 41,071
; REFERENCE/DOCKET NUMBER: TAMK:189
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 512-418-3000
; TELEFAX: 512-474-7577
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; US-09-010-317-9

Query Match 92.5%; Score 111; DB 4; Length 21;

Best Local Similarity 95.2%; Pred. No. 4.5e-11; Mismatches 1; Indels 0; Gaps 0;

QY 1 KPSYQFGHNSPDFFEDTLPK 21
|||||

Db 1 KPSYQFGHNSVDFFEDTLPK 21

RESULT 3

US-08-234-622A-4
; Sequence 4, Application US/08234622A
; Patent No. 5440014
; GENERAL INFORMATION:
; APPLICANT: Hook, Magnus
; APPLICANT: McGavin, Martin
; APPLICANT: RAUCCI, Giuseppe
; TITLE OF INVENTION: A FIBRONECTIN BINDING PEPTIDE

NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Burns, Doane, Swecker & Mathis
STREET: P.O. Box 1404
CITY: Alexandria
STATE: Virginia
COUNTRY: United States
ZIP: 22313-1404

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/234,622A

FILING DATE: 28-APR-1994

CLASSIFICATION: 530

PRIOR APPLICATION DATA:

APPLICATION NUMBER: SE 9002617-0

FILING DATE: 10-AUG-1990

PRIOR APPLICATION DATA:

APPLICATION NUMBER: WO PCT/SE91/00534

FILING DATE: 09-AUG-1991

ATTORNEY/AGENT INFORMATION:

NAME: Meuth, Donna M

REGISTRATION NUMBER: 36,607

REFERENCE/DOCKET NUMBER: 012885-044

TELECOMMUNICATION INFORMATION:

TELEPHONE: (703) 836-6620

TELEFAX: (703) 836-2021

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 37 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-234-622A-4

Query Match 92.5%; Score 111; DB 1; Length 37;

Best Local Similarity 95.2%; Pred. No. 8.6e-11; Mismatches 1; Indels 0; Gaps 0;

QY 1 KPSYQFGHNSPDFFEDTLPK 21
|||||

Db 16 KPSYQFGHNSVDFFEDTLPK 36

RESULT 4

US-08-294-189-8
; Sequence 8, Application US/08294189
; Patent No. 5707822
; GENERAL INFORMATION:
; APPLICANT: Fischetti, Vincent A.
; APPLICANT: Rakonjac, Jasna
; APPLICANT: Robbins, John
; TITLE OF INVENTION: GENE SERUM OPACITY FACTOR
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klauber & Jackson
; STREET: 411 Hackensack Avenue
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/294,189
; FILING DATE: 22-AUG-1994

CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-118
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 487-5800
TELEFAX: 201 343-1684
TELEX: 133521
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
ORGANISM: Streptococcus pyogenes
STRAIN: D734
INDIVIDUAL ISOLATE: 22
IMMEDIATE SOURCE:
CLONE: SAU3a
US-08-294-189-8

Query Match 92.5%; Score 111; DB 1; Length 38;
Best Local Similarity 95.2%; Pred. No. 8,9e-11;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KPSYQFGHNSVPDEDTLPK 21
Db 10 KPSYQFGHNSVPDEDTLPK 30

RESULT 5
US-08-729-767-5
Sequence 5, Application US/08729767
Patent No. 5770702
GENERAL INFORMATION:
APPLICANT: HOOK, Magnus
APPLICANT: LINDBERG, Martin Kjell
APPLICANT: SIGNAS, Lars Christer
APPLICANT: WADSTROM, Torkel Mikael
APPLICANT: FROMAN, Gunnar
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN AS WELL AS
TITLE OF INVENTION: ITS PREPARATION
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Burns, Doane, Swecker & Mathis, L.L.P.
STREET: P.O. Box 1404
CITY: Alexandria
STATE: Virginia
COUNTRY: United States
ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/729,767
FILING DATE: 07-OCT-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/259,000
FILING DATE: 13-JUN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/007,817
FILING DATE: 22-JAN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/201,028
FILING DATE: 01-JUN-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: SE 8702272-9

FILING DATE: 01-JUN-1987
ATTORNEY/AGENT INFORMATION:
NAME: McGowan, Malcolm K.
REGISTRATION NUMBER: 39,300
REFERENCE/DOCKET NUMBER: 012889-036
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-729-767-5

Query Match 92.5%; Score 111; DB 1; Length 38;
Best Local Similarity 95.2%; Pred. No. 8,9e-11;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KPSYQFGHNSVPDEDTLPK 21
Db 17 KPSYQFGHNSVPDEDTLPK 37

RESULT 6
US-08-259-000-3
Sequence 3, Application US/08259000
Patent No. 5571514
GENERAL INFORMATION:
APPLICANT: HOOK, Magnus
APPLICANT: LINDBERG, Martin Kjell
APPLICANT: SIGNAS, Lars Christer
APPLICANT: WADSTROM, Torkel Mikael
APPLICANT: FROMAN, Gunnar
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN AS WELL AS
TITLE OF INVENTION: ITS PREPARATION
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Burns, Doane, Swecker & Mathis
STREET: P.O. Box 1404
CITY: Alexandria
STATE: Virginia
COUNTRY: United States
ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/259,000
FILING DATE: 13-JUN-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: SE 8702272-9
FILING DATE: 01-JUN-1987
ATTORNEY/AGENT INFORMATION:
NAME: Meuth, Donna M
REGISTRATION NUMBER: 36,607
REFERENCE/DOCKET NUMBER: 012885-062
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 114 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-259-000-3

Query Match 92.5%; Score 111; DB 1; Length 114;
Best Local Similarity 95.2%; Pred. No. 3.1e-10;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 KPSYQFGHNSVPFEDTLPK 21
DB 93 KPSYQFGHNSVPFEDTLPK 113

RESULT 7
US-08-856-253-8
Sequence 8, Application US/08856253
Patent No. 6288214
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
APPLICANT: Patti, Joseph M.
APPLICANT: House-Pompeo, Karen
APPLICANT: Stranam, Narayana
APPLICANT: Symersky, Jindrich
TITLE OF INVENTION: COLLAGEN BINDING PROTEIN COMPOSITIONS
TITLE OF INVENTION: AND METHODS OF USE
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P O. Box 4433
CITY: Houston
STATE: Texas
COUNTRY: U.S.
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/856,253
FILING DATE: Concurrently Herewith
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/017,678
FILING DATE: 16-MAY-1996
ATTORNEY/AGENT INFORMATION:
NAME: Kitchell, Barbara S.
REGISTRATION NUMBER: 33,928
REFERENCE/DOCKET NUMBER: TAMR:193
TELEPHONE: (512) 418-3000
TELEFAX: (512) 474-7577
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 139 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-08-856-253-8

Query Match 92.5%; Score 111; DB 3; Length 139;
Best Local Similarity 95.2%; Pred. No. 3.9e-10;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 KPSYQFGHNSVPFEDTLPK 21
DB 107 KPSYQFGHNSVPFEDTLPK 127

RESULT 8
US-08-459-135A-12
Sequence 12, Application US/08459135A
Patent No. 595078
GENERAL INFORMATION:
APPLICANT: BURHAM, Martin Karl Russel
APPLICANT: CHOPRA, Ian

APPLICANT: CRITCHLEY, Ian Alfred
APPLICANT: KNOWLES, David Justin Charles
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN: MONOCLONAL ANTIBODY AND THEIR US
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
STATE: PA
COUNTRY: U.S.A.
ZIP: 19406-0939
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: PasteSeq, Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/459,135A
FILING DATE: 02-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB/94/00215
FILING DATE: 04-Feb-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Gimmil, Edward R.
REGISTRATION NUMBER: 38,891
REFERENCE/DOCKET NUMBER: P30591C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-4478
TELEFAX: 610-270-5090
TELEX:
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 178 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: Protein
US-08-459-135A-12

Query Match 92.5%; Score 111; DB 2; Length 178;
Best Local Similarity 95.2%; Pred. No. 5.2e-10;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 KPSYQFGHNSVPFEDTLPK 21
DB 93 KPSYQFGHNSVPFEDTLPK 113

RESULT 9
US-08-495-559-12
Sequence 12, Application US/08495559A
Patent No. 6054572
GENERAL INFORMATION:
APPLICANT: BURHAM, Martin Karl Russel
APPLICANT: CHOPRA, Ian
APPLICANT: CRITCHLEY, Ian Alfred
APPLICANT: KNOWLES, David Justin Charles
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN: MONOCLONAL
TITLE OF INVENTION: ANTIBODY AND THEIR USE IN PREVENTING BACTERIAL ADHESION
FILE REFERENCE: P30591
CURRENT APPLICATION NUMBER: US/08/495,559A
CURRENT FILING DATE: 1995-08-03
EARLIER APPLICATION NUMBER: GB 9302289.5
EARLIER FILING DATE: 1993-02-05
EARLIER APPLICATION NUMBER: GB 9321592.9
EARLIER FILING DATE: 1993-10-20
NUMBER OF SEQ ID NOS: 13
SOFTWARE: PasteSeq for Windows Version 3.0
SEQ ID NO 12
LENGTH: 178
TYPE: PRT

ORGANISM: Staphylococcus aureus
US-08-495-559-12

Query Match 92.5%; Score 111; DB 3; Length 178;
Best Local Similarity 95.2%; Pred. No. 5,2e-10;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KPSYQFGHNSPDPEDTLPK 21
Db 93 KPSYQFGHNSVDPEDTLPK 113

RESULT 10
US-08-956-171E-5254

Sequence 5254, Application US/08956171E
Patent No. 6593114

GENERAL INFORMATION:

APPLICANT: Charles Kunsch

Gil H. Choi

Patrick S. Dillon

Craig A. Rosen

Steven C. Barash

Michael R. Fannon

TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences

NUMBER OF SEQUENCES: 5256

CORRESPONDENCE ADDRESS:

ADDRESSEE: Human Genome Sciences, Inc.

STREET: 9410 Key West Avenue

CITY: Rockville

STATE: Maryland

COUNTRY: USA

ZIP: 20850

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage

COMPUTER: HP Vectra 486/33

OPERATING SYSTEM: MSDOS version 6.2

SOFTWARE: ASCII Text

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/956,171E

FILING DATE: 20-Oct-1997

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 60/009,861

FILING DATE: January 5, 1996

APPLICATION NUMBER: 08/781,986

FILING DATE: January 3, 1997

ATTORNEY/AGENT INFORMATION:

NAME: Mark J. Hyman

REGISTRATION NUMBER: 46,789

REFERENCE/DOCKET NUMBER: PB248P1

TELECOMMUNICATION INFORMATION:

TELEPHONE: (240) 314-1224

TELEFAX: (301) 309-8439

INFORMATION FOR SEQ ID NO: 5254:

SEQUENCE CHARACTERISTICS:

LENGTH: 1027 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 5254:

US-08-956-171E-5254

Query Match 92.5%; Score 111; DB 4; Length 1027;
Best Local Similarity 95.2%; Pred. No. 3.9e-09;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KPSYQFGHNSPDPEDTLPK 21
Db 846 KPSYQFGHNSVDPEDTLPK 866

RESULT 11

US-08-781-986A-5254
Sequence 5254, Application US/08781986A

Patent No. 6737248

GENERAL INFORMATION:

APPLICANT: Charles Kunsch

TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences

NUMBER OF SEQUENCES: 5255

CORRESPONDENCE ADDRESS:

ADDRESSEE: Human Genome Sciences, Inc.

STREET: 9410 Key West Avenue

CITY: Rockville

STATE: Maryland

COUNTRY: USA

ZIP: 20850

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage

COMPUTER: HP Vectra 486/33

OPERATING SYSTEM: MSDOS version 6.2

SOFTWARE: ASCII Text

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/781,986A

FILING DATE:

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Benson, Bob

REGISTRATION NUMBER: 30,446

REFERENCE/DOCKET NUMBER: PB248PP

TELECOMMUNICATION INFORMATION:

TELEPHONE: (301) 309-8504

TELEFAX: (301) 309-8512

INFORMATION FOR SEQ ID NO: 5254:

SEQUENCE CHARACTERISTICS:

LENGTH: 1027 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-781-986A-5254

Query Match 92.5%; Score 111; DB 4; Length 1027;
Best Local Similarity 95.2%; Pred. No. 3.9e-09;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KPSYQFGHNSPDPEDTLPK 21
Db 846 KPSYQFGHNSVDPEDTLPK 866

RESULT 12

US-09-010-317-14

Sequence 14, Application US/09010317

Patent No. 6685943

GENERAL INFORMATION:

APPLICANT: Hook, Magnus

APPLICANT: Patti, Joseph M.

APPLICANT: House-Pompeo, Karen L.

APPLICANT: Speziale, Pietro

APPLICANT: Joh, Danny

APPLICANT: McGavin, Martin J.

TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS

NUMBER OF SEQUENCES: 105

CORRESPONDENCE ADDRESS:

ADDRESSEE: Arnold, White & Durkee

STREET: P.O. Box 4433

CITY: Houston

STATE: TX

COUNTRY: USA

ZIP: 77210-4433

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-09-010-317-14

Query Match 88.3%; Score 106; DB 4; Length 21;
Best Local Similarity 95.0%; Pred. No. 2,8e-10;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 PSYQFGHNSPDEEDTLPK 21
Db 2 PSYQFGHNSVDFEEDTLPK 21

RESULT 13
US-09-010-317-16
Sequence 16, Application US/09010317
Patent No. 6685943
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
APPLICANT: Patti, Joseph M.
APPLICANT: House-Pompeo, Karen L.
APPLICANT: Speziale, Pietro
APPLICANT: John, Danny
APPLICANT: McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAMK:189
TELECOMMUNICATION INFORMATION:

TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-09-010-317-16

Query Match 88.3%; Score 106; DB 4; Length 21;
Best Local Similarity 90.5%; Pred. No. 2,8e-10;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 KPSPYQFGHNSPDEEDTLPK 21
Db 1 KPSPYQFGHNSVDFEEDTLPK 21

RESULT 14
US-09-010-317-23
Sequence 23, Application US/09010317
Patent No. 6685943
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
APPLICANT: Patti, Joseph M.
APPLICANT: House-Pompeo, Karen L.
APPLICANT: Speziale, Pietro
APPLICANT: John, Danny
APPLICANT: McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAMK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-09-010-317-23

Query Match 88.3%; Score 106; DB 4; Length 21;
Best Local Similarity 90.5%; Pred. No. 2,8e-10;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 KPSPYQFGHNSPDEEDTLPK 21
Db 1 KPSPYQFGHNSVDFEEDTLPK 21

Db 1 KPSYQFGHNPVDFEEDTLPK 21

RESULT 15
US-09-010-317-33

/ Sequence 33, Application US/09010317
/ Patent No. 6685943
/ GENERAL INFORMATION:
/ APPLICANT: Hook, Magnus
/ APPLICANT: Patti, Joseph M.
/ APPLICANT: House-Pompeo, Karen L.
/ APPLICANT: Speziale, Pietro
/ APPLICANT: McGavin, Martin J.
/ TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
/ NUMBER OF SEQUENCES: 105
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Arnold, White & Durkee
/ STREET: P.O. Box 4433
/ CITY: Houston
/ STATE: TX
/ COUNTRY: USA
/ ZIP: 77210-4433
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patentin Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/010.317
/ FILING DATE:
/ CLASSIFICATION:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 60/036,139
/ FILING DATE: 21-JAN-1997
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Hibler, David W.
/ REGISTRATION NUMBER: 41,071
/ REFERENCE/DOCKET NUMBER: TAMK.189
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 512-418-3000
/ TELEFAX: 512-474-7577
/ INFORMATION FOR SEQ ID NO: 33:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 21 amino acids
/ TYPE: amino acid
/ STRANDEDNESS:
/ TOPOLOGY: linear
/ US-09-010-317-33

Query Match 88.3%; Score 106; DB 4; Length 21;
Best Local Similarity 95.0%; Pred. No. 2.8e-10;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KPSYQFGHNSPDPEEDTLP 20
| | | | | | | | | | | | | | | | | | | | | |
Db 1 KPSYQFGHNSVDPEEDTLP 20

Search completed: October 22, 2005, 03:51:12
Job time : 15.9358 secs

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GenCore version 5.1.6
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OM protein - protein search, using SW model

Run on: October 22, 2005, 10:49:15 ; Search time 59.2367 Seconds
(without alignments)
148.005 Million cell updates/sec

Title: US-10-731-238-24

Perfect score: 120
Sequence: 1 KPSYQFGHNSPDEEDTLRK 21

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 1862951 seqs, 417491010 residues

Total number of hits satisfying chosen parameters: 1862951

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA:*

- 1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/2/pubpaa/PTCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
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- 6: /cgn2_6/ptodata/2/pubpaa/PTCTUS_PUBCOMB.pep.*
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- 8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
- 9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep.*
- 10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep.*
- 12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
- 13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
- 14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
- 15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pep.*
- 17: /cgn2_6/ptodata/2/pubpaa/US10E_PUBCOMB.pep.*
- 18: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
- 19: /cgn2_6/ptodata/2/pubpaa/US11A_PUBCOMB.pep.*
- 20: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep.*
- 21: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
- 22: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	120	100.0	21	US-10-731-238-24	Sequence 24, Appl
2	111	92.5	21	US-10-731-238-9	Sequence 9, Appl
3	111	92.5	37	US-11-066-697-1134	Sequence 1134, Ap
4	111	92.5	139	US-09-813-820-8	Sequence 8, Appl
5	111	92.5	1018	US-09-815-242-5797	Sequence 5797, Ap
6	111	92.5	1018	US-09-815-242-12838	Sequence 12838, A
7	111	92.5	1018	US-10-470-048B-68	Sequence 68, Appl
8	111	92.5	1027	US-08-781-986A-5254	Sequence 5254, Ap
9	111	92.5	1027	US-10-329-624-5254	Sequence 5254, Ap
10	108	90.0	961	US-10-283-122A-13778	Sequence 43778, A
11	108	90.0	978	US-09-815-242-5456	Sequence 5456, Ap

12	108	90.0	1001	US-09-815-242-12686	Sequence 12686, A
13	108	90.0	1038	US-10-282-122A-43827	Sequence 43827, A
14	106	88.3	21	US-10-731-238-14	Sequence 14, Appl
15	106	88.3	21	US-10-731-238-16	Sequence 16, Appl
16	106	88.3	21	US-10-731-238-23	Sequence 23, Appl
17	106	88.3	21	US-10-731-238-33	Sequence 33, Appl
18	105	87.5	21	US-10-731-238-18	Sequence 18, Appl
19	105	87.5	21	US-10-731-238-27	Sequence 27, Appl
20	105	87.5	21	US-10-731-238-28	Sequence 28, Appl
21	105	87.5	21	US-10-731-238-30	Sequence 30, Appl
22	104	86.7	21	US-10-731-238-25	Sequence 25, Appl
23	104	86.7	21	US-10-731-238-29	Sequence 29, Appl
24	104	86.7	21	US-10-731-238-31	Sequence 31, Appl
25	104	86.7	388	US-08-901-062-1	Sequence 1, Appl
26	104	86.7	559	US-08-781-986A-5251	Sequence 5251, Ap
27	104	86.7	559	US-10-329-624-5251	Sequence 5251, Ap
28	104	86.7	940	US-10-470-048B-424	Sequence 424, Ap
29	104	86.7	948	US-10-470-048B-69	Sequence 69, Appl
30	103	85.8	21	US-10-731-238-15	Sequence 15, Appl
31	103	85.8	21	US-10-731-238-10	Sequence 10, Appl
32	103	85.8	21	US-10-731-238-20	Sequence 20, Appl
33	103	85.8	21	US-10-731-238-22	Sequence 22, Appl
34	103	85.8	21	US-10-731-238-32	Sequence 32, Appl
35	103	85.8	22	US-10-731-238-13	Sequence 13, Appl
36	101	84.2	21	US-10-731-238-17	Sequence 17, Appl
37	101	84.2	21	US-10-731-238-21	Sequence 21, Appl
38	101	84.2	21	US-10-731-238-26	Sequence 26, Appl
39	101	84.2	21	US-10-731-238-34	Sequence 34, Appl
40	83	69.2	14	US-10-731-238-61	Sequence 61, Appl
41	72	60.0	18	US-10-731-238-96	Sequence 96, Appl
42	59	49.2	10	US-10-731-238-95	Sequence 95, Appl
43	55	45.0	196	US-11-097-143-13923	Sequence 13923, A
44	54	45.0	10	US-10-731-238-95	Sequence 95, Appl
45	53	44.2	215	US-10-437-963-145484	Sequence 145484, A

ALIGNMENTS

RESULT 1
US-10-731-238-24
Sequence 24, Application US/10731238
Publication No. US20050123552A1
GENERAL INFORMATION:
APPLICANT: Hook, Magneue
Fattl, Joseph M.
House-Pompeo, Karen L.
Speziale, Pietro
Joh, Danny
McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/731,238
FILING DATE: 10-Dec-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE: 21-Jan-1998
APPLICATION NUMBER: US 60/036,139

FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAMK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 24:
US-10-731-238-24

Query Match 100.0%; Score 120; DB 18; Length 21;
Best Local Similarity 100.0%; Pred. No. 6e-11;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KPSYQFGHNSPDEEDTLPK 21
1 KPSYQFGHNSPDEEDTLPK 21

RESULT 2
US-10-731-238-9
Sequence 9, Application US/10731238
Publication No. US20050123552A1
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
Patli, Joseph M.
House-Pompeo, Karen L.
Speziale, Pietro
Joh, Danny
McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/10/731,238
APPLICATION NUMBER: US/10/731,238
FILING DATE: 10-Dec-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE: 21-Jan-1998
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAMK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>

TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 9:
US-10-731-238-9

Query Match 92.5%; Score 111; DB 18; Length 21;
Best Local Similarity 95.2%; Pred. No. 1.4e-09;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KPSYQFGHNSPDEEDTLPK 21
1 KPSYQFGHNSVDFEEDTLPK 21

RESULT 3
US-11-066-697-1134
Sequence 1134, Application US/11066697
Publication No. US20050187159A1
GENERAL INFORMATION:
APPLICANT: Bridon, Dominique P.
APPLICANT: Ezrin, Alan M.
APPLICANT: Milner, Peter G.
APPLICANT: Holmes, Darren L.
APPLICANT: Thibaudau, Karen
TITLE OF INVENTION: PROTECTION OF ENDOGENOUS THERAPEUTIC PEPTIDES FROM
TITLE OF INVENTION: PEPTIDASE ACTIVITY THROUGH CONJUGATION TO BLOOD
FILE REFERENCE: 500862002301
CURRENT APPLICATION NUMBER: US/11/066,697
CURRENT FILING DATE: 2005-02-25
PRIOR APPLICATION NUMBER: 09/657,276
PRIOR FILING DATE: 2000-09-07
PRIOR APPLICATION NUMBER: 60/153,406
PRIOR FILING DATE: 1999-09-10
PRIOR APPLICATION NUMBER: 60/159,783
PRIOR FILING DATE: 1999-10-15
NUMBER OF SEQ ID NOS: 1617
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 1134
LENGTH: 37
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-11-066-697-1134

Query Match 92.5%; Score 111; DB 20; Length 37;
Best Local Similarity 95.2%; Pred. No. 2.5e-09;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KPSYQFGHNSPDEEDTLPK 21
16 KPSYQFGHNSVDFEEDTLPK 36

RESULT 4
US-09-813-820-8
Sequence 8, Application US/09813820
Patent No. US20020102262A1
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
Patli, Joseph M.
House-Pompeo, Karen
Sthanam, Narayana
Symeisky, Jindrich
TITLE OF INVENTION: COLLAGEN BINDING PROTEIN COMPOSITIONS
AND METHODS OF USE
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: Texas

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; COUNTRY: U.S.
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/813,820
; FILING DATE: 22-Mar-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/856,253
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Kitchell, Barbara S.
; REGISTRATION NUMBER: 33,928
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (512) 418-3000
; TELEFAX: (512) 474-7577
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 139 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-09-813-820-8

Query Match      92.5%; Score 111; DB 9; Length 139;
Best Local Similarity 95.2%; Pred. No. 1e-08;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Q# 1 KPSYQFGHNSPDEEDTLPK 21
Db 107 KPSYQFGHNSVDFEEDTLPK 127

RESULT 5
US-09-815-242-5797
; Sequence 5797, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari L.
; APPLICANT: Zysek, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; FILE REFERENCE: ELITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version 4.0
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; SEQ ID NO 5797
; LENGTH: 1018
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-09-815-242-5797

Query Match      92.5%; Score 111; DB 9; Length 1018;
Best Local Similarity 95.2%; Pred. No. 9e-08;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Q# 1 KPSYQFGHNSPDEEDTLPK 21
Db 837 KPSYQFGHNSVDFEEDTLPK 857

RESULT 6
US-09-815-242-12838
; Sequence 12838, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari L.
; APPLICANT: Zysek, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; FILE REFERENCE: ELITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12838
; LENGTH: 1018
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-09-815-242-12838

Query Match      92.5%; Score 111; DB 9; Length 1018;
Best Local Similarity 95.2%; Pred. No. 9e-08;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Q# 1 KPSYQFGHNSPDEEDTLPK 21
Db 837 KPSYQFGHNSVDFEEDTLPK 857

RESULT 7
US-10-470-048B-68
; Sequence 68, Application US/10470048B
; Publication No. US2005003744A1
; GENERAL INFORMATION:
; APPLICANT: MEINKE ET AL.
; TITLE OF INVENTION: A METHOD FOR IDENTIFICATION, ISOLATION AND PRODUCTION OF
; FILE REFERENCE: SOINN.035US
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;; CURRENT APPLICATION NUMBER: US/10/470,0488
;; CURRENT FILING DATE: 2003-07-25
;; NUMBER OF SEQ ID NOS: 603
;; SOFTWARE: PatentIn version 3.1
;; SEQ ID NO 68
;; LENGTH: 1018
;; TYPE: PRT
;; ORGANISM: Staphylococcus aureus
US-10-470-0488-68

Query Match 92.5%; Score 111; DB 17; Length 1018;
Best Local Similarity 95.2%; Pred. No. 9e-08;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 KPSYFGGHSVPDEEDTLPK 21
|||
Db 837 KPSYFGGHSVPDEEDTLPK 857

RESULT 8
US-08-781-986A-5254
; Sequence 5254, Application US/08781986A
; Publication No. US20030054436A1
; GENERAL INFORMATION:
; APPLICANT: Charles Kunach
; TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
; NUMBER OF SEQUENCES: 5255
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/781,986A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Benson, Bob
; REGISTRATION NUMBER: 30,446
; REFERENCE/DOCKET NUMBER: PB248BP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 5254:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1027 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-781-986A-5254

Query Match 92.5%; Score 111; DB 8; Length 1027;
Best Local Similarity 95.2%; Pred. No. 9.1e-08;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 KPSYFGGHSVPDEEDTLPK 21
|||
Db 846 KPSYFGGHSVPDEEDTLPK 866

RESULT 9
US-10-329-624-5254

; Sequence 5254, Application US/10329624
; Publication No. US20040043037A1
; GENERAL INFORMATION:
; APPLICANT: Charles Kunach
; GIL H. Choi
; Patrick S. Dillon
; Craig A. Rosen
; Steven C. Barash
; Michael R. Fannon

;; TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
;; NUMBER OF SEQUENCES: 5256
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Human Genome Sciences, Inc.
;; STREET: 9410 Key West Avenue
;; CITY: Rockville
;; STATE: Maryland
;; COUNTRY: USA
;; ZIP: 20850

;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
;; COMPUTER: HP Vectra 486/33
;; OPERATING SYSTEM: MSDOS version 6.2
;; SOFTWARE: ASCII Text
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/10/329,624
;; FILING DATE: 27-Dec-2002
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 08/956,171
;; FILING DATE: October 20, 1997
;; APPLICATION NUMBER: 60/009,861
;; FILING DATE: January 5, 1996
;; APPLICATION NUMBER: 08/781,986
;; FILING DATE: January 3, 1997

;; ATTORNEY/AGENT INFORMATION:
;; NAME: Mark J. Hyman

;; REGISTRATION NUMBER: 46,789
;; REFERENCE/DOCKET NUMBER: PB248P1D1
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (240) 314-1224
;; TELEFAX: (301) 309-8439
;; INFORMATION FOR SEQ ID NO: 5254:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 1027 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; SEQUENCE DESCRIPTION: SEQ ID NO: 5254:

US-10-329-624-5254

Query Match 92.5%; Score 111; DB 15; Length 1027;
Best Local Similarity 95.2%; Pred. No. 9.1e-08;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 KPSYFGGHSVPDEEDTLPK 21
|||
Db 846 KPSYFGGHSVPDEEDTLPK 866

RESULT 10
US-10-282-122A-43778
; Sequence 43778, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyckind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant

```
/ APPLICANT: Yamamoto, Robert
/ APPLICANT: Foreyth, R.
/ TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
/ FILE REFERENCE: ELITRA.013A
/ CURRENT FILING DATE: 2003-02-20
/ PRIOR APPLICATION NUMBER: 60/191,078
/ PRIOR FILING DATE: 2000-03-21
/ PRIOR APPLICATION NUMBER: 60/206,848
/ PRIOR FILING DATE: 2000-05-23
/ PRIOR APPLICATION NUMBER: 60/207,727
/ PRIOR FILING DATE: 2000-05-26
/ PRIOR APPLICATION NUMBER: 60/230,335
/ PRIOR FILING DATE: 2000-09-06
/ PRIOR APPLICATION NUMBER: 60/230,347
/ PRIOR FILING DATE: 2000-09-09
/ PRIOR APPLICATION NUMBER: 60/242,578
/ PRIOR FILING DATE: 2000-10-23
/ PRIOR APPLICATION NUMBER: 60/253,625
/ PRIOR FILING DATE: 2000-11-27
/ PRIOR APPLICATION NUMBER: 60/257,931
/ PRIOR FILING DATE: 2000-12-22
/ PRIOR APPLICATION NUMBER: 60/267,636
/ PRIOR FILING DATE: 2001-02-09
/ PRIOR APPLICATION NUMBER: 60/269,308
/ PRIOR FILING DATE: 2001-02-16
/ Remaining Prior Application data removed - See File Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 78614
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 43778
/ LENGTH: 961
/ TYPE: PRT
/ ORGANISM: Staphylococcus aureus
/ US-10-282-122A-43778

Query Match          90.0%; Score 108; DB 15; Length 961;
Best Local Similarity 90.5%; Pred. No. 2.4e-07;
Matches 19; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1 KPSYOGGHNSPDFEDTLPK 21
DB      784 KPNYOGGHNsyVDFEDTLPK 804

RESULT 11
US-09-815-242-5456
/ Sequence 5456, Application US/09815242
/ Patent No. US20020061569A1
/ GENERAL INFORMATION:
/ APPLICANT: Haselbeck, Robert
/ APPLICANT: Ohlsen, Karl L.
/ APPLICANT: Zyskind, Judith W.
/ APPLICANT: Wall, Daniel
/ APPLICANT: Trawick, John D.
/ APPLICANT: Carr, Grant J.
/ APPLICANT: Yamamoto, Robert T.
/ APPLICANT: Xu, H. Howard
/ TITLE OF INVENTION: Identification of Essential Genes in
/ TITLE OF INVENTION: Prokaryotes
/ FILE REFERENCE: ELITRA.011A
/ CURRENT APPLICATION NUMBER: US/09/815,242
/ CURRENT FILING DATE: 2001-03-21
/ PRIOR APPLICATION NUMBER: 60/191,078
/ PRIOR FILING DATE: 2000-03-21
/ PRIOR APPLICATION NUMBER: 60/206,848
/ PRIOR FILING DATE: 2000-05-23
/ PRIOR APPLICATION NUMBER: 60/207,727
/ PRIOR FILING DATE: 2000-05-26
/ PRIOR APPLICATION NUMBER: 60/242,578
/ PRIOR FILING DATE: 2000-10-23
/ PRIOR APPLICATION NUMBER: 60/253,625
/ PRIOR FILING DATE: 2000-11-27
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/ PRIOR APPLICATION NUMBER: 60/257,931
/ PRIOR FILING DATE: 2000-12-22
/ PRIOR APPLICATION NUMBER: 60/269,308
/ PRIOR FILING DATE: 2001-02-16
/ NUMBER OF SEQ ID NOS: 14110
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 5456
/ LENGTH: 978
/ TYPE: PRT
/ ORGANISM: Staphylococcus aureus
/ US-09-815-242-5456

Query Match          90.0%; Score 108; DB 9; Length 978;
Best Local Similarity 90.5%; Pred. No. 2.4e-07;
Matches 19; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1 KPSYOGGHNSPDFEDTLPK 21
DB      815 KPNYOGGHNsyVDFEDTLPK 835

RESULT 12
US-09-815-242-12686
/ Sequence 12686, Application US/09815242
/ Patent No. US20020061569A1
/ GENERAL INFORMATION:
/ APPLICANT: Haselbeck, Robert
/ APPLICANT: Ohlsen, Karl L.
/ APPLICANT: Zyskind, Judith W.
/ APPLICANT: Wall, Daniel
/ APPLICANT: Trawick, John D.
/ APPLICANT: Carr, Grant J.
/ APPLICANT: Yamamoto, Robert T.
/ APPLICANT: Xu, H. Howard
/ TITLE OF INVENTION: Identification of Essential Genes in
/ TITLE OF INVENTION: Prokaryotes
/ FILE REFERENCE: ELITRA.011A
/ CURRENT APPLICATION NUMBER: US/09/815,242
/ CURRENT FILING DATE: 2001-03-21
/ PRIOR APPLICATION NUMBER: 60/191,078
/ PRIOR FILING DATE: 2000-03-21
/ PRIOR APPLICATION NUMBER: 60/206,848
/ PRIOR FILING DATE: 2000-05-23
/ PRIOR APPLICATION NUMBER: 60/207,727
/ PRIOR FILING DATE: 2000-05-26
/ PRIOR APPLICATION NUMBER: 60/242,578
/ PRIOR FILING DATE: 2000-10-23
/ PRIOR APPLICATION NUMBER: 60/253,625
/ PRIOR FILING DATE: 2000-11-27
/ PRIOR APPLICATION NUMBER: 60/257,931
/ PRIOR FILING DATE: 2000-12-22
/ PRIOR APPLICATION NUMBER: 60/269,308
/ PRIOR FILING DATE: 2001-02-16
/ NUMBER OF SEQ ID NOS: 14110
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 12686
/ LENGTH: 1001
/ TYPE: PRT
/ ORGANISM: Staphylococcus aureus
/ US-09-815-242-12686

Query Match          90.0%; Score 108; DB 9; Length 1001;
Best Local Similarity 90.5%; Pred. No. 2.5e-07;
Matches 19; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1 KPSYOGGHNSPDFEDTLPK 21
DB      838 KPNYOGGHNsyVDFEDTLPK 858

RESULT 13
US-10-282-122A-43827
/ Sequence 43827, Application US/10282122A
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Publication No. US20040029129A1
GENERAL INFORMATION:
APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari
APPLICANT: Zykkind, Judith
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John
APPLICANT: Carr, Grant
APPLICANT: Yamamoto, Robert
APPLICANT: Forsyth, R.
TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REFERENCE: ELITRA.034A
CURRENT FILING DATE: 2003-02-20
PRIORITY FILING DATE: 2003-02-20
PRIORITY FILING DATE: 2000-03-21
PRIORITY FILING DATE: 2000-03-21
PRIORITY FILING DATE: 2000-05-23
PRIORITY FILING DATE: 2000-05-23
PRIORITY FILING DATE: 2000-05-26
PRIORITY FILING DATE: 2000-05-26
PRIORITY FILING DATE: 2000-09-06
PRIORITY FILING DATE: 2000-09-06
PRIORITY FILING DATE: 2000-09-09
PRIORITY FILING DATE: 2000-09-09
PRIORITY FILING DATE: 2000-10-23
PRIORITY FILING DATE: 2000-10-23
PRIORITY FILING DATE: 2000-11-27
PRIORITY FILING DATE: 2000-11-27
PRIORITY FILING DATE: 2000-12-22
PRIORITY FILING DATE: 2000-12-22
PRIORITY FILING DATE: 2001-02-09
PRIORITY FILING DATE: 2001-02-09
PRIORITY FILING DATE: 2001-02-16
PRIORITY FILING DATE: 2001-02-16
REMAINING PRIORITY APPLICATION DATA REMOVED - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 78614
SOFTWARE: PatentIn version 3.1
SEQ ID NO 43827
LENGTH: 1038
TYPE: PRT
ORGANISM: Staphylococcus aureus
US-10-282-122A-43827
Query Match 90.0%; Score 108; DB 15; Length 1038;
Best Local Similarity 90.5%; Pred. No. 2,6e-07;
Matches 19; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 KPSYQFGHNSPDPEDTLPK 21
DB 833 KPNYQFGHNSVDFEEDTLPK 853
RESULT 14
US-10-731-238-14
Sequence 14, Application US/10731238
Publication No. US20050123552A1
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
APPLICANT: Patti, Joseph M.
APPLICANT: House-Pompeo, Karen L.
APPLICANT: Speziale, Pietro
APPLICANT: Joh, Danny
APPLICANT: McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESSES:
ADDRESS: Arnold, White & Durkee
STREET: P. O. Box 4433

CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/731,238
FILING DATE: 10-Dec-2003
CLASSIFICATION: <Unknown>
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE: 21-Jan-1998
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TMMK.189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 14:
US-10-731-238-14
Query Match 88.3%; Score 106; DB 18; Length 21;
Best Local Similarity 95.0%; Pred. No. 7,8e-09;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2 PSYQFGHNSPDPEDTLPK 21
DB 2 PSYQFGHNSVDFEEDTLPK 21
RESULT 15
US-10-731-238-16
Sequence 16, Application US/10731238
Publication No. US20050123552A1
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
APPLICANT: Patti, Joseph M.
APPLICANT: House-Pompeo, Karen L.
APPLICANT: Speziale, Pietro
APPLICANT: Joh, Danny
APPLICANT: McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESSES:
ADDRESS: Arnold, White & Durkee
STREET: P. O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/731,238
FILING DATE: 10-Dec-2003
CLASSIFICATION: <Unknown>

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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/010.317
; FILING DATE: 21-Jan-1998
; APPLICATION NUMBER: US 60/036,139
; FILING DATE: 21-JAN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Hibler, David W.
; REGISTRATION NUMBER: 41,071
; REFERENCE/DOCKET NUMBER: TANK:189
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 512-418-3000
; TELEFAX: 512-474-7577
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 16:
US-10-731-238-16

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Query Match      88.3% Score 106; DB 18; Length 21;
Best Local Similarity 90.5%; Pred No. 7,8e-09;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY      1 KPSYQFGGHSVPFEEDTLPK 21
        |||||||
DB      1 KPSYQFGGHSVPFEEDTLPK 21

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Search completed: October 22, 2005, 11:34:41
Job time : 60.2367 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 22, 2005, 02:23:36 ; Search time 10.5465 seconds
(without alignments)
191.586 Million cell updates/sec

Title: US-10-731-238-24
Perfect score: 120
Sequence: 1 KPSYQFGHNSPDEFDTLPK 21

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :
1: p1r1: *
2: p1r2: *
3: p1r3: *
4: p1r4: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	111	92.5	1018	2	A32192	fibronectin-binding
2	108	90.0	961	2	G90053	hypothetical prote
3	108	90.0	1038	2	H90053	hypothetical prote
4	104	86.7	940	2	S19702	fibronectin-binding
5	49	40.8	468	2	T26081	hypothetical prote
6	48.5	40.4	1091	2	S33850	fibronectin-binding
7	48	40.0	474	2	B84357	serine-CRNA synth
8	48	40.0	2723	2	T03221	probable polykeid
9	46	38.3	216	2	A39926	hypothetical prote
10	46	38.3	364	2	E71433	probable metallopr
11	46	38.3	607	2	T40906	probable ATP-depen
12	46	38.3	665	2	AG1117	transketolase homo
13	46	38.3	665	2	AG1117	transketolase homo
14	45	37.5	188	2	E97318	transcription regu
15	45	37.5	433	2	T01405	vesicle-associated
16	45	37.5	445	2	P90562	hypothetical prote
17	45	37.5	579	1	W2BR34	gene 34 protein -
18	45	37.5	596	2	T26950	hypothetical prote
19	45	37.5	688	2	AH2294	protease II (imp
20	45	37.5	698	2	B97049	anaerobic ribonuc
21	45	37.5	702	2	A96959	oxygen-sensitive r
22	45	37.5	1322	2	A59288	myosin heavy chain
23	45	37.5	1926	2	UC4842	DNA-binding nuclea
24	44.5	37.1	510	1	W2BR47	protein-serine/thr
25	44.5	37.1	1038	2	T15098	hypothetical prote
26	44	36.7	256	2	AE2068	hypothetical prote
27	44	36.7	685	1	HPMS	haemoglobin precur
28	44	36.7	685	1	UC6331	rho-type guanine e
29	44	36.7	781	2	T49472	hormone-sensitive

30	44	36.7	811	2	T36581	probable transmembr
31	44	36.7	928	1	VC6BMC	glycoprotein B pre
32	43	35.8	158	2	F96579	hypothetical prote
33	43	35.8	181	2	A71094	probable 3-octapre
34	43	35.8	303	2	B75485	fructokinase - Dei
35	43	35.8	368	2	T15492	hypothetical prote
36	43	35.8	371	2	A88520	41.8K hypothetical
37	43	35.8	459	2	D34791	interleukin-7 rece
38	43	35.8	486	1	H5E15	betralysin (RC 3.4
39	43	35.8	503	2	T51908	glutathione-disulf
40	43	35.8	504	2	S12164	serralysin (EC 3.4
41	43	35.8	648	2	T43337	polo-like kinase-1
42	43	35.8	690	2	T33321	hypothetical prote
43	43	35.8	705	2	C64406	hypothetical prote
44	43	35.8	758	2	T38811	hypothetical prote
45	43	35.8	823	2	C81835	probable F-type ca

ALIGNMENTS

RESULT 1
A32192
fibronectin-binding protein - Staphylococcus aureus
C/Species: Staphylococcus aureus
C/Date: 31-Jul-1989 #sequence_revision 31-Jul-1989 #text_change 16-Feb-1997
C/Accession: A32192
R/Signaes, C.; Raucel, G.; Joensson, K.; Lindgren, P.E.; Anantharamiah, G.M.; Hoecek, M.
Proc. Natl. Acad. Sci. U.S.A. 86, 699-703, 1989
A/Title: Nucleotide sequence of the gene for a fibronectin-binding protein from Staphyloc
A/Reference number: A32192; MUID:89089898; PMID:2521391
A/Accession: A32192
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-1018 <SIG>
A/Cross-references: GB:J04151
C/Keywords: fibronectin binding

Query Match 92.5%; Score 111; DB 2; Length 1018;
Best Local Similarity 95.2%; Pred. No. 3.6e-09;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KPSYQFGHNSPDEFDTLPK 21
DB 837 KPSYQFGHNSVDFEDTLPK 857

RESULT 2

G90053
hypothetical protein fmb (imported) - Staphylococcus aureus (strain N315)
C/Species: Staphylococcus aureus
C/Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
R/Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguc
ma, A.; Mizutani-U, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.; i
C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
A/Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.
A/Reference number: A89758; MUID:21311952; PMID:11418146
A/Accession: G90053
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-961 <MUR>
A/Cross-references: UNIPROT:Q99RD3; GB:BA000018; PID:G13702452; PIDN:BA843593.1; GSPDB:G
C/Experimental source: strain N315
C/Genetics:
A/Genes: fmb

Query Match 90.0%; Score 108; DB 2; Length 961;
Best Local Similarity 90.5%; Pred. No. 9.9e-09;
Matches 19; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 KPSYQFGHNSPDEFDTLPK 21

Db 784 KPNYQFGHNSVDPEEDTLPK 804

RESULT 3

H90053 hypothetical protein fnb [imported] - Staphylococcus aureus (strain N315)

C:Species: Staphylococcus aureus

C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004

C:Accession: H90053

R:Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Ogura, A.; Mizutani-Uji, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.;

C:Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramoto, K.

Lancet 357, 1225-1240, 2001

A:Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.

A:Reference number: A89758; MUID:21311952; PMID:11418146

A:Accession: H90053

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-1038 <KUR>

A:Cross-references: UNIPROT:Q99RD2; GB:BA000018; PID:g13702453; PIDN:BA843594.1; GSPDB:G

A:Experimental source: strain N315

C:Genetics:

A:Gene: fnb

Query Match 90.0%; Score 108; DB 2; Length 1038;

Best Local Similarity 90.5%; Pred. No. 1.1e-08;

Matches 19; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 KPSYQFGHNSDPFEDTLPK 21

Db 833 KPNYQFGHNSVDPEEDTLPK 853

RESULT 4

S19702 fibronectin-binding protein B - Staphylococcus aureus

C:Species: Staphylococcus aureus

C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004

C:Accession: S19702

R:Joensson, K.; Signaes, C.; Mueller, H.P.; Lindberg, M.

Eur. J. Biochem. 202, 1041-1048, 1991

A:Title: Two different genes encode fibronectin binding proteins in Staphylococcus aureus

A:Reference number: S19702; MUID:92111475; PMID:1837266

A:Accession: S19702

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-940 <JOB>

A:Cross-references: UNIPROT:Q53682; EMBL:X62992; NID:g49040; PIDN:CAA44726.1; PID:G58156

C:Keywords: fibronectin binding

Query Match 86.7%; Score 104; DB 2; Length 940;

Best Local Similarity 85.7%; Pred. No. 4.1e-08;

Matches 18; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 1 KPSYQFGHNSDPFEDTLPK 21

Db 773 KPNYQFGHNSVDPEEDTLPK 793

RESULT 5

T26081 hypothetical protein W02A2.7 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004

C:Accession: T26081

R:Ainscough, R.

Submitted to the EMBL Data Library, November 1996

A:Reference number: Z20148

A:Accession: T26081

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-468 <WIL>

A:Cross-references: UNIPROT:Q9XUB2; EMBL:Z82286; PIDN:CA805310.1; GSPDB:GN00022; CESP:W0;

A:Experimental source: clone W02A2

C:Genetics:

A:Gene: CESP:W02A2.7

A:Map position: 4

A:Introns: 38/3; 212/2; 353/3; 403/2

Query Match 40.8%; Score 49; DB 2; Length 468;

Best Local Similarity 35.0%; Pred. No. 8.9;

Matches 7; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

OY 2 PSYQFGHNSDPFEDTLPK 21

Db 351 PPYQRMHDDDDYQDVPE 370

RESULT 6

S33850 fibronectin-binding protein - Streptococcus dysgalactiae

C:Species: Streptococcus dysgalactiae

C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Jul-2004

C:Accession: S33850, S32632

R:Lindgren, P.E.; McGavin, M.J.; Signaes, C.; Guss, B.; Gurusiddappa, S.; Hoecek, M.; Lit

Eur. J. Biochem. 214, 819-827, 1993

A:Title: Two different genes coding for fibronectin-binding proteins from Streptococcus

A:Reference number: S33850; MUID:93307299; PMID:8319691

A:Accession: S33850

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-1091 <LIN>

A:Cross-references: UNIPROT:Q06556; EMBL:Z22150; NID:g288968; PIDN:CAA80121.1; PID:g28896

Query Match 40.4%; Score 48.5; DB 2; Length 1091;

Best Local Similarity 52.4%; Pred. No. 27;

Matches 11; Conservative 1; Mismatches 8; Indels 1; Gaps 1;

OY 1 KPSYQFGHNSP-DFEEDTLPK 20

Db 977 KPEIMGQSDPDMVEDTLPK 997

RESULT 7

B84357 serine-tRNA synthetase [imported] - Halobacterium sp. NRC-1

C:Species: Halobacterium sp. NRC-1

C:Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004

C:Accession: B84357

R:Ng, W.V.; Kennedy, S.P.; Mahairas, G.G.; Bergquist, B.; Pan, M.; Shukla, H.D.; Lasky, S.

Jung, K.H.; Alam, M.; Freitas, T.

Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000

A:Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ehardt, H.; Lowe, T.M.; Lit

A:Title: Genome sequence of Halobacterium species NRC-1.

A:Reference number: A84160; MUID:20504483; PMID:11016950

A:Accession: B84357

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-474 <STO>

A:Cross-references: UNIPROT:Q9HNU8; GB:AE004437; NID:g10581491; PIDN:AA020222.1; GSPDB:G

C:Genetics:

A:Gene: serS

C:Superfamily: serine-tRNA ligase

Query Match 40.0%; Score 48; DB 2; Length 474;

Best Local Similarity 41.2%; Pred. No. 13;

Matches 7; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

OY 3 SYQFGHNSDPFEDTL 19

Db 234 AYRIGENDADYDDDL 250

RESULT 8

T03221
probable polyketide synthase module 1 - Streptomyces hygroscopicus
C/Species: Streptomyces hygroscopicus
C/Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 12-Jul-2004
C/Accession: T03221
R/Ruan, X.; Stead, D.; Lax, S.; Katz, L.
Gene 203, 1-9, 1997
A/Title: A second type-I PKS gene cluster isolated from Streptomyces hygroscopicus ATCC
A/Reference number: Z14848; MUID:98085969; PMID:9426000
C/Accession: T03221
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-2723 <RUA>
A/Cross-references: UNIPROT:O30479; EMBL:AF007101; NID:g2624946; PIDN:AA38061.1; PID:g2
A/Experimental source: ATCC 29253
C/Keywords: carrier protein
F/54-504/Domain: acetate-CoA ligase homology <ACU>
F/81-949/Domain: acyl carrier protein homology <ACP1>
F/96-1397/Domain: 3-oxoacyl-(acyl-carrier-protein) synthase I homology <OAS>
F/1509-1794/Domain: [acyl-carrier-protein] S-malonyltransferase homology <AMT>
F/2568-2639/Domain: acyl carrier protein homology <ACP2>

Query Match 40.0%; Score 48; DB 2; Length 2723;
Best Local Similarity 45.0%; Pred. No. 90;
Matches 9; Conservative 2; Mismatches 9; Indels 0; Gaps 0;

OY 2 PSYOGGHNPPFEDTLPK 21
DB 367 PSLMVGYNQPEATAPR 386

RESULT 9
A39926
hypothetical protein 1 - chicken anemia virus
C/Species: chicken anemia virus, CAV
C/Date: 17-Jan-1992 #sequence_revision 17-Jan-1992 #text_change 09-Jul-2004
C/Accession: A39926
R/Notoborn, M.H.M.; de Boer, G.F.; van Roozelaar, D.J.; Karreman, C.; Kranenburg, O.; Vo
J. Virol. 65, 3131-3139, 1991
A/Title: Characterization of cloned chicken anemia virus DNA that contains all elements
A/Reference number: A39926; MUID:91237831; PMID:1851873
A/Accession: A39926
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-216 <NOT>
A/Cross-references: UNIPROT:Q99151; GB:M55918; NID:g323250; PIDN:AAA91822.1; PID:g323251
C/Comment: This virus is unclassified.

Query Match 38.3%; Score 46; DB 2; Length 216;
Best Local Similarity 56.2%; Pred. No. 11;
Matches 9; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

OY 2 PSYOGGHNPPFEDTLPK 17
DB 172 PSEEDGTTSSDFED 187

RESULT 10
E71433
probable metalloproteinase (EC 3.4.24.-) - Arabidopsis thaliana
C/Species: Arabidopsis thaliana (mouse-ear cress)
A/Variety: Columbia
C/Date: 03-Aug-1998 #sequence_revision 03-Aug-1998 #text_change 09-Jul-2004
C/Accession: E71433
R/Bevan, M.; Bancroft, I.; Bent, E.; Love, K.; Goodman, H.; Dean, C.; Bergkamp, R.; Dirk
P.; Wedler, H.; Wedler, E.; Wamhoff, R.; Weitzengraber, T.; Pohl, T.M.; Terry, N.; Giel
avanagh, T.; Hempel, S.; Kotter, P.; Entian, K.D.; Kieger, M.; Schaeffer, M.; Funk, B.
Nature 391, 485-488, 1998
A/Authors: Mueller-Auer, S.; Silvey, M.; James, R.; Montfort, A.; Pons, A.; Puigdomenech
erhoff, A.; Moores, T.; Jones, J.D.G.; Eneva, T.; Palme, K.; Benes, V.; Rechman, S.; Ans
C.; Chalwatzis, N.
A/Title: Analysis of 1.9 Mb of contiguous sequence from chromosome 4 of Arabidopsis thal
A/Reference number: A71400; MUID:98121113; PMID:9461215

A/Accession: E71433
A/Status: preliminary; nucleic acid sequence not shown; translation not shown
A/Molecule type: DNA
A/Residues: 1-364 <BEV>
A/Cross-references: UNIPROT:O23507; GB:Z97341; NID:g2244991; PID:e327511; PID:g2245019
C/Genetics:
A/Map position: 4COP9-4G3845
C/Keywords: hydrolase; metalloproteinase; zinc
F/98-315/Domain: matrix metalloproteinase homology <MMP>
F/130-275,279,285/Binding site: zinc, catalytic (Cys, His, His, His) (inhibited) #status
F/275,279,285/Binding site: zinc, catalytic (His) #status predicted
F/276/Active site: Glu #status predicted

Query Match 38.3%; Score 46; DB 2; Length 364;
Best Local Similarity 46.7%; Pred. No. 20;
Matches 7; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

OY 4 YQFGGHNPPFEDTLPK 18
DB 24 YRFKARNTPEAGST 38

RESULT 11
T40906
probable ATP-dependent DNA helicase - fission yeast (Schizosaccharomyces pombe)
C/Species: Schizosaccharomyces pombe
C/Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 04-Apr-2004
C/Accession: T40906
R/Murphy, L.; Harris, D.; Lyne, M.; Rajandream, M.A.; Barrell, B.G.
submitted to the EMBL Data Library, December 1998
A/Reference number: Z21956
A/Accession: T40906
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-607 <MUR>
A/Cross-references: EMBL:AL034490; PIDN:CAA22471.1; GSPDB:GN00068; SPDB:SPCC126.02c
A/Experimental source: strain 972h-; cosmid c126
C/Genetics:
A/Gene: SPDB:SPCC126.02c
A/Map position: 3
A/Introns: 11/3; 72/3; 105/1; 501/3; 571/3
C/Superfamily: Ku70 autoantigen

Query Match 38.3%; Score 46; DB 2; Length 607;
Best Local Similarity 30.8%; Pred. No. 35;
Matches 12; Conservative 4; Mismatches 3; Indels 20; Gaps 1;

OY 3 SYQFGHNPPFEDTLPK 21
DB 457 SYQFGHNPPFEDTLPK 495

RESULT 12
AG1117
transketolase homolog lmo0342 [imported] - Listeria monocytogenes (strain EGD-e)
C/Species: Listeria monocytogenes
C/Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
C/Accession: AG1117
R/Glaeser, P.; Frangoul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloeker,
D.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Duesurget, O.; Entian, K.D.; Fslh, H.;
Science 294, 849-852, 2001
D.; Jones, L.M.; Karst, U.
A/Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapat, G.; Madueno, E.; Maitournam, A.; Mat
ok, C.; Schueller, T.; Simoes, N.; Tietz, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland,
A/Title: Comparative Genomics of Listeria species.
A/Reference number: AB1077; MUID:21537279; PMID:11679669
C/Accession: AG1117
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-665 <GLA>
A/Cross-references: UNIPROT:Q8YA23; GB:NC_003210; PIDN:CAC98421.1; PID:g16409720; GSPDB:C
A/Experimental source: strain EGD-e
C/Genetics:

A:Gene: lnc0342
C:Superfamily: transketolase; thiamin pyrophosphate-binding domain homology

Query Match 38.3%; Score 46; DB 2; Length 665;
Best Local Similarity 40.0%; Pred. No. 39;
Matches 8; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

QY 2 PSYQFGHNSPDPEDTLPK 21
||:|||||
DB 586 PSFPLFDKQSPYKESILPK 605

RESULT 13

A11477
transketolase homolog lnc0360 (imported) - *Listeria innocua* (strain C11P11262)

C:Species: *Listeria innocua*
C>Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004

C/Accession: A11477
R/Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloeker, D.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Feihl, H.; Jones, L.M.; Karet, U.
Science 294, 849-852, 2001

A:Authors: Kretz, J.; Kunz, M.; Kunst, F.; Kurapat, G.; Madueno, E.; Maitournam, A.; Maok, C.; Schlueder, T.; Simoes, N.; Tietzer, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, A./Title: Comparative genomics of *Listeria* species.
A/Reference number: AB1077; MUID:21537279; PMID:11679669

A/Accession: A11477

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-665 <GUA>

A/Cross-references: UNIPROT:Q92RU9; GB:AL592022; PIND:CA095593.1; PID:g16412789; GSPDB:C

A/Experimental source: strain C11P11262

C/Genetics:

A:Gene: lnc0360
C:Superfamily: transketolase; thiamin pyrophosphate-binding domain homology

Query Match 38.3%; Score 46; DB 2; Length 665;
Best Local Similarity 40.0%; Pred. No. 39;
Matches 8; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

QY 2 PSYQFGHNSPDPEDTLPK 21
||:|||||
DB 586 PSFPLFDKQSPYKESILPK 605

RESULT 14

E97318
transcription regulator, MarR/EmrR family (imported) - *Clostridium acetobutylicum*

C:Species: *Clostridium acetobutylicum*
C/Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 09-Jul-2004

C/Accession: E97318
R/Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee, J.; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.
J. Bacteriol. 183, 4823-4839, 2001

A/Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium *Clostridium acetobutylicum*

A/Reference number: A96900; MUID:21359325; PMID:21359325

A/Accession: E97318

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-188 <KUR>

A/Cross-references: UNIPROT:Q97DB6; GB:AE001437; PIND:AAK81336.1; PID:g15026492; GSPDB:C

A/Experimental source: *Clostridium acetobutylicum* ATCC824

C/Genetics:

A:Gene: CAC3406

Query Match 37.5%; Score 45; DB 2; Length 188;
Best Local Similarity 45.0%; Pred. No. 14;
Matches 9; Conservative 1; Mismatches 10; Indels 0; Gaps 0;

QY 1 KPSYQFGHNSPDPEDTLPK 20
||:|||||
DB 143 KULYRFDEGEODGFEDANP 162

RESULT 15

T01405
vesicle-associated protein 1 - sea urchin (*Strongylocentrotus purpuratus*) (fragment)

C:Species: *Strongylocentrotus purpuratus* (purple urchin)
C/Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 09-Jul-2004

C/Accession: T01405

R/Barton, N.R.; Bonder, E.M.; Fishkind, D.J.; Warren, R.H.; Pratt, M.M.

J. Cell Sci. 103, 797-809, 1992

A/Title: A novel vesicle-associated protein (VAP-1) in sea urchin eggs containing multiple

A/Reference number: Z14315; MUID:93123402; PMID:1478972

A/Accession: T01405

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: mRNA

A/Residues: 1-433 <BAR>

A/Cross-references: UNIPROT:Q06155; EMBL:SS2403; NID:9263072; PID:g263073

C/Genetics:

A:Gene: VAP-1

C:Superfamily: loricrin

Query Match 37.5%; Score 45; DB 2; Length 433;
Best Local Similarity 43.8%; Pred. No. 35;
Matches 7; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 2 PSYQFGHNSPDPED 17
||:|||||
DB 288 PTFQFGHGKQDIDVD 303

Search completed: October 22, 2005, 04:13:53
Job time : 11.5465 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: October 22, 2005, 02:23:35 ; Search time 51.4314 Seconds
(without alignments)
209.087 Million cell updates/sec

Title: US-10-731-238-24
Perfect score: 120
Sequence: 1 KPSYQFGHNSPDEEDTLPK 21

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_03:*
1: UniProt_sprot:*
2: UniProt_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	111	92.5	1018	1 FNBA_STRAU	P14738 staphylococ
2	108	90.0	961	2 Q99RD3	Q99RD3 staphylococ
3	108	90.0	961	2 Q7A3J8	Q7A3J8 staphylococ
4	108	90.0	965	2 Q6GJUS	Q6GJUS staphylococ
5	108	90.0	1015	2 Q8NNU7	Q8NNU7 staphylococ
6	108	90.0	1015	2 Q6GCH3	Q6GCH3 staphylococ
7	108	90.0	1038	2 Q99RD2	Q99RD2 staphylococ
8	108	90.0	1038	2 Q7A3J7	Q7A3J7 staphylococ
9	104	86.7	940	2 Q53682	Q53682 staphylococ
10	104	86.7	943	2 Q8NNU8	Q8NNU8 staphylococ
11	104	86.7	957	2 Q6GCH4	Q6GCH4 staphylococ
12	99	82.5	152	2 Q9AEP9	Q9AEP9 staphylococ
13	99	82.5	152	2 Q8KNC4	Q8KNC4 staphylococ
14	54	45.0	500	2 Q7KTI6	Q7KTI6 staphylococ
15	54	45.0	1679	2 Q8VLA5	Q8VLA5 actinobacill
16	53.5	44.6	177	2 Q8VLA2	Q8VLA2 actinobacill
17	53.5	44.6	177	2 Q8VLA4	Q8VLA4 actinobacill
18	53.5	44.6	177	2 Q8VLA2	Q8VLA2 actinobacill
19	53.5	44.6	177	2 Q8VLA2	Q8VLA2 actinobacill
20	52	43.3	190	2 Q8VLA2	Q8VLA2 actinobacill
21	52	43.3	191	2 Q7S7L2	Q7S7L2 neurospora
22	52	43.3	365	2 Q6WST6	Q6WST6 onychomys a
23	52	43.3	369	2 Q6WST5	Q6WST5 onychomys l
24	51.5	42.9	178	2 Q7VND4	Q7VND4 haemophilus
25	51	42.5	812	2 Q7ZP04	Q7ZP04 leprospira
26	51	42.5	812	2 Q8FET0	Q8FET0 leprospira
27	50	41.7	381	2 Q7XXQ8	Q7XXQ8 oryza sativ
28	49	40.8	354	2 Q6V7K6	Q6V7K6 trypanosoma
29	49	40.8	468	2 Q9XUB2	Q9XUB2 caenorhabdi
30	48.5	40.4	1091	2 Q06556	Q06556 streptococ
31	48	40.0	460	1 SYS_HALM1	Q9HJ8 halobacteri

32	48	40.0	466	2 Q6GN22	Q6GN22 xenopus lae
33	48	40.0	476	2 Q97044	Q97044 halocynthia
34	48	40.0	482	2 Q76K22	Q76K22 streptococ
35	48	40.0	668	2 Q75C56	Q75C56 aethya gos
36	48	40.0	2723	2 Q30479	Q30479 streptomyc
37	47.5	39.6	183	2 Q9D8U6	Q9D8U6 mus muscu
38	47	39.2	58	2 Q8BAG9	Q8BAG9 chicken ane
39	47	39.2	118	2 Q91N88	Q91N88 chicken ane
40	47	39.2	118	2 Q91N94	Q91N94 chicken ane
41	47	39.2	118	2 Q91N96	Q91N96 chicken ane
42	47	39.2	118	2 Q91NB5	Q91NB5 chicken ane
43	47	39.2	118	2 Q91NC1	Q91NC1 chicken ane
44	47	39.2	196	2 Q82GD7	Q82GD7 streptomyc
45	47	39.2	216	2 Q91N82	Q91N82 chicken ane

ALIGNMENTS

```

RESULT 1
FNBA_STRAU ID FNBA_STRAU STANDARD; PRT; 1018 AA.
AC P14738;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Fibronectin-binding protein precursor (FNBP).
GN Name=fnbp;
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1280;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NCTC 8325-4;
RX MEDLINE=89098998; PubMed=2521391;
RA Signaes C., Raucel G., Joensson K., Lindgren P.-E.,
  Anantharamaiah G.M., Hoceek M., Lindberg M.;
RT Nucleotide sequence of the gene for a fibronectin-binding protein
RT from Staphylococcus aureus: use of this peptide sequence in the
RT synthesis of biologically active peptides."
RL Proc. Natl. Acad. Sci. U.S.A. 86:699-703(1989).
CC -!- FUNCTION: The ability of bacteria to bind fibronectin has been
  proposed as a virulence factor enabling bacteria to colonize wound
  tissues and blood clots. Binding of plasma fibronectin to the
  bacterial surface might block adhesion receptors on S.aureus, thus
  representing an important defense mechanism against tissue
  invasion.
CC -!- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
  an amide bond (Potential).
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@sib-sib.ch).
CC -----
CC EMBL: J04151; AAA2632.1; -.
CC InterPro: IPR004237; Fn_bind.
CC InterPro: IPR005877; Gpos_YsIRK.
CC InterPro: IPR001899; Gram_pos_anchor.
CC Pfam: PF02986; Fn_bind; 1.
CC Pfam: PF04650; YsIRK_signal; 1.
CC TIGRfam: TIGR01167; LpYTG_anchor; 1.
CC TIGRfam: TIGR01168; YsIRK_signal; 1.
CC PROSITE: PS50847; GRAM_POS_ANCHORING; 1.
CC Cell adhesion; Cell wall; Peptidoglycan-anchor; Repeat; Signal;
  Virulence.
FT SIGNAL 1 36
FT CHAIN 37 985
FT PROPEP 986 1018
  Fibronectin-binding protein.
  Removed by sortase (Potential).

```



```
FT REPEAT 545 574 B-1.
FT REPEAT 575 604 B-2.
FT DOMAIN 745 878 4 X approximate tandem repeats,
  fibronectin-binding domain.
FT REPEAT 745 782 D-1.
FT REPEAT 783 820 D-2.
FT REPEAT 821 859 D-3.
FT DOMAIN 860 878 D-4 (incomplete).
FT REPEAT 879 948 5 X tandem repeats, Pro-rich (WR).
FT REPEAT 893 906 WR 1.
FT REPEAT 907 920 WR 2.
FT REPEAT 921 934 WR 3.
FT REPEAT 935 948 WR 4.
FT SITE 982 986 WR 5.
FT MOD_RES 985 985 LeuXtg scoring signal (Potential).
  pentaglycyl murein peptidoglycan amidated
  threonine (Potential).
SQ SEQUENCE 1018 AA; 111780 MW; 58175E0020E81F1F CRC64;

Query Match 92.5%; Score 111; DB 1; Length 1018;
Best Local Similarity 95.2%; Pred. No. 2.3e-08;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KPSYQFGHNSVDFEEDTLPK 21
Db 837 KPSYQFGHNSVDFEEDTLPK 857

RESULT 2
Q99RD3 PRELIMINARY; PRT; 961 AA.
ID Q99RD3
AC Q99RD3;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE Fibronectin-binding protein homolog.
DE Name=fnb3; OrderedLocNames=SAV2502;
OS Staphylococcus aureus (strain Mu50 / ATCC 700699).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=158879;
  [1]
  SEQUENCE FROM N.A.
  MEDLINE=21311952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2;
  Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
  Cui L., Oguchi A., Aoki K.-I., Nagai Y., Iian J.-Q., Ito T.,
  Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,
  Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
  Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
  Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
  Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
  "Whole genome sequencing of methicillin-resistant Staphylococcus
  aureus.";
  Lancet 357:1225-1240(2001).
  -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
  an amide bond (By similarity).
  EMBL; AP003365; BAB5864.1; -.
  CC CC
  DR GO; GO:0009986; C:cell surface; IEA.
  DR GO; GO:0005618; C:cell wall; IEA.
  DR GO; GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
  DR GO; GO:0016020; C:membrane; IEA.
  DR GO; GO:0007155; P:cell adhesion; IEA.
  DR InterPro; IPR008966; Adhes_bact.
  DR InterPro; IPR004237; Fn_bind.
  DR InterPro; IPR005877; Gpos_YsIRK.
  DR Pfam; PF02986; Fn_bind; 1.
  DR Pfam; PF00746; Gram_pos_anchor; 1.
  DR TIGRFAMS; TIGR01167; LpXTG_anchor; 1.
  DR TIGRFAMS; TIGR01168; YsIRK_signal; 1.
  DR PROSITE; PS0847; GRAM_POS_ANCHORING; 1.
  KW Cell wall; Complete proteome; Peptidoglycan-anchor.
  SQ SEQUENCE 961 AA; 106010 MW; 364940F884EA4101 CRC64;

Query Match 90.0%; Score 108; DB 2; Length 961;
Best Local Similarity 90.5%; Pred. No. 6.2e-08;
Matches 19; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KPSYQFGHNSVDFEEDTLPK 21
Db 784 KPSYQFGHNSVDFEEDTLPK 804

RESULT 3
Q7A3J8 PRELIMINARY; PRT; 961 AA.
ID Q7A3J8
AC Q7A3J8;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE FmbB protein.
DE Name=fnb3; OrderedLocNames=SA2290;
OS Staphylococcus aureus (strain N315).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=158879;
  [1]
  SEQUENCE FROM N.A.
  MEDLINE=21311952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2;
  Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
  Cui L., Oguchi A., Aoki K.-I., Nagai Y., Iian J.-Q., Ito T.,
  Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,
  Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
  Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
  Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
  Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
  "Whole genome sequencing of methicillin-resistant Staphylococcus
  aureus.";
  Lancet 357:1225-1240(2001).
  -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
  an amide bond (By similarity).
  EMBL; AP003365; BAB43593.1; -.
  CC CC
  DR GO; GO:0009986; C:cell surface; IEA.
  DR GO; GO:0005618; C:cell wall; IEA.
  DR GO; GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
  DR GO; GO:0016020; C:membrane; IEA.
  DR GO; GO:0007155; P:cell adhesion; IEA.
  DR InterPro; IPR008966; Adhes_bact.
  DR InterPro; IPR005877; Fn_bind.
  DR InterPro; IPR004237; Gpos_YsIRK.
  DR Pfam; PF02986; Fn_bind; 1.
  DR Pfam; PF00746; Gram_pos_anchor; 1.
  DR TIGRFAMS; TIGR01167; LpXTG_anchor; 1.
  DR TIGRFAMS; TIGR01168; YsIRK_signal; 1.
  DR PROSITE; PS0847; GRAM_POS_ANCHORING; 1.
  KW Cell wall; Complete proteome; Peptidoglycan-anchor.
  SQ SEQUENCE 961 AA; 106010 MW; 364940F884EA4101 CRC64;

Query Match 90.0%; Score 108; DB 2; Length 961;
Best Local Similarity 90.5%; Pred. No. 6.2e-08;
Matches 19; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KPSYQFGHNSVDFEEDTLPK 21
Db 784 KPSYQFGHNSVDFEEDTLPK 804

RESULT 4
Q6GDUS PRELIMINARY; PRT; 965 AA.
ID Q6GDUS
AC Q6GDUS;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
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```
DR PROSITE; PS50847; GRAM_POS_ANCHORING; 1.
KW Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ SEQUENCE 961 AA; 106010 MW; 364940F884EA4101 CRC64;

Query Match 90.0%; Score 108; DB 2; Length 961;
Best Local Similarity 90.5%; Pred. No. 6.2e-08;
Matches 19; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KPSYQFGHNSVDFEEDTLPK 21
Db 784 KPSYQFGHNSVDFEEDTLPK 804

RESULT 3
Q7A3J8 PRELIMINARY; PRT; 961 AA.
ID Q7A3J8
AC Q7A3J8;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE FmbB protein.
DE Name=fnb3; OrderedLocNames=SA2290;
OS Staphylococcus aureus (strain N315).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=158879;
  [1]
  SEQUENCE FROM N.A.
  MEDLINE=21311952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2;
  Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
  Cui L., Oguchi A., Aoki K.-I., Nagai Y., Iian J.-Q., Ito T.,
  Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,
  Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
  Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
  Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
  Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
  "Whole genome sequencing of methicillin-resistant Staphylococcus
  aureus.";
  Lancet 357:1225-1240(2001).
  -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
  an amide bond (By similarity).
  EMBL; AP003365; BAB43593.1; -.
  CC CC
  DR GO; GO:0009986; C:cell surface; IEA.
  DR GO; GO:0005618; C:cell wall; IEA.
  DR GO; GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
  DR GO; GO:0016020; C:membrane; IEA.
  DR GO; GO:0007155; P:cell adhesion; IEA.
  DR InterPro; IPR008966; Adhes_bact.
  DR InterPro; IPR005877; Fn_bind.
  DR InterPro; IPR004237; Gpos_YsIRK.
  DR Pfam; PF02986; Fn_bind; 1.
  DR Pfam; PF00746; Gram_pos_anchor; 1.
  DR TIGRFAMS; TIGR01167; LpXTG_anchor; 1.
  DR TIGRFAMS; TIGR01168; YsIRK_signal; 1.
  DR PROSITE; PS0847; GRAM_POS_ANCHORING; 1.
  KW Cell wall; Complete proteome; Peptidoglycan-anchor.
  SQ SEQUENCE 961 AA; 106010 MW; 364940F884EA4101 CRC64;

Query Match 90.0%; Score 108; DB 2; Length 961;
Best Local Similarity 90.5%; Pred. No. 6.2e-08;
Matches 19; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KPSYQFGHNSVDFEEDTLPK 21
Db 784 KPSYQFGHNSVDFEEDTLPK 804

RESULT 4
Q6GDUS PRELIMINARY; PRT; 965 AA.
ID Q6GDUS
AC Q6GDUS;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
```

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DR 05-JUL-2004 (TREMblrel. 27, Last sequence update)
DE Fibronectin-binding protein.
OS Name=fndb; OrderedLocuNames=SB2580;
OC Staphylococcus aureus (strain MRSA252).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OK NCBI_TaxID=282458;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=15213324; DOI=10.1073/pnas.0402521101;
RA Holden M.T.G., Fell E.J., Lindsey J.A., Peacock S.J., Day N.P.J.,
RA Enright M.C., Foster T.J., Moore C.E., Hurst L., Atkin R., Barron A.,
RA Bason N., Bentley S.D., Chillingworth C., Chillingworth T.,
RA Churcher C., Clark L., Corton C., Cronin A., Doggett J., Dowd L.,
RA Felwell T., Hance Z., Harris B., Hauser H., Holtroyd S., Jagels K.,
RA James K.D., Leonard N., Line A., Mayes R., Moulé S., Mungall K.,
RA Ormond D., Quail M.A., Rabinowitch E., Rutherford K.M., Sanders M.,
RA Sharp S., Simmonds M., Stevens K., Whitehead S., Barrett B.G.,
RA Spratt B.G., Parkhill J.;
RT "Complete genomes of two clinical Staphylococcus aureus strains:
RT evidence for the rapid evolution of virulence and drug resistance.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:9786-9791(2004).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC an amide bond (By similarity).
CC EMBL: BX571856; CAG41560.1; -.
DR GO: GO:0009986; C:cell surface; IEA.
DR GO: GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO: GO:0016020; C:membrane; IEA.
DR GO: GO:007155; P:cell adhesion; IEA.
DR InterPro: IPR008966; Adhes_bact.
DR InterPro: IPR004237; Fn_bind.
DR InterPro: IPR001899; Gram_pos_anchor.
DR Pfam: PF02986; Fn_bind; 1.
DR Pfam: PF00746; Gram_pos_anchor; 1.
DR TIGRFAMs: TIGR01167; LPXTG_anchor; 1.
DR TIGRFAMs: TIGR01168; YSIRK_signal; 1.
DR PROSITE: PS50847; GRAM_POS_ANCHORING; 1.
KM Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ SEQUENCE 965 AA; 10561 MW; 2982E32164D0551 CRC64;

Query Match 90.0%; Score 108; DB 2; Length 965;
Best Local Similarity 90.5%; Pred. No. 6.3e-08;
Matches 19; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 KPSYQFGHNSVDFEDTLPK 21
DB 802 KENYQFGHNSVDFEDTLPK 822

RESULT 5
ID Q8NUU7 PRELIMINARY; PRT; 1015 AA.
AC Q8NUU7;
DT 01-OCT-2002 (TREMblrel. 22, Created)
DT 01-OCT-2002 (TREMblrel. 22, Last sequence update)
DT 01-OCT-2003 (TREMblrel. 25, Last annotation update)
DE Fnb protein.
GN Name=fndb; OrderedLocuNames=NM2421;
OS Staphylococcus aureus (strain NM2).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OK NCBI_TaxID=196620;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=NM2;
RX MEDLINE=22040717; PubMed=12044378; DOI=10.1016/S0140-6736(02)08713-5;
RA Baba T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Ogunchi A.,
RA Nagai Y., Iwama N., Amano K., Naito T., Kuroda H., Cui L.,
RA Yamamoto K., Hiramatsu K.;
RA "Genome and virulence determinants of high virulence community-
RT acquired MRSA.";
RL Lancet 359:1819-1827(2002).

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CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC an amide bond (By similarity).
CC EMBL: AP004830; BAB96286.1; -.
DR GO: GO:0009986; C:cell surface; IEA.
DR GO: GO:0005618; C:cell wall; IEA.
DR GO: GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO: GO:0016020; C:membrane; IEA.
DR GO: GO:007155; P:cell adhesion; IEA.
DR InterPro: IPR008966; Adhes_bact.
DR InterPro: IPR004237; Fn_bind.
DR InterPro: IPR005877; Gpos_YSIRK.
DR InterPro: IPR001899; Gram_pos_anchor.
DR Pfam: PF02986; Fn_bind; 1.
DR Pfam: PF00746; Gram_pos_anchor; 1.
DR TIGRFAMs: TIGR01167; LPXTG_anchor; 1.
DR TIGRFAMs: TIGR01168; YSIRK_signal; 1.
DR PROSITE: PS50847; GRAM_POS_ANCHORING; 1.
KM Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ SEQUENCE 1015 AA; 11145 MW; D0F9281BB64D4D2 CRC64;

Query Match 90.0%; Score 108; DB 2; Length 1015;
Best Local Similarity 90.5%; Pred. No. 6.7e-08;
Matches 19; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 KPSYQFGHNSVDFEDTLPK 21
DB 838 KENYQFGHNSVDFEDTLPK 858

RESULT 6
ID Q6G6H3 PRELIMINARY; PRT; 1015 AA.
AC Q6G6H3;
DT 05-JUL-2004 (TREMblrel. 27, Created)
DT 05-JUL-2004 (TREMblrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMblrel. 27, Last annotation update)
DE Fibronectin-binding protein.
GN OrderedLocuNames=SA52388;
OS Staphylococcus aureus (strain MSSA476).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OK NCBI_TaxID=282459;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=15213324; DOI=10.1073/pnas.0402521101;
RA Holden M.T.G., Fell E.J., Lindsey J.A., Peacock S.J., Day N.P.J.,
RA Enright M.C., Foster T.J., Moore C.E., Hurst L., Atkin R., Barron A.,
RA Bason N., Bentley S.D., Chillingworth C., Chillingworth T.,
RA Churcher C., Clark L., Corton C., Cronin A., Doggett J., Dowd L.,
RA Felwell T., Hance Z., Harris B., Hauser H., Holtroyd S., Jagels K.,
RA James K.D., Leonard N., Line A., Mayes R., Moulé S., Mungall K.,
RA Ormond D., Quail M.A., Rabinowitch E., Rutherford K.M., Sanders M.,
RA Sharp S., Simmonds M., Stevens K., Whitehead S., Barrett B.G.,
RA Spratt B.G., Parkhill J.;
RT "Complete genomes of two clinical Staphylococcus aureus strains:
RT evidence for the rapid evolution of virulence and drug resistance.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:9786-9791(2004).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC an amide bond (By similarity).
CC EMBL: BX571857; CAG44202.1; -.
DR GO: GO:0009986; C:cell surface; IEA.
DR GO: GO:0005618; C:cell wall; IEA.
DR GO: GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO: GO:0016020; C:membrane; IEA.
DR GO: GO:007155; P:cell adhesion; IEA.
DR InterPro: IPR008966; Adhes_bact.
DR InterPro: IPR004237; Fn_bind.
DR InterPro: IPR005877; Gpos_YSIRK.
DR InterPro: IPR001899; Gram_pos_anchor.
DR Pfam: PF02986; Fn_bind; 1.
DR Pfam: PF00746; Gram_pos_anchor; 1.
DR TIGRFAMs: TIGR01167; LPXTG_anchor; 1.

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DR TIGRFAMS; TIGR01168; YSIRK_signal; 1.
AC PROSITE; PS50847; GRAM_POS_ANCHORING; 1.
DR Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ SEQUENCE 1015 AA; 111145 MW; D0F9281BB64D4D2 CRC64;

Query Match 90.0%; Score 108; DB 2; Length 1015;
Best Local Similarity 90.5%; Pred. No. 6.7e-08;
Matches 19; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KPSYQFGHNSVDFEEDTLPK 21
Db 833 KPNYQFGHNSVDFEEDTLPK 853

RESULT 7
Q99RD2 PRELIMINARY; PRT; 1038 AA.
ID 099RD2;
AC 099RD2;
DT 01-JUN-2001 (TRENBLrel. 17, Last sequence update)
DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)
DE Fibronectin-binding protein homolog.
GN Name=fnb; OrderedLocustNames=SAV2503;
OS Staphylococcus aureus (strain Mu50 / ATCC 700639).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
CX NCBI_TaxID=158878;

SEQUENCE FROM N.A.
RP STRAIN=Mu50 / ATCC 700639;
RX MEDLINE=21311952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2;
RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Iino J.-O., Ito T.,
RA Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hoshoyama A.,
RA Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
RA Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
RA Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
RA Hattori M., Ogasawara N., Hayashi H., Hiramoto K.;
RA "Whole genome sequencing of methicillin-resistant Staphylococcus
RT aureus.";
RT Lancet 357:1225-1240(2001).
RL -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC an amide bond (by similarity).
CC EMBL; AP003137; BAB3594.1; -.
DR PIR; H90053; H90053.
DR GO; GO:0009986; C:cell surface; IEA.
DR GO; GO:0005618; C:cell wall; IEA.
DR GO; GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0007155; P:cell adhesion; IEA.
DR InterPro; IPR008966; Adhes_bact.
DR InterPro; IPR004237; Fn_bind.
DR InterPro; IPR005877; Gpos_YSIRK.
DR InterPro; IPR001899; Gram_pos_anchor.
DR Pfam; PF02986; Fn_bind; 1.
DR Pfam; PF00746; Gram_pos_anchor; 1.
DR TIGRFAMS; TIGR01167; LpxTG_signal; 1.
DR TIGRFAMS; TIGR01168; YSIRK_signal; 1.
DR PROSITE; PS50847; GRAM_POS_ANCHORING; 1.
DR Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ SEQUENCE 1038 AA; 113618 MW; 666BF6BF2BFEB12 CRC64;

Query Match 90.0%; Score 108; DB 2; Length 1038;
Best Local Similarity 90.5%; Pred. No. 6.8e-08;
Matches 19; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KPSYQFGHNSVDFEEDTLPK 21
Db 833 KPNYQFGHNSVDFEEDTLPK 853

RESULT 8
Q7A3J7

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ID Q7A3J7 PRELIMINARY; PRT; 1038 AA.
AC Q7A3J7;
DT 05-JUL-2004 (TRENBLrel. 27, Created)
DT 05-JUL-2004 (TRENBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TRENBLrel. 27, Last annotation update)
DE Fnb protein.
GN Name=fnb; OrderedLocustNames=SA2291;
OS Staphylococcus aureus (strain N315).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
CX NCBI_TaxID=158878;

SEQUENCE FROM N.A.
RP MEDLINE=21311952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2;
RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Iino J.-O., Ito T.,
RA Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hoshoyama A.,
RA Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
RA Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
RA Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
RA Hattori M., Ogasawara N., Hayashi H., Hiramoto K.;
RA "Whole genome sequencing of methicillin-resistant Staphylococcus
RT aureus.";
RT Lancet 357:1225-1240(2001).
RL -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC an amide bond (by similarity).
CC EMBL; AP003137; BAB3594.1; -.
DR GO; GO:0009986; C:cell surface; IEA.
DR GO; GO:0005618; C:cell wall; IEA.
DR GO; GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0007155; P:cell adhesion; IEA.
DR InterPro; IPR008966; Adhes_bact.
DR InterPro; IPR004237; Fn_bind.
DR InterPro; IPR005877; Gpos_YSIRK.
DR InterPro; IPR001899; Gram_pos_anchor.
DR Pfam; PF02986; Fn_bind; 1.
DR Pfam; PF00746; Gram_pos_anchor; 1.
DR TIGRFAMS; TIGR01167; LpxTG_signal; 1.
DR TIGRFAMS; TIGR01168; YSIRK_signal; 1.
DR PROSITE; PS50847; GRAM_POS_ANCHORING; 1.
DR Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ SEQUENCE 1038 AA; 113618 MW; 666BF6BF2BFEB12 CRC64;

Query Match 90.0%; Score 108; DB 2; Length 1038;
Best Local Similarity 90.5%; Pred. No. 6.8e-08;
Matches 19; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KPSYQFGHNSVDFEEDTLPK 21
Db 833 KPNYQFGHNSVDFEEDTLPK 853

RESULT 9
Q53682 PRELIMINARY; PRT; 940 AA.
ID Q53682;
AC Q53682;
DT 01-NOV-1996 (TRENBLrel. 01, Created)
DT 01-NOV-1996 (TRENBLrel. 01, Last sequence update)
DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)
DE Fibronectin binding protein B.
GN Name=fnbB;
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
CX NCBI_TaxID=1280;

SEQUENCE FROM N.A.
RP STRAIN=8325-4;
RX MEDLINE=92111475; PubMed=1837266;
RA Jonsson K., Sigas C., Muller H.P., Lindberg M.;
RA "Two different genes encode fibronectin binding proteins in
RT Staphylococcus aureus. The complete nucleotide sequence and
RT characterization of the second gene.";
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RL Eur. J. Biochem. 202;1041-1048(1991).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC an amide bond (By similarity).
DR EMBL, X62992; CAA44726.1; -.
DR PIR, S19702; S19702.
DR HSSP, Q53653; IN67.
DR GO, GO:0009986; C:cell surface; IEA.
DR GO, GO:0005618; C:cell wall; IEA.
DR GO, GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO, GO:0016020; C:membrane; IEA.
DR GO, GO:0007155; P:cell adhesion; IEA.
DR InterPro, IPR008966; Adhes_bact.
DR InterPro, IPR004237; Fn_bind.
DR InterPro, IPR005877; Gpos_YsIRK.
DR Pfam, PF02986; Fn_bind; 2
DR Pfam, PF00746; Gram_pos_anchor; 1.
DR Pfam, PF04650; YsIRK_signal; 1.
DR TIGRFAMs, TIGR01167; LPXTG_anchor; 1.
DR TIGRFAMs, TIGR01168; YsIRK_signal; 1.
DR PROSITE, PSS0847; GRAM_POS_ANCHORING; 1.
DR Cell wall, Peptidoglycan-anchor.
SQ SEQUENCE 940 AA; 10355 MW; E35FBBCA907AE345 CRC64;

Query Match 86.7%; Score 104; DB 2; Length 940;
Best Local Similarity 85.7%; Pred. No. 2.6e-07;
Matches 18; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KPSYQFGHNSPDFFEDTLPK 21
Db 773 KENYQFGHNSVDFEDTLQ 793

RESULT 10
Q8NU8 PRELIMINARY; PRT; 943 AA.
ID Q8NU8;
AC Q8NU8; 01-OCT-2002 (T-EMBLrel. 22, Created)
DT 01-OCT-2002 (T-EMBLrel. 22, Last sequence update)
DT 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)
DE FnBb protein.
GN Name=fnbB; OrderedlocusNames=MW2420;
OS Staphylococcus aureus (strain MW2).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=196620;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MW2;
RX MEDLINE=22040717; PubMed=12044378; DOI=10.1016/S0140-6736(02)08713-5;
RA Baba T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Oguchi A.,
RA Nagai Y., Iwano N., Asano K., Naimi T., Kuroda H., Cui L.,
RA Yamamoto K., Hiratake K.;
RT "Genome and virulence determinants of high virulence community-
RT acquired MRSA."
RL Lancet 359:1819-1827(2002).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC an amide bond (By similarity).
DR EMBL, AB004830; BAB96285.1; -.
DR HSSP, Q53653; IN67.
DR GO, GO:0009986; C:cell surface; IEA.
DR GO, GO:0005618; C:cell wall; IEA.
DR GO, GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO, GO:0016020; C:membrane; IEA.
DR GO, GO:0007155; P:cell adhesion; IEA.
DR InterPro, IPR008966; Adhes_bact.
DR InterPro, IPR004237; Fn_bind.
DR InterPro, IPR005877; Gpos_YsIRK.
DR Pfam, PF02986; Fn_bind; 1.
DR Pfam, PF00746; Gram_pos_anchor; 1.
DR TIGRFAMs, TIGR01167; LPXTG_anchor; 1.
DR TIGRFAMs, TIGR01168; YsIRK_signal; 1.

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DR PROSITE, PSS0847; GRAM_POS_ANCHORING; 1.
KW Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ SEQUENCE 943 AA; 104537 MW; DA8A5F31947E1B8A CRC64;

Query Match 86.7%; Score 104; DB 2; Length 943;
Best Local Similarity 85.7%; Pred. No. 2.6e-07;
Matches 18; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KPSYQFGHNSPDFFEDTLPK 21
Db 780 KENYQFGHNSVDFEDTLQ 800

RESULT 11
Q6G6H4 PRELIMINARY; PRT; 957 AA.
ID Q6G6H4;
AC Q6G6H4; 05-JUL-2004 (T-EMBLrel. 27, Created)
DT 05-JUL-2004 (T-EMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (T-EMBLrel. 27, Last annotation update)
DE Fibronectin-binding protein.
GN Name=fnbB; OrderedlocusNames=SAS2387;
OS Staphylococcus aureus (strain MSSA476).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=282459;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=15213324; DOI=10.1073/pnas.0402521101;
RA Holden M.T.G., Fell E.J., Lindsey J.A., Peacock S.J., Day N.P.J.,
RA Enright M.C., Foster T.J., Moore C.E., Hurst L., Atkin R., Barron A.,
RA Bason N., Bentley S.D., Chillingworth C., Chillingworth T.,
RA Churcher C., Clark L., Corton C., Cronin A., Doggett J., Dowd L.,
RA Felwell T., Hance Z., Harris B., Hauser H., Holtroyd S., Jagels K.,
RA James K.D., Lennard N., Line A., Mayes R., Moule S., Mungall K.,
RA Ormond D., Quail M.A., Rabinowitsch E., Rutherford K.M., Sanders M.,
RA Sharp S., Simmonds M., Stevens K., Whitehead S., Barrett B.G.,
RA Spratt B.G., Parkhill J.;
RT "Complete genomes of two clinical Staphylococcus aureus strains:
RT evidence for the rapid evolution of virulence and drug resistance."
RL Proc. Natl. Acad. Sci. U.S.A. 101:9786-9791(2004).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC an amide bond (By similarity).
DR EMBL, BS71857; CAG44201.1; -.
DR GO, GO:0009986; C:cell surface; IEA.
DR GO, GO:0005618; C:cell wall; IEA.
DR GO, GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO, GO:0016020; C:membrane; IEA.
DR GO, GO:0007155; P:cell adhesion; IEA.
DR InterPro, IPR008966; Adhes_bact.
DR InterPro, IPR004237; Fn_bind.
DR InterPro, IPR005877; Gpos_YsIRK.
DR InterPro, IPR001899; Gram_pos_anchor.
DR Pfam, PF02986; Fn_bind; 1.
DR Pfam, PF00746; Gram_pos_anchor; 1.
DR Pfam, PF04650; YsIRK_signal; 1.
DR TIGRFAMs, TIGR01167; LPXTG_anchor; 1.
DR TIGRFAMs, TIGR01168; YsIRK_signal; 1.
DR PROSITE, PSS0847; GRAM_POS_ANCHORING; 1.
KW Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ SEQUENCE 957 AA; 105980 MW; 28F8BA7FFDFD3EAF CRC64;

Query Match 86.7%; Score 104; DB 2; Length 957;
Best Local Similarity 85.7%; Pred. No. 2.6e-07;
Matches 18; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KPSYQFGHNSPDFFEDTLPK 21
Db 780 KENYQFGHNSVDFEDTLQ 800

RESULT 12
Q9AEP9 PRELIMINARY; PRT; 152 AA.
ID Q9AEP9

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AC 09AEP9:
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE Fibronectin-binding protein (Fragment).
GN Name=fnb;
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1280;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CMRSA-1;
RX MEDLINE=21246681; PubMed=11349044;
RX DOI=10.1128/IAI.59.6.3791-3799.2001;
RX Rice K., Huebner M., Vaz D., McGavin M.J.;
RT "Variance in fibronectin binding and fnb locus polymorphisms in
RT Staphylococcus aureus: identification of antigenic variation in a
RT fibronectin binding protein adhesion of the epidemic CMRSA-1 strain of
RT methicillin-resistant S. aureus."
RL Infect. Immun. 69:3791-3799(2001).
DR EMBL; AY029184; AKJ1588.1; -.
FT NON TER 1
FT 152
SQ SEQUENCE 152 AA; 17193 MW; CFA3913CB11C025 CRC64;

Query Match 82.5%; Score 99; DB 2; Length 152;
Best Local Similarity 85.7%; Pred. No. 1.9e-07;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 1 KPSYQFGCHNSPDEDTLPK 21
    |||||
Db 130 KPSYQFGCHNGDFVEDTLPK 150

RESULT 13
08KNCA PRELIMINARY; PRT; 500 AA.
ID 08KNCA
AC 08KNCA:
DT 01-OCT-2002 (TREMBlrel. 22, Created)
DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE Calu22.
GN Name=calu22;
OS Micromonospora echinospora (Micromonospora purpurea).
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Micromonosporineae; Micromonosporaceae; Micromonospora.
OX NCBI_TaxID=1877;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NRRL 15839;
RX MEDLINE=22171114; PubMed=12183629; DOI=10.1126/science.1072105;
RX Ahlert J., Shepard E., Lomovskaya N., Zazopoulos E., Scalfa A.,
RX Bachmann B.O., Huang K., Fomstein L., Cziorny A., Whitwam R.E.,
RX Farret C.M., Thorson J.S.;
RT "The calicheamicin gene cluster and its iterative type I enediynes
RT PKS."
RL Science 297:1173-1176(2002).
DR EMBL; AF497482; AAM94801.1; -.
DR GO; GO:0003824; P:catalytic activity; IEA.
DR GO; GO:0050897; P:cobalt ion binding; IEA.
DR GO; GO:0005506; P:iron ion binding; IEA.
DR InterPro; IPR006158; B12-binding.
DR InterPro; IPR011007; B12-binding.
DR InterPro; IPR000345; CytC_heme_BS.
DR InterPro; IPR006638; E1p3/MlaB/NifB.
DR InterPro; IPR007197; Radical SAM.
DR Pfam; PF02310; B12-binding; I.
DR Pfam; PF04055; Radical SAM; I.
DR SMART; SM00729; E1p3; I.
DR PROSITE; PS00190; CYTOCHROME_C; UNKNOWN_1.
SQ SEQUENCE 500 AA; 55211 MW; 7C7D42827AF4713A CRC64;

Query Match 45.0%; Score 54; DB 2; Length 500;
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Best Local Similarity 69.2%; Pred. No. 9.2;
Matches 9; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Oy 7 GCHNSPDEDTLPK 19
    |||||
Db 443 GCHNSPDEDTLPK 455

RESULT 14
07KTI6 PRELIMINARY; PRT; 1679 AA.
ID 07KTI6
AC 07KTI6:
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE CG8086-PD.
GN ORFNames=CG8086;
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;
RX Adams M.D., Celnik S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RX Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,
RX George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RX Sutton G.G., Wortman J.R., Blazer V.H., Yandell M.D., Zhang Q., Chen L.X.,
RX Brandon R.C., Rogers Y.H., Blazer R.G., Champe M., Pfeiffer B.D.,
RX Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Gabor G.L.,
RX Abril J.F., Agbayani A., An H.J., Andrews-Fiankoch C., Baldwin D.,
RX Ballew R.M., Bau A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RX Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RX Borkova D., Botchan M.R., Bouck J., Brokstein P., Broctier P.,
RX Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RX Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RX de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RX Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RX Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RX Foster C., Gabrielian A.B., Garg N.S., Gelbart W.M., Glasser K.,
RX Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RX Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RX Hostin D., Houston K.A., Howland T.J., Wei M.H., Ibegwam C.,
RX Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RX Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RX Laeko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RX Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RX Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RX Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RX Nelson D.R., Nelson K.A., Nixon K., Pollard J., Puri V., Reese M.G.,
RX Palazzolo M., Pittman G.S., Pan S., Saunders R.D., Scheefer F., Shen H.,
RX Reiter K., Remington K., Sanders M., Skupski M.P., Smith T.,
RX Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RX Splitter E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RX Svrtkars R., Tecor C., Turner R., Venter E., Wang A.H., Wang X.,
RX Wang Z.Y., Wasserman D.A., Weinstein G.M., Weisenbach J.,
RX Williams S.M., Woodgerter, Worley K.C., Wu D., Yang S., Yao Q.A., Ye J.,
RX Yeh R.P., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RX Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RX Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster."
RL Science 287:2185-2195(2000).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=22426065; PubMed=12537568;
RX Celisner S.E., Wheeler D.A., Krommiller B., Carlson J.W., Halpern A.,
RX Patel S., Adams M., Champagne M., Dugan M., Prie E., Hodgson A.,
RX George R.A., Hoskins R.A., Laverly T., Muzny D.M., Nelson C.R.,
RX Pacled J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,
RX Svrtkars R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,
RX Weinstein G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.;
RT "Finishing a whole-genome shotgun: Release 3 of the Drosophila
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RT melanogaster euchromatic genome sequence."
RL Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=22426070; PubMed=12537573;
RA Kaminker J.S., Bergman C.M., Krommiller B., Carlson J., Svirskas R.,
RA Patel S., Fries E., Wheeler D.A., Lewis S.E., Rubin G.M.,
RA Ashburner M., Celisner S.E.;
RT "The transposable elements of the Drosophila melanogaster euchromatin:
RT a genomics perspective."
RL Genome Biol. 3:RESEARCH0084-RESEARCH0084(2002).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=22426069; PubMed=12537572;
RA Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
RA Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochuk S.E.,
RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,
RA Betencourt B.R., Celisner S.E., de Grey A.D., Drysdale R.A.,
RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
RA Lewis S.E.;
RT "Annotation of the Drosophila melanogaster euchromatic genome: a
RT systematic review."
RL Genome Biol. 3:RESEARCH0083-RESEARCH0083(2002).
RN [5]
RP SEQUENCE FROM N.A.
RG FlyBase;
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
RN [6]
RP SEQUENCE FROM N.A.
RG FlyBase;
RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AE003620; AAS64658.1; -.
DR InterPro: IPR010736; DUF1309.
DR Pfam: PF07004; DUF1309; 36.
SQ SEQUENCE 1679 AA; 183390 MW; 7EAD11800F72AF1 CRC64;

Query Match 45.0%; Score 54; DB 2; Length 1679;
Best Local Similarity 52.9%; Pred. No. 38;
Matches 9; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 2 PSYFGGHSPPDEEDT 18
DB 643 PAYSFGKNDPKVENNT 659

RESULT 15
Q8VL45 PRELIMINARY; PRT; 177 AA.
AC Q8VL45;
DT 01-MAR-2002 (TREMBlrel. 20, Created)
DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE Disulfide bond formation protein E.
GN Name=dbpE;
OS Actinobacillus pleuropneumoniae (Haemophilus pleuropneumoniae).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
OC Pasteurellaceae; Actinobacillus.
OX NCBT_Taxid=715;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21442124; PubMed=11557155; DOI=10.1016/S0378-1135(01)00414-X;
RA Chiers K., Van Overbeke I., Donne E., Baele M., Ducatelle R.,
RA De Baere T., Hasebrouck F.;
RT "Detection of Actinobacillus pleuropneumoniae in cultures from nasal
RT and tonsillar swabs of pigs by a PCR assay based on the nucleotide
RT sequence of a dsbE-like gene."
RL Vet. Microbiol. 83:147-159(2001).
RN [2]
RP SEQUENCE FROM N.A.
RA Chiers K., Van Overbeke I., Ducatelle R., Hasebrouck F.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF458433; AAL67774.1; -.

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DR EMBL; AF458430; AAL67768.1; -.
DR EMBL; AF458432; AAL67772.1; -.
DR GO; GO:0005489; F:electron transporter activity; IEA.
DR GO; GO:0006118; P:electron transport; IEA.
DR PRINTS; PR00421; THIOREDOXIN.
DR Prodom; PD003679; Thioredoxin like; 1.
DR PROSITE; PS00194; THIOREDOXIN; UNKNOWN_1.
KM Redox-active center.
SQ SEQUENCE 177 AA; 20447 MW; E20E2609326405A2 CRC64;

Query Match 44.6%; Score 53.5; DB 2; Length 177;
Best Local Similarity 61.1%; Pred. No. 3.3;
Matches 11; Conservative 3; Mismatches 3; Indels 1; Gaps 1;

QY 4 YQFGGHSPPDEEDTLPK 21
DB 153 YQKGGYN-PDFEODFLPR 169

Search completed: October 22, 2005, 04:10:12
Job time : 55.4314 secs

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OM protein - protein search, using SW model

Run on: October 25, 2005, 18:43:07 ; Search time 59.0973 Seconds
(without alignments)
137.434 Million cell updates/sec

Title: US-10-731-238-25

Perfect score: 118
Sequence: 1 KPSYQFGHNSVPFEDTLPK 21

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	118	100.0	21	AAW65681 Fibronec
2	110	93.2	21	AAW65665 Fibronec
3	110	93.2	22	AAW65679 Fibronec
4	110	93.2	37	AAW65672 Fibronec
5	110	93.2	38	AAW65682 Fibronec
6	110	93.2	134	AAW65687 S. aureus
7	110	93.2	139	AAW65688 Fibronec
8	110	93.2	1018	AAW65689 Fibronec
9	110	93.2	1018	AAW65690 Fibronec
10	110	93.2	1018	AAW65691 Fibronec
11	110	93.2	1018	AAW65692 Fibronec
12	110	93.2	1018	AAW65693 Fibronec
13	110	93.2	1018	AAW65694 Fibronec
14	110	93.2	1018	AAW65695 Fibronec
15	110	93.2	1018	AAW65696 Fibronec
16	110	93.2	1018	AAW65697 Fibronec
17	110	93.2	1018	AAW65698 Fibronec
18	110	93.2	1018	AAW65699 Fibronec
19	110	93.2	1018	AAW65700 Fibronec
20	110	93.2	1018	AAW65701 Fibronec
21	110	93.2	1018	AAW65702 Fibronec
22	110	93.2	1018	AAW65703 Fibronec
23	110	93.2	1018	AAW65704 Fibronec
24	110	93.2	1018	AAW65705 Fibronec
25	110	93.2	1018	AAW65706 Fibronec

26	104	88.1	21	AAW65674	AAW65674 Fibronec
27	103	87.3	21	AAW65685	AAW65685 Fibronec
28	103	87.3	21	AAW65687	AAW65687 Fibronec
29	103	87.3	77	AAW65679	AAW65679 S. aureus
30	103	87.3	101	AAW65672	AAW65672 D3D4 poly
31	103	87.3	113	AAW65679	AAW65679 D3D4 poly
32	103	87.3	124	AAW65682	AAW65682 D3D4 poly
33	103	87.3	128	AAW65687	AAW65687 D3D4 poly
34	103	87.3	130	AAW65688	AAW65688 Fibronec
35	103	87.3	130	AAW65689	AAW65689 Fibronec
36	103	87.3	130	AAW65690	AAW65690 Fibronec
37	103	87.3	130	AAW65691	AAW65691 Fibronec
38	103	87.3	134	AAW65692	AAW65692 S. aureus
39	103	87.3	162	AAW65693	AAW65693 D3D4 poly
40	103	87.3	164	AAW65694	AAW65694 Fibronec
41	103	87.3	174	AAW65695	AAW65695 Fibronec
42	103	87.3	174	AAW65696	AAW65696 Fibronec
43	103	87.3	181	AAW65697	AAW65697 Fibronec
44	103	87.3	181	AAW65698	AAW65698 Fibronec
45	103	87.3	559	AAW65683	AAW65683 Staphyloc

ALIGNMENTS

RESULT 1
AAW65681
AAW65681 standard; peptide; 21 AA.
XX
AC AAW65681;
XX
DT 16-OCT-1998 (first entry)
XX
DE Fibronecin binding protein-derived peptide #25.
XX
KW microbial surface components recognising adhesive matrix molecule;
KW MSCRAMM; fibronecin; fibronecin-binding protein; antibody; epitope;
KW antibiotic; bacterial infection; antibiotic-resistant strain.
XX
OS Synthetic.
OS Staphylococcus aureus.
XX
PN MO9813389-A2.
XX
PD 23-JUL-1998.
XX
PF 21-JAN-1998; 98WC-US001222.
XX
PR 21-JAN-1997; 97US-0036139P.
XX
PA (TEXA) UNTV TEXAS A & M SYSTEM.
XX
PI Hoeoek M, Patti JM, House-Pompeo KL, Speciale P, Joh D;
PI Mogavin MJ;
XX
XX WPI, 1998-413816/35.
XX
XX Example 8; Page 101; 201pp; English.
XX
XX The invention relates to antibodies that bind to a fibronecin-binding
XX domain of a fibronecin-binding protein, and inhibit binding of the
XX protein to a fibronecin. Also claimed are: (1) isolated peptides of a
XX fibronecin-binding protein that do not bind to fibronecin; (2) fusion
XX protein containing at least one peptide of a fibronecin-binding protein
XX linked to a second amino acid sequence; (3) nucleic acid encoding the
XX isolated peptide of (1). Antibodies, the isolated peptides of (1) and the
XX nucleic acids are all useful for immunisation (active or passive) and (by
XX inhibiting binding of bacteria to fibronecin) for preventing or treating
XX infection in humans or other animals, particularly by staphylococci or

CC streptococci, e.g. meningitis, otitis media, pneumonia, endocarditis,
 CC mastitis in cattle, abortion in horses and many others. Since the
 CC antibodies block binding of bacteria, they should be effective against
 CC antibiotic-resistant strains, and may replace antibiotic therapy or
 CC increase its effectiveness. Sequences AAW65670-90 represent a series of
 CC synthetic peptides based on the D3 repeat of *S. aureus* fibronectin
 CC binding protein A. They were synthesised to contain a proline residue at
 CC each position throughout the sequence (ie a proline scan)

SO Sequence 21 AA;

Query Match 100.0%; Score 118; DB 2; Length 21;
 Best Local Similarity 100.0%; Pred. No. 2.9e-12;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 KPSYQFGHNSVPFEEDTLPK 21
 |||||
 1 KPSYQFGHNSVPFEEDTLPK 21

RESULT 2
 ID AAW65665
 AAW65665 standard; peptide; 21 AA.

AC AAW65665;
 DT 16-OCT-1998 (first entry)

DE Fibronectin binding protein-derived peptide #9.

KM microbial surface components recognising adhesive matrix molecule;
 KM MSCRAMM; fibronectin; fibronectin-binding protein; antibody; epitope;
 KM antibiotic; bacterial infection; antibiotic-resistant strain.

OS Synthetic.
 OS *Staphylococcus aureus*.

PN WO9831389-A2.

PD 23-JUL-1998.

PF 21-JAN-1998; 98WO-US001222.

PR 21-JAN-1997; 97US-0036139P.

PA (TEXA) UNIV TEXAS A & M SYSTEM.

PI Hoecek M, Patti JM, House-Pompeo KL, Speciale P, Joh D;
 PI McGavin MJ;

DR WPI; 1998-413816/35.

PT Antibody that binds to fibronectin-binding protein, preventing its
 PT binding to fibronectin - used to treat or prevent bacterial infection,
 PT especially by *Staphylococci* and *Streptococci*.

PS Example 2; Page 92; 201pp; English.

CC The invention relates to antibodies that bind to a fibronectin-binding
 CC domain of a fibronectin-binding protein, and inhibit binding of the
 CC protein to fibronectin. Also claimed are: (1) isolated peptides of a
 CC fibronectin-binding protein that do not bind to fibronectin; (2) fusion
 CC protein containing at least one peptide of a fibronectin-binding protein
 CC linked to a second amino acid sequence; (3) nucleic acid encoding the
 CC isolated peptide of (1). Antibodies, the isolated peptides of (1) and the
 CC nucleic acids are all useful for immunisation (active or passive) and (by
 CC inhibiting binding of bacteria to fibronectin) for preventing or treating
 CC infection in humans or other animals, particularly by *Staphylococci* or
 CC streptococci, e.g. meningitis, otitis media, pneumonia, endocarditis,
 CC mastitis in cattle, abortion in horses and many others. Since the
 CC antibodies block binding of bacteria, they should be effective against
 CC antibiotic-resistant strains, and may replace antibiotic therapy or
 CC increase its effectiveness. Sequences AAW65659-68 represent synthetic

CC epitopes from the fibronectin binding domains DU and DI-D4 of the S.

CC *aureus* fnbA gene

XX Sequence 21 AA;

SO Query Match 93.2%; Score 110; DB 2; Length 21;
 Best Local Similarity 95.2%; Pred. No. 6.2e-11;
 Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 KPSYQFGHNSVPFEEDTLPK 21
 |||||
 1 KPSYQFGHNSVPFEEDTLPK 21

RESULT 3
 ID AAR21340
 AAR21340 standard; peptide; 22 AA.

AC AAR21340;

DT 25-MAR-2003 (revised)

DT 15-JUN-1992 (first entry)

DE Fibronectin binding protein.

KM FMBP; wound infection reduction; vaccination; mastitis;
 KM *Staphylococcal* infections; D3.

OS Synthetic.

PN WO9202555-A.

PD 20-FEB-1992.

PF 10-AUG-1990; 90SE-00002617.

PR 10-AUG-1990; 90SE-00002617.

PA (ALFA) ALFA LAVAL AGRIC INT AB.

PI Hook M, McGavin M, Raucel G;

DR WPI; 1992-080035/10.

PT New fibronectin binding peptide - combines with fusion peptide to form
 PT large antigen, used in immunisation, diagnosis and for treating wounds.

PS Claim 1; Page 22; 33pp; English.

CC The sequence comprises amino acids 17-33 of a tandem repeat, designated
 CC D3 of the fibronectin binding site of *Staphylococcus aureus* 8325-4 FMBP.
 CC The N-terminal DK may be replaced with H or K, and the C-terminal LKP may
 CC be replaced by either L, LP, or OH. The peptides were synthesised using
 CC standard methods and purified using reverse phase HPLC. The appropriate
 CC fractions were dialysed and lyophilised. Peptide sequencing was performed
 CC and the peptides digested and chemically modified by dihydroxypropylation
 CC of the amino side chain of lysine. The carboxylic side chains were
 CC converted to glycine methyl esters. The phenyl side chains of tyrosine
 CC residues were oxidised. Chemically modified peptide D3 was compared to
 CC unmodified D3. Lysine and tyrosine modifications only partially
 CC diminished its activity whereas modification of aspartic/glutamic
 CC residues resulted in complete loss of activity. The peptide can be used
 CC for the prevention or reduction of the risk of wound infection. The
 CC peptide can be used to create a large antigen for vaccinating ruminants
 CC against mastitis caused by *Staphylococcal* infections. It can also be used
 CC to diagnose *Staphylococcal* infections using ELISA or DNA probes. (Updated
 CC on 25-MAR-2003 to correct PA field.)

SO Sequence 22 AA;

Query Match 93.2%; Score 110; DB 2; Length 22;
 Best Local Similarity 95.2%; Pred. No. 6.5e-11;
 Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KPSYQFGHNSVPFEDTLPK 21
 |||||
 DB 2 KPSYQFGHNSVPFEDTLPK 22

RESULT 4
 AAB91958
 ID AAB91958 standard; peptide; 37 AA.
 AC AAB91958;
 XX
 DT 22-JUN-2001 (first entry)
 XX
 DE Fibrinectin fragment and fibrin related peptide SEQ ID NO:1134.
 XX
 KM Protection; endogenous therapeutic peptide; peptidase; conjugation;
 KM blood component; modification; succinimidy; maleimido group; amino;
 KM hydroxyl; thiol; hormone; growth factor; neurotransmitter.
 XX
 OS Homo sapiens.
 OS Synthetic.
 PN WO200069900-A2.
 XX
 PD 23-NOV-2000.
 XX
 PF 17-MAY-2000; 2000WO-US013576.
 XX
 PR 17-MAY-1999; 99US-0134406P.
 PR 10-SEP-1999; 99US-0153406P.
 PR 15-OCT-1999; 99US-0159783P.
 XX
 PA (CONJ-) CONJUCHEM INC.
 XX
 PI Brion DP, Ezrin AM, Milner PG, Holmes DL, Thibaudau K;
 XX
 DR WPI; 2001-112059/12.
 XX
 PT Modifying and attaching therapeutic peptides to albumin prevents
 PT peptidase degradation, useful for increasing length of in vivo activity.
 XX
 PS Disclosure; Page 566; 733pp; English.
 XX
 CC The present invention describes a modified therapeutic peptide (I)
 CC comprising a therapeutically active amino acid region (II) and a
 CC reactive group (II') (e.g. succinimidy) and maleimido groups) attached to
 CC a less therapeutically active amino acid region (IV), which covalently
 CC bonds with amino/hydroxyl/thiol groups on blood components to form a
 CC peptidase stabilised therapeutic peptide composed of 3-50 amino acids.
 CC (I) are useful for modifying therapeutic peptides e.g. hormones, growth
 CC factors and neurotransmitters, to protect them from peptidase activity in
 CC vivo for the treatment of various disorders. Endogenous therapeutic
 CC peptides are not suitable as drug candidates as they require frequent
 CC administration due to rapid degradation by peptidases in the body.
 CC Modifying and attaching therapeutic peptides to albumin prevents or
 CC reduces the action of peptidases to increase length of activity (half
 CC life) and specificity as bonding to large molecules decreases
 CC intracellular uptake and interference with physiological processes.
 CC AAB90829 to AAB92441 represent peptides which can be used in the
 CC exemplification of the present invention
 CC
 SQ Sequence 37 AA;

Query Match 93.2%; Score 110; DB 4; Length 37;
 Best Local Similarity 95.2%; Pred. No. 1.2e-10;
 Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KPSYQFGHNSVPFEDTLPK 21
 |||||
 DB 16 KPSYQFGHNSVPFEDTLPK 36

RESULT 5
 AAP80662
 ID AAP80662 standard; protein; 38 AA.
 XX
 AC AAP80662;
 XX
 DT 25-MAR-2003 (revised)
 DT 07-OCT-1990 (first entry)
 XX
 DE Protein with fibronectin binding ability.
 XX
 KM Hybrid DNA molecule; fibronectin binding; mastitis; ruminants;
 KM wound infection.
 XX
 OS Staphylococcus aureus.
 XX
 PN EP294349-A.
 XX
 PD 07-DEC-1988.
 XX
 PF 30-MAY-1988; 88EP-00850188.
 XX
 PR 01-JUN-1987; 87SE-00002272.
 XX
 PA (ALFA) ALFA LAVAL AGRIC INT AB.
 XX
 PI Lindberg MK, Signas LC, Wadstrom TM, Froman G;
 XX
 DR WPI; 1988-347978/49.
 DR N-PSDB; AAN81099.
 XX
 PT Hybrid DNA encoding Staphylococcus aureus fibronectin binding protein -
 PT useful for immunisation and topical application to prevent staphylococcal
 PT infections.
 XX
 PS Claim 11; Page 12; 23pp; English.
 XX
 CC The peptide has fibronectin binding ability. It is useful for immunising
 CC ruminants against staphylococcal mastitis, pref. when used at 0.5-5
 CC micrograms/kg, using 3 doses given at 1-3 week intervals; for topical
 CC application to prevent wound infection, using an isotonic saline soln. of
 CC concn. 25-250 micrograms/ml; and, when immobilised on a carrier, for
 CC diagnosing staphylococcal infections. (Updated on 25-MAR-2003 to correct
 CC PF field.) (Updated on 25-MAR-2003 to correct PA field.)
 CC
 SQ Sequence 38 AA;

Query Match 93.2%; Score 110; DB 1; Length 38;
 Best Local Similarity 95.2%; Pred. No. 1.2e-10;
 Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KPSYQFGHNSVPFEDTLPK 21
 |||||
 DB 17 KPSYQFGHNSVPFEDTLPK 37

RESULT 6
 AAY29087
 ID AAY29087 standard; protein; 134 AA.
 XX
 AC AAY29087;
 XX
 DT 28-SEP-1999 (first entry)
 XX
 DE S. aureus fibronectin binding protein A (FnBA) binding domain.
 XX
 KM Bovine herpes virus-2; BHV-2; cytokine; immune response; immunogen; IL;
 KM interleukin; colony stimulating factor; CSF; interferon; IFN; TNF;
 KM tumour necrosis factor; recombinant virus; vaccine; mucosal disease;
 KM mastitis; breast cancer; stress-induced disease; binding domain; FnBA;
 KM fibronectin binding protein.
 XX
 OS Staphylococcus aureus.

XX MO9916892-A1.
 XX 08-APR-1999.
 XX 29-SEP-1998; 98MO-GB002927.
 XX 29-SEP-1997; 97GB-00020633.
 XX (UYBR-) UNIV BRISTOL.
 XX Bradley AJ, Duffae WPH;
 XX WPI; 1999-255101/21.
 XX N-PSDB; AAX91504.
 XX New bovine herpes virus-2 vectors.
 XX Example 2; Fig 8A-B; 130pp; English.
 XX The invention provides bovine herpes virus-2 (BHV-2) based vectors that
 CC comprise at least one cytokine-encoding DNA sequence. The expression of
 CC cytokines in mammals can up-regulate immune responses to the immunogens.
 CC The cytokine is selected from interleukins (IL), colony stimulating
 CC factors (CSF), interferons (IFN) and tumour necrosis factors (TNF). The
 CC BHV-2 based vector or recombinant virus can be used as vaccines. They can
 CC be used for preventing or treating a mucosal disease in a subject, e.g.
 CC ruminants, cattle, sheep, goats, dogs, cats, horses, or man, particularly
 CC mastitis in cows or breast cancers in humans. They can also be used for
 CC preventing or treating a stress-induced disease. The present sequence
 CC represents the binding domain of a previously published S. aureus
 CC fibronectin binding protein A (FnBA) sequence. The FnB binding domain
 CC gene sequence FNBA, cloned for use in this invention has 97.8 percent
 CC identity when compared to the previously published FNBA and FNBB gene
 CC sequences

XX Sequence 134 AA;

Query Match 93.2%; Score 110; DB 2; Length 134;
 Best Local Similarity 95.2%; Pred. No. 5.3e-10;
 Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 KPSYQFGGHSVPFEDTLPK 21
 |||||
 DB 93 KPSYQFGGHSVPFEDTLPK 113

RESULT 7

AAW31556
 ID AAW31556 standard; protein; 139 AA.

AAW31556;

DT 27-AUG-2003 (revised)
 DT 25-MAR-2003 (revised)
 DT 21-MAY-1998 (first entry)

DE Fibronectin-binding MSCRAMM derivative pOD.

XX Fibronectin; pOD; collagen binding protein; sepsis; infection;
 KW microbial surface component recognising adhesive matrix molecule; MSCRAMM;
 KW adhesin; vaccine; immunisation; diagnosis; therapy; mastitis.

OS Staphylococcus aureus.

XX Key Location/Qualifiers

FT Peptide 1..12 /note= "vector pOE30-derived peptide"

PN MO9743314-A2.

XX 20-NOV-1997.

XX

PF 14-MAY-1997; 97MO-US0080210.
 XX 16-MAY-1996; 96US-0017678P.
 XX (TEXA) UNIV TEXAS A & M SYSTEM.
 PA (UABR-) UAB RES FOUND.
 XX Hoeoek W, Patti JM, House-Pompeo K, Sthanam N, Symersky J;
 XX WPI; 1998-008801/01.
 XX Antibody that interacts with collagen binding domain of Staphylococcal
 PT cna gene product - useful to prevent bacterial sepsis in animal infected
 PT with Staphylococcus aureus.
 XX Disclosure; Page 91; 143pp; English.

XX This protein comprises Staphylococcus aureus fibronectin-binding
 CC microbial surface component recognising adhesive matrix molecule (MSCRAMM)
 CC derivative pOD, plus a vector-derived N-terminal peptide. The invention
 CC relates to claimed nucleic acid sequences (see AAT93436-38) encoding S.
 CC aureus collagen binding protein (CBP) epitopes M17, M31 and M55 (see
 CC AAW31552-54) that confer protection against S. aureus infection. CBP
 CC protein and antigenic epitopes are contemplated for use in the treatment
 CC of pathological infections, especially to prevent bacterial adhesion to
 CC collagen. The epitopes are also contemplated for use in the preparation
 CC of vaccines and as carrier proteins for the prevention of S. aureus
 CC in the formulation of compositions for the prevention of S. aureus
 CC infection. pOF33 and pOD (see AAW31556) were used to raise anti-MSCRAMM
 CC polyclonal antibodies used in passive immunisation against bovine
 CC mastitis. (Updated on 25-MAR-2003 to correct PI field.) (Updated on 27-
 CC AUG-2003 to correct OS field.)

XX Sequence 139 AA;

Query Match 93.2%; Score 110; DB 2; Length 139;
 Best Local Similarity 95.2%; Pred. No. 5.5e-10;
 Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 KPSYQFGGHSVPFEDTLPK 21
 |||||
 DB 107 KPSYQFGGHSVPFEDTLPK 127

RESULT 8

AAP82115
 ID AAP82115 standard; protein; 1018 AA.

AAP82115;

DT 25-MAR-2003 (revised)
 DT 05-JAN-1990 (first entry)

DE Fibronectin binding protein.

XX Fibronectin binding protein; S. aureus; immunisation; mastitis; ruminants;
 KW wound infection; diagnosis.

OS Staphylococcus aureus.

XX EP294349-A.

PD 07-DEC-1988.

PF 30-MAY-1988; 88EP-00850188.

PR 01-JUN-1987; 87SE-00002272.

PA (ALFA) ALFA LAVAL AGRIC INT AB.

XX Lindberg MK, Signas LC, Wadstrom TM, Froman G;

XX WPI; 1988-347978/49.

XX

DR P-PSDB; AAP82115.

XX Hybrid DNA encoding Staphylococcus aureus fibronectin binding protein -
PT useful for immunisation and topical application to prevent staphylococcal
PT infections.

XX Disclosure; Fig. 8A.1-8A.2; 23pp; English.

XX The S.aureus fibronectin binding protein may be included in a hybrid
CC protein. The protein may be used to immunise ruminants against
CC staphylococcal mastitis, pref. when given at 0.5-5 microg/kg, using 3
CC doses at 1-3 week intervals; and for topical applicn. to prevent wound
CC infection, pref. using isotonic saline soln. of concn. 25-250 microg/mg.
CC The DNA encoding the binding protein and the hybrid protein may be
CC immobilised on a carrier and used to diagnose staphylococcal infections.
CC (updated on 25-MAR-2003 to correct PA field.)

XX Sequence 1018 AA;

Query Match 93.2%; Score 110; DB 1; Length 1018;
Best Local Similarity 95.2%; Pred. No. 5.6e-09;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KPSYQFGCHNSVDFEEDTLPK 21
DB 837 KPSYQFGCHNSVDFEEDTLPK 857

RESULT 9
AAU37245
ID AAU37245 standard; protein; 1018 AA.

XX AAU37245;
XX 14-FEB-2002 (first entry)

DE Staphylococcus aureus cellular proliferation protein #415.

XX Antisense; prokaryotic cellular proliferation protein; antibiotic;
KW antibacterial; drug design.

XX Staphylococcus aureus.

XX WO200170955-A2.

XX 27-SEP-2001.

XX 21-MAR-2001; 2001WO-US009180.

XX 21-MAR-2000; 2000US-0191078P.

XX 23-MAY-2000; 2000US-0206848P.

XX 26-MAY-2000; 2000US-0207727P.

XX 23-OCT-2000; 2000US-0242578P.

XX 27-NOV-2000; 2000US-0253625P.

XX 22-DEC-2000; 2000US-0257931P.

XX 16-FEB-2001; 2001US-0269308P.

XX (ELIT-) ELITRA PHARM INC.

XX Haselbeck R, Ohlsen KL, Zyskind JW, Wall D, Trawick JD, Carr GJ;
PI Yamamoto RT, Xu HH;
XX WPI; 2001-611495/70.
XX N-PSDB; AASS5104.

PS Example 3; SEQ ID NO 12838; 511pp; English.

CC The invention relates to antisense inhibitors of genes essential to
CC prokaryotic cellular proliferation, their use in identifying the genes,
CC their use in the discovery of novel antibiotics, the essential genes

CC themselves and the encoded proteins. The prokaryotes used are Escherichia
CC coli, Staphylococcus aureus, Salmonella typhi, Klebsiella pneumoniae,
CC pseudomonas aeruginosa and Enterococcus faecalis. The invention is also
CC useful for the identification of potential new targets for antibiotic
CC development. The antisense nucleic acids can also be used to identify
CC proteins used in proliferation, to express these proteins, and to obtain
CC antibodies capable of binding to the expressed proteins. The proteins can
CC be used to screen compounds in rational drug discovery programmes. The
CC antisense nucleic acid sequence is also useful to screen for homologous
CC nucleic acids which are required for cell proliferation in a wide variety
CC of organisms. The present sequence represents an essential prokaryotic
CC cellular proliferation protein. Note: The sequence data for this patent
CC did not form part of the printed specification, but was obtained in
CC electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences

XX Sequence 1018 AA;

Query Match 93.2%; Score 110; DB 4; Length 1018;
Best Local Similarity 95.2%; Pred. No. 5.6e-09;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KPSYQFGCHNSVDFEEDTLPK 21
DB 837 KPSYQFGCHNSVDFEEDTLPK 857

RESULT 10
AAU34301
ID AAU34301 standard; protein; 1018 AA.

XX AAU34301;

XX 14-FEB-2002 (first entry)

DE Staphylococcus aureus cellular proliferation protein #577.

XX Antisense; prokaryotic cellular proliferation protein; antibiotic;
KW antibacterial; drug design.

XX Staphylococcus aureus.

XX WO200170955-A2.

XX 27-SEP-2001.

XX 21-MAR-2001; 2001WO-US009180.

XX 21-MAR-2000; 2000US-0191078P.

XX 23-MAY-2000; 2000US-0206848P.

XX 26-MAY-2000; 2000US-0207727P.

XX 23-OCT-2000; 2000US-0242578P.

XX 27-NOV-2000; 2000US-0253625P.

XX 22-DEC-2000; 2000US-0257931P.

XX 16-FEB-2001; 2001US-0269308P.

XX (ELIT-) ELITRA PHARM INC.

XX Haselbeck R, Ohlsen KL, Zyskind JW, Wall D, Trawick JD, Carr GJ;
PI Yamamoto RT, Xu HH;
XX WPI; 2001-611495/70.
XX N-PSDB; AASS2160.

PS Example 3; SEQ ID NO 5797; 511pp; English.

CC The invention relates to antisense inhibitors of genes essential to
CC prokaryotic cellular proliferation, their use in identifying the genes,
CC their use in the discovery of novel antibiotics, the essential genes
CC themselves and the encoded proteins. The prokaryotes used are Escherichia

CC coli, *Staphylococcus aureus*, *Salmonella typhi*, *Klebsiella pneumoniae*,
 CC *Pseudomonas aeruginosa* and *Enterococcus faecalis*. The invention is also
 CC useful for the identification of potential new targets for antibiotic
 CC development. The antisense nucleic acids can also be used to identify
 CC proteins used in proliferation, to express these proteins, and to obtain
 CC antibodies capable of binding to the expressed proteins. The proteins can
 CC be used to screen compounds in rational drug discovery programmes. The
 CC antisense nucleic acid sequence is also useful to screen for homologous
 CC nucleic acids which are required for cell proliferation in a wide variety
 CC of organisms. The present sequence represents an essential prokaryotic
 CC cellular proliferation protein. Note: The sequence data for this patent
 CC did not form part of the printed specification, but was obtained in
 CC electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 1018 AA;

Query Match 93.2%; Score 110; DB 4; Length 1018;
 Best Local Similarity 95.2%; Pred. No. 5.6e-09;
 Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KPSYQFGGHSVPFEEDTLPK 21
 |||||
 Db 837 KPSYQFGGHSVPFEEDTLPK 857

RESULT 11
 ID ABJ18922 standard; protein; 1018 AA.

XX AC ABJ18922;
 XX 06-MAR-2003 (first entry)

DE Pathogen specific antigen related staphylococcal protein SEQ ID No 68.
 XX
 XX Antibacterial; virucide; fungicide; protozoaside; cytostatic; anti-HIV;
 KW hyperimmune; serum-reactive; antigen; pathogen; tumour; allergen;
 KW auto-immunity; vaccine; staphylococcal infection; antibody; cancer;
 KW autoimmune disease; HIV; hepatitis.

XX OS Staphylococcus sp.
 XX PN WO200259148-A2.
 XX PD 01-AUG-2002.
 XX PF 21-JAN-2002; 2002WO-EP000546.
 XX PR 26-JAN-2001; 2001AT-00000130.
 XX PA (CIST-) CISTEM BIOTECHNOLOGIES GMBH.

PI Meinke A, Nagy E, Von Ahse U, Klade C, Henics T, Zauner W;
 PI Mih D, Vytvyetka O, Etz H, Dyla A, Weichart T, Hafner M;
 PI Tempelmaier B;
 XX WPI; 2003-075410/07.

XX Identifying, isolating and producing hyperimmune serum-reactive antigens
 PT from a pathogen, for preparing vaccine or medicament for treating or
 PT preventing e.g. staphylococcal infections, comprises providing antibody
 PT preparation.

XX Example 7; Page 157; 252pp; English.

XX The invention relates to a novel method for identifying, isolating and
 CC producing hyperimmune serum-reactive antigens from a pathogen, tumour,
 CC allergen, a tissue or host prone to auto-immunity, where the antigens are
 CC used in a vaccine, comprises providing antibody preparation from a plasma
 CC pool of a type of animal, or individual sera with antibodies against the
 CC specific pathogen, tumour, allergen, tissue or host prone to auto-
 CC immunity. The hyperimmune serum-reactive antigens comprising any of the

CC 62 sequences of 53-2261 amino acids fully defined in the specification,
 CC or their hyperimmune fragments are useful for the manufacture of a
 CC pharmaceutical preparation, particularly a vaccine against staphylococcal
 CC infections or colonisation against *S. aureus* or *S. epidermidis*. The
 CC preparation of antibodies is useful for the manufacture of a medicament
 CC for treating or preventing staphylococcal infections or colonisation
 CC against *S. aureus* or *S. epidermidis*. The antibody preparations may also
 CC be used for diagnostic and imaging purposes. Other conditions that can be
 CC treated include cancer, autoimmune diseases or infections caused by viral
 CC (e.g. HIV, hepatitis A, B or C), fungal or protozoan pathogens. This
 CC sequence represents a staphylococcal protein relating to the method for
 CC identifying and producing pathogen specific antigens of the invention

XX SQ Sequence 1018 AA;

Query Match 93.2%; Score 110; DB 6; Length 1018;
 Best Local Similarity 95.2%; Pred. No. 5.6e-09;
 Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KPSYQFGGHSVPFEEDTLPK 21
 |||||
 Db 837 KPSYQFGGHSVPFEEDTLPK 857

RESULT 12
 ID ABM72537 standard; protein; 1018 AA.

XX AC ABM72537;
 XX 20-NOV-2003 (first entry)

DE Staphylococcus aureus protein #1777.
 XX
 XX Antibacterial; vaccine; gene therapy; infection; sepsis; diagnosis;
 KW enzymatic assay; antibiotic target.

XX OS Staphylococcus aureus.
 XX PN WO200294868-A2.
 XX PD 28-NOV-2002.
 XX PF 27-MAR-2002; 2002WO-IB002637.
 XX PR 27-MAR-2001; 2001GB-00007661.
 XX PA (CHIR-) CHIRON SPA.

PI Maignani V, Mora M, Scarselli M;
 DR WPI; 2003-120786/11.
 DR N-PSDB; ACF74097.

XX New Staphylococcus aureus protein, useful as a vaccine for treating or
 PT preventing Staphylococcal infection, specifically an infection caused by
 PT *S. aureus*, e.g. sepsis.

XX Claim 1; SEQ ID NO 3554; 49pp; English.

XX The invention relates to novel genes and encoded proteins from
 CC Staphylococcus aureus. A composition comprising the *S. aureus* protein, a
 CC nucleic acid encoding the protein, or an antibody to the protein, is
 CC useful as a pharmaceutical, particularly as a vaccine for treating or
 CC preventing infection due to Staphylococcus bacteria, specifically an
 CC infection caused by *S. aureus*. The composition is particularly useful for
 CC treating or preventing sepsis in a patient. The composition can also be
 CC used for diagnostics. The protein is also used in an assay for enzymatic
 CC studies and as a target for antibiotics. This sequence represents one of
 CC the novel *S. aureus* proteins of the invention

XX SQ Sequence 1018 AA;

Query Match 93.2%; Score 110; DB 6; Length 1018;
 Best Local Similarity 95.2%; Pred. No. 5,6e-09;
 Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KPSYQFGHNSVPFEDTLPK 21
 |||||
 DB 837 KPSYQFGHNSVPFEDTLPK 857

RESULT 13
 AAM89806
 ID AAM89806 standard; protein; 1027 AA.

AC AAM89806;

DT 16-MAR-1999 (first entry)

XX Staphylococcus aureus protein SEQ ID #5254.

XX Computer readable medium; vaccine; S. aureus infection; immunodetection;
 XX cellulitis; eyelid infection; food poisoning; osteomyelitis; therapy;
 KW skin infection; surgical wound infection; scalded skin syndrome;
 KW toxic shock syndrome.

XX Staphylococcus aureus.

XX EP786519-A2.

XX 30-JUL-1997.

XX 07-JAN-1997; 97EP-00100117.

XX 05-JAN-1996; 96US-0009861P.

XX (HUMA-) HUMAN GENOME SCI INC.

XX Kunech CA, Choi GH, Barash SC, Dillon PJ, Fannon MR, Rosen CA;

XX WPI; 1997-374922/35.

PT Polynucleotide(s) and proteins derived from Staphylococcus aureus -
 PT stored on computer readable medium and used in the production of anti-
 PT S. aureus vaccines.

PS Claim 23; Page 3263-3267; 3271pp; English.

XX This sequence represents a Staphylococcus aureus protein sequence of the
 CC invention. The DNA sequences encoding the S. aureus proteins are recorded
 CC on a computer readable medium, preferably selected from a floppy or hard
 CC disk, random access memory (RAM), read-only memory (ROM) or CD-ROM.
 CC Homology searches using the S. aureus DNA sequences allows putative
 CC functions to be assigned so that protein-encoding or regulatory regions
 CC of commercial, therapeutic or industrial importance can be obtained.
 CC Specifically, sequences which are likely to encode antigens have been
 CC identified and these polypeptides can be used in a vaccine composition
 CC against S. aureus infection. The polypeptides can also be used in a kit
 CC for the immunodetection of S. aureus in a sample. S. aureus is implicated
 CC in numerous human diseases, including cellulitis, eyelid infections, food
 CC poisoning, osteomyelitis, skin and surgical wound infections, scalded
 CC skin syndrome, toxic shock syndrome, etc. Organisms transformed with the
 CC DNA sequences can be used for recombinant production of the polypeptides.
 CC The new DNA sequences (and their fragments) are useful as primers or
 CC probes for isolating homologues of any of the 5191 S. aureus DNA sequences
 CC contained on the computer readable medium

XX Sequence 1027 AA;

QY Query Match 93.2%; Score 110; DB 2; Length 1027;
 Best Local Similarity 95.2%; Pred. No. 5,6e-09;
 Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KPSYQFGHNSVPFEDTLPK 21
 |||||

DB 846 KPSYQFGHNSVPFEDTLPK 866

RESULT 14

ABU15854
 ID ABU15854 standard; protein; 961 AA.

XX ABU15854;

XX 19-JUN-2003 (first entry)

XX Protein encoded by Prokaryotic essential gene #1381.

XX Antisense; prokaryotic essential gene; cell proliferation; drug design.

XX Staphylococcus aureus.

XX WO20027183-A2.

XX 03-OCT-2002.

XX 21-MAR-2002; 2002WO-US0009107.

XX 21-MAR-2001; 2001US-00815242.

XX 06-SEP-2001; 2001US-00948993.

XX 25-OCT-2001; 2001US-0342923P.

XX 08-FEB-2002; 2002US-00072851.

XX 06-MAR-2002; 2002US-0362699P.

XX (ELIT-) ELITRA PHARM INC.

XX Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;

XX Wall D, Trawick JD, Carr GU, Yamamoto R, Forsyth RA, Xu HH;

XX WPI; 2003-029926/02.

XX N-PSDB; ACAL9724.

XX Claim 25; SEQ ID NO 43778; 1766pp; English.

XX The invention relates to an isolated nucleic acid comprising any one of
 CC the 623 antisense sequences given in the specification where expression
 CC of the nucleic acid inhibits proliferation of a cell. Also included are:
 CC (1) a vector comprising a promoter operably linked to the nucleic acid
 CC encoding a polypeptide whose expression is inhibited by the antisense
 CC nucleic acid; (2) a host cell containing the vector; (3) an isolated
 CC polypeptide or its fragment whose expression is inhibited by the
 CC antisense nucleic acid; (4) an antibody capable of specifically binding
 CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular
 CC proliferation or the activity of a gene in an operon required for
 CC proliferation; (7) identifying a compound that influences the activity of
 CC the gene product or that has an activity against a biological pathway
 CC required for proliferation, or that inhibits cellular proliferation; (8)
 CC identifying a gene required for cellular proliferation or the biological
 CC pathway in which a proliferation-regulated gene or its gene product lies
 CC or a gene on which the test compound that inhibits proliferation of an
 CC organism acts; (9) manufacturing an antibiotic; (10) profiling a
 CC compound's activity; (11) a culture comprising strains in which the gene
 CC product is overexpressed or underexpressed; (12) determining the extent
 CC to which each of the strains is present in a culture or collection of
 CC strains; or (13) identifying the target of a compound that inhibits the
 CC proliferation of an organism. The antisense nucleic acids are useful for
 CC identifying proteins or screening for homologous nucleic acids required
 CC for cellular proliferation to isolate candidate molecules for rational
 CC drug discovery programs, or for screening homologous nucleic acids
 CC required for proliferation in cells other than S. aureus, S. typhimurium,
 CC K. pneumoniae or P. aeruginosa. The present sequence is encoded by one of
 CC the target prokaryotic essential genes. Note: The sequence data for this
 CC patent did not form part of the printed specification, but was obtained
 CC in electronic format directly from WIPO at

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CC      ftp.wipo.int/pub/published_pct_sequences
XX      SQ      Sequence 961 AA;
Query Match      90.7%; Score 107; DB 6; Length 961;
Best Local Similarity 90.5%; Pred. No. 1.6e-08;
Matches 19; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY      1 KPSYQFGHNSVDFEEDTLPK 21
      ||:|||||
DB      784 KPNYQFGHNSVDFEEDTLPK 804

RESULT 15
AU033960 standard; protein; 978 AA.
XX      AC      AU033960;
XX      DT      14-FEB-2002 (first entry)
XX      DE      Staphylococcus aureus cellular proliferation protein #236.
XX      KW      Antisense; prokaryotic cellular proliferation protein; antibiotic;
XX      OS      antibacterial; drug design.
XX      Staphylococcus aureus.
XX      PN      WO200170955-A2.
XX      PD      27-SEP-2001.
XX      PF      21-MAR-2001; 2001WO-US009180.
XX      PR      21-MAR-2000; 2000US-0191078P.
XX      PR      23-MAY-2000; 2000US-0206848P.
XX      PR      26-MAY-2000; 2000US-0207727P.
XX      PR      23-OCT-2000; 2000US-0242578P.
XX      PR      27-NOV-2000; 2000US-0253625P.
XX      PR      22-DEC-2000; 2000US-0257931P.
XX      PR      16-FEB-2001; 2001US-0269308P.
XX      PA      (ELITRA PHARM INC.
XX      PI      Haeelbeck R, Ohlsen KL, Zyskind JW, Wall D, Trawick JD, Carr GT;
XX      PI      Yamamoto RT, Xu HH;
XX      DR      N-PSDB; AAS51819.
XX      WIPI; 2001-611495/70.
XX      N-PSDB; AAS51819.
XX      PT      New polynucleotides for the identification and development of
XX      PT      antibiotics, comprise sequences of antisense nucleic acids.
XX      PS      Example 3; SEQ ID NO 5456; 511pp; English.
XX      CC      The invention relates to antisense inhibitors of genes essential to
XX      CC      prokaryotic cellular proliferation, their use in identifying the genes,
XX      CC      their use in the discovery of novel antibiotics, the essential genes
XX      CC      themselves and the encoded proteins. The prokaryotes used are Escherichia
XX      CC      coli, Staphylococcus aureus, Salmonella typhi, Klebsiella pneumoniae,
XX      CC      Pseudomonas aeruginosa and Enterococcus faecalis. The invention is also
XX      CC      useful for the identification of potential new targets for antibiotic
XX      CC      development. The antisense nucleic acids can also be used to identify
XX      CC      proteins used in proliferation, to express these proteins, and to obtain
XX      CC      antibodies capable of binding to the expressed proteins. The proteins can
XX      CC      be used to screen compounds in rational drug discovery programmes. The
XX      CC      antisense nucleic acid sequence is also useful to screen for homologous
XX      CC      nucleic acids which are required for cell proliferation in a wide variety
XX      CC      of organisms. The present sequence represents an essential prokaryotic
XX      CC      cellular proliferation protein. Note: The sequence data for this patent
XX      CC      did not form part of the printed specification, but was obtained in
XX      CC      ftp.wipo.int/pub/published_pct_sequences

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XX      SQ      Sequence 978 AA;
Query Match      90.7%; Score 107; DB 4; Length 978;
Best Local Similarity 90.5%; Pred. No. 1.7e-08;
Matches 19; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY      1 KPSYQFGHNSVDFEEDTLPK 21
      ||:|||||
DB      815 KPNYQFGHNSVDFEEDTLPK 835

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Job time : 59.1473 secs

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OM protein - protein search, using sw model

Run on: October 22, 2005, 02:23:36 ; Search time 15.9358 Seconds
(without alignments)
98.371 Million cell updates/sec

Title: US-10-731-238-25
Perfect score: 118
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Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues
Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-Processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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3: /cgn2_6/prodata/1/1aa/6A_COMB.pep: *
4: /cgn2_6/prodata/1/1aa/6B_COMB.pep: *
5: /cgn2_6/prodata/1/1aa/PCOTUS_COMB.pep: *
6: /cgn2_6/prodata/1/1aa/backfill1.pep: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	118	100.0	21	4	US-09-010-317-25 Sequence 25, Appl
2	110	93.2	21	4	US-09-010-317-9 Sequence 9, Appl
3	110	93.2	37	1	US-08-234-622A-4 Sequence 4, Appl
4	110	93.2	38	1	US-08-294-189-8 Sequence 8, Appl
5	110	93.2	38	1	US-08-729-767-5 Sequence 5, Appl
6	110	93.2	114	1	US-08-259-000-3 Sequence 3, Appl
7	110	93.2	139	3	US-08-856-253-8 Sequence 8, Appl
8	110	93.2	178	3	US-08-459-135A-12 Sequence 12, Appl
9	110	93.2	178	3	US-08-495-559-12 Sequence 12, Appl
10	110	93.2	1027	4	US-08-956-171E-5254 Sequence 5254, Ap
11	110	93.2	1027	4	US-08-781-986A-5254 Sequence 5254, Ap
12	105	89.0	21	4	US-09-010-317-14 Sequence 14, Appl
13	105	89.0	21	4	US-09-010-317-16 Sequence 16, Appl
14	105	89.0	21	4	US-09-010-317-23 Sequence 23, Appl
15	105	89.0	21	4	US-09-010-317-33 Sequence 33, Appl
16	104	88.1	21	4	US-09-010-317-18 Sequence 18, Appl
17	104	88.1	21	4	US-09-010-317-24 Sequence 24, Appl
18	104	88.1	21	4	US-09-010-317-27 Sequence 27, Appl
19	104	88.1	21	4	US-09-010-317-28 Sequence 28, Appl
20	104	88.1	21	4	US-09-010-317-30 Sequence 30, Appl
21	103	87.3	21	4	US-09-010-317-29 Sequence 29, Appl
22	103	87.3	21	4	US-09-010-317-31 Sequence 31, Appl
23	103	87.3	130	2	US-08-459-135A-7 Sequence 7, Appl
24	103	87.3	130	2	US-08-459-135A-8 Sequence 8, Appl
25	103	87.3	130	3	US-08-495-559-7 Sequence 7, Appl
26	103	87.3	130	3	US-08-495-559-8 Sequence 8, Appl
27	103	87.3	174	2	US-08-459-135A-10 Sequence 10, Appl

ALIGNMENTS

28	103	87.3	174	2	US-08-459-135A-13	Sequence 13, Appl
29	103	87.3	174	3	US-08-495-559-10	Sequence 10, Appl
30	103	87.3	176	3	US-08-495-559-13	Sequence 13, Appl
31	103	87.3	176	3	US-08-495-559-6	Sequence 6, Appl
32	103	87.3	181	2	US-08-459-135A-6	Sequence 6, Appl
33	103	87.3	559	4	US-08-956-171E-5251	Sequence 5251, Ap
34	103	87.3	559	4	US-08-781-986A-5251	Sequence 5251, Ap
35	102	86.4	21	4	US-09-010-317-10	Sequence 10, Appl
36	102	86.4	21	4	US-09-010-317-15	Sequence 15, Appl
37	102	86.4	21	4	US-09-010-317-20	Sequence 20, Appl
38	102	86.4	21	4	US-09-010-317-22	Sequence 22, Appl
39	102	86.4	21	4	US-09-010-317-32	Sequence 32, Appl
40	102	86.4	22	4	US-09-010-317-13	Sequence 13, Appl
41	100	84.7	21	4	US-09-010-317-17	Sequence 17, Appl
42	100	84.7	21	4	US-09-010-317-19	Sequence 19, Appl
43	100	84.7	21	4	US-09-010-317-21	Sequence 21, Appl
44	100	84.7	21	4	US-09-010-317-26	Sequence 26, Appl
45	89	75.4	19	1	US-08-234-622A-1	Sequence 1, Appl

RESULT 1
US-09-010-317-25
Sequence 25, Application US/09010317
Patent No. 6685943
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
APPLICANT: Patti, Joseph M.
APPLICANT: House-Pompeo, Karen L.
APPLICANT: Speziale, Pietro
APPLICANT: John, Danny
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
TITLE OF INVENTION: AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAMK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: amino acid
STRANDEDNESS: linear
TOPOLOGY: linear
US-09-010-317-25
Query Match 100.0%; Score 118; DB 4; Length 21;
Best Local Similarity 100.0%; Pred. No. 3.6e-12;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 KPSYQFGHNSVDFEEDTLPK 21
Db 1 KPSYQFGHNSVDFEEDTLPK 21

RESULT 2

US-09-010-317-9
; Sequence 9, Application US/09010317
; Patent No. 6685943
; GENERAL INFORMATION:
; APPLICANT: Hook, Magnus
; APPLICANT: Patti, Joseph M.
; APPLICANT: House-Pompeo, Karen L.
; APPLICANT: Speziale, Pietro
; APPLICANT: Joh, Danny
; APPLICANT: McGavin, Martin J.
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
; TITLE OF INVENTION: AND METHODS OF USE
; NUMBER OF SEQUENCES: 105
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: TX
; COUNTRY: USA
; ZIP: 77210-4433
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/010.317
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/036,139
; FILING DATE: 21-JAN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Hibley, David W.
; REGISTRATION NUMBER: 41,071
; REFERENCE/DOCKET NUMBER: TANK:189
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 512-418-3000
; TELEFAX: 512-474-7577
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
US-09-010-317-9

Query Match 93.2%; Score 110; DB 4; Length 21;
Best Local Similarity 95.2%; Pred. No. 6,7e-11;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 KPSYQFGHNSVDFEEDTLPK 21
Db 1 KPSYQFGHNSVDFEEDTLPK 21

RESULT 3

US-08-234-622A-4
; Sequence 4, Application US/08234622A
; Patent No. 5460014
; GENERAL INFORMATION:
; APPLICANT: Hook, Magnus
; APPLICANT: MCGAVIN, Martin
; APPLICANT: RAUCCI, Giuseppe
; TITLE OF INVENTION: A FIBRONECTIN BINDING PEPTIDE

NUMBER OF SEQUENCES: 4

CORRESPONDENCE ADDRESS:

ADDRESSEE: Burns, Doane, Swecker & Mathis

STREET: P.O. Box 1404

CITY: Alexandria

STATE: Virginia

COUNTRY: United States

ZIP: 22133-1404

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/234,622A

FILING DATE: 28-APR-1994

CLASSIFICATION: 530

PRIOR APPLICATION DATA:

APPLICATION NUMBER: SE 9002617-0

FILING DATE: 10-AUG-1990

PRIOR APPLICATION DATA:

APPLICATION NUMBER: WO PCT/SE91/00534

FILING DATE: 09-AUG-1991

ATTORNEY/AGENT INFORMATION:

NAME: Meuth, Donna M

REGISTRATION NUMBER: 36,607

REFERENCE/DOCKET NUMBER: 012885-044

TELECOMMUNICATION INFORMATION:

TELEPHONE: (703) 836-6620

TELEFAX: (703) 836-6620

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 37 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-234-622A-4

Query Match 93.2%; Score 110; DB 1; Length 37;
Best Local Similarity 95.2%; Pred. No. 1.3e-10;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 KPSYQFGHNSVDFEEDTLPK 21
Db 16 KPSYQFGHNSVDFEEDTLPK 36

RESULT 4

US-08-294-189-8
; Sequence 8, Application US/08294189
; Patent No. 5707822
; GENERAL INFORMATION:
; APPLICANT: Fischetti, Vincent A.
; APPLICANT: Rakonjac, Jasna
; APPLICANT: Robbins, John
; TITLE OF INVENTION: GENE SERUM OPACITY FACTOR
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klauber & Jackson
; STREET: 411 Hackensack Avenue
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/294,189
; FILING DATE: 22-AUG-1994

CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-118
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 487-5800
TELEFAX: 201 343-1684
TELEX: 133521
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
ORGANISM: Streptococcus pyogenes
STRAIN: D734
INDIVIDUAL ISOLATE: 22
IMMEDIATE SOURCE:
CLONE: SAU3a
US-08-294-189-8

Query Match 93.2%; Score 110; DB 1; Length 38;
Best Local Similarity 95.2%; Pred. No. 1.3e-10;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KPSYQFGHNSVDFEDTLPK 21
DB 10 KPSYQFGHNSVDFEDTLPK 30

RESULT 5
US-08-729-767-5
Sequence 5, Application US/08729767
Patent No. 5770702
GENERAL INFORMATION:
APPLICANT: HOOK, Magnus
APPLICANT: LINDBERG, Martin Kjell
APPLICANT: SIGNAS, Lars Christer
APPLICANT: MADSTROM, Torkel Mikael
APPLICANT: FROMAN, Gunnar
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN AS WELL AS
TITLE OF INVENTION: ITS PREPARATION
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Burns, Doane, Swecker & Mathis, L.L.P.
STREET: P.O. Box 1404
CITY: Alexandria
STATE: Virginia
COUNTRY: United States
ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/729,767
FILING DATE: 07-OCT-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/259,000
FILING DATE: 13-JUN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/007,817
FILING DATE: 22-JAN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/201,028
FILING DATE: 01-JUN-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: SE 8702272-9

FILING DATE: 01-JUN-1987
ATTORNEY/AGENT INFORMATION:
NAME: McGowan, Malcolm K.
REGISTRATION NUMBER: 39,300
REFERENCE/DOCKET NUMBER: 012889-036
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-729-767-5

Query Match 93.2%; Score 110; DB 1; Length 38;
Best Local Similarity 95.2%; Pred. No. 1.3e-10;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KPSYQFGHNSVDFEDTLPK 21
DB 17 KPSYQFGHNSVDFEDTLPK 37

RESULT 6
US-08-259-000-3
Sequence 3, Application US/08259000
Patent No. 5571514
GENERAL INFORMATION:
APPLICANT: HOOK, Magnus
APPLICANT: LINDBERG, Martin Kjell
APPLICANT: SIGNAS, Lars Christer
APPLICANT: MADSTROM, Torkel Mikael
APPLICANT: FROMAN, Gunnar
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN AS WELL AS
TITLE OF INVENTION: ITS PREPARATION
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Burns, Doane, Swecker & Mathis
STREET: P.O. Box 1404
CITY: Alexandria
STATE: Virginia
COUNTRY: United States
ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/259,000
FILING DATE: 13-JUN-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: SE 8702272-9
FILING DATE: 01-JUN-1987
ATTORNEY/AGENT INFORMATION:
NAME: Meuth, Donna M
REGISTRATION NUMBER: 36,607
REFERENCE/DOCKET NUMBER: 012885-062
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 114 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-259-000-3

Query Match 93.2%; Score 110; DB 1; Length 114;
Best Local Similarity 95.2%; Pred. No. 4,6e-10;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KPSYQFGHNSVDFEEDTLPK 21
Db 93 KPSYQFGHNSVDFEEDTLPK 113

RESULT 7
US-08-856-253-8

; Sequence 8, Application US/08856253
; Patent No. 6288214
; GENERAL INFORMATION:
; APPLICANT: Hook, Magnus
; APPLICANT: Patti, Joseph M.
; APPLICANT: House-Pompeo, Karen
; APPLICANT: Shanan, Narayana
; APPLICANT: Symerek, Jindrich
; TITLE OF INVENTION: COLLAGEN BINDING PROTEIN COMPOSITIONS
; TITLE OF INVENTION: AND METHODS OF USE
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: U.S.
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/856,253
; FILING DATE: Concurrently Herewith
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/017,678
; FILING DATE: 16-MAY-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Kitchell, Barbara S.
; REGISTRATION NUMBER: 33,928
; REFERENCE/DOCKET NUMBER: TANK:193
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (512) 418-3000
; TELEFAX: (512) 474-7577
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 139 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; US-08-856-253-8

Query Match 93.2%; Score 110; DB 3; Length 139;
Best Local Similarity 95.2%; Pred. No. 5.7e-10;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KPSYQFGHNSVDFEEDTLPK 21
Db 107 KPSYQFGHNSVDFEEDTLPK 127

RESULT 8
US-08-459-135A-12

; Sequence 12, Application US/08459135A
; Patent No. 5955078
; GENERAL INFORMATION:
; APPLICANT: BURHAM, Martin Karl Russel
; APPLICANT: CHOPRA, Ian

; APPLICANT: CRITCHLEY, Ian Alfred
; APPLICANT: KNOWLES, David Justin Charles
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN: MONOCLONAL ANTIBODY AND THEIR US
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corporation
; STREET: 709 Swedeland Road
; CITY: King of Prussia
; STATE: PA

COUNTRY: U.S.A.

ZIP: 19406-0939

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: PastSeq, Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/459,135A

FILING DATE: 02-JUN-1995

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/GB/94/00215

FILING DATE: 04-Feb-1994

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Gimm, Edward R.

REGISTRATION NUMBER: 38,891

REFERENCE/DOCKET NUMBER: P30591C2

TELECOMMUNICATION INFORMATION:

TELEPHONE: 610-270-4478

TELEFAX: 610-270-5090

TELEX:

INFORMATION FOR SEQ ID NO: 12:

SEQUENCE CHARACTERISTICS:

LENGTH: 178 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: Protein

Query Match 93.2%; Score 110; DB 2; Length 178;
Best Local Similarity 95.2%; Pred. No. 7.6e-10;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KPSYQFGHNSVDFEEDTLPK 21
Db 93 KPSYQFGHNSVDFEEDTLPK 113

RESULT 9
US-08-495-559-12

; Sequence 12, Application US/08495559A
; Patent No. 6054572
; GENERAL INFORMATION:
; APPLICANT: BURHAM, Martin Karl Russel
; APPLICANT: CHOPRA, Ian
; APPLICANT: CRITCHLEY, Ian Alfred
; APPLICANT: KNOWLES, David Justin Charles
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN: MONOCLONAL
; TITLE OF INVENTION: ANTIBODY AND THEIR USE IN PREVENTING BACTERIAL ADHESION
; FILE REFERENCE: P30591
; CURRENT APPLICATION NUMBER: US/08/495,559A
; CURRENT FILING DATE: 1995-08-03
; EARLIER APPLICATION NUMBER: GB 9302289.5
; EARLIER FILING DATE: 1993-02-05
; EARLIER APPLICATION NUMBER: GB 9321592.9
; EARLIER FILING DATE: 1993-10-20
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PastSeq for Windows Version 3.0
; SEQ ID NO 12
; LENGTH: 178
; TYPE: PRT

ORGANISM: Staphylococcus aureus
US-08-495-559-12

Query Match 93.2%; Score 110; DB 3; Length 178;
Best Local Similarity 95.2%; Pred. No. 7,6e-10;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KPSYOGGHN5VPFEDTLPK 21
DB 93 KPSYOGGHN5VPFEDTLPK 113

RESULT 10
US-08-956-171E-5254

Sequence 5254, Application US/08956171E
Patent No. 6593114
GENERAL INFORMATION:

APPLICANT: Charles Kunesh

Gil H. Choi

Patrick S. Dillon

Craig A. Rosen

Steven C. Barash

Michael R. Fannon

TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences

NUMBER OF SEQUENCES: 5256

CORRESPONDENCE ADDRESSES:

ADDRESSEE: Human Genome Sciences, Inc.

STREET: 9410 Key West Avenue

CITY: Rockville

STATE: Maryland

COUNTRY: USA

ZIP: 20850

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.50 inch, 1.4mb storage

COMPUTER: HP Vectra 486/33

OPERATING SYSTEM: MSDOS version 6.2

SOFTWARE: ASCII Text

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/956,171E

FILING DATE: 20-Oct-1997

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 60/009,861

FILING DATE: January 5, 1996

APPLICATION NUMBER: 08/781,986

FILING DATE: January 3, 1997

ATTORNEY/AGENT INFORMATION:

NAME: Mark J. Hyman

REGISTRATION NUMBER: 46,789

REFERENCE/DOCKET NUMBER: PB248P1

TELECOMMUNICATION INFORMATION:

TELEPHONE: (240) 314-1224

TELEFAX: (301) 309-8439

INFORMATION FOR SEQ ID NO: 5254:

SEQUENCE CHARACTERISTICS:

LENGTH: 1027 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 5254:

US-08-956-171E-5254

Query Match 93.2%; Score 110; DB 4; Length 1027;
Best Local Similarity 95.2%; Pred. No. 5.5e-09;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KPSYOGGHN5VPFEDTLPK 21
DB 846 KPSYOGGHN5VPFEDTLPK 866

RESULT 11

US-08-781-986A-5254

Sequence 5254, Application US/08781986A

Patent No. 6737248

GENERAL INFORMATION:

APPLICANT: Charles Kunesh

TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences

NUMBER OF SEQUENCES: 5255

CORRESPONDENCE ADDRESSES:

ADDRESSEE: Human Genome Sciences, Inc.

STREET: 9410 Key West Avenue

CITY: Rockville

STATE: Maryland

COUNTRY: USA

ZIP: 20850

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.50 inch, 1.4mb storage

COMPUTER: HP Vectra 486/33

OPERATING SYSTEM: MSDOS version 6.2

SOFTWARE: ASCII Text

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/781,986A

FILING DATE:

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER:

ATTORNEY/AGENT INFORMATION:

NAME: Benson, Bob

REGISTRATION NUMBER: 30,446

REFERENCE/DOCKET NUMBER: PB248PP

TELECOMMUNICATION INFORMATION:

TELEPHONE: (301) 309-8504

TELEFAX: (301) 309-8512

INFORMATION FOR SEQ ID NO: 5254:

SEQUENCE CHARACTERISTICS:

LENGTH: 1027 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-781-986A-5254

Query Match 93.2%; Score 110; DB 4; Length 1027;
Best Local Similarity 95.2%; Pred. No. 5.5e-09;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KPSYOGGHN5VPFEDTLPK 21
DB 846 KPSYOGGHN5VPFEDTLPK 866

RESULT 12

US-09-010-317-14

Sequence 14, Application US/09010317

Patent No. 6685943

GENERAL INFORMATION:

APPLICANT: Hook, Magnus

APPLICANT: Patti, Joseph M.

APPLICANT: House-Pompeo, Karen L.

APPLICANT: Speziale, Pietro

APPLICANT: Joh, Danny

APPLICANT: McGavin, Martin J.

TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS

NUMBER OF SEQUENCES: 105

CORRESPONDENCE ADDRESSES:

ADDRESSEE: Arnold, White & Durkee

STREET: P.O. Box 4433

CITY: Houston

STATE: TX

COUNTRY: USA

ZIP: 77210-4433

COMPUTER READABLE FORM:

```

; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/010,317
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/036,139
; FILING DATE: 21-JAN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Hibler, David W.
; REGISTRATION NUMBER: 41,071
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 512-418-3000
; TELEFAX: 512-474-7577
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
;
US-09-010-317-14

Query Match      89.0%; Score 105; DB 4; Length 21;
Best Local Similarity 95.0%; Pred. No. 4.2e-10;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      2 PSYQFGHNSVPFEEDTLPK 21
Db      2 PSYQFGHNSVDFEEDTLPK 21

RESULT 13
US-09-010-317-16
; Sequence 16, Application US/09010317
; Patent No. 6685943
; GENERAL INFORMATION:
; APPLICANT: Hook, Magnus
; APPLICANT: Patti, Joseph M.
; APPLICANT: House-Pompeo, Karen L.
; APPLICANT: Speziale, Pietro
; APPLICANT: Jhon, Danny
; APPLICANT: McGavin, Martin J.
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
; NUMBER OF SEQUENCES: 105
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P. O. Box 4433
; CITY: Houston
; STATE: TX
; COUNTRY: USA
; ZIP: 77210-4433
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/010,317
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/036,139
; FILING DATE: 21-JAN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Hibler, David W.
; REGISTRATION NUMBER: 41,071
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 512-418-3000
; TELEFAX: 512-474-7577
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
;
US-09-010-317-23

Query Match      89.0%; Score 105; DB 4; Length 21;
Best Local Similarity 95.0%; Pred. No. 4.2e-10;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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; TELEPHONE: 512-418-3000
; TELEFAX: 512-474-7577
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
;
US-09-010-317-16

Query Match      89.0%; Score 105; DB 4; Length 21;
Best Local Similarity 90.5%; Pred. No. 4.2e-10;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      1 KPQYQFGHNSVPFEEDTLPK 21
Db      1 KPQYQFGHNSVDFEEDTLPK 21

RESULT 14
US-09-010-317-23
; Sequence 23, Application US/09010317
; Patent No. 6685943
; GENERAL INFORMATION:
; APPLICANT: Hook, Magnus
; APPLICANT: Patti, Joseph M.
; APPLICANT: House-Pompeo, Karen L.
; APPLICANT: Speziale, Pietro
; APPLICANT: Jhon, Danny
; APPLICANT: McGavin, Martin J.
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
; NUMBER OF SEQUENCES: 105
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P. O. Box 4433
; CITY: Houston
; STATE: TX
; COUNTRY: USA
; ZIP: 77210-4433
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/010,317
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/036,139
; FILING DATE: 21-JAN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Hibler, David W.
; REGISTRATION NUMBER: 41,071
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 512-418-3000
; TELEFAX: 512-474-7577
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
;
US-09-010-317-23

Query Match      89.0%; Score 105; DB 4; Length 21;
Best Local Similarity 90.5%; Pred. No. 4.2e-10;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      1 KPQYQFGHNSVPFEEDTLPK 21
Db      1 KPQYQFGHNSVDFEEDTLPK 21
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Db 1 KPSYQFGHNPVDFEEDTLP 21

RESULT 15
US-09-010-317-33

; Sequence 33, Application US/09010317
; Patent No. 6685943

; GENERAL INFORMATION:

; APPLICANT: Hook, Magnus

; APPLICANT: Patti, Joseph M.

; APPLICANT: House-Pompeo, Karen L.

; APPLICANT: Speziale, Pietro

; APPLICANT: John, Danny

; APPLICANT: McGavin, Martin J.

; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS

; TITLE OF INVENTION: AND METHODS OF USE

; NUMBER OF SEQUENCES: 105

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Arnold, White & Durkee

; STREET: P.O. Box 4433

; CITY: Houston

; STATE: TX

; COUNTRY: USA

; ZIP: 77210-4433

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/010,317

; FILING DATE:

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 60/036,139

; FILING DATE: 21-JAN-1997

; ATTORNEY/AGENT INFORMATION:

; NAME: Habler, David W.

; REGISTRATION NUMBER: 41,071

; REFERENCE/DOCKET NUMBER: TAMK:189

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 512-418-3000

; TELEFAX: 512-474-7577

; INFORMATION FOR SEQ ID NO: 33:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 21 amino acids

; TYPE: amino acid

; STRANDEDNESS:

; TOPOLOGY: linear

US-09-010-317-33

Query Match 89.0%; Score 105; DB 4; Length 21;
Best Local Similarity 95.0%; Pred. No. 4.2e-10;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KPSYQFGHNSVPFEEDTLP 20
DB 1 KPSYQFGHNSVPFEEDTLP 20

Search completed: October 22, 2005, 03:51:13
Job time: 16.9358 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 22, 2005, 10:49:15 ; Search time 59.2367 Seconds
(without alignments)
148.005 Million cell updates/sec

Title: US-10-731-238-25

Perfect score: 118.
Sequence: 1 KPSYQFGCHNSVFEEDTLRK 21

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1862951 seqs, 417491010 residues

Total number of hits satisfying chosen parameters: 1862951

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

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6: /cgn2_6/prodata/2/pubppaa/PCTUS_PUBCOMB.pep.*
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11: /cgn2_6/prodata/2/pubppaa/US09C_PUBCOMB.pep.*
12: /cgn2_6/prodata/2/pubppaa/US09_NEW_PUB.pep.*
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17: /cgn2_6/prodata/2/pubppaa/US10F_PUBCOMB.pep.*
18: /cgn2_6/prodata/2/pubppaa/US10_NEW_PUB.pep.*
19: /cgn2_6/prodata/2/pubppaa/US11A_PUBCOMB.pep.*
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22: /cgn2_6/prodata/2/pubppaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	118	100.0	21	18	US-10-731-238-25
2	110	93.2	21	18	US-10-731-238-9
3	110	93.2	37	20	US-11-066-697-1114
4	110	93.2	139	9	US-08-813-820-8
5	110	93.2	1018	9	US-08-815-242-5797
6	110	93.2	1018	9	US-09-815-242-12838
7	110	93.2	1018	17	US-10-470-0488-68
8	110	93.2	1027	8	US-08-781-9864-5254
9	110	93.2	1027	15	US-10-329-624-5254
10	107	90.7	961	15	US-10-282-1224-43778
11	107	90.7	978	9	US-09-815-242-5456

12	107	90.7	1001	9	US-09-815-242-12686	Sequence 12686, A
13	107	90.7	1038	15	US-10-282-1224-43827	Sequence 43827, A
14	105	89.0	21	18	US-10-731-238-14	Sequence 14, Appl
15	105	89.0	21	18	US-10-731-238-16	Sequence 16, Appl
16	105	89.0	21	18	US-10-731-238-23	Sequence 23, Appl
17	105	89.0	21	18	US-10-731-238-33	Sequence 33, Appl
18	104	88.1	21	18	US-10-731-238-18	Sequence 18, Appl
19	104	88.1	21	18	US-10-731-238-24	Sequence 24, Appl
20	104	88.1	21	18	US-10-731-238-27	Sequence 27, Appl
21	104	88.1	21	18	US-10-731-238-28	Sequence 28, Appl
22	104	88.1	21	18	US-10-731-238-30	Sequence 30, Appl
23	103	87.3	21	18	US-10-731-238-39	Sequence 39, Appl
24	103	87.3	21	18	US-10-731-238-31	Sequence 31, Appl
25	103	87.3	388	8	US-08-901-062-1	Sequence 1, Appl
26	103	87.3	559	8	US-08-781-9864-5251	Sequence 5251, Ap
27	103	87.3	559	15	US-10-329-624-5251	Sequence 5251, Ap
28	103	87.3	940	17	US-10-470-0488-424	Sequence 424, App
29	103	87.3	948	17	US-10-470-0488-69	Sequence 69, Appl
30	102	86.4	21	18	US-10-731-238-15	Sequence 10, Appl
31	102	86.4	21	18	US-10-731-238-10	Sequence 15, Appl
32	102	86.4	21	18	US-10-731-238-20	Sequence 20, Appl
33	102	86.4	21	18	US-10-731-238-22	Sequence 22, Appl
34	102	86.4	21	18	US-10-731-238-32	Sequence 32, Appl
35	102	86.4	22	18	US-10-731-238-13	Sequence 13, Appl
36	100	84.7	21	18	US-10-731-238-17	Sequence 17, Appl
37	100	84.7	21	18	US-10-731-238-19	Sequence 19, Appl
38	100	84.7	21	18	US-10-731-238-21	Sequence 21, Appl
39	100	84.7	21	18	US-10-731-238-26	Sequence 26, Appl
40	82	69.5	21	18	US-10-731-238-34	Sequence 34, Appl
41	71	60.2	14	18	US-10-731-238-61	Sequence 61, Appl
42	59	50.0	10	18	US-10-731-238-96	Sequence 96, Appl
43	54	45.8	10	18	US-10-731-238-95	Sequence 95, Appl
44	52	44.1	10	18	US-10-731-238-97	Sequence 97, Appl
45	51	43.2	49	14	US-10-029-386-28259	Sequence 28259, A

ALIGNMENTS

RESULT 1
US-10-731-238-25
Sequence 25, Application US/10731238
Publication No. US20050123552A1
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
Pacifi, Joseph M.
House-Pompeo, Karen L.
Speziale, Pietro
McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSER: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/731,238
FILING DATE: 10-Dec-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE: 21-Jan-1998
APPLICATION NUMBER: US 60/036,139

FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TANK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 25:
US-10-731-238-25

Query Match 100.0%; Score 118; DB 18; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.7e-11;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KPSYQFGHNSVPEEDTLPK 21
DB 1 KPSYQFGHNSVPEEDTLPK 21

RESULT 2
US-10-731-238-9
Sequence 9, Application US/10731238
Publication No. US20050123552A1
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
Patti, Joseph M.
House-Pompeo, Karen L.
Speziale, Pietro
Joh, Danny
McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/731,238
FILING DATE: 10-Dec-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE: 21-Jan-1998
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TANK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>

TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 9:
US-10-731-238-9

Query Match 93.2%; Score 110; DB 18; Length 21;
Best Local Similarity 95.2%; Pred. No. 3.2e-10;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KPSYQFGHNSVPEEDTLPK 21
DB 1 KPSYQFGHNSVPEEDTLPK 21

RESULT 3
US-11-066-697-1134
Sequence 1134, Application US/11066697
Publication No. US20050187159A1
GENERAL INFORMATION:
APPLICANT: Bridon, Dominique P.
APPLICANT: Ezrin, Alan M.
APPLICANT: Milner, Peter G.
APPLICANT: Holmes, Darren L.
APPLICANT: Thibodeau, Karen
TITLE OF INVENTION: PROTECTION OF ENDOGENOUS THERAPEUTIC PEPTIDES FROM
TITLE OF INVENTION: PEPTIDASE ACTIVITY THROUGH CONJUGATION TO BLOOD
FILE REFERENCE: 500862002301
CURRENT APPLICATION NUMBER: US/11/066,697
CURRENT FILING DATE: 2005-02-25
PRIOR APPLICATION NUMBER: 09/657,276
PRIOR FILING DATE: 2000-09-07
PRIOR APPLICATION NUMBER: 60/153,406
PRIOR FILING DATE: 1999-09-10
PRIOR APPLICATION NUMBER: 60/159,783
PRIOR FILING DATE: 1999-10-15
NUMBER OF SEQ ID NOS: 1617
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 1134
LENGTH: 37
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-11-066-697-1134

Query Match 93.2%; Score 110; DB 20; Length 37;
Best Local Similarity 95.2%; Pred. No. 6.1e-10;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KPSYQFGHNSVPEEDTLPK 21
DB 16 KPSYQFGHNSVPEEDTLPK 36

RESULT 4
US-09-813-820-8
Sequence 8, Application US/09813820
Patent No. US20020102262A1
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
Patti, Joseph M.
House-Pompeo, Karen
Strhanam, Narayana
Sytersky, Jindrich
TITLE OF INVENTION: COLLAGEN BINDING PROTEIN COMPOSITIONS
AND METHODS OF USE
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: Texas

```

; COUNTRY: U.S.
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION NUMBER: US/09/813,820
; APPLICATION NUMBER: US/09/813,820
; FILING DATE: 22-Mar-2001
; CLASSIFICATION: <Unknown>
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: 08/856,253
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Kirchell, Barbara S.
; REGISTRATION NUMBER: 33,928
; REFERENCE/DOCKET NUMBER: TAMK:193
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (512) 418-3000
; TELEFAX: (512) 474-7577
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 139 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-09-813-820-8

Query Match      93.2%; Score 110; DB 9; Length 139;
Best Local Similarity 95.2%; Pred. No. 2.6e-09;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 KPSYQFGHNSVPFEEDTLPK 21
Db      107 KPSYQFGHNSVPFEEDTLPK 127

RESULT 5
US-09-815-242-5797
; Sequence 5797, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari L.
; APPLICANT: Zysek, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; FILE REFERENCE: ELITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; PRIORITY FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version 4.0
; FILE REFERENCE: FastSeq for Windows Version 4.0
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; SEQ ID NO 5797
; LENGTH: 1018
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-09-815-242-5797

Query Match      93.2%; Score 110; DB 9; Length 1018;
Best Local Similarity 95.2%; Pred. No. 2.4e-08;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 KPSYQFGHNSVPFEEDTLPK 21
Db      837 KPSYQFGHNSVPFEEDTLPK 857

RESULT 6
US-09-815-242-12838
; Sequence 12838, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari L.
; APPLICANT: Zysek, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; FILE REFERENCE: ELITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; PRIORITY FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12838
; LENGTH: 1018
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-09-815-242-12838

Query Match      93.2%; Score 110; DB 9; Length 1018;
Best Local Similarity 95.2%; Pred. No. 2.4e-08;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 KPSYQFGHNSVPFEEDTLPK 21
Db      837 KPSYQFGHNSVPFEEDTLPK 857

RESULT 7
US-10-470-048B-68
; Sequence 68, Application US/10470048B
; Publication No. US2005003744A1
; GENERAL INFORMATION:
; APPLICANT: MEINKE ET AL.
; TITLE OF INVENTION: A METHOD FOR IDENTIFICATION, ISOLATION AND PRODUCTION OF
; FILE REFERENCE: SONN.035US
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CURRENT APPLICATION NUMBER: US/10/470,048B
CURRENT FILING DATE: 2003-07-25
NUMBER OF SEQ ID NOS: 603
SOFTWARE: PatentIn version 3.1
SEQ ID NO: 68
LENGTH: 1018
TYPE: PRT
ORGANISM: Staphylococcus aureus
US-10-470-048B-68

Query Match 93.2%; Score 110; DB 17; Length 1018;
Best Local Similarity 95.2%; Pred. No. 2.4e-08;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KPSYQFGHNSVDFEEDTLPK 21
Db 837 KPSYQFGHNSVDFEEDTLPK 857

RESULT 8
US-08-781-986A-5254
Sequence 5254, Application US/08781986A
Publication No. US20030054436A1
GENERAL INFORMATION:
APPLICANT: Charles Kunach
TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
NUMBER OF SEQUENCES: 5255
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COUNTRY: USA
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/781,986A
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Benson, Bob
REGISTRATION NUMBER: 30,446
REFERENCE/DOCKET NUMBER: PB248BP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 5254:
SEQUENCE CHARACTERISTICS:
LENGTH: 1027 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-781-986A-5254

Query Match 93.2%; Score 110; DB 8; Length 1027;
Best Local Similarity 95.2%; Pred. No. 2.4e-08;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KPSYQFGHNSVDFEEDTLPK 21
Db 846 KPSYQFGHNSVDFEEDTLPK 866

RESULT 9
US-10-329-624-5254

Sequence 5254, Application US/10329624
Publication No. US20040043037A1
GENERAL INFORMATION:
APPLICANT: Charles Kunach
Gill H. Choi
Patrick S. Dillon
Craig A. Rosen
Steven C. Barash
Michael R. Fannon
TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
NUMBER OF SEQUENCES: 5256
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COUNTRY: USA
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/329,624
FILING DATE: 27-Dec-2002
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/956,171
FILING DATE: October 20, 1997
APPLICATION NUMBER: 60/009,861
FILING DATE: January 5, 1996
APPLICATION NUMBER: 08/781,986
FILING DATE: January 3, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Mark J. Hyman
REGISTRATION NUMBER: 46,789
REFERENCE/DOCKET NUMBER: PB248P1D1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (240) 314-1224
TELEFAX: (301) 309-8439
INFORMATION FOR SEQ ID NO: 5254:
SEQUENCE CHARACTERISTICS:
LENGTH: 1027 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 5254:
US-10-329-624-5254

Query Match 93.2%; Score 110; DB 15; Length 1027;
Best Local Similarity 95.2%; Pred. No. 2.4e-08;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KPSYQFGHNSVDFEEDTLPK 21
Db 846 KPSYQFGHNSVDFEEDTLPK 866

RESULT 10
US-10-282-122A-43778
Sequence 43778, Application US/10282122A
Publication No. US20040029129A1
GENERAL INFORMATION:
APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari
APPLICANT: Zykkind, Judith
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John
APPLICANT: Carr, Grant

```

; APPLICANT: Yamamoto, Robert
; APPLICANT: Foreyth, R.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 43778
; LENGTH: 961
; TYPE: PRF
; ORGANISM: Staphylococcus aureus
; US-10-282-122A-43778

Query Match          90.7%; Score 107; DB 15; Length 961;
Best Local Similarity 90.5%; Pred. No. 6.6e-08;
Matches 19; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1 KPSYOGGHSVDFEEDTLPK 21
DB      784 KPNYOGGHSVDFEEDTLPK 804

RESULT 11
US-09-815-242-5456
; Sequence 5456, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Karl L.
; APPLICANT: Zysek, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; TITLE OF INVENTION: Prokaryotes
; FILE REFERENCE: ELITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12686
; LENGTH: 1001
; TYPE: PRF
; ORGANISM: Staphylococcus aureus
; US-09-815-242-12686

Query Match          90.7%; Score 107; DB 15; Length 1001;
Best Local Similarity 90.5%; Pred. No. 7e-08;
Matches 19; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
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; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5456
; LENGTH: 978
; TYPE: PRF
; ORGANISM: Staphylococcus aureus
; US-09-815-242-5456

Query Match          90.7%; Score 107; DB 9; Length 978;
Best Local Similarity 90.5%; Pred. No. 6.8e-08;
Matches 19; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1 KPSYOGGHSVDFEEDTLPK 21
DB      815 KPNYOGGHSVDFEEDTLPK 835

RESULT 12
US-09-815-242-12686
; Sequence 12686, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Karl L.
; APPLICANT: Zysek, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; TITLE OF INVENTION: Prokaryotes
; FILE REFERENCE: ELITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12686
; LENGTH: 1001
; TYPE: PRF
; ORGANISM: Staphylococcus aureus
; US-09-815-242-12686

Query Match          90.7%; Score 107; DB 9; Length 1001;
Best Local Similarity 90.5%; Pred. No. 7e-08;
Matches 19; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1 KPSYOGGHSVDFEEDTLPK 21
DB      838 KPNYOGGHSVDFEEDTLPK 858

RESULT 13
US-10-282-122A-43827
; Sequence 43827, Application US/10282122A
```

Publication No. US20040029129A1
GENERAL INFORMATION:
APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haeselbeck, Robert
APPLICANT: Ohlsen, Karl
APPLICANT: Zykend, Judith
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John
APPLICANT: Carr, Grant
APPLICANT: Yamamoto, Robert
APPLICANT: Foreyth, R.
APPLICANT: Xu, H.
TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REFERENCE: ELITRA.034A
CURRENT APPLICATION NUMBER: US/10/282.122A
CURRENT FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/230,335
PRIOR FILING DATE: 2000-09-06
PRIOR APPLICATION NUMBER: 60/230,347
PRIOR FILING DATE: 2000-09-09
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/267,636
PRIOR FILING DATE: 2001-02-09
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 78614
SOFTWARE: Patent version 3.1
SEQ ID NO 43827
LENGTH: 1038
TYPE: PRT
ORGANISM: Staphylococcus aureus
US-10-282-122A-43827
Query Match 90.7%; Score 107; DB 15; Length 1038;
Best Local Similarity 90.5%; Pred. No. 7, 2e-08;
Matches 19; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 KPSYQFGHNSVDFEEDTLPK 21
DB 833 KPNYQFGHNSVDFEEDTLPK 853
RESULT 14
US-10-731-238-14
Sequence 14, Application US/10731238
Publication No. US20050123552A1
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
Patti, Joseph M.
House-Pompeo, Karen L.
Speziale, Pietro
Joh, Danny
McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433

CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/731,238
FILING DATE: 10-Dec-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE: 21-Jan-1998
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAMK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 14:
US-10-731-238-14
Query Match 89.0%; Score 105; DB 18; Length 21;
Best Local Similarity 95.0%; Pred. No. 2e-09;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2 PSYQFGHNSVDFEEDTLPK 21
DB 2 PSYQFGHNSVDFEEDTLPK 21
RESULT 15
US-10-731-238-16
Sequence 16, Application US/10731238
Publication No. US20050123552A1
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
Patti, Joseph M.
House-Pompeo, Karen L.
Speziale, Pietro
Joh, Danny
McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/731,238
FILING DATE: 10-Dec-2003
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE: 21-Jan-1998
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAMK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 16:
US-10-731-238-16

Query Match 89.0%; Score 105; DB 18; Length 21;
Best Local Similarity 90.5%; Pred. No. 2e-09;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 KPSPYQFGHNSVDFEEDTLPK 21
|||
Db 1 KPSPYQFGHNSVDFEEDTLPK 21

Search completed: October 22, 2005, 11:34:41
Job time : 59.2367 secs

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GenCore version 5.1.6
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OM protein - protein search, using SW model

Run on: October 22, 2005, 02:23:36 ; Search time 10.5465 Seconds
(without alignment)
191.586 Million cell updates/sec

Title: US-10-731-238-25

Perfect score: 118
Sequence: 1 KPSYQFGHNSVPFEEDTLPK 21

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :
1: p1r1: *
2: p1r2: *
3: p1r3: *
4: p1r4: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	110	93.2	1018	2 A32192	fibronectin-binding
2	107	90.7	961	2 G90053	hypothetical prote
3	107	90.7	1038	2 H90053	hypothetical prote
4	103	87.3	940	2 S19702	fibronectin-binding
5	51	43.2	928	1 VGBMC	glycoprotein B pre
6	50	42.4	987	2 A64474	hypothetical prote
7	49	41.5	739	2 T12964	subtilisin homolog
8	47	39.8	257	2 A36057	MHC class I histoc
9	47	39.8	462	1 A39356	3-oxoacyl-lacyl-ca
10	47	39.8	2508	2 S61441	surface-associated
11	46	39.0	1127	2 T25804	hypothetical prote
12	45	38.1	302	2 C83000	dTDP-4-dehydroxam
13	45	38.1	469	2 T10061	3-oxoacyl-lacyl-ca
14	45	38.1	1322	2 A59288	myosin heavy chain
15	45	38.1	1827	1 UHHY	sucrose alpha-gluc
16	44.5	37.7	376	2 S59418	hypothetical prote
17	44	37.3	445	2 P90562	hypothetical prote
18	44	37.3	517	2 T43358	hmf-3/forhead tra
19	44	37.3	705	2 C84406	hypothetical prote
20	43.5	36.9	374	2 D81328	probable aminotran
21	43	36.4	65	2 H95280	conserved hypotet
22	43	36.4	326	2 P64431	capsular polysacch
23	43	36.4	371	2 A88520	41.8k hypothetical
24	43	36.4	453	2 H70333	conserved hypotet
25	43	36.4	495	2 S47074	3-oxoacyl-lacyl-ca
26	43	36.4	648	2 T41337	polo-like kinase-1
27	43	36.4	808	2 P81180	conserved hypotet
28	43	36.4	1783	2 AC2091	serine/threonine k
29	42	35.6	169	2 G82520	hypothetical prote

30	42	35.6	183	2 A10023	conserved hypotet
31	42	35.6	188	2 B97318	transcription regu
32	42	35.6	322	2 D55078	transcription regu
33	42	35.6	348	2 A97946	regulatory functio
34	42	35.6	459	2 D34791	interleukin-7 rece
35	42	35.6	474	2 B84357	serine-trna synthe
36	42	35.6	489	1 S47076	3-oxoacyl-lacyl-ca
37	42	35.6	751	1 SYBYMT	methionine-trna 11
38	42	35.2	496	2 A49930	carb protein homol
39	41.5	35.2	1115	2 A70990	cardamoyl phosphat
40	41.5	35.2	1129	2 H86975	probable cardamoyl
41	41	34.7	197	2 C69779	NAD(P)H oxidoreduc
42	41	34.7	283	2 T42665	hypothetical prote
43	41	34.7	295	2 A41241	ubiquitin-conjugat
44	41	34.7	300	2 H70879	dihydrodipicolinat
45	41	34.7	306	2 A81156	hypothetical prote

ALIGNMENTS

RESULT 1

A32192
fibronectin-binding protein - Staphylococcus aureus
C:Species: Staphylococcus aureus
C:Date: 31-Jul-1989 #sequence_revision 31-Jul-1989 #text_change 16-Feb-1997
C:Accession: A32192
R:Signaes, C.; Raucel, G.; Joensson, K.; Lindgren, P.E.; Anantharamaiah, G.M.; Hoocek, M.
Proc. Natl. Acad. Sci. U.S.A. 86, 699-703, 1989
A:Title: Nucleotide sequence of the gene for a fibronectin-binding protein from Staphyloc
A:Reference number: A32192; MUID:89098998; PMID:2521391
A:Accession: A32192
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1018 <SIG>
A:Cross-references: GB:J04151
C:Keywords: fibronectin binding

Query Match 93.2%; Score 110; DB 2; Length 1018;
Best Local Similarity 95.2%; Pred. No. 3.1e-09;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KPSYQFGHNSVPFEEDTLPK 21
DB 837 KPSYQFGHNSVPFEEDTLPK 857

RESULT 2

G90053
hypothetical protein fnbB (imported) - Staphylococcus aureus (strain N315)
C:Species: Staphylococcus aureus
C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C:Accession: G90053
R:Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguchi
ma, A.; Mizutani-U, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.;
C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiratsuku, K.
Lancet 357, 1225-1240, 2001
A:Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.
A:Reference number: A89758; MUID:21311952; PMID:11418146
A:Accession: G90053
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-961 <KUR>
A:Cross-references: UNIPROT:Q99RD3; GB:BA000018; PTD:G13702452; PTDN:BA843593.1; GSPDB:G
A:Experimental source: strain N315
C:Genetics:
A:Gene: fnbB

Query Match 90.7%; Score 107; DB 2; Length 961;
Best Local Similarity 90.5%; Pred. No. 8.8e-09;
Matches 19; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 KPSYQFGHNSVPFEEDTLPK 21

Db 784 KPNYQFGHNSVDFEEDTLPK 804

RESULT 3

hypothetical protein fmb [imported] - Staphylococcus aureus (strain N315)

C:Species: Staphylococcus aureus
C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004

A:Accession: H90053
R:Kurrod, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Ogura, A.; Mutant-11, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramoto, K.
Lancet 357, 1225-1240, 2001

A:Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.
A:Reference number: A89758; MUID:21311952; PMID:11418146

A:Accession: H90053

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-1038 <KUR>

A:Cross-references: UNIPROT:Q99RD2; GB:BA000018; PID:g13702453; PIDN:BA043594.1; GSPDB:C

A:Experimental source: strain N315

C:Genetics:

A:Gene: fmb

Query Match 90.7%; Score 107; DB 2; Length 1038;
Best Local Similarity 90.5%; Pred. No. 9.6e-09;
Matches 19; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 KPSYQFGHNSVDFEEDTLPK 21

Db 833 KPNYQFGHNSVDFEEDTLPK 853

RESULT 4

fibronectin-binding protein B - Staphylococcus aureus

C:Species: Staphylococcus aureus

C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004

C:Accession: S19702

R:Johnson, K.; Signaes, C.; Mueller, H.P.; Lindberg, M.

Eur. J. Biochem. 202, 1041-1048, 1991

A:Title: Two different genes encode fibronectin binding proteins in Staphylococcus aureus

A:Reference number: S19702; MUID:92111475; PMID:1837266

A:Accession: S19702

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-940 <JOB>

A:Cross-references: UNIPROT:Q53682; EMBL:X62392; NID:g49040; PIDN:CAA44726.1; PID:g58156

C:Keywords: fibronectin binding

Query Match 87.3%; Score 103; DB 2; Length 940;
Best Local Similarity 85.7%; Pred. No. 3.7e-08;
Matches 18; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 1 KPSYQFGHNSVDFEEDTLPK 21

Db 773 KPNYQFGHNSVDFEEDTLPK 793

RESULT 5

glycoprotein B precursor - murine cytomegalovirus (strain Smith [ATCC VR-194])

C:Species: murine cytomegalovirus, murine herpesvirus 1

C:Date: 30-Jun-1992 #sequence_revision 30-Jun-1993 #text_change 09-Jul-2004

C:Accession: A41992; A40780; S23220

R:Rapp, M.; Messerle, M.; Buehler, B.; Tammheimer, M.; Kell, G.M.; Koszinowski, U.H.

J. Virol. 66, 4339-4406, 1992

A:Title: Identification of the murine cytomegalovirus glycoprotein B gene and its expression

A:Reference number: A41992; MUID:92292266; PMID:1318410

A:Accession: A41992

A:Molecule type: mRNA

A:Residues: 1-928 <RAP>

A:Cross-references: UNIPROT:P27171; GB:M86302

R:Elliot, R.; Clark, C.; Jaquish, D.; Spector, D.H.

Virology 165, 169-186, 1991

A:Title: Transcription analysis and sequence of the putative murine cytomegalovirus DNA I

A:Reference number: A40780; MUID:92024072; PMID:1718083

A:Accession: A40780

A:Molecule type: DNA

A:Residues: 514-521, 'R', 523-526, 'E', 528-555, 'T', 557-561, 'V', 563-582, 'Q', 584-586, 'K', 588-6

A:Cross-references: GB:M73549

C:Superfamily: herpesvirus glycoprotein B

C:Keywords: glycoprotein; transmembrane protein

F:1-36/Domain: signal sequence #status predicted <SIG>

F:37-928/Product: glycoprotein B #status predicted <GPB>

F:757-804/Domain: transmembrane #status predicted <TMN>

F:93,223,315,354,398,423,470,487,618,667/Binding site: carbohydrate (Aa) (covalent) #str

Query Match 43.2%; Score 51; DB 1; Length 928;
Best Local Similarity 69.2%; Pred. No. 7.8;
Matches 9; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 6 FCGHNSVDFEEDTL 18

Db 295 YNGENSEPFEEDT 307

RESULT 6

hypothetical protein MJ1394 - Methanococcus jannaschii

C:Species: Methanococcus jannaschii

C:Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004

C:Accession: A64474

R:Bult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blake, C.

Reich, C.I.; Overbeek, R.; Kirsch, E.F.; Weissbach, K.G.; Merrick, J.M.; Glodek, A.;

Leon, J.D.; Sadow, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hureb, M.A.

Science 273, 1058-1073, 1996

A:Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Frazer, C.M.; Smith, H.O.; Woese, C.

A:Title: Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschii.

A:Reference number: A64300; MUID:96337999; PMID:8688087

A:Accession: A64474

A:Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-987 <BDL>

A:Cross-references: UNIPROT:Q58789; GB:U67579; GB:L77117; NID:g1592037; PIDN:AAB99404.1;

C:Genetics:

A:Map position: FOR1343894-1346857

A:Start codon: GTG

Query Match 42.4%; Score 50; DB 2; Length 987;
Best Local Similarity 44.0%; Pred. No. 12;
Matches 11; Conservative 5; Mismatches 3; Indels 6; Gaps 2;

OY 1 KPSYQFG--GH---NSVDFEEDTL 19

Db 241 KTNYSYGLTGHIIIENTAPYKEDTL 265

RESULT 7

subtilisin homolog T6H20.130 - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)

C:Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 09-Jul-2004

C:Accession: T12964

R:Chisane, N.; Robert, C.; Brottier, P.; Wincker, P.; Catcollin, L.; Artiguenave, F.; Sav

submitted to the Protein Sequence Database, July 1999

A:Reference number: T12964

A:Accession: T12964

A:Molecule type: DNA

A:Residues: 1-739 <CHO>

A:Cross-references: UNIPROT:Q9STF6; EMBL:AL096859; GSPDB:GN00061; ATSP:T6H20.130

A:Experimental source: cultivar Columbia; BAC clone T6H20

C:Genetics:

A:Gene: ATSP:T6H20.130

A:Map position: 3

A:introns: 33/3; 65/2; 96/1; 180/2; 350/3; 382/2; 454/2; 491/3; 561/1
 C:Superfamily: subtilisin-like proteinase ag12; subtilisin homology

Query Match 41.5%; Score 49; DB 2; Length 739;
 Best Local Similarity 69.2%; Pred. No. 13;
 Matches 9; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 7 GGHNSVPFEEDTL 19
 DB 278 GGDNSPFEEDPI 290

RESULT 8

A36057
 MHC class I histocompatibility antigen alpha chain 1 (clone-lambdaTLAI-1) - common carp
 C:Species: Cyprinus carpio (common carp)
 C>Date: 18-Jan-1991 #sequence_revision 18-Jan-1991 #text_change 09-Jul-2004
 C:Accession: A36057; Nakaniishi, T.; Kurokawa, Y.
 R:Hashimoto, K.; Nakaniishi, T.; Kurokawa, Y.
 Proc. Natl. Acad. Sci. U.S.A. 87, 6863-6867, 1990
 A>Title: Isolation of carp genes encoding major histocompatibility complex antigens.
 A:Reference number: A36057; MUID:90370884; PMID:2395879
 A:Accession: A36057
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-257 <HAS>
 A:Cross-references: UNIPROT:Q95589; GB:M37106

Query Match 39.8%; Score 47; DB 2; Length 257;
 Best Local Similarity 56.2%; Pred. No. 7.8;
 Matches 9; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 4 YQFGHNSVPFEEDTL 19
 DB 108 YGFGEDCAFRSDTL 123

RESULT 9

A39356
 3-oxoacyl-[acyl-carrier-protein] synthase (EC 2.3.1.41) I beta chain precursor, chlorophyll
 N:Alternate names: beta-ketoacyl-[acyl carrier protein] synthase I
 C:Species: Hordeum vulgare (barley)
 C>Date: 06-Mar-1992 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
 C:Accession: A39356; A45129
 R:Siggaard-Andersen, M.; Kauppinen, S.; von Wettstein-Knowles, P.
 Proc. Natl. Acad. Sci. U.S.A. 88, 4114-4118, 1991
 A>Title: Primary structure of a cerulenin-binding beta-ketoacyl-[acyl carrier protein] S
 A:Reference number: A39356; MUID:91239517; PMID:2034657
 A:Accession: A39356
 A:Molecule type: mRNA
 A:Residues: 1-462 <SIG>

A:Cross-references: UNIPROT:P23902; GB:M60410; NID:g167064; PIDN:AAA32968.1; PID:g167065
 A:Experimental source: cv. Bonus, leaf
 A>Note: parts of this sequence, including the amino end of the mature protein, were conf
 R:Kauppinen, S.
 J. Biol. Chem. 267, 23999-24006, 1992

A>Title: Structure and expression of the Kas12 gene encoding a beta-ketoacyl-acyl carrie
 A:Reference number: A45129; MUID:93054767; PMID:1429736
 A:Accession: A45129

A:Molecule type: DNA
 A:Residues: 1-395,397-414, 'T', 415-462 <KAU>
 A:Experimental source: cv. Bonus
 A>Note: sequence inconsistent with the nucleotide translation; translation agrees with B
 A>Note: sequence extracted from NCBI backbone (NCBIP:118934)
 C:Genetics:

A:Gene: Kas12
 A:Map position: 2
 A:introns: 144/3; 288/3; 346/3; 384/3; 418/3; 441/1
 C:Complex: homodimer or heterodimer with alpha chain
 C:Superfamily: 3-oxoacyl-[acyl-carrier-protein] synthase I; 3-oxoacyl-[acyl-carrier-pro] C:Keyw
 F1-36/Domain: transit peptide (chloroplast) #status predicted <TNP>
 F136-462/Product: 3-oxoacyl-[acyl-carrier-protein] synthase I beta chain #status experim

F:68-457/Domain: 3-oxoacyl-[acyl-carrier-protein] synthase I homology <OAS>
 F:213/Active site: Cys #status experimental

Query Match 39.8%; Score 47; DB 1; Length 462;
 Best Local Similarity 58.8%; Pred. No. 15;
 Matches 10; Conservative 2; Mismatches 1; Indels 4; Gaps 1;

QY 3 SYQFGHNSV----PFE 15
 DB 445 SFGFGHNSVVVAPFK 461

RESULT 10

S61441
 surface-associated protein cshA precursor - Streptococcus gordonii
 N:Alternate names: adhesin
 C:Species: Streptococcus gordonii
 C>Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
 C:Accession: S61441; S61454; S27982
 R:McNab, R.; Jenkinson, H.F.; Loach, D.M.; Tannock, G.W.
 Mol. Microbiol. 14, 743-754, 1994
 A>Title: Cell-surface-associated polypeptides CshA and CshB of high molecular mass are c
 A:Reference number: S61441; MUID:95198547; PMID:7891560
 A:Accession: S61441
 A:Status: nucleic acid sequence not shown

A:Molecule type: DNA
 A:Residues: 1-2508 <MCN>
 A:Cross-references: UNIPROT:Q54194; EMBL:X65164; NID:g1808670; PIDN:CAA46281.1; PID:g457.
 A:Accession: S61454

A:Molecule type: protein
 A:Residues: 42-43, 'Y', 45-51 <MCN2>
 R:McNab, R.; Jenkinson, H.F.
 Mol. Microbiol. 6, 2939-2949, 1992
 A>Title: Gene disruption identifies a 290 kDa cell-surface polypeptide conferring hydrop
 A:Reference number: S27982; MUID:93125117; PMID:1479886
 A:Accession: S27982

A:Molecule type: DNA
 A:Residues: 2026-2508 <MC2>
 A:Cross-references: EMBL:X65164
 C:Genetics:

A:Gene: cshA
 F:1-41/Domain: signal sequence #status predicted <SIG>
 F:42-2508/Product: surface-associated protein cshA #status experimental <MAT>

Query Match 39.8%; Score 47; DB 2; Length 2508;
 Best Local Similarity 61.5%; Pred. No. 1.1e+02;
 Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 8 GHNVPFEEDTL 20
 DB 1450 GHDSVPFADSTP 1462

RESULT 11

T25804
 hypothetical protein H03E18.1 - Caenorhabditis elegans
 C:Species: Caenorhabditis elegans
 C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
 C:Accession: T25804

R:Bentley, D.
 submitted to the EMBL Data Library, August 1996
 A:Description: The sequence of C. elegans cosmid H03E18.
 A:Reference number: Z20090
 A:Accession: T25804

A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-1127 <BEN>

A:Cross-references: UNIPROT:Q94248; EMBL:U67947; PIDN:AA07557.1; GSPDB:GM00028; CESP:H0;
 A:Experimental source: strain Bristol N2; clone H03E18
 C:Genetics:

A:Gene: CESP:H03E18.1
 A:Map position: X
 A:introns: 112/3; 217/1; 282/2; 304/1; 424/1; 461/2; 579/3; 615/2; 831/1; 999/2; 1088/1

A;Description: oligo-1,6-glucosidase catalyzes the hydrolysis of 1,6-alpha-D-glucosidic
 A;Pathway: carbohydrate digestion
 C;Function: <SUC>
 A;Description: sucrose alpha-glucosidase catalyzes the hydrolysis of the 1,2-alpha-D-glu
 A;Pathway: carbohydrate digestion
 C;Superfamily: sucrase/isomaltase; sucrase/isomaltase homology; trefoil homology
 C;Keywords: carbohydrate digestion; duplication; glycoprotein; glycosidase; hydrolase; m
 F;2-1007/Product: oligo-1,6-glucosidase (isomaltase chain) #status experimental <MAT1>
 F;13-32/Domain: membrane associated #status predicted <TMM>
 F;42-60/Region: serine/threonine-rich
 F;63-109/Domain: trefoil homology <TRF1>
 F;189-840/Domain: sucrase/isomaltase homology <SIM>
 F;931-977/Domain: trefoil homology <TRF2>
 F;1008-1827/Product: sucrase alpha-glucosidase (sucrase chain) #status experimental <MAT
 F;1062-1734/Domain: sucrase/isomaltase homology <SIM2>
 F;12/Binding site: carbohydrate (Ser) (covalent) #status absent
 F;99,437,455,823,855,904,926,1235,1303,1340,1354,1403,1535,1572,1675,1748,1763,1815/Bind
 F;1007-1008/Cleavage site: Arg-116 (trypsin) #status predicted

Query Match 38.1%; Score 45; DB 1; Length 1827;

Best Local Similarity 66.7%; Pred. No. 1.5e+02;

Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 7 GGHNSVPPEEDT 18

DB 1791 GNKNSLPFNEEDT 1802

Search completed: October 22, 2005, 04:13:54
 Job time : 11.5465 secs

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FT REPEAT 545 574 B-1.
FT REPEAT 575 604 B-2.
FT DOMAIN 745 878 4 X approximate tandem repeats,
  fibronectin-binding domain.
FT REPEAT 745 782 D-1.
FT REPEAT 783 820 D-2.
FT REPEAT 821 859 D-3.
FT REPEAT 860 878 D-4 (incomplete).
FT DOMAIN 879 948 5 X tandem repeats, Pro-rich (WR).
FT REPEAT 879 892 WR 1.
FT REPEAT 893 906 WR 2.
FT REPEAT 907 920 WR 3.
FT REPEAT 921 934 WR 4.
FT REPEAT 935 948 WR 5.
FT SITE 982 986 LPXTG sorting signal (Potential).
FT MOD_RES 985 985 Pentaglycyl murein peptidoglycan amidated
  threonine (Potential).
SQ SEQUENCE 1018 AA; 111780 MW; 58175E0020E81F1F CRC64;

Query Match 93.2%; Score 110; DB 1; Length 1018;
Best Local Similarity 95.2%; Pred. No. 1.8e-08;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy 1 KPSYQFGHNSVPPEEDTLRK 21
Db 837 KPSYQFGHNSVPPEEDTLRK 857

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RESULT 2
ID 099RD3 PRELIMINARY; PRT; 961 AA.
AC 099RD3;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Fibronectin-binding protein hemolig.
GN Name=fnb3; OrderedLocusNames=SAV2502;
OS Staphylococcus aureus (strain Mu50 / ATCC 700699).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=158878;
RN [1]
RP SEQUENCE FROM N.A.
RC STEADY-STATE / ATCC 700699;
RX MEDLINE=21311952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2;
RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
  Cui L., Oguchi A., Aoki K.-I., Nagai Y., Lian J.-Q., Ito T.,
  Kanamori M., Matsunaru H., Maruyama A., Murakami H., Hoshiyama A.,
  Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
  Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
  Kanehisa M., Yamashta A., Oshima K., Furuya K., Yoshino C., Shiba T.,
  Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
  "Whole genome sequencing of methicillin-resistant Staphylococcus
  aureus."
RT Lancel 357:1225-1240(2001).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
  an amide bond (By similarity).
DR EMBL; AP003365; BAB58664.1; -.
DR FTR; G90053; G90053.
DR HSP; Q53653; I167.
DR GO; GO:0009986; C:cell surface; IEA.
DR GO; GO:0005618; C:cell wall; IEA.
DR GO; GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0007155; P:cell adhesion; IEA.
DR InterPro; IPR008966; Adhes_bact.
DR InterPro; IPR004237; Fn_bind.
DR InterPro; IPR005877; Gpos_YsIRK.
DR InterPro; IPR001899; Gram_pos_anchor.
DR Pfam; PF02986; Fn_bind; 1.
DR Pfam; PF00746; Gram_pos_anchor; 1.
DR Pfam; PF04650; YsIRK_signal; 1.
DR TIGRfams; TIGR01167; LPXTG_anchor; 1.
DR TIGRfams; TIGR01168; YsIRK_signal; 1.

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DR PROSITE; PSS0847; GRAM_POS_ANCHORING; 1.
KW Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ SEQUENCE 961 AA; 106010 MW; 364940F884BA4101 CRC64;

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Qy 1 KPSYQFGHNSVPPEEDTLRK 21
Db 784 KPSYQFGHNSVPPEEDTLRK 804

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RESULT 3
ID 07A3J8 PRELIMINARY; PRT; 961 AA.
AC 07A3J8;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE FmbB protein.
GN Name=fnb3; OrderedLocusNames=SA2290;
OS Staphylococcus aureus (strain N315).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=158879;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21311952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2;
RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
  Cui L., Oguchi A., Aoki K.-I., Nagai Y., Lian J.-Q., Ito T.,
  Kanamori M., Matsunaru H., Maruyama A., Murakami H., Hoshiyama A.,
  Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
  Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
  Kanehisa M., Yamashta A., Oshima K., Furuya K., Yoshino C., Shiba T.,
  Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
  "Whole genome sequencing of methicillin-resistant Staphylococcus
  aureus."
RT Lancel 357:1225-1240(2001).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
  an amide bond (By similarity).
DR EMBL; AP003365; BAB58664.1; -.
DR GO; GO:0009986; C:cell surface; IEA.
DR GO; GO:0005618; C:cell wall; IEA.
DR GO; GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0007155; P:cell adhesion; IEA.
DR InterPro; IPR008966; Adhes_bact.
DR InterPro; IPR004237; Fn_bind.
DR InterPro; IPR005877; Gpos_YsIRK.
DR InterPro; IPR001899; Gram_pos_anchor.
DR Pfam; PF02986; Fn_bind; 1.
DR Pfam; PF00746; Gram_pos_anchor; 1.
DR Pfam; PF04650; YsIRK_signal; 1.
DR TIGRfams; TIGR01167; LPXTG_anchor; 1.
DR TIGRfams; TIGR01168; YsIRK_signal; 1.
DR PROSITE; PSS0847; GRAM_POS_ANCHORING; 1.
KW Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ SEQUENCE 961 AA; 106010 MW; 364940F884BA4101 CRC64;

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Query Match 90.7%; Score 107; DB 2; Length 961;
Best Local Similarity 90.5%; Pred. No. 5.1e-08;
Matches 19; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KPSYQFGHNSVPPEEDTLRK 21
Db 784 KPSYQFGHNSVPPEEDTLRK 804

RESULT 4
ID 06GDUS PRELIMINARY; PRT; 965 AA.
AC 06GDUS;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)

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DT 05-JUN-2004 (TREMblrel. 27, Last sequence update)
DR 05-JUN-2004 (TREMblrel. 27, Last annotation update)
DN Fibronectin-binding protein.
GN Name=fnbA; OrderedLocNames=SAR2580;
OS Staphylococcus aureus (strain MRSA2525).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
CX NCBI_TaxID=282458;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed:15213324; DOI=10.1073/pnas.0402521101;
RA Holden M.T.G., Fell E.J., Lindsay J.A., Peacock S.J., Day N.P.J.,
RA Enright M.C., Foster T.J., Moore C.E., Hurst L., Atkin R., Barron A.,
RA Baason N., Bentley S.D., Chillingworth C., Chillingworth T.,
RA Churcher C., Clark L., Corbin A., Doggett J., Dowd L.,
RA Felwell T., Hance Z., Harris B., Hauser H., Holroyd S., Jagels K.,
RA James K.D., Leonard N., Line A., Mayes R., Moutie S., Mungall K.,
RA Ormond D., Quail M.A., Rabinowitch E., Rutherford K.M., Sanders M.,
RA Sharp S., Simmonds M., Stevens K., Whitehead S., Barrell B.G.,
RA Spratt B.G., Parthill J.;
RT "Complete genomes of two clinical Staphylococcus aureus strains:
RT evidence for the rapid evolution of virulence and drug resistance.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:9786-9791(2004).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC an amide bond (by similarity).
DR EMBL; BX571856; CAG41560.1; -.
DR GO; GO:0009986; C:cell surface; IEA.
DR GO; GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0007155; P:cell adhesion; IEA.
DR InterPro; IPR008966; Adhes_bact.
DR InterPro; IPR004237; Fm_bind.
DR InterPro; IPR001899; Gram_pos_anchor.
DR Pfam; PF02986; Fm_bind_1.
DR Pfam; PF00746; Gram_pos_anchor; 1.
DR Pfam; PF04650; YSIRK_signal; 1.
DR TIGRfams; TIGR01167; LpXTG_anchor; 1.
DR TIGRfams; TIGR01168; YSIRK_signal; 1.
DR PROSITE; PS50847; GRAM_POS_ANCHORING; 1.
KW Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ SEQUENCE 965 AA; 105691 MW; 2582E132164D0551 CRC64;

Query Match 90.7%; Score 107; DB 2; Length 965;
Best Local Similarity 90.5%; Pred. No. 5,1e-08;
Matches 19; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 KPSYQFGHNSVDFEDTLPK 21
DB 802 KPNYQFGHNSVDFEDTLPK 822

RESULT 5
Q8NUU7 PRELIMINARY; PRT; 1015 AA.
AC Q8NUU7;
DT 01-OCT-2002 (TREMblrel. 22, Created)
DT 01-OCT-2002 (TREMblrel. 22, Last sequence update)
DT 01-OCT-2003 (TREMblrel. 25, Last annotation update)
DE Fnb protein.
GN Name=fnb; OrderedLocNames=MM2421;
OS Staphylococcus aureus (strain MM2).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
CX NCBI_TaxID=196620;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=MM2;
RC MEDLINE=22040717; PubMed=12044378; DOI=10.1016/S0140-6736(02)08713-5;
RA Baba T., Takeuchi F., Yuzawa M., Yuzawa H., Aoki K.-I., Oguchi A.,
RA Nagai Y., Iwano K., Asano K., Naimi T., Kuroda H., Cui L.,
RA Yamamoto K., Hiratake K.;
RT "Genome and virulence determinants of high virulence community-
RT acquired MRSA.";
RL Lancet 359:1819-1827(2002).
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CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC an amide bond (by similarity).
DR EMBL; AP004830; BAB96286.1; -.
DR GO; GO:0009986; C:cell surface; IEA.
DR GO; GO:0005618; C:cell wall; IEA.
DR GO; GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0007155; P:cell adhesion; IEA.
DR InterPro; IPR008966; Adhes_bact.
DR InterPro; IPR004237; Fm_bind.
DR InterPro; IPR005877; Gpos_YSIRK.
DR InterPro; IPR001899; Gram_pos_anchor.
DR Pfam; PF02986; Fm_bind_1.
DR Pfam; PF00746; Gram_pos_anchor; 1.
DR Pfam; PF04650; YSIRK_signal; 1.
DR TIGRfams; TIGR01167; LpXTG_anchor; 1.
DR TIGRfams; TIGR01168; YSIRK_signal; 1.
DR PROSITE; PS50847; GRAM_POS_ANCHORING; 1.
KW Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ SEQUENCE 1015 AA; 111145 MW; D0F9281BB64D4D2 CRC64;

Query Match 90.7%; Score 107; DB 2; Length 1015;
Best Local Similarity 90.5%; Pred. No. 5,4e-08;
Matches 19; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 KPSYQFGHNSVDFEDTLPK 21
DB 838 KPNYQFGHNSVDFEDTLPK 858

RESULT 6
Q6G6H3 PRELIMINARY; PRT; 1015 AA.
AC Q6G6H3;
DT 05-JUN-2004 (TREMblrel. 27, Created)
DT 05-JUN-2004 (TREMblrel. 27, Last sequence update)
DT 05-JUN-2004 (TREMblrel. 27, Last annotation update)
DN Fibronectin-binding protein.
GN OrderedLocNames=SAS2388;
OS Staphylococcus aureus (strain MSSA476).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
CX NCBI_TaxID=282459;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed:15213324; DOI=10.1073/pnas.0402521101;
RA Holden M.T.G., Fell E.J., Lindsay J.A., Peacock S.J., Day N.P.J.,
RA Enright M.C., Foster T.J., Moore C.E., Hurst L., Atkin R., Barron A.,
RA Baason N., Bentley S.D., Chillingworth C., Chillingworth T.,
RA Churcher C., Clark L., Corbin A., Doggett J., Dowd L.,
RA Felwell T., Hance Z., Harris B., Hauser H., Holroyd S., Jagels K.,
RA James K.D., Leonard N., Line A., Mayes R., Moutie S., Mungall K.,
RA Ormond D., Quail M.A., Rabinowitch E., Rutherford K.M., Sanders M.,
RA Sharp S., Simmonds M., Stevens K., Whitehead S., Barrell B.G.,
RA Spratt B.G., Parthill J.;
RT "Complete genomes of two clinical Staphylococcus aureus strains:
RT evidence for the rapid evolution of virulence and drug resistance.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:9786-9791(2004).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC an amide bond (by similarity).
DR EMBL; BX571857; CAG44202.1; -.
DR GO; GO:0009986; C:cell surface; IEA.
DR GO; GO:0005618; C:cell wall; IEA.
DR GO; GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0007155; P:cell adhesion; IEA.
DR InterPro; IPR008966; Adhes_bact.
DR InterPro; IPR004237; Fm_bind.
DR InterPro; IPR005877; Gpos_YSIRK.
DR InterPro; IPR001899; Gram_pos_anchor.
DR Pfam; PF02986; Fm_bind_1.
DR Pfam; PF00746; Gram_pos_anchor; 1.
DR Pfam; PF04650; YSIRK_signal; 1.
DR TIGRfams; TIGR01167; LpXTG_anchor; 1.
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DR TIGRFAMs; TIGR01168; YSIRK signal; 1.
 DR PROSITE; PSS0847; GRAM_POS_ANCHORING; 1.
 DR Cell wall; Complete proteome; Peptidoglycan-anchor.
 SQ SEQUENCE 1015 AA; 11145 MW; D0F9281BB4D4D2 CRC64;

Query Match 90.7%; Score 107; DB 2; Length 1015;
 Best Local Similarity 90.5%; Pred. No. 5.4e-08;

Matches 19; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 KPSYQFGHNSVDFEEDTLPK 21
 ||:|||||
 DB 838 KPNYQFGHNSVDFEEDTLPK 858

RESULT 7

Q99RD2 PRELIMINARY; PRT; 1038 AA.
 AC Q99RD2;
 DT 01-JUN-2001 (TIGR01167, 17, Created)
 DT 01-JUN-2001 (TIGR01167, 17, Last sequence update)
 DT 01-MAR-2004 (TIGR01167, 26, Last annotation update)
 DE Fibronectin-binding protein homolog.
 GN Name=fnb; OrderedLocuNames=SAV2503;
 OS Staphylococcus aureus (strain Mu50 / ATCC 700699).
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 NC NCBI_TaxID=158878;

SEQUENCE FROM N.A.
 RC STRAIN=Mu50 / ATCC 700699;
 RX MEDLINE=21311952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2;
 RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
 RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Iian J.-O., Ito T.,
 RA Kanamori M., Matsunaru H., Maruyama A., Murakami H., Hosoyama A.,
 RA Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kato C.,
 RA Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
 RA Kamehisa M., Yamaoka A., Oshima K., Furuya K., Yoshino C., Shiba T.,
 RA Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
 RT "Whole genome sequencing of methicillin-resistant Staphylococcus
 aureus.";
 RL Lancet 357:1225-1240(2001).
 CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
 an amide bond (By similarity).
 DR EMBL; AP003137; BAB43594.1; -;
 DR PIR; H90053; H90053.

DR GO; GO:0009986; C:cell surface; IEA.
 DR GO; GO:0005618; C:cell wall; IEA.
 DR GO; GO:0009215; C:cell wall (sensu Gram-positive Bacteria); IEA.
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0007155; P:cell adhesion; IEA.
 DR InterPro; IPR008966; Adhes_bact.
 DR InterPro; IPR004237; Fn_bind.
 DR InterPro; IPR005877; Gpos_YsIRK.
 DR InterPro; IPR001899; Gram_pos_anchor.
 DR Pfam; PF02986; Fn_bind; 1.
 DR Pfam; PF00746; Gram_pos_anchor; 1.
 DR Pfam; PF04650; YSIRK_signal; 1.
 DR TIGRFAMs; TIGR01167; LPTXG_anchor; 1.
 DR TIGRFAMs; TIGR01168; YSIRK_signal; 1.
 DR PROSITE; PSS0847; GRAM_POS_ANCHORING; 1.
 DR Cell wall; Complete proteome; Peptidoglycan-anchor.
 SQ SEQUENCE 1038 AA; 113618 MW; 666BF6BF2FBEB12 CRC64;

Query Match 90.7%; Score 107; DB 2; Length 1038;
 Best Local Similarity 90.5%; Pred. No. 5.6e-08;
 Matches 19; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 KPSYQFGHNSVDFEEDTLPK 21
 ||:|||||
 DB 833 KPNYQFGHNSVDFEEDTLPK 853

RESULT 8

Q7A3J7

ID Q7A3J7 PRELIMINARY; PRT; 1038 AA.
 AC Q7A3J7;
 DT 05-JUL-2004 (TIGR01167, 27, Created)
 DT 05-JUL-2004 (TIGR01167, 27, Last sequence update)
 DT 05-JUL-2004 (TIGR01167, 27, Last annotation update)
 DE Fnb protein.
 GN Name=fnb; OrderedLocuNames=SA2291;
 OS Staphylococcus aureus (strain N315).
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 NC NCBI_TaxID=158879;

SEQUENCE FROM N.A.
 RX MEDLINE=21311952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2;
 RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
 RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Iian J.-O., Ito T.,
 RA Kanamori M., Matsunaru H., Maruyama A., Murakami H., Hosoyama A.,
 RA Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kato C.,
 RA Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
 RA Kamehisa M., Yamaoka A., Oshima K., Furuya K., Yoshino C., Shiba T.,
 RA Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
 RT "Whole genome sequencing of methicillin-resistant Staphylococcus
 aureus.";
 RL Lancet 357:1225-1240(2001).
 CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
 an amide bond (By similarity).
 DR EMBL; AP003137; BAB43594.1; -;
 DR PIR; H90053; H90053.

DR GO; GO:0009986; C:cell surface; IEA.
 DR GO; GO:0005618; C:cell wall; IEA.
 DR GO; GO:0009215; C:cell wall (sensu Gram-positive Bacteria); IEA.
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0007155; P:cell adhesion; IEA.
 DR InterPro; IPR008966; Adhes_bact.
 DR InterPro; IPR004237; Fn_bind.
 DR InterPro; IPR005877; Gpos_YsIRK.
 DR InterPro; IPR001899; Gram_pos_anchor.
 DR Pfam; PF02986; Fn_bind; 1.
 DR Pfam; PF00746; Gram_pos_anchor; 1.
 DR Pfam; PF04650; YSIRK_signal; 1.
 DR TIGRFAMs; TIGR01167; LPTXG_anchor; 1.
 DR TIGRFAMs; TIGR01168; YSIRK_signal; 1.
 DR PROSITE; PSS0847; GRAM_POS_ANCHORING; 1.
 DR Cell wall; Complete proteome; Peptidoglycan-anchor.
 SQ SEQUENCE 1038 AA; 113618 MW; 666BF6BF2FBEB12 CRC64;

Query Match 90.7%; Score 107; DB 2; Length 1038;
 Best Local Similarity 90.5%; Pred. No. 5.6e-08;
 Matches 19; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 KPSYQFGHNSVDFEEDTLPK 21
 ||:|||||
 DB 833 KPNYQFGHNSVDFEEDTLPK 853

RESULT 9

Q53682 PRELIMINARY; PRT; 940 AA.
 AC Q53682;
 DT 01-NOV-1996 (TIGR01167, 01, Created)
 DT 01-NOV-1996 (TIGR01167, 01, Last sequence update)
 DT 01-MAR-2004 (TIGR01167, 26, Last annotation update)
 DE Fibronectin binding protein B.
 GN Name=fnbB;
 OS Staphylococcus aureus.
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 NC NCBI_TaxID=1280;

SEQUENCE FROM N.A.
 RC STRAIN=8325-4;
 RX MEDLINE=92111475; PubMed=1837266;
 RA Johnson K., Sigman C., Muller H.P., Lindberg M.;
 RT "Two different genes encode fibronectin binding proteins in
 Staphylococcus aureus. The complete nucleotide sequence and
 characterization of the second gene.";

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RL Eur. J. Biochem. 202:1041-1048(1991).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
   an amide bond (By similarity).
DR EMBL: X62992; CAA44726.1; -.
DR PIR: S19702; S19702.
DR HSSP: Q53653; 1N67.
DR GO: GO:0009986; C:cell surface; IEA.
DR GO: GO:0005618; C:cell wall; IEA.
DR GO: GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO: GO:0016020; C:membrane; IEA.
DR GO: GO:0007155; P:cell adhesion; IEA.
DR InterPro: IPR008966; Adhes_Bact.
DR InterPro: IPR004237; Fn_bind.
DR InterPro: IPR001899; Gram_pos_anchor.
DR Pfam: PF02986; Fn_bind_2.
DR Pfam: PF00746; Gram_pos_anchor_1.
DR Pfam: PF04650; YSIRK_signal_1.
DR TIGRfams: TIGR01167; LpXTG_anchor_1.
DR TIGRfams: TIGR01168; YSIRK_signal_1.
DR PROSITE: PS0847; GRAM_POS_ANCHORING; 1.
KW Cell wall, Peptidoglycan-anchor.
SQ SEQUENCE 940 AA; 10355 MW; E5FBBCA907AE345 CRC64;

Query Match      87.3%; Score 103; DB 2; Length 940;
Best Local Similarity 85.7%; Pred. No. 2.2e-07;
Matches 18; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 1 KPSYQFGHNSVDFEEDTLPK 21
Db 773 KENYQFGHNSVDFEEDTLPO 793

RESULT 10
ID Q8NU08 PRELIMINARY; PRT; 943 AA.
Q8NU08
AC 01-OCT-2002 (TREMBLrel. 22, Created)
DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DS FnBb protein.
OS Name=fnbB; OrderedLocuNames=WM2420;
OS Staphylococcus aureus (strain WM2).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
CX NCBI_TaxId=196620;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=WM2;
RX MEDLINE=22040717; PubMed=12044378; DOI=10.1016/S0140-6736(02)08713-5;
RX Baba T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Oguchi A.,
RX Nagai Y., Iwama N., Asano K., Naim T., Kuroda H., Cui L.,
RX Yamamoto K., Hizamatsu K.,
RT "Genome and virulence determinants of high virulence community-
RT acquired MRSA."
RT Lancet 359;1819-1827(2002).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
   an amide bond (By similarity).
DR EMBL: AP004830; BAB96285.1; -.
DR HSSP: Q53653; 1N67.
DR GO: GO:0009986; C:cell surface; IEA.
DR GO: GO:0005618; C:cell wall; IEA.
DR GO: GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO: GO:0016020; C:membrane; IEA.
DR GO: GO:0007155; P:cell adhesion; IEA.
DR InterPro: IPR008966; Adhes_Bact.
DR InterPro: IPR004237; Fn_bind.
DR InterPro: IPR005877; Gpos_YSIRK.
DR InterPro: IPR001899; Gram_pos_anchor.
DR Pfam: PF02986; Fn_bind_1.
DR Pfam: PF00746; Gram_pos_anchor_1.
DR TIGRfams: TIGR01167; LpXTG_anchor_1.
DR TIGRfams: TIGR01168; YSIRK_signal_1.
DR PROSITE: PS0847; GRAM_POS_ANCHORING; 1.
KW Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ SEQUENCE 957 AA; 105980 MW; 28F8BA7FFDFD3EAF CRC64;

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DR PROSITE: PS0847; GRAM_POS_ANCHORING; 1.
KW Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ SEQUENCE 943 AA; 104537 MW; DAB5F31947E1B6A CRC64;

Query Match      87.3%; Score 103; DB 2; Length 943;
Best Local Similarity 85.7%; Pred. No. 2.2e-07;
Matches 18; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 1 KPSYQFGHNSVDFEEDTLPK 21
Db 780 KENYQFGHNSVDFEEDTLPO 800

RESULT 11
ID Q6G6H4 PRELIMINARY; PRT; 957 AA.
Q6G6H4
AC Q6G6H4;
DT 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE Fibrinectin-binding protein.
DE Name=fnbB; OrderedLocuNames=SAS2387;
OS Staphylococcus aureus (strain MSSA476).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
CX NCBI_TaxId=282459;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=1521324; DOI=10.1073/pnas.0402521101;
RX Holden M.T.G., Fell E.J., Lindsay J.A., Peacock S.J., Day N.P.J.,
RX Enright M.C., Foster T.J., Moore C.E., Hurst L., Atkin R., Barron A.,
RX Baon N., Bentley S.D., Chillingworth C., Chillingworth T.,
RX Churcher C., Clark L., Cotton C., Cronin A., Doggett J., Dowd L.,
RX James K.D., Lennard N., Line A., Mayes R., Moulis S., Mungall K.,
RX Ormond D., Quail M.A., Rabinowitsch E., Rutherford K.M., Sanders M.,
RX Sharp S., Simmonds M., Stevens K., Whitehead S., Barrell B.G.,
RX Spratt B.G., Parkhill J.,
RT "Complete genomes of two clinical Staphylococcus aureus strains:
RT evidence for the rapid evolution of virulence and drug resistance."
RT Proc. Natl. Acad. Sci. U.S.A. 101:9786-9791(2004).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
   an amide bond (By similarity).
DR EMBL: BX571857; CAG44201.1; -.
DR GO: GO:0009986; C:cell surface; IEA.
DR GO: GO:0005618; C:cell wall; IEA.
DR GO: GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO: GO:0016020; C:membrane; IEA.
DR GO: GO:0007155; P:cell adhesion; IEA.
DR InterPro: IPR008966; Adhes_bact.
DR InterPro: IPR004237; Fn_bind.
DR InterPro: IPR005877; Gpos_YSIRK.
DR InterPro: IPR001899; Gram_pos_anchor.
DR Pfam: PF02986; Fn_bind_1.
DR Pfam: PF00746; Gram_pos_anchor_1.
DR TIGRfams: TIGR01167; LpXTG_anchor_1.
DR TIGRfams: TIGR01168; YSIRK_signal_1.
DR PROSITE: PS0847; GRAM_POS_ANCHORING; 1.
KW Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ SEQUENCE 957 AA; 105980 MW; 28F8BA7FFDFD3EAF CRC64;

Query Match      87.3%; Score 103; DB 2; Length 957;
Best Local Similarity 85.7%; Pred. No. 2.2e-07;
Matches 18; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 1 KPSYQFGHNSVDFEEDTLPK 21
Db 780 KENYQFGHNSVDFEEDTLPO 800

RESULT 12
O9AEP9 PRELIMINARY; PRT; 152 AA.
O9AEP9

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AC Q9ABP9;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Fibronectin-binding protein (Fragment).
GN Name=fnb;
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1280;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CMRSA-1;
RX MEDLINE=21246681; PubMed=11349044;
DOI=10.1128/IAI.69.6.3791-3799.2001;
RA Rice K., Huebner M., Vaz D., McGavin M.J.;
RT "Variance in fibronectin binding and fnb locus polymorphisms in
RT Staphylococcus aureus: identification of antigenic variation in a
RT fibronectin binding protein adhesion of the epidemic CMRSA-1 strain of
RT methicillin-resistant S. aureus.";
RL Infect. Immun. 69:3791-3799(2001).
DR EMBL; AY029184; AAK3188.1; -.
FT NON TER 1
FT NON TER 152
SQ SEQUENCE 152 AA; 17193 MW; CFA3913C2B11C025 CRC64;

Query Match 83.1%; Score 98; DB 2; Length 152;
Best Local Similarity 81.0%; Pred. No. 1.7e-07;
Matches 17; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 KPSYQFGHNSVPEEDTLRK 21
| | | | | | | | | | | | | | | | | | | | | |
DB 130 KPSYQFGHNSVPEEDTLRK 150

RESULT 13
Q75C56 PRELIMINARY; PRT; 668 AA.
AC Q75C56;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE AC06060P.
GN ORNNames=ACR060W;
OS Aeshby goesypli (yeast) (Bremothecium goesypli).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Bremothecium.
OX NCBI_TaxID=33169;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 10895;
RA Brachet S., Voegelé S.E., Dietrich F.S., Lerch A., Gaffney T.,
RA Philpott P.;
RL Submitted (SEP-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AE016816; AAS51287.1; -.
DR AGD; ACR060W; -.
GN GO: GO:0005643; C:nuclear pore; IEA.
DR GO: GO:0017056; F:structural constituent of nuclear pore; IEA.
DR InterPro; IPR007758; Np1_C.
DR Pfam; PF05064; Np1_C; 1.
SQ SEQUENCE 668 AA; 69310 MW; 194CCD0B302F3FF6 CRC64;

Query Match 46.6%; Score 55; DB 2; Length 668;
Best Local Similarity 42.9%; Pred. No. 6.9;
Matches 9; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

QY 1 KPSYQFGHNSVPEEDTLRK 21
| | | | | | | | | | | | | | | | | | | | | |
DB 276 KPSYQFGHNSVPEEDTLRK 236

RESULT 14
Q8SSA9 PRELIMINARY; PRT; 933 AA.
ID Q8SSA9

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AC Q8SSA9;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE UNIDENTIFIED CARBOXY-TERMINAL HYDROLASE.
GN Name=EC03_0580;
OS Encephalitozoon cuniculi GB-M1.
OC Eukaryota; Fungi; Microsporidia; Unikaryonidae; Encephalitozoon.
OX NCBI_TaxID=264813;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=GB-M1;
RX MEDLINE=21576510; PubMed=11719806; DOI=10.1038/35106579;
RA Katinka M.D., Duprat S., Cornillot E., Metenier G., Thomarac F.,
RA Prenster G., Barbe V., Peyretrallade E., Broctier P., Wincker P.,
RA Delbac F., El Alaoui H., Peyret P., Saurin W., Gouy M.,
RA Weissensbach J., Vivares C.P.;
RT "genome sequence and gene compaction of the eukaryote parasite
RT Encephalitozoon cuniculi.";
RL Nature 414:450-453(2001).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=GB-M1;
RA Genoscope;
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL590443; CAD26204.1; -.
DR HSSP; Q93009; INB8.
DR GO: GO:0004197; F:cysteine-type endopeptidase activity; IEA.
DR GO: GO:0016787; F:hydrolase activity; IEA.
DR GO: GO:0004221; F:ubiquitin thioesterase activity; IEA.
DR GO: GO:0006511; P:ubiquitin-dependent protein catabolism; IEA.
DR InterPro; IPR001394; Peptidase_C19.
DR InterPro; IPR008974; Traf_Like.
DR Pfam; PF00443; UCH; 1.
DR PROSITE; PS00972; UCH_2_1; 1.
DR PROSITE; PS50235; UCH_2_3; 1.
KM Hydrolase.
SQ SEQUENCE 933 AA; 108184 MW; ABA872AED8F7EB0D CRC64;

Query Match 45.8%; Score 54; DB 2; Length 933;
Best Local Similarity 44.4%; Pred. No. 15;
Matches 12; Conservative 2; Mismatches 5; Indels 8; Gaps 1;

QY 2 PSYQFGHNSVPEEDTLRK 20
| | | | | | | | | | | | | | | | | | | | | |
DB 580 PSYQFGHNSVPEEDTLRK 606

RESULT 15
VGLB_MCMVS STANDARD; PRT; 928 AA.
ID VGLB_MCMVS
AC P27171;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Glycoprotein B precursor.
GN Name=GB; Synonyms=UL55;
OS Murine cytomegalovirus (strain Smith).
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Betaherpesvirinae; Muromegalovirus.
OX NCBI_TaxID=10367;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=92292265; PubMed=1318410;
RA Rapp M., Messerle M., Buehler B., Tanheimer M., Keil G.M.,
RA Koszinowski U.H.;
RT "Identification of the murine cytomegalovirus glycoprotein B gene and
RT its expression by recombinant vaccinia virus.";
RL J. Virol. 66:4399-4406(1992).
RN [2]
RP SEQUENCE OF 1-280 FROM N.A.
RX MEDLINE=93031129; PubMed=1329325;
RA Messerle M., Keil G.M., Schneider K., Koszinowski U.H.;

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RT "Characterization of the murine cytomegalovirus genes encoding the
RT major DNA binding protein and the ICPI8.5 homolog."
RL Virology 191:355-367(1992).
RN [3]
RP SEQUENCE OF 514-928 FROM N.A.
RX MEDLINE=92024072; PubMed=1718083;
RA Elliott R., Clark C., Jagush D., Spector D.H.;
RT "Transcription analysis and sequence of the putative murine
RT cytomegalovirus DNA polymerase gene."
RL Virology 185:169-186(1991).
CC -1- FUNCTION: Important determinant of virus infectivity.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@sib-sib.ch).
CC -----
CC EMBL: M86302; AAA45936.1; -
CC EMBL: X67021; CAA47416.1; -
CC EMBL: M73549; AAA45939.1; -
CC PIR: A4192; VGBEMC.
CC InterPro: IPR000234; Glycoprot_B.
CC Pfam: PF00606; Glycoprotein_B; 1.
CC Glycoprotein; Signal; Transmembrane.
CC SIGNAL 1 36
CC CHAIN 37 928 Potential.
CC DOMAIN 37 739 Glycoprotein B.
CC TRANSMEM 740 755 Extracellular (Potential).
CC TRANSMEM 761 780 Potential.
CC TRANSMEM 784 804 Potential.
CC DOMAIN 805 928 Cytosolic (Potential).
CC CARBOHYD 93 93 N-linked (GlcNAc...) (Potential).
CC CARBOHYD 223 223 N-linked (GlcNAc...) (Potential).
CC CARBOHYD 315 315 N-linked (GlcNAc...) (Potential).
CC CARBOHYD 354 354 N-linked (GlcNAc...) (Potential).
CC CARBOHYD 398 398 N-linked (GlcNAc...) (Potential).
CC CARBOHYD 429 429 N-linked (GlcNAc...) (Potential).
CC CARBOHYD 470 470 N-linked (GlcNAc...) (Potential).
CC CARBOHYD 487 487 N-linked (GlcNAc...) (Potential).
CC CARBOHYD 618 618 N-linked (GlcNAc...) (Potential).
CC CARBOHYD 667 667 N-linked (GlcNAc...) (Potential).
CC CARBOHYD 667 667 N-linked (GlcNAc...) (Potential).
CC CONFLICT 522 522 K -> R (in Ref. 3).
CC CONFLICT 527 527 D -> E (in Ref. 3).
CC CONFLICT 556 556 S -> T (in Ref. 3).
CC CONFLICT 562 562 I -> V (in Ref. 3).
CC CONFLICT 583 583 K -> Q (in Ref. 3).
CC CONFLICT 587 587 S -> K (in Ref. 3).
CC CONFLICT 617 617 I -> V (in Ref. 3).
CC CONFLICT 672 672 E -> D (in Ref. 3).
CC CONFLICT 675 675 D -> Q (in Ref. 3).
CC CONFLICT 806 806 R -> KQSAAR (in Ref. 3).
CC CONFLICT 890 890 N -> T (in Ref. 3).
SQ SEQUENCE 928 AA; 104109 MW; 0EDBF3FB7A43810D CRC64;
```

```
Query Match 43.2%; Score 51; DB 1; Length 928;
Best Local Similarity 69.2%; Pred. No. 44;
Matches 9; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
```

```
OY 6 FCGHNSVPEEDT 18
DB 295 YNGENSEPFEEDT 307
```

Search completed: October 22, 2005, 04:10:14
Job time : 53.4314 secs

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CC streptococci, e.g. meningitis, otitis media, pneumonia, endocarditis,
 CC mastitis in cattle, abortion in horses and many others. Since the
 CC antibodies block binding of bacteria, they should be effective against
 CC antibiotic-resistant strains, and may replace antibiotic therapy or
 CC increase its effectiveness. Sequences AAW65670-90 represent a series of
 CC synthetic peptides based on the D3 repeat of *S. aureus* fibronectin
 CC binding protein A. They were synthesised to contain a proline residue at
 CC each position through the sequence (ie a proline scan)

XX
 SQ Sequence 21 AA;
 Query Match 100.0%; Score 118; DB 2; Length 21;
 Best Local Similarity 100.0%; Pred. No. 2.5e-11;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KPSYQFGHNSVDPEDTLPK 21
 DB 1 KPSYQFGHNSVDPEDTLPK 21

RESULT 2
 AAW65665
 ID AAW65665 standard; peptide; 21 AA.
 AC AAW65665;
 XX
 DT 16-OCT-1998 (first entry)
 XX
 DE Fibronectin binding protein-derived peptide #9.
 XX
 KM microbial surface components recognising adhesive matrix molecule;
 KM MSCRAMM; fibronectin; fibronectin-binding protein; antibody; epitope;
 KM antibiotic; bacterial infection; antibiotic-resistant strain.
 OS Synthetic.
 OS Staphylococcus aureus.
 XX
 PN WO9831389-A2.
 PD
 XX 23-JUL-1998.
 PF 21-JAN-1998; 98WO-US001222.
 PR 21-JAN-1997; 97US-0036139P.
 XX
 PA (TEXA) UNIV TEXAS A & M SYSTEM.
 PI
 PI Hoeoek M, Patti JM, House-Pompeo KL, Speziale P, Joh D;
 PI McGavin MJ;
 XX
 XX WPI; 1998-413816/35.
 DR
 XX
 PT Antibody that binds to fibronectin-binding protein, preventing its
 PT binding to fibronectin - used to treat or prevent bacterial infection,
 PT especially by Staphylococci and Streptococci.
 XX
 PS Example 2; Page 92; 201pp; English.

CC epitopes from the fibronectin binding domains DU and DI-D4 of the *S.*
 CC *aureus* fnbA gene
 XX
 SQ Sequence 21 AA;
 Query Match 90.7%; Score 107; DB 2; Length 21;
 Best Local Similarity 95.2%; Pred. No. 1.4e-09;
 Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KPSYQFGHNSVDPEDTLPK 21
 DB 1 KPSYQFGHNSVDPEDTLPK 21

RESULT 3
 AAR21340
 ID AAR21340 standard; peptide; 22 AA.
 AC AAR21340;
 XX
 DT 25-MAR-2003 (revised)
 DT 15-JUN-1992 (first entry)
 XX
 DE Fibronectin binding protein.
 XX
 KM FMBP; wound infection reduction; vaccination; mastitis;
 KM Staphylococcal infections; D3.
 XX
 OS Synthetic.
 OS WO9202555-A.
 XX
 PN WO9202555-A.
 PD 20-FEB-1992.
 PF 10-AUG-1990; 90SE-00002617.
 XX
 PR 10-AUG-1990; 90SE-00002617.
 XX
 PA (ALFA) ALFA LAVAL AGRIC INT AB.
 XX
 XX Hook M, McGavin M, Rauczi G;
 PI
 DR WPI; 1992-080035/10.
 XX
 PT New fibronectin binding peptide - combines with fusion peptide to form
 PT large antigen, used in immunisation, diagnosis and for treating wounds.
 XX
 XX Claim 1; Page 22; 33pp; English.

CC The sequence comprises amino acids 17-33 of a tandem repeat, designated
 CC D3 of the fibronectin binding site of Staphylococcus aureus 8325-4 FMBP.
 CC The N-terminal DK may be replaced with H or K, and the C-terminal LKP may
 CC be replaced by either L, LP, or OH. The peptides were synthesised using
 CC standard methods and purified using reverse phase HPLC. The appropriate
 CC fractions were dialysed and lyophilised. Peptide sequencing was performed
 CC and the peptides digested and chemically modified by dihydroxypropylation
 CC of the amino side chain of lysine. The carboxylic side chains were
 CC converted to glycine methyl esters. The phenyl side chains of tyrosine
 CC residues were oxidised. Chemically modified peptide D3 was compared to
 CC unmodified D3. Lysine and tyrosine modifications only partially
 CC diminished D3 activity whereas modification of aspartic/glutamic
 CC residues resulted in complete loss of activity. The peptide can be used
 CC for the prevention or reduction of the risk of wound infection. The
 CC peptide can be used to create a large antigen for vaccinating ruminants
 CC against mastitis caused by Staphylococcal infections. It can also be used
 CC to diagnose Staphylococcal infections using ELISA or DNA probes. (Updated
 CC on 25-MAR-2003 to correct PA field.)

XX
 SQ Sequence 22 AA;
 Query Match 90.7%; Score 107; DB 2; Length 22;
 Best Local Similarity 95.2%; Pred. No. 1.4e-09;
 Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 KPSYQFGHNSVDPEDTLPK 21
 |||||
 DB 2 KPSYQFGHNSVDPEDTLPK 22

RESULT 4
 AAB91958
 ID AAB91958 standard; peptide; 37 AA.

AC AAB91958;
 DT 22-JUN-2001 (first entry)

DE Fibronectin fragment and fibrin related peptide SEQ ID NO:1134.

XX Protection; endogenous therapeutic peptide; peptidase; conjugation;
 KM blood component; modification; succinimidy; maleimido group; amino;
 KM hydroxyl; thiol; hormone; growth factor; neurotransmitter.

XX Homo sapiens.
 OS Synthetic.

XX WO200069900-A2.

XX 23-NOV-2000.

XX 17-MAY-2000; 2000WO-US013576.

XX 17-MAY-1999; 99US-0134406P.

XX 10-SEP-1999; 99US-0153406P.

XX 15-OCT-1999; 99US-0159783P.

XX (CONJ-) CONJUCHEM INC.

XX Bridon DP, Errin AM, Milner PG, Holmes DL, Thibaudau K;

XX WPI; 2001-112059/12.

PT Modifying and attaching therapeutic peptides to albumin prevents
 PT peptidase degradation, useful for increasing length of in vivo activity.

PS Disclosure; Page 566; 733pp; English.

XX The present invention describes a modified therapeutic peptide (I)
 CC comprising a therapeutically active amino acid region (III) and a
 CC reactive group (II) (e.g. succinimidy and maleimido groups) attached to
 CC a less therapeutically active amino acid region (IV), which covalently
 CC bonds with amino/hydroxyl/thiol groups on blood components to form a
 CC peptidase stabilised therapeutic peptide composed of 3-50 amino acids.
 CC (I) are useful for modifying therapeutic peptides e.g. hormones, growth
 CC factors and neurotransmitters, to protect them from peptidase activity in
 CC vivo for the treatment of various disorders. Endogenous therapeutic
 CC peptides are not suitable as drug candidates as they require frequent
 CC administration due to rapid degradation by peptidases in the body.
 CC Modifying and attaching therapeutic peptides to albumin prevents or
 CC reduces the action of peptidases to increase length of activity (half
 CC life) and specificity as bonding to large molecules decreases
 CC intracellular uptake and interference with physiological processes.
 CC AAB90829 to AAB92441 represent peptides which can be used in the
 CC exemplification of the present invention

XX Sequence 37 AA;

Query Match 90.7%; Score 107; DB 4; Length 37;

Best Local Similarity 95.2%; Pred. No. 2.6e-09;

Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 KPSYQFGHNSVDPEDTLPK 21
 |||||
 DB 16 KPSYQFGHNSVDPEDTLPK 36

RESULT 5
 AAP80662
 ID AAP80662 standard; protein; 38 AA.

XX AAP80662;
 AC AAP80662;

DT 25-MAR-2003 (revised)

DT 07-OCT-1990 (first entry)

DE Protein with fibronectin binding ability.

XX Hybrid DNA molecule; fibronectin binding; mastitis; ruminants;
 KM wound infection.

XX Staphylococcus aureus.

XX EP294349-A.

XX 07-DEC-1988.

XX 30-MAY-1988; 88EP-00850188.

XX 01-JUN-1987; 87SB-00002272.

XX (ALFA) ALFA LAVAL AGRIC INT AB.

XX Lindberg MK, Signas LC, Wadstrom TM, Froman G;

XX WPI; 1988-347978/49.

XX N-PSDB; AAN81099.

PT Hybrid DNA encoding Staphylococcus aureus fibronectin binding protein -
 PT useful for immunisation and topical application to prevent staphylococcal
 PT infections.

XX Claim 11; Page 12; 23pp; English.

XX The peptide has fibronectin binding ability. It is useful for immunising
 CC ruminants against staphylococcal mastitis, pre: when used at 0.5-5
 CC micrograms/kg, using 3 doses given at 1-3 week intervals; for topical
 CC application to prevent wound infection, using an isotonic saline soln. of
 CC connn. 25-250 micrograms/ml; and, when immobilised on a carrier, for
 CC diagnosing staphylococcal infections. (Updated on 25-MAR-2003 to correct
 CC PF field.) (Updated on 25-MAR-2003 to correct PA field.)

XX Sequence 38 AA;

Query Match 90.7%; Score 107; DB 1; Length 38;

Best Local Similarity 95.2%; Pred. No. 2.7e-09;

Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 KPSYQFGHNSVDPEDTLPK 21
 |||||
 DB 17 KPSYQFGHNSVDPEDTLPK 37

RESULT 6
 AAY29087

ID AAY29087 standard; protein; 134 AA.

XX AAY29087;

XX 28-SEP-1999 (first entry)

DE S. aureus fibronectin binding protein A (FnBA) binding domain.

XX Bovine herpes virus-2; BHV-2; cytokine; immune response; immunogen; IL;

XX Interleukin; colony stimulating factor; CSF; interferon; IFN; TNF;

XX tumour necrosis factor; recombinant virus; vaccine; mucosal disease;

XX mastitis; breast cancer; stress-induced disease; binding domain; FnBA;

XX fibronectin binding protein.

OS Staphylococcus aureus.


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XX  MO9916892-A1.
PN
XX  08-APR-1999.
PD
XX  29-SEP-1998; 98WO-GB002927.
XX  29-SEP-1997; 97GB-00020633.
XX  (UTBR-) UNIV BRISTOL.
PA
XX  Bradley AJ, Duffas WPJ,
PI
XX  WPI: 1999-255101/21.
DR  N-PSDB: AAX91504.
XX
XX  New bovine herpes virus-2 vectors.
PT
XX  Example 2; Fig 8A-B; 130pp; English.
PS
XX  The invention provides bovine herpes virus-2 (BHV-2) based vectors that
CC  comprise at least one cytokine-encoding DNA sequence. The expression of
CC  cytokines in mammals can up-regulate immune responses to the immunogens.
CC  The cytokine is selected from interleukins (IL), colony stimulating
CC  factors (CSF), interferons (IFN) and tumour necrosis factors (TNF). The
CC  BHV-2 based vector or recombinant virus can be used as vaccines. They can
CC  be used for preventing or treating a mucosal disease in a subject, e.g.
CC  runts, cattle, sheep, goats, dogs, cats, horses, or man, particularly
CC  mastitis in cows or breast cancers in humans. They can also be used for
CC  preventing or treating a stress-induced disease. The present sequence
CC  represents the binding domain of a previously published S. aureus
CC  fibronectin binding protein A (FnBA) sequence. The FnB binding domain
CC  gene sequence FNBA, cloned for use in this invention has 97.8 percent
CC  identity when compared to the previously published FnBA and FnBB gene
CC  sequences
XX
SQ  Sequence 134 AA;

Query Match          90.7%; Score 107; DB 2; Length 134;
Best Local Similarity 95.2%; Pred. No. 1.1e-08;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY  1 KPSYQFGHNSVDPEDTLPK 21
    |||||
DB  93 KPSYQFGHNSVDPEDTLPK 113

RESULT 7
AAW31556
ID  AAW31556 standard; protein; 139 AA.
XX
AC  AAW31556;
XX
XX  27-AUG-2003 (revised)
DT  25-MAR-2003 (revised)
DT  21-MAY-1998 (first entry)
XX
XX  Fibronectin-binding MSCRAMM derivative PQD.
DE
XX  Fibronectin; PQD; collagen binding protein; sepsis; infection;
KW  microbial surface component recognising adhesive matrix molecule; MSCRAMM;
KW  adhesin; vaccine; immunisation; diagnosis; therapy; mastitis.
XX
OS  Staphylococcus aureus.
XX
XX  Key Location/Qualifiers
FT  Peptide 1..12
FT  /note= "vector pQE30-derived peptide"
XX
XX  MO9743314-A2.
XX
XX  20-NOV-1997.
XX

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PF  14-MAY-1997; 97WO-US008210.
XX
XX  16-MAY-1996; 96US-0017678P.
XX
XX  (TEXA ) UNIV TEXAS A & M SYSTEM.
PA  (UABR-) UAB RES FOUND.
XX
XX  Hoeoek M, Patil JM, House-Pompeo K, Sthanam N, Symersky J;
PI  WPI: 1998-008801/01.
XX
XX  Antibody that interacts with collagen binding domain of Staphylococcal
PT  cna gene product - useful to prevent bacterial sepsis in animal infected
PT  with Staphylococcus aureus.
XX
XX  Disclosure; Page 91; 143pp; English.
PS
XX  This protein comprises Staphylococcus aureus fibronectin-binding
CC  microbial surface component recognising adhesive matrix molecule (MSCRAMM)
CC  derivative PQD, plus a vector-derived N-terminal peptide. The invention
CC  relates to claimed nucleic acid sequences (see AAT93436-38) encoding S.
CC  aureus collagen binding protein (CBP) epitopes M17, M31 and M55 (see
CC  AAW31552-54) that confer protection against S. aureus infection. CBP
CC  protein and antigenic epitopes are contemplated for use in the treatment
CC  of pathological infections, especially to prevent bacterial adhesion to
CC  collagen. The epitopes are also contemplated for use in the preparation
CC  of vaccines and as carrier proteins in vaccine formulations, as well as
CC  in the formulation of compositions for the prevention of S. aureus
CC  infection. pCF33 and PQD (see AAW31556) were used to raise anti-MSCRAMM
CC  polyclonal antibodies used in passive immunisation against bovine
CC  mastitis. (Updated on 25-MAR-2003 to correct PI field.) (Updated on 27-
CC  AUG-2003 to correct OS field.)
XX
SQ  Sequence 139 AA;

Query Match          90.7%; Score 107; DB 2; Length 139;
Best Local Similarity 95.2%; Pred. No. 1.2e-08;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY  1 KPSYQFGHNSVDPEDTLPK 21
    |||||
DB  107 KPSYQFGHNSVDPEDTLPK 127

RESULT 8
AAP82115
ID  AAP82115 standard; protein; 1018 AA.
XX
XX  AAP82115;
XX
XX  25-MAR-2003 (revised)
DT  05-JAN-1990 (first entry)
XX
XX  Fibronectin binding protein.
DE
XX  Fibronectin binding protein; S. aureus; immunisation; mastitis; runts;
KW  wound infection; diagnosis.
XX
XX  Staphylococcus aureus.
OS
XX  EP294349-A.
XX
XX  07-DEC-1988.
PD
XX  30-MAY-1988; 88EP-00850188.
XX
XX  01-JUN-1987; 87SR-00002272.
XX
XX  (ALFA ) ALFA LAVAL AGRIC INT AB.
PA
XX  Lindberg MK, Signas LC, Wadstrom TM, Froman G;
PI  WPI: 1988-347978/49.
XX

```

DR P-PSDB; AAP82115.
XX Hybrid DNA encoding Staphylococcus aureus fibronectin binding protein -
PT useful for immunisation and topical application to prevent staphylococcal
PT infections.
XX Disclousure; Fig. 8A:1-8A:2; 23pp; English.
XX The S.aureus fibronectin binding protein may be included in a hybrid
XX protein. The protein may be used to immunise ruminants against
CC staphylococcal mastitis, pref. when given at 0.5-5 microg/kg, using 3
CC doses at 1-3 week intervals and for topical applicn. to prevent wound
CC infection, pref. using isotonic saline soln. of concn. 25-250 microg/mg.
CC The DNA encoding the binding protein and the hybrid protein may be
CC immobilised on a carrier and used to diagnose staphylococcal infections.
CC (Updated on 25-MAR-2003 to correct PA field.)
XX
SQ Sequence 1018 AA;

Query Match 90.7%; Score 107; DB 1; Length 1018;
Best Local Similarity 95.2%; Pred. No. 1.2e-07;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KPSYQFGGHSVDPEDTLPK 21
Db 837 KPSYQFGGHSVDPEDTLPK 857
|||||

RESULT 9
AAU37245
ID AAU37245 standard; protein; 1018 AA.
XX
AC AAU37245;
XX
DT 14-FEB-2002 (first entry)
XX
DE Staphylococcus aureus cellular proliferation protein #1415.
XX
KW Antisense; prokaryotic cellular proliferation protein; antibiotic;
XX antibacterial; drug design.
XX
OS Staphylococcus aureus.
XX
PN WO200170955-A2.
XX
PD 27-SEP-2001.
XX
PF 21-MAR-2001; 2001WO-US009180.
XX
PR 21-MAR-2000; 2000US-0191078P.
XX
PR 23-MAY-2000; 2000US-0206848P.
XX
PR 26-MAY-2000; 2000US-0207727P.
XX
PR 23-OCT-2000; 2000US-0242578P.
XX
PR 27-NOV-2000; 2000US-0253625P.
XX
PR 22-DEC-2000; 2000US-0257931P.
XX
PR 16-FEB-2001; 2001US-0269308P.
XX
PA (ELIT-) ELITRA PHARM INC.
XX
PI Haselbeck R, Ohlsen KL, Zyskind JW, Wall D, Trawick JD, Carr GJ;
PI Yamamoto RT, Xu HH;
XX
XX WPI; 2001-611495/70.
XX
DR N-PSDB; AAS55104.
XX
PT New polynucleotides for the identification and development of
PT antibiotics, comprise sequences of antisense nucleic acids.
XX
PS Example 3; SEQ ID NO 12838; 511pp; English.
XX
CC The invention relates to antisense inhibitors of genes essential to
CC prokaryotic cellular proliferation, their use in identifying the genes,
CC their use in the discovery of novel antibiotics, the essential genes

CC themselves and the encoded proteins. The prokaryotes used are Escherichia
CC coli, Staphylococcus aureus, Salmonella typhi, Klebsiella pneumoniae,
CC pseudomonas aeruginosa and Enterococcus faecalis. The invention is also
CC useful for the identification of potential new targets for antibiotic
CC development. The antisense nucleic acids can also be used to identify
CC proteins used in proliferation, to express these proteins, and to obtain
CC antibodies capable of binding to the expressed proteins. The proteins can
CC be used to screen compounds in rational drug discovery programmes. The
CC antisense nucleic acid sequence is also useful to screen for homologous
CC nucleic acids which are required for cell proliferation in a wide variety
CC of organisms. The present sequence represents an essential prokaryotic
CC cellular proliferation protein. Note: The sequence data for this patent
CC did not form part of the printed specification, but was obtained in
CC electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pcc_sequences
XX
SQ Sequence 1018 AA;

Query Match 90.7%; Score 107; DB 4; Length 1018;
Best Local Similarity 95.2%; Pred. No. 1.2e-07;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KPSYQFGGHSVDPEDTLPK 21
Db 837 KPSYQFGGHSVDPEDTLPK 857
|||||

RESULT 10
AAU34301
ID AAU34301 standard; protein; 1018 AA.
XX
AC AAU34301;
XX
DT 14-FEB-2002 (first entry)
XX
DE Staphylococcus aureus cellular proliferation protein #577.
XX
KW Antisense; prokaryotic cellular proliferation protein; antibiotic;
XX antibacterial; drug design.
XX
OS Staphylococcus aureus.
XX
PN WO200170955-A2.
XX
PD 27-SEP-2001.
XX
PF 21-MAR-2001; 2001WO-US009180.
XX
PR 21-MAR-2000; 2000US-0191078P.
XX
PR 23-MAY-2000; 2000US-0206848P.
XX
PR 26-MAY-2000; 2000US-0207727P.
XX
PR 23-OCT-2000; 2000US-0242578P.
XX
PR 27-NOV-2000; 2000US-0253625P.
XX
PR 22-DEC-2000; 2000US-0257931P.
XX
PR 16-FEB-2001; 2001US-0269308P.
XX
PA (ELIT-) ELITRA PHARM INC.
XX
PI Haselbeck R, Ohlsen KL, Zyskind JW, Wall D, Trawick JD, Carr GJ;
PI Yamamoto RT, Xu HH;
XX
XX WPI; 2001-611495/70.
XX
DR N-PSDB; AAS52160.
XX
PT New polynucleotides for the identification and development of
PT antibiotics, comprise sequences of antisense nucleic acids.
XX
PS Example 3; SEQ ID NO 5797; 511pp; English.
XX
CC The invention relates to antisense inhibitors of genes essential to
CC prokaryotic cellular proliferation, their use in identifying the genes,
CC their use in the discovery of novel antibiotics, the essential genes
CC themselves and the encoded proteins. The prokaryotes used are Escherichia

coli, *Staphylococcus aureus*, *Salmonella typhi*, *Klebsiella pneumoniae*,
CC *Pseudomonas aeruginosa* and *Enterococcus faecalis*. The invention is also
CC useful for the identification of potential new targets for antibiotic
CC development. The antisense nucleic acids can also be used to identify
CC proteins used in proliferation, to express these proteins, and to obtain
CC antibodies capable of binding to the expressed proteins. The proteins can
CC be used to screen compounds in rational drug discovery programmes. The
CC antisense nucleic acid sequence is also useful to screen for homologous
CC nucleic acids which are required for cell proliferation in a wide variety
CC of organisms. The present sequence represents an essential prokaryotic
CC cellular proliferation protein. Note: The sequence data for this patent
CC did not form part of the printed specification, but was obtained in
CC electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 1018 AA;
XX
Query Match 90.7%; Score 107; DB 4; Length 1018;
Best Local Similarity 95.2%; Pred. No. 1.2e-07;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 1 KPSYQFGGHSVDPEDTLPK 21
DB 837 KPSYQFGGHSVDPEDTLPK 857
XX
RESULT 11
ABJ18922
ID ABJ18922 standard; protein; 1018 AA.
XX
AC ABJ18922;
XX
DT 06-MAR-2003 (first entry)
XX
DE Pathogen specific antigen related staphylococcal protein SEQ ID No 68.
XX
DE Antibacterial; virucide; fungicide; protozoacide; cytostatic; anti-HIV;
KM hyperimmune; serum-reactive; antigen; pathogen; tumour; allergen;
KM auto-immunity; vaccine; staphylococcal infection; antibody; cancer;
KM autoimmune disease; HIV; hepatitis.
XX
OS *Staphylococcus* sp.
XX
OS WO200259148-A2.
XX
PN 01-AUG-2002.
XX
PD 21-JAN-2002; 2002WO-EP000546.
XX
PF 26-JAN-2001; 2001AT-00000130.
XX
PR (CIST-) CISTEM BIOTECHNOLOGIES GMBH.
XX
PI Meinke A, Nagy E, Von Ahnen U, Klade C, Henics T, Zauner W;
PI Mihh DB, Vytvyetka O, Etz H, Dryla A, Weichardt T, Hafner M;
PI Tempelmeier B;
XX
XX WPI; 2003-075410/07.
XX
XX Identifying, isolating and producing hyperimmune serum-reactive antigens
XX from a pathogen, for preparing vaccine or medicament for treating or
XX preventing e.g. staphylococcal infections, comprises providing antibody
XX preparation.
XX
XX Example 7; Page 157; 252pp; English.
XX
XX The invention relates to a novel method for identifying, isolating and
XX producing hyperimmune serum-reactive antigens from a pathogen, tumour,
XX allergen, a tissue or host prone to auto-immunity, where the antigens are
XX used in a vaccine, comprises providing antibody preparation from a plasma
XX pool of a type of animal, or individual sera with antibodies against the
XX specific pathogen, tumour, allergen, tissue or host prone to auto-
XX immunity. The hyperimmune serum-reactive antigens comprising any of the

CC 62 sequences of 53-2261 amino acids fully defined in the specification,
CC or their hyperimmune fragments are useful for the manufacture of a
CC pharmaceutical preparation, particularly a vaccine against staphylococcal
CC infections or colonisation against *S. aureus* or *S. epidermidis*. The
CC preparation of antibodies is useful for the manufacture of a medicament
CC for treating or preventing staphylococcal infections or colonisation
CC against *S. aureus* or *S. epidermidis*. The antibody preparations may also
CC be used for diagnostic and imaging purposes. Other conditions that can be
CC treated include cancer, autoimmune diseases or infections caused by viral
CC (e.g. HIV, hepatitis A, B or C), fungal or protozoan pathogens. This
CC sequence represents a staphylococcal protein relating to the method for
CC identifying and producing pathogen specific antigens of the invention
XX
SQ Sequence 1018 AA;
XX
Query Match 90.7%; Score 107; DB 6; Length 1018;
Best Local Similarity 95.2%; Pred. No. 1.2e-07;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 1 KPSYQFGGHSVDPEDTLPK 21
DB 837 KPSYQFGGHSVDPEDTLPK 857
XX
RESULT 12
ABM72537
ID ABM72537 standard; protein; 1018 AA.
XX
AC ABM72537;
XX
DT 20-NOV-2003 (first entry)
XX
DE *Staphylococcus aureus* protein #1777.
XX
DE Antibacterial; vaccine; gene therapy; infection; sepsis; diagnosis;
KM enzymatic assay; antibiotic target.
XX
OS *Staphylococcus aureus*.
XX
PN WO200294868-A2.
XX
XX 28-NOV-2002.
XX
PD 27-MAR-2002; 2002WO-IB002637.
XX
PF 27-MAR-2001; 2001GB-00007661.
XX
PR (CHIR-) CHIRON SPA.
XX
PI Masignani V, Mora M, Scarselli M;
XX
XX WPI; 2003-120786/11.
XX
DR N-PSDB; ACF74097.
XX
XX New *Staphylococcus aureus* protein, useful as a vaccine for treating or
XX preventing *Staphylococcal* infection, specifically an infection caused by
XX *S. aureus*, e.g. sepsis.
XX
XX Claim 1; SEQ ID NO 3554; 49pp; English.
XX
XX The invention relates to novel genes and encoded proteins from
XX *Staphylococcus aureus*. A composition comprising the *S. aureus* protein, a
XX nucleic acid encoding the protein, or an antibody to the protein, is
XX useful as a pharmaceutical, particularly as a vaccine for treating or
XX preventing infection due to *Staphylococcus* bacteria, specifically an
XX infection caused by *S. aureus*. The composition is particularly useful for
XX treating or preventing sepsis in a patient. The composition can also be
XX used for diagnostics. The protein is also used in an assay for enzymatic
XX studies and as a target for antibiotics. This sequence represents one of
XX the novel *S. aureus* proteins of the invention
XX
SQ Sequence 1018 AA;

Query Match 90.7%; Score 107; DB 6; Length 1018;
Best Local Similarity 95.2%; Pred. No. 1.2e-07;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KPSYQFGHNSVDFEEDTLPK 21
DB 837 KPSYQFGHNSVDFEEDTLPK 857

RESULT 13

AAW89806
ID AAW89806 standard; protein; 1027 AA.

AC AAW89806;

DT 16-MAR-1999 (first entry)

DE Staphylococcus aureus protein SEQ ID #5254.

XX Computer readable medium; vaccine; S. aureus infection; immunodetection;
XX cellulitis; eyelid infection; food poisoning; osteomyelitis; therapy;
XX skin infection; surgical wound infection; scalded skin syndrome;
XX toxic shock syndrome.

OS Staphylococcus aureus.

PN EP76519-A2.

PD 30-JUL-1997.

PF 07-JAN-1997; 97EP-00100117.

PR 05-JAN-1996; 96US-0009861P.

XX (HUMA-) HUMAN GENOME SCI INC.

XX Kunach CA, Choi GH, Barash SC, Dillon PJ, Fannon ME, Rosen CA;

XX MPI; 1997-374922/35.

XX Polynucleotide(s) and proteins derived from Staphylococcus aureus -
XX stored on computer readable medium and used in the production of anti-
XX S. aureus vaccines.

PS Claim 23; Page 3263-3267; 3271pp; English.

XX This sequence represents a Staphylococcus aureus protein sequence of the
XX invention. The DNA sequences encoding the S. aureus proteins are recorded
XX on a computer readable medium, preferably selected from a floppy or hard
XX disk, random access memory (RAM), read-only memory (ROM) or CD-ROM.
XX Homology searches using the S. aureus DNA sequences allows putative
XX functions to be assigned so that protein-encoding or regulatory regions
XX of commercial, therapeutic or industrial importance can be obtained.
XX Specifically, sequences which are likely to encode antigens have been
XX identified and these polypeptides can be used in a vaccine composition
XX against S. aureus infection. The polypeptides can also be used in a kit
XX for the immunodetection of S. aureus in a sample. S. aureus is implicated
XX in numerous human diseases, including cellulitis, eyelid infections, food
XX poisoning, osteomyelitis, skin and surgical wound infections, scalded
XX skin syndrome, toxic shock syndrome, etc. Organisms transformed with the
XX DNA sequences can be used for recombinant production of the polypeptides.
XX The new DNA sequences (and their fragments) are useful as primers or
XX probes for isolating homologues of any of the 5191 S. aureus DNA sequences
XX contained on the computer readable medium

XX Sequence 1027 AA;

QY Query Match 90.7%; Score 107; DB 2; Length 1027;
Best Local Similarity 95.2%; Pred. No. 1.2e-07;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KPSYQFGHNSVDFEEDTLPK 21
|||||

DB 846 KPSYQFGHNSVDFEEDTLPK 866

RESULT 14

ABU15854
ID ABU15854 standard; protein; 961 AA.

XX AC ABU15854;

DT 19-JUN-2003 (first entry)

DE Protein encoded by Prokaryotic essential gene #1381.

XX Antisense; prokaryotic essential gene; cell proliferation; drug design.

XX Staphylococcus aureus.

XX WO200277183-A2.

XX 03-OCT-2002.

XX 21-MAR-2002; 2002WO-US009107.

XX 21-MAR-2001; 2001US-00815242.

XX 06-SEP-2001; 2001US-00948993.

XX 25-OCT-2001; 2001US-0342923P.

XX 08-FEB-2002; 2002US-00072851.

XX 06-MAR-2002; 2002US-0362699P.

XX (ELIT-) ELITRA PHARM INC.

XX Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zykkind JW;

XX Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;

XX MPI; 2003-029926/02.

XX N-PSDB; ACAL9724.

XX New antisense nucleic acids, useful for identifying proteins or screening
XX PT for homologous nucleic acids required for cellular proliferation to
XX isolate candidate molecules for rational drug discovery programs.

PS Claim 25; SEQ ID NO 43778; 1766pp; English.

XX The invention relates to an isolated nucleic acid comprising any one of
XX the 623 antisense sequences given in the specification where expression
XX of the nucleic acid inhibits proliferation of a cell. Also included are:
XX (1) a vector comprising a promoter operably linked to the nucleic acid
XX encoding a polypeptide whose expression is inhibited by the antisense
XX nucleic acid; (2) a host cell containing the vector; (3) an isolated
XX polypeptide or its fragment whose expression is inhibited by the
XX antisense nucleic acid; (4) an antibody capable of specifically binding
XX the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular
XX proliferation or the activity of a gene in an operon required for
XX proliferation; (7) identifying a compound that influences the activity of
XX the gene product or that has an activity against a biological pathway of
XX required for proliferation, or that inhibits cellular proliferation; (8)
XX identifying a gene required for cellular proliferation or the biological
XX pathway in which a proliferation-regulated gene or its gene product lies
XX or a gene on which the test compound that inhibits proliferation of an
XX organism acts; (9) manufacturing an antibiotic; (10) profiling a
XX compound's activity; (11) a culture comprising strains in which the gene
XX product is overexpressed or underexpressed; (12) determining the extent
XX to which each of the strains is present in a culture or collection of
XX strains; or (13) identifying the target of a compound that inhibits the
XX proliferation of an organism. The antisense nucleic acids are useful for
XX identifying proteins or screening for homologous nucleic acids required
XX for cellular proliferation to isolate candidate molecules for rational
XX drug discovery programs, or for screening homologous nucleic acids
XX required for proliferation in cells other than S. aureus, S. typhimurium,
XX K. pneumoniae or P. aeruginosa. The present sequence is encoded by one of
XX the target prokaryotic essential genes. Note: The sequence data for this
XX patent did not form part of the printed specification, but was obtained
XX in electronic format directly from WIPO at

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CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 961 AA;
Query Match 88.1%; Score 104; DB 6; Length 961;
Best Local Similarity 90.5%; Pred. No. 3.3e-07;
Matches 19; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 KPSYQFGHNSVDPEDTLPK 21
DB 784 KPNYQFGHNSVDPEDTLPK 804

RESULT 15
AAU33960
ID AAU33960 standard; protein, 978 AA.
XX
AC AAU33960;
XX
DT 14-FEB-2002 (first entry)
DE Staphylococcus aureus cellular proliferation protein #236.
XX
KM Antisense; prokaryotic cellular proliferation protein; antibiotic;
XX antibacterial; drug design.
OS Staphylococcus aureus.
XX
PN WO200170955-A2.
PD 27-SEP-2001.
XX
PF 21-MAR-2001; 2001WO-US009180.
XX
PR 21-MAR-2000; 2000US-0191078P.
PR 23-MAY-2000; 2000US-0206848P.
PR 26-MAY-2000; 2000US-0207727P.
PR 23-OCT-2000; 2000US-0242578P.
PR 27-NOV-2000; 2000US-0253625P.
PR 22-DEC-2000; 2000US-0257931P.
PR 16-FEB-2001; 2001US-0269308P.
XX
PA (ELIT-) ELITRA PHARM INC.
XX
PI Haselbeck R, Ohlsen KI, Zyekind JW, Wall D, Trawick JD, Carr GJ;
PI Yamamoto RT, Xu HH;
XX
DR N-PSDB; AAS51819.
XX
WPI; 2001-611495/70.
XX
PT New polynucleotides for the identification and development of
PT antibiotics, comprise sequences of antisense nucleic acids.
XX
PS Example 3; SEQ ID NO 5456; 511p; English.
XX
XX The invention relates to antisense inhibitors of genes essential to
CC prokaryotic cellular proliferation, their use in identifying the genes,
CC their use in the discovery of novel antibiotics, the essential genes
CC themselves and the encoded proteins. The prokaryotes used are Escherichia
CC coli, Staphylococcus aureus, Salmonella typhi, Klebsiella pneumoniae,
CC Pseudomonas aeruginosa and Enterococcus faecalis. The invention is also
CC useful for the identification of potential new targets for antibiotic
CC development. The antisense nucleic acids can also be used to identify
CC proteins used in proliferation, to express these proteins, and to obtain
CC antibodies capable of binding to the expressed proteins. The proteins can
CC be used to screen compounds in rational drug discovery programmes. The
CC antisense nucleic acid sequence is also useful to screen for homologous
CC nucleic acids which are required for cell proliferation in a variety
CC of organisms. The present sequence represents an essential prokaryotic
CC cellular proliferation protein. Note: The sequence data for this patent
CC did not form part of the printed specification, but was obtained in
CC electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
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XX
SQ Sequence 978 AA;
Query Match 88.1%; Score 104; DB 4; Length 978;
Best Local Similarity 90.5%; Pred. No. 3.4e-07;
Matches 19; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 KPSYQFGHNSVDPEDTLPK 21
DB 815 KPNYQFGHNSVDPEDTLPK 835
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Search completed: October 25, 2005, 19:38:29
Job time : 59.1473 secs

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OM protein - protein search, using SW model

Run on: October 22, 2005, 02:23:36 ; Search time 15.9358 Seconds
(without alignments)
98.371 Million cell updates/sec

Title: US-10-731-238-26

Perfect score: 118
Sequence: 1 KPSYQFGGNSVDEPDLTPK 21

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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5: /cgn2_6/ptodata/1/1aa/6CCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/1aa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	118	100.0	21	4	US-09-010-317-26
2	107	90.7	21	4	US-09-010-317-9
3	107	90.7	37	1	US-08-234-622A-4
4	107	90.7	38	1	US-08-294-189-8
5	107	90.7	38	1	US-08-729-767-5
6	107	90.7	114	1	US-08-259-000-3
7	107	90.7	139	3	US-08-856-253-8
8	107	90.7	178	3	US-08-459-135A-12
9	107	90.7	178	3	US-08-495-559-12
10	107	90.7	1027	4	US-08-956-171B-5254
11	107	90.7	1027	4	US-08-781-986A-5254
12	102	86.4	21	4	US-09-010-317-14
13	102	86.4	21	4	US-09-010-317-16
14	102	86.4	21	4	US-09-010-317-23
15	102	86.4	21	4	US-09-010-317-33
16	101	85.6	21	4	US-09-010-317-18
17	101	85.6	21	4	US-09-010-317-24
18	101	85.6	21	4	US-09-010-317-27
19	101	85.6	21	4	US-09-010-317-28
20	101	85.6	21	4	US-09-010-317-30
21	100	84.7	21	4	US-09-010-317-25
22	100	84.7	21	4	US-09-010-317-29
23	100	84.7	21	4	US-09-010-317-31
24	100	84.7	130	2	US-08-459-135A-7
25	100	84.7	130	2	US-08-459-135A-8
26	100	84.7	130	3	US-08-495-559-7
27	100	84.7	130	3	US-08-495-559-8

28	100	84.7	174	2	US-08-459-135A-10	Sequence 10, Appl
29	100	84.7	174	2	US-08-459-135A-13	Sequence 13, Appl
30	100	84.7	174	3	US-08-495-559-10	Sequence 10, Appl
31	100	84.7	174	3	US-08-495-559-13	Sequence 13, Appl
32	100	84.7	176	3	US-08-495-559-6	Sequence 6, Appl
33	100	84.7	181	2	US-08-459-135A-6	Sequence 6, Appl
34	100	84.7	559	4	US-08-956-171B-5251	Sequence 5251, Ap
35	100	84.7	559	4	US-08-781-986A-5251	Sequence 5251, Ap
36	99	83.9	21	4	US-09-010-317-10	Sequence 10, Appl
37	99	83.9	21	4	US-09-010-317-15	Sequence 15, Appl
38	99	83.9	21	4	US-09-010-317-20	Sequence 20, Appl
39	99	83.9	21	4	US-09-010-317-22	Sequence 22, Appl
40	99	83.9	21	4	US-09-010-317-32	Sequence 32, Appl
41	99	83.9	22	4	US-09-010-317-13	Sequence 13, Appl
42	97	82.2	21	4	US-09-010-317-17	Sequence 17, Appl
43	97	82.2	21	4	US-09-010-317-19	Sequence 19, Appl
44	97	82.2	21	4	US-09-010-317-21	Sequence 21, Appl
45	86	72.9	19	1	US-08-234-622A-1	Sequence 1, Appl

ALIGNMENTS

RESULT 1
; Sequence 26, Application US/09010317
; Patent No. 6685943
; GENERAL INFORMATION:
; APPLICANT: Hook, Magnus
; APPLICANT: Patti, Joseph M.
; APPLICANT: House-Pompeo, Karen L.
; APPLICANT: Speziale, Pietro
; APPLICANT: Joh, Danny
; APPLICANT: McGavin, Martin J.
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
; NUMBER OF SEQUENCES: 105
; CORRESPONDENCE ADDRESSES:
; ADDRESSER: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: TX
; COUNTRY: USA
; ZIP: 77210-4433
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/010.317
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/036,139
; FILING DATE: 21-JAN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Hibler, David W.
; REGISTRATION NUMBER: 41,071
; REFERENCE/DOCKET NUMBER: TANK:189
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 512-418-3000
; TELEFAX: 512-474-7577
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; US-09-010-317-26
; Query Match 100.0%; Score 118; DB 4; Length 21;
; Best Local Similarity 100.0%; Pred. No. 4.9e-12;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KPSYFGGHSVDPEDTLPK 21
Db 1 KPSYFGGHSVDPEDTLPK 21

RESULT 2

US-09-010-317-9
Sequence 9, Application US/09010317
Patent No. 6685943
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
APPLICANT: Patti, Joseph M.
APPLICANT: House-Pompeo, Karen L.
APPLICANT: Speziale, Pietro
APPLICANT: Joh, Danny
APPLICANT: McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
TITLE OF INVENTION: AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/010.317
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/036.139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibley, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAMK.189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-09-010-317-9

Query Match 90.7%; Score 107; DB 4; Length 21;
Best Local Similarity 95.2%; Pred. No. 2.7e-10;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KPSYFGGHSVDPEDTLPK 21
Db 1 KPSYFGGHSVDPEDTLPK 21

RESULT 3

US-08-234-622A-4
Sequence 4, Application US/08234622A
Patent No. 5440014
GENERAL INFORMATION:
APPLICANT: HOOK, Magnus
APPLICANT: MCGAVIN, Martin
APPLICANT: RAUCCI, Giuseppe
TITLE OF INVENTION: A FIBRONECTIN BINDING PEPTIDE

NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:

ADDRESSEE: Burns, Doane, Swecker & Mathis
STREET: P.O. Box 1404

CITY: Alexandria
STATE: Virginia

COUNTRY: United States
ZIP: 22313-1404

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/234.622A
FILING DATE: 28-APR-1994

CLASSIFICATION: 530

PRIOR APPLICATION DATA:
APPLICATION NUMBER: SE 9002617-0
FILING DATE: 10-AUG-1990

PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/SE91/00534
FILING DATE: 09-AUG-1991

ATTORNEY/AGENT INFORMATION:
NAME: Meuth, Donna M

REGISTRATION NUMBER: 36,607
REFERENCE/DOCKET NUMBER: 012885-044

TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021

INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:

LENGTH: 37 amino acids
TYPE: amino acid

STRANDEDNESS: single
TOPOLOGY: linear

MOLECULE TYPE: peptide
US-08-234-622A-4

Query Match 90.7%; Score 107; DB 1; Length 37;
Best Local Similarity 95.2%; Pred. No. 5.1e-10;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KPSYFGGHSVDPEDTLPK 21
Db 16 KPSYFGGHSVDPEDTLPK 36

RESULT 4

US-08-294-189-8
Sequence 8, Application US/08294189
Patent No. 5707822
GENERAL INFORMATION:
APPLICANT: Fischetti, Vincent A.
APPLICANT: Rakonjac, Jasna
APPLICANT: Robbins, John
TITLE OF INVENTION: GENE SERUM OPACITY FACTOR
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack Avenue
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/294.189
FILING DATE: 22-AUG-1994

CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-118
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 487-5800
TELEFAX: 201 343-1684
TELEX: 133521
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
ORGANISM: Streptococcus pyogenes
STRAIN: D734
INDIVIDUAL ISOLATE: 22
IMMEDIATE SOURCE:
CLONE: SAU3a
US-08-294-189-8

Query Match 90.7%; Score 107; DB 1; Length 38;
Best Local Similarity 95.2%; Pred. No. 5.3e-10;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KPSYQFGHNSVDPEDTLPK 21
DB 10 KPSYQFGHNSVDPEDTLPK 30

RESULT 5
US-08-729-767-5
Sequence 5, Application US/08729767
Patent No. 5770702
GENERAL INFORMATION:
APPLICANT: HOOK, Magnus
APPLICANT: LINDBERG, Martin Kjell
APPLICANT: SIGNAS, Lars Christer
APPLICANT: WADSTROM, Torkel Mikael
APPLICANT: FROMAN, Gunnar
TITLE OF INVENTION: FIBROECTIN BINDING PROTEIN AS WELL AS
TITLE OF INVENTION: ITS PREPARATION
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Burns, Doane, Swecker & Mathis, L.L.P.
STREET: P.O. Box 1404
CITY: Alexandria
STATE: Virginia
COUNTRY: United States
ZIP: 22133-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/729,767
FILING DATE: 07-OCT-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/259,000
FILING DATE: 13-JUN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/007,817
FILING DATE: 22-JAN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/201,028
FILING DATE: 01-JUN-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: SE 8702272-9

FILING DATE: 01-JUN-1987
ATTORNEY/AGENT INFORMATION:
NAME: McGowan, Malcolm K.
REGISTRATION NUMBER: 39,300
REFERENCE/DOCKET NUMBER: 012889-036
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-729-767-5

Query Match 90.7%; Score 107; DB 1; Length 38;
Best Local Similarity 95.2%; Pred. No. 5.3e-10;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KPSYQFGHNSVDPEDTLPK 21
DB 17 KPSYQFGHNSVDPEDTLPK 37

RESULT 6
US-08-259-000-3
Sequence 3, Application US/08259000
Patent No. 5571514
GENERAL INFORMATION:
APPLICANT: HOOK, Magnus
APPLICANT: LINDBERG, Martin Kjell
APPLICANT: SIGNAS, Lars Christer
APPLICANT: WADSTROM, Torkel Mikael
APPLICANT: FROMAN, Gunnar
TITLE OF INVENTION: FIBROECTIN BINDING PROTEIN AS WELL AS
TITLE OF INVENTION: ITS PREPARATION
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Burns, Doane, Swecker & Mathis
STREET: P.O. Box 1404
CITY: Alexandria
STATE: Virginia
COUNTRY: United States
ZIP: 22133-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/259,000
FILING DATE: 13-JUN-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: SE 8702272-9
FILING DATE: 01-JUN-1987
ATTORNEY/AGENT INFORMATION:
NAME: Meuth, Donna M
REGISTRATION NUMBER: 36,607
REFERENCE/DOCKET NUMBER: 012885-062
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 114 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-259-000-3

Query Match 90.7%; Score 107; DB 1; Length 114;
Best Local Similarity 95.2%; Pred. No. 1.9e-09;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 KPSYQFGHNSVDPEDTLPK 21
Db 93 KPSYQFGHNSVDPEDTLPK 113

RESULT 7

US-08-856-253-8
; Sequence 8, Application US/08856253
; Patent No. 6288214
; GENERAL INFORMATION:
; APPLICANT: Hook, Magnus
; APPLICANT: Patti, Joseph M.
; APPLICANT: House-Pompeo, Karen
; APPLICANT: Schanaw, Narayana
; APPLICANT: Symersky, Jindrich
; TITLE OF INVENTION: COLLAGEN BINDING PROTEIN COMPOSITIONS
; NUMBER OF SEQUENCES: 8
; NUMBER OF INVENTIONS: AND METHODS OF USE
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: U.S.
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/856,253
; FILING DATE: Concurrently Herewith
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/017,678
; FILING DATE: 16-MAY-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Kitchell, Barbara S.
; REGISTRATION NUMBER: 33,928
; REFERENCE/DOCKET NUMBER: TAWK:193
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (512) 418-3000
; TELEFAX: (512) 474-7577
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 139 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
US-08-856-253-8

Query Match 90.7%; Score 107; DB 3; Length 139;
Best Local Similarity 95.2%; Pred. No. 2.3e-09;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 KPSYQFGHNSVDPEDTLPK 21
Db 107 KPSYQFGHNSVDPEDTLPK 127

RESULT 8

US-08-459-135A-12
; Sequence 12, Application US/08459135A
; Patent No. 5955078
; GENERAL INFORMATION:
; APPLICANT: BURHAM, Martin Karl Ruseel
; APPLICANT: CHOPRA, Ian

APPLICANT: CRITCHLEY, Ian Alfred
APPLICANT: KNOWLES, David Justin Charles
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN: MONOCLONAL ANTIBODY AND THEIR US
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
STATE: PA

COUNTRY: U.S.A.
ZIP: 19406-0939

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS

SOFTWARE: FastSeq, Version 2.0
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/459,135A
FILING DATE: 02-JUN-1995

CLASSIFICATION: 435
PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/GB/94/00215
FILING DATE: 04-Feb-1994

CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:

NAME: Gimmi, Edward R.
REGISTRATION NUMBER: 38,891

REFERENCE/DOCKET NUMBER: P30591C2
TELECOMMUNICATION INFORMATION:

TELEPHONE: 610-270-4478
TELEFAX: 610-270-5090

TELEX:
INFORMATION FOR SEQ ID NO: 12:

SEQUENCE CHARACTERISTICS:
LENGTH: 178 amino acids

TYPE: amino acid
STRANDEDNESS: single

TOPOLOGY: linear
MOLECULE TYPE: Protein

US-08-459-135A-12

Query Match 90.7%; Score 107; DB 2; Length 178;
Best Local Similarity 95.2%; Pred. No. 3.1e-09;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 KPSYQFGHNSVDPEDTLPK 21
Db 93 KPSYQFGHNSVDPEDTLPK 113

RESULT 9

US-08-495-559-12
; Sequence 12, Application US/08495559A
; Patent No. 6054572
; GENERAL INFORMATION:
; APPLICANT: BURHAM, Martin Karl Ruseel
; APPLICANT: CHOPRA, Ian
; APPLICANT: CRITCHLEY, Ian Alfred
; APPLICANT: KNOWLES, David Justin Charles
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN: MONOCLONAL
; TITLE OF INVENTION: ANTIBODY AND THEIR USE IN PREVENTING BACTERIAL ADHESION
; FILE REFERENCE: P30591
; CURRENT APPLICATION NUMBER: US/08/495,559A
; CURRENT FILING DATE: 1995-08-03
; EARLIER APPLICATION NUMBER: GB 9302289.5
; EARLIER FILING DATE: 1993-02-05
; EARLIER APPLICATION NUMBER: GB 9321592.9
; EARLIER FILING DATE: 1993-10-20
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 12
; LENGTH: 178
; TYPE: PRT

ORGANISM: Staphylococcus aureus
US-08-495-559-12

Query Match 90.7%; Score 107; DB 3; Length 178;
Best Local Similarity 95.2%; Pred. No. 3.1e-09;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KPSYQFGHNSVDFEEDTLPK 21
DB 93 KPSYQFGHNSVDFEEDTLPK 113

RESULT 10
US-08-956-171E-5254
Sequence 5254, Application US/08956171E
Patent No. 6593114

GENERAL INFORMATION:
APPLICANT: Charles Kunach

Gail H. Choi

Patrick S. Dillon

Craig A. Rosen

Steven C. Barash

Michael R. Fannon

ADDRESS: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue

CITY: Rockville
STATE: Maryland

COUNTRY: USA
ZIP: 20850

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage

COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2

SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/956,171E

FILING DATE: 20-Oct-1997
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/009,861

FILING DATE: January 5, 1996
APPLICATION NUMBER: 08/781,986

FILING DATE: January 3, 1997
ATTORNEY/AGENT INFORMATION:

NAME: Mark J. Hyman
REGISTRATION NUMBER: 46,789

REFERENCE/DOCKET NUMBER: PB248P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (240) 314-1224

TELEFAX: (301) 309-8439
INFORMATION FOR SEQ ID NO: 5254:

SEQUENCE CHARACTERISTICS:
LENGTH: 1027 amino acids

TYPE: amino acid
STRANDEDNESS: single

TOPOLOGY: linear
MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 5254:
US-08-956-171E-5254

Query Match 90.7%; Score 107; DB 4; Length 1027;
Best Local Similarity 95.2%; Pred. No. 2.3e-08;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KPSYQFGHNSVDFEEDTLPK 21
DB 846 KPSYQFGHNSVDFEEDTLPK 866

RESULT 11

US-08-781-986A-5254
Sequence 5254, Application US/08781986A
Patent No. 6737248

GENERAL INFORMATION:
APPLICANT: Charles Kunach

TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
NUMBER OF SEQUENCES: 5255

CORRESPONDENCE ADDRESS:
ADDRESS: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue

CITY: Rockville
STATE: Maryland

COUNTRY: USA
ZIP: 20850

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage

COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2

SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/781,986A

FILING DATE:
CLASSIFICATION: 435

PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:

ATTORNEY/AGENT INFORMATION:
NAME: Benson, Bob

REGISTRATION NUMBER: 30,446
REFERENCE/DOCKET NUMBER: PB248BP

TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504

TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 5254:

SEQUENCE CHARACTERISTICS:
LENGTH: 1027 amino acids

TYPE: amino acid
STRANDEDNESS: single

TOPOLOGY: linear
MOLECULE TYPE: protein

US-08-781-986A-5254

Query Match 90.7%; Score 107; DB 4; Length 1027;
Best Local Similarity 95.2%; Pred. No. 2.3e-08;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KPSYQFGHNSVDFEEDTLPK 21
DB 846 KPSYQFGHNSVDFEEDTLPK 866

RESULT 12

US-09-010-317-14
Sequence 14, Application US/09010317

Patent No. 6685943
GENERAL INFORMATION:

APPLICANT: Hook, Magnus
APPLICANT: Patil, Joseph M.

APPLICANT: House-Pompeo, Karen L.
APPLICANT: Speziale, Pietro

APPLICANT: Juh, Danny
APPLICANT: McGavin, Martin J.

TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
NUMBER OF SEQUENCES: 105

CORRESPONDENCE ADDRESS:
ADDRESSES: Arnold, White & Durkee
STREET: P.O. Box 4433

CITY: Houston
STATE: TX
COUNTRY: USA

ZIP: 77210-4433
COMPUTER READABLE FORM:

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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/010.317
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-09-010-317-14

Query Match      86.4%; Score 102; DB 4; Length 21;
Best Local Similarity 95.0%; Pred. No. 1.7e-09;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2 PSYQFGHNSVDPEDTLPK 21
DB      2 PSYQFGHNSVDPEDTLPK 21

RESULT 13
US-09-010-317-16
Sequence 16, Application US/09010317
Patent No. 6685943
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
APPLICANT: Patti, Joseph M.
APPLICANT: House-Pompeo, Karen L.
APPLICANT: Speziale, Pietro
APPLICANT: John, Danny
APPLICANT: McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/010.317
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-09-010-317-23

Query Match      86.4%; Score 102; DB 4; Length 21;
Best Local Similarity 90.5%; Pred. No. 1.7e-09;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-09-010-317-16

Query Match      86.4%; Score 102; DB 4; Length 21;
Best Local Similarity 90.5%; Pred. No. 1.7e-09;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 KPSPYQFGHNSVDPEDTLPK 21
DB      1 KPSPYQFGHNSVDPEDTLPK 21

RESULT 14
US-09-010-317-23
Sequence 23, Application US/09010317
Patent No. 6685943
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
APPLICANT: Patti, Joseph M.
APPLICANT: House-Pompeo, Karen L.
APPLICANT: Speziale, Pietro
APPLICANT: John, Danny
APPLICANT: McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/010.317
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-09-010-317-23

Query Match      86.4%; Score 102; DB 4; Length 21;
Best Local Similarity 90.5%; Pred. No. 1.7e-09;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 KPSPYQFGHNSVDPEDTLPK 21
DB      1 KPSPYQFGHNSVDPEDTLPK 21
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Db 1 KPSYQFGHNPVDFEEDTLPK 21

RESULT 15

US-09-010-317-33
 ; Sequence 33, Application US/09010317
 ; Patent No. 6685943
 ; GENERAL INFORMATION:
 ; APPLICANT: Hook, Magnus
 ; APPLICANT: Patti, Joseph M.
 ; APPLICANT: House, Pompeo, Karen L.
 ; APPLICANT: Speziale, Pietro
 ; APPLICANT: Joh, Danny
 ; APPLICANT: McGavin, Martin J.
 ; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
 ; TITLE OF INVENTION: AND METHODS OF USE
 ; NUMBER OF SEQUENCES: 105
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Arnold, White & Durkee
 ; STREET: P.O. Box 4433
 ; CITY: Houston
 ; STATE: TX
 ; COUNTRY: USA
 ; ZIP: 77210-4433
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patentin Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/010,317
 ; FILING DATE:
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 60/036,139
 ; FILING DATE: 21-JAN-1997
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Hibler, David W.
 ; REGISTRATION NUMBER: 41,071
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 512-418-3000
 ; TELEFAX: 512-474-7577
 ; INFORMATION FOR SEQ ID NO: 33:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 21 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS:
 ; TOPOLOGY: linear
 ; US-09-010-317-33

Query Match 86.4%; Score 102; DB 4; Length 21;
 Best Local Similarity 95.0%; Pred. No. 1.7e-09;
 Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KPSYQFGHNSVDFEEDTLPK 20
 |||||
 Db 1 KPSYQFGHNSVDFEEDTLPK 20

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 22, 2005, 10:49:15 ; Search time 59.2367 Seconds
(without alignments)
148.005 Million cell updates/sec

Title: US-10-731-238-26

Perfect score: 118
Sequence: 1 KPSYQFGHNSVDEPDLTPK 21

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1862951 seqs, 417491010 residues

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Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
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2	107	90.7	21	18	US-10-731-238-9
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4	107	90.7	139	9	US-09-813-820-8
5	107	90.7	1018	9	US-09-815-242-5797
6	107	90.7	1018	17	US-09-815-242-12838
7	107	90.7	1018	17	US-10-470-048B-68
8	107	90.7	1027	8	US-08-781-986A-5254
9	107	90.7	1027	15	US-10-329-62A-5254
10	104	88.1	961	15	US-10-282-122A-43778
11	104	88.1	978	9	US-09-815-242-5456

12	104	88.1	1001	9	US-09-815-242-12686	Sequence 12686, A
13	104	88.1	1038	15	US-10-282-122A-43827	Sequence 43827, A
14	102	86.4	21	18	US-10-731-238-14	Sequence 14, App1
15	102	86.4	21	18	US-10-731-238-16	Sequence 16, App1
16	102	86.4	21	18	US-10-731-238-23	Sequence 23, App1
17	102	86.4	21	18	US-10-731-238-33	Sequence 33, App1
18	101	85.6	21	18	US-10-731-238-18	Sequence 18, App1
19	101	85.6	21	18	US-10-731-238-24	Sequence 24, App1
20	101	85.6	21	18	US-10-731-238-27	Sequence 27, App1
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22	101	85.6	21	18	US-10-731-238-30	Sequence 30, App1
23	100	84.7	21	18	US-10-731-238-25	Sequence 25, App1
24	100	84.7	21	18	US-10-731-238-29	Sequence 29, App1
25	100	84.7	21	18	US-10-731-238-31	Sequence 31, App1
26	100	84.7	388	8	US-08-901-062-1	Sequence 1, App1
27	100	84.7	559	8	US-08-781-986A-5251	Sequence 5251, Ap
28	100	84.7	559	15	US-10-329-62A-5251	Sequence 5251, Ap
29	100	84.7	940	17	US-10-470-048B-424	Sequence 424, App
30	100	84.7	948	17	US-10-470-048B-69	Sequence 69, App1
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32	99	83.9	21	18	US-10-731-238-15	Sequence 15, App1
33	99	83.9	21	18	US-10-731-238-20	Sequence 20, App1
34	99	83.9	21	18	US-10-731-238-22	Sequence 22, App1
35	99	83.9	21	18	US-10-731-238-32	Sequence 32, App1
36	99	83.9	22	18	US-10-731-238-13	Sequence 13, App1
37	97	82.2	21	18	US-10-731-238-17	Sequence 17, App1
38	97	82.2	21	18	US-10-731-238-19	Sequence 19, App1
39	97	82.2	21	18	US-10-731-238-21	Sequence 21, App1
40	79	66.9	21	18	US-10-731-238-34	Sequence 34, App1
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42	59	50.0	10	18	US-10-731-238-96	Sequence 96, App1
43	58	49.2	10	18	US-10-731-238-97	Sequence 97, App1
44	54	45.8	10	18	US-10-731-238-95	Sequence 95, App1
45	52	44.1	49	16	US-10-437-963-171086	Sequence 171086,

ALIGNMENTS

RESULT 1
US-10-731-238-26
; Sequence 26, Application US/10731238
; Publication No. US20050123552A1
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
Patli, Joseph M.
House-Pompeo, Karen L.
Speziale, Pietro
Uoh, Danny
McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESSES:
ADDRESSER: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/731,238
FILING DATE: 10-Dec-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE: 21-Jan-1998
APPLICATION NUMBER: US 60/036,139

FLING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TANK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
US-10-731-238-26
SEQUENCE DESCRIPTION: SEQ ID NO: 26:
Query Match 100.0%; Score 118; DB 18; Length 21;
Best Local Similarity 100.0%; Pred. No. 9,1e-11;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 KPSYQFGHNSVDPEDTLPK 21
Db 1 KPSYQFGHNSVDPEDTLPK 21
RESULT 2
US-10-731-238-9
Sequence 9, Application US/10731238
Publication No. US20050123552A1
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
Patti, Joseph M.
House-Pompeo, Karen L.
Speziale, Pietro
Joh, Danny
McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/731,238
FLING DATE: 10-Dec-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FLING DATE: 21-Jan-1998
APPLICATION NUMBER: US 60/036,139
FLING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TANK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>

TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 9:
US-10-731-238-9
Query Match 90.7%; Score 107; DB 18; Length 21;
Best Local Similarity 95.2%; Pred. No. 4,3e-09;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 KPSYQFGHNSVDPEDTLPK 21
Db 1 KPSYQFGHNSVDPEDTLPK 21
RESULT 3
US-11-066-697-1134
Sequence 1134, Application US/11066697
Publication No. US20050187159A1
GENERAL INFORMATION:
APPLICANT: Bridon, Dominique P.
APPLICANT: Ezrin, Alan M.
APPLICANT: Milner, Peter G.
APPLICANT: Holmes, Darren L.
APPLICANT: Thibaudau, Karen
TITLE OF INVENTION: PROTECTION OF ENDOGENOUS THERAPEUTIC PEPTIDES FROM
TITLE OF INVENTION: PEPTIDASE ACTIVITY THROUGH COMUAGTATION TO BLOOD
FILE REFERENCE: 500862002301
CURRENT APPLICATION NUMBER: US/11/066,697
CURRENT FILING DATE: 2005-02-25
PRIOR APPLICATION NUMBER: 09/657,276
PRIOR FILING DATE: 2000-09-07
PRIOR APPLICATION NUMBER: 60/153,406
PRIOR FILING DATE: 1999-09-10
PRIOR APPLICATION NUMBER: 60/159,783
PRIOR FILING DATE: 1999-10-15
NUMBER OF SEQ ID NOS: 1617
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 1134
LENGTH: 37
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-11-066-697-1134
Query Match 90.7%; Score 107; DB 20; Length 37;
Best Local Similarity 95.2%; Pred. No. 8e-09; 1; Indels 0; Gaps 0;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 KPSYQFGHNSVDPEDTLPK 21
Db 16 KPSYQFGHNSVDPEDTLPK 36
RESULT 4
US-09-813-820-8
Sequence 8, Application US/09813820
Patent No. US20020102262A1
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
Patti, Joseph M.
House-Pompeo, Karen
Schanam, Narayana
Symerky, Jindrich
TITLE OF INVENTION: COLLAGEN BINDING PROTEIN COMPOSITIONS
AND METHODS OF USE
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: Texas

```

; COUNTRY: U.S.
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/813,820
; FILING DATE: 22-Mar-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/856,253
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Kitchell, Barbara S.
; REGISTRATION NUMBER: 33,928
; REFERENCE/DOCKET NUMBER: TAMK:193
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (512) 418-3000
; TELEFAX: (512) 474-7577
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 139 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-09-813-820-8

Query Match          90.7%; Score 107; DB 9; Length 139;
Best Local Similarity 95.2%; Pred. No. 3.4e-08;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Q# 1 KPSYQFGHNSVDPEDTLPK 21
Db 107 KPSYQFGHNSVDPEDTLPK 127

RESULT 5
US-09-815-242-5797
; Sequence 5797, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; FILE REFERENCE: ELITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version 4.0
; FILE REFERENCE: FastSeq for Windows Version 4.0
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; SEQ ID NO 5797
; LENGTH: 1018
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-09-815-242-5797

Query Match          90.7%; Score 107; DB 9; Length 1018;
Best Local Similarity 95.2%; Pred. No. 3.1e-07;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Q# 1 KPSYQFGHNSVDPEDTLPK 21
Db 837 KPSYQFGHNSVDPEDTLPK 857

RESULT 6
US-09-815-242-12838
; Sequence 12838, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; FILE REFERENCE: ELITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12838
; LENGTH: 1018
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-09-815-242-12838

Query Match          90.7%; Score 107; DB 9; Length 1018;
Best Local Similarity 95.2%; Pred. No. 3.1e-07;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Q# 1 KPSYQFGHNSVDPEDTLPK 21
Db 837 KPSYQFGHNSVDPEDTLPK 857

RESULT 7
US-10-470-048B-68
; Sequence 68, Application US/10470048B
; Publication No. US2005003744A1
; GENERAL INFORMATION:
; APPLICANT: MEINKE ET AL.
; TITLE OF INVENTION: A METHOD FOR IDENTIFICATION, ISOLATION AND PRODUCTION OF
; FILE REFERENCE: SONN.035US
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;; CURRENT APPLICATION NUMBER: US/10/470,048B
;; CURRENT FILING DATE: 2003-07-25
;; NUMBER OF SEQ ID NOS: 603
;; SOFTWARE: PatentIn version 3.1
;; SEQ ID NO: 68
;; LENGTH: 1018
;; TYPE: PRT
;; ORGANISM: Staphylococcus aureus
US-10-470-048B-68

Query Match 90.7%; Score 107; DB 17; Length 1018;
Best Local Similarity 95.2%; Pred. No. 3.1e-07;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KPSYFGGHSVDPEDTLPK 21
DB 837 KPSYFGGHSVDPEDTLPK 857

RESULT 8
US-08-781-986A-5254
; Sequence 5254, Application US/08781986A
; Publication No. US2003005436A1
; GENERAL INFORMATION:
; APPLICANT: Charles Kunach
; TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
; NUMBER OF SEQUENCES: 5255
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/781,986A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Benson, Bob
; REGISTRATION NUMBER: 30,446
; REFERENCE/DOCKET NUMBER: PB248BP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 5254:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1027 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-781-986A-5254

Query Match 90.7%; Score 107; DB 8; Length 1027;
Best Local Similarity 95.2%; Pred. No. 3.1e-07;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KPSYFGGHSVDPEDTLPK 21
DB 846 KPSYFGGHSVDPEDTLPK 866

RESULT 9
US-10-329-624-5254

;; Sequence 5254, Application US/10329624
;; Publication No. US20040043037A1
;; GENERAL INFORMATION:
;; APPLICANT: Charles Kunach
;; Gil H. Choi
;; Patrick S. Dillon
;; Craig A. Rosen
;; Steven C. Barash
;; Michael R. Fannon
;; TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
;; NUMBER OF SEQUENCES: 5256
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Human Genome Sciences, Inc.
;; STREET: 9410 Key West Avenue
;; CITY: Rockville
;; STATE: Maryland
;; COUNTRY: USA
;; ZIP: 20850
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
;; COMPUTER: HP Vectra 486/33
;; OPERATING SYSTEM: MSDOS version 6.2
;; SOFTWARE: ASCII Text
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/10/329,624
;; FILING DATE: 27-Dec-2002
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 08/956,171
;; FILING DATE: October 20, 1997
;; APPLICATION NUMBER: 60/009,861
;; FILING DATE: January 5, 1996
;; APPLICATION NUMBER: 08/781,986
;; FILING DATE: January 3, 1997
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Mark J. Hyman
;; REGISTRATION NUMBER: 46,789
;; REFERENCE/DOCKET NUMBER: PB248P1D1
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (240) 314-1224
;; TELEFAX: (301) 309-8439
;; INFORMATION FOR SEQ ID NO: 5254:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 1027 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; SEQUENCE DESCRIPTION: SEQ ID NO: 5254:
US-10-329-624-5254

Query Match 90.7%; Score 107; DB 15; Length 1027;
Best Local Similarity 95.2%; Pred. No. 3.1e-07;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KPSYFGGHSVDPEDTLPK 21
DB 846 KPSYFGGHSVDPEDTLPK 866

RESULT 10
US-10-282-122A-43778
; Sequence 43778, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zykkind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant

```

; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.039A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; REMAINING PRIOR APPLICATION DATA REMOVED - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 43778
; LENGTH: 961
; TYPE: prt
; ORGANISM: Staphylococcus aureus
; US-10-282-122A-43778

Query Match      88.1%; Score 104; DB 15; Length 961;
Best Local Similarity 90.5%; Pred. No. 8.2e-07;
Matches 19; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1 KPSYOGGHSVDPEDTLPK 21
DB      784 KPNYOGGHSVDPEDTLPK 804

RESULT 11
US-09-815-242-5456
; Sequence 5456, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; TITLE OF INVENTION: Prokaryotes
; FILE REFERENCE: ELITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
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; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5456
; LENGTH: 978
; TYPE: prt
; ORGANISM: Staphylococcus aureus
; US-09-815-242-5456

Query Match      88.1%; Score 104; DB 9; Length 978;
Best Local Similarity 90.5%; Pred. No. 8.4e-07;
Matches 19; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1 KPSYOGGHSVDPEDTLPK 21
DB      815 KPNYOGGHSVDPEDTLPK 835

RESULT 12
US-09-815-242-12686
; Sequence 12686, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; TITLE OF INVENTION: Prokaryotes
; FILE REFERENCE: ELITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12686
; LENGTH: 1001
; TYPE: prt
; ORGANISM: Staphylococcus aureus
; US-09-815-242-12686

Query Match      88.1%; Score 104; DB 9; Length 1001;
Best Local Similarity 90.5%; Pred. No. 8.6e-07;
Matches 19; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1 KPSYOGGHSVDPEDTLPK 21
DB      838 KPNYOGGHSVDPEDTLPK 858

RESULT 13
US-10-282-122A-43827
; Sequence 43827, Application US/10282122A
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Publication No. US20040029129A1
GENERAL INFORMATION:
APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari
APPLICANT: Zykand, Judith
APPLICANT: Wall, Daniel
APPLICANT: Trewick, John
APPLICANT: Carr, Grant
APPLICANT: Yamamoto, Robert
APPLICANT: Forsyth, R.
APPLICANT: Xu, H.
TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REFERENCE: ELITRA.034A
CURRENT APPLICATION NUMBER: US/10/282.122A
CURRENT FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/230,335
PRIOR FILING DATE: 2000-09-06
PRIOR APPLICATION NUMBER: 60/230,347
PRIOR FILING DATE: 2000-09-09
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/267,636
PRIOR FILING DATE: 2001-02-09
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 78614
SOFTWARE: PatentIn version 3.1
SEQ ID NO 43827
LENGTH: 1038
TYPE: PRT
ORGANISM: Staphylococcus aureus
US-10-282-122A-43827
Query Match 88.1%; Score 104; DB 15; Length 1038;
Best Local Similarity 90.5%; Pred. No. 9e-07;
Matches 19; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
Qy 1 KPSYFGGHSVDPEDTLPK 21
Db 833 KPNYQFGGHSVDPEDTLPK 853
US-10-731-238-14
Sequence 14, Application US/10731238
Publication No. US20050123552A1
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
Patel, Joseph M.
House-Pompeo, Karen L.
Speziale, Pietro
Joh, Danny
McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Arnold, White & Durkee
STREET: P. O. Box 4433

CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/731.238
FILING DATE: 10-Dec-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/010.317
FILING DATE: 21-Jan-1998
APPLICATION NUMBER: US 60/036.139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TLMK.189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 14:
US-10-731-238-14
Query Match 86.4%; Score 102; DB 18; Length 21;
Best Local Similarity 95.0%; Pred. No. 2.5e-08;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 2 PSYQFGGHSVDPEDTLPK 21
Db 2 PSYQFGGHSVDPEDTLPK 21
US-10-731-238-16
Sequence 16, Application US/10731238
Publication No. US20050123552A1
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
Patel, Joseph M.
House-Pompeo, Karen L.
Speziale, Pietro
Joh, Danny
McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Arnold, White & Durkee
STREET: P. O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/731.238
FILING DATE: 10-Dec-2003
CLASSIFICATION: <Unknown>

```

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/010,317
; FILING DATE: 21-Jan-1998
; APPLICATION NUMBER: US 60/036,139
; FILING DATE: 21-JAN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Hibler, David W.
; REGISTRATION NUMBER: 41,071
; REFERENCE/DOCKET NUMBER: TANK:189
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 512-418-3000
; TELEFAX: 512-474-7577
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 16:
; US-10-731-238-16

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Query Match      86.4%; Score 102; DB 18; Length 21;
Best Local Similarity 90.5%; Pred. No. 2,5e-08;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Qy      1 KPSYQFGHNSVDPEDTLPK 21
      |||||
Db      1 KPYYQFGHNSVDPEDTLPK 21

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Search completed: October 22, 2005, 11:34:41
 Job time : 59.2367 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 22, 2005, 02:23:36 ; Search time 10.5465 Seconds
(without alignments)
191.586 Million cell updates/sec

Title: US-10-731-238-26

Perfect score: 118
Sequence: 1 KPSYQFGHNSVDPEDTLPK 21

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: p1r1: *
2: p1r2: *
3: p1r3: *
4: p1r4: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	107	90.7	1018	2 A32192	fibronectin-binding
2	104	88.1	961	2 G90053	hypothetical prote
3	104	88.1	1038	2 H90053	hypothetical prote
4	100	84.7	940	2 S19702	fibronectin-binding
5	46.5	39.4	918	2 JC4361	scavenger receptor
6	46	39.0	342	2 S76463	hypothetical prote
7	46	39.0	344	2 S73188	pyruvate dehydroge
8	46	39.0	344	2 AE2144	pyruvate dehydroge
9	46	39.0	445	2 F90562	hypothetical prote
10	46	39.0	623	2 T18892	hypothetical prote
11	45.5	38.6	176	2 T15953	beta-amylose (EC 3
12	45.5	38.6	548	2 T52556	3-phosphoshikimate
13	45	38.1	427	2 D95159	3-phosphoshikimate
14	45	38.1	431	2 D98025	3-oxoacyl-lacyl-ca
15	45	38.1	462	2 A39356	3-oxoacyl-lacyl-ca
16	45	38.1	469	2 T10061	myosin heavy chain
17	45	38.1	1322	2 A59288	protein-tyrosine k
18	45	38.1	1584	2 T18276	cag island protein
19	44.5	37.7	1167	2 B71924	cag pathogenicity
20	44.5	37.7	1186	2 C64588	cytotoxin-associated
21	44.5	37.7	1215	2 B48281	29k serine protein
22	44	37.3	251	2 PC1235	flagellar motor sw
23	44	37.3	349	2 H82116	extracellular prote
24	44	37.3	387	2 I38449	transforming prote
25	44	37.3	429	2 A36420	S-receptor kinase
26	44	37.3	849	1 T05181	probable secreted
27	43.5	36.9	417	2 T34930	pyruvate dehydroge
28	43	36.4	409	2 T38417	hypothetical prote
29	43	36.4	416	2 T46123	hypothetical prote

30	43	36.4	443	1 DERBPA	pyruvate dehydroge
31	43	36.4	474	2 B84357	serine-tRNA synthe
32	43	36.4	576	2 S16693	Gly-X carboxypepti
33	43	36.4	578	2 S52913	nuclear receptor R
34	43	36.4	869	2 A55384	transcription fact
35	43	36.4	1052	2 T04439	hypothetical prote
36	42.5	36.0	380	1 S73751	high affinity tran
37	42.5	36.0	720	2 S51340	nucleoporin NUP2 -
38	42.5	36.0	759	2 B83474	probable type II b
39	42.5	36.0	1034	2 S63536	aminomethyltransfe
40	42.5	36.0	1035	2 T07826	aminomethyltransfe
41	42.5	36.0	1037	2 S63535	aminomethyltransfe
42	42.5	36.0	1038	2 T15098	hypothetical prote
43	42.5	36.0	1091	2 S33850	fibronectin-binding
44	42	35.6	237	2 A70672	hypothetical prote
45	42	35.6	390	2 JC7256	L-pipecolate oxida

ALIGNMENTS

RESULT 1

A32192
fibronectin-binding protein - Staphylococcus aureus
C:Species: Staphylococcus aureus
C:Date: 31-Jul-1989 #sequence_revision 31-Jul-1989 #text_change 16-Feb-1997
C:Accession: A32192
R:Signaess, C.; Raucel, G.; Joensson, K.; Lindgren, P.E.; Anantharamiah, G.M.; Hoesoek, M.
Proc. Natl. Acad. Sci. U.S.A. 86, 699-703, 1989
A:Title: Nucleotide sequence of the gene for a fibronectin-binding protein from Staphyloc
A:Reference number: A32192; MUID:89098998; PMID:2521391
A:Accession: A32192
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1018 <SIG>
A:Cross-references: GB:J04151
A:Keywords: fibronectin binding

Query Match 90.7%; Score 107; DB 2; Length 1018;
Best Local Similarity 95.2%; Pred. No. 1.1e-08;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KPSYQFGHNSVDPEDTLPK 21

DB 837 KPSYQFGHNSVDPEDTLPK 857

RESULT 2

G90053
hypothetical protein fnb [Imported] - Staphylococcus aureus (strain N315)
C:Species: Staphylococcus aureus
C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C:Accession: G90053
R:Kurda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguc
ma, A.; Mizutani-Ut, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.;
C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
A:Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.
A:Reference number: A69758; MUID:21311952; PMID:11418146
A:Accession: G90053
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-961 <KUR>
A:Cross-references: UNIPROT:Q99RD3; GB:BA000018; PID:G13702452; PIDN:BA843593.1; GSPDB:G
A:Experimental source: strain N315
A:Genetics:
A:Gene: fnb

Query Match 88.1%; Score 104; DB 2; Length 961;
Best Local Similarity 90.5%; Pred. No. 3.2e-08;
Matches 19; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 KPSYQFGHNSVDPEDTLPK 21

Db 784 KPNYFGGHSVDPEDTLPPK 804

RESULT 3

hypothetical protein fnb [imported] - Staphylococcus aureus (strain N315)
H90053
C:Species: Staphylococcus aureus
C>Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C:Accession: H90053
R:Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Ogura, A.; Mizutani-Uji, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.; C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
A:Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.
A:Reference number: A89758; MUID:21311952; PMID:11418146
A:Accession: H90053
A:Status: Preliminary
A:Molecule type: DNA
A:Residues: 1-1038 <KUR>
A:Cross-references: UNIPROT:Q99RD2; GB:BA000018; PID:g13702453; PIDN:BA843594.1; GSPDB:C
A:Experimental source: Strain N315
C:Genetics:
A:Gene: fnb

Query Match 88.1%; Score 104; DB 2; Length 1038;
Best Local Similarity 90.5%; Pred. No. 3.4e-08;
Matches 19; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 KPSYFGGHSVDPEDTLPPK 21
Db 833 KPNYFGGHSVDPEDTLPPK 853

RESULT 4

fibronectin-binding protein B - Staphylococcus aureus
S19702
C:Species: Staphylococcus aureus
C>Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
C:Accession: S19702
R:Joensson, K.; Signaes, C.; Mueller, H.P.; Lindberg, M.
Eur. J. Biochem. 202, 1041-1048, 1991
A:Title: Two different genes encode fibronectin binding proteins in Staphylococcus aureus
A:Reference number: S19702; MUID:92111475; PMID:1837266
A:Accession: S19702
A:Status: Preliminary
A:Molecule type: DNA
A:Residues: 1-940 <JOB>
A:Cross-references: UNIPROT:Q53682; EMBL:X62392; NID:g49040; PIDN:CAA44726.1; PID:G58156
C:Keywords: fibronectin binding

Query Match 84.7%; Score 100; DB 2; Length 940;
Best Local Similarity 85.7%; Pred. No. 1.3e-07;
Matches 18; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 KPSYFGGHSVDPEDTLPPK 21
Db 773 KPNYFGGHSVDPEDTLPPK 793

RESULT 5

scavenger receptor Cys-rich epidermal growth factor precursor - sea lamprey
JC4361
C:Species: Petromyzon marinus (sea lamprey)
C>Date: 08-Jan-1996 #sequence_revision 08-Feb-1996 #text_change 09-Jul-2004
C:Accession: JC4361
R:Mayer, W.B.; Tichy, H.
Gene 164, 267-271, 1995
A:Title: A cDNA clone from the sea lamprey Petromyzon marinus coding for a scavenger receptor
A:Reference number: JC4361; MUID:96069593; PMID:7590341
A:Molecule type: mRNA
A:Residues: 1-918 <MAY>

A:Cross-references: UNIPROT:Q92098; GB:U20652; NID:g790233; PIDN:AAA90990.1; PID:g790234
C:Comment: This protein is rich in cysteine and plays a role in intercellular contacts at
C:Keywords: glycoprotein; growth factor; receptor; transmembrane protein
F:1-24/Domain: signal sequence #status predicted <SIG>
F:25-918/Product: scavenger receptor Cys-rich epidermal growth factor #status predicted <F>
F:15-157/Domain: scavenger receptor Cys-rich epidermal growth factor #status predicted <F>
F:179-212/Domain: EGF homology <EG1>
F:234-267/Domain: EGF homology <EG2>
F:325-328/Domain: EGF homology <EG3>
F:355-389/Domain: EGF homology <EG4>
F:410-443/Domain: EGF homology <EG5>
F:463-565/Domain: scavenger receptor cysteine-rich domain homology <SRC2>
F:876-895/Domain: transmembrane #status predicted <TM>
F:896-918/Domain: intracellular #status predicted <INT>
F:40,545,575,585,814/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 39.4%; Score 46.5; DB 2; Length 918;
Best Local Similarity 37.0%; Pred. No. 45;
Matches 10; Conservative 4; Mismatches 6; Indels 7; Gaps 1;

QY 2 PSY-----QFGGHSVDPEDTLPPK 21
Db 259 PSYWMGNCERYGASHDAPEDTLPPK 285

RESULT 6

hypothetical protein - Synechocystis sp. (strain PCC 6803)
S76463
C:Species: Synechocystis sp.
A:Variety: PCC 6803
C>Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004
C:Accession: S76463
R:Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.; O. K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda, DNA Res. 3, 109-136, 1996
A:Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis sp.
A:Reference number: S74322; MUID:97061201; PMID:8905231
A:Accession: S76463
A:Status: Preliminary
A:Molecule type: DNA
A:Residues: 1-342 <KAN>
A:Cross-references: UNIPROT:P74490; EMBL:D90915; GB:AB001339; NID:g1653604; PIDN:BA1859;
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
C:Superfamily: pyruvate dehydrogenase (lipoamide) alpha chain; thiamin pyrophosphate-binc
F:155-205/Domain: thiamin pyrophosphate-binding domain homology <TPB>

Query Match 39.0%; Score 46; DB 2; Length 342;
Best Local Similarity 50.0%; Pred. No. 17;
Matches 7; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 3 SYRFGGHSVDPED 16
Db 259 TYRFRGSHLADPE 272

RESULT 7

pyruvate dehydrogenase E1 component alpha chain - red alga (Porphyra purpurea) chloroplast
S73188
C:Species: Chloroplast Porphyra purpurea
C>Date: 19-Mar-1997 #sequence_revision 09-May-1997 #text_change 09-Jul-2004
C:Accession: S73188
R:Reith, M.; Munholland, J.
Plant Mol. Biol. Rep. 13, 333-335, 1995
A:Title: Complete nucleotide sequence of the Porphyra purpurea chloroplast genome.
A:Reference number: S73108
A:Accession: S73188
A:Status: Preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-344 <RET>
A:Cross-references: UNIPROT:P51267; EMBL:U38804; NID:g1276652; PIDN:AAC08153.1; PID:g1276
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1995
C:Genetics:

A:Gene: odba
 A:Genome: chloroplast
 C:Superfamily: pyruvate dehydrogenase (lipoamide) alpha chain; thiamin pyrophosphate-bin
 C:Keywords: chloroplast

Query Match 39.0%; Score 46; DB 2; Length 344;
 Best Local Similarity 50.0%; Pred. No. 18;
 Matches 7; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 3 SYQFGHNSVDPPE 16
 DB 260 TYRFRGSHLADPDE 273

RESULT 8
 AE2144
 Pyruvate dehydrogenase E1 component, alpha chain [imported] - Nostoc sp. (strain PCC 7120
 C:Species: Nostoc sp. PCC 7120
 A:Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
 C:Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004
 C:Accession: AE2144
 R:Kaneko, T.; Nakamura, Y.; Molk, C.P.; Kurita, T.; Sasamoto, S.; Matanabe, A.; Iriyuchi, S.; Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S.
 DNA Res. 8, 205-213, 2001
 A:Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Anabaena
 A:Reference number: AB1807; MUID:21595285; PMID:11759840
 A:Accession: AE2144
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-344 <KUR>
 A:Cross-references: UNIPROT:Q8YTK9; GB:BA000019; PIDN:BAW74407.1; PID:G17131801; GSPDB:C
 A:Experimental source: strain PCC 7120
 C:Genetics:
 A:Gene: alr2708
 C:Superfamily: pyruvate dehydrogenase (lipoamide) alpha chain; thiamin pyrophosphate-bin

Query Match 39.0%; Score 46; DB 2; Length 344;
 Best Local Similarity 50.0%; Pred. No. 18;
 Matches 7; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 3 SYQFGHNSVDPPE 16
 DB 259 TYRFRGSHLADPDE 272

RESULT 9
 F90562
 Hypothetical protein MYPV 4060 [imported] - Mycoplasma pulmonis (strain UAB CTIP)
 C:Species: Mycoplasma pulmonis
 C:Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 09-Jul-2004
 C:Accession: F90562
 R:Chambaud, I.; Heilig, R.; Ferris, S.; Barbe, V.; Samson, D.; Galisson, F.; Moszer, I.; Nucleic Acids Res. 29, 2145-2153, 2001
 A:Title: The complete genome sequence of the murine respiratory pathogen Mycoplasma pulmonis
 A:Reference number: A99512; MUID:21267165; PMID:11353084
 A:Accession: F90562
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-445 <KUR>
 A:Cross-references: UNIPROT:Q98QGO; GB:AL445566; PID:G14089620; PIDN:CAC13579.1; GSPDB:C
 A:Experimental source: strain UAB CTIP
 C:Genetics:
 A:Gene: MYPV 4060
 A:Genetic code: SGC3

Query Match 39.0%; Score 46; DB 2; Length 445;
 Best Local Similarity 43.8%; Pred. No. 24;
 Matches 7; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 1 KPSYQFGHNSVDPPE 16
 DB 334 KPDPVAGHNTYEHQE 349

RESULT 10
 T18932
 Hypothetical protein C03E10.5 - Caenorhabditis elegans
 C:Species: Caenorhabditis elegans
 C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
 C:Accession: T18932
 R:Kershaw, J. submitted to the EMBL Data Library, November 1996
 A:Reference number: Z19039
 A:Accession: T18932
 A:Molecule type: DNA
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Residues: 1-623 <ML>
 A:Cross-references: UNIPROT:O17662; EMBL:Z81458; PIDN:CAB03824.1; GSPDB:GN00023; CESP:C03
 A:Experimental source: clone C03E10
 C:Genetics:
 A:Gene: CESP:C03E10.5
 A:Map position: 5
 A:introns: 284/1; 327/3; 352/2; 381/2; 436/1; 541/3; 569/2

Query Match 39.0%; Score 46; DB 2; Length 623;
 Best Local Similarity 61.5%; Pred. No. 35;
 Matches 8; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 8 GHSVDPEDTLP 20
 DB 399 GHEGVCPPESTIP 411

RESULT 11
 T15953
 Hypothetical protein F01F1.2 - Caenorhabditis elegans
 C:Species: Caenorhabditis elegans
 C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
 C:Accession: T15953
 R:Miller, N. submitted to the EMBL Data Library, July 1995
 A:Description: The sequence of C. elegans cosmid F01F1.
 A:Reference number: Z18435
 A:Accession: T15953
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-176 <ML>
 A:Cross-references: UNIPROT:Q19093; EMBL:U13070; NID:G529697; PID:G529699; PIDN:AAC46636.
 A:Experimental source: strain Bristol N2
 C:Genetics:
 A:Gene: CESP:F01F1.2
 A:introns: 49/1; 84/1
 C:Superfamily: Caenorhabditis elegans hypothetical protein F01F1.2

Query Match 38.6%; Score 45.5; DB 2; Length 176;
 Best Local Similarity 52.4%; Pred. No. 9.8;
 Matches 11; Conservative 1; Mismatches 8; Indels 1; Gaps 1;

QY 2 PSYQFGHNSVDPEDTLP 21
 DB 38 PHYSAGPHGLDPPEDTLPK 58

RESULT 12
 T52556
 beta-amylase (EC 3.2.1.2) precursor, chloroplast [validated] - Arabidopsis thaliana
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C:Date: 24-Oct-2000 #sequence_revision 24-Oct-2000 #text_change 09-Jul-2004
 C:Accession: T52556
 R:Yao, N.T.; Schoneveld, O.; Mould, R.M.; Hibberd, J.M.; Gray, J.C.; Kavanagh, T.A.
 Plant J. 20, 519-527, 1999
 A:Title: An Arabidopsis gene encoding a chloroplast-targeted b-amylase.
 A:Reference number: Z26113
 A:Accession: T52556
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA


```

FT REPEAT 545 574 B-1.
FT REPEAT 575 604 B-2.
FT DOMAIN 745 878 4 X approximate tandem repeats,
  fibronectin-binding domain.
FT REPEAT 745 782 D-1.
FT REPEAT 783 820 D-2.
FT REPEAT 821 859 D-3.
FT REPEAT 860 878 D-4 (incomplete).
FT DOMAIN 879 948 5 X tandem repeats, Pro-rich (WR).
FT REPEAT 879 892 WR 1.
FT REPEAT 893 906 WR 2.
FT REPEAT 907 920 WR 3.
FT REPEAT 921 934 WR 4.
FT REPEAT 935 948 WR 5.
FT SITE 982 986 LPXTG sorting signal (Potential).
FT MOD_RRS 985 985 Pentaglycyl murein peptidoglycan amidated
  threonine (Potential).
SQ SEQUENCE 1018 AA; 11780 MW; 58175E0020B81F1F CRC64;

Query Match 90.7%; Score 107; DB 1; Length 1018;
Best Local Similarity 95.2%; Pred. No. 1e-07;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 KPSYQFGHNSVDPEDTLPK 21
Db 837 KPSYQFGHNSVDPEDTLPK 857

RESULT 2
O99RD3 PRELIMINARY; PRT; 961 AA.
AC O99RD3
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE Fibronectin-binding protein homolog.
GN Name=fnb3; OrderedLocuNames=SAV2502;
OS Staphylococcus aureus (strain Mu50 / ATCC 700689).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=158878;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=21311952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2;
RX Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
  RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Iian J.-Q., Ito T.,
  RA Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosooyama A.,
  RA Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
  RA Sekimizu K., Hiraoka H., Kuhara S., Goto S., Yabuzaki J.,
  RA Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
  RA Hattori M., Ogasawara N., Hayashi H., Hiratake K.;
  RT "Whole genome sequencing of methicillin-resistant Staphylococcus
  aureus."
  RL Lancet 357:1225-1240(2001).
  CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
  an amide bond (By similarity).
  DR EMBL; AP003365; BAB58664.1; -.
  DR HSSP; Q53653; 1N67.
  DR GO; GO:0009986; C:cell surface; IEA.
  DR GO; GO:0005618; C:cell wall; IEA.
  DR GO; GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
  DR GO; GO:0016020; C:membrane; IEA.
  DR GO; GO:0071155; P:cell adhesion; IEA.
  DR InterPro; IPR008966; Adhes_bact.
  DR InterPro; IPR004237; Fn_bind.
  DR InterPro; IPR005877; Gpos_YsIRK.
  DR Pfam; PF02986; Gram_pos_anchor.
  DR Pfam; PF00746; Gram_pos_anchor; 1.
  DR Pfam; PF04650; YsIRK_signal; 1.
  DR TIGRfams; TIGR01167; LPXTG_anchor; 1.
  DR TIGRfams; TIGR01168; YsIRK_signal; 1.
  DR PROSITE; PS50847; GRAM_POS_ANCHORING; 1.
  KW Cell wall; Complete proteome; Peptidoglycan-anchor.
  SQ SEQUENCE 961 AA; 106010 MW; 364940F884NA4101 CRC64;

Query Match 88.1%; Score 104; DB 2; Length 961;
Best Local Similarity 90.5%; Pred. No. 2.9e-07;
Matches 19; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Oy 1 KPSYQFGHNSVDPEDTLPK 21
Db 784 KPSYQFGHNSVDPEDTLPK 804

RESULT 3
O7A3J8 PRELIMINARY; PRT; 961 AA.
AC O7A3J8
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE FnbB protein.
GN Name=fnbB; OrderedLocuNames=SA2290;
OS Staphylococcus aureus (strain N315).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=158879;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=21311952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2;
RX Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
  RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Iian J.-Q., Ito T.,
  RA Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosooyama A.,
  RA Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
  RA Sekimizu K., Hiraoka H., Kuhara S., Goto S., Yabuzaki J.,
  RA Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
  RA Hattori M., Ogasawara N., Hayashi H., Hiratake K.;
  RT "Whole genome sequencing of methicillin-resistant Staphylococcus
  aureus."
  RL Lancet 357:1225-1240(2001).
  CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
  an amide bond (By similarity).
  DR EMBL; AP003137; BAB43593.1; -.
  DR GO; GO:0009986; C:cell surface; IEA.
  DR GO; GO:0005618; C:cell wall; IEA.
  DR GO; GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
  DR GO; GO:0016020; C:membrane; IEA.
  DR GO; GO:0071155; P:cell adhesion; IEA.
  DR InterPro; IPR008966; Adhes_bact.
  DR InterPro; IPR004237; Fn_bind.
  DR InterPro; IPR005877; Gpos_YsIRK.
  DR InterPro; IPR001899; Gram_pos_anchor.
  DR Pfam; PF02986; Fn_bind; 1.
  DR Pfam; PF00746; Gram_pos_anchor; 1.
  DR Pfam; PF04650; YsIRK_signal; 1.
  DR TIGRfams; TIGR01167; LPXTG_anchor; 1.
  DR TIGRfams; TIGR01168; YsIRK_signal; 1.
  DR PROSITE; PS50847; GRAM_POS_ANCHORING; 1.
  KW Cell wall; Complete proteome; Peptidoglycan-anchor.
  SQ SEQUENCE 961 AA; 106010 MW; 364940F884NA4101 CRC64;

Query Match 88.1%; Score 104; DB 2; Length 961;
Best Local Similarity 90.5%; Pred. No. 2.9e-07;
Matches 19; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Oy 1 KPSYQFGHNSVDPEDTLPK 21
Db 784 KPSYQFGHNSVDPEDTLPK 804

RESULT 4
O6GDUS PRELIMINARY; PRT; 965 AA.
AC O6GDUS
DT 05-JUL-2004 (TREMBlrel. 27, Created)

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DR PROSITE; PS50847; GRAM_POS_ANCHORING; 1.
KW Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ SEQUENCE 961 AA; 106010 MW; 364940F884NA4101 CRC64;

Query Match 88.1%; Score 104; DB 2; Length 961;
Best Local Similarity 90.5%; Pred. No. 2.9e-07;
Matches 19; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Oy 1 KPSYQFGHNSVDPEDTLPK 21
Db 784 KPSYQFGHNSVDPEDTLPK 804

RESULT 3
O7A3J8 PRELIMINARY; PRT; 961 AA.
AC O7A3J8
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE FnbB protein.
GN Name=fnbB; OrderedLocuNames=SA2290;
OS Staphylococcus aureus (strain N315).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=158879;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=21311952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2;
RX Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
  RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Iian J.-Q., Ito T.,
  RA Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosooyama A.,
  RA Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
  RA Sekimizu K., Hiraoka H., Kuhara S., Goto S., Yabuzaki J.,
  RA Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
  RA Hattori M., Ogasawara N., Hayashi H., Hiratake K.;
  RT "Whole genome sequencing of methicillin-resistant Staphylococcus
  aureus."
  RL Lancet 357:1225-1240(2001).
  CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
  an amide bond (By similarity).
  DR EMBL; AP003137; BAB43593.1; -.
  DR GO; GO:0009986; C:cell surface; IEA.
  DR GO; GO:0005618; C:cell wall; IEA.
  DR GO; GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
  DR GO; GO:0016020; C:membrane; IEA.
  DR GO; GO:0071155; P:cell adhesion; IEA.
  DR InterPro; IPR008966; Adhes_bact.
  DR InterPro; IPR004237; Fn_bind.
  DR InterPro; IPR005877; Gpos_YsIRK.
  DR InterPro; IPR001899; Gram_pos_anchor.
  DR Pfam; PF02986; Fn_bind; 1.
  DR Pfam; PF00746; Gram_pos_anchor; 1.
  DR Pfam; PF04650; YsIRK_signal; 1.
  DR TIGRfams; TIGR01167; LPXTG_anchor; 1.
  DR TIGRfams; TIGR01168; YsIRK_signal; 1.
  DR PROSITE; PS50847; GRAM_POS_ANCHORING; 1.
  KW Cell wall; Complete proteome; Peptidoglycan-anchor.
  SQ SEQUENCE 961 AA; 106010 MW; 364940F884NA4101 CRC64;

Query Match 88.1%; Score 104; DB 2; Length 961;
Best Local Similarity 90.5%; Pred. No. 2.9e-07;
Matches 19; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Oy 1 KPSYQFGHNSVDPEDTLPK 21
Db 784 KPSYQFGHNSVDPEDTLPK 804

RESULT 4
O6GDUS PRELIMINARY; PRT; 965 AA.
AC O6GDUS
DT 05-JUL-2004 (TREMBlrel. 27, Created)

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05-JUL-2004 (TREMblrel. 27, Last sequence update)
 05-JUL-2004 (TREMblrel. 27, Last annotation update)
 Fibronectin-binding protein.
 Name=fmba; OrderedlocusNames=SR2580;
 Staphylococcus aureus (strain MRSA252).
 Bacteria; Firmicutes; Bacillales; Staphylococcus.
 NCBI_TaxID=282458;
 [1]
 SEQUENCE FROM N.A.
 PubMed=15213324; DOI=10.1073/pnas.0402521101;
 Holden M.T.G., Fell E.J., Lindsey J.A., Peacock S.J., Day N.P.J.,
 Enright M.C., Foster T.J., Moore C.E., Hurst L., Atkin R., Barron A.,
 Baason N., Bentley S.D., Chillingworth C., Chillingworth T.,
 Churcher C., Clark L., Corton C., Cronin A., Doggett J., Dowd L.,
 Felwell T., Hance Z., Harris B., Hauser H., Holroyd S., Jagels K.,
 James K.D., Leonard N., Line A., Mayes R., Moule S., Mungall K.,
 Ormond D., Quail M.A., Rabinowitch E., Rutherford K.M., Sanders M.,
 Sharp S., Simmonds M., Stevens K., Whitehead S., Barrett B.G.,
 Spratt B.G., Parkhill J.;
 "Complete genomes of two clinical Staphylococcus aureus strains:
 evidence for the rapid evolution of virulence and drug resistance";
 Proc. Natl. Acad. Sci. U.S.A. 101:9786-9791(2004).
 -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
 an amide bond (By similarity).
 EMBL; BX571856; CAG41560.1; -;
 GO; GO:0009986; C:cell surface; IEA.
 GO; GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
 GO; GO:0016020; C:membrane; IEA.
 GO; GO:0007155; P:cell adhesion; IEA.
 InterPro; IPR008966; Adhes_bact.
 InterPro; IPR004237; Fb_bind.
 InterPro; IPR005877; Gpos_YsIRK.
 InterPro; IPR001899; Gram_pos_anchor.
 Pfam; PF02986; Fb_bind.1.
 Pfam; PF00746; Gram_pos_anchor.1.
 Pfam; PF04650; YsIRK_signal.1.
 TIGRFAMs; TIGR01167; LPXTG_anchor.1.
 TIGRFAMs; TIGR01168; YsIRK_signal.1.
 PROSITE; PS50847; GRAM_POS_ANCHORING.1.
 Cell wall; Complete proteome; Peptidoglycan-anchor.
 SEQUENCE 965 AA; 105691 MW; 29828132164D0551 CRC64;
 SQ

Query Match 88.1%; Score 104; DB 2; Length 965;
 Best Local Similarity 90.5%; Pred. No. 2.9e-07;
 Matches 19; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 KPSYQFGHNSVDPEDTLPK 21
 DB 802 KENYQFGHNSVDPEDTLPK 822

RESULT 5
 Q8NUU7 PRELIMINARY; PRT; 1015 AA.
 AC Q8NUU7;
 DT 01-OCT-2002 (TREMblrel. 22, Created)
 DT 01-OCT-2002 (TREMblrel. 22, Last sequence update)
 DT 01-OCT-2003 (TREMblrel. 25, Last annotation update)
 DE Fnb protein.
 GN Name=fnb; OrderedlocusNames=MM2421;
 OS Staphylococcus aureus (strain MM2).
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 NCBI_TaxID=196620;
 [1]
 SEQUENCE FROM N.A.
 STRAIN=MM2;
 MEDLINE=22040717; PubMed=12044378; DOI=10.1016/S0140-6736(02)08713-5;
 Baba T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Oguchi A.,
 Nagai Y., Iwano K., Amano K., Naito T., Kuroda H., Cui L.,
 Yamamoto K., Hiramoto K.;
 "Genome and virulence determinants of high virulence community-
 acquired MRSA";
 Lancet 359:1819-1827(2002).
 RL

-1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
 an amide bond (By similarity).
 EMBL; AP004830; BAB96286.1; -;
 GO; GO:0009986; C:cell surface; IEA.
 GO; GO:0005618; C:cell wall; IEA.
 GO; GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
 GO; GO:0016020; C:membrane; IEA.
 GO; GO:0007155; P:cell adhesion; IEA.
 InterPro; IPR008966; Adhes_bact.
 InterPro; IPR004237; Fb_bind.
 InterPro; IPR005877; Gpos_YsIRK.
 InterPro; IPR001899; Gram_pos_anchor.
 Pfam; PF02986; Fb_bind.1.
 Pfam; PF00746; Gram_pos_anchor.1.
 Pfam; PF04650; YsIRK_signal.1.
 TIGRFAMs; TIGR01167; LPXTG_anchor.1.
 TIGRFAMs; TIGR01168; YsIRK_signal.1.
 PROSITE; PS50847; GRAM_POS_ANCHORING.1.
 Cell wall; Complete proteome; Peptidoglycan-anchor.
 SEQUENCE 1015 AA; 111145 MW; D0F9281B864D44D2 CRC64;
 SQ

Query Match 88.1%; Score 104; DB 2; Length 1015;
 Best Local Similarity 90.5%; Pred. No. 3.1e-07;
 Matches 19; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 KPSYQFGHNSVDPEDTLPK 21
 DB 838 KENYQFGHNSVDPEDTLPK 858

RESULT 6
 Q6G6H3 PRELIMINARY; PRT; 1015 AA.
 AC Q6G6H3;
 DT 05-JUL-2004 (TREMblrel. 27, Created)
 DT 05-JUL-2004 (TREMblrel. 27, Last sequence update)
 DT 05-JUL-2004 (TREMblrel. 27, Last annotation update)
 DE Fibronectin-binding protein.
 GN OrderedlocusNames=SA52388;
 OS Staphylococcus aureus (strain MSSA476).
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 NCBI_TaxID=282459;
 [1]
 SEQUENCE FROM N.A.
 PubMed=15213324; DOI=10.1073/pnas.0402521101;
 Holden M.T.G., Fell E.J., Lindsey J.A., Peacock S.J., Day N.P.J.,
 Enright M.C., Foster T.J., Moore C.E., Hurst L., Atkin R., Barron A.,
 Baason N., Bentley S.D., Chillingworth C., Chillingworth T.,
 Churcher C., Clark L., Corton C., Cronin A., Doggett J., Dowd L.,
 Felwell T., Hance Z., Harris B., Hauser H., Holroyd S., Jagels K.,
 James K.D., Leonard N., Line A., Mayes R., Moule S., Mungall K.,
 Ormond D., Quail M.A., Rabinowitch E., Rutherford K.M., Sanders M.,
 Sharp S., Simmonds M., Stevens K., Whitehead S., Barrett B.G.,
 Spratt B.G., Parkhill J.;
 "Complete genomes of two clinical Staphylococcus aureus strains:
 evidence for the rapid evolution of virulence and drug resistance";
 Proc. Natl. Acad. Sci. U.S.A. 101:9786-9791(2004).
 -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
 an amide bond (By similarity).
 EMBL; BX571857; CAG44202.1; -;
 GO; GO:0009986; C:cell surface; IEA.
 GO; GO:0005618; C:cell wall; IEA.
 GO; GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
 GO; GO:0016020; C:membrane; IEA.
 GO; GO:0007155; P:cell adhesion; IEA.
 InterPro; IPR008966; Adhes_bact.
 InterPro; IPR004237; Fb_bind.
 InterPro; IPR005877; Gpos_YsIRK.
 InterPro; IPR001899; Gram_pos_anchor.
 Pfam; PF02986; Fb_bind.1.
 Pfam; PF00746; Gram_pos_anchor.1.
 Pfam; PF04650; YsIRK_signal.1.
 TIGRFAMs; TIGR01167; LPXTG_anchor.1.
 RL

DR TIGRFAMs; TIGR01168; YSIRK signal; 1.
 DR PROSITE; PS50847; GRAM_POS_ANCHORING; 1.
 KW Cell wall; Complete proteome; Peptidoglycan-anchor.
 SQ SEQUENCE 1015 AA; 111145 MW; D0F9281BB64D4D2 CRC64;

Query Match 88.1%; Score 104; DB 2; Length 1015;
 Best Local Similarity 90.5%; Pred. No. 3,1e-07;
 Matches 19; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 KPSYQFGHNSVDPEDTLPK 21
 DB 838 KPNYQFGHNSVDPEDTLPK 858

RESULT 7
 ID 099RD2 PRELIMINARY; PRT; 1038 AA.
 AC 099RD2;
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Fibronectin-binding protein homolog.
 GN Name=fnb; OrderedLocustNames=SAV2503;
 OS Staphylococcus aureus (strain Muso / ATCC 700699).
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 NC NCB1_TaxID=158878;
 RX MEDLINE=21311952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2;
 RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
 RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Iian J.-Q., Ito T.,
 RA Kanamori M., Matsunaru H., Maruyama A., Murakami H., Hoshoyama A.,
 RA Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
 RA Sekimizu K., Hiraoka H., Kuhara S., Goto S., Yabuzaki J.,
 RA Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
 RA Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
 RT "Whole genome sequencing of methicillin-resistant Staphylococcus
 aureus.";
 RL Lancet 357:1225-1240(2001).
 CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
 an amide bond (By similarity).
 DR EMBL; AP003137; BAB5865.1; -;
 DR PIR; H90053; H90053.
 DR GO; GO:0009986; C:cell surface; IEA.
 DR GO; GO:0005618; C:cell wall; IEA.
 DR GO; GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0007155; P:cell adhesion; IEA.
 DR InterPro; IPR008966; Adhes_bact.
 DR InterPro; IPR004237; Fn_bind.
 DR InterPro; IPR005877; GPos_YSIRK.
 DR InterPro; IPR001899; Gram_pos_anchor.
 DR Pfam; PF02986; Fn_bind; 1.
 DR Pfam; PF00746; Gram_pos_anchor; 1.
 DR Pfam; PF04650; YSIRK_signal; 1.
 DR TIGRFAMs; TIGR01167; LPTXG_anchor; 1.
 DR TIGRFAMs; TIGR01168; YSIRK_signal; 1.
 DR PROSITE; PS50847; GRAM_POS_ANCHORING; 1.
 KW Cell wall; Complete proteome; Peptidoglycan-anchor.
 SQ SEQUENCE 1038 AA; 113618 MW; 666BF6B2BFBB12 CRC64;

Query Match 88.1%; Score 104; DB 2; Length 1038;
 Best Local Similarity 90.5%; Pred. No. 3,1e-07;
 Matches 19; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 KPSYQFGHNSVDPEDTLPK 21
 DB 833 KPNYQFGHNSVDPEDTLPK 853

RESULT 8
 Q7A3J7

ID 07A3J7 PRELIMINARY; PRT; 1038 AA.
 AC 07A3J7;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Fnb protein.
 GN Name=fnb; OrderedLocustNames=SA2291;
 OS Staphylococcus aureus (strain N315).
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 NC NCB1_TaxID=158879;
 RX MEDLINE=21311952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2;
 RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
 RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Iian J.-Q., Ito T.,
 RA Kanamori M., Matsunaru H., Maruyama A., Murakami H., Hoshoyama A.,
 RA Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
 RA Sekimizu K., Hiraoka H., Kuhara S., Goto S., Yabuzaki J.,
 RA Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
 RA Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
 RT "Whole genome sequencing of methicillin-resistant Staphylococcus
 aureus.";
 RL Lancet 357:1225-1240(2001).
 CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
 an amide bond (By similarity).
 DR EMBL; AP003137; BAB43594.1; -;
 DR GO; GO:0009986; C:cell surface; IEA.
 DR GO; GO:0005618; C:cell wall; IEA.
 DR GO; GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0007155; P:cell adhesion; IEA.
 DR InterPro; IPR008966; Adhes_bact.
 DR InterPro; IPR004237; Fn_bind.
 DR InterPro; IPR005877; GPos_YSIRK.
 DR InterPro; IPR001899; Gram_pos_anchor.
 DR Pfam; PF02986; Fn_bind; 1.
 DR Pfam; PF00746; Gram_pos_anchor; 1.
 DR Pfam; PF04650; YSIRK_signal; 1.
 DR TIGRFAMs; TIGR01167; LPTXG_anchor; 1.
 DR TIGRFAMs; TIGR01168; YSIRK_signal; 1.
 DR PROSITE; PS50847; GRAM_POS_ANCHORING; 1.
 KW Cell wall; Complete proteome; Peptidoglycan-anchor.
 SQ SEQUENCE 1038 AA; 113618 MW; 666BF6B2BFBB12 CRC64;

Query Match 88.1%; Score 104; DB 2; Length 1038;
 Best Local Similarity 90.5%; Pred. No. 3,1e-07;
 Matches 19; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 KPSYQFGHNSVDPEDTLPK 21
 DB 833 KPNYQFGHNSVDPEDTLPK 853

RESULT 9
 ID 053682 PRELIMINARY; PRT; 940 AA.
 AC 053682;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Fibronectin binding protein B.
 GN Name=fnbB;
 OS Staphylococcus aureus.
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 NC NCB1_TaxID=1280;
 RX MEDLINE=92111475; PubMed=1837266;
 RA Jonsson K., Sigmas C., Muller H.P., Lindberg M.;
 RT "Two different genes encode fibronectin binding proteins in
 Staphylococcus aureus. The complete nucleotide sequence and
 characterization of the second gene.";

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RL Eur. J. Biochem. 202;1041-1048(1991).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC an amide bond (By similarity).
EMBL, X62992; CAA44726.1; -.
DR PIR, S19702; S19702.
DR HSSP, Q53653; IN67.
DR GO, GO:0009986; C:cell surface; IEA.
DR GO, GO:0005618; C:cell wall; IEA.
DR GO, GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO, GO:0016020; C:membrane; IEA.
DR GO, GO:0007155; P:cell adhesion; IEA.
DR InterPro, IPR008966; Adhes_Dact.
DR InterPro, IPR004237; Fn_bind.
DR InterPro, IPR005877; Gpos_YsIRK.
DR Pfam, PF02986; Fn_bind; 2
DR Pfam, PF00746; Gram_pos_anchor; 1.
DR Pfam, PF04650; YsIRK_signal; 1.
DR TIGRfams, TIGR01167; LpXTG_anchor; 1.
DR TIGRfams, TIGR01168; YsIRK_signal; 1.
DR PROSITE, PS50847; GRAM_POS_ANCHORING; 1.
KW Cell wall, Peptidoglycan-anchor.
SQ SEQUENCE 940 AA; 10355 MW; E35FBBCA907AE345 CRC64;

Query Match 84.7%; Score 100; DB 2; Length 940;
Best Local Similarity 85.7%; Pred. No. 1.2e-06;
Matches 18; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 KPSYQFGHNSVDFEEDTLPK 21
Db 773 KPNYQFGHNSVDFEEDTLQ 793

RESULT 10
ID Q8NUU8 PRELIMINARY; PRT; 943 AA.
AC Q8NUU8;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE FnBb protein.
GN Name=fnBb; OrderedLocustNames=MW2420;
OS Staphylococcus aureus (strain MW2).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=196620;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MW2;
RX MEDLINE=22040717; PubMed=12044378; DOI=10.1016/S0140-6736(02)08713-5;
RA Baba T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Oguchi A.,
RA Nagai Y., Iwama N., Amano K., Naito T., Kuroda H., Cui L.,
RA Yamamoto K., Hiramoto K.;
RT "Genome and virulence determinants of high virulence community-
acquired MRSA."
RL Lancet 359:1819-1827(2002).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC an amide bond (By similarity).
EMBL, AP004830; BAB96285.1; -.
DR HSSP, Q53653; IN67.
DR GO, GO:0009986; C:cell surface; IEA.
DR GO, GO:0005618; C:cell wall; IEA.
DR GO, GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO, GO:0016020; C:membrane; IEA.
DR GO, GO:0007155; P:cell adhesion; IEA.
DR InterPro, IPR008966; Adhes_Dact.
DR InterPro, IPR004237; Fn_bind.
DR InterPro, IPR005877; Gpos_YsIRK.
DR Pfam, PF02986; Fn_bind; 1.
DR Pfam, PF00746; Gram_pos_anchor; 1.
DR TIGRfams, TIGR01167; LpXTG_anchor; 1.
DR TIGRfams, TIGR01168; YsIRK_signal; 1.

```

```

DR PROSITE, PS50847; GRAM_POS_ANCHORING; 1.
KW Cell wall, Complete proteome, Peptidoglycan-anchor.
SQ SEQUENCE 943 AA; 104537 MW; DA8A5F3194F1B6A CRC64;

Query Match 84.7%; Score 100; DB 2; Length 943;
Best Local Similarity 85.7%; Pred. No. 1.2e-06;
Matches 18; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 KPSYQFGHNSVDFEEDTLPK 21
Db 780 KPNYQFGHNSVDFEEDTLQ 800

RESULT 11
ID Q6G6H4 PRELIMINARY; PRT; 957 AA.
AC Q6G6H4;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Fibronectin-binding protein.
GN Name=fnBb; OrderedLocustNames=SAS2387;
OS Staphylococcus aureus (strain MSSA476).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=282459;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=15213324; DOI=10.1073/pnas.0402521101;
RA Holden M.T.G., Fell E.J., Lindsey J.A., Peacock S.J., Day N.P.J.,
RA Enright M.C., Foster T.J., Moore C.E., Hurst L., Atkin R., Barton A.,
RA Bason N., Bentley S.D., Chillingworth C., Chillingworth T.,
RA Churcher C., Clark L., Corton C., Cronin A., Doggett J., Dowd L.,
RA Felwell T., Hance Z., Harris B., Hauser H., Holtroyd S., Jagsels K.,
RA James K.D., Lennard N., Line A., Mayes R., Moulé S., Mungall K.,
RA Ormond D., Quail M.A., Rabinowitch E., Rutherford K.M., Sanders M.,
RA Sharp S., Simmonds M., Stevens K., Whitehead S., Barrell B.G.,
RA Spratt B.G., Parkhill J.;
RT "Complete genomes of two clinical Staphylococcus aureus strains:
evidence for the rapid evolution of virulence and drug resistance."
RL Proc. Natl. Acad. Sci. U.S.A. 101:9786-9791(2004).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC an amide bond (By similarity).
EMBL, BX571857; CAG44201.1; -.
DR GO, GO:0009986; C:cell surface; IEA.
DR GO, GO:0005618; C:cell wall; IEA.
DR GO, GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO, GO:0016020; C:membrane; IEA.
DR GO, GO:0007155; P:cell adhesion; IEA.
DR InterPro, IPR008966; Adhes_Dact.
DR InterPro, IPR004237; Fn_bind.
DR InterPro, IPR005877; Gpos_YsIRK.
DR InterPro, IPR001899; Gram_pos_anchor.
DR Pfam, PF02986; Fn_bind; 1.
DR Pfam, PF00746; Gram_pos_anchor; 1.
DR Pfam, PF04650; YsIRK_signal; 1.
DR TIGRfams, TIGR01167; LpXTG_anchor; 1.
DR TIGRfams, TIGR01168; YsIRK_signal; 1.
DR PROSITE, PS50847; GRAM_POS_ANCHORING; 1.
KW Cell wall, Complete proteome, Peptidoglycan-anchor.
SQ SEQUENCE 957 AA; 105980 MW; 28F8BA7FFDFD3EAF CRC64;

Query Match 84.7%; Score 100; DB 2; Length 957;
Best Local Similarity 85.7%; Pred. No. 1.2e-06;
Matches 18; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 KPSYQFGHNSVDFEEDTLPK 21
Db 780 KPNYQFGHNSVDFEEDTLQ 800

RESULT 12
ID Q9AEP9 PRELIMINARY; PRT; 152 AA.

```

```

AC 09AEP9;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE Fibronectin-binding protein (Fragment).
GN Name:fnb;
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1280;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CMRSA-1;
RX MEDLINE=21246681; PubMed=11349044;
RX DOI=10.1128/TAI.69.6.3791-3799.2001;
RA Rice K., Huebner M., Vaz D., McGavin M.J.;
RT "Variance in fibronectin binding and fnb locus polymorphisms in
RT Staphylococcus aureus: identification of antigenic variation in a
RT fibronectin binding protein adhesin of the epidemic CMRSA-1 strain of
RT methicillin-resistant S. aureus."
RL Infect.Immun. 69:3791-3799(2001).
DR EMBL; AY029184; AAKJ1588.1; -.
FT NON TER 1
FT 152
SQ SEQUENCE 152 AA; 17193 MW; CFA3913C2B11C025 CRC64;

Query Match 80.5%; Score 95; DB 2; Length 152;
Best Local Similarity 81.0%; Pred. No. 8.9e-07;
Matches 17; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Oy 1 KPSYQFGHNSVDPEDTLPK 21
    |||||
Db 130 KPSYQFGHNGIDPFEDTLPK 150

RESULT 13
MYCS MOUSE STANDARD; PRT; 431 AA.
ID MYCS_MOUSE
AC 09Z304;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE S-myc protein.
GN Name=Myes;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BAAB/C; TISSUE=Liver;
RX MEDLINE=99132300; PubMed=9911502; DOI=10.1016/S0378-1119(98)00547-2;
RX Sugiyama A., Noguchi K., Kitahara C., Katou N., Tashiro F., Ono T.,
RX Yoshida M.C., Kuchino Y.;
RT "Molecular cloning and chromosomal mapping of mouse intronless myc
RT gene acting as a potent apoptosis inducer."
RL Gene 226:273-283(1999).
CC -1- FUNCTION: Has apoptosis-inducing activity.
CC -1- SUBUNIT: Efficient DNA binding requires dimerization with another
CC bHLH protein.
CC -1- SUBCELLULAR LOCATION: Nuclear (Potential).
CC -1- SIMILARITY: Contains 1 basic helix-loop-helix (bHLH) domain.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; AB016289; BAAJ7155.1; -.
CC HSSP; P25912; INLM.
DR MGD; MGI:1332242; Myes.

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DR InterPro; IPR001092; HLH basic.
DR InterPro; IPR002418; TF_Myc.
DR Pfam; PF00010; HLH; 1.
DR Pfam; PF01056; MYC_N; 1.
DR PRINTS; PR00044; LEUZIPPRMYC.
DR SMART; SM00353; HLH; 1.
DR PROSITE; PS50888; HLH; 1.
KW Apoptosis; DNA-binding; Nuclear protein; Phosphorylation.
FT DNA_BIND 349 361
FT DOMAIN 362 401
FT DOMAIN 400 421
FT MOD_RES 36 36
FT 36
FT similarity).
SQ SEQUENCE 431 AA; 47663 MW; AD69FDAAB13A4F52 CRC64;

Query Match 44.1%; Score 52; DB 1; Length 431;
Best Local Similarity 62.5%; Pred. No. 18;
Matches 10; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Oy 6 FGHNSTPFGEDTWK 21
    |||||
Db 37 FGHNSTPFGEDTWK 52

RESULT 14
O9AUV6 PRELIMINARY; PRT; 480 AA.
ID O9AUV6
AC 09AUV6;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Putative UDP-glucose dehydrogenase.
GN Name=OSJNB0040E01.8;
OS Oryza sativa (Japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaceae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
RP SEQUENCE FROM N.A.
RA Buell C.R., Yuan Q., Ouyang S., Moffat K.S., Hill J.N., Burr P.C.,
RA Hsiao J., Zisemann V., Pal G., Bowman C.L., Fujii C.Y., Vanden S.E.,
RA Bowman C.L., Craven B., Utechtack T.R., Kalak H., Feldlyum T.V.,
RA Quackenbush J., White O., Salzberg S.L., Fraser C.M.;
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Buell R.;
RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC079887; AAK16194.1; -.
DR Gramene; O9AUV6; -.
DR GO; GO:0006118; P:electron transport; IEA.
DR InterPro; IPR008927; 6DGDH_C-like.
DR InterPro; IPR001732; UDPG_MGDP_dh.
DR Pfam; PF00984; UDPG_MGDP_dh; 1.
DR Pfam; PF03720; UDPG_MGDP_dh; 1.
DR Pfam; PF03721; UDPG_MGDP_dh; 1.
DR SEQUENCE 480 AA; 52898 MW; 3E36BFCAB97DF7C6 CRC64;

Query Match 44.1%; Score 52; DB 2; Length 480;
Best Local Similarity 56.2%; Pred. No. 20;
Matches 9; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Oy 1 KPSYQFGHNSVDPBE 16
    ||:|
Db 439 KPAVFQGRNVDPBK 454

RESULT 15
O98ED8 PRELIMINARY; PRT; 356 AA.
ID O98ED8;
AC O98ED8;
DT 01-OCT-2001 (TREMBlrel. 18, Created)

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Query Match	43.2%	Score 51	DB 2	Length 356
Best Local Similarity	50.0%	Pred. No. 20		
Matches 10	Conservative 2	Mismatches 8	Indels 0	Gaps 0

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Oy      1 KPSYQFGGHNVDPEEDTLR 20
          :|||: |||
Db      91 QPSYLFGTMTDPRVTTLP 110

```

Search completed: October 22, 2005, 04:10:16
Job time : 53.4314 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 25, 2005, 18:43:07 ; Search time 59.0973 Seconds
(without alignments)
137.434 Million cell updates/sec

Title: US-10-731-238-27
Perfect score: 119
Sequence: 1 KPSYQFGGNSVDPEDTLPK 21

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: _Geneseq_1dDec04: *
2: geneseqp1980s: *
3: geneseqp1990s: *
4: geneseqp2000s: *
5: geneseqp2001s: *
6: geneseqp2002s: *
7: geneseqp2003s: *
8: geneseqp2004s: *

pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	119	100.0	21	2	AAW65683
2	111	93.3	21	2	AAW65685
3	111	93.3	22	2	AAW65687
4	111	93.3	37	4	AAW65681
5	111	93.3	38	1	AAW65682
6	111	93.3	134	2	AAW65684
7	111	93.3	139	2	AAW65686
8	111	93.3	1018	1	AAW65688
9	111	93.3	1018	4	AAW65690
10	111	93.3	1018	4	AAW65692
11	111	93.3	1018	4	AAW65694
12	111	93.3	1018	4	AAW65696
13	111	93.3	1018	4	AAW65698
14	111	93.3	1018	4	AAW65700
15	111	93.3	1018	4	AAW65702
16	111	93.3	1018	4	AAW65704
17	111	93.3	1018	4	AAW65706
18	111	93.3	1018	4	AAW65708
19	111	93.3	1018	4	AAW65710
20	111	93.3	1018	4	AAW65712
21	111	93.3	1018	4	AAW65714
22	111	93.3	1018	4	AAW65716
23	111	93.3	1018	4	AAW65718
24	111	93.3	1018	4	AAW65720
25	111	93.3	1018	4	AAW65722

26	104	87.4	21	2	AAW65685	AAW65685 Fibronect
27	104	87.4	21	2	AAW65687	AAW65687 Fibronect
28	104	87.4	21	2	AAW65681	AAW65681 Fibronect
29	104	87.4	77	2	AAW65689	AAW65689 S. aureus
30	104	87.4	101	2	AAW65693	AAW65693 D3D4 poly
31	104	87.4	113	2	AAW65697	AAW65697 D3D4 poly
32	104	87.4	124	2	AAW65701	AAW65701 D3D4 poly
33	104	87.4	128	2	AAW65705	AAW65705 D3D4 poly
34	104	87.4	130	2	AAW65709	AAW65709 D3D4 poly
35	104	87.4	130	2	AAW65713	AAW65713 D3D4 poly
36	104	87.4	130	2	AAW65717	AAW65717 D3D4 poly
37	104	87.4	130	2	AAW65721	AAW65721 D3D4 poly
38	104	87.4	134	2	AAW65725	AAW65725 D3D4 poly
39	104	87.4	162	2	AAW65729	AAW65729 D3D4 poly
40	104	87.4	164	2	AAW65733	AAW65733 D3D4 poly
41	104	87.4	174	2	AAW65737	AAW65737 D3D4 poly
42	104	87.4	181	2	AAW65741	AAW65741 D3D4 poly
43	104	87.4	181	2	AAW65745	AAW65745 D3D4 poly
44	104	87.4	181	2	AAW65749	AAW65749 D3D4 poly
45	104	87.4	559	2	AAW65753	AAW65753 D3D4 poly

ALIGNMENTS

RESULT 1
AAW65683
ID AAW65683 standard; peptide; 21 AA.
XX
AC AAW65683;
XX
DT 16-OCT-1998 (first entry)
XX
DE Fibronectin binding protein-derived peptide #27.
XX
KW microbial surface components recognising adhesive matrix molecule;
XX MSCRAMM; fibronectin-binding protein; antibody; epitope;
KW antibiotic; bacterial infection; antibiotic-resistant strain.
XX
OS Synthetic.
OS Staphylococcus aureus.
OS
PN MO9831389-A2.
XX
PD 23-JUL-1998.
XX
PF 21-JAN-1998; 98WO-US001222.
XX
PR 21-JAN-1997; 97US-0036139P.
XX
PA (TEXA) UNITV TEXAS A & M SYSTEM.
XX
PI Hoeek M, Patti JM, House-Pompeo KL, Speziale P, Joh D;
PI Mcgavin MJ;
XX
DR WPI, 1998-413816/35.
XX
PT Antibody that binds to fibronectin-binding protein, preventing its
PT binding to fibronectin - used to treat or prevent bacterial infection,
PT especially by Staphylococci and Streptococci.
XX
PS Example 8, Page 101, 201pp; English.
XX
CC The invention relates to antibodies that bind to a fibronectin-binding
CC domain of a fibronectin-binding protein, and inhibit binding of the
CC protein to fibronectin. Also claimed are: (1) isolated peptides of a
CC fibronectin-binding protein that do not bind to fibronectin; (2) fusion
CC protein containing at least one peptide of a fibronectin-binding protein
CC linked to a second amino acid sequence; (3) nucleic acid encoding the
CC isolated peptide of (1). Antibodies, the isolated peptides of (1) and the
CC nucleic acids are all useful for immunisation (active or passive) and (b)
CC inhibiting binding of bacteria to fibronectin for preventing or treating
CC infection in humans or other animals, particularly by staphylococci or

streptococci, e.g. meningitis, otitis media, pneumonia, endocarditis, CC
CC mactilis in cattle, abortion in horses and many others. Since the CC
CC antibodies block binding of bacteria, they should be effective against CC
CC antibiotic-resistant strains, and may replace antibiotic therapy or CC
CC increase its effectiveness. Sequences AAW65570-90 represent a series of CC
CC synthetic peptides based on the D3 repeat of *S. aureus* fibronectin CC
CC binding protein A. They were synthesised to contain a proline residue at CC
CC each position through the sequence (le a proline scan)

XX Sequence 21 AA;
SQ

Query Match 100.0%; Score 119; DB 2; Length 21;
Best Local Similarity 100.0%; Pred. No. 2,1e-11;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0

OY 1 KPSYQFGGHSVDPEDTLTPK 21
Db 1 KPSYQFGGHSVDPEDTLTPK 21

RESULT 2
AAW65665
ID AAW65665 standard; peptide; 21 AA.
XX
AC AAW65665;
XX
DT 16-OCT-1998 (first entry)
XX
DE Fibronectin binding protein-derived peptide #9.

KM microbial surface components recognising adhesive matrix molecule;
KW MSCRAMM; fibronectin; fibronectin-binding protein; antibody; epitope;
KM antibiotic; bacterial infection; antibiotic-resistant strain.
XX
OS Synthetic.
OS Staphylococcus aureus.
XX
PN MO9831389-A2.
XX
PD 23-JUL-1998.
XX
PF 21-JAN-1998; 98WO-US001222.
XX
PR 21-JAN-1997; 97US-0036139P.
XX
PA (TEXA) UNIV TEXAS A & M SYSTEM.
XX
PI Hooeok M, Patti JM, House-Pompeo KL, Speciale P, Joh D;
PI McGavin MJ;
XX
DR WPI; 1998-413816/35.
XX
PT Antibody that binds to fibronectin-binding protein, preventing its
PT binding to fibronectin - used to treat or prevent bacterial infection,
PT especially by Staphylococci and Streptococci.
XX
PS Example 2; Page 92; 201JP; English.

The invention relates to antibodies that bind to a fibronectin-binding domain of a fibronectin-binding protein, and inhibit binding of the protein to fibronectin. Also claimed are: (1) isolated peptides of a fibronectin-binding protein that do not bind to fibronectin; (2) fusion protein containing at least one peptide of a fibronectin-binding protein linked to a second amino acid sequence; (3) nucleic acid encoding the CC isolated peptide of (1). Antibodies, the isolated peptides of (1) and the CC nucleic acids are all useful for immunisation (active or passive) and (by CC inhibiting binding of bacteria to fibronectin) for preventing or treating CC infection in humans or other animals, particularly by staphylococci or streptococci, e.g. meningitis, otitis media, pneumonia, endocarditis, CC mactilis in cattle, abortion in horses and many others. Since the CC antibodies block binding of bacteria, they should be effective against CC antibiotic-resistant strains, and may replace antibiotic therapy or CC increase its effectiveness. Sequences AAW65659-68 represent synthetic

```

CC  eptlopes from the fibronectin binding domains DU and D1-D4 of the S.
CC  aureus fnbA gene
XX
SQ  Sequence 21 AA;
Query Match          93.3%; Score 111; DB 2; Length 21;
Best Local Similarity 95.2%; Pred. No. 3.8e-10;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY  1 KPSYQFGGHSVPPEPTLPK 21
    |||||
DB  1 KPSYQFGGHSVPFEEDLPK 21
    |||||

RESULT 3
ID  AAR21340 standard; peptide: 22 AA.
XX
XX  AAR21340;
XX
XX  25-MAR-2003 (revised)
DT  15-JUN-1992 (first entry)
XX
XX  Fibronectin binding protein.
DE
XX  FnBP; wound infection reduction; vaccination; mastitis;
XX  Staphylococcal infections; D3.
XX
XX  Synthetic.
XX  OS
XX  FN
XX  MO9202555-A.
XX
XX  20-FEB-1992.
PD
XX
XX  10-AUG-1990; 90SE-00002617.
PF
XX
XX  10-AUG-1990; 90SE-00002617.
PR
XX
XX  (ALFA ) ALFA LAVAL AGRIC INT AB.
PA
XX
XX  Hook M, McGavin M, Raucel G;
PI
XX
XX  WPI: 1992-080035/10.
DR
XX
XX  New fibronectin binding peptide - combines with fusion peptide to form
PT  large antigen, used in immunisation, diagnosis and for treating wounds.
XX
XX
XX  Claim 1; Page 22; 33pp; English.
XX
XX  The sequence comprises amino acids 17-33 of a tandem repeat, designated
CC  D3 of the fibronectin binding site of Staphylococcus aureus 8325-4 FnBP.
CC  The N-terminal DK may be replaced with H or K, and the C-terminal LKP may
CC  be replaced by either L, LP, or OH. The peptides were synthesised using
CC  standard methods and purified using reverse phase HPLC. The appropriate
CC  fractions were dialysed and lyophilised. Peptide sequencing was performed
CC  and the peptides digested and chemically modified by dihydroxypropylation
CC  of the amino side chain of lysine. The carboxylic side chains were
CC  converted to glycine methyl esters. The phenyl side chains of tyrosine
CC  residues were oxidised. Chemically modified peptide D3 was compared to
CC  unmodified D3. Lysine and tyrosine modifications only partially
CC  diminished its activity whereas modification of aspartic/glutamic
CC  residues resulted in complete loss of activity. The peptide can be used
CC  for the prevention or reduction of the risk of wound infection. The
CC  peptide can be used to create a large antigen for vaccinating ruminants
CC  against mastitis caused by Staphylococcal infections. It can also be used
CC  to diagnose Staphylococcal infections using ELISA or DNA probes. (Updated
CC  on 25-MAR-2003 to correct PA field.)
XX
XX
SQ  Sequence 22 AA;
Query Match          93.3%; Score 111; DB 2; Length 22;
Best Local Similarity 95.2%; Pred. No. 4e-10;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

OY 1 KPSYQFGHNSVDFEDTLPK 21
 |||||
 DB 2 KPSYQFGHNSVDFEDTLPK 22

RESULT 4
 AAB91958
 ID AAB91958 standard; peptide; 37 AA.
 XX AAB91958;
 AC

XX 22-JUN-2001 (first entry)
 DT

XX Fibrinectin fragment and fibrin related peptide SEQ ID NO:1134.
 DE

XX Protection; endogenous therapeutic peptide; peptidase; conjugation;
 KM blood component; modification; succinimidyl; maleimido group; amino;
 KM hydroxyl; thiol; hormone; growth factor; neurotransmitter.

XX Homo sapiens.
 OS Synthetic.
 OS

XX WO200069900-A2.
 PN

XX 23-NOV-2000.
 PD

XX 17-MAY-2000; 2000WO-US013576.
 PF

XX 17-MAY-1999; 99US-0134406P.
 PR

XX 10-SEP-1999; 99US-0153406P.
 PR

XX 15-OCT-1999; 99US-0159783P.
 PR

XX (CONJ-) CONJUCHEM INC.
 PA

XX Bridon DP, Ezrin AM, Milner PG, Holmes DL, Thibaudeau K;
 PI

XX WPI; 2001-112059/12.
 DR

XX Modifying and attaching therapeutic peptides to albumin prevents
 PT peptidase degradation, useful for increasing length of in vivo activity.

XX Disclosure; Page 566; 733pp; English.
 PS

XX The present invention describes a modified therapeutic peptide (I)
 CC comprising a therapeutically active amino acid region (III) and a
 CC reactive group (II) (e.g. succinimidyl and maleimido groups) attached to
 CC a less therapeutically active amino acid region (IV), which covalently
 CC bonds with amino/hydroxyl/thiol groups on blood components to form a
 CC peptidase stabilised therapeutic peptide composed of 3-50 amino acids.
 CC (I) are useful for modifying therapeutic peptides e.g. hormones, growth
 CC factors and neurotransmitters, to protect them from peptidase activity in
 CC vivo for the treatment of various disorders. Endogenous therapeutic
 CC peptides are not suitable as drug candidates as they require frequent
 CC administration due to rapid degradation by peptidases in the body.
 CC Modifying and attaching therapeutic peptides to albumin prevents or
 CC reduces the action of peptidases to increase length of activity (half
 CC life) and specificity as bonding to large molecules decreases
 CC intracellular uptake and interference with physiological processes.
 CC AAB90829 to AAB92441 represent peptide which can be used in the
 CC exemplification of the present invention
 CC

XX Sequence 37 AA;
 SQ

Query Match 93.3%; Score 111; DB 4; Length 37;
 Best Local Similarity 95.2%; Pred. No. 7.1e-10;

Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 KPSYQFGHNSVDFEDTLPK 21
 |||||
 DB 16 KPSYQFGHNSVDFEDTLPK 36

RESULT 5
 AAP80662
 ID AAP80662 standard; protein; 38 AA.
 XX AAP80662;
 AC

XX 25-MAR-2003 (revised)
 DT

XX 07-OCT-1990 (first entry)
 DT

XX Protein with fibronectin binding ability.
 DE

XX Hybrid DNA molecule; fibronectin binding; mastitis; ruminants;
 KM wound infection.

XX Staphylococcus aureus.
 OS

XX EP294349-A.
 PN

XX 07-DEC-1988.
 PD

XX 30-MAY-1988; 88EP-00850188.
 PF

XX 01-JUN-1987; 87SE-00002272.
 PR

XX (ALFA) ALFA LAVAL AGRIC INT AB.
 PA

XX Lindberg MK, Signas LC, Wadstrom TM, Froman G;
 PI

XX WPI; 1988-347978/49.
 DR

XX N-PSDB; AAN81099.
 DR

XX Hybrid DNA encoding Staphylococcus aureus fibronectin binding protein -
 PT useful for immunisation and topical application to prevent staphylococcal
 PT infections.

XX Claim 11; Page 12; 23pp; English.
 PS

XX The peptide has fibronectin binding ability. It is useful for immunising
 CC ruminants against staphylococcal mastitis, pref. when used at 0.5-5
 CC micrograms/kg, using 3 doses given at 1-3 week intervals; for topical
 CC application to prevent wound infection, using an isotonic saline soln. of
 CC concn. 25-250 micrograms/ml; and, when immobilised on a carrier, for
 CC diagnosing staphylococcal infections. (Updated on 25-MAR-2003 to correct
 CC PF field.) (Updated on 25-MAR-2003 to correct PA field.)
 CC

XX Sequence 38 AA;
 SQ

Query Match 93.3%; Score 111; DB 1; Length 38;
 Best Local Similarity 95.2%; Pred. No. 7.3e-10;

Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 KPSYQFGHNSVDFEDTLPK 21
 |||||
 DB 17 KPSYQFGHNSVDFEDTLPK 37

RESULT 6
 AAY29087
 ID AAY29087 standard; protein; 134 AA.
 XX AAY29087;
 AC

XX 28-SEP-1999 (first entry)
 DT

XX S. aureus fibronectin binding protein A (FnBA) binding domain.
 DE

XX Bovine herpes virus-2; BHV-2; cytokine; immune response; immunogen; IL;
 KM Interleukin; colony stimulating factor; CSF; interferon; IFN; TNF;
 KM tumour necrosis factor; recombinant virus; vaccine; mucosal disease;
 KM mastitis; breast cancer; stress-induced disease; binding domain; FnBA;
 KM fibronectin binding protein.
 KM

XX Staphylococcus aureus.
 OS

```
XX  W09916892-A1.
PN
XX
PD  08-APR-1999.
XX
PF  29-SEP-1998; 98WO-GB002927.
XX
PR  29-SEP-1997; 97GB-00020633.
XX
PA  (UYBR-) UNIV BRISTOL.
XX
PI  Bradley AJ, Duffas WPJ,
XX
DR  WPI; 1999-255101/21.
XX
DR  N-PSDB; AAX91504.
XX
PT  New bovine herpes virus-2 vectors.
XX
PS  Example 2; Fig 8A-B; 10pp; English.
XX
CC  The invention provides bovine herpes virus-2 (BHV-2) based vectors that
CC  comprise at least one cytokine-encoding DNA sequence. The expression of
CC  cytokines in mammals can up-regulate immune responses to the immunogens.
CC  The cytokine is selected from interleukins (IL), colony stimulating
CC  factors (CSF), interferons (IFN) and tumour necrosis factors (TNF). The
CC  BHV-2 based vector or recombinant virus can be used as vaccines. They can
CC  be used for preventing or treating a mucosal disease in a subject, e.g.
CC  ruminants, cattle, sheep, goats, dogs, cats, horses, or man, particularly
CC  mastitis in cows or breast cancers in humans. They can also be used for
CC  preventing or treating a stress-induced disease. The present sequence
CC  represents the binding domain of a previously published S. aureus
CC  fibronectin binding protein A (FnBA) sequence. The FnB binding domain
CC  gene sequence FnBAB, cloned for use in this invention has 97.8 percent
CC  identity when compared to the previously published FnBA and FnBB gene
CC  sequences
XX
SQ  Sequence 134 AA;

Query Match          93.3%; Score 111; DB 2; Length 134;
Best Local Similarity 95.2%; Pred. No. 2.9e-09;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY  1 KPSYQFGGHSVDPEDTLPK 21
DB  93 KPSYQFGGHSVDPEDTLPK 113

RESULT 7
AAW31556
ID  AAW31556 standard; protein; 139 AA.
XX
AC  AAW31556;
XX
DT  27-AUG-2003 (revised)
DT  25-MAR-2003 (revised)
DT  21-MAY-1998 (first entry)
XX
DE  Fibronectin-binding MSCRAMM derivative POD.
XX
KW  Fibronectin; POD; collagen binding protein; sepsis; infection;
KW  microbial surface component recognising adhesive matrix molecule; MSCRAMM;
KW  adhesin; vaccine; immunisation; diagnosis; therapy; mastitis.
XX
OS  Staphylococcus aureus.
XX
XX
FH  Key
FT  Peptide
XX  Location/Qualifiers
XX  1..12
XX  /note= "vector pQE30-derived peptide"
XX  W09743314-A2.
XX  20-NOV-1997.
XX
```

```
PF  14-MAY-1997; 97WO-US008210.
XX
XX  16-MAY-1996; 96US-0017678P.
XX
PA  (TEXA ) UNIV TEXAS A & M SYSTEM.
XX
PA  (UABR-) UAB RES FOUND.
XX
PI  Hoeoek M, Patel JM, House-Pompeo K, Sthanam N, Symersky J;
XX
DR  WPI; 1998-008801/01.
XX
PT  Antibody that interacts with collagen binding domain of Staphylococcal
PT  cna gene product - useful to prevent bacterial sepsis in animal infected
PT  with Staphylococcus aureus.
XX
PS  Disclosure; Page 91; 143pp; English.
XX
CC  This protein comprises Staphylococcus aureus fibronectin-binding
CC  microbial surface component recognising adhesive matrix molecule (MSCRAMM)
CC  derivative POD, plus a vector-derived N-terminal peptide. The invention
CC  relates to claimed nucleic acid sequences (see AAT93436-38) encoding S.
CC  aureus collagen binding protein (CBP) epitopes M17, M31 and M55 (see
CC  AAW31552-54) that confer protection against S. aureus infection. CBP
CC  protein and antigenic epitopes are contemplated for use in the treatment
CC  of pathological infections, especially to prevent bacterial adhesion to
CC  collagen. The epitopes are also contemplated for use in the preparation
CC  of vaccines and as carrier proteins in vaccine formulations, as well as
CC  in the formulation of compositions for the prevention of S. aureus
CC  infection. pCF33 and POD (see AAW31556) were used to raise anti-MSCRAMM
CC  polyclonal antibodies used in passive immunisation against bovine
CC  mastitis. (Updated on 25-MAR-2003 to correct PI field.) (Updated on 27-
CC  AUG-2003 to correct OS field.)
XX
SQ  Sequence 139 AA;

Query Match          93.3%; Score 111; DB 2; Length 139;
Best Local Similarity 95.2%; Pred. No. 3e-09;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY  1 KPSYQFGGHSVDPEDTLPK 21
DB  107 KPSYQFGGHSVDPEDTLPK 127

RESULT 8
AAP82115
ID  AAP82115 standard; protein; 1018 AA.
XX
AC  AAP82115;
XX
DT  25-MAR-2003 (revised)
DT  05-JAN-1990 (first entry)
XX
DE  Fibronectin binding protein.
XX
KW  Fibronectin binding protein; S.aureus; immunisation; mastitis; ruminants;
KW  wound infection; diagnosis.
XX
OS  Staphylococcus aureus.
XX
XX
EP294349-A.
XX  07-DEC-1988.
XX
XX  30-MAY-1988; 88EP-00850188.
XX
XX  01-JUN-1987; 87SE-00002272.
XX
PA  (ALFA ) ALFA LAVAL AGRIC INT AB.
XX
PI  Lindberg MK, Signas LC, Wadstrom TM, Froman G;
XX
DR  WPI; 1988-347978/49.
XX
```

DR P-PSDB; AAP82115.
XX Hybrid DNA encoding Staphylococcus aureus fibronectin binding protein -
PT useful for immunisation and topical application to prevent staphylococcal
PT infections.
XX
XX Disclosure; Fig. 8A.1-8A.2; 23pp; English.
XX
XX The S. aureus fibronectin binding protein may be included in a hybrid
CC protein. The protein may be used to immunise ruminants against
CC staphylococcal mastitis, pref. when given at 0.5-5 microg/kg, using 3
CC doses at 1-3 week intervals; and for topical applicn. to prevent wound
CC infection, pref. using isotonic saline soln. of concn. 25-250 microg/mg.
CC The DNA encoding the binding protein and the hybrid protein may be
CC immobilised on a carrier and used to diagnose staphylococcal infections.
CC (updated on 25-MAR-2003 to correct PA field.)
XX
SQ Sequence 1018 AA;

Query Match 93.3%; Score 111; DB 1; Length 1018;
Best Local Similarity 95.2%; Pred. No. 2.7e-08;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KPSYQFGHNSVDFPBDTLPK 21
DB 837 KPSYQFGHNSVDFPBDTLPK 857
|||||

RESULT 9
AAU37245
ID AAU37245 standard; protein; 1018 AA.
XX
XX AAU37245;
AC
XX 14-FEB-2002 (first entry)
DT
XX
XX Staphylococcus aureus cellular proliferation protein #1415.
DE
XX
XX Antisense; prokaryotic cellular proliferation protein; antibiotic;
KW antibacterial; drug design.
XX
XX Staphylococcus aureus.
OS
XX
XX WO200170955-A2.
PN
XX
XX 27-SEP-2001.
PD
XX
XX
XX 21-MAR-2001; 2001WO-US009180.
PF
XX
XX 21-MAR-2000; 2000US-0191078P.
PR
XX 23-MAY-2000; 2000US-0206848P.
PR
XX 26-MAY-2000; 2000US-0207727P.
PR
XX 23-OCT-2000; 2000US-0242578P.
PR
XX 27-NOV-2000; 2000US-0253625P.
PR
XX 22-DEC-2000; 2000US-0257931P.
PR
XX 16-FEB-2001; 2001US-0269308P.
XX
XX (ELIT-) ELITRA PHARM INC.
PA
XX
XX Haselbeck R, Ohlsen KL, Zyskind JW, Wall D, Trawick JD, Carr GU;
PI Yamamoto RT, Xu HH;
PI
XX
XX WPI; 2001-611495/70.
DR
XX N-PSDB; AAS55104.
XX
XX New polynucleotides for the identification and development of
PT antibiotics, comprise sequences of antisense nucleic acids.
PT
XX
XX Example 3; SEQ ID NO 12838; 511pp; English.
PS
XX
XX The invention relates to antisense inhibitors of genes essential to
CC prokaryotic cellular proliferation, their use in identifying the genes,
CC their use in the discovery of novel antibiotics, the essential genes

CC themselves and the encoded proteins. The prokaryotes used are Escherichia
CC coli, Staphylococcus aureus, Salmonella typhi, Klebsiella pneumoniae,
CC pseudomonas aeruginosa and Enterococcus faecalis. The invention is also
CC useful for the identification of potential new targets for antibiotic
CC development. The antisense nucleic acids can also be used to identify
CC proteins used in proliferation, to express these proteins, and to obtain
CC antibodies capable of binding to the expressed proteins. The proteins can
CC be used to screen compounds in rational drug discovery programmes. The
CC antisense nucleic acid sequence is also useful to screen for homologous
CC nucleic acids which are required for cell proliferation in a wide variety
CC of organisms. The present sequence represents an essential prokaryotic
CC cellular proliferation protein. Note: The sequence data for this patent
CC did not form part of the printed specification, but was obtained in
CC electronic format directly from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 1018 AA;

Query Match 93.3%; Score 111; DB 4; Length 1018;
Best Local Similarity 95.2%; Pred. No. 2.7e-08;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KPSYQFGHNSVDFPBDTLPK 21
DB 837 KPSYQFGHNSVDFPBDTLPK 857
|||||

RESULT 10
AAU34301
ID AAU34301 standard; protein; 1018 AA.
XX
XX AAU34301;
AC
XX
XX 14-FEB-2002 (first entry)
DT
XX
XX Staphylococcus aureus cellular proliferation protein #577.
DE
XX
XX Antisense; prokaryotic cellular proliferation protein; antibiotic;
KW antibacterial; drug design.
XX
XX Staphylococcus aureus.
OS
XX
XX WO200170955-A2.
PN
XX
XX 27-SEP-2001.
PD
XX
XX
XX 21-MAR-2001; 2001WO-US009180.
PF
XX
XX 21-MAR-2000; 2000US-0191078P.
PR
XX 23-MAY-2000; 2000US-0206848P.
PR
XX 26-MAY-2000; 2000US-0207727P.
PR
XX 23-OCT-2000; 2000US-0242578P.
PR
XX 27-NOV-2000; 2000US-0253625P.
PR
XX 22-DEC-2000; 2000US-0257931P.
PR
XX 16-FEB-2001; 2001US-0269308P.
XX
XX (ELIT-) ELITRA PHARM INC.
PA
XX
XX Haselbeck R, Ohlsen KL, Zyskind JW, Wall D, Trawick JD, Carr GU;
PI Yamamoto RT, Xu HH;
PI
XX
XX WPI; 2001-611495/70.
DR
XX N-PSDB; AAS52160.
XX
XX New polynucleotides for the identification and development of
PT antibiotics, comprise sequences of antisense nucleic acids.
PT
XX
XX Example 3; SEQ ID NO 5797; 511pp; English.
PS
XX
XX The invention relates to antisense inhibitors of genes essential to
CC prokaryotic cellular proliferation, their use in identifying the genes,
CC their use in the discovery of novel antibiotics, the essential genes
CC themselves and the encoded proteins. The prokaryotes used are Escherichia

coli, *Staphylococcus aureus*, *Salmonella typhi*, *Klebsiella pneumoniae*,
CC *Pseudomonas aeruginosa* and *Enterococcus faecalis*. The invention is also
CC useful for the identification of potential new targets for antibiotic
CC development. The antisense nucleic acids can also be used to identify
CC antibodies used in proliferation, to express these proteins, and to obtain
CC antibodies capable of binding to the expressed proteins. The proteins can
CC be used to screen compounds in rational drug discovery programmes. The
CC antisense nucleic acid sequence is also useful to screen for homologous
CC nucleic acids which are required for cell proliferation in a wide variety
CC of organisms. The present sequence represents an essential prokaryotic
CC cellular proliferation protein. Note: The sequence data for this patent
CC did not form part of the printed specification, but was obtained in
CC electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pcc_sequences
XX
SQ Sequence 1018 AA;
Query Match 93.3%; Score 111; DB 4; Length 1018;
Best Local Similarity 95.2%; Pred. No. 2.7e-08;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 KPSYQFGGHSVDPEDTLRK 21
DB 837 KPSYQFGGHSVDPEDTLRK 857
RESULT 11
ABJ18922 ID ABJ18922 standard; protein; 1018 AA.
XX
AC ABJ18922;
DT 06-MAR-2003 (first entry)
XX
DE Pathogen specific antigen related staphylococcal protein SEQ ID No 68.
XX
KM Antibacterial; virucide; fungicide; protozoacide; cytostatic; anti-HIV;
KM hyperimmune; serum-reactive; antigen; pathogen; tumour; allergen;
KM auto-immunity; vaccine; staphylococcal infection; antibody; cancer;
KM autoimmune disease; HIV; hepatitis.
XX
OS *Staphylococcus* sp.
XX
XX WO200259148-A2.
PN 01-AUG-2002.
XX
PD 21-JAN-2002; 2002WO-EP000546.
XX
PF 26-JAN-2001; 2001AT-00000130.
PR
PA (CIST-) CISTEM BIOTECHNOLOGIES GMBH.
XX
PI Meinke A, Nagy E, Von Ahesen U, Klade C, Henice T, Zauner W;
PI Mihh DB, Vyrvyska O, Etz H, Dryla A, Weichart T, Hafner M;
PI Tempelmeier B;
XX
DR WPI; 2003-075410/07.
XX
PT Identifying, isolating and producing hyperimmune serum-reactive antigens
PT from a pathogen, for preparing vaccine or medicament for treating or
PT preventing e.g. staphylococcal infections, comprises providing antibody
PT preparation.
XX
XX Example 7; Page 157; 252pp; English.
XX
PS The invention relates to a novel method for identifying, isolating and
CC producing hyperimmune serum-reactive antigens from a pathogen, tumour,
CC allergen, a tissue or host prone to auto-immunity, where the antigens are
CC used in a vaccine, comprises providing antibody preparation from a plasma
CC pool of a type of animal, or individual sera with antibodies against the
CC specific pathogen, tumour, allergen, tissue or host prone to auto-
CC immunity. The hyperimmune serum-reactive antigens comprising any of the

CC 62 sequences of 53-2261 amino acids fully defined in the specification,
CC or their hyperimmune fragments are useful for the manufacture of a
CC pharmaceutical preparation, particularly a vaccine against staphylococcal
CC infections or colonisation against *S. aureus* or *S. epidermidis*. The
CC preparation of antibodies is useful for the manufacture of a medicament
CC for treating or preventing staphylococcal infections or colonisation
CC against *S. aureus* or *S. epidermidis*. The antibody preparations may also
CC be used for diagnostic and imaging purposes. Other conditions that can be
CC treated include cancer, autoimmune diseases or infections caused by viral
CC (e.g. HIV, hepatitis A, B or C), fungal or protozoan pathogens. This
CC sequence represents a staphylococcal protein relating to the method for
CC identifying and producing pathogen specific antigens of the invention
XX
SQ Sequence 1018 AA;
Query Match 93.3%; Score 111; DB 6; Length 1018;
Best Local Similarity 95.2%; Pred. No. 2.7e-08;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 KPSYQFGGHSVDPEDTLRK 21
DB 837 KPSYQFGGHSVDPEDTLRK 857
RESULT 12
ABM72537 ID ABM72537 standard; protein; 1018 AA.
XX
AC ABM72537;
DT 20-NOV-2003 (first entry)
XX
DE *Staphylococcus aureus* protein #1777.
XX
KM Antibacterial; vaccine; gene therapy; infection; sepsis; diagnosis;
KM enzymatic assay; antibiotic target.
XX
OS *Staphylococcus aureus*.
XX
PN WO200294868-A2.
XX
XX 28-NOV-2002.
PD 27-MAR-2002; 2002WO-IB002637.
XX
PF 27-MAR-2001; 2001GB-00007661.
PR
PA (CHIR-) CHIRON SPA.
XX
PI Masignani V, Mora M, Scarselli M;
XX
DR WPI; 2003-120786/11.
DR N-PSDB; ACF74097.
XX
PT New *Staphylococcus aureus* protein, useful as a vaccine for treating or
PT preventing staphylococcal infection, specifically an infection caused by
PT *S. aureus*, e.g. sepsis.
XX
XX Claim 1; SEQ ID NO 3554; 49pp; English.
XX
PS The invention relates to novel genes and encoded proteins from
CC *Staphylococcus aureus*. A composition comprising the *S. aureus* protein, a
CC nucleic acid encoding the protein, or an antibody to the protein, is
CC useful as a pharmaceutical, particularly as a vaccine for treating or
CC preventing infection due to *Staphylococcus* bacteria, specifically an
CC infection caused by *S. aureus*. The composition is particularly useful for
CC treating or preventing sepsis in a patient. The composition can also be
CC used for diagnostics. The protein is also used in an assay for enzymatic
CC studies and as a target for antibiotics. This sequence represents one of
CC the novel *S. aureus* proteins of the invention
XX
SQ Sequence 1018 AA;

Query Match 93.3%; Score 111; DB 6; Length 1018;
 Best Local Similarity 95.2%; Pred. No. 2.7e-08;
 Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KPSYQFGHNSVDFEDTLPK 21
 DB 837 KPSYQFGHNSVDFEDTLPK 857

RESULT 13

AAW89806
 ID AAW89806 standard; protein; 1027 AA.

AC AAW89806;

DT 16-MAR-1999 (first entry)

DE Staphylococcus aureus protein SEQ ID #5254.

XX Computer readable medium; vaccine; S. aureus infection; immunodetection;
 XX cellulitis; eyelid infection; food poisoning; osteomyelitis; therapy;
 KM skin infection; surgical wound infection; scalded skin syndrome;
 KM toxic shock syndrome.

XX Staphylococcus aureus.

XX EP76519-A2.

XX 30-JUL-1997.

XX 07-JAN-1997; 97EP-00100117.

XX 05-JAN-1996; 96US-0009861P.

XX (HUMA-) HUMAN GENOME SCI INC.

XX Kunsch CA, Choi GH, Barash SC, Dillon PJ, Fannon MR, Rosen CA;

XX WPI; 1997-374922/35.

PT Polynucleotide(s) and proteins derived from Staphylococcus aureus -
 PT stored on computer readable medium and used in the production of anti-
 PT S. aureus vaccines.

XX Claim 23; Page 3263-3267; 3271pp; English.

CC This sequence represents a Staphylococcus aureus protein sequence of the
 CC invention. The DNA sequences encoding the S. aureus proteins are recorded
 CC on a computer readable medium, preferably selected from a floppy or hard
 CC disk, random access memory (RAM), read-only memory (ROM) or CD-ROM.
 CC Homology searches using the S. aureus DNA sequences allows putative
 CC functions to be assigned so that protein-encoding or regulatory regions
 CC of commercial, therapeutic or industrial importance can be obtained.
 CC Specifically, sequences which are likely to encode antigens have been
 CC identified and these polypeptides can be used in a vaccine composition
 CC against S. aureus infection. The polypeptides can also be used in a kit
 CC for the immunodetection of S. aureus in a sample. S. aureus is implicated
 CC in numerous human diseases, including cellulitis, eyelid infections, food
 CC poisoning, osteomyelitis, skin and surgical wound infections, scalded
 CC skin syndrome, toxic shock syndrome, etc. Organisms transformed with the
 CC DNA sequences can be used for recombinant production of the polypeptides.
 CC The new DNA sequences (and their fragments) are useful as primers or
 CC probes for isolating homologues of any of the 5191 S. aureus DNA sequences
 CC contained on the computer readable medium

XX Sequence 1027 AA;

QY Query Match 93.3%; Score 111; DB 2; Length 1027;

Best Local Similarity 95.2%; Pred. No. 2.7e-08;
 Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KPSYQFGHNSVDFEDTLPK 21
 |||||

DB 846 KPSYQFGHNSVDFEDTLPK 866

RESULT 14

ABU15854
 ID ABU15854 standard; protein; 961 AA.

XX AC ABU15854;

DT 19-JUN-2003 (first entry)

DE Protein encoded by Prokaryotic essential gene #1381.

XX Antisense; prokaryotic essential gene; cell proliferation; drug design.

XX Staphylococcus aureus.

XX WO20027183-A2.

XX 03-OCT-2002.

XX 21-MAR-2002; 2002WO-US009107.

XX 21-MAR-2001; 2001US-00815242.

XX 06-SEP-2001; 2001US-00948993.

XX 25-OCT-2001; 2001US-0342922P.

XX 08-FEB-2002; 2002US-00072851.

XX 06-MAR-2002; 2002US-0362699P.

XX (ELIT-) ELITRA PHARM INC.

XX Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zykkind JW;

XX Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;

XX N-PSDB; ACA19724.

XX WPI; 2003-029926/02.

XX Claim 25; SEQ ID NO 43778; 1766pp; English.

CC The invention relates to an isolated nucleic acid comprising any one of
 CC the 623 antisense sequences given in the specification where expression
 CC of the nucleic acid inhibits proliferation of a cell. Also included are:
 CC (1) a vector comprising a promoter operably linked to the nucleic acid
 CC encoding a polypeptide whose expression is inhibited by the antisense
 CC nucleic acid; (2) a host cell containing the vector; (3) an isolated
 CC polypeptide or its fragment whose expression is inhibited by the
 CC antisense nucleic acid; (4) an antibody capable of specifically binding
 CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular
 CC proliferation or the activity of a gene in an operon required for
 CC proliferation; (7) identifying a compound that influences the activity of
 CC the gene product or that has an activity against a biological pathway;
 CC required for proliferation, or that inhibits cellular proliferation; (8)
 CC identifying a gene required for cellular proliferation or the biological
 CC pathway in which a proliferation-regulated gene or its gene product lies
 CC or a gene on which the test compound that inhibits proliferation of an
 CC organism acts; (9) manufacturing an antibiotic; (10) profiling a
 CC compound's activity; (11) a culture comprising strains in which the gene
 CC product is overexpressed or underexpressed; (12) determining the extent
 CC to which each of the strains is present in a culture or collection of
 CC strains; or (13) identifying the target of a compound that inhibits the
 CC proliferation of an organism. The antisense nucleic acids are useful for
 CC identifying proteins or screening for homologous nucleic acids required
 CC for cellular proliferation to isolate candidate molecules for rational
 CC drug discovery programs, or for screening homologous nucleic acids
 CC required for proliferation in cells other than S. aureus, S. typhimurium,
 CC K. pneumoniae or P. aeruginosa. The present sequence is encoded by one of
 CC the target prokaryotic essential genes. Note: The sequence data for this
 CC patent did not form part of the printed specification, but was obtained
 CC in electronic format directly from WIPO at


```
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 961 AA;
Query Match 90.8%; Score 108; DB 6; Length 961;
Best Local Similarity 90.5%; Pred. No. 7.4e-08;
Matches 19; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 KPSYQFGGHSVDPEDTLPK 21
DB 784 KPNYQFGGHSVDPEDTLPK 804

RESULT 15
AAU33960
ID AAU33960 standard; protein; 978 AA.
XX
AC AAU33960;
XX
DT 14-FEB-2002 (first entry)
XX
DE Staphylococcus aureus cellular proliferation protein #236.
XX
KW Antisense; prokaryotic cellular proliferation protein; antibiotic;
KM antibacterial; drug design.
XX
CS Staphylococcus aureus.
XX
MO200170955-A2.
XX
PD 27-SEP-2001.
XX
PF 21-MAR-2001; 2001WO-US009180.
XX
PR 21-MAR-2000; 2000US-0191078P.
PR 23-MAY-2000; 2000US-0206848P.
PR 26-MAY-2000; 2000US-0207272P.
PR 23-OCT-2000; 2000US-0242578P.
PR 27-NOV-2000; 2000US-0253625P.
PR 22-DEC-2000; 2000US-0257931P.
PR 16-FEB-2001; 2001US-0269308P.
XX
PA (ELIT-) ELITRA PHARM INC.
XX
PI Haselbeck R, Ohlsen KL, Zyskind JW, Wall D, Trawick JD, Carr GJ;
PI Yamamoto RT, Xu HH;
XX
DR N-PSDB; AAS51819.
XX
WPI; 2001-611495/70.
XX
New polynucleotides for the identification and development of
PT antibiotics, comprise sequences of antisense nucleic acids.
XX
PS Example 3; SEQ ID NO 5456; 511p; English.
XX
The invention relates to antisense inhibitors of genes essential to
CC prokaryotic cellular proliferation, their use in identifying the genes,
CC their use in the discovery of novel antibiotics, the essential genes
CC themselves and the encoded proteins. The prokaryotes used are Escherichia
CC coli, Staphylococcus aureus, Salmonella typhi, Klebsiella pneumoniae,
CC Pseudomonas aeruginosa and Enterococcus faecalis. The invention is also
CC useful for the identification of potential new targets for antibiotic
CC development. The antisense nucleic acids can also be used to identify
CC proteins used in proliferation, to express these proteins, and to obtain
CC antibodies capable of binding to the expressed proteins. The proteins can
CC be used to screen compounds in rational drug discovery programmes. The
CC antisense nucleic acid sequence is also useful to screen for homologous
CC nucleic acids which are required for cell proliferation in a wide variety
CC of organisms. The present sequence represents an essential prokaryotic
CC cellular proliferation protein. Note: The sequence data for this patent
CC did not form part of the printed specification, but was obtained in
CC electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
```

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XX
SQ Sequence 978 AA;
Query Match 90.8%; Score 108; DB 4; Length 978;
Best Local Similarity 90.5%; Pred. No. 7.6e-08;
Matches 19; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 KPSYQFGGHSVDPEDTLPK 21
DB 815 KPNYQFGGHSVDPEDTLPK 835
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Search completed: October 25, 2005, 19:38:30
Job time : 60.1473 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 22, 2005, 02:23:36 ; Search time 15.9358 seconds
(without alignments)
98.371 Million cell updates/sec

Title: US-10-731-238-27

Perfect score: 119
Sequence: 1 KPSYQFGHNSVDPEDTLPK 21

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :
1: /cgn2_6/prodata/1/1aa/5A_COMB.pep:*
2: /cgn2_6/prodata/1/1aa/5B_COMB.pep:*
3: /cgn2_6/prodata/1/1aa/5A_COMB.pep:*
4: /cgn2_6/prodata/1/1aa/5B_COMB.pep:*
5: /cgn2_6/prodata/1/1aa/PCTUS_COMB.pep:*
6: /cgn2_6/prodata/1/1aa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	119	100.0	21	4	US-09-010-317-27
2	111	93.3	21	4	US-09-010-317-9
3	111	93.3	37	1	US-08-234-622A-4
4	111	93.3	38	1	US-08-294-189-8
5	111	93.3	38	1	US-08-729-767-5
6	111	93.3	114	1	US-08-259-000-3
7	111	93.3	139	3	US-08-856-253-8
8	111	93.3	178	3	US-08-459-135A-12
9	111	93.3	178	3	US-08-495-559-12
10	111	93.3	1027	4	US-08-956-171E-5254
11	111	93.3	1027	4	US-08-781-986A-5254
12	106	89.1	21	4	US-09-010-317-14
13	106	89.1	21	4	US-09-010-317-16
14	106	89.1	21	4	US-09-010-317-23
15	106	89.1	21	4	US-09-010-317-33
16	105	88.2	21	4	US-09-010-317-18
17	105	88.2	21	4	US-09-010-317-24
18	105	88.2	21	4	US-09-010-317-28
19	105	88.2	21	4	US-09-010-317-30
20	104	87.4	21	4	US-09-010-317-25
21	104	87.4	21	4	US-09-010-317-29
22	104	87.4	21	4	US-09-010-317-31
23	104	87.4	130	2	US-08-459-135A-7
24	104	87.4	130	2	US-08-459-135A-8
25	104	87.4	130	3	US-08-495-559-7
26	104	87.4	130	3	US-08-495-559-8
27	104	87.4	174	2	US-08-459-135A-10

28	104	87.4	174	2	US-08-459-135A-13	Sequence 13, Appl
29	104	87.4	174	3	US-08-495-559-10	Sequence 10, Appl
30	104	87.4	176	3	US-08-495-559-13	Sequence 13, Appl
31	104	87.4	176	3	US-08-495-559-6	Sequence 6, Appl
32	104	87.4	181	2	US-08-459-135A-6	Sequence 6, Appl
33	104	87.4	559	4	US-08-956-171E-5251	Sequence 5251, Ap
34	104	87.4	559	4	US-08-781-986A-5251	Sequence 5251, Ap
35	103	86.6	21	4	US-09-010-317-10	Sequence 10, Appl
36	103	86.6	21	4	US-09-010-317-15	Sequence 15, Appl
37	103	86.6	21	4	US-09-010-317-20	Sequence 20, Appl
38	103	86.6	21	4	US-09-010-317-22	Sequence 22, Appl
39	103	86.6	21	4	US-09-010-317-32	Sequence 32, Appl
40	103	86.6	22	4	US-09-010-317-13	Sequence 13, Appl
41	101	84.9	21	4	US-09-010-317-17	Sequence 17, Appl
42	101	84.9	21	4	US-09-010-317-19	Sequence 19, Appl
43	101	84.9	21	4	US-09-010-317-21	Sequence 21, Appl
44	101	84.9	21	4	US-09-010-317-26	Sequence 26, Appl
45	90	75.6	19	1	US-08-234-622A-1	Sequence 1, Appl

ALIGNMENTS

RESULT 1
US-09-010-317-27
Sequence 27, Application US/09010317
Patent No. 6685943
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
APPLICANT: Patti, Joseph M.
APPLICANT: House-Pompeo, Karen L.
APPLICANT: Speziale, Pietro
APPLICANT: Joh, Danny
APPLICANT: McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
TITLE OF INVENTION: AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSER: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-09-010-317-27
Query Match 100.0%; Score 119; DB 4; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.9e-12;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KPSYQFGHNSVDFPDLTPK 21
Db 1 KPSYQFGHNSVDFPDLTPK 21

RESULT 2
US-09-010-317-9

; Sequence 9, Application US/09010317
; Patent No. 6685943
; GENERAL INFORMATION:
; APPLICANT: Hook, Magnus
; APPLICANT: Patti, Joseph M.
; APPLICANT: House-Pompeo, Karen L.
; APPLICANT: Speziale, Pietro
; APPLICANT: Joh, Danny
; APPLICANT: McGavin, Martin J.
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
; TITLE OF INVENTION: AND METHODS OF USE
; NUMBER OF SEQUENCES: 105
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: TX
; COUNTRY: USA
; ZIP: 77210-4433
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/010,317
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/036,139
; FILING DATE: 21-JAN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Hibley, David W.
; REGISTRATION NUMBER: 41, 071
; REFERENCE/DOCKET NUMBER: TANK:189
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 512-418-3000
; TELEFAX: 512-474-7577
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; US-09-010-317-9

Query Match 93.3%; Score 111; DB 4; Length 21;
Best Local Similarity 95.2%; Pred. No. 3.6e-11;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KPSYQFGHNSVDFPDLTPK 21
Db 1 KPSYQFGHNSVDFPDLTPK 21

RESULT 3
US-08-234-622A-4
; Sequence 4, Application US/08234622A
; Patent No. 5440014
; GENERAL INFORMATION:
; APPLICANT: Hook, Magnus
; APPLICANT: MCGAVIN, Martin
; APPLICANT: RAUCCI, Giuseppe
; TITLE OF INVENTION: A FIBRONECTIN BINDING PEPTIDE

; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Doane, Swecker & Mathis
; STREET: P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 2213-1404

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/234,622A
; FILING DATE: 28-APR-1994
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: SE 9002617-0
; FILING DATE: 10-AUG-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/SB91/00534
; FILING DATE: 09-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Meuth, Donna M
; REGISTRATION NUMBER: 36,607
; REFERENCE/DOCKET NUMBER: 012885-044
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 37 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-234-622A-4

Query Match 93.3%; Score 111; DB 1; Length 37;
Best Local Similarity 95.2%; Pred. No. 6.9e-11;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KPSYQFGHNSVDFPDLTPK 21
Db 16 KPSYQFGHNSVDFPDLTPK 36

RESULT 4
US-08-234-189-8
; Sequence 8, Application US/08294189
; Patent No. 5707822
; GENERAL INFORMATION:
; APPLICANT: Fischetti, Vincent A.
; APPLICANT: Rakonjac, Jasna
; APPLICANT: Robbins, John
; TITLE OF INVENTION: GENE SERUM OPACITY FACTOR
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klauber & Jackson
; STREET: 411 Hackensack Avenue
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/294,189
; FILING DATE: 22-AUG-1994

CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-118
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 487-5800
TELEFAX: 201 343-1684
TELEX: 133521
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
ORGANISM: Streptococcus pyogenes
STRAIN: D734
INDIVIDUAL ISOLATE: 22
IMMEDIATE SOURCE:
CLONE: SAU3a
US-08-294-189-8

Query Match 93.3%; Score 111; DB 1; Length 38;
Best Local Similarity 95.2%; Pred. No. 7,1e-11;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KPSYQFGHNSVDFEDTLPK 21
DB 10 KPSYQFGHNSVDFEDTLPK 30

RESULT 5
US-08-729-767-5
Sequence 5, Application US/08729767
Patent No. 5770702
GENERAL INFORMATION:
APPLICANT: HOOK, Magnus
APPLICANT: LINDBERG, Martin Kjell
APPLICANT: SIGNAS, Lars Christer
APPLICANT: WADSTROM, Torkel Mikael
APPLICANT: FROMAN, Gunnar
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN AS WELL AS
TITLE OF INVENTION: ITS PREPARATION
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Burns, Doane, Swecker & Mathis, L.L.P.
STREET: P.O. Box 1404
CITY: Alexandria
STATE: Virginia
COUNTRY: United States
ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/729,767
FILING DATE: 07-OCT-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/259,000
FILING DATE: 13-JUN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/007,817
FILING DATE: 22-JAN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/201,028
FILING DATE: 01-JUN-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: SE 8702272-9

FILING DATE: 01-JUN-1987
ATTORNEY/AGENT INFORMATION:
NAME: McGowan, Malcolm K.
REGISTRATION NUMBER: 39,300
REFERENCE/DOCKET NUMBER: 012889-036
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-729-767-5

Query Match 93.3%; Score 111; DB 1; Length 38;
Best Local Similarity 95.2%; Pred. No. 7,1e-11;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KPSYQFGHNSVDFEDTLPK 21
DB 17 KPSYQFGHNSVDFEDTLPK 37

RESULT 6
US-08-259-000-3
Sequence 3, Application US/08259000
Patent No. 5571514
GENERAL INFORMATION:
APPLICANT: HOOK, Magnus
APPLICANT: LINDBERG, Martin Kjell
APPLICANT: SIGNAS, Lars Christer
APPLICANT: WADSTROM, Torkel Mikael
APPLICANT: FROMAN, Gunnar
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN AS WELL AS
TITLE OF INVENTION: ITS PREPARATION
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Burns, Doane, Swecker & Mathis
STREET: P.O. Box 1404
CITY: Alexandria
STATE: Virginia
COUNTRY: United States
ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/259,000
FILING DATE: 13-JUN-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: SE 8702272-9
FILING DATE: 01-JUN-1987
ATTORNEY/AGENT INFORMATION:
NAME: Meuth, Donna M.
REGISTRATION NUMBER: 36,607
REFERENCE/DOCKET NUMBER: 012885-062
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 114 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-259-000-3

Query Match 93.3%; Score 111; DB 1; Length 114;
Best Local Similarity 95.2%; Pred. No. 2,5e-10;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KPSYQFGHNSVDFEEDTLPK 21
Db 93 KPSYQFGHNSVDFEEDTLPK 113

RESULT 7

US-08-856-253-8
Sequence 8, Application US/08856253
Patent No. 6288214
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
APPLICANT: Patti, Joseph M.
APPLICANT: House-Pompeo, Karen
APPLICANT: Schanam, Narayana
APPLICANT: Symersky, Jindrich
TITLE OF INVENTION: COLLAGEN BINDING PROTEIN COMPOSITIONS
NUMBER OF SEQUENCES: 8
METHODS OF USE
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: Texas
COUNTRY: U.S.
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/856,253
FILING DATE: Concurrently Herewith
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/017,678
FILING DATE: 16-MAY-1996
ATTORNEY/AGENT INFORMATION:
NAME: Kitchell, Barbara S.
REGISTRATION NUMBER: 33,928
REFERENCE/DOCKET NUMBER: TANK:193
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
TELEFAX: (512) 474-7577
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 139 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-08-856-253-8

Query Match 93.3%; Score 111; DB 3; Length 139;
Best Local Similarity 95.2%; Pred. No. 3,1e-10;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KPSYQFGHNSVDFEEDTLPK 21
Db 107 KPSYQFGHNSVDFEEDTLPK 127

RESULT 8

US-08-459-135A-12
Sequence 12, Application US/08459135A
Patent No. 5955078
GENERAL INFORMATION:
APPLICANT: BURHAM, Martin Karl Russel
APPLICANT: CHOPRA, Ian

APPLICANT: CRITCHLEY, Ian Alfred
APPLICANT: KNOWLES, David Justin Charles
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN: MONOCLONAL ANTIBODY AND THEIR US
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
STATE: PA

COUNTRY: U.S.A.
ZIP: 19406-0939

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS

SOFTWARE: Fastseq, Version 2.0
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/459,135A
FILING DATE: 02-JUN-1995

CLASSIFICATION: 435
PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/GB/94/00215
FILING DATE: 04-Feb-1994

CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:

NAME: Gimmi, Edward R.
REGISTRATION NUMBER: 38,891

REFERENCE/DOCKET NUMBER: P30591C2
TELECOMMUNICATION INFORMATION:

TELEPHONE: 610-270-4478
TELEFAX: 610-270-5090

TELEX:
INFORMATION FOR SEQ ID NO: 12:

SEQUENCE CHARACTERISTICS:
LENGTH: 178 amino acids

TYPE: amino acid
STRANDEDNESS: single

TOPOLOGY: linear
MOLECULE TYPE: Protein

US-08-459-135A-12

Query Match 93.3%; Score 111; DB 2; Length 178;
Best Local Similarity 95.2%; Pred. No. 4,1e-10;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KPSYQFGHNSVDFEEDTLPK 21
Db 93 KPSYQFGHNSVDFEEDTLPK 113

RESULT 9

US-08-495-559-12
Sequence 12, Application US/08495559A
Patent No. 6054572
GENERAL INFORMATION:
APPLICANT: BURHAM, Martin Karl Russel
APPLICANT: CHOPRA, Ian
APPLICANT: CRITCHLEY, Ian Alfred
APPLICANT: KNOWLES, David Justin Charles
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN: MONOCLONAL
TITLE OF INVENTION: ANTIBODY AND THEIR USE IN PREVENTING BACTERIAL ADHESION
FILE REFERENCE: P30591
CURRENT APPLICATION NUMBER: US/08/495,559A
CURRENT FILING DATE: 1995-08-03
EARLIER APPLICATION NUMBER: GB 9302289.5
EARLIER FILING DATE: 1993-02-05
EARLIER APPLICATION NUMBER: GB 9321592.9
EARLIER FILING DATE: 1993-10-20
NUMBER OF SEQ ID NOS: 13
SOFTWARE: Fastseq for Windows Version 3.0
SEQ ID NO 12
LENGTH: 178
TYPE: PRT

ORGANISM: Staphylococcus aureus
US-08-495-559-12

Query Match 93.3%; Score 111; DB 3; Length 178;
Best Local Similarity 95.2%; Pred. No. 4.1e-10;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KPSYOGGHSVDPEDTLPK 21
Db 93 KPSYOGGHSVDPEDTLPK 113

RESULT 10
US-08-956-171E-5254
Sequence 5254, Application US/08956171E
Patent No. 6593114

GENERAL INFORMATION:
APPLICANT: Charles Kunach

Gil H. Choi
Patrick S. Dillon
Craig A. Rosen
Steven C. Barash
Michael R. Fannon

TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
NUMBER OF SEQUENCES: 5256
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COUNTRY: USA
ZIP: 20850

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/956,171E
FILING DATE: 20-Oct-1997
CLASSIFICATION: <unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/009,861
FILING DATE: January 5, 1996
APPLICATION NUMBER: 08/781,986
FILING DATE: January 3, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Mark J. Hyman
REGISTRATION NUMBER: 46,789
REFERENCE/DOCKET NUMBER: PB248P1

TELECOMMUNICATION INFORMATION:
TELEPHONE: (240) 314-1224
TELEFAX: (301) 309-8439
INFORMATION FOR SEQ ID NO: 5254:
SEQUENCE CHARACTERISTICS:
LENGTH: 1027 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 5254:
US-08-956-171E-5254

Query Match 93.3%; Score 111; DB 4; Length 1027;
Best Local Similarity 95.2%; Pred. No. 3e-09;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KPSYOGGHSVDPEDTLPK 21
Db 846 KPSYOGGHSVDPEDTLPK 866

RESULT 11

US-08-781-986A-5254
Sequence 5254, Application US/08781986A
Patent No. 6737248

GENERAL INFORMATION:
APPLICANT: Charles Kunach
TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
NUMBER OF SEQUENCES: 5255
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COUNTRY: USA
ZIP: 20850

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/781,986A
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:

ATTORNEY/AGENT INFORMATION:
NAME: Benson, Bob
REGISTRATION NUMBER: 30,446
REFERENCE/DOCKET NUMBER: PB248PP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 5254:
SEQUENCE CHARACTERISTICS:
LENGTH: 1027 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-781-986A-5254

Query Match 93.3%; Score 111; DB 4; Length 1027;
Best Local Similarity 95.2%; Pred. No. 3e-09;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KPSYOGGHSVDPEDTLPK 21
Db 846 KPSYOGGHSVDPEDTLPK 866

RESULT 12
US-09-010-317-14
Sequence 14, Application US/09010317
Patent No. 6685943

GENERAL INFORMATION:
APPLICANT: Hook, Magnus
APPLICANT: Patil, Joseph M.
APPLICANT: House-Pompeo, Karen L.
APPLICANT: Speziale, Pietro
APPLICANT: Uhn, Danny
APPLICANT: McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/010.317
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-09-010-317-14

Query Match 89.1%; Score 106; DB 4; Length 21;
Best Local Similarity 95.0%; Pred. No. 2.3e-10;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 PSYFGGHSVDFPDLTPK 21
DB 2 PSYFGGHSVDFPDLTPK 21

RESULT 13
US-09-010-317-16

Sequence 16, Application US/09010317
Patent No. 6685943
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
APPLICANT: Patti, Joseph M.
APPLICANT: House-Pompeo, Karen L.
APPLICANT: Speziale, Pietro
APPLICANT: John, Danny
APPLICANT: McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/010.317
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAMK.189
TELECOMMUNICATION INFORMATION:

TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-09-010-317-16

Query Match 89.1%; Score 106; DB 4; Length 21;
Best Local Similarity 90.5%; Pred. No. 2.3e-10;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 KPSYFGGHSVDFPDLTPK 21
DB 1 KPSYFGGHSVDFPDLTPK 21

RESULT 14
US-09-010-317-23

Sequence 23, Application US/09010317
Patent No. 6685943
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
APPLICANT: Patti, Joseph M.
APPLICANT: House-Pompeo, Karen L.
APPLICANT: Speziale, Pietro
APPLICANT: John, Danny
APPLICANT: McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/010.317
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAMK.189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-09-010-317-23

Query Match 89.1%; Score 106; DB 4; Length 21;
Best Local Similarity 90.5%; Pred. No. 2.3e-10;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 KPSYFGGHSVDFPDLTPK 21

Db 1 KPSYQFGGHNPVDEBTLTPK 21

RESULT 15

US-09-010-317-33
 ; Sequence 33, Application US/09010317
 ; Patent No. 6685943
 ; GENERAL INFORMATION:
 ; APPLICANT: Hook, Magnus
 ; APPLICANT: Patl. Joseph M.
 ; APPLICANT: House-Pompeo, Karen L.
 ; APPLICANT: Speziale, Pietro
 ; APPLICANT: Joh, Danny
 ; APPLICANT: McGavin, Martin J.
 ; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
 ; TITLE OF INVENTION: AND METHODS OF USE
 ; NUMBER OF SEQUENCES: 105
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Arnold, White & Durkee
 ; STREET: P.O. Box 4433
 ; CITY: Houston
 ; STATE: TX
 ; COUNTRY: USA
 ; ZIP: 77210-4433
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patentin Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/010,317
 ; FILING DATE:
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 60/036,139
 ; FILING DATE: 21-JAN-1997
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Hibley, David W.
 ; REGISTRATION NUMBER: 41,071
 ; REFERENCE/DOCKET NUMBER: TAMK:189
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 512-418-3000
 ; TELEFAX: 512-474-7577
 ; INFORMATION FOR SEQ ID NO: 33:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 21 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS:
 ; TOPOLOGY: linear
 ; US-09-010-317-33

Query Match 89.1%; Score 106; DB 4; Length 21;
 Best Local Similarity 95.0%; Pred. No. 2.3e-10;
 Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 KPSYQFGGHNSVDFEETLP 20
 |||||
 Db 1 KPSYQFGGHNSVDFEETLP 20

Search completed: October 22, 2005, 03:51:13
 Job time : 15.9358 secs

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OM protein - protein search, using sw model

Run on: October 22, 2005, 10:49:15 ; Search time 59.2367 Seconds
(without alignments)
148.005 Million cell updates/sec

Title: US-10-731-238-27
Perfect score: 119
Sequence: 1 KPSYQFGHNSVDPEEDTLPK 21

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Gapop 10.0 , Gapext 0.5

Searched: 1862951 seqs, 417491010 residues

Total number of hits satisfying chosen parameters: 1862951

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA.*
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12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
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19: /cgn2_6/ptodata/2/pubpaa/US11A_PUBCOMB.pep.*
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22: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	119	100.0	21	US-10-731-238-27	Sequence 27, Appl
2	111	93.3	21	US-10-731-238-9	Sequence 9, Appl
3	111	93.3	37	US-11-066-697-1134	Sequence 1134, Ap
4	111	93.3	139	US-09-813-820-9	Sequence 8, Appl
5	111	93.3	1018	US-09-815-242-5797	Sequence 5797, Ap
6	111	93.3	1018	US-09-815-242-12838	Sequence 12838, A
7	111	93.3	1018	US-10-470-048B-68	Sequence 68, Appl
8	111	93.3	1027	US-08-781-986A-5254	Sequence 5254, Ap
9	111	93.3	1027	US-10-329-624-5254	Sequence 5254, Ap
10	108	90.8	961	US-10-282-122A-43778	Sequence 43778, A
11	108	90.8	978	US-09-815-242-5456	Sequence 5456, Ap

12	108	90.8	1001	US-09-815-242-12686	Sequence 12686, A
13	108	90.8	1038	US-10-282-122A-43827	Sequence 43827, A
14	106	89.1	21	US-10-731-238-14	Sequence 14, Appl
15	106	89.1	21	US-10-731-238-16	Sequence 16, Appl
16	106	89.1	21	US-10-731-238-23	Sequence 23, Appl
17	106	89.1	21	US-10-731-238-33	Sequence 33, Appl
18	105	88.2	21	US-10-731-238-18	Sequence 18, Appl
19	105	88.2	21	US-10-731-238-28	Sequence 28, Appl
20	105	88.2	21	US-10-731-238-28	Sequence 28, Appl
21	105	88.2	21	US-10-731-238-30	Sequence 30, Appl
22	104	87.4	21	US-10-731-238-25	Sequence 25, Appl
23	104	87.4	21	US-10-731-238-29	Sequence 29, Appl
24	104	87.4	21	US-10-731-238-31	Sequence 31, Appl
25	104	87.4	388	US-08-901-062-1	Sequence 1, Appl
26	104	87.4	559	US-08-781-986A-5251	Sequence 5251, Ap
27	104	87.4	559	US-10-329-624-5251	Sequence 5251, Ap
28	104	87.4	940	US-10-470-048B-424	Sequence 424, Appl
29	104	87.4	948	US-10-470-048B-69	Sequence 69, Appl
30	103	86.6	21	US-10-731-238-15	Sequence 15, Appl
31	103	86.6	21	US-10-731-238-15	Sequence 15, Appl
32	103	86.6	21	US-10-731-238-20	Sequence 20, Appl
33	103	86.6	21	US-10-731-238-22	Sequence 22, Appl
34	103	86.6	21	US-10-731-238-32	Sequence 32, Appl
35	103	86.6	22	US-10-731-238-13	Sequence 13, Appl
36	101	84.9	21	US-10-731-238-17	Sequence 17, Appl
37	101	84.9	21	US-10-731-238-19	Sequence 19, Appl
38	101	84.9	21	US-10-731-238-21	Sequence 21, Appl
39	101	84.9	21	US-10-731-238-26	Sequence 26, Appl
40	83	69.7	21	US-10-731-238-34	Sequence 34, Appl
41	72	60.5	14	US-10-731-238-61	Sequence 61, Appl
42	59	49.6	10	US-10-731-238-96	Sequence 96, Appl
43	58	48.7	10	US-10-731-238-97	Sequence 97, Appl
44	54	45.4	10	US-10-731-238-85	Sequence 85, Appl
45	53	44.5	14	US-10-340-811-3	Sequence 3, Appl

ALIGNMENTS

RESULT 1
US-10-731-238-27
Sequence 27, Application US/10731238
Publication No. US20050123552A1
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
Patli, Joseph M.
House-Pompeo, Karen L.
Speziale, Pietro
Jon, Danny
McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSER: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/731,238
FILING DATE: 10-Dec-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE: 21-Jan-1998
APPLICATION NUMBER: US 60/036,139

FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TANK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 27:
US-10-731-238-27

Query Match 100.0%; Score 119; DB 18; Length 21;
Best Local Similarity 100.0%; Pred. No. 1,3e-11;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KPSYQFGGHSVDPEDTLPK 21
|||
Db 1 KPSYQFGGHSVDPEDTLPK 21

RESULT 2
US-10-731-238-9
Sequence 9, Application US/10731238
Publication No. US20050123552A1
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
Patti, Joseph M.
House-Pompeo, Karen L.
Speziale, Pietro
Joh, Danny
McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/731,238
FILING DATE: 10-Dec-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE: 21-Jan-1998
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TANK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>

TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 9:
US-10-731-238-9

Query Match 93.3%; Score 111; DB 18; Length 21;
Best Local Similarity 95.2%; Pred. No. 2,3e-10;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KPSYQFGGHSVDPEDTLPK 21
|||
Db 1 KPSYQFGGHSVDPEDTLPK 21

RESULT 3
US-11-066-697-1134
Sequence 1134, Application US/11066697
Publication No. US20050187159A1
GENERAL INFORMATION:
APPLICANT: Bridon, Dominique P.
APPLICANT: Ezrin, Alan M.
APPLICANT: Milner, Peter G.
APPLICANT: Holmes, Darren L.
APPLICANT: Thibaudau, Karen
TITLE OF INVENTION: PROTECTION OF ENDOGENOUS THERAPEUTIC PEPTIDES FROM
TITLE OF INVENTION: PEPTIDASE ACTIVITY THROUGH COMUGATION TO BLOOD
FILE REFERENCE: 500862002301
CURRENT APPLICATION NUMBER: US/11/066,697
CURRENT FILING DATE: 2005-02-25
PRIOR APPLICATION NUMBER: 09/657,276
PRIOR FILING DATE: 2000-09-07
PRIOR APPLICATION NUMBER: 60/153,406
PRIOR FILING DATE: 1999-09-10
PRIOR APPLICATION NUMBER: 60/159,783
PRIOR FILING DATE: 1999-10-15
NUMBER OF SEQ ID NOS: 1617
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1134
LENGTH: 37
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-11-066-697-1134

Query Match 93.3%; Score 111; DB 20; Length 37;
Best Local Similarity 95.2%; Pred. No. 4,4e-10;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KPSYQFGGHSVDPEDTLPK 21
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Db 16 KPSYQFGGHSVDPEDTLPK 36

RESULT 4
US-09-813-820-8
Sequence 8, Application US/09813820
Patent No. US200201026262A1
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
Patti, Joseph M.
House-Pompeo, Karen
Schanam, Narayana
Sytersky, Jindrich
TITLE OF INVENTION: COLLAGEN BINDING PROTEIN COMPOSITIONS
AND METHODS OF USE
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: Texas

```

; COUNTRY: U.S.
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION NUMBER: US/09/813,820
; FILING DATE: 22-Mar-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/856,253
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Kitchell, Barbara S.
; REGISTRATION NUMBER: 33,928
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (512) 418-3000
; TELEFAX: (512) 474-7577
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 139 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-09-813-820-8

Query Match      93.3%; Score 111; DB 9; Length 139;
Best Local Similarity 95.2%; Pred. No. 1.9e-09;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 KPSYQFGHNSVDPEDTLPK 21
Db      107 KPSYQFGHNSVDPEDTLPK 127

RESULT 5
US-09-815-242-5797
; Sequence 5797, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Karl L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; FILE OF INVENTION: Prokaryotes
; FILE REFERENCE: ELITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version 4.0
; FILE REFERENCE: FastSeq for Windows Version 4.0

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; SEQ ID NO 5797
; LENGTH: 1018
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-09-815-242-5797

Query Match      93.3%; Score 111; DB 9; Length 1018;
Best Local Similarity 95.2%; Pred. No. 1.8e-08;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 KPSYQFGHNSVDPEDTLPK 21
Db      837 KPSYQFGHNSVDPEDTLPK 857

RESULT 6
US-09-815-242-12838
; Sequence 12838, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Karl L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; FILE OF INVENTION: Prokaryotes
; FILE REFERENCE: ELITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12838
; LENGTH: 1018
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-09-815-242-12838

RESULT 7
US-10-470-048B-68
; Sequence 68, Application US/10470048B
; Publication No. US2005003744A1
; GENERAL INFORMATION:
; APPLICANT: MEINKE ET AL.
; TITLE OF INVENTION: A METHOD FOR IDENTIFICATION, ISOLATION AND PRODUCTION OF
; FILE OF INVENTION: ANTIGENS TO A SPECIFIC PATHOGEN
; FILE REFERENCE: SONN.035US

```

;; CURRENT APPLICATION NUMBER: US/10/470,048B
;; CURRENT FILING DATE: 2003-07-25
;; NUMBER OF SEQ ID NOS: 603
;; SOFTWARE: PatentIn version 3.1
;; SEQ ID NO: 68
;; LENGTH: 1018
;; TYPE: PR1
;; ORGANISM: Staphylococcus aureus
US-10-470-048B-68

Query Match 93.3%; Score 111; DB 17; Length 1018;
Best Local Similarity 95.2%; Pred. No. 1.8e-08;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KPSYQFGHNSVDPEDTLPK 21
Db 837 KPSYQFGHNSVDPEDTLPK 857

RESULT 8
US-08-781-986A-5254
; Sequence 5254, Application US/08781986A
; Publication No. US20030054436A1
; GENERAL INFORMATION:
; APPLICANT: Charles Kunsch
; TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
; NUMBER OF SEQUENCES: 5255
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/781,986A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Benson, Bob
; REGISTRATION NUMBER: 30,446
; REFERENCE/DOCKET NUMBER: PB248PP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 5254:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1027 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-781-986A-5254

Query Match 93.3%; Score 111; DB 8; Length 1027;
Best Local Similarity 95.2%; Pred. No. 1.8e-08;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KPSYQFGHNSVDPEDTLPK 21
Db 846 KPSYQFGHNSVDPEDTLPK 866

RESULT 9
US-10-329-624-5254

;; Sequence 5254, Application US/10329624
;; Publication No. US20040043037A1
;; GENERAL INFORMATION:
;; APPLICANT: Charles Kunsch
;; Gil H. Choi
;; Patrick S. Dillon
;; Craig A. Rosen
;; Steven C. Barash
;; Michael R. Fannon
;; TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
;; NUMBER OF SEQUENCES: 5256
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Human Genome Sciences, Inc.
;; STREET: 9410 Key West Avenue
;; CITY: Rockville
;; STATE: Maryland
;; COUNTRY: USA
;; ZIP: 20850
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
;; COMPUTER: HP Vectra 486/33
;; OPERATING SYSTEM: MSDOS version 6.2
;; SOFTWARE: ASCII Text
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/10/329,624
;; FILING DATE: 27-Dec-2002
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 08/956,171
;; FILING DATE: October 20, 1997
;; APPLICATION NUMBER: 60/009,861
;; FILING DATE: January 5, 1996
;; APPLICATION NUMBER: 08/781,986
;; FILING DATE: January 3, 1997
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Mark J. Hyman
;; REGISTRATION NUMBER: 46,789
;; REFERENCE/DOCKET NUMBER: PB248P1D1
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (240) 314-1224
;; TELEFAX: (301) 309-8439
;; INFORMATION FOR SEQ ID NO: 5254:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 1027 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; SEQUENCE DESCRIPTION: SEQ ID NO: 5254:
US-10-329-624-5254

Query Match 93.3%; Score 111; DB 15; Length 1027;
Best Local Similarity 95.2%; Pred. No. 1.8e-08;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KPSYQFGHNSVDPEDTLPK 21
Db 846 KPSYQFGHNSVDPEDTLPK 866

RESULT 10
US-10-282-122A-43778
; Sequence 43778, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Wall, Daniel
; APPLICANT: Zyskind, Judith
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant

```
APPLICANT: Yamamoto, Robert
APPLICANT: Foreyth, R.
TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REFERENCE: ELITRA.034A US/10/282,122A
CURRENT APPLICATION NUMBER: 2003-02-20
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/230,335
PRIOR FILING DATE: 2000-09-06
PRIOR APPLICATION NUMBER: 60/230,347
PRIOR FILING DATE: 2000-09-09
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/267,636
PRIOR FILING DATE: 2001-02-09
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 78614
SOFTWARE: PatentIn version 3.1
SEQ ID NO 43778
LENGTH: 961
TYPE: PRT
ORGANISM: Staphylococcus aureus
US-10-282-122A-43778
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```
Query Match          90.8%; Score 108; DB 15; Length 961;
Best Local Similarity 90.5%; Pred. No. 4.9e-08;
Matches 19; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 1 KPSYQFGHNSVDPEDTLPK 21
DB 784 KPNYQFGHNSVDPEDTLPK 804
```

```
RESULT 11
US-09-815-242-5456
Sequence 5456, Application US/09815242
Patent No. US20020061569A1
GENERAL INFORMATION:
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Karl L.
APPLICANT: Zyskind, Judith W.
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John D.
APPLICANT: Carr, Grant J.
APPLICANT: Yamamoto, Robert T.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in
Prokaryotes
FILE REFERENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: US/09/815,242
PRIOR FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
```

```
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 5456
LENGTH: 978
TYPE: PRT
ORGANISM: Staphylococcus aureus
US-09-815-242-5456
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```
Query Match          90.8%; Score 108; DB 9; Length 978;
Best Local Similarity 90.5%; Pred. No. 5e-08;
Matches 19; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
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```
QY 1 KPSYQFGHNSVDPEDTLPK 21
DB 815 KPNYQFGHNSVDPEDTLPK 835
```

```
RESULT 12
US-09-815-242-12686
Sequence 12686, Application US/09815242
Patent No. US20020061569A1
GENERAL INFORMATION:
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Karl L.
APPLICANT: Zyskind, Judith W.
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John D.
APPLICANT: Carr, Grant J.
APPLICANT: Yamamoto, Robert T.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in
Prokaryotes
FILE REFERENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: US/09/815,242
PRIOR FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 12686
LENGTH: 1001
TYPE: PRT
ORGANISM: Staphylococcus aureus
US-09-815-242-12686
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Query Match          90.8%; Score 108; DB 9; Length 1001;
Best Local Similarity 90.5%; Pred. No. 5.1e-08;
Matches 19; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
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QY 1 KPSYQFGHNSVDPEDTLPK 21
DB 838 KPNYQFGHNSVDPEDTLPK 858
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RESULT 13
US-10-282-122A-43827
Sequence 43827, Application US/10282122A
```

Publication No. US20040029129A1
GENERAL INFORMATION:
APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari
APPLICANT: Zyglid, Judith
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John
APPLICANT: Carr, Grant
APPLICANT: Yamamoto, Robert
APPLICANT: Forsyth, R.
APPLICANT: Xu, H.
TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REFERENCE: ELITRA.034A
CURRENT APPLICATION NUMBER: US/10/282.122A
CURRENT FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/230,335
PRIOR FILING DATE: 2000-09-06
PRIOR APPLICATION NUMBER: 60/230,347
PRIOR FILING DATE: 2000-09-09
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/267,636
PRIOR FILING DATE: 2001-02-09
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 78614
SOFTWARE: PatentIn version 3.1
SEQ ID NO: 43827
LENGTH: 1038
TYPE: PRT
ORGANISM: Staphylococcus aureus
US-10-282-122A-43827
Query Match 90.8%; Score 108; DB 15; Length 1038;
Best Local Similarity 90.5%; Pred. No. 5, 4e-08;
Matches 19; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KPSYQFGHNSVDFEPTLPK 21
Db 833 KPNYQFGHNSVDFEPTLPK 853

RESULT 14
US-10-731-238-14
Sequence 14, Application US/10731238
Publication No. US20050123552A1
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
Pattl, Joseph M.
House-Pompeo, Karen L.
Speziale, Pietro
Joh, Danny
McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433

CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/731,238
FILING DATE: 10-Dec-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE: 21-Jan-1998
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TMMK.189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 14:
US-10-731-238-14
Query Match 89.1%; Score 106; DB 18; Length 21;
Best Local Similarity 95.0%; Pred. No. 1, 5e-09;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 PSYQFGHNSVDFEPTLPK 21
Db 2 PSYQFGHNSVDFEPTLPK 21

RESULT 15
US-10-731-238-16
Sequence 16, Application US/10731238
Publication No. US20050123552A1
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
Pattl, Joseph M.
House-Pompeo, Karen L.
Speziale, Pietro
Joh, Danny
McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/731,238
FILING DATE: 10-Dec-2003
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE: 21-Jan-1998
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAMK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 16:
US-10-731-238-16

Query Match 89.1%; Score 106; DB 18; Length 21;
Best Local Similarity 90.5%; Pred No. 1.5e-09;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 KPSPYQFGHNSVDFPEDTLPK 21
|||
DB 1 KPSPYQFGHNSVDFPEDTLPK 21

Search completed: October 22, 2005, 11:34:42
Job time : 60.2367 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 22, 2005, 02:23:36 ; Search time 10.5465 Seconds
(without alignments)
191.586 Million cell updates/sec

Title: US-10-731-238-27
Perfect score: 119
Sequence: 1 KPSYQFGHNSVDFPDLTPK 21

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	111	93.3	A32192	fibronectin-bindin
2	108	90.8	G90053	hypothetical prote
3	108	90.8	H90053	hypothetical prote
4	104	87.4	S19702	fibronectin-bindin
5	52.5	44.1	T34930	probable secreted
6	52	43.7	C84406	hypothetical prote
7	47	39.5	T05894	probable oxoglutar
8	47	39.5	T47680	probable oxoglutar
9	47	39.5	T50644	oxoglutarate dehyd
10	47	39.5	S61441	surface-associated
11	46	38.7	T49278	hypothetical prote
12	46	38.7	B84357	serine-tRNA synthe
13	46	38.7	C84965	oxoglutarate dehyd
14	45	37.8	S49156	HagC hemagglutinin
15	45	37.8	S52213	HagB hemagglutinin
16	45	37.8	D69462	pyruvate synthase
17	45	37.8	A39356	3-oxoacyl-[acyl-ca
18	45	37.8	T26081	hypothetical prote
19	45	37.8	T10061	3-oxoacyl-[acyl-ca
20	45	37.8	T27672	hypothetical prote
21	45	37.8	A59288	myosin heavy chain
22	44.5	37.4	AG3069	phosphoenolpyruvat
23	44.5	37.4	C98217	enzyme I-nlr prote
24	44.5	37.4	S33850	fibronectin-binding
25	44.5	37.4	S31853	laminin alpha-1 ch
26	44	37.0	C257	MHC class I histoc
27	44	37.0	T38449	extracellular prote
28	44	37.0	P90562	hypothetical prote
29	44	37.0	A45259	desmoyokin - human

30	43.5	36.6	781	2	A38973	beta-catenin - hum
31	43.5	36.6	781	2	S35091	beta-catenin - mou
32	43.5	36.6	1890	2	T04556	hypothetical prote
33	43	36.1	65	2	H95280	conserved hypothet
34	43	36.1	175	2	S42095	capsid protein - o
35	43	36.1	229	2	AG0698	probable pathogeni
36	43	36.1	346	2	C72353	hypothetical prote
37	43	36.1	368	2	G87637	hypothetical prote
38	43	36.1	410	2	AC3603	3-methyl-2-oxobuta
39	43	36.1	444	2	T19855	hypothetical prote
40	43	36.1	454	2	T24455	hypothetical prote
41	43	36.1	1011	2	JC8059	semaphorin 6D-1 -
42	42.5	35.7	666	2	I58169	semaphorin III - m
43	42.5	35.7	759	2	B83474	probable type II s
44	42.5	35.7	771	2	D49423	semaphorin IRI pre
45	42.5	35.7	772	2	I48747	semaphorin D - mou

ALIGNMENTS

RESULT 1
A32192
fibronectin-binding protein - Staphylococcus aureus
C/Species: Staphylococcus aureus
C/Date: 31-Jul-1989 #sequence_revision 31-Jul-1989 #text_change 16-Feb-1997
C/Accession: A32192
R/Sigmaes, C.; Raucel, G.; Joensson, K.; Lindgren, P.E.; Anantharamiah, G.M.; Hoecek, M.
Proc. Natl. Acad. Sci. U.S.A. 86, 699-703, 1989
A/Title: Nucleotide sequence of the gene for a fibronectin-binding protein from Staphyloc
A/Reference number: A32192; MUID:89089898; PMID:2521391
A/Accession: A32192
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-1018 <SIG>
A/Cross-references: GB:J04151
C/Keywords: fibronectin binding

Query Match 93.3%; Score 111; DB 2; Length 1018;
Best Local Similarity 95.2%; Pred. No. 4.5e-09;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KPSYQFGHNSVDFPDLTPK 21
DB 837 KPSYQFGHNSVDFPDLTPK 857

RESULT 2

G90053
hypothetical protein fnb [imported] - Staphylococcus aureus (strain N315)
C/Species: Staphylococcus aureus
C/Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C/Accession: G90053
R/Kuroda, M.; Ohira, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Gui, L.; Oguchi
ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.; f
C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hirataesu, K.
Lancet 357, 1225-1240, 2001
A/Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.
A/Reference number: A89758; MUID:2111952; PMID:11418146
A/Accession: G90053
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-961 <KUR>
A/Cross-references: UNIPROT:Q99RD3; GB:BA000018; PID:G13702452; PIDN:BA843593.1; GSPDB:G
A/Experimental source: strain N315
C/Genetics: fnbB
A/Genes: fnbB

Query Match 90.8%; Score 108; DB 2; Length 961;
Best Local Similarity 90.5%; Pred. No. 1.2e-08;
Matches 19; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 KPSYQFGHNSVDFPDLTPK 21

Db 784 KPNYFGGHSVDPEDTLPK 804

RESULT 3

H90053

hypothetical protein fnb [imported] - Staphylococcus aureus (strain N315)

C:Species: Staphylococcus aureus

C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004

C:Accession: H90053

R:Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguc

ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.;

C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.

Lancet 357, 1225-1240, 2001

A:Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.

A:Reference number: A89758; MUID:21311952; PMID:11418146

A:Accession: H90053

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-1038 <KUR>

A:Cross-references: UNIPROT:Q99RD2; GB:BA000018; PID:g13702453; PIDN:BA843594.1; GSPDB:C

A:Experimental source: strain N315

C:Genetics:

A:Gene: fnb

Query Match 90.8%; Score 108; DB 2; Length 1038;

Best Local Similarity 90.5%; Pred. No. 1.3e-08;

Matches 19; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 KPSYFGGHSVDPEDTLPK 21

Db 833 KPNYFGGHSVDPEDTLPK 853

RESULT 4

S19702

fibronectin-binding protein B - Staphylococcus aureus

C:Species: Staphylococcus aureus

C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004

C:Accession: S19702

R:Joenson, K.; Signaes, C.; Mueller, H.P.; Lindberg, M.

Eur. J. Biochem. 202, 1041-1048, 1991

A:Title: Two different genes encode fibronectin binding proteins in Staphylococcus aure

A:Reference number: S19702; MUID:92111475; PMID:1837266

A:Accession: S19702

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-940 <JOB>

A:Cross-references: UNIPROT:Q53682; EMBL:X62392; NID:g49040; PIDN:CAA44726.1; PID:G58156

C:Keywords: fibronectin binding

Query Match 87.4%; Score 104; DB 2; Length 940;

Best Local Similarity 85.7%; Pred. No. 5.1e-08;

Matches 18; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 KPSYFGGHSVDPEDTLPK 21

Db 773 KPNYFGGHSVDPEDTLPK 793

RESULT 5

T34930

probable secreted protein - Streptomyces coelicolor

C:Species: Streptomyces coelicolor

C:Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 09-Jul-2004

C:Accession: T34930

R:Seeger, K.J.; Harris, D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.

submitted to the EMBL Data Library, June 1998

A:Reference number: Z21562

A:Accession: T34930

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-417 <SEB>

A:Cross-references: UNIPROT:O69948; EMBL:AL023862; PIDN:CAA19631.1; GSPDB:GN00070; SCOEDB

A:Experimental source: strain A3(2)

C:Genetics:

C:Superfamily: myo-inositol-1-phosphate synthase

Query Match 44.1%; Score 52.5; DB 2; Length 417;

Best Local Similarity 55.0%; Pred. No. 2.4;

Matches 11; Conservative 3; Mismatches 3; Indels 3; Gaps 1;

QY 2 PSYFGGHSVDPEDTLPK 21

Db 62 PALVFGGHDTVDCP---LPK 78

RESULT 6

C84406

hypothetical protein Vng2556th [imported] - Halobacterium sp. NRC-1

C:Species: Halobacterium sp. NRC-1

C:Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004

C:Accession: C84406

R:Ng, W.V.; Kennedy, S.P.; Mahire, G.G.; Bergqvist, B.; Pan, M.; Shukla, H.D.; Laeky, S.

; Leithauser, B.; Keller, K.; Cruz, R.; Danson, M.D.; Hough, D.W.; Maddocks, D.G.; Jablor

Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000

A:Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ehardt, H.; Lowe, T.M.; Li

A:Title: Genome sequence of Halobacterium species NRC-1.

A:Reference number: A84160; MUID:20504483; PMID:11016950

A:Accession: C84406

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-705 <STO>

A:Cross-references: UNIPROT:Q9HMF6; GB:AE004437; NID:g10581952; PIDN:AAG20615.1; GSPDB:G

C:Genetics:

A:Gene: VNG2556th

Query Match 43.7%; Score 52; DB 2; Length 705;

Best Local Similarity 55.6%; Pred. No. 5.2;

Matches 10; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 2 PSYFGGHSVDPEDTL 19

Db 235 PSYVAGGHQIATFPRDL 252

RESULT 7

T05894

probable oxoglutarate dehydrogenase (lipoamide) (EC 1.2.4.2) - Arabidopsis thaliana

N:Alternate names: protein F6H1.130

C:Species: Arabidopsis thaliana (mouse-ear cress)

C:Date: 09-Apr-1999 #sequence_revision 09-Apr-1999 #text_change 09-Jul-2004

C:Accession: T05894

R:Bevan, M.; Brandt, P.; Dose, S.; Jakke, D.; Scharfe, M.; Schon, O.; Bancroft, I.; Mew

submitted to the Protein Sequence Database, April 1998

A:Reference number: Z15456

A:Accession: T05894

A:Molecule type: DNA

A:Residues: 1-973 <BEV>

A:Cross-references: UNIPROT:Q49541; EMBL:AL021684; GSPDB:GN00063; ATSP:F6H1.130

A:Experimental source: cultivar Columbia; BAC clone F6H1

C:Genetics:

A:Gene: ATSP:F6H1.130

A:Map position: 5

A:Genome: nuclear

A:Introns: 520/3; 596/2; 707/2; 789/3; 832/3; 894/1

C:Superfamily: oxoglutarate dehydrogenase (lipoamide); thiamin pyrophosphate-binding dom

C:Keywords: mitochondrion; oxidoreductase; thiamin pyrophosphate; tricarboxylic acid cycl

F;399-444/Domain: thiamin pyrophosphate-binding domain homology <TPB>

Query Match 39.5%; Score 47; DB 2; Length 973;

Best Local Similarity 50.0%; Pred. No. 45;

Matches 9; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

QY 4 YQFGHNSVDFPDLTPK 21
 Db 500 YRRFGHNEIDPSFTQPK 517

RESULT 8
 T47680
 probable oxoglutarate dehydrogenase (lipoamide) (EC 1.2.4.2) E1 chain - Arabidopsis thaliana
 N.Alternate names: protein T22816.70
 C.Species: Arabidopsis thaliana (mouse-ear cress)
 C.Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 09-Jul-2004
 C.Accession: T47680
 R.Benes, V.; Wirtzbach, E.; Drzonek, H.; Ansoerge, W.; Mewes, H.W.; Lemcke, K.; Mayer, K.F.
 submitted to the Protein Sequence Database, February 2000
 A.Reference number: 224472
 A.Accession: T47680
 A.Status: preliminary
 A.Molecule type: DNA
 A.Residues: 1-1009 <BEN>
 A.Cross-references: UNIPROT:Q9M2T8; EMBL:AL132975
 A.Experimental source: cultivar Columbia; BAC clone T22816
 C.Genetics:
 A.Map position: 3
 A.Introns: 516/3; 592/2; 703/2; 785/3; 828/3; 900/3; 942/1
 A.Note: T22816.70
 C.Superfamily: oxoglutarate dehydrogenase (lipoamide); thiamin pyrophosphate-binding domain
 C.Keywords: oxidoreductase

Query Match 39.5%; Score 47; DB 2; Length 1009;
 Best Local Similarity 50.0%; Pred. No. 47;
 Matches 9; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

QY 4 YQFGHNSVDFPDLTPK 21
 Db 486 YRRFGHNEIDPSFTQPK 513

RESULT 9
 T50644
 oxoglutarate dehydrogenase (lipoamide) (EC 1.2.4.2) E1 chain [imported] - Arabidopsis thaliana
 C.Species: Arabidopsis thaliana (mouse-ear cress)
 C.Date: 21-Jul-2000 #sequence_revision 21-Jul-2000 #text_change 09-Jul-2004
 C.Accession: T50644
 R.Machuy, N.; Klein, M.; Mueller-Roeber, B.
 submitted to the EMBL Data Library, January 1998
 A.Description: Cloning and characterization of 2-Oxoglutarate dehydrogenase from Arabidopsis
 A.Reference number: 225151
 A.Accession: T50644
 A.Status: preliminary
 A.Molecule type: mRNA
 A.Experimental source: translated from GB/EMBL/DBJ
 A.Residues: 1-1027 <MAC>
 A.Cross-references: UNIPROT:Q9ZKQ2; EMBL:AJ223802; P1DN:CAA11552.1
 A.Superfamily: oxoglutarate dehydrogenase (lipoamide); thiamin pyrophosphate-binding domain
 C.Keywords: oxidoreductase

Query Match 39.5%; Score 47; DB 2; Length 1027;
 Best Local Similarity 50.0%; Pred. No. 48;
 Matches 9; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

QY 4 YQFGHNSVDFPDLTPK 21
 Db 500 YRRFGHNEIDPSFTQPK 517

RESULT 10
 S61441
 surface-associated protein csha precursor - Streptococcus gordonii
 N.Alternate names: adhesin
 C.Species: Streptococcus gordonii
 C.Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
 C.Accession: S61441; S61454; S27982
 R.McNab, R.; Jenkinson, H.F.; Loach, D.W.; Tannock, G.W.

Mol. Microbiol. 14, 743-754, 1994
 A.Title: Cell-surface-associated polypeptides Csha and CshB of high molecular mass are cc
 A.Reference number: S61441; MUID:95198547; PMID:7891560
 A.Accession: S61441
 A.Status: nucleic acid sequence not shown
 A.Molecule type: DNA
 A.Residues: 1-2508 <MCN>
 A.Cross-references: UNIPROT:Q54194; EMBL:X65164; NID:q1808670; P1DN:CAA46281.1; PID:9457;
 A.Accession: S61454
 A.Molecule type: protein
 A.Residues: 42-43; 'Y', 45-51 <MCN2>
 R.McNab, R.; Jenkinson, H.F.
 Mol. Microbiol. 6, 2919-2949, 1992
 A.Title: Gene disruption identifies a 290 kDa cell-surface polypeptide conferring hydrophobicity
 A.Reference number: S27982; MUID:93125117; PMID:1479886
 A.Accession: S27982
 A.Molecule type: DNA
 A.Residues: 2026-2508 <MC2>
 A.Cross-references: EMBL:X65164
 C.Genetics:
 A.Gene: csha
 F.1-41/Domain: signal sequence #status predicted <SIG>
 F.42-2508/Product: surface-associated protein csha #status experimental <MAT>

Query Match 39.5%; Score 47; DB 2; Length 2508;
 Best Local Similarity 61.5%; Pred. No. 1.3e+02;
 Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 8 GHNSVDFPDLTPK 20
 Db 1450 GHDSVFPADSTP 1462

RESULT 11
 T49278
 hypothetical protein T21J18.90 - Arabidopsis thaliana
 C.Species: Arabidopsis thaliana (mouse-ear cress)
 C.Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 09-Jul-2004
 C.Accession: T49278
 R.Rieger, M.; Gabel, C.; Mueller-Auer, S.; Schaefer, M.; Zipp, M.; Mewes, H.W.; Rudd, S.;
 submitted to the Protein Sequence Database, April 2000
 A.Reference number: 225021
 A.Accession: T49278
 A.Status: preliminary
 A.Molecule type: DNA
 A.Experimental source: UNIPROT:Q9M301; EMBL:AL132963; GSPDB:GN00061; ATSP:T21J18.90
 A.Cross-references: UNIPROT:Q9M301; EMBL:AL132963; GSPDB:GN00061; ATSP:T21J18.90
 A.Gene: ATSP:T21J18.90
 A.Map position: 3
 A.Introns: 35/2; 71/3; 123/3; 157/2; 174/2; 238/3; 269/1; 290/3; 342/2; 369/3; 406/2

Query Match 38.7%; Score 46; DB 2; Length 470;
 Best Local Similarity 63.6%; Pred. No. 29;
 Matches 7; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 11 SVDFPDLTPK 21
 Db 60 SINFPKDTVPK 70

RESULT 12
 B84357
 serine-tRNA synthetase [imported] - Halobacterium sp. NRC-1
 C.Species: Halobacterium sp. NRC-1
 C.Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
 C.Accession: B84357
 R.Ng, W.V.; Kennedy, S.P.; Mahatras, G.G.; Bergquist, B.; Pan, M.; Shukla, H.D.; Laaky, S.;
 Leitauer, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Jablor
 Jung, K.H.; Alam, M.; Freitas, T.
 Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000
 A.Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ebdardt, H.; Lowe, T.M.; Li

A;Title: Genome sequence of *Halobacterium* species NRC-1.
A;Reference number: A84160; MUID:20504483; PMID:11016950
A;Accession: B84357
A;Status: Preliminary
A;Molecule type: DNA
A;Residues: 1-474 <STO>
A;Cross-references: UNIPROT:Q9HNU8; GB:A8004437; NID:gi10581491; PIDN:AMG2022.1; GSPDB:C
C;Genetic:
A;Gene: *serS*
C;Superfamily: serine-tRNA ligase

Query Match 38.7%; Score 46; DB 2; Length 474;
Best Local Similarity 41.2%; Pred. No. 29;
Matches 7; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 3 YQFGHNSVDFPEDTL 19
: : | | | : : | |
Db 234 AYRIGENDADYDDDL 250

RESULT 13
C84965
oxoglutarate dehydrogenase (lipoamide) (EC 1.2.4.2) e1 component [imported] - *Buchnera* sp.
C;Species: *Buchnera* sp.
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 23-Mar-2001
C;Accession: C84965
R;Shigenobu, S.; Watanabe, H.; Hattori, M.; Sakaki, Y.; Ishikawa, H.
Nature 407, 81-86, 2000
A;Title: Genome sequence of the endocellular bacterial symbiont of aphids *Buchnera* sp. A
A;Reference number: A84930; MUID:20445173; PMID:10993077
A;Accession: C84965
A;Status: Preliminary
A;Molecule type: DNA
A;Residues: 1-909 <STO>
A;Cross-references: GB:AP00398; GSPDB:GN00144
A;Experimental source: strain APS
C;Genetic:
A;Gene: *sucA*; BU302
C;Superfamily: oxoglutarate dehydrogenase (lipoamide); thiamin pyrophosphate-binding dom
C;Keywords: oxidoreductase

Query Match 38.7%; Score 46; DB 2; Length 909;
Best Local Similarity 52.9%; Pred. No. 60;
Matches 9; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

QY 4 YQFGHNSVDFPEDTL 20
: : | | | | : : | | | |
Db 435 YRRNGHNEVDPSVTP 451

RESULT 14
S49156
HagC hemagglutinin protein - *Porphyromonas gingivalis*
C;Species: *Porphyromonas gingivalis*
C;Date: 16-Feb-1995 #sequence_revision 12-May-1995 #text_change 09-Jul-2004
C;Accession: S49156
R;Lepine, G.; Progulake-Fox, A.
submitted to the EMBL Data Library, November 1993
A;Description: Cloning and characterization of a third hemagglutinin gene from *Porphyromonas*
A;Reference number: S49156
A;Accession: S49156
A;Status: Preliminary
A;Molecule type: DNA
A;Residues: 1-350 <LEP>
A;Cross-references: UNIPROT:Q51830; EMBL:Z27394; NID:gs10187; PIDN:CAA81786.1; PID:gs101

Query Match 37.8%; Score 45; DB 2; Length 350;
Best Local Similarity 50.0%; Pred. No. 29;
Matches 9; Conservative 1; Mismatches 8; Indels 0; Gaps 0;

QY 4 YQFGHNSVDFPEDTL 21
: : | | | | : : | | | |
Db 291 YRINGEQLVVPEDEL 308

RESULT 15
S52213
HagB hemagglutinin protein - *Porphyromonas gingivalis*
C;Species: *Porphyromonas gingivalis*
C;Date: 07-May-1995 #sequence_revision 21-Jul-1995 #text_change 09-Jul-2004
C;Accession: S52213
R;Progulake-Fox, A.; Tumwaaron, S.; Lepine, G.; Whitlock, J.A.; Savett, D.A.; Ferretti, C.
submitted to the EMBL Data Library, July 1994
A;Description: The cloning, expression, and sequence analysis of a second *Porphyromonas* s
A;Reference number: S52213
A;Accession: S52213
A;Status: Preliminary
A;Molecule type: DNA
A;Residues: 1-350 <PRO>
A;Cross-references: UNIPROT:Q51828; EMBL:Z35494; NID:gs609182; PIDN:CAA84627.1; PID:gs60918

Query Match 37.8%; Score 45; DB 2; Length 350;
Best Local Similarity 50.0%; Pred. No. 29;
Matches 9; Conservative 1; Mismatches 8; Indels 0; Gaps 0;

QY 4 YQFGHNSVDFPEDTL 21
: : | | | | : : | | | |
Db 291 YRINGEQLVVPEDEL 308

Search completed: October 22, 2005, 04:13:56
Job time : 11.5465 secs

GenCore version 5.1.6
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OM protein - protein search, using SW model

Run on: October 22, 2005, 02:23:35 ; Search time 51.4314 Seconds
(without alignments)
209.087 Million cell updates/sec

Title: US-10-731-238-27
Perfect score: 119
Sequence: 1 KPSYQFGGHSVDPEDTLRK 21

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_03:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	111	93.3	1018	1	FNBA_STPAU	P14738 staphylococ
2	108	90.8	961	2	Q99RD3	Q99rd3 staphylococ
3	108	90.8	961	2	Q7A3J8	Q7a3j8 staphylococ
4	108	90.8	965	2	Q6GDU5	Q6gd5 staphylococ
5	108	90.8	1015	2	Q8NUT7	Q8nu7 staphylococ
6	108	90.8	1015	2	Q6G6H3	Q6g6h3 staphylococ
7	108	90.8	1038	2	Q99RD2	Q99rd2 staphylococ
8	108	90.8	1038	2	Q7A3J7	Q7a3j7 staphylococ
9	105	86.2	952	2	Q9AEP9	Q9aep9 staphylococ
10	104	87.4	940	2	Q53682	Q53682 staphylococ
11	104	87.4	943	2	Q8NUT8	Q8nu8 staphylococ
12	104	87.4	957	2	Q6G6H4	Q6g6h4 staphylococ
13	53	44.5	497	2	Q9FPU7	Q9fpu7 brasiica na
14	52.5	44.1	417	2	Q69948	Q69948 streptomyce
15	52	43.7	288	2	Q7P048	Q7p048 chromobacte
16	52	43.7	705	2	Q9HMF6	Q9hmf6 halobacteri
17	51	42.9	151	2	Q920M1	Q92qm1 rhicobium m
18	49	41.2	123	2	Q38257	Q38257 lactococcu
19	49	41.2	285	2	Q08866	Q08866 carassius a
20	49	41.2	249	2	Q6FZ83	Q6fz83 bartonella
21	49	41.2	638	2	Q7SGV4	Q7sgv4 neurospora
22	49	41.2	731	2	Q9KKE8	Q9kek8 streptococ
23	49	41.2	731	2	Q8E0Q5	Q8e0q5 streptococ
24	49	41.2	731	2	Q8E6C3	Q8e6c3 streptococ
25	49	41.2	1726	2	Q6G4Z9	Q6g4z9 bartonella
26	48	40.3	319	2	Q9SYW6	Q9syw6 gossypium h
27	48	40.3	326	2	Q8LSC8	Q8lsc8 gossypium h
28	48	40.3	354	2	Q6V7K6	Q6v7k6 trypanosoma
29	48	40.3	486	2	Q9LVF0	Q9lvf0 arbidopsia
30	48	40.3	1234	2	Q8R0N7	Q8rqn7 corynebacte
31	48	40.3	1257	2	P96746	P96746 corynebacte

32	48	40.3	1257	2	Q8NRG3	Q8nrg3 corynebacte
33	47.5	39.9	232	2	Q64QV5	Q64qv5 bacteroides
34	47	39.5	138	1	HFB_RALSO	Q8f0y3 ralsomia s
35	47	39.5	467	2	Q75HB3	Q75hb3 oryza sativ
36	47	39.5	933	2	Q8SSA9	Q8ssa9 encephalito
37	47	39.5	973	2	Q49541	Q49541 arabidopsis
38	47	39.5	1008	2	Q623X5	Q623x5 oryza sativ
39	47	39.5	1009	2	Q9M2T8	Q9m2t8 arabidopsis
40	47	39.5	1013	2	Q7PIB2	Q7pib2 anophelae g
41	47	39.5	1017	2	Q84VW8	Q84vw8 arabidopsis
42	47	39.5	1018	2	Q7PIB4	Q7pib4 anophelae g
43	47	39.5	1025	2	Q9FLH2	Q9flh2 arabidopsis
44	47	39.5	1027	2	Q9ZRO2	Q9zrq2 arabidopsis
45	47	39.5	1043	2	Q7Q5L5	Q7q5l5 anophelae g

ALIGNMENTS

```

RESULT 1
FNBA_STPAU          STANDARD:      PRT; 1018 AA.
ID      FNBA_STPAU
AC      P14738;
DT      01-APR-1990 (Rel. 14, Created)
DT      01-APR-1990 (Rel. 14, Last sequence update)
DT      25-OCT-2004 (Rel. 45, Last annotation update)
DE      Fibronectin-binding protein precursor (FNBP).
GN      Name=fnba;
OS      Staphylococcus aureus.
OC      Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX      NCBI_TaxId=1280;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN=NCTC 8325-4;
RX      MEDLINE=89098998; PubMed=2521391;
RA      Signaes C., Raucel G., Joensson K., Lindgren P.-E.,
      Anantharamiah G.M., Hoesok M., Lindberg M.;
      "Nucleotide sequence of the gene for a fibronectin-binding protein
      from Staphylococcus aureus: use of this peptide sequence in the
      synthesis of biologically active peptides.";
      Proc. Natl. Acad. Sci. U.S.A. 86:699-703(1989).
RT      -!- FUNCTION: The ability of bacteria to bind fibronectin has been
      proposed as a virulence factor enabling bacteria to colonize wound
      tissues and blood clots. Binding of plasma fibronectin to the
      bacterial surface might block adhesion receptors on S.aureus, thus
      representing an important defense mechanism against tissue
      invasion.
      -!- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
      an amide bond (Potential).
CC      -----
CC      This SWISS-PROT entry is copyright. It is produced through a collaboration
CC      between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC      the European Bioinformatics Institute. There are no restrictions on its
CC      use by non-profit institutions as long as its content is in no way
CC      modified and this statement is not removed. Usage by and for commercial
CC      entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC      or send an email to license@isb-sib.ch).
CC      -----
CC      EMBL: J04151; AAA26632.1; -
CC      InterPro: IPR004237; Fn_bind.
CC      InterPro: IPR005877; Gpos_Y5IRK.
CC      InterPro: IPR001899; Gram_pos_anchor.
CC      Pfam: PF02986; Fn_bind; 1.
CC      Pfam: PF00746; Gram_pos_anchor; 1.
CC      Pfam: PF04650; Y5IRK_signal; 1.
CC      TIGRPFAMS: TIGR01167; LpYTG_anchor; 1.
CC      TIGRPFAMS: TIGR01168; Y5IRK_signal; 1.
CC      PROSITE: PS50847; GRAM_POS_ANCHORING; 1.
CC      Cell adhesion; Cell wall; Peptidoglycan-anchor; Repeat; Signal;
CC      Virulence.
CC      FT      SIGNAL      1      36
CC      CHAIN      37      985      Fibronectin-binding protein.
CC      PROPEP      986      1018      Removed by sortase (Potential).

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FT REPEAT 545 574 B-1.
FT REPEAT 575 604 B-2.
FT DOMAIN 745 878 4 X approximate tandem repeats,
  fibronectin-binding domain.
FT REPEAT 745 782 D-1.
FT REPEAT 783 820 D-2.
FT REPEAT 821 859 D-3.
FT REPEAT 860 878 D-4 (incomplete).
FT DOMAIN 879 948 5 X tandem repeats, Pro-rich (WR).
FT REPEAT 879 892 WR 1.
FT REPEAT 893 906 WR 2.
FT REPEAT 907 920 WR 3.
FT REPEAT 921 934 WR 4.
FT REPEAT 935 948 WR 5.
FT SITE 982 986 LPTXG sorting signal (Potential).
FT MOD_RSS 985 985 Pentaglycyl murein peptidoglycan amidated
  chreonine (Potential).
SQ SEQUENCE 1018 AA; 11780 MW; 58175E0020E81F1F CRC64;

Query Match 93.3%; Score 111; DB 1; Length 1018;
Best Local Similarity 95.2%; Fred. No. 2.8e-08;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KPSYQFGGHSVDPEDTLPK 21
Db 837 KPSYQFGGHSVDPEDTLPK 857

RESULT 2
Q99RD3 PRELIMINARY; PRT; 961 AA.
AC Q99RD3
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DE 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE Fibronectin-binding protein homolog.
GN Name=fnb3; OrderedLocustNames=SAV2502;
OS Staphylococcus aureus (strain Mu50 / ATCC 700699).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=158879;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=21311952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2;
RX Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
  RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Iian J.-Q., Ito T.,
  RA Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosooyama A.,
  RA Mizutani-Ui Y., Takehashi N.K., Sawano T., Inoue R.-I., Kaito C.,
  RA Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
  RA Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
  RA Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
  RT "Whole genome sequencing of methicillin-resistant Staphylococcus
  aureus.";
  RL Lancet 357:1225-1240(2001).
  CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
  an amide bond (by similarity).
  CC EMBL; AP003365; BAB58664.1; -.
  CC PIR; G90053; G90053.
  DR HSSP; Q53653; 1N67.
  DR GO; GO:0009986; C:cell surface; IEA.
  DR GO; GO:0005618; C:cell wall; IEA.
  DR GO; GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
  DR GO; GO:0016020; C:membrane; IEA.
  DR GO; GO:0007155; P:cell adhesion; IEA.
  DR InterPro; IPR008966; Adhes_bact.
  DR InterPro; IPR004237; Fn_bind.
  DR InterPro; IPR005877; Gpos_YsIRK.
  DR Pfam; PF02986; Fn_bind; 1.
  DR Pfam; PF00746; Gram_pos_anchor; 1.
  DR Pfam; PF04650; YsIRK_signal; 1.
  DR TIGRFAMs; TIGR01167; LPTXG_anchor; 1.
  DR TIGRFAMs; TIGR01168; YsIRK_signal; 1.
  DR PROSITE; PS50847; GRAM_POS_ANCHORING; 1.
  KW Cell wall; Complete proteome; Peptidoglycan-anchor.
  SQ SEQUENCE 961 AA; 106010 MW; 364940F884DA4101 CRC64;
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DR PROSITE; PS50847; GRAM_POS_ANCHORING; 1.
KW Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ SEQUENCE 961 AA; 106010 MW; 364940F884EA4101 CRC64;

Query Match 90.8%; Score 108; DB 2; Length 961;
Best Local Similarity 90.5%; Fred. No. 7.7e-08;
Matches 19; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KPSYQFGGHSVDPEDTLPK 21
Db 784 KPSYQFGGHSVDPEDTLPK 804

RESULT 3
Q7A3J8 PRELIMINARY; PRT; 961 AA.
ID Q7A3J8
AC Q7A3J8
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DE 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE FnbB protein.
GN Name=fnbB; OrderedLocustNames=SA2290;
OS Staphylococcus aureus (strain N315).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=158879;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21311952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2;
RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
  RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Iian J.-Q., Ito T.,
  RA Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosooyama A.,
  RA Mizutani-Ui Y., Takehashi N.K., Sawano T., Inoue R.-I., Kaito C.,
  RA Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
  RA Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
  RA Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
  RT "Whole genome sequencing of methicillin-resistant Staphylococcus
  aureus.";
  RL Lancet 357:1225-1240(2001).
  CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
  an amide bond (by similarity).
  CC EMBL; AP003137; BAB43593.1; -.
  DR GO; GO:0009986; C:cell surface; IEA.
  DR GO; GO:0005618; C:cell wall; IEA.
  DR GO; GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
  DR GO; GO:0016020; C:membrane; IEA.
  DR GO; GO:0007155; P:cell adhesion; IEA.
  DR InterPro; IPR008966; Adhes_bact.
  DR InterPro; IPR004237; Fn_bind.
  DR InterPro; IPR005877; Gpos_YsIRK.
  DR InterPro; IPR001899; Gram_pos_anchor.
  DR Pfam; PF02986; Fn_bind; 1.
  DR Pfam; PF00746; Gram_pos_anchor; 1.
  DR Pfam; PF04650; YsIRK_signal; 1.
  DR TIGRFAMs; TIGR01167; LPTXG_anchor; 1.
  DR TIGRFAMs; TIGR01168; YsIRK_signal; 1.
  DR PROSITE; PS50847; GRAM_POS_ANCHORING; 1.
  KW Cell wall; Complete proteome; Peptidoglycan-anchor.
  SQ SEQUENCE 961 AA; 106010 MW; 364940F884DA4101 CRC64;

Query Match 90.8%; Score 108; DB 2; Length 961;
Best Local Similarity 90.5%; Fred. No. 7.7e-08;
Matches 19; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KPSYQFGGHSVDPEDTLPK 21
Db 784 KPSYQFGGHSVDPEDTLPK 804

RESULT 4
Q6GDUS PRELIMINARY; PRT; 965 AA.
ID Q6GDUS
AC Q6GDUS
DT 05-JUL-2004 (TREMBlrel. 27, Created)
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DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE Fibronectin-binding protein.
GN Name=fibA; OrderedLocusNames=SR2580;
OS Staphylococcus aureus (strain MRSA252).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=282458;
RN [1]
RP SEQUENCE FROM N.A.
RX Holden M.T.G., Fell E.J., Lindsey J.A., Peacock S.J., Day N.P.J.,
  Enright M.C., Foster T.J., Moore C.E., Hurst L., Atkin R., Barron A.,
  Bason N., Bentley S.D., Chillingworth C., Chillingworth T.,
  Churcher C., Clark L., Cotton C., Cronin A., Doggett J., Dowd L.,
  Felwell T., Hance Z., Harris B., Hauser H., Holtroyd S., Jagsels K.,
  James K.D., Leonard N., Line A., Mayes R., Moulé S., Mungall K.,
  Ormond D., Quail M.A., Rabinowitch E., Rutherford K.M., Sanders M.,
  Sharp S., Simmonds M., Stevens K., Whitehead S., Barrell B.G.,
  Spratt B.G., Parkhill J.;
  PubMed=15213324; DOI=10.1073/pnas.0402521101;
  EMBL; AP004830; BAB96286.1; -.
DR GO; GO:0009986; C:cell surface; IEA.
DR GO; GO:0005618; C:cell wall; IEA.
DR GO; GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0007155; P:cell adhesion; IEA.
DR InterPro; IPR008966; Adhes_bact.
DR InterPro; IPR004237; Fn_bind.
DR InterPro; IPR005877; Gpos_YsIRK.
DR InterPro; IPR001899; Gram_pos_anchor.
DR Pfam; PF02986; Fn_bind; 1.
DR Pfam; PF00746; Gram_pos_anchor; 1.
DR Pfam; PF04650; YsIRK_signal; 1.
DR TIGRFAMs; TIGR01167; LPXTG_anchor; 1.
DR TIGRFAMs; TIGR01168; YsIRK_signal; 1.
DR PROSITE; PS50847; GRAM_POS_ANCHORING; 1.
KW Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ SEQUENCE 965 AA; 10581 MW; 2982E312164D551 CRC64;

Query Match          90.8%; Score 108; DB 2; Length 965;
Best Local Similarity 90.5%; Pred. No. 7.7e-08;
Matches 19; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 KPSYFGGHSYDPEDTLPK 21
DB 802 KENYOFGGHSYDPEDTLPK 822

RESULT 5
Q8NUU7 PRELIMINARY; PRT; 1015 AA.
AC Q8NUU7;
DT 01-OCT-2002 (TREMBlrel. 22, Created)
DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Fmb protein.
GN Name=fmb; OrderedLocusNames=NM2421;
OS Staphylococcus aureus (strain NM2).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=196620;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=NM2;
  MEDLINE=220404717; PubMed=12044378; DOI=10.1016/S0140-6736(02)08713-5;
  Baba T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Oguchi A.,
  Nagai Y., Iwama N., Asano K., Naimi T., Kuroda H., Cui L.,
  Yamamoto K., Hiramatsu K.;
  Genome and virulence determinants of high virulence community-
  RT acquired MRSA.
  Lancet 359:1819-1827(2002).

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CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC an amide bond (by similarity).
DE EMBL; AP004830; BAB96286.1; -.
DR GO; GO:0009986; C:cell surface; IEA.
DR GO; GO:0005618; C:cell wall; IEA.
DR GO; GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0007155; P:cell adhesion; IEA.
DR InterPro; IPR008966; Adhes_bact.
DR InterPro; IPR004237; Fn_bind.
DR InterPro; IPR005877; Gpos_YsIRK.
DR InterPro; IPR001899; Gram_pos_anchor.
DR Pfam; PF02986; Fn_bind; 1.
DR Pfam; PF00746; Gram_pos_anchor; 1.
DR Pfam; PF04650; YsIRK_signal; 1.
DR TIGRFAMs; TIGR01167; LPXTG_anchor; 1.
DR TIGRFAMs; TIGR01168; YsIRK_signal; 1.
DR PROSITE; PS50847; GRAM_POS_ANCHORING; 1.
KW Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ SEQUENCE 1015 AA; 111145 MW; D0F281BB64D44D2 CRC64;

Query Match          90.8%; Score 108; DB 2; Length 1015;
Best Local Similarity 90.5%; Pred. No. 8.2e-08;
Matches 19; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 KPSYFGGHSYDPEDTLPK 21
DB 838 KENYOFGGHSYDPEDTLPK 858

RESULT 6
Q6G6H3 PRELIMINARY; PRT; 1015 AA.
AC Q6G6H3;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE Fibronectin-binding protein.
GN Name=fibA; OrderedLocusNames=SA52388;
OS Staphylococcus aureus (strain MSSA476).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=282459;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=15213324; DOI=10.1073/pnas.0402521101;
  Holden M.T.G., Fell E.J., Lindsey J.A., Peacock S.J., Day N.P.J.,
  Enright M.C., Foster T.J., Moore C.E., Hurst L., Atkin R., Barron A.,
  Bason N., Bentley S.D., Chillingworth C., Chillingworth T.,
  Churcher C., Clark L., Cotton C., Cronin A., Doggett J., Dowd L.,
  Felwell T., Hance Z., Harris B., Hauser H., Holtroyd S., Jagsels K.,
  James K.D., Leonard N., Line A., Mayes R., Moulé S., Mungall K.,
  Ormond D., Quail M.A., Rabinowitch E., Rutherford K.M., Sanders M.,
  Sharp S., Simmonds M., Stevens K., Whitehead S., Barrell B.G.,
  Spratt B.G., Parkhill J.;
  PubMed=15213324; DOI=10.1073/pnas.0402521101;
  EMBL; AP004830; BAB96286.1; -.
DR GO; GO:0009986; C:cell surface; IEA.
DR GO; GO:0005618; C:cell wall; IEA.
DR GO; GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0007155; P:cell adhesion; IEA.
DR InterPro; IPR008966; Adhes_bact.
DR InterPro; IPR004237; Fn_bind.
DR InterPro; IPR005877; Gpos_YsIRK.
DR InterPro; IPR001899; Gram_pos_anchor.
DR Pfam; PF02986; Fn_bind; 1.
DR Pfam; PF00746; Gram_pos_anchor; 1.
DR Pfam; PF04650; YsIRK_signal; 1.
DR TIGRFAMs; TIGR01167; LPXTG_anchor; 1.

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DR  TIGRFAMs; TIGR01168; YSIRK_signal; 1.
DR  PROSITE; PS50847; GRAM_POS_ANCHORING; 1.
DR  Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ  SEQUENCE 1015 AA; 111145 MW; D0F9281BB64D44D2 CRC64;

Query Match 90.8%; Score 108; DB 2; Length 1015;
Best Local Similarity 90.5%; Pred. No. 8.2e-08;
Matches 19; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KPSYQFGGHSVDFEEDTLPK 21
Db 838 KPNYQFGGHSVDFEEDTLPK 858

RESULT 7
Q999RD2 PRELIMINARY; PRT; 1038 AA.
ID 0999RD2
AC 0999RD2;
DT 01-JUN-2001 (TReMBLrel. 17, Created)
DT 01-JUN-2001 (TReMBLrel. 17, Last sequence update)
DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)
DE Fibronectin-binding protein homolog.
GN Name=fnb; OrderedLocustNames=SAV2503;
OS Staphylococcus aureus (strain Mu50 / ATCC 700699).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=158878;
[1]
SEQUENCE FROM N.A.
RP STRAIN=Mu50 / ATCC 700699;
RX MEDLINE=21311952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2;
RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Iian J.-Q., Ito T.,
RA Kanamori M., Matsunaru H., Maruyama A., Murakami H., Hoshiyama A.,
RA Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
RA Sekimizu K., Hiraoka H., Kuhara S., Goto S., Yabuzaki J.,
RA Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
RA Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
RT "Whole genome sequencing of methicillin-resistant Staphylococcus
RT aureus.";
RL Lancet 357:1225-1240(2001).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC an amide bond (By similarity).
DR EMBL; AP003137; BAB43594.1; -.
DR PIR; H90053; H90053.
DR GO; GO:0009986; C:cell surface; IEA.
DR GO; GO:0005618; C:cell wall; IEA.
DR GO; GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0007155; P:cell adhesion; IEA.
DR InterPro; IPR008966; Adhes_bact.
DR InterPro; IPR004237; Fn_bind.
DR InterPro; IPR005877; GPos_YSIRK.
DR InterPro; IPR001899; Gram_pos_anchor.
DR Pfam; PF02986; Fn_bind; 1.
DR Pfam; PF04650; YSIRK_signal; 1.
DR TIGRFAMs; TIGR01167; LpxTG_anchor; 1.
DR TIGRFAMs; TIGR01168; YSIRK_signal; 1.
DR PROSITE; PS50847; GRAM_POS_ANCHORING; 1.
DR Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ SEQUENCE 1038 AA; 113618 MW; 666BF6B2BFBEB12 CRC64;

Query Match 90.8%; Score 108; DB 2; Length 1038;
Best Local Similarity 90.5%; Pred. No. 8.4e-08;
Matches 19; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KPSYQFGGHSVDFEEDTLPK 21
Db 833 KPNYQFGGHSVDFEEDTLPK 853

RESULT 8
Q7A3J7 PRELIMINARY; PRT; 1038 AA.
ID 07A3J7
AC 07A3J7;
DT 05-JUL-2004 (TReMBLrel. 27, Created)
DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TReMBLrel. 27, Last annotation update)
DE Fnb protein.
GN Name=fnb; OrderedLocustNames=SA2291;
OS Staphylococcus aureus (strain N315).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=158879;
[1]
SEQUENCE FROM N.A.
RP STRAIN=CMRSA-1;
RX MEDLINE=21246681; PubMed=11349041;
RX DOI=10.1128/IAI.69.6.3791-3799.2001;
RA Rice K., Huesca M., Vaz D., McGavin M.D.;
RT "Variance in fibronectin binding and fnb locus polymorphisms in a
Staphylococcus aureus: identification of antigenic variation in a

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ID 07A3J7 PRELIMINARY; PRT; 1038 AA.
AC 07A3J7;
DT 05-JUL-2004 (TReMBLrel. 27, Created)
DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TReMBLrel. 27, Last annotation update)
DE Fnb protein.
GN Name=fnb; OrderedLocustNames=SA2291;
OS Staphylococcus aureus (strain N315).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=158879;
[1]
SEQUENCE FROM N.A.
RP STRAIN=CMRSA-1;
RX MEDLINE=21246681; PubMed=11349041;
RX DOI=10.1128/IAI.69.6.3791-3799.2001;
RA Rice K., Huesca M., Vaz D., McGavin M.D.;
RT "Variance in fibronectin binding and fnb locus polymorphisms in a
Staphylococcus aureus: identification of antigenic variation in a

Query Match 90.8%; Score 108; DB 2; Length 1038;
Best Local Similarity 90.5%; Pred. No. 8.4e-08;
Matches 19; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KPSYQFGGHSVDFEEDTLPK 21
Db 833 KPNYQFGGHSVDFEEDTLPK 853

RESULT 9
Q9AEP9 PRELIMINARY; PRT; 152 AA.
ID 09AEP9
AC 09AEP9;
DT 01-JUN-2001 (TReMBLrel. 17, Created)
DT 01-JUN-2001 (TReMBLrel. 17, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE Fibronectin-binding protein (fragment).
GN Name=fnb;
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1280;
[1]
SEQUENCE FROM N.A.
RP STRAIN=CMRSA-1;
RX MEDLINE=21246681; PubMed=11349041;
RX DOI=10.1128/IAI.69.6.3791-3799.2001;
RA Rice K., Huesca M., Vaz D., McGavin M.D.;
RT "Variance in fibronectin binding and fnb locus polymorphisms in a
Staphylococcus aureus: identification of antigenic variation in a

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RT fibronectin binding protein adhesin of the epidemic CMRSA-1 strain of
 RT methicillin-resistant *S. aureus*.
 RL Infect. Immun. 69:3791-3799(2001).
 DR EMBL: AY029184; AAK31588.1; --
 FT NON_TER 1 152
 FT NON_TER 1 152
 SO SEQUENCE 152 AA; 17193 MW; CFA3913CB11C025 CRC64;

Query Match 88.2%; Score 105; DB 2; Length 152;
 Best Local Similarity 85.7%; Pred. No. 2.8e-08;
 Matches 18; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 KPSYQFGHNSVDFPBDTLPK 21
 Db 130 KPSYQFGHNSVDFPBDTLPK 150

RESULT 10
 O53682 PRELIMINARY; PRT; 940 AA.
 AC O53682;
 DT 01-NOV-1996 (TREMblrel. 01, Created)
 DT 01-NOV-1996 (TREMblrel. 01, Last sequence update)
 DT 01-MAR-2004 (TREMblrel. 26, Last annotation update)
 DE Fibronectin binding protein B.
 GN Name=fnbB;
 OS Staphylococcus aureus.
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 OX NCBI_TaxId=1280;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=8325-4;
 RX MEDLINE=92111475; PubMed=1837266;
 RA Johnson K., Signas C., Muller H.P., Landberg M.;
 RT "Two different genes encode fibronectin binding proteins in
 Staphylococcus aureus. The complete nucleotide sequence and
 RT characterization of the second gene."
 RL Eur. J. Biochem. 202:1041-1048(1991).
 CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
 an amide bond (By similarity).
 DR EMBL: X62982; CAA44726.1; --
 DR PIR: S19702; S19702.
 DR HSP: O53653; IN67.
 DR GO: GO:0009986; C:cell surface; IEA.
 DR GO: GO:0005618; C:cell wall (sensu Gram-positive Bacteria); IEA.
 DR GO: GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
 DR GO: GO:0016020; C:membrane; IEA.
 DR GO: GO:007155; P:cell adhesion; IEA.
 DR InterPro: IPR008966; Adhes_Bact.
 DR InterPro: IPR004237; Fn_bind.
 DR InterPro: IPR005877; Gpos_YsIRK.
 DR InterPro: IPR001899; Gram_pos_anchor.
 DR Pfam: PF02986; Fn_bind; 2.
 DR Pfam: PF00746; Gram_pos_anchor; 1.
 DR Pfam: PF04650; YsIRK_signal; 1.
 DR TIGRFAms: TIGR01167; LPXTG_anchor; 1.
 DR TIGRFAms: TIGR01168; YsIRK_signal; 1.
 DR PROSITE: PS50847; GRAM_POS_ANCHORING; 1.
 KW Cell wall; Peptidoglycan-anchor.
 SQ SEQUENCE 940 AA; 10355 MW; E35FBBCA907A5345 CRC64;

Query Match 87.4%; Score 104; DB 2; Length 940;
 Best Local Similarity 85.7%; Pred. No. 3.2e-07;
 Matches 18; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KPSYQFGHNSVDFPBDTLPK 21
 Db 773 KPSYQFGHNSVDFPBDTLPK 793
 RESULT 11
 Q8NTU8 PRELIMINARY; PRT; 943 AA.

AC Q8NTU8;
 DT 01-OCT-2002 (TREMblrel. 22, Created)
 DT 01-OCT-2002 (TREMblrel. 22, Last sequence update)
 DT 01-OCT-2003 (TREMblrel. 25, Last annotation update)
 DE FnBb protein.
 GN Name=fnbB; OrderedLocNames=MM2420;
 OS Staphylococcus aureus (strain MM2).
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 OX NCBI_TaxId=196620;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=MM2;
 RX MEDLINE=224040717; PubMed=12044378; DOI=10.1016/S0140-6736(02)08713-5;
 RA Baba T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Oguchi A.,
 RA Nagai Y., Iwano N., Asano K., Naito T., Kuroda H., Cui L.,
 RA Yamamoto K., Hiramatsu K.;
 RT "Genome and virulence determinants of high virulence community-
 RT acquired MRSA."
 RL Lancet 359:1819-1827(2002).
 CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
 an amide bond (By similarity).
 DR EMBL: AP004830; BAB96285.1; --
 DR HSP: O53653; IN67.
 DR GO: GO:0009986; C:cell surface; IEA.
 DR GO: GO:0005618; C:cell wall; IEA.
 DR GO: GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
 DR GO: GO:0016020; C:membrane; IEA.
 DR GO: GO:007155; P:cell adhesion; IEA.
 DR InterPro: IPR008966; Adhes_Bact.
 DR InterPro: IPR004237; Fn_bind.
 DR InterPro: IPR005877; Gpos_YsIRK.
 DR InterPro: IPR001899; Gram_pos_anchor.
 DR Pfam: PF02986; Fn_bind; 1.
 DR Pfam: PF00746; Gram_pos_anchor; 1.
 DR Pfam: PF04650; YsIRK_signal; 1.
 DR TIGRFAms: TIGR01167; LPXTG_anchor; 1.
 DR TIGRFAms: TIGR01168; YsIRK_signal; 1.
 DR PROSITE: PS50847; GRAM_POS_ANCHORING; 1.
 KW Cell wall; Complete proteome; Peptidoglycan-anchor.
 SQ SEQUENCE 943 AA; 104537 MW; DA8A5F31947E1B6A CRC64;

Query Match 87.4%; Score 104; DB 2; Length 943;
 Best Local Similarity 85.7%; Pred. No. 3.2e-07;
 Matches 18; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KPSYQFGHNSVDFPBDTLPK 21
 Db 780 KPSYQFGHNSVDFPBDTLPK 800

RESULT 12
 O6G6H4 PRELIMINARY; PRT; 957 AA.
 AC O6G6H4;
 DT 05-JUL-2004 (TREMblrel. 27, Created)
 DT 05-JUL-2004 (TREMblrel. 27, Last sequence update)
 DT 05-JUL-2004 (TREMblrel. 27, Last annotation update)
 DE Fibronectin-binding protein.
 GN Name=fnbB; OrderedLocNames=SA52387;
 OS Staphylococcus aureus (strain MSSA476).
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 OX NCBI_TaxId=282459;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX PubMed=15213324; DOI=10.1073/pnas.0402521101;
 RA Holden M.T.G., Fell B.J., Lindsay J.A., Peacock S.J., Day N.P.J.,
 RA Enright M.C., Foster T.J., Moore C.E., Hurst L., Atkin R., Barron A.,
 RA Baason N., Bentley S.D., Chillingworth C., Chillingworth T., Dowd L.,
 RA Churcher C., Clark L., Cotton C., Cronin A., Doggett J., Dowd L.,
 RA Felwell T., Hance Z., Harris B., Hauser H., Holroyd S., Jagels K.,
 RA James K.D., Lennard N., Line A., Mayes R., Moulé S., Mungall K.,
 RA Ormond D., Quail M.A., Rabinowitch B., Rutherford K.M., Sanders M.,
 RA Sharp S., Simmonds M., Stevens K., Whitehead S., Barrett B.G.,

```
RA Spratt B.G., Parkhill J.;
RT "Complete genomes of two clinical Staphylococcus aureus strains:
RT evidence for the rapid evolution of virulence and drug resistance.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:9786-9791(2004).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC an amide bond (By similarity).
DR EMBL: BX571857; CAG4201.1; -.
DR GO: GO:0009986; C:cell surface; IEA.
DR GO: GO:0005618; C:cell wall; IEA.
DR GO: GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO: GO:0016020; C:membrane; IEA.
DR GO: GO:0007155; P:cell adhesion; IEA.
DR InterPro: IPR008966; Adhes_bact.
DR InterPro: IPR004237; Fn_bind.
DR InterPro: IPR005877; Gpos_SIRK.
DR InterPro: IPR001899; Gram_pos_anchor.
DR Pfam: PF02986; Fn_bind_1.
DR Pfam: PF00746; Gram_pos_anchor_1.
DR Pfam: PF04650; YSIRK_signal_1.
DR TIGRfams: TIGR01167; LPSATG_anchor_1.
DR TIGRfams: TIGR01168; YSIRK_signal_1.
DR PROSITE: PS50847; GRAM_POS_ANCHORING_1.
KW Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ SEQUENCE 957 AA; 105980 MW; 28F8BA7FFDFD3EAF CRC64;

Query Match 87.4%; Score 104; DB 2; Length 957;
Best Local Similarity 85.7%; Pred. No. 3; 2e-07;
Matches 18; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Oy 1 KPSYFGGHSVDPEDTLPK 21
Db 780 KPNYFGGHSVDPEDTLPQ 800

RESULT 13
O9FYU7 PRELIMINARY; PRT; 497 AA.
AC O9FYU7;
DT 01-MAR-2001 (TREMBlrel. 16; Created)
DT 01-MAR-2001 (TREMBlrel. 16; Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26; Last annotation update)
DE UDP-glucose:sinapate glucosyltransferase (EC 2.4.1.120).
GN Name:SGT1;
OS Brassica napus (rape).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eucosids II; Brassicales; Brassicaceae; Brassica.
OX NCBI_TaxID=3708;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Cotyledon;
RX MEDLINE=21017286; PubMed=11144274;
RA Milkowski C., Baumert A., Strack D.;
RT "Cloning and heterologous expression of a rape cDNA encoding UDP-
RT glucose:sinapate glucosyltransferase.";
RL Planta 211:883-886(2000).
CC -1- SIMILARITY: Belongs to the UDP-glycosyltransferase family.
DR EMBL: AF287143; AAF98390.1; -.
DR GO: GO:0005284; F:sinapate 1-glycosyltransferase activity; IEA.
DR GO: GO:0016758; F:transferase activity, transferring hexosyl . . .; IEA.
DR GO: GO:0008157; P:metabolism; IEA.
DR InterPro: IPR002213; UDP_glucose_trans.
DR Pfam: PF00201; UDPGT_1.
DR PROSITE: PS00375; UDPGT_1.
KW Glycosyltransferase; Transferase.
SQ SEQUENCE 497 AA; 55970 MW; 4D3312D921B7887 CRC64;

Query Match 44.5%; Score 53; DB 2; Length 497;
Best Local Similarity 52.6%; Pred. No. 14;
Matches 10; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

Oy 3 SYVFGGHSVDPEDTLPK 21
||:|||||:|
```

```
Db 157 SYYYNHKLVDPETETDPK 175

RESULT 14
O69948 PRELIMINARY; PRT; 417 AA.
ID O69948
AC O69948;
DT 01-AUG-1998 (TREMBlrel. 07; Created)
DT 01-AUG-1998 (TREMBlrel. 07; Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24; Last annotation update)
DE Putative secreted protein.
GN ORFNames=SC3F9.08;
OS Streptomyces coelicolor.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Streptomycinae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=1902;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=A3(2) / M145;
RX MEDLINE=2196410; PubMed=12000953; DOI=10.1038/417141a;
RA Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,
RA Thompson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,
RA Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
RA Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
RA Huang C.-H., Kieser T., Larke L., Murphy L.D., Oliver K., O'Neill S.,
RA Rabinowitsch E., Rajandream M.A., Rutherford K.M., Rutter S.,
RA Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,
RA Warren T., Wietzorrek A., Woodward J.R., Barrall B.G., Parkhill J.,
RA Hopwood D.A.;
RT "Complete genome sequence of the model actinomycete Streptomyces
RT coelicolor A3(2).";
RL Nature 417:141-147(2002).
DR EMBL: AL939128; CAI19631.1; -.
DR PIR: T34930; T34930.
DR GO: GO:0004512; F:inositol-3-phosphate synthase activity; IEA.
DR GO: GO:0006021; P:myo-inositol biosynthesis; IEA.
DR GO: GO:0008654; P:phospholipid biosynthesis; IEA.
DR InterPro: IPR002587; Inos-1-P_synth.
DR Pfam: PF01658; Inos-1-P_synth_1.
KW Complete proteome.
SQ SEQUENCE 417 AA; 41769 MW; D3B86872FADF5E4 CRC64;

Query Match 44.1%; Score 52.5; DB 2; Length 417;
Best Local Similarity 55.0%; Pred. No. 13;
Matches 11; Conservative 3; Mismatches 3; Indels 3; Gaps 1;

Oy 2 PSYFGGHSVDPEDTLPK 21
Db 62 PALVFGGHDTVDCP---LPK 78

RESULT 15
ID Q7P048 PRELIMINARY; PRT; 288 AA.
AC Q7P048;
DT 01-MAR-2004 (TREMBlrel. 26; Created)
DT 01-MAR-2004 (TREMBlrel. 26; Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26; Last annotation update)
DE Probable transcriptional regulator LysR family.
GN OrderedLocusNames=CV0720;
OS Chromobacterium violaceum.
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Chromobacterium.
OX NCBI_TaxID=536;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 12472 / DSM 30191;
RX MEDLINE=22882880; PubMed=14500782; DOI=10.1073/pnas.1832124100;
RA Vasconcelos A.T.R., de Almeida D.F., Hungria M., Guimaraes C.T.,
RA Antonio R.V., Almeida F.C., de Almeida L.G.P., de Almeida R.,
RA Alves-Gomes J.A., Andrade E.M., Aratijo J., de Araujo W.F.F.,
RA Assolfi-Filho S., Azevedo V., Baptista A.J., Bataus L.A.M.,
RA Batista J.S., Belo A., van den Berg C., Bogo M., Bonatto S.,
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RA Bordignon J., Brigido M.M., Brito C.A., Brocchi M., Burily H.A.,
 RA Camargo A.A., Cardoso D.D.P., Carneiro N.P., Carraro D.M.,
 RA Carvalho C.M.B., Cascardo J.C.M., Cavada B.S., Chueire L.M.O.,
 RA Creczynski-Pasa T.B., Cunha-Junior N.C., Fagundes N., Falcão C.L.,
 RA Fancinatti F., Farias I.P., Felipe M.S.S., Ferrari L.P., Ferro J.A.,
 RA Ferro M.I.T., Franco G.R., Freitas N.S.A., Furian L.R.,
 RA Gazzinelli R.T., Gomes E.A., Gonçalves P.R., Grangeiro T.B.,
 RA Grattapaglia D., Gilsard E.C., Hanna E.S., Jardim S.N., Laurino J.,
 RA Leoi L.C.T., Lima L.F.A., Loureiro M.F., Lyra M.C.C.P.,
 RA Madeira H.M.F., Manfio G.P., Maranhão A.O., Martins W.S.,
 RA di Mauro S.M.Z., de Medeiros S.R.B., Meisner R.V., Moreira M.A.M.,
 RA Nascimento F.F., Nicolae M.F., Oliveira J.G., Oliveira S.C.,
 RA Paixão R.F.C., Parente J.A., Pedrosa F.O., Pena S.D.U., Pereira J.O.,
 RA Pereira M., Pinto L.S.R.C., Pinto L.S., Porto J.I.R., Potrich D.P.,
 RA Ramalho-Neto C.E., Reis A.M.M., Rigo L.U., Rondinelli E.,
 RA Santos E.B.P., Santos F.R., Schneider M.P.C., Seunemann H.N.,
 RA Silva A.M.R., da Silva A.L.C., Silva D.W., Silva R., Simoes I.C.,
 RA Simon D., Soares C.M.A., Soares R.B.A., Souza E.M., Souza K.R.L.,
 RA Souza R.C., Steffens M.B.R., Steindel M., Teixeira S.R., Urmenyi T.,
 RA Vettore A., Wasseem R., Zaha A., Simpson A.J.G.,
 RT "The complete genome sequence of *Chromobacterium violaceum* reveals
 RT remarkable and exploitable bacterial adaptability";
 RT Proc. Natl. Acad. Sci. U.S.A. 100:11660-11665(2003).
 RL EMBL; AE016912; AAQ58396.1; -.
 DR GO; GO:0003700; F:transcription factor activity; IEA.
 DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
 DR InterPro; IPR000847; HTH_LYSR.
 DR InterPro; IPR005119; LysR_subf.
 DR InterPro; IPR009058; wing_hlx_DNA_bnd.
 DR Pfam; PF00126; HTH_1; 1.
 DR Pfam; PF03466; LysR_substrate; 1.
 DR PROSITE; PS50931; HTH_LYSR; 1.
 KW Complete proteome.
 SQ SEQUENCE 288 AA; 31603 MW; 12330EB2F0175BD1 CRC64;

Query Match 43.7%; Score 52; DB 2; Length 288;
 Best Local Similarity 45.0%; Pred. No. 11;
 Matches 9; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

QY 2 PSYQFGHNSVDPEDTLPK 21
 DB 179 PGDGFAGHLLMFPRDTVPR 198

Search completed: October 22, 2005, 04:10:18
 Job time : 53.4314 secs

11/11/11

CC streptococci, e.g. meningitis, otitis media, pneumonia, endocarditis,
 CC mastitis in cattle, abortion in horses and many others. Since the
 CC antibodies block binding of bacteria, they should be effective against
 CC antibiotic-resistant strains, and may replace antibiotic therapy or
 CC increase its effectiveness. Sequences AAW65670-90 represent a series of
 CC synthetic peptides based on the D3 repeat of *S. aureus* fibronectin
 CC binding protein A. They were synthesised to contain a proline residue at
 CC each position through the sequence (ie a proline scan)

XX
 SQ Sequence 21 AA;

Query Match 100.0%; Score 119; DB 2; Length 21;
 Best Local Similarity 100.0%; Pred. No. 1.2e-11;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KPSYQFGHNSVDFEPTLPK 21
 DB 1 KPSYQFGHNSVDFEPTLPK 21

RESULT 2
 AAW65665
 ID AAW65665 standard; peptide; 21 AA.
 AC AAW65665;
 XX
 DT 16-OCT-1998 (first entry)
 DE Fibronectin binding protein-derived peptide #9.
 XX
 XX microbial surface components recognising adhesive matrix molecule;
 KM MSCRAMM; fibronectin; fibronectin-binding protein; antibody; epitope;
 KM antibiotic; bacterial infection; antibiotic-resistant strain.
 OS Synthetic.
 OS Staphylococcus aureus.
 XX
 PN WO9831389-A2.
 PD 23-JUL-1998.
 XX
 PF 21-JAN-1998; 98WO-US001222.
 XX
 PR 21-JAN-1997; 97US-0036139P.
 XX
 PA (TEXA) UNIV TEXAS A & M SYSTEM.
 PI
 PI Hoseok M, Patti JM, House-Pompeo KL, Speciale P, Joh D;
 PI McGavin MJ;
 XX
 WP; 1998-413816/35.
 XX
 PT Antibody that binds to fibronectin-binding protein, preventing its
 PT binding to fibronectin - used to treat or prevent bacterial infection,
 PT especially by Staphylococci and Streptococci.
 PS
 PS Example 2; Page 92; 201pp; English.

XX The invention relates to antibodies that bind to a fibronectin-binding
 CC domain of a fibronectin-binding protein, and inhibit binding of the
 CC protein to fibronectin. Also claimed are: (1) isolated peptides of a
 CC fibronectin-binding protein that do not bind to fibronectin; (2) fusion
 CC protein containing at least one peptide of a fibronectin-binding protein
 CC linked to a second amino acid sequence; (3) nucleic acid encoding the
 CC isolated peptide of (1). Antibodies, the isolated peptides of (1) and the
 CC nucleic acids are all useful for immunisation (active or passive) and (by
 CC inhibiting binding of bacteria to fibronectin) for preventing or treating
 CC infection in humans or other animals, particularly by staphylococci or
 CC streptococci, e.g. meningitis, otitis media, pneumonia, endocarditis,
 CC mastitis in cattle, abortion in horses and many others. Since the
 CC antibodies block binding of bacteria, they should be effective against
 CC antibiotic-resistant strains, and may replace antibiotic therapy or
 CC increase its effectiveness. Sequences AAW65659-68 represent synthetic

CC epitopes from the fibronectin binding domains DU and D1-D4 of the S.
 CC aureus fbnA gene
 XX
 SQ Sequence 21 AA;

Query Match 93.3%; Score 111; DB 2; Length 21;
 Best Local Similarity 95.2%; Pred. No. 2.2e-10;
 Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KPSYQFGHNSVDFEPTLPK 21
 DB 1 KPSYQFGHNSVDFEPTLPK 21

RESULT 3
 AAR21340
 ID AAR21340 standard; peptide; 22 AA.
 AC AAR21340;
 XX
 DT 25-MAR-2003 (revised)
 DT 15-JUN-1992 (first entry)
 DE Fibronectin binding protein.
 DE FbBP; wound infection reduction; vaccination; mastitis;
 KM Staphylococcal infections; D3.
 KM
 XX Synthetic.
 OS
 PN WO9202555-A.
 XX
 PD 20-FEB-1992.
 XX
 PF 10-AUG-1990; 90SE-00002617.
 XX
 PR 10-AUG-1990; 90SE-00002617.
 XX
 PA (ALFA) ALFA LAVAL AGRIC INT AB.
 PI
 PI Hook M, McGavin M, Rauczi G;
 PI
 DR WP; 1992-080035/10.
 XX
 PT New fibronectin binding peptide - combines with fusion peptide to form
 PT large antigen, used in immunisation, diagnosis and for treating wounds.
 PS
 PS Claim 1; Page 22; 33pp; English.

XX The sequence comprises amino acids 17-33 of a tandem repeat, designated
 CC D3 of the fibronectin binding site of Staphylococcus aureus 8325-4 FbBP.
 CC The N-terminal DK may be replaced with H or K, and the C-terminal LKP may
 CC be replaced by either L, IP, or OH. The peptides were synthesised using
 CC standard methods and purified using reverse phase HPLC. The appropriate
 CC fractions were dialysed and lyophilised. Peptide sequencing was performed
 CC and the peptides digested and chemically modified by dihydroxypropylation
 CC of the amino side chain of lysine. The carboxylic side chains were
 CC converted to glycine methyl esters. The phenyl side chains of tyrosine
 CC residues were oxidised. Chemically modified peptide D3 was compared to
 CC unmodified D3. Lysine and tyrosine modifications only partially
 CC diminished its activity whereas modification of aspartic/glutamic
 CC residues resulted in complete loss of activity. The peptide can be used
 CC for the prevention or reduction of the risk of wound infection. The
 CC peptide can be used to create a large antigen for vaccinating ruminants
 CC against mastitis caused by Staphylococcal infections. It can also be used
 CC to diagnose Staphylococcal infections using ELISA or DNA probes. (Updated
 CC on 25-MAR-2003 to correct PA field.)

XX
 SQ Sequence 22 AA;

Query Match 93.3%; Score 111; DB 2; Length 22;
 Best Local Similarity 95.2%; Pred. No. 2.4e-10;
 Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;


```
XX  MO9916892-A1.
PN
XX  08-APR-1999.
PD
XX  29-SEP-1998; 98WO-GB002927.
PF
XX  29-SEP-1997; 97GB-00020633.
PR
XX  (UYBR-) UNIV BRISTOL.
PA
XX  Bradley AJ, Duffas WPJ;
PI
XX  WPI; 1999-255101/21.
DR
XX  N-PSDB; AAX91504.
XX
XX  New bovine herpes virus-2 vectors.
PT
XX  Example 2; Fig 8A-B; 130pp; English.
PS
XX  The invention provides bovine herpes virus-2 (BHV-2) based vectors that
CC  comprise at least one cytokine-encoding DNA sequence. The expression of
CC  cytokines in mammals can up-regulate immune responses to the immunogens.
CC  The cytokine is selected from interleukins (IL), colony stimulating
CC  factors (CSF), interferons (IFN) and tumour necrosis factors (TNF). The
CC  BHV-2 based vector or recombinant virus can be used as vaccines. They can
CC  be used for preventing or treating a mucosal disease in a subject, e.g.
CC  ruminants, cattle, sheep, goats, dogs, cats, horses, or man, particularly
CC  mastitis in cows or breast cancers in humans. They can also be used for
CC  preventing or treating a stress-induced disease. The present sequence
CC  represents the binding domain of a previously published S. aureus
CC  fibronectin binding protein A (FnBA) sequence. The FnB binding domain
CC  gene sequence FnBAB, cloned for use in this invention has 97.8 percent
CC  identity when compared to the previously published FnBA and FnBB gene
CC  sequences
XX
XX  Sequence 134 AA;
SQ
XX
XX  Query Match 93.3%; Score 111; DB 2; Length 134;
XX  Best Local Similarity 95.2%; Pred. No. 1.7e-09;
XX  Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 1 KPSYQFGGHNSVDFEEDTLPK 21
XX  |||||
DB 93 KPSYQFGGHNSVDFEEDTLPK 113
XX  |||||
XX
XX  RESULT 7
XX  AAW31556
ID AAW31556 standard; protein; 139 AA.
XX
XX  AAW31556;
AC
XX  27-AUG-2003 (revised)
XX  25-MAR-2003 (revised)
XX  21-MAY-1998 (first entry)
DT
XX
XX  Fibronectin-binding MSCRAMM derivative POD.
DE
XX  Fibronectin; POD; collagen binding protein; sepsis; infection;
XX  microbial surface component recognising adhesive matrix molecule; MSCRAMM;
XX  adhesin; vaccine; immunisation; diagnosis; therapy; mastitis.
XX
XX  Staphylococcus aureus.
OS
XX
XX  Key Location/Qualifiers
XX  Peptide 1..12
XX  /note= "vector pQE30-derived peptide"
XX
XX  MO9743314-A2.
PN
XX  20-NOV-1997.
PD
XX
```

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PF 14-MAY-1997; 97WO-US008210.
XX
XX  16-MAY-1996; 96US-0017678P.
PR
XX  (TEXA ) UNIV TEXAS A & M SYSTEM.
PA
XX  (UABR-) UAB RES FOUND.
XX
XX  Hoeoek M, Patil JM, House-Pompeo K, Sthanam N, Symersky J;
PI
XX  WPI; 1998-008801/01.
DR
XX
XX  Antibody that interacts with collagen binding domain of Staphylococcal
PT  cna gene product - useful to prevent bacterial sepsis in animal infected
XX  with Staphylococcus aureus.
XX
XX  Disclosure; Page 91; 143pp; English.
PS
XX
XX  This protein comprises Staphylococcus aureus fibronectin-binding
CC  microbial surface component recognising adhesive matrix molecule (MSCRAMM)
CC  derivative POD, plus a vector-derived N-terminal peptide. The invention
CC  relates to claimed nucleic acid sequences (see AAT93436-38) encoding S.
CC  aureus collagen binding protein (CBP) epitopes M17, M31 and M55 (see
CC  AAW31552-54) that confer protection against S. aureus infection. CBP
CC  protein and antigenic epitopes are contemplated for use in the treatment
CC  of pathological infections, especially to prevent bacterial adhesion to
CC  collagen. The epitopes are also contemplated for use in the preparation
CC  of vaccines and as carrier proteins in vaccine formulations, as well as
CC  in the formulation of compositions for the prevention of S. aureus
CC  infection. PCR33 and POD (see AAW31556) were used to raise anti-MSCRAMM
CC  polyclonal antibodies used in passive immunisation against bovine
CC  mastitis. (Updated on 25-MAR-2003 to correct PI field.) (Updated on 27-
CC  AUG-2003 to correct OS field.)
XX
XX  Sequence 139 AA;
SQ
XX
XX  Query Match 93.3%; Score 111; DB 2; Length 139;
XX  Best Local Similarity 95.2%; Pred. No. 1.8e-09;
XX  Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 1 KPSYQFGGHNSVDFEEDTLPK 21
XX  |||||
DB 107 KPSYQFGGHNSVDFEEDTLPK 127
XX  |||||
XX
XX  RESULT 8
XX  AAP82115
ID AAP82115 standard; protein; 1018 AA.
XX
XX  AAP82115;
AC
XX  25-MAR-2003 (revised)
XX  05-JAN-1990 (first entry)
DT
XX
XX  Fibronectin binding protein.
DE
XX  Fibronectin binding protein; S.aureus; immunisation; mastitis; ruminants;
XX  wound infection; diagnosis.
XX
XX  Staphylococcus aureus.
OS
XX
XX  EP294349-A.
XX  07-DEC-1988.
XX
XX  30-MAY-1988; 88BP-00850188.
XX  01-JUN-1987; 87SE-00002272.
XX
XX  (ALFA ) ALFA LAVAL AGRIC INT AB.
XX
XX  Lindberg MK, Signas LC, Wadstrom TM, Froman G;
PI
XX  WPI; 1988-347978/49.
DR
```

DR P-PSDB; AAP82115.
XX Hybrid DNA encoding Staphylococcus aureus fibronectin binding protein -
PT useful for immunisation and topical application to prevent staphylococcal
PT infections.
XX
PS Disclosure; Fig. 8A:1-8A:2; 23pp; English.
XX
CC The *S. aureus* fibronectin binding protein may be included in a hybrid
CC protein. The protein may be used to immunise ruminants against
CC staphylococcal mastitis, pref. when given at 0.5-5 microg/kg, using 3
CC doses at 1-3 week intervals; and for topical applicn. to prevent wound
CC infection, pref. using isotonic saline soln. of concn. 25-250 microg/mg.
CC The DNA encoding the binding protein and the hybrid protein may be
CC immobilised on a carrier and used to diagnose staphylococcal infections.
CC (Updated on 25-MAR-2003 to correct PA field.)
XX
SQ Sequence 1018 AA;
XX
Query Match 93.3%; Score 111; DB 1; Length 1018;
Best Local Similarity 95.2%; Pred. No. 1.6e-08;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Oy 1 KPSYQFGGHNVSVDPEDTLPK 21
DB 837 KPSYQFGGHNVSVDPEDTLPK 857
RESULT 9
AAU37245
ID AAU37245 standard; protein; 1018 AA.
XX
AC AAU37245;
XX
DT 14-FEB-2002 (first entry)
XX
DE Staphylococcus aureus cellular proliferation protein #1415.
XX
KW Antisense; prokaryotic cellular proliferation protein; antibiotic;
XX antibacterial; drug design.
XX
OS Staphylococcus aureus.
XX
PN WO200170955-A2.
XX
PD 27-SEP-2001.
XX
PF 21-MAR-2001; 2001WO-US009180.
XX
PR 21-MAR-2000; 2000US-0191078P.
XX
PR 23-MAY-2000; 2000US-0206848P.
XX
PR 26-MAY-2000; 2000US-0207727P.
XX
PR 23-OCT-2000; 2000US-0242578P.
XX
PR 27-NOV-2000; 2000US-0253625P.
XX
PR 22-DEC-2000; 2000US-0257931P.
XX
PR 16-FEB-2001; 2001US-0269308P.
XX
PA (ELIT-) ELITRA PHARM INC.
XX
PI Haselbeck R, Ohlsen KL, Zyskind JW, Wall D, Trawick JD, Carr GJ;
PI Yamamoto RT, Xu HH;
XX
XX WPI; 2001-611495/70.
XX
XX N-PSDB; AAS55104.
XX
PT New polynucleotides for the identification and development of
XX antibiotics, comprise sequences of antisense nucleic acids.
XX
PS Example 3; SEQ ID NO 12838; 511pp; English.
XX
CC The invention relates to antisense inhibitors of genes essential to
CC prokaryotic cellular proliferation, their use in identifying the genes,
CC their use in the discovery of novel antibiotics, the essential genes

CC themselves and the encoded proteins. The prokaryotes used are *Escherichia*
CC coli, *Staphylococcus aureus*, *Salmonella typhi*, *Klebsiella pneumoniae*,
CC *Pseudomonas aeruginosa* and *Enterococcus faecalis*. The invention is also
CC useful for the identification of potential new targets for antibiotic
CC development. The antisense nucleic acids can also be used to identify
CC proteins used in proliferation, to express these proteins, and to obtain
CC antibodies capable of binding to the expressed proteins. The proteins can
CC be used to screen compounds in rational drug discovery programmes. The
CC antisense nucleic acid sequence is also useful to screen for homologous
CC nucleic acids which are required for cell proliferation in a wide variety
CC of organisms. The present sequence represents an essential prokaryotic
CC cellular proliferation protein. Note: The sequence data for this patent
CC did not form part of the printed specification, but was obtained in
CC electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 1018 AA;
XX
Query Match 93.3%; Score 111; DB 4; Length 1018;
Best Local Similarity 95.2%; Pred. No. 1.6e-08;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Oy 1 KPSYQFGGHNVSVDPEDTLPK 21
DB 837 KPSYQFGGHNVSVDPEDTLPK 857
RESULT 10
AAU34301
ID AAU34301 standard; protein; 1018 AA.
XX
AC AAU34301;
XX
DT 14-FEB-2002 (first entry)
XX
DE Staphylococcus aureus cellular proliferation protein #577.
XX
KW Antisense; prokaryotic cellular proliferation protein; antibiotic;
XX antibacterial; drug design.
XX
OS Staphylococcus aureus.
XX
PN WO200170955-A2.
XX
PD 27-SEP-2001.
XX
PF 21-MAR-2001; 2001WO-US009180.
XX
PR 21-MAR-2000; 2000US-0191078P.
XX
PR 23-MAY-2000; 2000US-0206848P.
XX
PR 26-MAY-2000; 2000US-0207727P.
XX
PR 23-OCT-2000; 2000US-0242578P.
XX
PR 27-NOV-2000; 2000US-0253625P.
XX
PR 22-DEC-2000; 2000US-0257931P.
XX
PR 16-FEB-2001; 2001US-0269308P.
XX
PA (ELIT-) ELITRA PHARM INC.
XX
PI Haselbeck R, Ohlsen KL, Zyskind JW, Wall D, Trawick JD, Carr GJ;
PI Yamamoto RT, Xu HH;
XX
XX WPI; 2001-611495/70.
XX
XX N-PSDB; AAS52160.
XX
PT New polynucleotides for the identification and development of
XX antibiotics, comprise sequences of antisense nucleic acids.
XX
PS Example 3; SEQ ID NO 5797; 511pp; English.
XX
CC The invention relates to antisense inhibitors of genes essential to
CC prokaryotic cellular proliferation, their use in identifying the genes,
CC their use in the discovery of novel antibiotics, the essential genes
CC themselves and the encoded proteins. The prokaryotes used are *Escherichia*

CC coli, *Staphylococcus aureus*, *Salmonella typhi*, *Klebsiella pneumoniae*,
CC *Pseudomonas aeruginosa* and *Enterococcus faecalis*. The invention is also
CC useful for the identification of potential new targets for antibiotic
CC development. The antisense nucleic acids can also be used to identify
CC antibodies used in proliferation, to express these proteins, and to obtain
CC antibodies capable of binding to the expressed proteins. The proteins can
CC be used to screen compounds in rational drug discovery programmes. The
CC antisense nucleic acid sequence is also useful to screen for homologous
CC nucleic acids which are required for cell proliferation in a wide variety
CC of organisms. The present sequence represents an essential prokaryotic
CC cellular proliferation protein. Note: The sequence data for this patent
CC did not form part of the printed specification, but was obtained in
CC electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
CC
XX Sequence 1018 AA;
SQ
Query Match 93.3%; Score 111; DB 4; Length 1018;
Best Local Similarity 95.2%; Pred. No. 1.6e-08;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 KPSYQFGGHSVDPEDTLPK 21
Db 837 KPSYQFGGHSVDPEDTLPK 857
RESULT 11
ABJ18922
ID ABJ18922 standard; protein; 1018 AA.
AC
XX ABJ18922;
XX
DT 06-MAR-2003 (first entry)
DE
XX Pathogen specific antigen related staphylococcal protein SEQ ID No 68.
XX
XX Antibacterial; virucide; fungicide; protozoacide; cytostatic; anti-HIV;
XX hyperimmune; serum-reactive; antigen; pathogen; tumour; allergen;
XX auto-immunity; vaccine; staphylococcal infection; antibody; cancer;
XX autoimmune disease; HIV; hepatitis.
XX
XX *Staphylococcus* sp.
XX OS
XX WO200259148-A2.
XX PN
XX 01-AUG-2002.
XX PD
XX 21-JAN-2002; 2002WO-EP000546.
XX PF
XX 26-JAN-2001; 2001AT-00000130.
XX PR
XX (CIST-) CISTEM BIOTECHNOLOGIES GMBH.
XX PA
XX Meinke A, Nagy E, Von Ahnen U, Klade C, Henics T, Zauner W;
XX Mih DB, Vycvyetka O, Etz H, Dryla A, Weichardt T, Hafner M;
XX Tempelmeier B;
XX PI
XX WPI; 2003-075410/07.
XX DR
XX
XX Identifying, isolating and producing hyperimmune serum-reactive antigens
XX from a pathogen, for preparing vaccine or medicament for treating or
XX preventing e.g. staphylococcal infections, comprises providing antibody
XX preparation.
XX PT
XX
XX Example 7; Page 157; 252pp; English.
XX PS
XX The invention relates to a novel method for identifying, isolating and
XX producing hyperimmune serum-reactive antigens from a pathogen, tumour,
XX allergen, a tissue or host prone to auto-immunity, where the antigens are
XX used in a vaccine, comprises providing antibody preparation from a plasma
XX pool of a type of animal, or individual sera with antibodies against the
XX specific pathogen, tumour, allergen, tissue or host prone to auto-
XX immunity. The hyperimmune serum-reactive antigens comprising any of the

CC 62 sequences of 53-2261 amino acids fully defined in the specification,
CC or their hyperimmune fragments are useful for the manufacture of a
CC pharmaceutical preparation, particularly a vaccine against staphylococcal
CC infections or colonisation against *S. aureus* or *S. epidermidis*. The
CC preparation of antibodies is useful for the manufacture of a medicament
CC for treating or preventing staphylococcal infections or colonisation
CC against *S. aureus* or *S. epidermidis*. The antibody preparations may also
CC be used for diagnostic and imaging purposes. Other conditions that can be
CC treated include cancer, autoimmune diseases or infections caused by viral
CC (e.g. HIV, hepatitis A, B or C), fungal or protozoan pathogens. This
CC sequence represents a staphylococcal protein relating to the method for
CC identifying and producing pathogen specific antigens of the invention
CC
XX Sequence 1018 AA;
SQ
Query Match 93.3%; Score 111; DB 6; Length 1018;
Best Local Similarity 95.2%; Pred. No. 1.6e-08;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 KPSYQFGGHSVDPEDTLPK 21
Db 837 KPSYQFGGHSVDPEDTLPK 857
RESULT 12
ABM72537
ID ABM72537 standard; protein; 1018 AA.
XX
XX ABM72537;
XX AC
XX 20-NOV-2003 (first entry)
XX DT
XX
XX *Staphylococcus aureus* protein #1777.
XX DE
XX
XX Antibacterial; vaccine; gene therapy; infection; sepsis; diagnosis;
XX enzymatic assay; antibiotic target.
XX KW
XX
XX *Staphylococcus aureus*.
XX OS
XX WO200294868-A2.
XX PN
XX 28-NOV-2002.
XX XX
XX 27-MAR-2002; 2002WO-IB002637.
XX PF
XX 27-MAR-2001; 2001GB-00007661.
XX PR
XX (CHIR-) CHIRON SPA.
XX PA
XX Masignani V, Mora M, Scarselli M;
XX PI
XX WPI; 2003-120786/11.
XX DR
XX N-PSDB; ACF74097.
XX DT
XX
XX New *Staphylococcus aureus* protein, useful as a vaccine for treating or
XX preventing *Staphylococcal* infection, specifically an infection caused by
XX *S. aureus*, e.g. sepsis.
XX PT
XX
XX Claim 1; SEQ ID NO 3554; 49pp; English.
XX PS
XX
XX The invention relates to novel genes and encoded proteins from
XX *Staphylococcus aureus*. A composition comprising the *S. aureus* protein, a
XX nucleic acid encoding the protein, or an antibody to the protein, is
XX useful as a pharmaceutical, particularly as a vaccine for treating or
XX preventing infection due to *Staphylococcus* bacteria, specifically an
XX infection caused by *S. aureus*. The composition is particularly useful for
XX treating or preventing sepsis in a patient. The composition can also be
XX used for diagnostics. The protein is also used in an assay for enzymatic
XX studies and as a target for antibiotics. This sequence represents one of
XX the novel *S. aureus* proteins of the invention
XX
XX Sequence 1018 AA;
SQ

Query Match 93.3%; Score 111; DB 6; Length 1018;
 Best Local Similarity 95.2%; Pred. No. 1.6e-08;
 Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KPSYQFGHNSVDFEPTLPK 21
 DB 837 KPSYQFGHNSVDFEPTLPK 857

RESULT 13
 AAW89806
 ID AAW89806 standard; protein; 1027 AA.

AC AAW89806;
 DT 16-MAR-1999 (first entry)
 DE Staphylococcus aureus protein SEQ ID #5254.

XX Computer readable medium; vaccine; S. aureus infection; immunodetection;
 XX cellulitis; eyelid infection; food poisoning; osteomyelitis; therapy;
 KW skin infection; surgical wound infection; scalded skin syndrome;
 KW toxic shock syndrome.

XX Staphylococcus aureus.

XX EP76519-A2.

XX 30-JUL-1997.

XX 07-JAN-1997; 97EP-00100117.

XX 05-JAN-1996; 96US-0009861P.

XX (HUMA-) HUMAN GENOME SCI INC.

XX Kunach CA, Choi GH, Barash SC, Dillon PJ, Fannon MR, Rosen CA;
 PI WPI: 1997-374922/35.

PT Polynucleotide(s) and proteins derived from Staphylococcus aureus -
 PT stored on computer readable medium and used in the production of anti-
 PT S. aureus vaccines.

PS Claim 23; Page 3263-3267; 3271pp; English.

XX This sequence represents a Staphylococcus aureus protein sequence of the
 CC invention. The DNA sequences encoding the S. aureus proteins are recorded
 CC on a computer readable medium, preferably selected from a floppy or hard
 CC disk, random access memory (RAM), read-only memory (ROM) or CD-ROM.
 CC Homology searches using the S. aureus DNA sequences allows putative
 CC functions to be assigned so that protein-encoding or regulatory regions
 CC of commercial, therapeutic or industrial importance can be obtained.
 CC Specifically, sequences which are likely to encode antigens have been
 CC identified and these polypeptides can be used in a vaccine composition
 CC against S. aureus infection. The polypeptides can also be used in a kit
 CC for the immunodetection of S. aureus in a sample. S. aureus is implicated
 CC in numerous human diseases, including cellulitis, eyelid infections, food
 CC poisoning, osteomyelitis, skin and surgical wound infections, scalded
 CC skin syndrome, toxic shock syndrome, etc. Organisms transformed with the
 CC DNA sequences can be used for recombinant production of the polypeptides.
 CC The new DNA sequences (and their fragments) are useful as primers or
 CC probes for isolating homologues of any of the 5191 S. aureus DNA sequences
 CC contained on the computer readable medium

XX Sequence 1027 AA;

QY Query Match 93.3%; Score 111; DB 2; Length 1027;
 Best Local Similarity 95.2%; Pred. No. 1.6e-08;
 Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KPSYQFGHNSVDFEPTLPK 21
 DB 837 KPSYQFGHNSVDFEPTLPK 857

DB 846 KPSYQFGHNSVDFEPTLPK 866

RESULT 14
 ABU15854
 ID ABU15854 standard; protein; 961 AA.

AC ABU15854;

DT 19-JUN-2003 (first entry)

DE Protein encoded by Prokaryotic essential gene #1381.

XX Antisense; prokaryotic essential gene; cell proliferation; drug design.

XX Staphylococcus aureus.

XX WO20027183-A2.

XX 03-OCT-2002.

XX 21-MAR-2002; 2002WO-US009107.

XX 21-MAR-2001; 2001US-00815242.

XX 25-OCT-2001; 2001US-0342923P.

XX 08-FEB-2002; 2002US-00072851.

XX 06-MAR-2002; 2002US-0362695P.

XX (ELIT-) ELITRA PHARM INC.

XX Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zykkind JW;
 PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;

XX WPI: 2003-029926/02.

XX N-PSDB; ACA19724.

PT New antisense nucleic acid, useful for identifying proteins or screening
 PT for homologous nucleic acids required for cellular proliferation to
 PT isolate candidate molecules for rational drug discovery programs.

PS Claim 25; SEQ ID NO 43778; 1766pp; English.

XX The invention relates to an isolated nucleic acid comprising any one of
 CC the 623 antisense sequences given in the specification where expression
 CC of the nucleic acid inhibits proliferation of a cell. Also included are:
 CC (1) a vector comprising a promoter operably linked to the nucleic acid
 CC encoding a polypeptide whose expression is inhibited by the antisense
 CC nucleic acid; (2) a host cell containing the vector; (3) an isolated
 CC polypeptide or its fragment whose expression is inhibited by the
 CC antisense nucleic acid; (4) an antibody capable of specifically binding
 CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular
 CC proliferation or the activity of a gene in an operon required for
 CC proliferation; (7) identifying a compound that influences the activity of
 CC the gene product or that has an activity against a biological pathway
 CC required for proliferation, or that inhibits cellular proliferation; (8)
 CC identifying a gene required for cellular proliferation or the biological
 CC pathway in which a proliferation-regulated gene or its gene product lies
 CC or a gene on which the test compound that inhibits proliferation of an
 CC organism acts; (9) manufacturing an antibiotic; (10) profiling a
 CC compound's activity; (11) a culture comprising strains in which the gene
 CC product is overexpressed or underexpressed; (12) determining the extent
 CC to which each of the strains is present in a culture or collection of
 CC strains; or (13) identifying the target of a compound that inhibits the
 CC proliferation of an organism. The antisense nucleic acids are useful for
 CC identifying proteins or screening for homologous nucleic acids required
 CC for cellular proliferation to isolate candidate molecules for rational
 CC drug discovery programs, or for screening homologous nucleic acids
 CC required for proliferation in cells other than S. aureus, S. typhimurium,
 CC K. pneumoniae or P. aeruginosa. The present sequence is encoded by one of
 CC the target prokaryotic essential genes. Note: The sequence data for this
 CC patent did not form part of the printed specification, but was obtained
 CC in electronic format directly from WIPO at

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CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 961 AA;
Query Match 90.8%; Score 108; DB 6; Length 961;
Best Local Similarity 90.5%; Pred. No. 4.6e-08;
Matches 19; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
OY 1 KPSYQFGGHSVDPEDPTLPK 21
Db 784 KPNYQFGGHSVDPEDPTLPK 804

RESULT 15
AAU33960
ID AAU33960 standard; protein; 978 AA.
XX
AC AAU33960;
XX
DT 14-FEB-2002 (first entry)
XX
DE Staphylococcus aureus cellular proliferation protein #236.
XX
KM Antisense; prokaryotic cellular proliferation protein; antibiotic;
XX antibacterial; drug design.
XX
OS Staphylococcus aureus.
XX
PN MO200170955-A2.
XX
PD 27-SEP-2001.
XX
PF 21-MAR-2001; 2001WO-US009180.
XX
PR 21-MAR-2000; 2000US-0191078P.
XX
PR 23-MAY-2000; 2000US-0206848P.
XX
PR 26-MAY-2000; 2000US-0207727P.
XX
PR 23-OCT-2000; 2000US-0242578P.
XX
PR 27-NOV-2000; 2000US-0253625P.
XX
PR 22-DEC-2000; 2000US-0257931P.
XX
PR 16-FEB-2001; 2001US-0269308P.
XX
PA (ELIT-) ELITRA PHARM INC.
XX
PI Haselbeck R, Ohlsen KJ, Zyckind JW, Wall D, Trawick JD, Carr GT;
PI Yamamoto RT, Xu HH;
XX
DR N-PSDB; AAS51819.
XX
WPI; 2001-611495/70.
XX
PT New polynucleotides for the identification and development of
PT antibiotics, comprise sequences of antisense nucleic acids.
XX
PS Example 3; SEQ ID NO 5456; 511p; English.
XX
CC The invention relates to antisense inhibitors of genes essential to
CC prokaryotic cellular proliferation, their use in identifying the genes,
CC their use in the discovery of novel antibiotics, the essential genes
CC themselves and the encoded proteins. The prokaryotes used are Escherichia
CC coli, Staphylococcus aureus, Salmonella typhi, Klebsiella pneumoniae,
CC Pseudomonas aeruginosa and Enterococcus faecalis. The invention is also
CC useful for the identification of potential new targets for antibiotic
CC development. The antisense nucleic acids can also be used to identify
CC proteins used in proliferation, to express these proteins, and to obtain
CC antibodies capable of binding to the expressed proteins. The proteins can
CC be used to screen compounds in rational drug discovery programmes. The
CC antisense nucleic acid sequence is also useful to screen for homologous
CC nucleic acids which are required for cell proliferation in a wide variety
CC of organisms. The present sequence represents an essential prokaryotic
CC cellular proliferation protein. Note: The sequence data for this patent
CC did not form part of the printed specification, but was obtained in
CC electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
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SQ Sequence 978 AA;
Query Match 90.8%; Score 108; DB 4; Length 978;
Best Local Similarity 90.5%; Pred. No. 4.7e-08;
Matches 19; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
OY 1 KPSYQFGGHSVDPEDPTLPK 21
Db 815 KPNYQFGGHSVDPEDPTLPK 835

Search completed: October 25, 2005, 19:38:30
Job time : 59.1473 secs
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OW protein - protein search, using SW model

Run on: October 22, 2005, 02:23:36 ; Search time 15.9358 seconds
(without alignments)
98.371 Million cell updates/sec

Title: US-10-731-238-28

Sequence: 1 KPSYQFGHNSVDEPDTLPK 21

Scoring table: BLOSUM62

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Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

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6: /cgn2_6/prodata/1/1aa/Backfill1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	111	93.3	21	4	US-09-010-317-9
3	111	93.3	37	1	US-08-234-622A-4
4	111	93.3	38	1	US-08-294-189-8
5	111	93.3	38	1	US-08-729-767-5
6	111	93.3	134	1	US-08-259-000-3
7	111	93.3	139	3	US-08-856-253-8
8	111	93.3	178	3	US-08-459-135A-12
9	111	93.3	178	3	US-08-495-559-12
10	111	93.3	1027	4	US-08-956-171B-5254
11	111	93.3	1027	4	US-08-781-986A-5254
12	106	89.1	21	4	US-09-010-317-14
13	106	89.1	21	4	US-09-010-317-16
14	106	89.1	21	4	US-09-010-317-23
15	106	89.1	21	4	US-09-010-317-33
16	105	88.2	21	4	US-09-010-317-18
17	105	88.2	21	4	US-09-010-317-24
18	105	88.2	21	4	US-09-010-317-27
19	105	88.2	21	4	US-09-010-317-30
20	104	87.4	21	4	US-09-010-317-25
21	104	87.4	21	4	US-09-010-317-29
22	104	87.4	21	4	US-09-010-317-31
23	104	87.4	130	2	US-08-459-135A-7
24	104	87.4	130	2	US-08-459-135A-8
25	104	87.4	130	3	US-08-495-559-7
26	104	87.4	130	3	US-08-495-559-8
27	104	87.4	174	2	US-08-459-135A-10

28	104	87.4	174	2	US-08-459-135A-13	Sequence 13, Appl
29	104	87.4	174	3	US-08-495-559-10	Sequence 10, Appl
30	104	87.4	174	3	US-08-495-559-13	Sequence 13, Appl
31	104	87.4	176	3	US-08-495-559-6	Sequence 6, Appl
32	104	87.4	181	2	US-08-459-135A-6	Sequence 6, Appl
33	104	87.4	559	4	US-08-956-171B-5251	Sequence 5251, Ap
34	104	87.4	559	4	US-08-781-986A-5251	Sequence 5251, Ap
35	103	86.6	21	4	US-09-010-317-10	Sequence 10, Appl
36	103	86.6	21	4	US-09-010-317-15	Sequence 15, Appl
37	103	86.6	21	4	US-09-010-317-20	Sequence 20, Appl
38	103	86.6	21	4	US-09-010-317-22	Sequence 22, Appl
39	103	86.6	21	4	US-09-010-317-32	Sequence 32, Appl
40	103	86.6	22	4	US-09-010-317-13	Sequence 13, Appl
41	101	84.9	21	4	US-09-010-317-17	Sequence 17, Appl
42	101	84.9	21	4	US-09-010-317-19	Sequence 19, Appl
43	101	84.9	21	4	US-09-010-317-21	Sequence 21, Appl
44	101	84.9	21	4	US-09-010-317-26	Sequence 26, Appl
45	90	75.6	19	1	US-08-234-622A-1	Sequence 1, Appl

ALIGNMENTS

RESULT 1
US-09-010-317-28
Sequence 28, Application US/09010317
Patent No. 6685943
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
APPLICANT: Patti, Joseph M.
APPLICANT: House-Pompeo, Karen L.
APPLICANT: Speziale, Pietro
APPLICANT: Joh, Danny
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
TITLE OR INVENTION: AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSER: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE:
CLASSIFICATION:
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-09-010-317-28
Query Match 100.0%; Score 119; DB 4; Length 21;
Best Local Similarity 100.0%; Pred. No. 3.8e-12;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KPSYQFGHNSVDPEPDTLPK 21
Db 1 KPSYQFGHNSVDPEPDTLPK 21

RESULT 2

US-09-010-317-9

Sequence 9, Application US/09010317
Patent No. 6685943

GENERAL INFORMATION:

APPLICANT: Hook, Magnus

APPLICANT: Batt, Joseph M.

APPLICANT: House-Pompeo, Karen L.

APPLICANT: Speziale, Pietro

APPLICANT: Joh, Danny

APPLICANT: McGavin, Martin J.

TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS

TITLE OF INVENTION: AND METHODS OF USE

NUMBER OF SEQUENCES: 105

CORRESPONDENCE ADDRESS:

ADDRESSEE: Arnold, White & Durkee

STREET: P.O. Box 4433

CITY: Houston

STATE: TX

COUNTRY: USA

ZIP: 77210-4433

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/010.317

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 60/036,139

FILING DATE: 21-JAN-1997

ATTORNEY/AGENT INFORMATION:

NAME: Hibley, David W.

REGISTRATION NUMBER: 41,071

REFERENCE/DOCKET NUMBER: TAMK.189

TELECOMMUNICATION INFORMATION:

TELEPHONE: 512-418-3000

TELEFAX: 512-474-7577

INFORMATION FOR SEQ ID NO: 9:

SEQUENCE CHARACTERISTICS:

LENGTH: 21 amino acids

TYPE: amino acid

STRANDEDNESS:

TOPOLOGY: linear

US-09-010-317-9

Query Match 93.3%; Score 111; DB 4; Length 21;

Best Local Similarity 95.2%; Pred. No. 7e-11; 1; Indels 0; Gaps 0;

Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KPSYQFGHNSVDPEPDTLPK 21

Db 1 KPSYQFGHNSVDPEPDTLPK 21

RESULT 3

US-08-234-622A-4

Sequence 4, Application US/08234622A

Patent No. 5440014

GENERAL INFORMATION:

APPLICANT: Hook, Magnus

APPLICANT: McGavin, Martin

APPLICANT: RAUCCI, Giuseppe

TITLE OF INVENTION: A FIBRONECTIN BINDING PEPTIDE

NUMBER OF SEQUENCES: 4

CORRESPONDENCE ADDRESS:

ADDRESSEE: Burns, Doane, Swecker & Mathis

STREET: P.O. Box 1404

CITY: Alexandria

STATE: Virginia

COUNTRY: United States

ZIP: 22313-1404

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/234,622A

FILING DATE: 28-APR-1994

CLASSIFICATION: 530

PRIOR APPLICATION DATA:

APPLICATION NUMBER: SE 9002617-0

FILING DATE: 10-AUG-1990

PRIOR APPLICATION DATA:

APPLICATION NUMBER: WO PCT/SE91/00534

FILING DATE: 09-AUG-1991

ATTORNEY/AGENT INFORMATION:

NAME: Meuth, Donna M

REGISTRATION NUMBER: 36,607

REFERENCE/DOCKET NUMBER: 012885-044

TELECOMMUNICATION INFORMATION:

TELEPHONE: (703) 836-6620

TELEFAX: (703) 836-2021

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 37 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-234-622A-4

Query Match 93.3%; Score 111; DB 1; Length 37;

Best Local Similarity 95.2%; Pred. No. 1.3e-10; 1; Indels 0; Gaps 0;

Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KPSYQFGHNSVDPEPDTLPK 21

Db 16 KPSYQFGHNSVDPEPDTLPK 36

RESULT 4

US-08-294-189-8

Sequence 8, Application US/08294189

Patent No. 5707822

GENERAL INFORMATION:

APPLICANT: Fischetti, Vincent A.

APPLICANT: Rakonjac, Jasna

APPLICANT: Robbins, John

TITLE OF INVENTION: GENE SERUM OPACITY FACTOR

NUMBER OF SEQUENCES: 23

CORRESPONDENCE ADDRESS:

ADDRESSEE: Klauber & Jackson

STREET: 411 Hackensack Avenue

CITY: Hackensack

STATE: New Jersey

COUNTRY: USA

ZIP: 07601

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/294,189

FILING DATE: 22-AUG-1994

CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-118
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 487-5800
TELEFAX: 201 343-1684
TELEX: 133521
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
ORGANISM: Streptococcus pyogenes
STRAIN: D734
INDIVIDUAL ISOLATE: 22
IMMEDIATE SOURCE:
CLONE: SAU3a
US-08-294-189-8

Query Match 93.3%; Score 111; DB 1; Length 38;
Best Local Similarity 95.2%; Pred. No. 1.4e-10;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KPSYQFGHNSVDPEDTLPK 21
DB 10 KPSYQFGHNSVDPEDTLPK 30

RESULT 5
US-08-729-767-5
Sequence 5, Application US/08729767
Patent No. 5770702
GENERAL INFORMATION:
APPLICANT: HOOK, Magnus
APPLICANT: LINDBERG, Martin Kjell
APPLICANT: SIGNAS, Lars Christer
APPLICANT: WADSTROM, Torkel Mikael
APPLICANT: FROMAN, Gunnar
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN AS WELL AS
TITLE OF INVENTION: ITS PREPARATION
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Burns, Doane, Swecker & Mathis, L.L.P.
STREET: P.O. Box 1404
CITY: Alexandria
STATE: Virginia
COUNTRY: United States
ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/729,767
FILING DATE: 07-OCT-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/259,000
FILING DATE: 13-JUN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/007,817
FILING DATE: 22-JAN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/201,028
FILING DATE: 01-JUN-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: SE 8702272-9

FILING DATE: 01-JUN-1987
ATTORNEY/AGENT INFORMATION:
NAME: McGowan, Malcolm K.
REGISTRATION NUMBER: 39,300
REFERENCE/DOCKET NUMBER: 012889-036
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-729-767-5

Query Match 93.3%; Score 111; DB 1; Length 38;
Best Local Similarity 95.2%; Pred. No. 1.4e-10;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KPSYQFGHNSVDPEDTLPK 21
DB 17 KPSYQFGHNSVDPEDTLPK 37

RESULT 6
US-08-259-000-3
Sequence 3, Application US/08259000
Patent No. 5571514
GENERAL INFORMATION:
APPLICANT: HOOK, Magnus
APPLICANT: LINDBERG, Martin Kjell
APPLICANT: SIGNAS, Lars Christer
APPLICANT: WADSTROM, Torkel Mikael
APPLICANT: FROMAN, Gunnar
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN AS WELL AS
TITLE OF INVENTION: ITS PREPARATION
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Burns, Doane, Swecker & Mathis
STREET: P.O. Box 1404
CITY: Alexandria
STATE: Virginia
COUNTRY: United States
ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/259,000
FILING DATE: 13-JUN-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: SE 8702272-9
FILING DATE: 01-JUN-1987
ATTORNEY/AGENT INFORMATION:
NAME: Meuth, Donna M
REGISTRATION NUMBER: 36,607
REFERENCE/DOCKET NUMBER: 012885-062
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 114 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-259-000-3

	Query Match	93.3%;	Score 111;	DB 1;	Length 114;	
	Best Local Similarity	95.2%;	Pred. No. 4.7e-10;			
	Matches 20;	Conservative 0;	Mismatches 1;	Indels 0;	Gaps 0;	
OY	1 KPSYQFGGHSVDFEPTLPK 21					
Db	93 KPSYQFGGHSVDFEPTLPK 113					
	RESULT 7					
	US-08-856-253-8					
	; Sequence 8, Application US/08856253					
	; Patent No. 6288214					
	GENERAL INFORMATION:					
	APPLICANT: Hook, Magnus					
	APPLICANT: Patti, Joseph M.					
	APPLICANT: House-Pompeo, Karen					
	APPLICANT: Sthanam, Narayana					
	APPLICANT: Syversky, Jindrich					
	TITLE OF INVENTION: COLLAGEN BINDING PROTEIN COMPOSITIONS					
	TITLE OF INVENTION: AND METHODS OF USE					
	NUMBER OF SEQUENCES: 8					
	CORRESPONDENCE ADDRESSES:					
	ADDRESSEE: Arnold, White & Durkee					
	STREET: P.O. Box 4433					
	CITY: Houston					
	STATE: Texas					
	COUNTRY: U.S.					
	ZIP: 77210					
	COMPUTER READABLE FORM:					
	MEDIUM TYPE: Floppy disk					
	COMPUTER: IBM PC compatible					
	OPERATING SYSTEM: PC-DOS/MS-DOS					
	SOFTWARE: Patent Release #1.0, Version #1.30					
	CURRENT APPLICATION DATA:					
	APPLICATION NUMBER: US/08/856,253					
	FILING DATE: Concurrently Herewith					
	CLASSIFICATION: 514					
	PRIOR APPLICATION DATA:					
	APPLICATION NUMBER: US 60/017,678					
	FILING DATE: 16-MAY-1996					
	ATTORNEY/AGENT INFORMATION:					
	NAME: Kitchenl, Barbara S.					
	REGISTRATION NUMBER: 33,928					
	REFERENCE/DOCKET NUMBER: TAWK.193					
	TELECOMMUNICATION INFORMATION:					
	TELEPHONE: (512) 418-3000					
	TELEFAX: (512) 474-7577					
	INFORMATION FOR SEQ ID NO: 8:					
	SEQUENCE CHARACTERISTICS:					
	LENGTH: 139 amino acids					
	TYPE: amino acid					
	STRANDEDNESS:					
	TOPOLOGY: linear					
	US-08-856-253-8					
	Query Match	93.3%;	Score 111;	DB 3;	Length 139;	
	Best Local Similarity	95.2%;	Pred. No. 5.9e-10;			
	Matches 20;	Conservative 0;	Mismatches 1;	Indels 0;	Gaps 0;	
OY	1 KPSYQFGGHSVDFEPTLPK 21					
Db	107 KPSYQFGGHSVDFEPTLPK 127					
	RESULT 8					
	US-08-459-135A-12					
	; Sequence 12, Application US/08459135A					
	; Patent No. 5955078					
	GENERAL INFORMATION:					
	APPLICANT: BURHAM, Martin Karl Russel					
	APPLICANT: CHOPRA, Ian					

```

1  APPLICANT: CRITCHLEY, Ian Alfred
2  APPLICANT: KNOWLES, David Justin Charles
3  TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN: MONOCLONAL ANTIBODY AND THEIR USE
4  NUMBER OF SEQUENCES: 15
5  CORRESPONDENCE ADDRESS:
6  ADDRESSEE: SmithKline Beecham Corporation
7  STREET: 709 Swedeland Road
8  CITY: King of Prussia
9  STATE: PA
10 COUNTRY: U.S.A.
11 ZIP: 19406-0939
12 COMPUTER READABLE FORM:
13 MEDIUM TYPE: Diskette
14 COMPUTER: IBM Compatible
15 OPERATING SYSTEM: DOS
16 SOFTWARE: Fastseq, Version 2.0
17 CURRENT APPLICATION DATA:
18 APPLICATION NUMBER: US/08/459,135A
19 FILING DATE: 02-JUN-1995
20 CLASSIFICATION: 435
21 PRIOR APPLICATION DATA:
22 APPLICATION NUMBER: PCT/GB/94/00215
23 FILING DATE: 04-Feb-1994
24 CLASSIFICATION: 435
25 ATTORNEY/AGENT INFORMATION:
26 NAME: Gimmil, Edward R
27 REGISTRATION NUMBER: 38,891
28 REFERENCE/DOCKET NUMBER: P30591C2
29 TELECOMMUNICATION INFORMATION:
30 TELEPHONE: 610-270-4478
31 TELEFAX: 610-270-5090
32 TELEX:
33 INFORMATION FOR SEQ ID NO: 12:
34 SEQUENCE CHARACTERISTICS:
35 LENGTH: 178 amino acids
36 TYPE: amino acid
37 STRANDEDNESS: single
38 TOPOLOGY: linear
39 MOLECULE TYPE: Protein
40 US-08-459-135A-12
41
42 Query March 93.3%; Score 111; DB 2; Length 178;
43 Best Local Similarity 95.2%; Pred. No. 7,8e-10;
44 Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
45
46 QY 1 KPSYQFGGHSVDFEEDTLPK 21
47 |||||
48 |||||
49 |||||
50 |||||
51 |||||
52 |||||
53 KPSYQFGGHSVDFEEDTLPK 113
54
55 Db 93 KPSYQFGGHSVDFEEDTLPK 113
56
57 RESULT 9
58 US-08-495-559-12
59 ; Sequence 12, Application US/08495559A
60 ; Patent No. 6054572
61 ; GENERAL INFORMATION:
62 APPLICANT: BURMAN, Martin Karl Russel
63 APPLICANT: CHOPRA, Ian
64 APPLICANT: CRITCHLEY, Ian Alfred
65 APPLICANT: KNOWLES, David Justin Charles
66 TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN: MONOCLONAL
67 TITLE OF INVENTION: ANTIBODY AND THEIR USE IN PREVENTING BACTERIAL ADHESION
68 FILE REFERENCE: P30591
69 CURRENT APPLICATION NUMBER: US/08/495,559A
70 CURRENT FILING DATE: 1995-08-03
71 EARLIER APPLICATION NUMBER: GB 9302289.5
72 EARLIER FILING DATE: 1993-02-05
73 EARLIER APPLICATION NUMBER: GB 9321592.9
74 EARLIER FILING DATE: 1993-10-20
75 NUMBER OF SEQ ID NOS: 13
76 SOFTWARE: Fastseq for Windows Version 3.0
77 SEQ ID NO 12
78 LENGTH: 178
79 TYPE: PRT

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ORGANISM: Staphylococcus aureus
US-08-495-559-12

Query Match 93.3%; Score 111; DB 3; Length 178;
Best Local Similarity 95.2%; Pred. No. 7.8e-10;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KPSYOGGHSVDFEPTLPK 21
DB 93 KPSYOGGHSVDFEPTLPK 113

RESULT 10
US-08-956-171E-5254

Sequence 5254, Application US/08956171E
Patent No. 6593114

GENERAL INFORMATION:

APPLICANT: Charles Kunach

Gail H. Choi

Patrick S. Dillon

Craig A. Rosen

Steven C. Barash

Michael R. Pannan

TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences

NUMBER OF SEQUENCES: 5256

CORRESPONDENCE ADDRESS:

ADDRESSEE: Human Genome Sciences, Inc.

STREET: 9410 Key West Avenue

CITY: Rockville

STATE: Maryland

COUNTRY: USA

ZIP: 20850

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.50 inch, 1.4mb storage

COMPUTER: HP Vectra 486/33

OPERATING SYSTEM: MSDOS version 6.2

SOFTWARE: ASCII Text

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/956,171E

FILING DATE: 20-Oct-1997

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 60/009,861

FILING DATE: January 5, 1996

APPLICATION NUMBER: 08/781,986

FILING DATE: January 3, 1997

ATTORNEY/AGENT INFORMATION:

NAME: Mark J. Hyman

REGISTRATION NUMBER: 46,789

REFERENCE/DOCKET NUMBER: PB248P1

TELEPHONE: (240) 314-1224

TELEFAX: (301) 309-8439

INFORMATION FOR SEQ ID NO: 5254:

SEQUENCE CHARACTERISTICS:

LENGTH: 1027 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 5254:

US-08-956-171E-5254

Query Match 93.3%; Score 111; DB 4; Length 1027;
Best Local Similarity 95.2%; Pred. No. 5.7e-09;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KPSYOGGHSVDFEPTLPK 21
DB 846 KPSYOGGHSVDFEPTLPK 866

RESULT 11

US-08-781-986A-5254
Sequence 5254, Application US/08781986A

Patent No. 6737248

GENERAL INFORMATION:

APPLICANT: Charles Kunach

TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences

NUMBER OF SEQUENCES: 5255

CORRESPONDENCE ADDRESS:

ADDRESSEE: Human Genome Sciences, Inc.

STREET: 9410 Key West Avenue

CITY: Rockville

STATE: Maryland

COUNTRY: USA

ZIP: 20850

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.50 inch, 1.4mb storage

COMPUTER: HP Vectra 486/33

OPERATING SYSTEM: MSDOS version 6.2

SOFTWARE: ASCII Text

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/781,986A

FILING DATE:

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Benson, Bob

REGISTRATION NUMBER: 30,446

REFERENCE/DOCKET NUMBER: PB248PP

TELEPHONE: (301) 309-8504

TELEFAX: (301) 309-8512

INFORMATION FOR SEQ ID NO: 5254:

SEQUENCE CHARACTERISTICS:

LENGTH: 1027 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-781-986A-5254

Query Match 93.3%; Score 111; DB 4; Length 1027;
Best Local Similarity 95.2%; Pred. No. 5.7e-09;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KPSYOGGHSVDFEPTLPK 21
DB 846 KPSYOGGHSVDFEPTLPK 866

RESULT 12
US-09-010-317-14

Sequence 14, Application US/09010317

Patent No. 6685943

GENERAL INFORMATION:

APPLICANT: Hook, Magnus

APPLICANT: Patti, Joseph M.

APPLICANT: House-Pompeo, Karen L.

APPLICANT: Speziale, Pietro

APPLICANT: Jon, Danny

APPLICANT: McGavin, Martin J.

TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS

NUMBER OF SEQUENCES: 105

CORRESPONDENCE ADDRESS:

ADDRESSEE: Arnold, White & Durkee

STREET: P.O. Box 4433

CITY: Houston

STATE: TX

COUNTRY: USA

ZIP: 77210-4433

COMPUTER READABLE FORM:

```

; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/010.317
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/036.139
; FILING DATE: 21-JAN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Hibler, David W.
; REGISTRATION NUMBER: 41.071
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 512-418-3000
; TELEFAX: 512-474-7577
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
;
US-09-010-317-14

Query Match      89.1%; Score 106; DB 4; Length 21;
Best Local Similarity 95.0%; Pred. No. 4.3e-10;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      2 PSYFGGHSVDFEPTLPK 21
Db      2 PSYFGGHSVDFEPTLPK 21

RESULT 13
US-09-010-317-16
; Sequence 16, Application US/09010317
; Patent No. 6685943
; GENERAL INFORMATION:
; APPLICANT: Hook, Magnus
; APPLICANT: Patti, Joseph M.
; APPLICANT: House-Pompeo, Karen L.
; APPLICANT: Speziale, Pietro
; APPLICANT: Joh, Danny
; APPLICANT: McGavin, Martin J.
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
; NUMBER OF SEQUENCES: 105
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: TX
; COUNTRY: USA
; ZIP: 77210-4433
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/010.317
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/036.139
; FILING DATE: 21-JAN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Hibler, David W.
; REGISTRATION NUMBER: 41.071
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 512-418-3000
; TELEFAX: 512-474-7577
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
;
US-09-010-317-23

Query Match      89.1%; Score 106; DB 4; Length 21;
Best Local Similarity 90.5%; Pred. No. 4.3e-10;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```

; TELEPHONE: 512-418-3000
; TELEFAX: 512-474-7577
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
;
US-09-010-317-16

Query Match      89.1%; Score 106; DB 4; Length 21;
Best Local Similarity 90.5%; Pred. No. 4.3e-10;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      1 KPSYFGGHSVDFEPTLPK 21
Db      1 KPSYFGGHSVDFEPTLPK 21

RESULT 14
US-09-010-317-23
; Sequence 23, Application US/09010317
; Patent No. 6685943
; GENERAL INFORMATION:
; APPLICANT: Hook, Magnus
; APPLICANT: Patti, Joseph M.
; APPLICANT: House-Pompeo, Karen L.
; APPLICANT: Speziale, Pietro
; APPLICANT: Joh, Danny
; APPLICANT: McGavin, Martin J.
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
; NUMBER OF SEQUENCES: 105
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: TX
; COUNTRY: USA
; ZIP: 77210-4433
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/010.317
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/036.139
; FILING DATE: 21-JAN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Hibler, David W.
; REGISTRATION NUMBER: 41.071
; REFERENCE/DOCKET NUMBER: TAMK:189
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 512-418-3000
; TELEFAX: 512-474-7577
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
;
US-09-010-317-23

Query Match      89.1%; Score 106; DB 4; Length 21;
Best Local Similarity 90.5%; Pred. No. 4.3e-10;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      1 KPSYFGGHSVDFEPTLPK 21
Db      1 KPSYFGGHSVDFEPTLPK 21
```

Db 1 KPSYQFGGHNPDPEEDTLPK 21

RESULT 15

US-09-010-317-33
Sequence 33, Application US/09010317
Patent No. 6685943

GENERAL INFORMATION:

APPLICANT: Hook, Magnus

APPLICANT: Patti, Joseph M.

APPLICANT: House-Pompeo, Karen L.

APPLICANT: Speziale, Pietro

APPLICANT: Joh, Danny

APPLICANT: McGavin, Martin J.

TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS

TITLE OF INVENTION: AND METHODS OF USE

NUMBER OF SEQUENCES: 105

CORRESPONDENCE ADDRESS:

ADDRESSEE: Arnold, White & Durkee

STREET: P.O. Box 4433

CITY: Houston

STATE: TX

COUNTRY: USA

ZIP: 77210-4433

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA: US/09/010.317

APPLICATION NUMBER: US/09/010.317

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 60/036,139

FILING DATE: 21-JAN-1997

ATTORNEY/AGENT INFORMATION:

NAME: Hibler, David W.

REGISTRATION NUMBER: 41,071

REFERENCE/DOCKET NUMBER: TANK:189

TELECOMMUNICATION INFORMATION:

TELEPHONE: 512-418-3000

TELEFAX: 512-474-7577

INFORMATION FOR SEQ ID NO: 33:

SEQUENCE CHARACTERISTICS:

LENGTH: 21 amino acids

TYPE: amino acid

STRANDEDNESS:

TOPOLOGY: linear

US-09-010-317-33

Query Match 89.1%; Score 106; DB 4; Length 21;

Best Local Similarity 95.0%; Pred. No. 4.3e-10;

Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

1 KPSYQFGGHNPDPEEDTLPK 20

1 KPSYQFGGHNPDPEEDTLPK 20

Search completed: October 22, 2005, 03:51:14

Job time : 16.9358 secs

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OM protein - protein search, using BW model

Run on: October 22, 2005, 10:49:15 ; Search time 59.2367 Seconds
(without alignments)
148.005 Million cell updates/sec

Title: US-10-731-238-28

Perfect score: 119

Sequence: 1 KPSYQFGHNSVDEPDTLPK 21

Scoring table: BLOSUM62

Searched: 1862951 seqs, 417491010 residues

Total number of hits satisfying chosen parameters: 1862951

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing:

Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA.*
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2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
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20: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep.*
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22: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	119	100.0	21	18	US-10-731-238-28
2	111	93.3	21	18	US-10-731-238-9
3	111	93.3	37	20	US-11-066-697-1134
4	111	93.3	139	9	US-09-813-820-8
5	111	93.3	1018	9	US-09-815-242-5797
6	111	93.3	1018	9	US-09-815-242-12838
7	111	93.3	1018	17	US-10-470-048B-68
8	111	93.3	1027	8	US-08-781-986A-5254
9	111	93.3	1027	15	US-10-329-624-5254
10	108	90.8	961	15	US-10-282-122A-43778
11	108	90.8	978	9	US-09-815-242-5456

12	108	90.8	1001	9	US-09-815-242-12686	Sequence 12686, A
13	108	90.8	1038	15	US-10-282-122A-43827	Sequence 43827, A
14	106	89.1	21	18	US-10-731-238-14	Sequence 14, Appl
15	106	89.1	21	18	US-10-731-238-16	Sequence 16, Appl
16	106	89.1	21	18	US-10-731-238-18	Sequence 18, Appl
17	106	89.1	21	18	US-10-731-238-23	Sequence 23, Appl
18	105	88.2	21	18	US-10-731-238-33	Sequence 33, Appl
19	105	88.2	21	18	US-10-731-238-18	Sequence 18, Appl
20	105	88.2	21	18	US-10-731-238-24	Sequence 24, Appl
21	105	88.2	21	18	US-10-731-238-27	Sequence 27, Appl
22	105	88.2	21	18	US-10-731-238-30	Sequence 30, Appl
23	105	88.2	21	18	US-10-731-238-25	Sequence 25, Appl
24	104	87.4	21	18	US-10-731-238-31	Sequence 31, Appl
25	104	87.4	388	8	US-08-901-062-1	Sequence 1, Appl
26	104	87.4	559	8	US-08-781-986A-5251	Sequence 5251, Ap
27	104	87.4	559	15	US-10-329-624-5251	Sequence 5251, Ap
28	104	87.4	940	17	US-10-470-048B-424	Sequence 424, App
29	104	87.4	948	17	US-10-470-048B-69	Sequence 69, Appl
30	103	86.6	21	18	US-10-731-238-15	Sequence 15, Appl
31	103	86.6	21	18	US-10-731-238-10	Sequence 10, Appl
32	103	86.6	21	18	US-10-731-238-20	Sequence 20, Appl
33	103	86.6	21	18	US-10-731-238-22	Sequence 22, Appl
34	103	86.6	21	18	US-10-731-238-32	Sequence 32, Appl
35	103	86.6	22	18	US-10-731-238-13	Sequence 13, Appl
36	101	84.9	21	18	US-10-731-238-17	Sequence 17, Appl
37	101	84.9	21	18	US-10-731-238-19	Sequence 19, Appl
38	101	84.9	21	18	US-10-731-238-21	Sequence 21, Appl
39	101	84.9	21	18	US-10-731-238-26	Sequence 26, Appl
40	83	69.7	21	18	US-10-731-238-34	Sequence 34, Appl
41	72	60.5	14	18	US-10-731-238-61	Sequence 61, Appl
42	59	48.6	10	18	US-10-731-238-96	Sequence 96, Appl
43	58	48.7	10	18	US-10-731-238-97	Sequence 97, Appl
44	57	47.9	10	18	US-10-731-238-98	Sequence 98, Appl
45	54	45.4	10	18	US-10-731-238-95	Sequence 95, Appl

ALIGNMENTS

RESULT 1
US-10-731-238-28
; Sequence 28, Application US/10731238
; Publication No. US20050123552A1
; GENERAL INFORMATION:
; APPLICANT: Hook, Magnus
; Patli, Joseph M.
; House-Pompeo, Karen L.
; Speciale, Pietro
; John, Danny
; Mcdevlin, Martin J.
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
; AND METHODS OF USE
; NUMBER OF SEQUENCES: 105
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: TX
; COUNTRY: USA
; ZIP: 77210-4433
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/731,238
; FILING DATE: 10-Dec-2003
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/010,317
; FILING DATE: 21-Jan-1998
; APPLICATION NUMBER: US 60/036,139

FILED DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TANK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
US-10-731-238-28
SEQUENCE DESCRIPTION: SEQ ID NO: 28:
Query Match 100.0%; Score 119; DB 18; Length 21;
Best Local Similarity 100.0%; Pred. No. 4.5e-11;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 KPSYQFGHNSVDEPDTLPK 21
Db 1 KPSYQFGHNSVDEPDTLPK 21
RESULT 2
US-10-731-238-9
Sequence 9, Application US/10731238
Publication No. US20050123552A1
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
Patti, Joseph M.
House-Pompeo, Karen L.
Speziale, Pietro
Joh, Danny
McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/731,238
FILING DATE: 10-Dec-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE: 21-Jan-1998
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TANK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>

TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 9:
US-10-731-238-9
Query Match 93.3%; Score 111; DB 18; Length 21;
Best Local Similarity 95.2%; Pred. No. 7.6e-10;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 KPSYQFGHNSVDEPDTLPK 21
Db 1 KPSYQFGHNSVDEPDTLPK 21
RESULT 3
US-11-066-697-1134
Sequence 1134, Application US/11066697
Publication No. US20050187159A1
GENERAL INFORMATION:
APPLICANT: Bridon, Dominique P.
APPLICANT: Ezrin, Alan M.
APPLICANT: Milner, Peter G.
APPLICANT: Holmes, Darren L.
APPLICANT: Thibaudau, Karen
TITLE OF INVENTION: PROTECTION OF ENDOGENOUS THERAPEUTIC PEPTIDES FROM
TITLE OF INVENTION: PEPTIDASE ACTIVITY THROUGH CONJUGATION TO BLOOD
FILE REFERENCE: 500862002301
CURRENT APPLICATION NUMBER: US/11/066,697
CURRENT FILING DATE: 2005-02-25
PRIOR APPLICATION NUMBER: 09/657,276
PRIOR FILING DATE: 2000-09-07
PRIOR APPLICATION NUMBER: 60/153,406
PRIOR FILING DATE: 1999-09-10
PRIOR APPLICATION NUMBER: 60/159,783
PRIOR FILING DATE: 1999-10-15
NUMBER OF SEQ ID NOS: 1617
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1134
LENGTH: 37
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-11-066-697-1134
Query Match 93.3%; Score 111; DB 20; Length 37;
Best Local Similarity 95.2%; Pred. No. 1.4e-09;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 KPSYQFGHNSVDEPDTLPK 21
Db 16 KPSYQFGHNSVDEPDTLPK 36
RESULT 4
US-09-813-820-8
Sequence 8, Application US/09813820
Patent No. US20020102262A1
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
Patti, Joseph M.
House-Pompeo, Karen
Schanam, Narayana
Sytersky, Jindrich
TITLE OF INVENTION: COLLAGEN BINDING PROTEIN COMPOSITIONS
AND METHODS OF USE
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: Texas

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; COUNTRY: U.S.
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/813,820
; FILING DATE: 22-Mar-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/856,253
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Kitchell, Barbara S.
; REGISTRATION NUMBER: 33,928
; REFERENCE/DOCKET NUMBER: TAMK:193
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (512) 474-7577
; TELEFAX: (512) 474-7577
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 139 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-09-813-820-8

Query Match      93.3%; Score 111; DB 9; Length 139;
Best Local Similarity 95.2%; Pred. No. 5,6e-09;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1 KPSYQFGHNSVDFEPTLPK 21
Db      107 KPSYQFGHNSVDFEPTLPK 127

RESULT 5
US-09-815-242-5797
; Sequence 5797, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Karl L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; FILE REFERENCE: Prokaryotes
; CURRENT APPLICATION NUMBER: US/09/815,242
; FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version 4.0
; FILE REFERENCE: FastSeq for Windows Version 4.0

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; SEQ ID NO 5797
; LENGTH: 1018
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-09-815-242-5797

Query Match      93.3%; Score 111; DB 9; Length 1018;
Best Local Similarity 95.2%; Pred. No. 4,6e-08;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1 KPSYQFGHNSVDFEPTLPK 21
Db      837 KPSYQFGHNSVDFEPTLPK 857

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US-09-815-242-12838
; Sequence 12838, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Karl L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; FILE REFERENCE: Prokaryotes
; CURRENT APPLICATION NUMBER: US/09/815,242
; FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12838
; LENGTH: 1018
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-09-815-242-12838

Query Match      93.3%; Score 111; DB 9; Length 1018;
Best Local Similarity 95.2%; Pred. No. 4,6e-08;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1 KPSYQFGHNSVDFEPTLPK 21
Db      837 KPSYQFGHNSVDFEPTLPK 857

RESULT 7
US-10-470-048B-68
; Sequence 68, Application US/10470048B
; Publication No. US2005003744A1
; GENERAL INFORMATION:
; APPLICANT: MEINKE ET AL.
; TITLE OF INVENTION: A METHOD FOR IDENTIFICATION, ISOLATION AND PRODUCTION OF
; FILE REFERENCE: SONN:035US

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;; CURRENT APPLICATION NUMBER: US/10/470,048B
;; CURRENT FILING DATE: 2003-07-25
;; NUMBER OF SEQ ID NOS: 603
;; SOFTWARE: PatentIn version 3.1
;; SEQ ID NO 68
;; LENGTH: 1018
;; TYPE: PR1
;; ORGANISM: Staphylococcus aureus
US-10-470-048B-68

Query Match 93.3%; Score 111; DB 17; Length 1018;
Best Local Similarity 95.2%; Pred. No. 4.6e-08;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KPSYQFGHNSVDFEPTLPK 21
DB 837 KPSYQFGHNSVDFEPTLPK 857

RESULT 8
US-08-781-986A-5254
; Sequence 5254, Application US/08781986A
; Publication No. US20030054436A1
; GENERAL INFORMATION:
; APPLICANT: Charles Kunsch
; TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
; NUMBER OF SEQUENCES: 5255
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/781,986A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Benson, Bob
; REGISTRATION NUMBER: 30,446
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 5254:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1027 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-781-986A-5254

Query Match 93.3%; Score 111; DB 8; Length 1027;
Best Local Similarity 95.2%; Pred. No. 4.7e-08;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KPSYQFGHNSVDFEPTLPK 21
DB 846 KPSYQFGHNSVDFEPTLPK 866

RESULT 9
US-10-329-624-5254

; Sequence 5254, Application US/10329624
; Publication No. US20040043037A1
; GENERAL INFORMATION:
; APPLICANT: Charles Kunsch
; Gil H. Choi
; Patrick S. Dillon
; Craig A. Rosen
; Steven C. Barash
; Michael R. Fannon

; TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences

; NUMBER OF SEQUENCES: 5256

; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.

; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage

; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text

; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/329,624
; FILING DATE: 27-Dec-2002

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/956,171
; FILING DATE: October 20, 1997

; APPLICATION NUMBER: 60/009,861
; FILING DATE: January 5, 1996

; APPLICATION NUMBER: 08/781,986
; FILING DATE: January 3, 1997

; ATTORNEY/AGENT INFORMATION:
; NAME: Mark J. Hyman

; REGISTRATION NUMBER: 46,789
; REFERENCE/DOCKET NUMBER: PB248P1D1

; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (240) 314-1224
; TELEFAX: (301) 309-8439

; INFORMATION FOR SEQ ID NO: 5254:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1027 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 5254:

US-10-329-624-5254

Query Match 93.3%; Score 111; DB 15; Length 1027;
Best Local Similarity 95.2%; Pred. No. 4.7e-08;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KPSYQFGHNSVDFEPTLPK 21
DB 846 KPSYQFGHNSVDFEPTLPK 866

RESULT 10
US-10-282-122A-43778
; Sequence 43778, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zykkind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant

```
APPLICANT: Yamamoto, Robert
APPLICANT: Forsyth, R.
TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REFERENCE: ELITRA.014A
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/230,335
PRIOR FILING DATE: 2000-09-06
PRIOR APPLICATION NUMBER: 60/230,347
PRIOR FILING DATE: 2000-09-09
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/267,636
PRIOR FILING DATE: 2001-02-09
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 78614
SOFTWARE: PatentIn version 3.1
SEQ ID NO 43778
LENGTH: 961
TYPE: PR
ORGANISM: Staphylococcus aureus
US-10-282-122A-43778

Query Match
Best Local Similarity 90.8%; Score 108; DB 15; Length 961;
Matches 19; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
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```
QY 1 KPSYOGGHSVDPEPTLPK 21
DB 784 KPNYOGGHSVDPEPTLPK 804
```

```
RESULT 11
US-09-815-242-5456
```

```
Sequence 5456, Application US/09815242
Patent No. US20020061569A1
```

```
GENERAL INFORMATION:
```

```
APPLICANT: Haselbeck, Robert
```

```
APPLICANT: Ohlsen, Karl L.
```

```
APPLICANT: Zyskind, Judith W.
```

```
APPLICANT: Wall, Daniel
```

```
APPLICANT: Trawick, John D.
```

```
APPLICANT: Carr, Grant J.
```

```
APPLICANT: Yamamoto, Robert T.
```

```
APPLICANT: Xu, H. Howard
```

```
TITLE OF INVENTION: Identification of Essential Genes in
```

```
FILE REFERENCE: ELITRA.011A
```

```
CURRENT APPLICATION NUMBER: US/09/815,242
```

```
CURRENT FILING DATE: 2001-03-21
```

```
PRIOR APPLICATION NUMBER: 60/191,078
```

```
PRIOR FILING DATE: 2000-03-21
```

```
PRIOR APPLICATION NUMBER: 60/206,848
```

```
PRIOR FILING DATE: 2000-05-23
```

```
PRIOR APPLICATION NUMBER: 60/207,727
```

```
PRIOR FILING DATE: 2000-05-26
```

```
PRIOR APPLICATION NUMBER: 60/242,578
```

```
PRIOR FILING DATE: 2000-10-23
```

```
PRIOR APPLICATION NUMBER: 60/253,625
```

```
PRIOR FILING DATE: 2000-11-27
```

```
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 5456
LENGTH: 978
TYPE: PR
ORGANISM: Staphylococcus aureus
US-09-815-242-5456
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```
Query Match
Best Local Similarity 90.8%; Score 108; DB 9; Length 978;
Matches 19; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
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QY 1 KPSYOGGHSVDPEPTLPK 21
DB 815 KPNYOGGHSVDPEPTLPK 835
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RESULT 12
US-09-815-242-12686
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Sequence 12686, Application US/09815242
Patent No. US20020061569A1
```

```
GENERAL INFORMATION:
```

```
APPLICANT: Haselbeck, Robert
```

```
APPLICANT: Ohlsen, Karl L.
```

```
APPLICANT: Zyskind, Judith W.
```

```
APPLICANT: Wall, Daniel
```

```
APPLICANT: Trawick, John D.
```

```
APPLICANT: Carr, Grant J.
```

```
APPLICANT: Yamamoto, Robert T.
```

```
TITLE OF INVENTION: Identification of Essential Genes in
```

```
FILE REFERENCE: ELITRA.011A
```

```
CURRENT APPLICATION NUMBER: US/09/815,242
```

```
CURRENT FILING DATE: 2001-03-21
```

```
PRIOR APPLICATION NUMBER: 60/191,078
```

```
PRIOR FILING DATE: 2000-03-21
```

```
PRIOR APPLICATION NUMBER: 60/206,848
```

```
PRIOR FILING DATE: 2000-05-23
```

```
PRIOR APPLICATION NUMBER: 60/207,727
```

```
PRIOR FILING DATE: 2000-05-26
```

```
PRIOR APPLICATION NUMBER: 60/242,578
```

```
PRIOR FILING DATE: 2000-10-23
```

```
PRIOR APPLICATION NUMBER: 60/253,625
```

```
PRIOR FILING DATE: 2000-11-27
```

```
PRIOR APPLICATION NUMBER: 60/257,931
```

```
PRIOR FILING DATE: 2000-12-22
```

```
PRIOR APPLICATION NUMBER: 60/269,308
```

```
PRIOR FILING DATE: 2001-02-16
```

```
NUMBER OF SEQ ID NOS: 14110
```

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SOFTWARE: FastSeq for Windows Version 4.0
```

```
SEQ ID NO 12686
```

```
LENGTH: 1001
```

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TYPE: PR
```

```
ORGANISM: Staphylococcus aureus
```

```
US-09-815-242-12686
```

```
Query Match
Best Local Similarity 90.8%; Score 108; DB 9; Length 1001;
Matches 19; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
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```
QY 1 KPSYOGGHSVDPEPTLPK 21
DB 838 KPNYOGGHSVDPEPTLPK 858
```

```
RESULT 13
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```
US-10-282-122A-43827
```

```
Sequence 43827, Application US/10282122A
```

Publication No. US20040029129A1
GENERAL INFORMATION:
APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari
APPLICANT: Zykkind, Judith
APPLICANT: Wall, Daniel
APPLICANT: Trewick, John
APPLICANT: Carr, Grant
APPLICANT: Yamamoto, Robert
APPLICANT: Foreysch, R.
APPLICANT: Xu, H.
TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REFERENCE: ELITRA.034A
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/230,335
PRIOR FILING DATE: 2000-09-06
PRIOR APPLICATION NUMBER: 60/230,347
PRIOR FILING DATE: 2000-09-09
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/267,636
PRIOR FILING DATE: 2001-02-09
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 78614
SOFTWARE: PatentIn version 3.1
SEQ ID NO 43827
LENGTH: 1038
TYPE: PRT
ORGANISM: *Staphylococcus aureus*
US-10-282-122A-43827

Query Match 90.8%; Score 108; DB 15; Length 1038;
Best Local Similarity 90.5%; Pred. No. 1.4e-07;
Matches 19; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 KPSYQFGGHSVDPEDTLPK 21
DB 833 KPNYQFGGHSVDPEDTLPK 853

RESULT 14
US-10-731-238-14
Sequence 14, Application US/10731238
Publication No. US20050123552A1
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
APPLICANT: Patti, Joseph M.
APPLICANT: House-Pompeo, Karen L.
APPLICANT: Speziale, Pietro
APPLICANT: Joh, Danny
APPLICANT: McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESSES:
ADDRESSER: Arnold, White & Durkee
STREET: P. O. Box 4433

CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/731,238
FILING DATE: 10-Dec-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE: 21-Jan-1998
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TBMK.189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 14:
US-10-731-238-14

Query Match 89.1%; Score 106; DB 18; Length 21;
Best Local Similarity 95.0%; Pred. No. 4.5e-09;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 PSYQFGGHSVDPEDTLPK 21
DB 2 PSYQFGGHSVDPEDTLPK 21

RESULT 15
US-10-731-238-16
Sequence 16, Application US/10731238
Publication No. US20050123552A1
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
APPLICANT: Patti, Joseph M.
APPLICANT: House-Pompeo, Karen L.
APPLICANT: Speziale, Pietro
APPLICANT: Joh, Danny
APPLICANT: McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESSES:
ADDRESSER: Arnold, White & Durkee
STREET: P. O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/731,238
FILING DATE: 10-Dec-2003
CLASSIFICATION: <Unknown>

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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/010,317
; FILING DATE: 21-Jan-1998
; APPLICATION NUMBER: US 60/036,139
; FILING DATE: 21-JAN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Hibley, David W.
; REGISTRATION NUMBER: 41, 071
; REFERENCE/DOCKET NUMBER: TAWK:189
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 512-418-3000
; TELEFAX: 512-474-7577
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 16:
US-10-731-238-16

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Query Match      89.1%; Score 106; DB 18; Length 21;
Best Local Similarity 90.5%; Pred: No. 4,5e-09;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Oy      1 KPSYQFGHNSVDPEPTLPK 21
      1 KPYQFGHNSVDPEPTLPK 21
Db

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Search completed: October 22, 2005, 11:34:42
 Job time : 59.2367 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 22, 2005, 02:23:36 ; Search time 10.5465 Seconds
(without alignments)
191.586 Million cell updates/sec

Title: US-10-731-238-28
Perfect score: 119
Sequence: 1 KPSYQFGHNSVDFEPTLPK 21

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	111	93.3	1018	2 A32192	fibronectin-bindin
2	108	90.8	961	2 G90053	hypothetical prote
3	108	90.8	1038	2 H90053	hypothetical prote
4	104	87.4	940	2 S19702	fibronectin-bindin
5	52	43.7	303	2 B75485	fructokinase - Del
6	51.5	43.3	234	2 T10473	late expression fa
7	50.5	42.4	1038	2 T15098	hypothetical prote
8	50	42.0	288	2 T17395	probable 33.6k pro
9	50	42.0	288	2 A42518	AAR protein - vacc
10	49	41.2	216	2 S58652	hypothetical prote
11	49	41.2	2802	2 P97686	cyclic beta-(1-2)
12	49	41.2	2831	2 A12911	beta (1->2) glucan
13	47	39.5	954	2 AF2756	glycine cleavage s
14	47	39.5	954	2 E97537	glycine cleavage s
15	46	38.7	453	2 H70333	conserved hypothet
16	46	38.7	462	2 A39356	3-oxoacyl-lacyl-ca
17	46	38.7	474	2 B84357	serine-tRNA synthet
18	45	37.8	257	2 A36057	MHC class I histoc
19	45	37.8	468	2 T26081	hypothetical prote
20	45	37.8	469	2 T10061	3-oxoacyl-lacyl-ca
21	45	37.8	678	2 A70762	probable PPE prote
22	45	37.8	719	2 A96008	hypothetical prote
23	45	37.8	1322	2 A59288	myosin heavy chain
24	45	37.8	1354	2 T13930	tripeptidyl-peptid
25	45	37.8	2870	2 A35548	319k protein ndvb
26	44.5	37.4	345	2 AB1448	gpII (bacteriophag
27	44.5	37.4	417	2 T34930	probable secreted
28	44	37.0	347	1 HPMS	hapoglobin precur
29	44	37.0	433	2 T01405	vesicle-associated

30	44	37.0	533	2 C97324	beta-xylolase, f
31	43.5	36.6	852	2 A99790	hypothetical prote
32	43.5	36.6	852	2 D85650	hypothetical prote
33	43.5	36.6	985	2 E69850	formate dehydrogen
34	43	36.1	304	2 AG1837	WD-40 repeat prote
35	43	36.1	504	2 T34106	hypothetical prote
36	43	36.1	808	2 F81180	conserved hypochet
37	43	36.1	2831	2 T31419	cyclic beta 1-2 gl
38	43	36.1	2867	2 AG3481	cellulose-phospho
39	42.5	35.7	535	2 T10055	probable 3-oxoacyl
40	42.5	35.7	541	2 D96779	probable 3-ketocacy
41	42	35.3	259	2 S39664	hypothetical prote
42	42	35.3	288	2 F72164	AAR protein - vari
43	42	35.3	288	2 T28550	hypothetical prote
44	42	35.3	288	2 T36848	AAR protein - vari
45	42	35.3	339	2 S32624	INDC11 protein - f

ALIGNMENTS

RESULT 1
A32192
fibronectin-binding protein - Staphylococcus aureus
C:Species: Staphylococcus aureus
C:Date: 31-Jul-1989 #sequence_revision 31-Jul-1989 #text_change 16-Feb-1997
A:Accession: A32192
R:Signaes, C.; Rauccl, G.; Joensson, K.; Lindgren, P.E.; Anantharamiah, G.M.; Hoesock, M.
Proc. Natl. Acad. Sci. U.S.A. 86, 699-703, 1989
A:Title: Nucleotide sequence of the gene for a fibronectin-binding protein from Staphyloc
A:Reference number: A32192; MUID:89098996; PMID:2521391
A:Accession: A32192
A:Status: Preliminary
A:Molecule type: DNA
A:Residues: 1-1018 <SIG>
A:Cross-references: GB:J04151
C:Keywords: fibronectin binding

Query Match 93.3%; Score 111; DB 2; Length 1018;
Best Local Similarity 95.2%; Pred. No. 1.9e-09;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KPSYQFGHNSVDFEPTLPK 21
DB 837 KPSYQFGHNSVDFEPTLPK 857

RESULT 2

G90053
hypothetical protein fnb3 [imported] - Staphylococcus aureus (strain N315)
C:Species: Staphylococcus aureus
C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004

ma, A.; Mizutani-U, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.;
C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramoto, K.
Lancet 357, 1225-1240, 2001
A:Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.
A:Reference number: A69758; MUID:21311952; PMID:11418146
A:Accession: G90053
A:Status: Preliminary
A:Molecule type: DNA
A:Residues: 1-961 <KUN>
A:Cross-references: UNIPROT:Q99RD3; GB:BA000018; PID:g13702452; PTDN:BA83593.1; GSPDB:G

A:Experimental source: strain N315
C:Genetics:
A:Gene: fnb3

Query Match 90.8%; Score 108; DB 2; Length 961;
Best Local Similarity 90.5%; Pred. No. 5.4e-09;
Matches 19; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 KPSYQFGHNSVDFEPTLPK 21

Db 784 KPNYQFGGHSVDFEEDTLPK 804

RESULT 3

H90053

hypothetical protein fnb [imported] - Staphylococcus aureus (strain N315)

C/Species: Staphylococcus aureus

C/Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004

C/Accession: H90053

R/Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguc

ma, A.; Mitani-Ii, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.;

C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiratake, K.

Lancet 357, 1225-1240, 2001

A/Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.

A/Reference number: A89758; MUID:21311952; PMID:11418146

A/Accession: H90053

A/Status: Preliminary

A/Molecule type: DNA

A/Residues: 1-1038 <KUR>

A/Cross-references: UNIPROT:Q99RD2; GB:BA000018; PID:g13702453; PIDN:BA03594.1; GSPDB:C

A/Experimental source: strain N315

C/Genetics:

A/Gene: fnb

Query Match 90.8%; Score 108; DB 2; Length 1038;

Best Local Similarity 90.5%; Pred. No. 5.9e-09;

Matches 19; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 KPSYQFGGHSVDFEEDTLPK 21

Db 833 KPNYQFGGHSVDFEEDTLPK 853

RESULT 4

S19702

fibronectin-binding protein B - Staphylococcus aureus

C/Species: Staphylococcus aureus

C/Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004

C/Accession: S19702

R./Jensen, K.; Signaes, C.; Mueller, H.P.; Lindberg, M.

Eur. J. Biochem. 202, 1041-1048, 1991

A/Title: Two different genes encode fibronectin binding proteins in Staphylococcus aureu

A/Reference number: S19702; MUID:92111475; PMID:1837266

A/Accession: S19702

A/Status: Preliminary

A/Molecule type: DNA

A/Residues: 1-940 <JOB>

A/Cross-references: UNIPROT:Q53682; EMBL:X62992; NID:g49040; PIDN:CAA44726.1; PID:g58156

C/Keywords: fibronectin binding

Query Match 87.4%; Score 104; DB 2; Length 940;

Best Local Similarity 85.7%; Pred. No. 2.3e-08;

Matches 18; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 KPSYQFGGHSVDFEEDTLPK 21

Db 773 KPNYQFGGHSVDFEEDTLPK 793

RESULT 5

B75485

fructokinase - Deinococcus radiodurans (strain R1)

C/Species: Deinococcus radiodurans

C/Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004

C/Accession: B75485

R./White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;

S.; Smith, H.O.; Venter, J.C.; Frazer, C.M.

Science 286, 1571-1577, 1999

A/Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.

A/Reference number: A75250; MUID:20036896; PMID:10567266

A/Accession: B75485

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-303 <WHI>

A/Cross-references: UNIPROT:Q9RWE1; GB:AE001928; GB:AE000513; NID:g6458421; PIDN:AAF10301

A/Experimental source: strain R1

C/Genetics:

A/Gene: DR0728

A/Map position: 1

C/Superfamily: ribokinase

Query Match 43.7%; Score 52; DB 2; Length 303;

Best Local Similarity 52.4%; Pred. No. 1.4;

Matches 11; Conservative 2; Mismatches 6; Indels 2; Gaps 1;

QY 2 PSYQFGGHSVDFEEDTLPK 20

Db 94 PYRFLGNSADLHFDPTLRP 114

RESULT 6

T30473

late expression factor 1 - Lymantria dispar nuclear polyhedrosis virus

C/Species: Lymantria dispar nuclear polyhedrosis virus, LdMNPV

C/Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004

C/Accession: T30473

R./Kuzio, J.; Pearson, M.N.; Harwood, S.H.; Funk, C.J.; Evans, J.T.; Slavicek, J.M.; Rohm

Virology 253, 17-34, 1999

A/Title: Sequence and analysis of the genome of a baculovirus pathogenic for Lymantria di

A/Reference number: Z20836; MUID:99124785; PMID:9887315

A/Accession: T30473

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: DNA

A/Residues: 1-234 <KUZ>

A/Cross-references: UNIPROT:Q9YMK4; EMBL:AF081810; NID:g3822234; PIDN:AAC70309.1; PID:g38

C/Superfamily: viral DNA primase, Ief-1

Query Match 43.3%; Score 51.5; DB 2; Length 234;

Best Local Similarity 50.0%; Pred. No. 1.3;

Matches 12; Conservative 2; Mismatches 7; Indels 3; Gaps 1;

QY 1 KPSYQFGGHSVDFEEDTLPK 21

Db 67 KLPENCGRGWVLDVDFEEDTLPEPR 90

RESULT 7

T15098

hypothetical protein T22B11.5 - Caenorhabditis elegans

C/Species: Caenorhabditis elegans

C/Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004

C/Accession: T15098

R./König, T.; Wöhlmann, P.

submitted to the EMBL Data Library, December 1997

A/Description: The sequence of C. elegans cosmid T22B11.

A/Reference number: Z18292

A/Accession: T15098

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: DNA

A/Residues: 1-1038 <ROH>

A/Cross-references: UNIPROT:O61199; EMBL:AF039040; NID:g2736374; PID:g2736379; PIDN:AA894

A/Experimental source: strain Bristol N2; clone T22B11

C/Genetics:

A/Gene: CESP.T22B11.5

A/Map position: 4

A/Intons: 45/3; 128/2; 225/3; 659/3; 707/3; 820/3; 969/3

F/420-465/Domain: thiamin pyrophosphate dehydrogenase (lipoamide); thiamin pyrophosphate-binding dome

Query Match 42.4%; Score 50.5; DB 2; Length 1038;

Best Local Similarity 40.7%; Pred. No. 10;

Matches 11; Conservative 2; Mismatches 5; Indels 9; Gaps 1;

QY 3 SYQFGGHSVDFEEDTLPK 20

Db 156 SYQTRGNHIALDPLGINSADLDTIP 182

RESULT 8

Probable 33.6K protein - vaccinia virus (strain Ankara)

C:Species: vaccinia virus

A:Variety: strain Ankara

C:Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 09-Jul-2004

C:Accession: T37395

R:Antoine, G.; Scheiflinger, F.; Falkner, F.G.; Dörner, F.

Submitted to the EMBL Data Library, March 1997

A:Description: The complete genomic sequence of the Modified Vaccinia Ankara (MVA) strain

A:Reference number: 220877

A:Accession: T37395

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-288 <ANT>

A:Cross-references: UNIPROT:O57221; EMBL:U94848; PIDN:AA96520.1

A:Experimental source: strain Ankara

C:Genetics:

A:Note: MVA119R

C:Superfamily: vaccinia virus probable 33.6K protein

Query Match 42.0%; Score 50; DB 2; Length 288;

Best Local Similarity 56.2%; Pred. No. 2.9;

Matches 9; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 KPSTQFGHNSVDPEP 16

Db 141 KLGYQFGNHYHVDPEP 156

RESULT 9

A:2518

A:R protein - vaccinia virus (strain Copenhagen)

C:Species: vaccinia virus

A:Note: host Homo sapiens (man)

C:Date: 09-Nov-1990 #sequence_revision 09-Nov-1990 #text_change 09-Jul-2004

C:Accession: A42518

R:Johnson, G.P.

Submitted to GenBank, June 1990

A:Reference number: A33172

A:Accession: A42518

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-288 <JOH>

A:Cross-references: UNIPROT:P20986

C:Superfamily: vaccinia virus probable 33.6K protein

Query Match 42.0%; Score 50; DB 2; Length 288;

Best Local Similarity 56.2%; Pred. No. 2.9;

Matches 9; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 KPSTQFGHNSVDPEP 16

Db 141 KLGYQFGNHYHVDPEP 156

RESULT 10

S58652

Hypothetical protein YFR036w-a - yeast (Saccharomyces cerevisiae)

C:Species: Saccharomyces cerevisiae

C:Date: 27-Oct-1995 #sequence_revision 10-Nov-1995 #text_change 29-Oct-1999

C:Accession: S58652

R:Murakami, Y.; Naitou, M.; Hagiwara, H.; Shibata, T.; Ozawa, M.; Sasanuma, S.I.; Sasanuma, S.I.

Submitted to the EMBL Data Library, May 1995

A:Description: Analysis of the nucleotide sequence of chromosome VI from Saccharomyces cerevisiae

A:Reference number: S58652

A:Accession: S58652

A:Molecule type: DNA

A:Residues: 1-216 <MUR>

A:Cross-references: EMBL:D50617; GSPDB:GN00006; MIPS:YFR036w-a

C:Genetics:

A:Gene: MIPS:YFR036w-a

A:Map position: 6R

Query Match 41.2%; Score 49; DB 2; Length 216;

Best Local Similarity 72.7%; Pred. No. 3;

Matches 8; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 10 NSVDPEPDTLP 20

Db 188 HSNFEPDTLP 198

RESULT 11

F97686

Cyclic beta-(1-2) glucan synthetase [imported] - Agrobacterium tumefaciens (strain C58, C)

C:Species: Agrobacterium tumefaciens

C:Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 09-Jul-2004

C:Accession: F97686

R:Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman, A.; Liu, F.; Wollam, C.; Allinger, M.; Dougherty, D.; Scott, C.; Lappas, C.; Markelz, B.; Science 294, 2323-2328, 2001

A:Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tumefaciens

A:Reference number: A97359; MUID:21608551; PMID:117433194

A:Accession: F97686

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-2802 <KUR>

A:Cross-references: UNIPROT:Q8UBX0; GB:AE007869; PIDN:AAK88447.1; PID:G15157946; GSPDB:G

C:Genetics:

A:Gene: AGR_C_4949

A:Map position: circular chromosome

Query Match 41.2%; Score 49; DB 2; Length 2802;

Best Local Similarity 50.0%; Pred. No. 54;

Matches 8; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 5 QFGHNSVDPEPDTLP 20

Db 1422 QYFHDVDFPPTRPV 1437

RESULT 12

A12911

Beta (1->2) glucan biosynthesis protein [imported] - Agrobacterium tumefaciens (strain C)

C:Species: Agrobacterium tumefaciens

C:Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 09-Jul-2004

C:Accession: A12911

R:Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, L.

erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kutlyavin, T.; Levy, R.; Li, M.; McClellan, J.; Karp, P.; Romero, P.; Zhang, S.

Science 294, 2317-2323, 2001

A:Authors: Yoo, H.; Tso, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm, J.

ster, E.W.

A:Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.

A:Reference number: AB2577; MUID:21608550; PMID:117433193

A:Accession: A12911

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-2831 <KUR>

A:Cross-references: UNIPROT:Q8UBX0; GB:AE008688; PIDN:AA143711.1; PID:G17741241; GSPDB:G

A:Experimental source: strain C58 (Dupont)

C:Genetics:

A:Gene: chvB

A:Map position: circular chromosome

Query Match 41.2%; Score 49; DB 2; Length 2831;

Best Local Similarity 50.0%; Pred. No. 55;

Matches 8; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 5 QFGHNSVDPEPDTLP 20

Db 1422 QYFHDVDFPPTRPV 1437

Db 1451 QXGFHDAVDFPTTRVP 1466

RESULT 13

AF2756
glycine cleavage system protein P2 gcvp [imported] - Agrobacterium tumefaciens (strain C
C/Species: Agrobacterium tumefaciens
C/Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 09-Jul-2004
C/Accession: AF2756
R/Wood, D.W.; Secubal, J.C.; Kaul, R.; Monke, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, L.
erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kuttyavin, T.; Levy, R.; Li, M.; McCelli
Science 294, 2317-2323, 2001
A/Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
ster, E.W.
A/Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A/Reference number: AB2577; MUID:21608550; PMID:11743193
A/Accession: AF2756
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-954 <KUR>
A/Cross-references: UNIPROT:Q8UFD6; GB:AE008688; PIDN:AAL42468.1; PID:G17739884; GSPDB:C
A/Experimental source: strain C58 (Dupont)
C/Genetics:
A/Gene: gcvp
A/Map position: circular chromosome

Query Match 39.5%; Score 47; DB 2; Length 954;

Best Local Similarity 66.7%; Pred. No. 33;

Matches 12; Conservative 2; Mismatches 2; Indels 2; Gaps 2;

QY 6 FCGHNSV-DPEPD-TLPK 21

Db 444 FCGNFSISDFEYRLPK 461

RESULT 14

E97537
glycine cleavage system protein P2 (PA2445) [imported] - Agrobacterium tumefaciens (stra
C/Species: Agrobacterium tumefaciens
C/Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 09-Jul-2004
C/Accession: E97537
R/Goodner, B.; Hinkle, G.; Gatung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman,
A.; Liu, F.; Wollam, C.; Allinger, M.; Doughly, D.; Scott, C.; Lappas, C.; Markelz, B.;
Science 294, 2323-2328, 2001
A/Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum
A/Reference number: A97359; MUID:21608551; PMID:11743194
A/Accession: E97537
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-954 <KUR>
A/Cross-references: UNIPROT:Q8UFD6; GB:AE007869; PIDN:AAK87254.1; PID:G15156542; GSPDB:C
C/Genetics:
A/Gene: AGR_C_2699
A/Map position: circular chromosome

Query Match 39.5%; Score 47; DB 2; Length 954;

Best Local Similarity 66.7%; Pred. No. 33;

Matches 12; Conservative 2; Mismatches 2; Indels 2; Gaps 2;

QY 6 FCGHNSV-DPEPD-TLPK 21

Db 444 FCGNFSISDFEYRLPK 461

RESULT 15

H70333
conserved hypothetical protein aq_378 - Aquifex aeolicus
C/Species: Aquifex aeolicus
C/Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 09-Jul-2004
C/Accession: H70333
R/Decker, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.; Oy
V.

Nature 392, 353-358, 1998

A/Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.

A/Reference number: A70300; MUID:98196666; PMID:9537320

A/Accession: H70333

A/Status: preliminary; nucleic acid sequence not shown; translation not shown

A/Molecule type: DNA

A/Residues: 1-453 <AQF>

A/Cross-references: UNIPROT:O66700; GB:AE000687; NID:G2983050; PIDN:AAC06670.1; PID:G298;

A/Experimental source: strain VF5

C/Genetics:

A/Gene: aq_378

Query Match 38.7%; Score 46; DB 2; Length 453;

Best Local Similarity 53.8%; Pred. No. 21;

Matches 7; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 3 SYQFGHNSVDFE 15

Db 114 SYSGSYNTLEFE 126

Search completed: October 22, 2005, 04:13:57
Job time : 11.5465 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 22, 2005, 02:23:35 ; Search time 51.4314 Seconds
(without alignments)
209.087 Million cell updates/sec

Title: US-10-731-238-28
Perfect score: 119
Sequence: 1 KPSYQFGHNSVDEPPTLPK 21

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues
Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_03:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	111	93.3	1018 1	FNBA_STPAU P14738 staphylococ
2	108	90.8	961 2	Q99RD3 Q99d3 staphylococ
3	108	90.8	961 2	Q7A3J8 Q7a3j8 staphylococ
4	108	90.8	965 2	O6GDU5 O6gdu5 staphylococ
5	108	90.8	1015 2	O8NUU7 O8nuu7 staphylococ
6	108	90.8	1015 2	O6G6H3 O6g6h3 staphylococ
7	108	90.8	1038 2	Q99RD2 Q99rd2 staphylococ
8	108	90.8	1038 2	Q7A3J7 Q7a3j7 staphylococ
9	104	87.4	940 2	O53682 O53682 staphylococ
10	104	87.4	943 2	O8NUU8 O8nuu8 staphylococ
11	104	87.4	957 2	O6G6H4 O6g6h4 staphylococ
12	99	83.2	152 2	Q9AEP9 Q9aep9 staphylococ
13	53	44.5	500 2	O8KNC4 O8knc4 micromonosp
14	52	43.7	303 2	Q9RWE1 Q9rwe1 delnocoocus
15	52	43.7	598 1	LZT1_MOUSE LZt1 mouse
16	52	43.7	600 1	O8CFC9 O8cfc9 ratuus norv
17	51.5	43.3	234 2	O9YMK4 O9ymk4 lymantria d
18	51	42.9	305 2	Q7NY51 Q7ny51 chromobacte
19	50.5	42.4	1029 2	O61199 O61199 caenorhabdl
20	50	42.0	288 1	VA08_VACCC VA08 vaccina vi
21	50	42.0	288 2	O57221 O57221 vaccinia vi
22	50	42.0	288 2	O6RZHS O6rzh5 rabdltpox v
23	50	42.0	288 2	O77T16 O77t16 vaccinia vi
24	50	42.0	302 2	O6ZENA O6zena burkholderi
25	50	42.0	302 2	O63Y68 O63y68 burkholderi
26	50	42.0	302 2	O63Y68 O63y68 burkholderi
27	49	41.2	245 1	LZT1_HUMAN LZt1 homo sapien
28	49	41.2	245 1	O08866 O08866 carassius a
29	49	41.2	289 2	O6FZ83 O6fz83 bartonella
30	49	41.2	410 2	P72454 P72454 streptomyce
31	49	41.2	1726 2	O6G429 O6g429 bartonella
31	49	41.2	2802 2	Q7CWD9 Q7cwd9 agrobacteri

32	49	41.2	2831 2	O71ED3 O71ed3 agrobacteri
33	49	41.2	2831 2	O8UBX0 O8ubx0 agrobacteri
34	48	40.3	337 2	O6FS15 O6fs15 candida gla
35	48	40.3	436 2	O88PW8 O88pw8 pseudomonas
36	48	40.3	1767 2	Q7R2V4 Q7r2v4 giardia lam
37	47	39.5	229 2	O8HLO8 O8hlo8 diatomoides
38	47	39.5	466 2	O6GN22 O6gn22 xenopus lae
39	47	39.5	487 2	O8A9A4 O8a9a4 bacteroides
40	47	39.5	608 2	Q7QP79 Q7qp79 giardia lam
41	47	39.5	954 1	GCSP_AGR75 GCsp_agr75
42	47	39.5	1277 2	O6SLE3 O6sle3 cochllobol
43	46	38.7	208 1	URK_CLOPE URK_clope
44	46	38.7	243 1	S112_APATH S112_athap
45	46	38.7	442 2	Q7XUW9 Q7xuw9 oryza sativ

ALIGNMENTS

```

RESULT 1
FNBA_STPAU STANDARD; PRT; 1018 AA.
AC P14738;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Fibronectin-binding protein precursor (FNBP).
GN Name=fnba;
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxId=1280;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NTCT 8325-4;
RX MEDLINE=8908998; PubMed=2521391;
RA Signaes C., Raucel G., Joensson K., Lindgren P.-E.,
  Anantharamiah G.M., Hoeoek M., Lindberg M.;
  "Nucleotide sequence of the gene for a fibronectin-binding protein
  from Staphylococcus aureus: use of this peptide sequence in the
  synthesis of biologically active peptides.";
  Proc. Natl. Acad. Sci. U.S.A. 86:699-703(1989).
RT
RL
CC -I- FUNCTION: The ability of bacteria to bind fibronectin has been
  proposed as a virulence factor enabling bacteria to colonize wound
  tissues and blood clots. Binding of plasma fibronectin to the
  bacterial surface might block adhesion receptors on S.aureus, thus
  representing an important defense mechanism against tissue
  invasion.
CC -I- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
  an amide bond (Potential).
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
  between the Swiss Institute of Bioinformatics and the EMBL outstation -
  the European Bioinformatics Institute. There are no restrictions on its
  use by non-profit institutions as long as its content is in no way
  modified and this statement is not removed. Usage by and for commercial
  entities requires a license agreement (See http://www.isb-sib.ch/announce/
  or send an email to license@sib-sib.ch).
CC
CC EMBL: J04151; AAA2632.1; -.
DR InterPro: IPR004237; Fn_bind.
DR InterPro: IPR005877; Gpos_YsIRK.
DR InterPro: IPR001899; Gram_pos_anchor.
DR Pfam: PF02986; Fn_bind; 1.
DR Pfam: PF00746; Gram_pos_anchor; 1.
DR Pfam: PF04650; YsIRK_signal; 1.
DR TIGRfam: TIGR01167; LpxTG_anchor; 1.
DR TIGRfam: TIGR01168; YsIRK_signal; 1.
DR PROSITE: PS50847; GRAM_POS_ANCHORING; 1.
KW Cell adhesion; Cell wall; Peptidoglycan-anchor; Repeat; Signal;
  virulence.
FT SIGNAL 1 36
FT CHAIN 37 985 Fibronectin-binding protein.
FT PROPE 986 1018 Removed by sortase (Potential).

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FT REPEAT 545 574 B-1.
FT REPEAT 575 604 B-2.
FT DOMAIN 745 878 4 X approximate tandem repeats,
  fibronectin-binding domain.
FT REPEAT 745 782 D-1.
FT REPEAT 783 820 D-2.
FT REPEAT 821 859 D-3.
FT REPEAT 860 878 D-4 (incomplete).
FT DOMAIN 879 948 5 X tandem repeats, Pro-rich (WR).
FT REPEAT 879 892 WR 1.
FT REPEAT 893 906 WR 2.
FT REPEAT 907 920 WR 3.
FT REPEAT 921 934 WR 4.
FT REPEAT 935 948 WR 5.
FT SITE 982 986 LPXTG sorting signal (Potential).
FT MOD_RES 985 985 Pentaglycyl murein peptidoglycan amidated
  chreonine (Potential).
SQ SEQUENCE 1018 AA; 111780 MW; 58175E020E81F1F CRC64;

Query Match 93.3%; Score 111; DB 1; Length 1018;
Best Local Similarity 95.2%; Pred. No. 6.1e-09;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KPXYFGGHSVDFEPTLPK 21
Db 837 KPXYFGGHSVDFEPTLPK 857

RESULT 2
Q99RD3 PRELIMINARY; PRT; 961 AA.
AC Q99RD3 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE Fibronectin-binding protein homolog.
GN Name=fnb3; OrderedLocusNames=SAV2502;
OS Staphylococcus aureus (strain Mu50 / ATCC 700689).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=158878;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Mu50 / ATCC 700689;
RA MEDLINE=21311952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2;
RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
  Cui L., Oguchi A., Aoki K.-I., Nagai Y., Iian J.-Q., Ito T.,
  Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hoshiyama A.,
  Mitutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
  Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
  Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
  Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
  "Whole genome sequencing of methicillin-resistant Staphylococcus
  aureus."
RT Lancet 357:1225-1240(2001).
RL -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
  an amide bond (By similarity).
CC EMBL; AP003365; BAB58664.1; -.
CC PIR; G90053; G90053.
DR HSSP; Q53653; IN67.
DR GO; GO:0009986; C:cell surface; IEA.
DR GO; GO:0005618; C:cell wall; IEA.
DR GO; GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:007155; P:cell adhesion; IEA.
DR InterPro; IPR008966; Adhes_bact.
DR InterPro; IPR004237; Fn_bind.
DR InterPro; IPR005877; Gpos_YsIRK.
DR Pfam; PF02986; Fn_bind; 1.
DR Pfam; PF00746; Gram_pos_anchor; 1.
DR Pfam; PF04650; YsIRK_signal; 1.
DR TIGRfams; TIGR01167; LPXTG_anchor; 1.
DR TIGRfams; TIGR01167; LPXTG_anchor; 1.
DR TIGRfams; TIGR01168; YsIRK_signal; 1.
DR TIGRfams; TIGR01168; YsIRK_signal; 1.
```

```
DR PROSITE; PS50847; GRAM_POS_ANCHORING; 1.
KW Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ SEQUENCE 961 AA; 106010 MW; 364940F884EA4101 CRC64;

Query Match 90.8%; Score 108; DB 2; Length 961;
Best Local Similarity 90.5%; Pred. No. 1.8e-08;
Matches 19; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KPXYFGGHSVDFEPTLPK 21
Db 784 KPXYFGGHSVDFEPTLPK 804

RESULT 3
Q7A3J8 PRELIMINARY; PRT; 961 AA.
AC Q7A3J8 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE FnbB protein.
GN Name=fnb3; OrderedLocusNames=SA2290;
OS Staphylococcus aureus (strain N315).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=158879;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=21311952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2;
RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
  Cui L., Oguchi A., Aoki K.-I., Nagai Y., Iian J.-Q., Ito T.,
  Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hoshiyama A.,
  Mitutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
  Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
  Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
  Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
  "Whole genome sequencing of methicillin-resistant Staphylococcus
  aureus."
RT Lancet 357:1225-1240(2001).
RL -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
  an amide bond (By similarity).
CC EMBL; AP003137; BAB43593.1; -.
CC GO; GO:0009986; C:cell surface; IEA.
CC GO; GO:0005618; C:cell wall; IEA.
CC GO; GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
CC GO; GO:0016020; C:membrane; IEA.
CC GO; GO:007155; P:cell adhesion; IEA.
CC InterPro; IPR008966; Adhes_bact.
CC InterPro; IPR004237; Fn_bind.
CC InterPro; IPR005877; Gpos_YsIRK.
CC InterPro; IPR001899; Gram_pos_anchor.
CC Pfam; PF02986; Fn_bind; 1.
CC Pfam; PF00746; Gram_pos_anchor; 1.
CC Pfam; PF04650; YsIRK_signal; 1.
CC TIGRfams; TIGR01167; LPXTG_anchor; 1.
CC TIGRfams; TIGR01168; YsIRK_signal; 1.
CC PROSITE; PS50847; GRAM_POS_ANCHORING; 1.
KW Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ SEQUENCE 961 AA; 106010 MW; 364940F884EA4101 CRC64;

Query Match 90.8%; Score 108; DB 2; Length 961;
Best Local Similarity 90.5%; Pred. No. 1.8e-08;
Matches 19; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KPXYFGGHSVDFEPTLPK 21
Db 784 KPXYFGGHSVDFEPTLPK 804

RESULT 4
Q6GDUS PRELIMINARY; PRT; 965 AA.
ID Q6GDUS 05-JUL-2004 (TREMBlrel. 27, Created)
```

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DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE Fibronectin-binding protein.
GN Name=fnbA; OrderedLocustNames=SAR2580;
OS Staphylococcus aureus (strain MRSA252).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
CX NCBI_TaxID=282458;
RN (1)
RP SEQUENCE FROM N.A.
RX PubMed=15213324; DOI=10.1073/pnas.0402521101;
RA Holden M.T.G., Fell E.J., Lindsey J.A., Peacock S.J., Day N.P.J.,
RA Knight M.C., Foster T.J., Moore C.E., Hurst L., Atkin R., Barron A.,
RA Baeson N., Bentley S.D., Chillingworth C., Chillingworth T.,
RA Churcher C., Clark L., Corton C., Cronin A., Doggett J., Dowd L.,
RA Fellwell T., Hance Z., Harris B., Hauser H., Holroyd S., Jagels K.,
RA James K.D., Lennard N., Line A., Mayes R., Moule S., Mungall K.,
RA Ormond D., Quail M.A., Rabinowitsch E., Rutherford K.M., Sanders M.,
RA Sharp S., Simmonds M., Stevens K., Whitehead S., Barrett B.G.,
RA Spratt B.G., Parkhill J.;
RT "Complete genomes of two clinical Staphylococcus aureus strains:
RT evidence for the rapid evolution of virulence and drug resistance.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:9786-9791(2004).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC an amide bond (By similarity).
CC EMBL: BX571856; CAG41560.1; -.
DR GO: GO:0009986; C:cell surface; IEA.
DR GO: GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO: GO:0016020; C:membrane; IEA.
DR GO: GO:0007155; P:cell adhesion; IEA.
DR InterPro: IPR008966; Adhes_bact.
DR InterPro: IPR004237; Fn_bind.
DR InterPro: IPR005877; Gpos_YsIRK.
DR InterPro: IPR001899; Gram_pos_anchor.
DR Pfam: PF00746; Gram_pos_anchor; 1.
DR Pfam: PF04650; YsIRK_signal; 1.
DR TIGRfams: TIGR01167; LpxTG_anchor; 1.
DR TIGRfams: TIGR01168; YsIRK_signal; 1.
DR PROSITE: PS50847; GRAM_POS_ANCHORING; 1.
KW Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ SEQUENCE 965 AA; 105691 MW; 2982E132164D0551 CRC64;

Query Match 90.8%; Score 108; DB 2; Length 965;
Best Local Similarity 90.5%; Pred. No. 1.9e-08;
Matches 19; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 KPSYQFGCHNSVDFEEDTLPK 21
DB 802 KPNYQFGCHNSVDFEEDTLPK 822

RESULT 5
Q8NTU7 PRELIMINARY; PRT; 1015 AA.
AC Q8NTU7;
DT 01-OCT-2002 (TREMBlrel. 22, Created)
DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Pnb protein.
GN Name=fnb; OrderedLocustNames=MM2421;
OS Staphylococcus aureus (strain MM2).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
CX NCBI_TaxID=196620;
RN (1)
RP SEQUENCE FROM N.A.
RX STRAIN=MM2;
RX MEDLINE=22040717; PubMed=12044378; DOI=10.1016/S0140-6736(02)08713-5;
RA Baba T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Oguchi A.,
RA Nagai Y., Iwano N., Asano K., Naimi T., Kuroda H., Cui L.,
RA Yamamoto K., Hiramatsu K.;
RT "Genome and virulence determinants of high virulence community-
RT acquired MRSA.";
RL Lancet 359:1819-1827(2002).
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CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC an amide bond (By similarity).
CC EMBL: AF004830; BAB96286.1; -.
DR GO: GO:0009986; C:cell surface; IEA.
DR GO: GO:0005618; C:cell wall; IEA.
DR GO: GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO: GO:0016020; C:membrane; IEA.
DR GO: GO:0007155; P:cell adhesion; IEA.
DR InterPro: IPR008966; Adhes_bact.
DR InterPro: IPR004237; Fn_bind.
DR InterPro: IPR005877; Gpos_YsIRK.
DR InterPro: IPR001899; Gram_pos_anchor.
DR Pfam: PF02986; Fn_bind; 1.
DR Pfam: PF00746; Gram_pos_anchor; 1.
DR Pfam: PF04650; YsIRK_signal; 1.
DR TIGRfams: TIGR01167; LpxTG_anchor; 1.
DR TIGRfams: TIGR01168; YsIRK_signal; 1.
DR PROSITE: PS50847; GRAM_POS_ANCHORING; 1.
KW Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ SEQUENCE 1015 AA; 111145 MW; D0F9281BB64D4D2 CRC64;

Query Match 90.8%; Score 108; DB 2; Length 1015;
Best Local Similarity 90.5%; Pred. No. 1.9e-08;
Matches 19; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 KPSYQFGCHNSVDFEEDTLPK 21
DB 838 KPNYQFGCHNSVDFEEDTLPK 858

RESULT 6
Q6G6H3 PRELIMINARY; PRT; 1015 AA.
AC Q6G6H3;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE Fibronectin-binding protein.
GN OrderedLocustNames=SSA2388;
OS Staphylococcus aureus (strain MSSA476).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
CX NCBI_TaxID=282459;
RN (1)
RP SEQUENCE FROM N.A.
RX PubMed=15213324; DOI=10.1073/pnas.0402521101;
RA Holden M.T.G., Fell E.J., Lindsey J.A., Peacock S.J., Day N.P.J.,
RA Knight M.C., Foster T.J., Moore C.E., Hurst L., Atkin R., Barron A.,
RA Baeson N., Bentley S.D., Chillingworth C., Chillingworth T.,
RA Churcher C., Clark L., Corton C., Cronin A., Doggett J., Dowd L.,
RA Fellwell T., Hance Z., Harris B., Hauser H., Holroyd S., Jagels K.,
RA James K.D., Lennard N., Line A., Mayes R., Moule S., Mungall K.,
RA Ormond D., Quail M.A., Rabinowitsch E., Rutherford K.M., Sanders M.,
RA Sharp S., Simmonds M., Stevens K., Whitehead S., Barrett B.G.,
RA Spratt B.G., Parkhill J.;
RT "Complete genomes of two clinical Staphylococcus aureus strains:
RT evidence for the rapid evolution of virulence and drug resistance.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:9786-9791(2004).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC an amide bond (By similarity).
CC EMBL: BX571857; CAG44202.1; -.
DR GO: GO:0009986; C:cell surface; IEA.
DR GO: GO:0005618; C:cell wall; IEA.
DR GO: GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO: GO:0016020; C:membrane; IEA.
DR GO: GO:0007155; P:cell adhesion; IEA.
DR InterPro: IPR008966; Adhes_bact.
DR InterPro: IPR004237; Fn_bind.
DR InterPro: IPR005877; Gpos_YsIRK.
DR InterPro: IPR001899; Gram_pos_anchor.
DR Pfam: PF02986; Fn_bind; 1.
DR Pfam: PF00746; Gram_pos_anchor; 1.
DR TIGRfams: TIGR01167; LpxTG_anchor; 1.
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DR TIGRFAMS: TIGR01168; YSIRK signal; 1.
 DR PROSITE; PSS50847; GRAM_POS_ANCHORING; 1.
 KW Cell wall; Complete proteome; Peptidoglycan-anchor.
 SQ SEQUENCE 1015 AA; 111145 MW; D0F9281BB54D44D2 CRC64;

Query Match 90.8%; Score 108; DB 2; Length 1015;
 Best Local Similarity 90.5%; Pred. No. 1.9e-08;
 Matches 19; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 KPSYQFGHNSVDFEPTLPK 21
 DB 838 KPNYQFGHNSVDFEPTLPK 858
 ||:|||||
 ||:|||||

RESULT 7
 ID 099RD2 PRELIMINARY; PRT; 1038 AA.
 AC 099RD2;
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Fibronectin-binding protein homolog.
 GN Name=fnb; OrderedLocuNames=SAV2503;
 OS Staphylococcus aureus (strain Mu50 / ATCC 700699).
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 NC NCBI_TaxID=158878;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=M50 / ATCC 700699;
 RX MEDLINE=21311952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2;
 RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
 RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Iian J.-Q., Ito T.,
 RA Kanamori M., Matsunaru H., Maruyama A., Murakami H., Hoshiyama A.,
 RA Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
 RA Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
 RA Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
 RA Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
 RT "Whole genome sequencing of methicillin-resistant Staphylococcus
 aureus."
 RL Lancet 357:1225-1240(2001).
 CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
 an amide bond (By similarity).
 DR EMBL: AP003365; BAB58665.1; -.
 DR EIR; H90053; H90053.
 DR GO; GO:0009986; C:cell surface; IEA.
 DR GO; GO:0005618; C:cell wall; IEA.
 DR GO; GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0007155; P:cell adhesion; IEA.
 DR InterPro; IPR008966; Adhes_bact.
 DR InterPro; IPR004237; Fn_bind.
 DR InterPro; IPR005877; Gpos_YSIRK.
 DR Pfam; PF02986; Fn_bind; 1.
 DR Pfam; PF02986; Gram_pos_anchor; 1.
 DR Pfam; PF02986; Fn_bind; 1.
 DR Pfam; PF02986; Gram_pos_anchor; 1.
 DR TIGRFAMS; TIGR01167; LPXTG_anchor; 1.
 DR TIGRFAMS; TIGR01167; LPXTG_anchor; 1.
 DR TIGRFAMS; TIGR01168; YSIRK_signal; 1.
 DR PROSITE; PSS50847; GRAM_POS_ANCHORING; 1.
 KW Cell wall; Complete proteome; Peptidoglycan-anchor.
 SQ SEQUENCE 1038 AA; 113618 MW; 666BF6BF2BFBEB12 CRC64;

Query Match 90.8%; Score 108; DB 2; Length 1038;
 Best Local Similarity 90.5%; Pred. No. 1.9e-08;
 Matches 19; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 KPSYQFGHNSVDFEPTLPK 21
 DB 833 KPNYQFGHNSVDFEPTLPK 853
 ||:|||||
 ||:|||||

RESULT 8
 ID 07A3J7 PRELIMINARY; PRT; 1038 AA.
 AC 07A3J7;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Fnb protein.
 GN Name=fnb; OrderedLocuNames=SA2291;
 OS Staphylococcus aureus (strain N315).
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 NC NCBI_TaxID=158879;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC MEDLINE=21311952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2;
 RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
 RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Iian J.-Q., Ito T.,
 RA Kanamori M., Matsunaru H., Maruyama A., Murakami H., Hoshiyama A.,
 RA Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
 RA Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
 RA Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
 RA Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
 RT "Whole genome sequencing of methicillin-resistant Staphylococcus
 aureus."
 RL Lancet 357:1225-1240(2001).
 CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
 an amide bond (By similarity).
 DR EMBL: AP003337; BAB43594.1; -.
 DR GO; GO:0009986; C:cell surface; IEA.
 DR GO; GO:0005618; C:cell wall; IEA.
 DR GO; GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0007155; P:cell adhesion; IEA.
 DR InterPro; IPR008966; Adhes_bact.
 DR InterPro; IPR004237; Fn_bind.
 DR InterPro; IPR005877; Gpos_YSIRK.
 DR Pfam; PF02986; Fn_bind; 1.
 DR Pfam; PF02986; Gram_pos_anchor; 1.
 DR Pfam; PF02986; Fn_bind; 1.
 DR TIGRFAMS; TIGR01167; LPXTG_anchor; 1.
 DR TIGRFAMS; TIGR01168; YSIRK_signal; 1.
 DR PROSITE; PSS50847; GRAM_POS_ANCHORING; 1.
 KW Cell wall; Complete proteome; Peptidoglycan-anchor.
 SQ SEQUENCE 1038 AA; 113618 MW; 666BF6BF2BFBEB12 CRC64;

Query Match 90.8%; Score 108; DB 2; Length 1038;
 Best Local Similarity 90.5%; Pred. No. 1.9e-08;
 Matches 19; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 KPSYQFGHNSVDFEPTLPK 21
 DB 833 KPNYQFGHNSVDFEPTLPK 853
 ||:|||||
 ||:|||||

RESULT 9
 ID 053682 PRELIMINARY; PRT; 940 AA.
 AC 053682;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Fibronectin binding protein B.
 GN Name=fnbB;
 OS Staphylococcus aureus.
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 NC NCBI_TaxID=1280;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=8325-4;
 RX MEDLINE=92111475; PubMed=1837266;
 RA Jonsson K., Sigfus C., Muller H.-P., Lindberg M.;
 RT "Two different genes encode fibronectin binding proteins in
 Staphylococcus aureus. The complete nucleotide sequence and
 characterization of the second gene.";

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RL  Eur. J. Biochem. 202:1041-1048(1991).
CC  -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC  an amide bond (by similarity).
EMBL: X62992; CAA44726.1; -.
DR  PIR: S19702; S19702.
DR  HSSP: O53553; IN67.
DR  GO: GO:0009986; C:cell surface; IEA.
DR  GO: GO:0005618; C:cell wall; IEA.
DR  GO: GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR  GO: GO:0016020; C:membrane; IEA.
DR  GO: GO:0007155; P:cell adhesion; IEA.
DR  InterPro: IPR008966; Adhes_bact.
DR  InterPro: IPR004237; Fn_bind.
DR  InterPro: IPR005877; Gpos_YsIRK.
DR  InterPro: IPR001899; Gram_pos_anchor.
DR  Pfam: PF00746; Gram_pos_anchor; 1.
DR  Pfam: PF04650; YsIRK_signal; 1.
DR  TIGRfams: TIGR01167; LpxTG_anchor; 1.
DR  TIGRfams: TIGR01168; YsIRK_signal; 1.
DR  PROSITE: PS50847; GRAM_POS_ANCHORING; 1.
KW  Cell wall; Peptidoglycan-anchor.
SQ  SEQUENCE 940 AA; 10355 MW; E35FBBCA907AE345 CRC64;

Query Match      87.4%; Score 104; DB 2; Length 940;
Best Local Similarity 85.7%; Pred. No. 7.7e-08;
Matches 18; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY  1 KPSYQFGHNSVDPEPDLTPK 21
DB  773 KPNYQFGHNSVDPEPDLTPQ 793

RESULT 10
ID  Q8NTU8      PRELIMINARY;      PRT;      943 AA.
AC  Q8NTU8;
DT  01-OCT-2002 (TREMBLrel. 22, Created)
DT  01-OCT-2002 (TREMBLrel. 22, Last sequence update)
DT  01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE  FnBb protein.
OS  Name=fnbB; OrderedLocustNames=NM2420;
OS  Staphylococcus aureus (strain MW2).
OC  Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX  NCBI_TaxID=196620;
RN  [1]
RP  SEQUENCE FROM N.A.
RC  STRAIN=NM2;
RX  MEDLINE=22040717; PubMed=12044378; DOI=10.1016/S0140-6736(02)08713-5;
RA  Baba T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Oguchi A.,
RA  Nagai Y., Iwano N., Asano K., Naimi T., Kuroda H., Cui L.,
RA  Yamamoto K., Hiramoto K.;
RT  Genome and virulence determinants of high virulence community-
RT  acquired MRSA.
RL  Lancet 359:1819-1827(2002).
CC  -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC  an amide bond (by similarity).
EMBL: AB004830; BAB96285.1; -.
DR  HSSP: Q53553; IN67.
DR  GO: GO:0009986; C:cell surface; IEA.
DR  GO: GO:0005618; C:cell wall; IEA.
DR  GO: GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR  GO: GO:0016020; C:membrane; IEA.
DR  GO: GO:0007155; P:cell adhesion; IEA.
DR  InterPro: IPR008966; Adhes_bact.
DR  InterPro: IPR004237; Fn_bind.
DR  InterPro: IPR005877; Gpos_YsIRK.
DR  InterPro: IPR001899; Gram_pos_anchor.
DR  Pfam: PF02986; Fn_bind; 1.
DR  Pfam: PF00746; Gram_pos_anchor; 1.
DR  Pfam: PF04650; YsIRK_signal; 1.
DR  TIGRfams: TIGR01167; LpxTG_anchor; 1.
DR  TIGRfams: TIGR01168; YsIRK_signal; 1.

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DR  PROSITE: PS50847; GRAM_POS_ANCHORING; 1.
KW  Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ  SEQUENCE 943 AA; 104537 MW; DA6A5F31947E1B6A CRC64;

Query Match      87.4%; Score 104; DB 2; Length 943;
Best Local Similarity 85.7%; Pred. No. 7.7e-08;
Matches 18; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY  1 KPSYQFGHNSVDPEPDLTPK 21
DB  780 KPNYQFGHNSVDPEPDLTPQ 800

RESULT 11
ID  Q6G6H4      PRELIMINARY;      PRT;      957 AA.
AC  Q6G6H4;
DT  05-JUL-2004 (TREMBLrel. 27, Created)
DT  05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DT  05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE  Fibronectin-binding protein.
OS  Name=fnbB; OrderedLocustNames=SAS2387.
OS  Staphylococcus aureus (strain MSSA476).
OC  Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX  NCBI_TaxID=282459;
RN  [1]
RP  SEQUENCE FROM N.A.
RX  PubMed=15213324; DOI=10.1073/pnas.0402521101;
RA  Holden M.T.G., Fell E.J., Lindsay J.A., Peacock S.J., Day N.P.J.,
RA  Enright M.C., Foster T.J., Moore C.E., Hurst L., Atkin R., Barron A.,
RA  Baeson N., Bentley S.D., Chillingworth C., Chillingworth T.,
RA  Churcher C., Clark L., Cronin A., Doggett J., Dowd L.,
RA  Felwell T., Hance Z., Harris B., Hauser H., Holroyd S., Jagels K.,
RA  James K.D., Leonard N., Line A., Mayes R., Moutie S., Mungall K.,
RA  Ormond D., Quail M.A., Rabinowitsch E., Rutherford K.M., Sanders M.,
RA  Sharp S., Simmonds M., Stevens K., Whitehead S., Barrell B.G.,
RA  Spratt B.G., Parhill J.;
RT  Complete genomes of two clinical Staphylococcus aureus strains:
RT  evidence for the rapid evolution of virulence and drug resistance.
RL  Proc. Natl. Acad. Sci. U.S.A. 101:9786-9791(2004).
CC  -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC  an amide bond (by similarity).
EMBL: BX571857; CAG44201.1; -.
DR  GO: GO:0009986; C:cell surface; IEA.
DR  GO: GO:0005618; C:cell wall; IEA.
DR  GO: GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR  GO: GO:0016020; C:membrane; IEA.
DR  GO: GO:0007155; P:cell adhesion; IEA.
DR  InterPro: IPR008966; Adhes_bact.
DR  InterPro: IPR004237; Fn_bind.
DR  InterPro: IPR005877; Gpos_YsIRK.
DR  InterPro: IPR001899; Gram_pos_anchor.
DR  Pfam: PF02986; Fn_bind; 1.
DR  Pfam: PF00746; Gram_pos_anchor; 1.
DR  Pfam: PF04650; YsIRK_signal; 1.
DR  TIGRfams: TIGR01167; LpxTG_anchor; 1.
DR  TIGRfams: TIGR01168; YsIRK_signal; 1.
DR  PROSITE: PS50847; GRAM_POS_ANCHORING; 1.
KW  Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ  SEQUENCE 957 AA; 105980 MW; 28F8BA7FFDFD3EAF CRC64;

Query Match      87.4%; Score 104; DB 2; Length 957;
Best Local Similarity 85.7%; Pred. No. 7.8e-08;
Matches 18; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY  1 KPSYQFGHNSVDPEPDLTPK 21
DB  780 KPNYQFGHNSVDPEPDLTPQ 800

RESULT 12
ID  Q9AEP9      PRELIMINARY;      PRT;      152 AA.

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AC Q9AEP9;
DT 01-JUN-2001 (Tremblrel. 17, Created)
DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE Fibronectin-binding protein (fragment).
GN Name=fnb;
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1280;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CMRSA-1;
RX MEDLINE=21246681; PubMed=11349044;
RX DOI=10.1128/JAI.69.6.3791-3799.2001;
RA Rice K., Huesca M., Vaz D., McGavin M.J.;
RT "Variance in fibronectin binding and fnb locus polymorphisms in
RT Staphylococcus aureus: identification of antigenic variation in a
RT fibronectin binding protein adhesin of the epidemic CMRSA-1 strain of
RT methicillin-resistant S. aureus.";
RL Infect. Immun. 69:3791-3799(2001).
DR EMBL; AY029184; AAKJ1588.1; -.
FT NON_TER 1
FT TER 152
SQ SEQUENCE 152 AA; 17193 MW; CFA3913C2B11C025 CRC64;

Query Match 83.2%; Score 99; DB 2; Length 152;
Best Local Similarity 81.0%; Pred. No. 6.1e-08;
Matches 17; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 KPSYQFGHNSVDFEPTLPK 21
Db 130 KPSYQFGHNSVDFEPTLPK 150

RESULT 13
O8KNC4 PRELIMINARY; PRT; 500 AA.
AC O8KNC4;
DT 01-OCT-2002 (Tremblrel. 22, Created)
DT 01-OCT-2002 (Tremblrel. 22, Last sequence update)
DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)
DE Calu22.
GN Name=calu22;
OS Micromonospora echinospora (Micromonospora purpurea).
OC Bacteria; Actinobacteriia; Actinobacteridae; Actinomycetales;
OC Micromonosporineae; Micromonosporaceae; Micromonospora.
OX NCBI_TaxID=1877;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NRRL 15839;
RX MEDLINE=22171414; PubMed=12183629; DOI=10.1126/science.1072105;
RA Ahlert J., Shepard B., Lomovskaya N., Zazopoulos E., Scatfa A.,
RA Bachmann B.O., Huang K., Fongstein L., Csisny A., Whitlam R.E.,
RA Farnet C.M., Thorson J.S.;
RT "The calicheamicin gene cluster and its iterative type I enediynes
RT PKS.";
RL Science 297:1173-1176(2002).
DR EMBL; AF497482; AAM94801.1; -.
DR GO; GO:0003824; F:catalytic activity; IEA.
DR GO; GO:0050897; F:catalytic ion binding; IEA.
DR GO; GO:0005506; F:iron ion binding; IEA.
DR InterPro; IPR006158; B12-binding.
DR InterPro; IPR011007; B12-binding.
DR InterPro; IPR000345; CyC_heme_BS.
DR InterPro; IPR006638; EIP3/MlaB/Nlfb.
DR InterPro; IPR007197; Radical SAM.
DR Pfam; PF02310; B12-binding; I.
DR Pfam; PF04055; Radical SAM; I.
DR SMART; SM00729; EIP3; I.
DR PROSITE; PS00190; CYTOCHROME_C; UNKNOWN_1.
SQ SEQUENCE 500 AA; 55211 MW; 7C7D42827AF4713A CRC64;

Query Match 44.5%; Score 53; DB 2; Length 500;
```

```
Best Local Similarity 69.2%; Pred. No. 7.9;
Matches 9; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 7 GGHNSVDFEPTLP 19
Db 443 GGHNSVDFEPTLP 455

RESULT 14
Q9RWE1 PRELIMINARY; PRT; 303 AA.
AC Q9RWE1;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)
DE Fructokinase.
GN OrderedLocustNames=DR0728;
OS Deinococcus radiodurans.
OC Bacteria; Deinococcus-Thermus; Deinococci; Deinococcales;
OC Deinococcaceae; Deinococcus.
OX NCBI_TaxID=1299;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=R1 / ATCC 13939 / DSM 20539 / NCIB 9279;
RX MEDLINE=20036896; PubMed=10567266; DOI=10.1126/science.286.5444.1571;
RA White O., Eisen J.A., Heidelberg J.F., Hickey E.K., Peterson J.D.,
RA Dodson R.J., Haft D.H., Gwinn M.L., Nelson W.C., Richardson D.L.,
RA Moffat K.S., Qin H., Jiang L., Pamphile M., Crosby M., Shen M.,
RA Vamatheva J.J., Lam P., McDonald L.A., Ueberlack T.R., Zalewski C.,
RA Makarov K.S., Aravind L., Daly M.J., Minton K.W., Fleischmann R.D.,
RA Ketchum K.A., Nelson K.E., Salzberg S.L., Smith H.O., Venter J.C.,
RA Fraser C.M.;
RT "Genome sequence of the radioresistant bacterium Deinococcus
RT radiodurans R1.";
RL Science 286:1571-1577(1999).
DR EMBL; AE001928; AAF10301.1; -.
DR PIR; B75485; B75485.
DR TIGR; DR0728; -.
DR GO; GO:0016101; F:kinase activity; IEA.
DR InterPro; IPR002173; PKB_KINASES_1; UNKNOWN_1.
DR PROSITE; PS00583; PKB_KINASES_1; UNKNOWN_1.
DR PROSITE; PS00584; PKB_KINASES_2; 1.
KV Complete proteome; Kinase.
SQ SEQUENCE 303 AA; 31811 MW; 60B688ABA446EC3 CRC64;

Query Match 43.7%; Score 52; DB 2; Length 303;
Best Local Similarity 52.4%; Pred. No. 6.5;
Matches 11; Conservative 2; Mismatches 6; Indels 2; Gaps 1;

Qy 2 PSYQFGHNSVD--FEPTLP 20
Db 94 PSYQFGHNSVDHFDPTLP 114

RESULT 15
LZT1 MOUSE STANDARD; PRT; 598 AA.
AC P60853;
DT 05-JUL-2004 (Rel. 44, Created)
DT 05-JUL-2004 (Rel. 44, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Leucine zipper putative tumor suppressor 1 (F37/Esophageal cancer-
DE related gene-coding leucine-zipper motif) (Fesl).
GN Name=Lzts1; Synonyms=Fesl;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=129/J;
RX MEDLINE=99199287; PubMed=10097140; DOI=10.1073/pnas.96.7.3328;
RX Ishii H., Baffa R., Numata S.-I., Murakumo Y., Rattan S., Inoue H.,
```

RA Mori M., Fidanza V., Alder H., Croce C.M.;
 RT "The FEZ1 gene at chromosome 8p22 encodes a leucine-zipper protein,
 and its expression is altered in multiple human tumors."; Proc. Natl. Acad. Sci. U.S.A. 96:3928-3933(1999).
 CC -1- FUNCTION: Involved in the regulation of cell growth. May stabilize
 the active CDC2-cyclin B1 complex and thereby contribute to the
 regulation of the cell cycle and the prevention of uncontrolled
 cell proliferation. May act as tumor suppressor (By similarity).
 CC -1- SUBUNIT: Binds E2F1 and CDC2 (By similarity).
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic; associated with the plasma
 membrane and with microtubules. Detected in dendritic spines,
 especially in the postsynaptic density (By similarity).
 CC -1- PTM: Phosphorylated on serine residues. Hyperphosphorylated by the
 CAMP-dependent kinase PKA during cell-cycle progression (By
 similarity).
 CC -1- SIMILARITY: Belongs to the LZTS family.

 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 between the Swiss Institute of Bioinformatics and the EMBL outstation -
 the European Bioinformatics Institute. There are no restrictions on its
 use by non-profit institutions as long as its content is in no way
 modified and this statement is not removed. Usage by and for commercial
 entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 or send an email to license@isb-sib.ch).

 CC EMBL: AF288601; AA014349.1; -;
 DR Anti-oncogene; Cell cycle; Coiled coil; Lipoprotein; Membrane;
 KW Myristate; Phosphorylation.
 FT INIT_MET 0 0 By similarity.
 FT LIPID 1 1 N-myristoyl glycine (By similarity).
 FT DOMAIN 255 571 Coiled coil (Potential).
 SQ SEQUENCE 598 AA; 67176 MW; D45781BECF2A6C70 CRC64;

Query Match 43.7%; Score 52; DB 1; Length 598;

Best Local Similarity 40.7%; Pred.No. 14;

Matches 11; Conservative 2; Mismatches 8; Indels 6; Gaps 1;

QY 1 KPSY-----QFGHNSVDFPDTLPK 21

DB 78 RPDYRALSGDMGCGGCVDFDPATPPK 104

Search completed: October 22, 2005, 04:10:19
 Job time : 52.4314 secs

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CC streptococci, e.g. meningitis, otitis media, pneumonia, endocarditis,
 CC mastitis in cattle, abortion in horses and many others. Since the
 CC antibodies block binding of bacteria, they should be effective against
 CC antibiotic-resistant strains, and may replace antibiotic therapy or
 CC increase its effectiveness. Sequences AAW65670-90 represent a series of
 CC synthetic peptides based on the D3 repeat of *S. aureus* fibronectin
 CC binding protein A. They were synthesised to contain a proline residue at
 CC each position through the sequence (ie a proline scan)

XX Sequence 21 AA;

Query Match 100.0%; Score 118; DB 2; Length 21;
 Best Local Similarity 100.0%; Pred. No. 4e-11;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KPSYQFGGHSVDFEPTLPK 21
 |||||
 DB 1 KPSYQFGGHSVDFEPTLPK 21

RESULT 2
 AAW65665
 ID AAW65665 standard; peptide; 21 AA.

XX AAW65665;

DT 16-OCT-1998 (first entry)

XX Fibronectin binding protein-derived peptide #9.

XX microbial surface components recognising adhesive matrix molecule;

XX MSCRAMM; fibronectin; fibronectin-binding protein; antibody; epitope;

XX antibiotic; bacterial infection; antibiotic-resistant strain.

XX Synthetic.

XX Staphylococcus aureus.

XX WO9831389-A2.

XX 23-JUL-1998.

XX 21-JAN-1998; 98MO-US001222.

XX 21-JAN-1997; 97US-0036139P.

XX (TEXA) UNIV TEXAS A & M SYSTEM.

XX Hosook M, Patti JM, House-Pompeo KL, Speciale P, Joh D;
 PI Mcgavin M;

XX WPI; 1998-413816/35.

XX Antibody that binds to fibronectin-binding protein, preventing its
 PT binding to fibronectin - used to treat or prevent bacterial infection,
 PT especially by Staphylococci and Streptococci.

XX Example 2; Page 92; 201pp; English.

XX The invention relates to antibodies that bind to a fibronectin-binding
 CC domain of a fibronectin-binding protein, and inhibit binding of the
 CC protein to fibronectin. Also claimed are: (1) isolated peptides of a
 CC fibronectin-binding protein that do not bind to fibronectin; (2) fusion
 CC protein containing at least one peptide of a fibronectin-binding protein
 CC linked to a second amino acid sequence; (3) nucleic acid encoding the
 CC isolated peptide of (1). Antibodies, the isolated peptides of (1) and the
 CC nucleic acids are all useful for immunisation (active or passive) and (by
 CC inhibiting binding of bacteria to fibronectin) for preventing or treating
 CC infection in humans or other animals, particularly by Staphylococci or
 CC streptococci, e.g. meningitis, otitis media, pneumonia, endocarditis,
 CC mastitis in cattle, abortion in horses and many others. Since the
 CC antibodies block binding of bacteria, they should be effective against
 CC antibiotic-resistant strains, and may replace antibiotic therapy or
 CC increase its effectiveness. Sequences AAW65659-68 represent synthetic

CC epitopes from the fibronectin binding domains DU and D1-D4 of the *S.*
 CC *aureus* fnbA gene

XX Sequence 21 AA;

QY Query Match 93.2%; Score 110; DB 2; Length 21;
 |||||
 DB 1 KPSYQFGGHSVDFEPTLPK 21

XX Best Local Similarity 95.2%; Pred. No. 7.1e-10;
 XX Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KPSYQFGGHSVDFEPTLPK 21
 |||||
 DB 1 KPSYQFGGHSVDFEPTLPK 21

RESULT 3
 AAR21340
 ID AAR21340 standard; peptide; 22 AA.

XX AAR21340;

DT 25-MAR-2003 (revised)

DT 15-JUN-1992 (first entry)

XX Fibronectin binding protein.

XX FbBP; wound infection reduction; vaccination; mastitis;

XX Staphylococcal infections; D3.

XX Synthetic.

XX WO9202555-A.

XX 20-FEB-1992.

XX 10-AUG-1990; 90SE-00002617.

XX 10-AUG-1990; 90SE-00002617.

XX (ALFA) ALFA LAVAL AGRIC INT AB.

XX Hook M, Mcgavin M, Raucsi G;

XX WPI; 1992-080035/10.

XX Claim 1; Page 22; 33pp; English.

XX The sequence comprises amino acids 17-33 of a tandem repeat, designated
 CC D3 of the fibronectin binding site of *Staphylococcus aureus* 8325-4 FbBP.
 CC The N-terminal DK may be replaced with H or K, and the C-terminal LKP may
 CC be replaced by either L, LP, or OH. The peptides were synthesised using
 CC standard methods and purified using reverse phase HPLC. The appropriate
 CC fractions were dialysed and lyophilised. Peptide sequencing was performed
 CC and the peptides digested and chemically modified by dihydroxypropylation
 CC of the amino side chain of lysine. The carboxylic side chains were
 CC converted to glycine methyl esters. The phenyl side chains of tyrosine
 CC residues were oxidised. Chemically modified peptide D3 was compared to
 CC unmodified D3. Lysine and tyrosine modifications only partially
 CC diminished its activity whereas modification of aspartic/glutamic
 CC residues resulted in complete loss of activity. The peptide can be used
 CC for the prevention or reduction of the risk of wound infection. The
 CC peptide can be used to create a large antigen for vaccinating humans
 CC against mastitis caused by *Staphylococcal* infections. It can also be used
 CC to diagnose *Staphylococcal* infections using ELISA or DNA probes. (Updated
 CC on 25-MAR-2003 to correct PA field.)

XX Sequence 22 AA;

Query Match 93.2%; Score 110; DB 2; Length 22;
 Best Local Similarity 95.2%; Pred. No. 7.5e-10;

Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KPSYQFGHNSVDPEEPTLPK 21
 ID |||||
 DB 2 KPSYQFGHNSVDPEEDTLPK 22

RESULT 4
 AAB91958
 ID AAB91958 standard; peptide; 37 AA.
 XX
 AC AAB91958;
 XX
 DT 22-JUN-2001 (first entry)
 XX
 DE Fibrinectin fragment and fibrin related peptide SEQ ID NO:1134.
 XX
 KM Protection; endogenous therapeutic peptide; peptidase; conjugation;
 KM blood component; modification; succinimidy; maleimido group; amino;
 KM hydroxyl; thiol; hormone; growth factor; neurotransmitter.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 PN WO20069900-A2.
 XX
 PD 23-NOV-2000.
 XX
 PE 17-MAY-2000; 2000WO-US013576.
 XX
 PR 17-MAY-1999; 99US-0134406P.
 PR 10-SEP-1999; 99US-0153406P.
 PR 15-OCT-1999; 99US-0159783P.
 XX
 PA (CONJ-) CONJUCHEM INC.
 XX
 PI Bridon DP, Errin AM, Milner PG, Holmes DL, Thibaudau K;
 XX
 DR WPI; 2001-112059/12.
 XX
 PT Modifying and attaching therapeutic peptides to albumin prevents
 PT peptidase degradation, useful for increasing length of in vivo activity.
 XX
 PS Disclosure; Page 566; 73pp; English.

CC The present invention describes a modified therapeutic peptide (I)
 CC comprising a therapeutically active amino acid region (III) and a
 CC reactive group (II) (e.g. succinimidy) and maleimido groups) attached to
 CC a less therapeutically active amino acid region (IV), which covalently
 CC bonds with amino/hydroxyl/thiol groups on blood components to form a
 CC peptidease stabilised therapeutic peptide composed of 3-50 amino acids.
 CC (I) are useful for modifying therapeutic peptides e.g. hormones, growth
 CC factors and neurotransmitters, to protect them from peptidase activity in
 CC vivo for the treatment of various disorders. Endogenous therapeutic
 CC peptides are not suitable as drug candidates as they require frequent
 CC administration due to rapid degradation by peptidases in the body.
 CC Modifying and attaching therapeutic peptides to albumin prevents or
 CC reduces the action of peptidases to increase length of activity (half
 CC life) and specificity as bonding to large molecules decreases
 CC intracellular uptake and interference with physiological processes.
 CC AAB90829 to AAB92441 represent peptides which can be used in the
 CC exemplification of the present invention
 CC
 SO Sequence 37 AA;

Query Match 93.2%; Score 110; DB 4; Length 37;
 Best Local Similarity 95.2%; Pred. No. 1.3e-09;
 Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KPSYQFGHNSVDPEEPTLPK 21
 ID |||||
 DB 16 KPSYQFGHNSVDPEEDTLPK 36

RESULT 5
 AAP80662
 ID AAP80662 standard; protein; 38 AA.
 XX
 AC AAP80662;
 XX
 DT 25-MAR-2003 (revised)
 DT 07-OCT-1990 (first entry)
 XX
 DE Protein with fibrinectin binding ability.
 XX
 KM Hybrid DNA molecule; fibrinectin binding; mastitis; ruminants;
 KM wound infection.
 XX
 OS Staphylococcus aureus.
 XX
 PN EP294349-A.
 XX
 PD 07-DEC-1998.
 XX
 PE 30-MAY-1998; 88EP-00850188.
 XX
 PR 01-JUN-1987; 87SE-00002272.
 XX
 PA (ALFA) ALFA LAVAL AGRIC INT AB.
 XX
 PI Lindberg MK, Signas LC, Wadstrom TM, Froman G;
 XX
 DR WPI; 1988-347978/49.
 XX
 DR N-PSDB; AAN81099.
 XX
 PT Hybrid DNA encoding Staphylococcus aureus fibrinectin binding protein -
 PT useful for immunisation and topical application to prevent staphylococcal
 PT infections.
 XX
 PS Claim 11; Page 12; 23pp; English.

CC The peptide has fibrinectin binding ability. It is useful for immunising
 CC ruminants against staphylococcal mastitis, pref. when used at 0.5-5
 CC micrograms/kg, using 3 doses given at 1-3 week intervals; for topical
 CC application to prevent wound infection, using an isotonic saline soln. of
 CC concn. 25-250 micrograms/ml; and, when immobilised on a carrier, for
 CC diagnosing staphylococcal infections. (Updated on 25-MAR-2003 to correct
 CC PF field.) (Updated on 25-MAR-2003 to correct PA field.)
 CC
 SO Sequence 38 AA;

Query Match 93.2%; Score 110; DB 1; Length 38;
 Best Local Similarity 95.2%; Pred. No. 1.3e-09;
 Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KPSYQFGHNSVDPEEPTLPK 21
 ID |||||
 DB 17 KPSYQFGHNSVDPEEDTLPK 37

RESULT 6
 AAY29087
 ID AAY29087 standard; protein; 134 AA.
 XX
 AC AAY29087;
 XX
 DT 28-SEP-1999 (first entry)
 XX
 DE S. aureus fibrinectin binding protein A (FnBA) binding domain.
 XX
 KM Bovine herpes virus-2; BHV-2; cytokine; immune response; immunogen; IL;
 KM interleukin; colony stimulating factor; CSF; interferon; IFN; TNF;
 KM tumour necrosis factor; recombinant virus; vaccine; mucosal disease;
 KM mastitis; breast cancer; stress-induced disease; binding domain; FnBA;
 KM fibrinectin binding protein.
 XX
 OS Staphylococcus aureus.

QY 1 KPSYQFGHNSVDPEEPTLPK 21
 ID |||||
 DB 16 KPSYQFGHNSVDPEEDTLPK 36

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XX  MN  MO9916892-A1.
XX  PD  08-APR-1999.
XX  PF  29-SEP-1998; 98WO-GB002927.
XX  PR  29-SEP-1997; 97GB-00020633.
XX  PA  (UYBR-) UNIV BRISTOL.
XX  PI  Bradley AJ, Duffas WPJ;
XX  WP1: 1999-255101/21.
XX  DR  N-PSDB; AAX91504.
XX  PT  New bovine herpes virus-2 vectors.
XX  PS  Example 2; Fig 8A-B; 130pp; English.
XX  CC  The invention provides bovine herpes virus-2 (BHV-2) based vectors that
CC  comprise at least one cytokine-encoding DNA sequence. The expression of
CC  cytokines in mammals can up-regulate immune responses to the immunogens.
CC  The cytokine is selected from interleukins (IL), colony stimulating
CC  factors (CSF), interferons (IFN) and tumour necrosis factors (TNF). The
CC  BHV-2 based vector or recombinant virus can be used as vaccines. They can
CC  be used for preventing or treating a mucosal disease in a subject, e.g.
CC  ruminants, cattle, sheep, goats, dogs, cats, horses, or man, particularly
CC  mastitis in cows or breast cancers in humans. They can also be used for
CC  preventing or treating a stress-induced disease. The present sequence
CC  represents the binding domain of a previously published S. aureus
CC  fibronectin binding protein A (FnBA) sequence. The FnB binding domain
CC  gene sequence FnBAB, cloned for use in this invention has 97.8 percent
CC  identity when compared to the previously published FnBA and FnBB gene
CC  sequences
XX  SQ  Sequence 134 AA;

Query Match          93.2%; Score 110; DB 2; Length 134;
Best Local Similarity 95.2%; Pred. No. 5.2e-09;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY  1 KPSYQFGGHSVDFEEDTLRK 21
DB  93 KPSYQFGGHSVDFEEDTLRK 113

RESULT 7
AAM31556
ID  AAM31556 standard; protein; 139 AA.
XX  AC  AAM31556;
XX  DT  27-AUG-2003 (revised)
XX  DT  25-MAR-2003 (revised)
XX  DT  21-MAY-1998 (first entry)
XX  DE  Fibronectin-binding MSCRAMM derivative POD.
XX  KW  Fibronectin; POD; collagen binding protein; sepsis; infection;
XX  KW  microbial surface component recognising adhesive matrix molecule; MSCRAMM;
XX  KW  adhesin; vaccine; immunisation; diagnosis; therapy; mastitis.
XX  OS  Staphylococcus aureus.
XX  FH  Key
XX  FT  Peptide
XX  Location/Qualifiers
XX  1..12
XX  /note= "vector pOE30-derived peptide"
XX  MN  MO9743314-A2.
XX  PD  20-NOV-1997.

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PF  14-MAY-1997; 97WO-US008210.
XX  BR  16-MAY-1996; 96US-0017678P.
XX  PA  (TEXA ) UNIV TEXAS A & M SYSTEM.
XX  PA  (UABR-) UAB RES FOUND.
XX  PI  Hoeoek M, Patil JM, House-Pompeo K, Sthanam N, Symersky J;
XX  WP1: 1998-008801/01.
XX  PT  Antibody that interacts with collagen binding domain of Staphylococcal
XX  PT  cna gene product - useful to prevent bacterial sepsis in animal infected
XX  PT  with Staphylococcus aureus.
XX  PS  Disclosure; Page 91; 143pp; English.
XX  CC  This protein comprises Staphylococcus aureus fibronectin-binding
XX  CC  microbial surface component recognising adhesive matrix molecule (MSCRAMM)
XX  CC  derivative POD, plus a vector-derived N-terminal peptide. The invention
XX  CC  relates to claimed nucleic acid sequences (see AAT93436-38) encoding S.
XX  CC  aureus collagen binding protein (CBP) epitopes M17, M31 and M55 (see
XX  CC  AAM31552-54) that confer protection against S. aureus infection. CBP
XX  CC  of pathologic and antigenic epitopes are contemplated for use in the treatment
XX  CC  of pathological infections, especially to prevent bacterial adhesion to
XX  CC  collagen. The epitopes are also contemplated for use in the preparation
XX  CC  of vaccines and as carrier proteins in vaccine formulations, as well as
XX  CC  in the formulation of compositions for the prevention of S. aureus
XX  CC  infection. pOF33 and pOD (see AAM31556) were used to raise anti-MSCRAMM
XX  CC  polyclonal antibodies used in passive immunisation against bovine
XX  CC  mastitis. (Updated on 25-MAR-2003 to correct PI field.) (Updated on 27-
XX  CC  AUG-2003 to correct OS field.)
XX  SQ  Sequence 139 AA;

Query Match          93.2%; Score 110; DB 2; Length 139;
Best Local Similarity 95.2%; Pred. No. 5.4e-09;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY  1 KPSYQFGGHSVDFEEDTLRK 21
DB  107 KPSYQFGGHSVDFEEDTLRK 127

RESULT 8
AAP82115
ID  AAP82115 standard; protein; 1018 AA.
XX  AC  AAP82115;
XX  DT  25-MAR-2003 (revised)
XX  DT  05-JUN-1990 (first entry)
XX  DE  Fibronectin binding protein.
XX  KW  Fibronectin binding protein; S. aureus; immunisation; mastitis; ruminants;
XX  KW  wound infection; diagnosis.
XX  OS  Staphylococcus aureus.
XX  PN  EP294349-A.
XX  PD  07-DEC-1988.
XX  PF  30-MAY-1988; 88EP-00850188.
XX  PR  01-JUN-1987; 87SE-00002272.
XX  PA  (ALFA ) ALFA LAVAL AGRIC INT AB.
XX  PI  Lindberg MK, Signas LC, Wadstrom TM, Froman G;
XX  WP1: 1988-347976/49.

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DR P-PSDB; AAP82115.
XX Hybrid DNA encoding *Staphylococcus aureus* fibronectin binding protein -
PT useful for immunisation and topical application to prevent staphylococcal
PT infections.
XX Disclousure; Fig. 8A:1-8A:2; 23pp; English.
PS The *S. aureus* fibronectin binding protein may be included in a hybrid
CC streptolococcal mastitis, pref. when given at 0.5-5 microg/kg, using 3
CC doses at 1-3 week intervals; and for topical applicn. to prevent wound
CC infection, pref. using isotonic saline soln. of concn. 25-250 microg/mg.
CC The DNA encoding the binding protein and the hybrid protein may be
CC immobilised on a carrier and used to diagnose staphylococcal infections.
CC (Updated on 25-MAR-2003 to correct PA field.)
XX Sequence 1018 AA:
SQ
Query Match 93.2%; Score 110; DB 1; Length 1018;
Best Local Similarity 95.2%; Pred. No. 4.6e-08;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 1 KPSYQFGGHSVDFEEDTLPK 21
DB 837 KPSYQFGGHSVDFEEDTLPK 857
RESULT 9
AAU37245
ID AAU37245 standard; protein, 1018 AA.
XX AAU37245;
AC 14-FEB-2002 (first entry)
XX DT
XX Staphylococcus aureus cellular proliferation protein #1415.
DE
XX Antisense; prokaryotic cellular proliferation protein; antibiotic;
KW antibacterial; drug design.
XX OS
XX Staphylococcus aureus.
XX PN
XX WO200170955-A2.
XX PD
XX 27-SEP-2001.
XX PF
XX 21-MAR-2001; 2001WO-US009180.
XX PR
XX 21-MAR-2000; 2000US-0191078P.
XX PR 23-MAY-2000; 2000US-0206848P.
XX PR 26-MAY-2000; 2000US-0207272P.
XX PR 23-OCT-2000; 2000US-0242578P.
XX PR 27-NOV-2000; 2000US-0253625P.
XX PR 22-DEC-2000; 2000US-0257931P.
XX PR 16-FEB-2001; 2001US-0269308P.
XX PA
XX (ELIT-) ELITRA PHARM INC.
XX PI
XX Haselbeck R, Ohlsen KL, Zyskind JW, Wall D, Trawick JD, Carr GJ;
XX Yamamoto RT, Xu HH;
XX WPI; 2001-611495/70.
XX DR N-PSDB; AAS55104.
XX DR
XX New polynucleotides for the identification and development of
PT antibiotics, comprise sequences of antisense nucleic acids.
XX PT
XX Example 3; SEQ ID NO 12838; 511pp; English.
XX PS
XX The invention relates to antisense inhibitors of genes essential to
CC prokaryotic cellular proliferation, their use in identifying the genes,
CC their use in the discovery of novel antibiotics, the essential genes

CC themselves and the encoded proteins. The prokaryotes used are *Escherichia*
CC coli, *Staphylococcus aureus*, *Salmonella typhi*, *Klebsiella pneumoniae*,
CC *Pseudomonas aeruginosa* and *Enterococcus faecalis*. The invention is also
CC useful for the identification of potential new targets for antibiotic
CC development. The antisense nucleic acids can also be used to identify
CC proteins used in proliferation, to express these proteins, and to obtain
CC antibodies capable of binding to the expressed proteins. The proteins can
CC be used to screen compounds in rational drug discovery programmes. The
CC antisense nucleic acid sequence is also useful to screen for homologous
CC nucleic acids which are required for cell proliferation in a wide variety
CC of organisms. The present sequence represents an essential prokaryotic
CC cellular proliferation protein. Note: The sequence data for this patent
CC did not form part of the printed specification, but was obtained in
CC electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX Sequence 1018 AA:
SQ
Query Match 93.2%; Score 110; DB 4; Length 1018;
Best Local Similarity 95.2%; Pred. No. 4.6e-08;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 1 KPSYQFGGHSVDFEEDTLPK 21
DB 837 KPSYQFGGHSVDFEEDTLPK 857
RESULT 10
AAU34301
ID AAU34301 standard; protein, 1018 AA.
XX AAU34301;
AC 14-FEB-2002 (first entry)
XX DT
XX Staphylococcus aureus cellular proliferation protein #577.
DE
XX Antisense; prokaryotic cellular proliferation protein; antibiotic;
KW antibacterial; drug design.
XX OS
XX Staphylococcus aureus.
XX PN
XX WO200170955-A2.
XX PD
XX 27-SEP-2001.
XX PF
XX 21-MAR-2001; 2001WO-US009180.
XX PR
XX 21-MAR-2000; 2000US-0191078P.
XX PR 23-MAY-2000; 2000US-0206848P.
XX PR 26-MAY-2000; 2000US-0207272P.
XX PR 23-OCT-2000; 2000US-0242578P.
XX PR 27-NOV-2000; 2000US-0253625P.
XX PR 22-DEC-2000; 2000US-0257931P.
XX PR 16-FEB-2001; 2001US-0269308P.
XX PA
XX (ELIT-) ELITRA PHARM INC.
XX PI
XX Haselbeck R, Ohlsen KL, Zyskind JW, Wall D, Trawick JD, Carr GJ;
XX Yamamoto RT, Xu HH;
XX WPI; 2001-611495/70.
XX DR N-PSDB; AAS52160.
XX DR
XX New polynucleotides for the identification and development of
PT antibiotics, comprise sequences of antisense nucleic acids.
XX PT
XX Example 3; SEQ ID NO 5797; 511pp; English.
XX PS
XX The invention relates to antisense inhibitors of genes essential to
CC prokaryotic cellular proliferation, their use in identifying the genes,
CC their use in the discovery of novel antibiotics, the essential genes
CC themselves and the encoded proteins. The prokaryotes used are *Escherichia*

coli, *Staphylococcus aureus*, *Salmonella typhi*, *Klebsiella pneumoniae*,
CC *Pseudomonas aeruginosa* and *Enterococcus faecalis*. The invention is also
CC useful for the identification of potential new targets for antibiotic
CC development. The antisense nucleic acids can also be used to identify
CC proteins used in proliferation, to express these proteins, and to obtain
CC antibodies capable of binding to the expressed proteins. The proteins can
CC be used to screen compounds in rational drug discovery programmes. The
CC antisense nucleic acid sequence is also useful to screen for homologous
CC nucleic acids which are required for cell proliferation in a wide variety
CC of organisms. The present sequence represents an essential prokaryotic
CC cellular proliferation protein. Note: The sequence data for this patent
CC did not form part of the printed specification, but was obtained in
CC electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pcc_sequences
XX
SQ Sequence 1018 AA;
XX
Query Match 93.2%; Score 110; DB 4; Length 1018;
Best Local Similarity 95.2%; Pred. No. 4.6e-08;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 KPSYQFGGHSVDPFEEDTLPK 21
DB 837 KPSYQFGGHSVDPFEEDTLPK 857
XX
RESULT 11
ABU18922
ID ABU18922 standard; protein; 1018 AA.
XX
AC ABU18922;
XX
DT 06-MAR-2003 (first entry)
XX
DE Pathogen specific antigen related staphylococcal protein SEQ ID No 68.
XX
XX Antibacterial; virucide; fungicide; protozoacide; cytostatic; anti-HIV;
XX hyperimmune; serum-reactive; antigen; pathogen; tumour; allergen;
XX auto-immunity; vaccine; staphylococcal infection; antibody; cancer;
XX autoimmune disease; HIV; hepatitis.
XX
OS *Staphylococcus* sp.
XX
XX WO200259148-A2.
XX
PN 01-AUG-2002.
XX
PD 21-JAN-2002; 2002WO-EP000546.
XX
PF 26-JAN-2001; 2001AT-00000130.
XX
PR (CIST-) CISTEM BIOTECHNOLOGIES GMBH.
XX
PA Meinke A, Nagy E, Von Ahesen U, Klade C, Henice T, Zauner W;
PI Minh DB, Vyrvyrtka O, Ecz H, Dyla A, Weichart T, Hafner M;
PI Tempelmeier B;
XX
XX WPI; 2003-075410/07.
XX
PT Identifying, isolating and producing hyperimmune serum-reactive antigens
PT from a pathogen, for preparing vaccine or medicament for treating or
PT preventing e.g. staphylococcal infections, comprises providing antibody
PT preparation.
XX
XX Example 7; Page 157; 252pp; English.
XX
XX The invention relates to a novel method for identifying, isolating and
XX producing hyperimmune serum-reactive antigens from a pathogen, tumour,
XX allergen, a tissue or host prone to auto-immunity, where the antigens are
XX used in a vaccine, comprises providing antibody preparation from a plasma
XX pool of a type of animal, or individual sera with antibodies against the
XX specific pathogen, tumour, allergen, tissue or host prone to auto-
XX immunity. The hyperimmune serum-reactive antigens comprising any of the

CC 62 sequences of 53-2261 amino acids fully defined in the specification,
CC or their hyperimmune fragments are useful for the manufacture of a
CC pharmaceutical preparation, particularly a vaccine against staphylococcal
CC infections or colonisation against *S. aureus* or *S. epidermidis*. The
CC preparation of antibodies is useful for the manufacture of a medicament
CC for treating or preventing staphylococcal infections or colonisation
CC against *S. aureus* or *S. epidermidis*. The antibody preparations may also
CC be used for diagnostic and imaging purposes. Other conditions that can be
CC treated include cancer, autoimmune diseases or infections caused by viral
CC (e.g. HIV, hepatitis A, B or C), fungal or protozoan pathogens. This
CC sequence represents a staphylococcal protein relating to the method for
CC identifying and producing pathogen specific antigens of the invention
XX
SQ Sequence 1018 AA;
XX
Query Match 93.2%; Score 110; DB 6; Length 1018;
Best Local Similarity 95.2%; Pred. No. 4.6e-08;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 KPSYQFGGHSVDPFEEDTLPK 21
DB 837 KPSYQFGGHSVDPFEEDTLPK 857
XX
RESULT 12
ABM72537
ID ABM72537 standard; protein; 1018 AA.
XX
AC ABM72537;
XX
DT 20-NOV-2003 (first entry)
XX
DE *Staphylococcus aureus* protein #1777.
XX
XX Antibacterial; vaccine; gene therapy; infection; sepsis; diagnosis;
XX enzymatic assay; antibiotic target.
XX
XX *Staphylococcus aureus*.
XX
XX WO200294868-A2.
XX
PN 28-NOV-2002.
XX
PD 27-MAR-2002; 2002WO-IB002637.
XX
PF 27-MAR-2001; 2001GB-00007661.
XX
PR (CHIR-) CHIRON SPA.
XX
PA Maignani V, Mora M, Scarselli M;
PI WPI; 2003-120786/11.
PI N-PSDB; ACF74097.
XX
XX New *Staphylococcus aureus* protein, useful as a vaccine for treating or
XX preventing *Staphylococcal* infection, specifically an infection caused by
XX *S. aureus*, e.g. sepsis.
XX
XX Claim 1; SEQ ID NO 3554; 49pp; English.
XX
XX The invention relates to novel genes and encoded proteins from
XX *Staphylococcus aureus*. A composition comprising the *S. aureus* protein, a
XX nucleic acid encoding the protein, or an antibody to the protein, is
XX useful as a pharmaceutical, particularly as a vaccine for treating or
XX preventing infection due to *Staphylococcus* bacteria, specifically an
XX infection caused by *S. aureus*. The composition is particularly useful for
XX treating or preventing sepsis in a patient. The composition can also be
XX used for diagnostics. The protein is also used in an assay for enzymatic
XX studies and as a target for antibiotics. This sequence represents one of
XX the novel *S. aureus* proteins of the invention
XX
SQ Sequence 1018 AA;

Query Match 93.2%; Score 110; DB 6; Length 1018;
Best Local Similarity 95.2%; Pred. No. 4.6e-08;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 KPSYQFGHNSVDPEPTLPK 21
DB 837 KPSYQFGHNSVDPEPTLPK 857

RESULT 13
AAW89806
ID AAW89806 standard; protein; 1027 AA.
AC AAW89806;
XX
XX 16-MAR-1999 (first entry)
DT
XX Staphylococcus aureus protein SEQ ID #5254.
DE
XX
XX Computer readable medium; vaccine; S. aureus infection; immunodetection;
KW cellulitis; eyelid infection; food poisoning; osteomyelitis; therapy;
KW skin infection; surgical wound infection; scalded skin syndrome;
KW toxic shock syndrome.
XX Staphylococcus aureus.
OS
XX EP786519-A2.
XX 30-JUL-1997.
PD
XX 07-JAN-1997; 97BP-00100117.
PF
XX 05-JAN-1996; 96US-0009861P.
PR
XX (HUMA-) HUMAN GENOME SCT INC.
XX
XX Kunech CA, Choi GH, Barash SC, Dillon PJ, Fannon MR, Rosen CA;
PI WPI: 1997-374922/35.
XX
XX Polynucleotide(s) and proteins derived from Staphylococcus aureus -
PT stored on computer readable medium and used in the production of anti-
S. aureus vaccines.
XX
XX Claim 23; Page 3263-3267; 3271pp; English.

This sequence represents a Staphylococcus aureus protein sequence of the invention. The DNA sequences encoding the S. aureus proteins are recorded on a computer readable medium, preferably selected from a floppy or hard disk, random access memory (RAM), read-only memory (ROM) or CD-ROM. Homology searches using the S. aureus DNA sequences allows putative functions to be assigned so that protein-encoding or regulatory regions of commercial, therapeutic or industrial importance can be obtained. Specifically, sequences which are likely to encode antigens have been identified and these polypeptides can be used in a vaccine composition against S. aureus infection. The polypeptides can also be used in a kit for the immunodetection of S. aureus in a sample. S. aureus is implicated in numerous human diseases, including cellulitis, eyelid infections, food poisoning, osteomyelitis, skin and surgical wound infections, scalded skin syndrome, toxic shock syndrome, etc. Organisms transformed with the DNA sequences can be used for recombinant production of the polypeptides. The new DNA sequences (and their fragments) are useful as primers or probes for isolating homologues of any of the 5191 S. aureus DNA sequences contained on the computer readable medium

Sequence 1027 AA;

Query Match 93.2%; Score 110; DB 2; Length 1027;
Best Local Similarity 95.2%; Pred. No. 4.7e-08;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 KPSYQFGHNSVDPEPTLPK 21
|||||

DB 846 KPSYQFGHNSVDPEPTLPK 866

RESULT 14
ABU15854
ID ABU15854 standard; protein; 961 AA.
XX
XX ABU15854;
AC
XX
XX 19-JUN-2003 (first entry)
DT
XX
XX Protein encoded by Prokaryotic essential gene #1381.
DE
XX
XX Antisense; prokaryotic essential gene; cell proliferation; drug design.
XX
XX Staphylococcus aureus.
OS
XX WO200277183-A2.
XX
XX 03-OCT-2002.
DT
XX 21-MAR-2002; 2002WO-US009107.
PD
XX 21-MAR-2001; 2001US-00815242.
PF
XX 26-SEP-2001; 2001US-00948993.
PR 25-OCT-2001; 2001US-0342923P.
PR 08-FEB-2002; 2002US-00072851.
PR 06-MAR-2002; 2002US-0362699P.
XX
XX (ELIT-) ELITRA PHARM INC.
XX
XX Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;
PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;
XX
XX WPI: 2003-029926/02.
XX
XX N-PSDB; ACA19724.
DR
XX
XX New antisense nucleic acid, useful for identifying proteins or screening
PT for homologous nucleic acids required for cellular proliferation to
PT isolate candidate molecules for rational drug discovery programs.
XX
XX Claim 25; SEQ ID NO 43778; 1766pp; English.

The invention relates to an isolated nucleic acid comprising any one of the 623 antisense sequences given in the specification where expression of the nucleic acid inhibits proliferation of a cell. Also included are: (1) a vector comprising a promoter operably linked to the nucleic acid encoding a polypeptide whose expression is inhibited by the antisense nucleic acid; (2) a host cell containing the vector; (3) an isolated polypeptide or its fragment whose expression is inhibited by the antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular proliferation or the activity of a gene in an operon required for proliferation; (7) identifying a compound that influences the activity of the gene product or that has an activity against a biological pathway of the cell required for proliferation, or that inhibits cellular proliferation; (8) identifying a gene required for cellular proliferation or the biological pathway in which a proliferation-regulated gene or its gene product lies or a gene on which the test compound that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound's activity; (11) a culture comprising strains in which the gene product is overexpressed or underexpressed; (12) determining the extent to which each of the strains is present in a culture or collection of strains; or (13) identifying the target of a compound that inhibits the proliferation of an organism. The antisense nucleic acids are useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs, or for screening homologous nucleic acids required for proliferation in cells other than S. aureus, S. typhimurium, K. pneumoniae or P. aeruginosa. The present sequence is encoded by one of the target prokaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at


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CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 961 AA;
Query Match 90.7%; Score 107; DB 6; Length 961;
Best Local Similarity 90.5%; Pred. No. 1.3e-07;
Matches 19; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 KPSYQFGGHSVDFEPTLPK 21
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Db 784 KPNYQFGGHSVDFEPTLPK 804

RESULT 15
AAU33960
ID AAU33960 standard; protein; 978 AA.
XX
AC AAU33960;
XX
DT 14-FEB-2002 (first entry)
XX
DE Staphylococcus aureus cellular proliferation protein #236.
XX
KM Antisense; prokaryotic cellular proliferation protein; antibiotic;
XX antibiotic; drug design.
XX
OS Staphylococcus aureus.
XX
PN MO200170955-A2.
XX
PD 27-SEP-2001.
XX
PI 21-MAR-2001; 2001WO-US009180.
XX
PR 21-MAR-2000; 2000US-0191078P.
XX
PR 23-MAY-2000; 2000US-0206848P.
XX
PR 26-MAY-2000; 2000US-0207727P.
XX
PR 23-OCT-2000; 2000US-0242578P.
XX
PR 27-NOV-2000; 2000US-0253625P.
XX
PR 22-DEC-2000; 2000US-0257931P.
XX
PR 16-FEB-2001; 2001US-0269308P.
XX
PA (ELIT-) ELITRA PHARM INC.
XX
PI Haeelbeck R, Ohlsen KL, Zyskind JW, Wall D, Trawick JD, Jarr GJ;
PI Yamamoto RT, Xu HH;
XX
DR N-PSDB; AAS51819.
XX
WPI: 2001-611495/70.
XX
PT New polynucleotides for the identification and development of
PT antibiotics, comprise sequences of antisense nucleic acids.
XX
PS Example 3; SEQ ID NO 5456; 511P; English.
XX
XX
CC The invention relates to antisense inhibitors of genes essential to
CC prokaryotic cellular proliferation, their use in identifying the genes,
CC their use in the discovery of novel antibiotics, the essential genes
CC themselves and the encoded proteins. The prokaryotes used are Escherichia
CC coli, Staphylococcus aureus, Salmonella typhi, Klebsiella pneumoniae,
CC Pseudomonas aeruginosa and Enterococcus faecalis. The invention is also
CC useful for the identification of potential new targets for antibiotic
CC development. The antisense nucleic acids can also be used to identify
CC proteins used in proliferation, to express these proteins, and to obtain
CC antibodies capable of binding to the expressed proteins. The proteins can
CC be used to screen compounds in rational drug discovery programmes. The
CC antisense nucleic acid sequence is also useful to screen for homologous
CC nucleic acids which are required for cell proliferation in a wide variety
CC of organisms. The present sequence represents an essential prokaryotic
CC cellular proliferation protein. Note: The sequence data for this patent
CC did not form part of the printed specification, but was obtained in
CC electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
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XX
SQ Sequence 978 AA;
Query Match 90.7%; Score 107; DB 4; Length 978;
Best Local Similarity 90.5%; Pred. No. 1.3e-07;
Matches 19; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 KPSYQFGGHSVDFEPTLPK 21
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Db 815 KPNYQFGGHSVDFEPTLPK 835

Search completed: October 25, 2005, 19:38:30
Job time : 59.1473 secs
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OM protein - protein search, using SW model

Run on: October 22, 2005, 02:23:36 ; Search time 15.9358 Seconds
(without alignments)
98.371 Million cell updates/sec

Title: US-10-731-238-29

Perfect score: 118
Sequence: 1 KPSYQFGHNSVDPEPTLPK 21

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Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	118	100.0	21 4 US-09-010-317-29	Sequence 29, Appl
2	110	93.2	21 4 US-09-010-317-9	Sequence 9, Appl
3	110	93.2	37 1 US-08-234-622A-4	Sequence 4, Appl
4	110	93.2	38 1 US-08-294-189-8	Sequence 8, Appl
5	110	93.2	38 1 US-08-729-767-5	Sequence 5, Appl
6	110	93.2	114 1 US-08-259-000-3	Sequence 3, Appl
7	110	93.2	139 3 US-08-856-253-8	Sequence 8, Appl
8	110	93.2	178 3 US-08-459-135A-12	Sequence 12, Appl
9	110	93.2	178 3 US-08-495-559-12	Sequence 12, Appl
10	110	93.2	1027 4 US-08-956-171E-5254	Sequence 5254, Ap
11	110	93.2	1027 4 US-08-781-986A-5254	Sequence 5254, Ap
12	105	89.0	21 4 US-09-010-317-14	Sequence 14, Appl
13	105	89.0	21 4 US-09-010-317-16	Sequence 16, Appl
14	105	89.0	21 4 US-09-010-317-23	Sequence 23, Appl
15	105	89.0	21 4 US-09-010-317-33	Sequence 33, Appl
16	104	88.1	21 4 US-09-010-317-18	Sequence 18, Appl
17	104	88.1	21 4 US-09-010-317-24	Sequence 24, Appl
18	104	88.1	21 4 US-09-010-317-27	Sequence 27, Appl
19	104	88.1	21 4 US-09-010-317-28	Sequence 28, Appl
20	104	88.1	21 4 US-09-010-317-30	Sequence 30, Appl
21	103	87.3	21 4 US-09-010-317-25	Sequence 25, Appl
22	103	87.3	21 4 US-09-010-317-31	Sequence 31, Appl
23	103	87.3	130 2 US-08-459-135A-7	Sequence 7, Appl
24	103	87.3	130 2 US-08-459-135A-8	Sequence 8, Appl
25	103	87.3	130 3 US-08-495-559-7	Sequence 7, Appl
26	103	87.3	130 3 US-08-495-559-8	Sequence 8, Appl
27	103	87.3	174 2 US-08-459-135A-10	Sequence 10, Appl

28	103	87.3	174 2 US-08-459-135A-13	Sequence 13, Appl
29	103	87.3	174 3 US-08-495-559-10	Sequence 10, Appl
30	103	87.3	174 3 US-08-495-559-13	Sequence 13, Appl
31	103	87.3	176 3 US-08-495-559-6	Sequence 6, Appl
32	103	87.3	181 2 US-08-459-135A-6	Sequence 6, Appl
33	103	87.3	559 4 US-08-956-171E-5251	Sequence 5251, Ap
34	103	87.3	559 4 US-08-781-986A-5251	Sequence 5251, Ap
35	102	86.4	21 4 US-09-010-317-10	Sequence 10, Appl
36	102	86.4	21 4 US-09-010-317-15	Sequence 15, Appl
37	102	86.4	21 4 US-09-010-317-20	Sequence 20, Appl
38	102	86.4	21 4 US-09-010-317-22	Sequence 22, Appl
39	102	86.4	21 4 US-09-010-317-32	Sequence 32, Appl
40	102	86.4	22 4 US-09-010-317-13	Sequence 13, Appl
41	100	84.7	21 4 US-09-010-317-17	Sequence 17, Appl
42	100	84.7	21 4 US-09-010-317-19	Sequence 19, Appl
43	100	84.7	21 4 US-09-010-317-21	Sequence 21, Appl
44	100	84.7	21 4 US-09-010-317-26	Sequence 26, Appl
45	89	75.4	19 1 US-08-234-622A-1	Sequence 1, Appl

ALIGNMENTS

RESULT 1
US-09-010-317-29
Sequence 29, Application US/09010317
Patent No. 6685943
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
APPLICANT: Patti, Joseph M.
APPLICANT: House-Pompeo, Karen L.
APPLICANT: Speziale, Pietro
APPLICANT: Joh, Danny
APPLICANT: McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
TITLE OF INVENTION: AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESSES:
ADDRESSES: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US-60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hihler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TANK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 29:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-09-010-317-29
Query Match 100.0%; Score 118; DB 4; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.6e-12;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KPSYFGGHSVDFEPTLPK 21
Db 1 KPSYFGGHSVDFEPTLPK 21

RESULT 2

US-09-010-317-9
; Sequence 9, Application US/09010317
; Patent No. 6685943
; GENERAL INFORMATION:
; APPLICANT: Hook, Magnus
; APPLICANT: Patti, Joseph M.
; APPLICANT: House-Pompeo, Karen L.
; APPLICANT: Speziale, Pietro
; APPLICANT: McGavin, Martin J.
; APPLICANT: Joh, Danny
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
; TITLE OF INVENTION: AND METHODS OF USE
; NUMBER OF SEQUENCES: 105
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: TX
; COUNTRY: USA
; ZIP: 77210-4433
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/010.317
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/036,139
; FILING DATE: 21-JAN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Hieber, David W.
; REGISTRATION NUMBER: 41,071
; REFERENCE/DOCKET NUMBER: TAMK:189
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 512-418-3000
; TELEFAX: 512-474-7577
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; US-09-010-317-9

Query Match 93.2%; Score 110; DB 4; Length 21;
Best Local Similarity 95.2%; Pred. No. 3.3e-11;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KPSYFGGHSVDFEPTLPK 21
Db 1 KPSYFGGHSVDFEPTLPK 21

RESULT 3

US-08-234-622A-4
; Sequence 4, Application US/08234622A
; Patent No. 5440014
; GENERAL INFORMATION:
; APPLICANT: HOOK, Magnus
; APPLICANT: MCGAVIN, Martin
; APPLICANT: RAUCCI, Giuseppe
; TITLE OF INVENTION: A FIBRONECTIN BINDING PEPTIDE

NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Burns, Doane, Swecker & Mathis
STREET: P.O. Box 1404
CITY: Alexandria
STATE: Virginia
COUNTRY: United States
ZIP: 22313-1404

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/234,622A
FILING DATE: 28-APR-1994
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: SE 9002617-0
FILING DATE: 10-AUG-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/SE91/00534
FILING DATE: 09-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: Meuth, Donna M
REGISTRATION NUMBER: 36,607
REFERENCE/DOCKET NUMBER: 012885-044
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 37 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-234-622A-4

Query Match 93.2%; Score 110; DB 1; Length 37;
Best Local Similarity 95.2%; Pred. No. 6.3e-11;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KPSYFGGHSVDFEPTLPK 21
Db 16 KPSYFGGHSVDFEPTLPK 36

RESULT 4

US-08-294-189-8
; Sequence 8, Application US/08294189
; Patent No. 5707822
; GENERAL INFORMATION:
; APPLICANT: Fischetti, Vincent A.
; APPLICANT: Rakonjac, Jasna
; APPLICANT: Robbing, John
; TITLE OF INVENTION: GENE SERUM OPACITY FACTOR
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klauder & Jackson
; STREET: 411 Hackensack Avenue
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/294,189
; FILING DATE: 22-AUG-1994

CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-118
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 487-5800
TELEFAX: 201 343-1684
TELEX: 133521
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
ORGANISM: Streptococcus pyogenes
STRAIN: D734
INDIVIDUAL ISOLATE: 22
IMMEDIATE SOURCE:
CLONE: SAUSA
US-08-294-189-8

Query Match 93.2%; Score 110; DB 1; Length 38;
Best Local Similarity 95.2%; Pred. No. 6.5e-11;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KPSYQFGHNSVDFEPTLPK 21
DB 10 KPSYQFGHNSVDFEPTLPK 30

RESULT 5
US-08-729-767-5
Sequence 5, Application US/08729767
Patent No. 5770702
GENERAL INFORMATION:
APPLICANT: HOOK, Magnus
APPLICANT: LINDBERG, Martin Kjell
APPLICANT: SIGNAS, Lars Christer
APPLICANT: WADSTROM, Torkel Mikael
APPLICANT: FROMAN, Gunnar
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN AS WELL AS
TITLE OF INVENTION: ITS PREPARATION
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Burns, Doane, Swecker & Mathis, L.L.P.
STREET: P.O. Box 1404
CITY: Alexandria
STATE: Virginia
COUNTRY: United States
ZIP: 22113-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/729,767
FILING DATE: 07-OCT-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/259,000
FILING DATE: 13-JUN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/007,817
FILING DATE: 22-JAN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/201,028
FILING DATE: 01-JUN-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: SE 8702272-9

FILING DATE: 01-JUN-1987
ATTORNEY/AGENT INFORMATION:
NAME: McGowan, Malcolm K.
REGISTRATION NUMBER: 39,300
REFERENCE/DOCKET NUMBER: 012889-036
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-729-767-5

Query Match 93.2%; Score 110; DB 1; Length 38;
Best Local Similarity 95.2%; Pred. No. 6.5e-11;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KPSYQFGHNSVDFEPTLPK 21
DB 17 KPSYQFGHNSVDFEPTLPK 37

RESULT 6
US-08-259-000-3
Sequence 3, Application US/08259000
Patent No. 5571514
GENERAL INFORMATION:
APPLICANT: HOOK, Magnus
APPLICANT: LINDBERG, Martin Kjell
APPLICANT: SIGNAS, Lars Christer
APPLICANT: WADSTROM, Torkel Mikael
APPLICANT: FROMAN, Gunnar
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN AS WELL AS
TITLE OF INVENTION: ITS PREPARATION
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Burns, Doane, Swecker & Mathis
STREET: P.O. Box 1404
CITY: Alexandria
STATE: Virginia
COUNTRY: United States
ZIP: 22113-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/259,000
FILING DATE: 13-JUN-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: SE 8702272-9
FILING DATE: 01-JUN-1987
ATTORNEY/AGENT INFORMATION:
NAME: Meuth, Donna M
REGISTRATION NUMBER: 36,607
REFERENCE/DOCKET NUMBER: 012885-062
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 114 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-259-000-3

Query Match 93.2%; Score 110; DB 1; Length 114;
Best Local Similarity 95.2%; Pred. No. 2.3e-10;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KPSYQFGHNSVDPDEPTLPK 21
Db 93 KPSYQFGHNSVDPDEPTLPK 113

RESULT 7

US-08-856-253-8
; Sequence 8, Application US/08856253
; Patent No. 6288214
; GENERAL INFORMATION:
; APPLICANT: Hook, Magnus
; APPLICANT: Patli, Joseph M.
; APPLICANT: House-Pompeo, Karen
; APPLICANT: Sthanam, Narayana
; APPLICANT: Symersky, Jindrich
; TITLE OF INVENTION: COLLAGEN BINDING PROTEIN COMPOSITIONS
; TITLE OF INVENTION: AND METHODS OF USE
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: U.S.
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/856,253
; FILING DATE: Concurrently Herewith
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/017,678
; FILING DATE: 16-MAY-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Kitchell, Barbara S.
; REGISTRATION NUMBER: 33,928
; REFERENCE/DOCKET NUMBER: TAWK:193
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (512) 418-3000
; TELEFAX: (512) 474-7577
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 119 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
US-08-856-253-8

Query Match 93.2%; Score 110; DB 3; Length 139;
Best Local Similarity 95.2%; Pred. No. 2.9e-10;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KPSYQFGHNSVDPDEPTLPK 21
Db 107 KPSYQFGHNSVDPDEPTLPK 127

RESULT 8

US-08-459-135A-12
; Sequence 12, Application US/08459135A
; Patent No. 5955078
; GENERAL INFORMATION:
; APPLICANT: BURHAM, Martin Karl Russel
; APPLICANT: CHOPRA, Ian

APPLICANT: CRITCHLEY, Ian Alfred
APPLICANT: KNOWLES, David Justin Charles
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN: MONOCLONAL ANTIBODY AND THEIR US
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
STATE: PA

COUNTRY: U.S.A.

ZIP: 19406-0939

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: Fastseq, Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/459,135A

FILING DATE: 02-JUN-1995

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/GB/94/00215

FILING DATE: 04-Feb-1994

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Gimml, Edward R

REGISTRATION NUMBER: 38,891

REFERENCE/DOCKET NUMBER: P30591C2

TELECOMMUNICATION INFORMATION:

TELEPHONE: 610-270-4478

TELEFAX: 610-270-5090

TELEX:

INFORMATION FOR SEQ ID NO: 12:

SEQUENCE CHARACTERISTICS:

LENGTH: 178 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: Protein

US-08-459-135A-12

Query Match 93.2%; Score 110; DB 2; Length 178;
Best Local Similarity 95.2%; Pred. No. 3.8e-10;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KPSYQFGHNSVDPDEPTLPK 21
Db 93 KPSYQFGHNSVDPDEPTLPK 113

RESULT 9

US-08-495-559-12
; Sequence 12, Application US/08495559A
; Patent No. 6054572
; GENERAL INFORMATION:
; APPLICANT: BURHAM, Martin Karl Russel
; APPLICANT: CHOPRA, Ian
; APPLICANT: CRITCHLEY, Ian Alfred
; APPLICANT: KNOWLES, David Justin Charles
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN: MONOCLONAL
; TITLE OF INVENTION: ANTIBODY AND THEIR USE IN PREVENTING BACTERIAL ADHESION
; FILE REFERENCE: P30591
; CURRENT APPLICATION NUMBER: US/08/495,559A
; CURRENT FILING DATE: 1995-08-03
; EARLIER APPLICATION NUMBER: GB 9302289.5
; EARLIER FILING DATE: 1993-02-05
; EARLIER APPLICATION NUMBER: GB 9321592.9
; EARLIER FILING DATE: 1993-10-20
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: Fastseq for Windows Version 3.0
; SEQ ID NO 12
; LENGTH: 178
; TYPE: PRT

ORGANISM: Staphylococcus aureus
US-08-495-559-12

Query Match 93.2%; Score 110; DB 3; Length 178;
Best Local Similarity 95.2%; Pred. No. 3.8e-10;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KPSYOGGHSVDPEEPTLPK 21
Db 93 KPSYOGGHSVDPEEPTLPK 113

RESULT 10
US-08-956-171E-5254

Sequence 5254, Application US/08956171E
Patent No. 6593114

GENERAL INFORMATION:

APPLICANT: Charles Kunsch

Gil H. Choi

Patrick S. Dillon

Craig A. Rosen

Steven C. Barash

Michael R. Rannon

TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences

NUMBER OF SEQUENCES: 5256

CORRESPONDENCE ADDRESS:

ADDRESSEE: Human Genome Sciences, Inc.

STREET: 9410 Key West Avenue

CITY: Rockville

STATE: Maryland

COUNTRY: USA

ZIP: 20850

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.50 inch, 1.4mb storage

COMPUTER: HP Vectra 486/33

OPERATING SYSTEM: MSDOS version 6.2

SOFTWARE: ASCII text

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/956,171E

FILING DATE: 20-Oct-1997

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 60/009,861

FILING DATE: January 5, 1996

APPLICATION NUMBER: 08/781,986

FILING DATE: January 3, 1997

ATTORNEY/AGENT INFORMATION:

NAME: Mark J. Hyman

REGISTRATION NUMBER: 46,789

REFERENCE/DOCKET NUMBER: PB248P1

TELECOMMUNICATION INFORMATION:

TELEPHONE: (240) 314-1224

TELEFAX: (301) 309-8439

INFORMATION FOR SEQ ID NO: 5254:

SEQUENCE CHARACTERISTICS:

LENGTH: 1027 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 5254:

US-08-956-171E-5254

Query Match 93.2%; Score 110; DB 4; Length 1027;
Best Local Similarity 95.2%; Pred. No. 2.8e-09;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KPSYOGGHSVDPEEPTLPK 21
Db 846 KPSYOGGHSVDPEEPTLPK 866

RESULT 11

US-08-781-986A-5254
Sequence 5254, Application US/08781986A
Patent No. 6737248

GENERAL INFORMATION:

APPLICANT: Charles Kunsch

TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences

NUMBER OF SEQUENCES: 5255

CORRESPONDENCE ADDRESS:

ADDRESSEE: Human Genome Sciences, Inc.

STREET: 9410 Key West Avenue

CITY: Rockville

STATE: Maryland

COUNTRY: USA

ZIP: 20850

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.50 inch, 1.4mb storage

COMPUTER: HP Vectra 486/33

OPERATING SYSTEM: MSDOS version 6.2

SOFTWARE: ASCII text

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/781,986A

FILING DATE:

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Benson, Bob

REGISTRATION NUMBER: 30,446

REFERENCE/DOCKET NUMBER: PB248PP

TELECOMMUNICATION INFORMATION:

TELEPHONE: (301) 309-8504

TELEFAX: (301) 309-8512

INFORMATION FOR SEQ ID NO: 5254:

SEQUENCE CHARACTERISTICS:

LENGTH: 1027 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-781-986A-5254

Qy 1 KPSYOGGHSVDPEEPTLPK 21
Db 846 KPSYOGGHSVDPEEPTLPK 866

RESULT 12
US-09-010-317-14
Sequence 14, Application US/09010317
Patent No. 6685943

GENERAL INFORMATION:

APPLICANT: Hook, Magnus

APPLICANT: Patil, Joseph M.

APPLICANT: House-Pompeo, Karen L.

APPLICANT: Speziale, Pietro

APPLICANT: Joh, Danny

APPLICANT: McGavin, Martin J.

TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS

NUMBER OF SEQUENCES: 105

CORRESPONDENCE ADDRESS:

ADDRESSEE: Arnold, White & Durkee

STREET: P.O. Box 4433

CITY: Houston

STATE: TX

COUNTRY: USA

ZIP: 77210-4433

COMPUTER READABLE FORM:

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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-09-010-317-14

Query Match      89.0%; Score 105; DB 4; Length 21;
Best Local Similarity 95.0%; Pred. No. 2,1e-10;
Matches 19; Conservative 0; Mismatches 1; Indels 0 Gaps 0;

QY      2 PSYFGGHSVDFEPTLPK 21
DB      2 PSYFGGHSVDFEPTLPK 21

RESULT 13
US-09-010-317-16
Sequence 16, Application US/09010317
Patent No. 6685943
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
APPLICANT: Patti, Joseph M.
APPLICANT: House-Pompeo, Karen L.
APPLICANT: Speziale, Pietro
APPLICANT: Joh, Danny
APPLICANT: McGavin, Martin J.
TITLE OF INVENTION: FIBROECTIN BINDING PROTEIN COMPOSITIONS
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESS: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAMK:189
TELECOMMUNICATION INFORMATION:
```

```

TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-09-010-317-16

Query Match      89.0%; Score 105; DB 4; Length 21;
Best Local Similarity 90.5%; Pred. No. 2,1e-10;
Matches 19; Conservative 0; Mismatches 2; Indels 0 Gaps 0;

QY      1 KPSYFGGHSVDFEPTLPK 21
DB      1 KPSYFGGHSVDFEPTLPK 21

RESULT 14
US-09-010-317-23
Sequence 23, Application US/09010317
Patent No. 6685943
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
APPLICANT: Patti, Joseph M.
APPLICANT: House-Pompeo, Karen L.
APPLICANT: Speziale, Pietro
APPLICANT: Joh, Danny
APPLICANT: McGavin, Martin J.
TITLE OF INVENTION: FIBROECTIN BINDING PROTEIN COMPOSITIONS
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESS: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAMK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-09-010-317-23

Query Match      89.0%; Score 105; DB 4; Length 21;
Best Local Similarity 90.5%; Pred. No. 2,1e-10;
Matches 19; Conservative 0; Mismatches 2; Indels 0 Gaps 0;

QY      1 KPSYFGGHSVDFEPTLPK 21
DB      1 KPSYFGGHSVDFEPTLPK 21
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 22, 2005, 10:49:15 ; Search time 59.2367 Seconds
(without alignments)
148.005 Million cell updates/sec

Title: US-10-731-238-29
Perfect score: 118
Sequence: 1 KPSYGFCHNSYDFEPTLPK 21

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1862951 seqs, 417491010 residues
Total number of hits satisfying chosen parameters: 1862951

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

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2: /cgn2_6/ptodata/2/pubppa/PCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/2/pubppa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/2/pubppa/US06_PUBCOMB.pep.*
5: /cgn2_6/ptodata/2/pubppa/US07_NEW_PUB.pep.*
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7: /cgn2_6/ptodata/2/pubppa/US08_NEW_PUB.pep.*
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9: /cgn2_6/ptodata/2/pubppa/US09_PUBCOMB.pep.*
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11: /cgn2_6/ptodata/2/pubppa/US09C_PUBCOMB.pep.*
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16: /cgn2_6/ptodata/2/pubppa/US10D_PUBCOMB.pep.*
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19: /cgn2_6/ptodata/2/pubppa/US11A_PUBCOMB.pep.*
20: /cgn2_6/ptodata/2/pubppa/US11B_PUBCOMB.pep.*
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22: /cgn2_6/ptodata/2/pubppa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	118	100.0	21	18	US-10-731-238-29
2	110	93.2	21	18	US-10-731-238-9
3	110	93.2	37	20	US-11-066-697-1134
4	110	93.2	139	9	US-09-813-820-8
5	110	93.2	1018	9	US-09-815-242-5797
6	110	93.2	1018	9	US-09-815-242-12838
7	110	93.2	1018	17	US-10-470-048B-68
8	110	93.2	1027	8	US-08-781-986A-5254
9	110	93.2	1027	15	US-10-329-624-5254
10	107	90.7	961	15	US-10-282-122A-43778
11	107	90.7	978	9	US-09-815-242-5456

12	107	90.7	1001	9	US-09-815-242-12686	Sequence 12686, A
13	107	90.7	1038	15	US-10-282-122A-43827	Sequence 43827, A
14	105	89.0	21	18	US-10-731-238-14	Sequence 14, Appl
15	105	89.0	21	18	US-10-731-238-16	Sequence 16, Appl
16	105	89.0	21	18	US-10-731-238-23	Sequence 23, Appl
17	105	89.0	21	18	US-10-731-238-33	Sequence 33, Appl
18	104	88.1	21	18	US-10-731-238-18	Sequence 18, Appl
19	104	88.1	21	18	US-10-731-238-24	Sequence 24, Appl
20	104	88.1	21	18	US-10-731-238-27	Sequence 27, Appl
21	104	88.1	21	18	US-10-731-238-28	Sequence 28, Appl
22	104	88.1	21	18	US-10-731-238-30	Sequence 30, Appl
23	103	87.3	21	18	US-10-731-238-35	Sequence 35, Appl
24	103	87.3	21	18	US-10-731-238-31	Sequence 31, Appl
25	103	87.3	388	8	US-08-901-062-1	Sequence 1, Appl
26	103	87.3	559	8	US-08-781-986A-5251	Sequence 5251, Ap
27	103	87.3	559	15	US-10-329-624-5251	Sequence 5251, Ap
28	103	87.3	940	17	US-10-470-048B-424	Sequence 424, App
29	103	87.3	948	17	US-10-470-048B-69	Sequence 69, Appl
30	102	86.4	21	18	US-10-731-238-10	Sequence 10, Appl
31	102	86.4	21	18	US-10-731-238-15	Sequence 15, Appl
32	102	86.4	21	18	US-10-731-238-20	Sequence 20, Appl
33	102	86.4	21	18	US-10-731-238-22	Sequence 22, Appl
34	102	86.4	21	18	US-10-731-238-32	Sequence 32, Appl
35	102	86.4	22	18	US-10-731-238-13	Sequence 13, Appl
36	100	84.7	21	18	US-10-731-238-17	Sequence 17, Appl
37	100	84.7	21	18	US-10-731-238-19	Sequence 19, Appl
38	100	84.7	21	18	US-10-731-238-21	Sequence 21, Appl
39	100	84.7	21	18	US-10-731-238-26	Sequence 26, Appl
40	82	69.5	21	18	US-10-731-238-34	Sequence 34, Appl
41	82	69.5	21	18	US-10-731-238-61	Sequence 61, Appl
42	59	50.0	10	18	US-10-731-238-96	Sequence 96, Appl
43	58	49.2	10	18	US-10-731-238-97	Sequence 97, Appl
44	57	48.3	10	18	US-10-731-238-98	Sequence 98, Appl
45	54	45.8	10	18	US-10-731-238-95	Sequence 95, Appl

ALIGNMENTS

RESULT 1
US-10-731-238-29
Sequence 29, Application US/10731238
Publication No. US20050123552A1
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
Pattl, Joseph M.
House-Pompeo, Karen L.
Speziale, Pietro
Joh, Danny
McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/731, 238
FILING DATE: 10-Dec-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/010, 317
FILING DATE: 21-Jan-1998
APPLICATION NUMBER: US 60/036, 139

FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TANK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 29:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 29:
US-10-731-238-29
Query Match 100.0%; Score 118; DB 18; Length 21;
Best Local Similarity 100.0%; Pred. No. 3,1e-11;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 KPSYQFGGHSVDPEEPTLPK 21
Db 1 KPSYQFGGHSVDPEEPTLPK 21
RESULT 2
US-10-731-238-9
Sequence 9, Application US/10731238
Publication No. US20050123552A1
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
Patti, Joseph M.
House-Pompeo, Karen L.
Speziale, Pietro
Joh, Danny
McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/731,238
FILING DATE: 10-Dec-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE: 21-Jan-1998
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TANK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>

TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 9:
US-10-731-238-9
Query Match 93.2%; Score 110; DB 18; Length 21;
Best Local Similarity 95.2%; Pred. No. 5,6e-10;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 KPSYQFGGHSVDPEEPTLPK 21
Db 1 KPSYQFGGHSVDPEEPTLPK 21
RESULT 3
US-11-066-697-1134
Sequence 1134, Application US/11066697
Publication No. US20050187159A1
GENERAL INFORMATION:
APPLICANT: Bridon, Dominique P.
APPLICANT: Ezrin, Alan M.
APPLICANT: Milner, Peter G.
APPLICANT: Holmes, Darren L.
APPLICANT: Thibaudau, Karen
TITLE OF INVENTION: PROTECTION OF ENDOGENOUS THERAPEUTIC PEPTIDES FROM
TITLE OF INVENTION: PEPTIDASE ACTIVITY THROUGH COMUUGATION TO BLOOD
FILE OF INVENTION: COMPONENTS
FILE REFERENCE: 500862002301
CURRENT APPLICATION NUMBER: US/11/066,697
CURRENT FILING DATE: 2005-02-25
PRIOR APPLICATION NUMBER: 09/657,276
PRIOR FILING DATE: 2000-09-07
PRIOR APPLICATION NUMBER: 60/153,406
PRIOR FILING DATE: 1999-09-10
PRIOR APPLICATION NUMBER: 60/159,783
PRIOR FILING DATE: 1999-10-15
NUMBER OF SEQ ID NOS: 1617
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1134
LENGTH: 37
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
OTHER INFORMATION: Peptide
US-11-066-697-1134
Query Match 93.2%; Score 110; DB 20; Length 37;
Best Local Similarity 95.2%; Pred. No. 1e-09;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 KPSYQFGGHSVDPEEPTLPK 21
Db 16 KPSYQFGGHSVDPEEPTLPK 36
RESULT 4
US-09-813-820-8
Sequence 8, Application US/09813820
Patent No. US2002010262A1
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
Patti, Joseph M.
House-Pompeo, Karen
Sthanam, Narayana
Sytersky, Jindrich
TITLE OF INVENTION: COLLAGEN BINDING PROTEIN COMPOSITIONS
AND METHODS OF USE
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: Texas

```

; COUNTRY: U.S.
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION NUMBER: US/09/813,820
; FILING DATE: 22-Mar-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/856,253
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Kitchell, Barbara S.
; REGISTRATION NUMBER: 33,928
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (512) 474-7577
; TELEFAX: (512) 474-7577
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 139 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-09-813-820-8

Query Match      93.2%; Score 110; DB 9; Length 139;
Best Local Similarity 95.2%; Pred. No. 4.3e-09;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1 KPSYOGGHSVDFEPTLPK 21
Db      107 KPSYOGGHSVDFEPTLPK 127

RESULT 5
US-09-815-242-5797
; Sequence 5797, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Karl L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; FILE OF INVENTION: Prokaryotes
; FILE REFERENCE: ELITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version 4.0
;

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; SEQ ID NO 5797
; LENGTH: 1018
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-09-815-242-5797

Query Match      93.2%; Score 110; DB 9; Length 1018;
Best Local Similarity 95.2%; Pred. No. 3.8e-08;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1 KPSYOGGHSVDFEPTLPK 21
Db      837 KPSYOGGHSVDFEPTLPK 857

RESULT 6
US-09-815-242-12838
; Sequence 12838, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Karl L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; FILE OF INVENTION: Prokaryotes
; FILE REFERENCE: ELITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12838
; LENGTH: 1018
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-09-815-242-12838

Query Match      93.2%; Score 110; DB 9; Length 1018;
Best Local Similarity 95.2%; Pred. No. 3.8e-08;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1 KPSYOGGHSVDFEPTLPK 21
Db      837 KPSYOGGHSVDFEPTLPK 857

RESULT 7
US-10-470-048B-68
; Sequence 68, Application US/10470048B
; Publication No. US2005003744A1
; GENERAL INFORMATION:
; APPLICANT: MEINKE ET AL.
; TITLE OF INVENTION: A METHOD FOR IDENTIFICATION, ISOLATION AND PRODUCTION OF
; FILE OF INVENTION: ANTIGENS TO A SPECIFIC PATHOGEN
; FILE REFERENCE: SONN:03505
;

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;; CURRENT APPLICATION NUMBER: US/10/470,048B
;; CURRENT FILING DATE: 2003-07-25
;; NUMBER OF SEQ ID NOS: 603
;; SOFTWARE: PatentIn version 3.1
;; SEQ ID NO: 68
;; LENGTH: 1018
;; TYPE: PRF
;; ORGANISM: Staphylococcus aureus
US-10-470-048B-68

Query Match 93.2%; Score 110; DB 17; Length 1018;
Best Local Similarity 95.2%; Pred. No. 3.8e-08;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 KPSYQFGGHSVDPFEEDTLPK 21
|||
Db 837 KPSYQFGGHSVDPFEEDTLPK 857

RESULT 8
US-08-781-986A-5254
; Sequence 5254, Application US/08/781986A
; Publication No. US2003005436A1
; GENERAL INFORMATION:
; APPLICANT: Charles Kunach
; TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
; NUMBER OF SEQUENCES: 5255
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/781,986A
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Benson, Bob
REGISTRATION NUMBER: 30,446
REFERENCE/DOCKET NUMBER: PB248BP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 5254:

SEQUENCE CHARACTERISTICS:
LENGTH: 1027 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-781-986A-5254

Query Match 93.2%; Score 110; DB 8; Length 1027;
Best Local Similarity 95.2%; Pred. No. 3.8e-08;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 KPSYQFGGHSVDPFEEDTLPK 21
|||
Db 846 KPSYQFGGHSVDPFEEDTLPK 866

RESULT 9
US-10-329-624-5254

; Sequence 5254, Application US/10329624
; Publication No. US20040043037A1
; GENERAL INFORMATION:
; APPLICANT: Charles Kunach
; Gil H. Choi
; Patrick S. Dillon
; Craig A. Rosen
; Steven C. Barash
; Michael R. Fannon

TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
NUMBER OF SEQUENCES: 5256
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COUNTRY: USA
ZIP: 20850

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/329,624
FILING DATE: 27-Dec-2002
PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/956,171
FILING DATE: October 20, 1997
APPLICATION NUMBER: 60/009,861
FILING DATE: January 5, 1996
APPLICATION NUMBER: 08/781,986
FILING DATE: January 3, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Mark J. Hyman
REGISTRATION NUMBER: 46,789
REFERENCE/DOCKET NUMBER: PB248B1D1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (240) 314-1224
TELEFAX: (301) 309-8439

INFORMATION FOR SEQ ID NO: 5254:
SEQUENCE CHARACTERISTICS:
LENGTH: 1027 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 5254:

US-10-329-624-5254

Query Match 93.2%; Score 110; DB 15; Length 1027;
Best Local Similarity 95.2%; Pred. No. 3.8e-08;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 KPSYQFGGHSVDPFEEDTLPK 21
|||
Db 846 KPSYQFGGHSVDPFEEDTLPK 866

RESULT 10
US-10-282-122A-43778

; Sequence 43778, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:

APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari
APPLICANT: Zyckind, Judith
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John
APPLICANT: Carr, Grant

APPLICANT: Yamamoto, Robert
APPLICANT: Forsyth, R.
TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REFERENCE: ELITRA.03A
CURRENT FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/230,335
PRIOR FILING DATE: 2000-09-06
PRIOR APPLICATION NUMBER: 60/230,347
PRIOR FILING DATE: 2000-09-09
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/267,636
PRIOR FILING DATE: 2001-02-09
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
Remaining Prior Application data removed - See File Wrapper or PAM.
NUMBER OF SEQ ID NOS: 78614
SOFTWARE: Patent version 3.1
SEQ ID NO 43778
LENGTH: 961
TYPE: PRT
ORGANISM: Staphylococcus aureus
US-10-282-122A-43778

Query Match
Best Local Similarity 90.7%; Score 107; DB 15; Length 961;
Pred. No. 1e-07;
Matches 19; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 KPSYOGGNSVDPEPTLPK 21
DB 784 KPNYOGGNSVDPEPTLPK 804

RESULT 11
US-09-815-242-5456
Sequence 5456, Application US/09815242
Patent No. US20020061569A1
GENERAL INFORMATION:
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Karl L.
APPLICANT: Zyskind, Judith W.
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John D.
APPLICANT: Carr, Grant J.
APPLICANT: Yamamoto, Robert T.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in Prokaryotes
FILE REFERENCE: ELITRA.01A
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27

PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 5456
LENGTH: 978
TYPE: PRT
ORGANISM: Staphylococcus aureus
US-09-815-242-5456

Query Match
Best Local Similarity 90.7%; Score 107; DB 9; Length 978;
Pred. No. 1.1e-07;
Matches 19; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 KPSYOGGNSVDPEPTLPK 21
DB 815 KPNYOGGNSVDPEPTLPK 835

RESULT 12
US-09-815-242-12686
Sequence 12686, Application US/09815242
Patent No. US20020061569A1
GENERAL INFORMATION:
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Karl L.
APPLICANT: Zyskind, Judith W.
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John D.
APPLICANT: Carr, Grant J.
APPLICANT: Yamamoto, Robert T.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in Prokaryotes
FILE REFERENCE: ELITRA.01A
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 12686
LENGTH: 1001
TYPE: PRT
ORGANISM: Staphylococcus aureus
US-09-815-242-12686

Query Match
Best Local Similarity 90.7%; Score 107; DB 9; Length 1001;
Pred. No. 1.1e-07;
Matches 19; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 KPSYOGGNSVDPEPTLPK 21
DB 838 KPNYOGGNSVDPEPTLPK 858

RESULT 13
US-10-282-122A-43827
Sequence 43827, Application US/10282122A

Publication No. US20040029129A1
GENERAL INFORMATION:
APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Karl
APPLICANT: Zykend, Judith
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John
APPLICANT: Carr, Grant
APPLICANT: Yamamoto, Robert
APPLICANT: Foreyth, R.
APPLICANT: Xu, H.
TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REFERENCE: ELITRA.034A
CURRENT APPLICATION NUMBER: US/10/282.122A
CURRENT FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/230,335
PRIOR FILING DATE: 2000-09-06
PRIOR APPLICATION NUMBER: 60/230,347
PRIOR FILING DATE: 2000-09-09
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/267,636
PRIOR FILING DATE: 2001-02-09
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
Remaining Prior Application data removed - See file Wrapper or PALM.
NUMBER OF SEQ ID NOS: 78614
SOFTWARE: PatentIn version 3.1
SEQ ID NO 43827
LENGTH: 1038
TYPE: PRT
ORGANISM: Staphylococcus aureus
US-10-282-122A-43827
Query Match 90.7%; Score 107; DB 15; Length 1038;
Best Local Similarity 90.5%; Pred. No. 1,1e-07;
Matches 19; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
CY 1 KPSYQFGHNSVDPEEPTLPK 21
DB 833 KPNYQFGHNSVDPEEPTLPK 853
US-10-731-238-14
Sequence 14, Application US/10731238
Publication No. US20050123552A1
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
Patil, Joseph M.
House-Pompeo, Karen L.
Speziale, Pietro
Joh, Danny
McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESSES:
ADDRESS: Arnold, White & Durkee
STREET: P. O. Box 4433

CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/731.238
FILING DATE: 10-Dec-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/010.317
FILING DATE: 21-Jan-1998
APPLICATION NUMBER: US 60/036.139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAMK.189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 14:
US-10-731-238-14
Query Match 89.0%; Score 105; DB 18; Length 21;
Best Local Similarity 95.0%; Pred. No. 3.4e-09;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
CY 2 PSYQFGHNSVDPEEPTLPK 21
DB 2 PSYQFGHNSVDPEEPTLPK 21
US-10-731-238-16
Sequence 16, Application US/10731238
Publication No. US20050123552A1
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
Patil, Joseph M.
House-Pompeo, Karen L.
Speziale, Pietro
Joh, Danny
McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESSES:
ADDRESS: Arnold, White & Durkee
STREET: P. O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/731.238
FILING DATE: 10-Dec-2003
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/09/010,317
 FILING DATE: 21-Jan-1998
 APPLICATION NUMBER: US 60/036,139
 FILING DATE: 21-JAN-1997
 ATTORNEY/AGENT INFORMATION:
 NAME: Hibler, David W.
 REGISTRATION NUMBER: 41,071
 REFERENCE/DOCKET NUMBER: TAMK:189
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 512-418-3000
 TELEFAX: 512-474-7577
 INFORMATION FOR SEQ ID NO: 16:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 21 amino acids
 TYPE: amino acid
 STRANDEDNESS: <Unknown>
 TOPOLOGY: linear
 SEQUENCE DESCRIPTION: SEQ ID NO: 16:
 US-10-731-238-16

Query Match 89.0%; Score 105; DB 18; Length 21;
 Best Local Similarity 90.5%; Pred. No. 3.4e-09;
 Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 1 KPSYQFGGNSVDPEEPTLPK 21
 ||||||||||||
 Db 1 KPPYQFGGNSVDPEEDTLPK 21

Search completed: October 22, 2005, 11:34:43
 Job time : 60.2367 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 22, 2005, 02:23:36 ; Search time 10.5465 Seconds
(without alignments)
191.586 Million cell updates/sec

Title: US-10-731-238-29

Perfect score: 118

Sequence: 1 KPSYQFGGHNVSVDPEPTLPK 21

Scoring table: BLOSUM62

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database: PIR_79:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	110	93.2	1018	2	A32192	fibronectin-binding
2	107	90.7	1038	2	H90053	hypothetical prote
3	103	87.3	940	2	S19702	fibronectin-binding
4	103	87.3	940	2	S19702	fibronectin-binding
5	49.5	41.9	720	2	S51340	nucleoporin NUP2 -
6	47	39.8	387	2	I38449	extracellular prote
7	47	39.8	445	2	F90562	hypothetical prote
8	47	39.8	462	1	A39356	3-oxoacyl-lacyl-ca
9	46	38.0	453	2	H70333	conserved hypothet
10	46	38.0	975	2	T29908	hypothetical prote
11	45.5	38.6	1123	2	A39962	kinase-related tra
12	45.5	38.6	1130	1	TVHUA	protein-tyrosine k
13	45	38.1	433	2	T01405	vesicle-associated
14	45	38.1	469	2	T10061	hypothetical-lacyl-ca
15	45	38.1	1271	2	T24008	hypothetical prote
16	45	38.1	1322	2	A59288	myosin heavy chain
17	44.5	37.7	417	2	T34930	probable secreted
18	44	37.3	303	2	B75485	fructokinase - Del
19	44	37.3	427	2	D95159	3-phosphoshikimate
20	44	37.3	431	2	D96025	ferredoxin-NADP re
21	44	37.3	440	1	S33479	ferredoxin-NADP re
22	44	37.3	440	2	AB2321	ferredoxin-NADP(+)
23	44	37.3	690	2	T33321	hypothetical prote
24	43	36.4	197	2	C69779	NAD(P)H oxidoreduc
25	43	36.4	288	2	T37395	probable 33.6k pro
26	43	36.4	288	2	A42518	A8R protein - vacc
27	43	36.4	407	2	S27794	hypothetical 46.7K
28	43	36.4	750	2	G81361	probable flagellin
29	43	36.4	1005	2	D95391	probable cation ef

30	43	36.4	1963	2	B98002	IGA-specific metal
31	42.5	36.0	459	2	SE9731	mRNA guanylyltrans
32	42.5	36.0	718	1	VCPVIM	coat protein VP1 -
33	42.5	36.0	722	1	VCPVME	coat protein VP1 -
34	42.5	36.0	727	1	VCPVIF	coat protein VP1 -
35	42.5	36.0	727	1	VCPVIF	coat protein VP1 -
36	42.5	36.0	729	1	AC0006	coat protein VP1 -
37	42.5	36.0	729	1	VCPVNA	coat protein VP1 -
38	42.5	36.0	748	1	VCPVCP	coat protein VP1 -
39	42.5	36.0	1037	2	AF0101	probable exported
40	42	35.6	222	2	S74066	hypothetical prote
41	42	35.6	284	2	S60250	mab-18 protein (tr
42	42	35.6	296	2	S60251	mab-18 protein (tr
43	42	35.6	363	2	T27388	hypothetical prote
44	42	35.6	431	2	B84031	trigger factor (pr
45	42	35.6	457	2	T29846	hypothetical prote

ALIGNMENTS

RESULT 1

A32192
fibronectin-binding protein - Staphylococcus aureus
C.Species: Staphylococcus aureus
C.Date: 31-Jul-1989 #sequence_revision 31-Jul-1989 #text_change 16-Feb-1997
R.Accession: A32192
R.Signaess, C.; Raucel, G.; Joensson, K.; Lindgren, P.E.; Anantharamiah, G.M.; Hoeseck, M.
Proc. Natl. Acad. Sci. U.S.A. 86, 699-703, 1989
A.Title: Nucleotide sequence of the gene for a fibronectin-binding protein from Staphyloc
A.Reference number: A32192; MUID:89098989; PMID:2521391
A.Accession: A32192
A.Status: preliminary
A.Molecule type: DNA
A.Residues: 1-1018 <SIG>
A.Cross-references: GB:J04151
C.Keywords: fibronectin binding

Query Match 93.2% Score 110; DB 2; Length 1018;
Best Local Similarity 95.2% Pred. No. 3.6e-09;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KPSYQFGGHNVSVDPEPTLPK 21

DB 837 KPSYQFGGHNVSVDPEPTLPK 857

RESULT 2

G90053
hypothetical protein fnb [imported] - Staphylococcus aureus (strain N315)
C.Species: Staphylococcus aureus
C.Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004

R.Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguc
ma, A.; Mizutani-U, Y.; Kobayashi, N.; Swano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.; I
C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiratake, K.
Lancet 357, 1225-1240, 2001

A.Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.
A.Reference number: AB9758; MUID:21311952; PMID:11418146

A.Accession: G90053
A.Status: preliminary
A.Molecule type: DNA

A.Residues: 1-961 <KUR>
A.Cross-references: UNIPROT:Q99RD3; GB:BA000018; PID:g13702452; PIDN:BA843593.1; GSPDB:G
A.Experimental source: strain N315

C.Genetics:
A.Gene: fnb
Query Match 90.7% Score 107; DB 2; Length 961;
Best Local Similarity 90.5% Pred. No. 1e-08;
Matches 19; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 KPSYQFGGHNVSVDPEPTLPK 21

Db 784 KPNTQFGHNSVDPDEEDTLPK 804

RESULT 3

H90053 hypothetical protein fnb [imported] - Staphylococcus aureus (strain N315)

C/Species: Staphylococcus aureus
C/Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change (9-Jul-2004
C/Accession: H90053
R/Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguc
ma, A.; Mutant-01, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kato, C.; Sekimizu, K.;
C/ Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
A/Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.
A/Reference number: A89758; MUID:21311952; PMID:11418146
A/Accession: H90053
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-1038 <KUR>
A/Cross-references: UNIPROT:Q99RD2; GB:BA000018; PID:g13702453; FIDN:BA043594.1; GSPDB:G
A/Experimental source: strain N315
C/Genetics:
A/Gene: fnb

Query Match 90.7%; Score 107; DB 2; Length 1038;
Best Local Similarity 90.5%; Pred. No. 1,1e-08;
Matches 19; Conservative 1; Mismatches 1; Indels 3; Gaps 0;

OY 1 KPSTQFGHNSVDPDEEDTLPK 21

Db 833 KPNTQFGHNSVDPDEEDTLPK 853

RESULT 4

S19702 fibronectin-binding protein B - Staphylococcus aureus

C/Species: Staphylococcus aureus
C/Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 0; Jul-2004
C/Accession: S19702
R/Johnson, K.; Signaes, C.; Mueller, H.P.; Lindberg, M.
Eur. J. Biochem. 202, 1041-1048, 1991
A/Title: Two different genes encode fibronectin binding proteins in Staphylococcus aureus
A/Reference number: S19702; MUID:92111475; PMID:1837266
A/Accession: S19702
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-940 <JOB>
A/Cross-references: UNIPROT:O53682; EMBL:X62992; NID:g49040; PIDN:CAA44726.1; PID:g58156
C/Keywords: fibronectin binding

Query Match 87.3%; Score 103; DB 2; Length 940;
Best Local Similarity 85.7%; Pred. No. 4.3e-08;
Matches 18; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 1 KPSTQFGHNSVDPDEEDTLPK 21

Db 773 KPNTQFGHNSVDPDEEDTLPK 793

RESULT 5

S51340 nucleoporin NUP2 - yeast (Saccharomyces cerevisiae)

N/Alternate names: protein L8300.9; protein YLR335W
C/Species: Saccharomyces cerevisiae
C/Date: 23-Feb-1995 #sequence_revision 11-Aug-1995 #text_change 23-Mar-2001
C/Accession: S51340; A47725; S31315
R/Du, Z.
submitted to the EMBL Data Library, December 1994
A/Description: The sequence of S. cerevisiae cosmid 8300.
A/Reference number: S51339
A/Accession: S51340
A/Molecule type: DNA

A/Residues: 1-720 <DUZ>
A/Cross-references: EMBL:U19028; NID:g609380; PID:g609388; MIPS:YLR335W
R/Loeb, J.D.; Davis, L.I.; Fink, G.R.
Mol. Biol. Cell 4, 209-222, 1993
A/Title: NUP2, a novel yeast nucleoporin, has functional overlap with other proteins of t

A/Reference number: A47725; MUID:93184405; PMID:8443417
A/Accession: A47725
A/Molecule type: DNA
A/Residues: 1-136, 'F', 138-369, 'N', 371-417, 'F', 419-720 <LOW>
A/Cross-references: EMBL:X69964; NID:g4048; PIDN:CAA49587.1; PID:g4049
A/Note: sequence extracted from NCBI backbone (NCBIN:126719, NCBIPI:126721)
C/Genetics:
A/Gene: SGD:NUP2
A/Cross-references: SGD:S0004327; MIPS:YLR335W
A/Map position: 12R

Query Match 41.9%; Score 49.5; DB 2; Length 720;
Best Local Similarity 43.5%; Pred. No. 11;
Matches 10; Conservative 5; Mismatches 5; Indels 3; Gaps 1;

OY 1 KPSTQFGHNSVDPDEEDTLPK 20

Db 435 KPSTQFGHNSVDPDEEDTLPK 457

RESULT 6

I38449 extracellular protein - human

C/Species: Homo sapiens (man)
C/Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 21-Jul-2000
C/Accession: I38449
R/Locka-Czerwik, B.; Lumpkin, C.K.
Mol. Cell. Biol. 15, 120-128, 1995
A/Title: An overexpressed gene transcript in senescent and quiescent human fibroblasts er
A/Reference number: I38449; MUID:9507985; PMID:779918
A/Accession: I38449
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-387 <RES>
A/Cross-references: EMBL:U03877; NID:g458227; PIDN:AAA65590.1; PID:g458228
C/Genetics:
A/Gene: SI-5

Query Match 39.8%; Score 47; DB 2; Length 387;
Best Local Similarity 47.4%; Pred. No. 13;
Matches 9; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

OY 2 PSTQFGHNSVDPDEEDTLPK 20

Db 97 PGTQKRGECVDEICTIP 115

RESULT 7

F90562 hypothetical protein MYPU 4060 [imported] - Mycoplasma pulmonis (strain UAB CTIP)

C/Species: Mycoplasma pulmonis
C/Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 09-Jul-2004
C/Accession: F90562
R/Chambaud, I.; Heilig, R.; Ferris, S.; Barbe, V.; Samson, D.; Gallison, F.; Moszer, I.;
Nucleic Acids Res. 29, 2145-2153, 2001
A/Title: The complete genome sequence of the murine respiratory pathogen Mycoplasma pulm
A/Reference number: A95512; MUID:21267165; PMID:11353084
A/Accession: F90562
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-445 <KUR>
A/Cross-references: UNIPROT:Q98QGO; GB:AL445566; PID:g14089820; PIDN:CAC13579.1; GSPDB:G

A/Experimental source: strain UAB CTIP
C/Genetics:
A/Gene: MYPU_4060
A/Genetic code: SGC3

Query Match 39.8%; Score 47; DB 2; Length 445;

Best Local Similarity 43.8%; Pred. No. 15;
Matches 7; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

Qy 1 KPSYFGGHSVDFEE 16
Db 334 KPFOVAGNHYEHQ 349

RESULT 8

A39356
3-oxoacyl-[acyl-carrier-protein] synthase (EC 2.3.1.41) I beta chain precursor, chloropl

N.Alternate names: beta-ketoacyl-[acyl carrier protein] synthase I

C.Species: Hordeum vulgare (barley)

C.Date: 06-Mar-1992 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004

C.Accession: A39356; A45129

R.Siggaard-Andersen, M.; Kauppinen, S.; von Wettstein-Knowles, P.

A.Title: Primary structure of a cerulenin-binding beta-ketoacyl-[acyl carrier protein] E

A.Reference number: A39356; MUID:91239517; PMID:2034657

A.Accession: A39356

A.Molecule type: mRNA

A.Residues: 1-462 <SIG>

A.Cross-references: UNIPROT:P23902; GB:M60410; NID:g167064; PIDN:AAA22968.1; PID:g167065

A.Experimental source: cv. Bonus, leaf

A.Note: parts of this sequence, including the amino end of the mature protein, were conf

R.Kauppinen, S.

J. Biol. Chem. 267, 23999-24006, 1992

A.Title: Structure and expression of the Kas12 gene encoding a beta-ketoacyl-acyl carrie

A.Reference number: A45129; MUID:93054767; PMID:1429736

A.Accession: A45129

A.Molecule type: DNA

A.Residues: 1-395,397-414,'T',415-462 <KAU>

A.Experimental source: cv. Bonus

A.Note: sequence inconsistent with the nucleotide translation; translation agrees with E

C.Genetics:

A.Gene: Kas12

A.Map position: 2

A.Introms: 144/3; 288/3; 346/3; 384/3; 418/3; 441/1

C.Complex: homodimer or heterodimer with alpha chain

C.Superfamily: 3-oxoacyl-[acyl-carrier-protein] synthase I; 3-oxoacyl-[acyl-carrier-prot

C.Keywords: acyltransferase; chloroplast; fatty acid biosynthesis; heterodimer; homodime

E.1-36/Domains: transit peptide (chloroplast) #status predicted <TNP>

F.36-462/Product: 3-oxoacyl-[acyl-carrier-protein] synthase I beta chain #status experim

F.68-462/Domains: 3-oxoacyl-[acyl-carrier-protein] synthase I homology <OAS>

F.213/Active site: Cys #status experimental

Query Match 39.8%; Score 47; DB 1; Length 462;

Best Local Similarity 55.6%; Pred. No. 16;

Matches 10; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

Qy 3 SYQFGGHSVDFEPTLP 20
Db 445 SFGFGHSVDFEPTLP 462

RESULT 9

H70333

conserved hypothetical protein aq_378 - Aquifex aeolicus

C.Species: Aquifex aeolicus

C.Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 09-Jul-2004

C.Accession: H70333

R.Decker, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.; Ov

V. Nature 392, 353-358, 1998

A.Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.

A.Reference number: A70300; MUID:98196666; PMID:9537320

A.Accession: H70333

A.Status: preliminary; nucleic acid sequence not shown; translation not shown

A.Molecule type: DNA

A.Residues: 1-453 <QOF>

A.Cross-references: UNIPROT:O66700; GB:AE000687; NID:g2963050; PIDN:AAC06670.1; PID:g296

A.Experimental source: strain VFS

C.Genetics:

A.Gene: aq_378

Query Match 39.0%; Score 46; DB 2; Length 453;

Best Local Similarity 53.8%; Pred. No. 23;

Matches 7; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 3 SYQFGGHSVDFE 15
Db 114 SYFGSYNTLEFE 126

RESULT 10

T29908

hypothetical protein F59A3.2 - Caenorhabditis elegans

C.Species: Caenorhabditis elegans

C.Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004

C.Accession: T29908

R.Wu, X.; Le, T.T

submitted to the EMBL Data Library, November 1996

A.Description: The sequence of C. elegans cosmid F59A3.

A.Reference number: 220707

A.Accession: T29908

A.Status: preliminary; translated from GB/EMBL/DBJ

A.Molecule type: DNA

A.Residues: 1-975 <WUX>

A.Cross-references: UNIPROT:P91357; EMBL:U80448; PIDN:AA837819.1; GSPDB:GN00019; CESP:F5

A.Experimental source: strain Bristol N2; clone F59A3

C.Genetics:

A.Gene: CESP:F59A3.2

A.Map position: 1

A.Introms: 15/1; 233/2; 347/2; 427/1; 504/3; 554/3; 678/3; 696/2; 744/3; 795/2; 831/3; 90

C.Superfamily: Caenorhabditis elegans hypothetical protein F59A3.2

Query Match 39.0%; Score 46; DB 2; Length 975;

Best Local Similarity 42.1%; Pred. No. 54;

Matches 8; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

Qy 1 KPSYFGGHSVDFEPTLP 19
Db 600 KKSFFNNHRSKANFSNPTL 618

RESULT 11

A39962

kinase-related transforming protein (abl) (EC 2.7.1.-) type I - mouse

C.Species: Mus musculus (house mouse)

C.Date: 08-Nov-1991 #sequence_revision 08-Nov-1991 #text_change 18-Jun-1999

C.Accession: A39962; A24773; S00771; A00626

R.Ogpi, C.; Shore, S.K.; Reddy, E.P.

Proc. Natl. Acad. Sci. U.S.A. 84, 8200-8204, 1987

A.Title: Nucleotide sequence of testis-derived c-abl cDNAs: implications for testis-speci

A.Reference number: A39962; MUID:88068561; PMID:3317402

A.Accession: A39962

A.Status: preliminary

A.Molecule type: mRNA

A.Residues: 1-1123 <OPP>

A.Cross-references: GB:J02995; NID:g191566; PIDN:AAA88241.1; PID:g309084

A.Experimental source: clone A16

R.Ben-Neriah, Y.; Bernard, A.; Paikind, M.; Daley, G.Q.; Baltimore, D.

Cell 44, 577-586, 1986

A.Title: Alternative 5' exons in c-abl mRNA.

A.Reference number: A90877; MUID:86133550; PMID:3512096

A.Accession: A24773

A.Molecule type: mRNA

A.Residues: 1-118 <BN>

R.Bernard, A.; Paikind, M.; Baltimore, D.

Oncogene 2, 297-304, 1988

A.Title: Four murine c-abl mRNAs arise by usage of two transcriptional promoters and alte

A.Reference number: S00771; MUID:88202920; PMID:3283651

A.Accession: S00771

A.Molecule type: DNA

A:Residues: 1-26 <BER>
A:Cross-references: EMBL:X07539; NID:949837; PION:CAA30411.1; PID:949838
R:Wang, J.Y.; J. Ledley, F.; Golf, S.; Dee, R.; Groner, Y.; Baltimore, D.
Cell 36, 349-356, 1984
A:Title: The mouse c-abl locus: molecular cloning and characterization.
A:Reference number: A00626; MUID:84106840; PMID:6319018
A:Accession: A00626
A:Molecule type: DNA
A:Residues: 85-127, 'C', 129-182 <MAN>
C:Genetics:
A:Gene: abl
C:Superfamily: human protein-tyrosine kinase abl; protein kinase homology; SH2 homology
C:Keywords: alternative splicing; ATP; autophosphorylation; nucleus; phosphoprotein; phos
F:68-116/Domain: SH3 homology <SH3>
F:127-217/Domain: SH2 homology <SH2>
F:240-500/Domain: protein kinase homology <KIN>
F:248-256/Region: protein kinase ATP-binding motif

Query Match 38.6%; Score 45.5; DB 2; Length 1123;
Best Local Similarity 52.6%; Pred. No. 76;
Matches 10; Conservative 2; Mismatches 4; Indels 3; Gaps 1;

QY 3 SYVFGGHSVDPEPTLPK 21
DB 748 SSTEFGHKS---EKPLDR 763

RESULT 12
TVHUA
protein-tyrosine kinase (EC 2.7.1.112) abl - human
N:Alternate names: kinase-related transforming protein p150
C:Species: Homo sapiens (man)
C:Date: 03-Aug-1984 #sequence_revision 17-Nov-1995 #text_change 05-Jul-2004
C:Accession: S08519; A25582; A00625; E38268
R:Faustein, E.; Blum, M.; Gokkel, E.; Marcelle, C.; Croce, C.M.; Gale, R.P.; Canaan
Oncogene 4, 1477-1481, 1989
A:Title: Nucleotide sequence analysis of human abl and bcr-abl cDNAs.
A:Reference number: S08519; MUID:90082420; PMID:2687768
A:Accession: S08519
A:Molecule type: mRNA
A:Residues: 1-1130 <FAI>
A:Cross-references: UNIPROT:P00519; EMBL:X16416
R:Shivelman, E.; Lifshitz, B.; Gale, R.P.; Roe, B.A.; Canaan, E.
Cell 47, 277-284, 1986
A:Title: Alternative splicing of RNAs transcribed from the human abl gene and from the b
A:Reference number: A25582; MUID:87028219; PMID:3021337
A:Accession: A25582
A:Molecule type: mRNA
A:Residues: 1-139, 'P', 141-158, 'S', 160-444, 'R', 446-458, 'K', 460-718, 'V', 720-836, 'W', 838-86
S', 1104-1130 <SH3>
A:Note: The authors translated the codon GAG for residues 279, 282, 527, 549, and 581 as
R:Groffen, J.; Heisterkamp, N.; Reynolds Jr., F.H.; Stephenson, J.R.
Nature 304, 167-169, 1983
A:Title: Homology between phosphotyrosine acceptor site of human c-abl and viral oncogen
A:Reference number: A00625; MUID:83245023; PMID:6191223
A:Accession: A00625
A:Molecule type: DNA
A:Residues: 360-423, 'GK', 426 <GRO>
R:Partanen, J.; Mäkelä, T.P.; Allitalo, R.; Lehtvaeslahti, H.; Allitalo, K.
Proc. Natl. Acad. Sci. U.S.A. 87, 8913-8917, 1990
A:Title: Putative tyrosine kinases expressed in K-562 human leukemia cells.
A:Reference number: A38268; MUID:91062389; PMID:2247464
A:Accession: E38268
A:Status: nucleic acid sequence not shown; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 365-420 <PAR>
C:Genetics:
A:Gene: GDB:ABU1
A:Cross-references: GDB:119640; OMIM:189980
A:Map position: 9q34.1-9q34.1
C:Function:
A:Description: catalyzes the phosphorylation of a peptidyl tyrosine residue by ATP
C:Superfamily: human protein-tyrosine kinase abl; protein kinase homology; SH2 homology;

```

C:Keywords: ATP autophosphorylation; glycoprotein; phosphoprotein; phosphotransferase;
F:68-116/Domain: SH3 homology <SH3>
F:127-217/Domain: SH2 homology <SH2>
F:240-500/Domain: protein kinase homology <KIN>
F:248-256/Region: protein kinase ATP-binding motif
F:146,770/Binding site: carboxylate (Asn) (covalent) #status predicted
F:271/Active site: Lys #status predicted
F:393/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status predicted

Query Match      38.6%; Score 45.5; DB 1; Length 1130;
Best Local Similarity 52.6%; Pred. No. 76;
Matches 10; Conservative 2; Mismatches 4; Indels 3; Gaps 1;

Oy      3 SYORGHNSVDFEPTLPK 21
Db      749 SSTRFGHKS--EKPALPR 764

RESULT 13
T01405
C:Species: Strongylocentrotus purpuratus (purple urchin)
C:Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #ext_change 09-Jul-2004
C:Accession: T01405
R:Baron, N.R.; Bonder, E.M.; Fishkind, D.J.; Warren, R.H.; Pratt, M.M.
J. Cell Sci. 103, 797-809, 1992
A:Title: A novel vesicle-associated protein (VAP-1) in sea urchin eggs containing multiple
A:Reference number: 214315; MUID:93123402; PMID:1478972
A:Accession: T01405
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-433 <BAR>
A:Cross-references: UNIPROT:006155; EMBL:S52403; NID:g263072; PID:g263073
C:Genetics:
A:Gene: VAP-1
C:Superfamily: lorixin

Query Match      38.1%; Score 45; DB 2; Length 433;
Best Local Similarity 38.5%; Pred. No. 31;
Matches 10; Conservative 1; Mismatches 7; Indels 8; Gaps 1;

Oy      2 PSYOGGHN-----SVDFEPTL 19
Db      69 PKFGFGHGKGDIDVADVDIERPDL 94

RESULT 14
T10061
C:Oxoacyl-[acyl-carrier-protein] synthase (EC 2.3.1.41) precursor, chloroplast - castor l
N:Alternate names: beta-ketoacyl-[acyl carrier protein] synthase
C:Species: Ricinus communis (castor bean)
C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #ext_change 09-Jul-2004
C:Accession: T10061
R:Genev, A.L.
submitted to the EMBL Data Library, April 1993
A:Description: Cloning and molecular characterisation of B-ketoacyl-ACP synthases from enc
A:Reference number: 216924
A:Accession: T10061
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-469 <GEN>
A:Cross-references: UNIPROT:Q41135; EMBL:L13242; NID:g294667; PID:g294668
C:Genetics:
A:Genome: nuclear
C:Function:
A:Pathway: fatty acid biosynthesis
C:Superfamily: 3-oxoacyl-[acyl-carrier-protein] synthase I; 3-oxoacyl-[acyl-carrier-prote
C:Keywords: acyltransferase; chloroplast; fatty acid biosynthesis
F:1-42/Domain: transit peptide (chloroplast) #status predicted <TNP>
F:143-469/Product: 3-oxoacyl-[acyl-carrier-protein] synthase #status predicted <MAT>
F:77-466/Domain: 3-oxoacyl-[acyl-carrier-protein] synthase I homology <OAS>

Query Match      38.1%; Score 45; DB 2; Length 469;

```

Best Local Similarity 80.0%; Pred. No. 34;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 3 SYFGGHNSV 12
|:|||||
Db 452 SFGFGHNSV 461

RESULT 15

T24008
hypochemical protein R07B5.8 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004

C:Accession: T24008

R:Kelly, P.
submitted to the EMBL Data Library, May 1996

A:Reference number: Z19829

A:Accession: T24008
A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-1271 <WIL>

A:Cross-references: UNIPROT:Q21789; EMBL:Z72512; PIDN:CAA96668.1; GSPDB:GN00023; CESP:R0

A:Experimental source: clone R07B5

C:Genetics:
A:Gene: CESP:R07B5.8
A:Map position: 5
A:Introns: 34/1; 67/3; 129/3; 193/3; 313/2; 446/1; 479/2; 513/3; 571/3; 631/1; 845/3; 10

Query Match 38.1%; Score 45; DB 2; Length 1271;
Best Local Similarity 42.1%; Pred. No. 1e+02;

Matches 8; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

OY 1 KPSYQFGHNSVDPEPTL 19
:||||:|||||
Db 1221 QPPYQNPYNQVDYQCPWL 1239

Search completed: October 22, 2005, 04:13:57
Job time : 10.5465 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 22, 2005, 02:23:35 ; Search time 51.4314 Seconds
(without alignments)
209.087 Million cell updates/sec

Title: US-10-731-238-29
Perfect score: 118
Sequence: 1 KPSYQPGGNSVDFEPTLPK 21

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_03: *
1: uniprot_sprot: *
2: uniprot_trembl: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	110	93.2	1018	1 FNA8_STRAU
2	107	90.7	961	Q99RD3 staphylococ
3	107	90.7	961	Q7A3J8 staphylococ
4	107	90.7	965	Q6GDU5 staphylococ
5	107	90.7	1015	Q8NUU7 staphylococ
6	107	90.7	1015	Q6G6H3 staphylococ
7	107	90.7	1038	Q99RD2 staphylococ
8	107	90.7	1038	Q7A3J7 staphylococ
9	103	87.3	940	Q53682 staphylococ
10	103	87.3	943	Q8NUU8 staphylococ
11	103	87.3	957	Q6G6H4 staphylococ
12	98	83.1	152	Q9AEP9 staphylococ
13	54	45.8	467	Q75HB3 oryza sativ
14	50.5	42.8	519	Q6LS97 oryza sativ
15	49.5	41.9	720	P32499 saccharomyc
16	48	40.7	229	Q8HUO8 staphylococ
17	48	40.7	280	Q81187 plasmodium
18	48	40.7	465	Q6F2M2 bartonella
19	48	40.7	1738	Q86Y16 homo sapien
20	48	40.7	1770	Q94820 homo sapien
21	47	39.8	102	Q8U155 virus phich
22	47	39.8	223	Q820N7 streptomyces
23	47	39.8	224	Q9D314 mus muscicu
24	47	39.8	275	Q61GY6 dirosophila
25	47	39.8	325	Q61EB9 oligotropha
26	47	39.8	328	Q8VCN2 mus muscicu
27	47	39.8	341	Q9CUJ2 mus muscicu
28	47	39.8	392	Q64P55 bacteroides
29	47	39.8	442	Q7XUW9 oryza sativ
30	47	39.8	445	Q98G50 mycoplasma
31	47	39.8	462	P23302 hordeum vul

ALIGNMENTS

32	47	39.8	465	2	Q69VA2	Q69VA2 oryza sativ
33	47	39.8	488	2	Q82520	Q82520 capsicum ch
34	47	39.8	493	1	FBL3_HUMAN	Q12805 homo sapien
35	47	39.8	493	2	Q7YQD7	Q7YQD7 macaca fasc
36	47	39.8	1075	2	Q8CUM7	Q8CUM7 oceanobacil
37	47	39.8	2360	2	Q7ZEP0	Q7ZEP0 eimeria max
38	46.5	39.4	485	2	Q93DB1	Q93DB1 streptococc
39	46.5	39.4	1045	2	Q6BZ26	Q6BZ26 debaryomyces
40	46	39.0	185	2	Q7R1K7	Q7R1K7 plasmodium
41	46	39.0	208	1	URK_CLOPE	Q8XJ17 clostridium
42	46	39.0	243	1	S112_ARATH	Q9FK43 arabidopsis
43	46	39.0	248	2	Q9MBE1	Q9MBE1 rosa rugosa
44	46	39.0	249	2	Q9MBE0	Q9MBE0 rosa rugosa
45	46	39.0	250	2	Q9MBD9	Q9MBD9 rosa rugosa

RESULT 1
FNA8_STRAU STANDARD; PRT; 1018 AA.
ID FNA8_STRAU

AC P14738:
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Fibronectin-binding protein precursor (FNBp).
GN Name=fnbA;
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OK NCBI_Taxid=1280;
RN (1)
RP SEQUENCE FROM N.A.

RC STRAIN=NCIT 8325-4;
RX MEDLINE=89098998; PubMed=2521391;
RA Signae C., Raucel G., Joensen K., Lindgren P.-E.,
RA Antharathanaiah G.M., Hoeck M., Lindberg M.;
RT "Nucleotide sequence of the gene for a fibronectin-binding protein
RT from Staphylococcus aureus: use of this peptide sequence in the
RT synthesis of biologically active peptides."
RT Proc. Natl. Acad. Sci. U.S.A. 86:699-703 (1989).

CC -!- FUNCTION: The ability of bacteria to bind fibronectin has been
CC proposed as a virulence factor enabling bacteria to colonize wound
CC tissues and blood clots. Binding of plasma fibronectin to the
CC bacterial surface might block adhesion receptors on S.aureus, thus
CC representing an important defense mechanism against tissue
CC invasion.

CC -!- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC an amide bond (potential).
CC
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).

CC -----
CC EMBL: J04151; AAA26632.1; -;
CC InterPro: IPR004237; Fn_bind.
CC InterPro: IPR005877; Gpos_Y5IRK.
CC InterPro: IPR001899; Gram_pos_anchor.
CC Pfam: PF02986; Fn_bind; 1.
CC Pfam: PF00746; Gram_pos_anchor; 1.
CC DR Pfam: PF04650; Y5IRK_signal; 1.
CC DR TIGRPFAM: TIGR01167; LpxTG_signal; 1.
CC DR TIGRPFAM: TIGR01168; Y5IRK_signal; 1.
CC DR PROSITE: PS50847; GRAM_POS_ANCHORING; 1.
CC Cell address: Cell wall; Peptidoglycan-anchor; Repeat; Signal;
CC Virulence.
CC KMW SIGNL 1 36
CC FT CHAIN 37 985 Fibronectin-binding protein.
CC FT PROPEP 986 1018 Removed by sortase (potential).
CC


```
FT REPEAT 545 574 B-1.
FT REPEAT 575 604 B-2.
FT DOMAIN 745 878 4 X approximate tandem repeats
  fibronectin-binding domain.
FT REPEAT 745 782 D-1.
FT REPEAT 783 820 D-2.
FT REPEAT 821 859 D-3.
FT REPEAT 860 878 D-4 (incomplete).
FT DOMAIN 879 948 5 X tandem repeats, Pro-rich (IR).
FT REPEAT 879 892 WR 1.
FT REPEAT 893 906 WR 2.
FT REPEAT 907 920 WR 3.
FT REPEAT 921 934 WR 4.
FT REPEAT 935 948 WR 5.
FT SITE 982 986 LPXTG sorting signal (Potentia.).
FT MOD_RES 985 985 PentaGlycyl murein peptidoglycan amidated
  .Chreonine (Potential).
SQ SEQUENCE 1018 AA; 111780 MW; 58175E0020E81F1F CRC64;

Query Match 93.2%; Score 110; DB 1; Length 1018;
Best Local Similarity 95.2%; Pred. No. 3.9e-08;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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```
Qy 1 KPSYFGGHSVDFEPTLPK 21
Db 837 KPSYFGGHSVDFEPTLPK 857
```

```
RESULT 2
ID 099RD3 PRELIMINARY; PRT; 961 AA.
AC 099RD3;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE Fibronectin-binding protein homolog.
GN Name=fnb3; OrderedLocNames=SAV2502;
OS Staphylococcus aureus (strain Muso / ATCC 700699).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
CX NCBI_TaxID=158879;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Muso / ATCC 700699;
RX MEDLINE=21311952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2;
  Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
  RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Lian J.-Q., Ito T.,
  RA Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,
  RA Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
  RA Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
  RA Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
  RA Hattori M., Ogaewara N., Hayashi H., Hiramatsu K.;
  RT "Whole genome sequencing of methicillin-resistant Staphylococcus
  aureus."
  RL Lancet 357:1225-1240(2001).
  CC -I- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
  an amide bond (By similarity).
  DR EMBL: AP003365; BAB5664.1; -.
  DR PIR: G90053; G90053.
  DR HSSP: Q53653; IN67.
  DR GO: GO:0009986; C:cell surface; IEA.
  DR GO: GO:0005618; C:cell wall; IEA.
  DR GO: GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
  DR GO: GO:0016020; C:membrane; IEA.
  DR GO: GO:007155; P:cell adhesion; IEA.
  DR InterPro: IPR008966; Adhes_bact.
  DR InterPro: IPR004237; Fn_bind.
  DR InterPro: IPR005877; Gpos_Ysirk.
  DR InterPro: IPR001899; Gram_pos_anchor.
  DR Pfam: PF02986; Fn_bind.1.
  DR Pfam: PF00746; Gram_pos_anchor.1.
  DR Pfam: PF04650; Ysirk_signal.1.
  DR TIGRFAMs: TIGR01167; LPXTG_anchor.1.
  DR TIGRFAMs: TIGR01167; LPXTG_signal.1.
  DR TIGRFAMs: TIGR01168; Ysirk_anchor.1.
  DR TIGRFAMs: TIGR01168; Ysirk_signal.1.
```

```
DR PROSITE; PS50847; GRAM_POS_ANCHORING; 1.
KW Cell wall, complete proteome; Peptidoglycan-anchor.
SQ SEQUENCE 961 AA; 106010 MW; 364940F84EA4101 CRC64;
```

```
Query Match 90.7%; Score 107; DB 2; Length 961;
Best Local Similarity 90.5%; Pred. No. 1.1e-07;
Matches 19; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
```

```
Qy 1 KPSYFGGHSVDFEPTLPK 21
Db 784 KPSYFGGHSVDFEPTLPK 804
```

```
RESULT 3
ID 07A3J8 PRELIMINARY; PRT; 961 AA.
AC 07A3J8;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE FnB protein.
GN Name=fnb3; OrderedLocNames=SA2290;
OS Staphylococcus aureus (strain N315).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
CX NCBI_TaxID=158879;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=21311952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2;
  Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
  RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Lian J.-Q., Ito T.,
  RA Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,
  RA Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
  RA Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
  RA Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
  RA Hattori M., Ogaewara N., Hayashi H., Hiramatsu K.;
  RT "Whole genome sequencing of methicillin-resistant Staphylococcus
  aureus."
  RL Lancet 357:1225-1240(2001).
  CC -I- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
  an amide bond (By similarity).
  DR EMBL: AP003137; BAB3593.1; -.
  DR GO: GO:0009986; C:cell surface; IEA.
  DR GO: GO:0005618; C:cell wall; IEA.
  DR GO: GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
  DR GO: GO:0016020; C:membrane; IEA.
  DR GO: GO:007155; P:cell adhesion; IEA.
  DR InterPro: IPR008966; Adhes_bact.
  DR InterPro: IPR004237; Gpos_Ysirk.
  DR InterPro: IPR005877; Gpos_Ysirk.
  DR InterPro: IPR001899; Gram_pos_anchor.
  DR Pfam: PF02986; Fn_bind.1.
  DR Pfam: PF00746; Gram_pos_anchor.1.
  DR Pfam: PF04650; Ysirk_signal.1.
  DR TIGRFAMs: TIGR01167; LPXTG_anchor.1.
  DR TIGRFAMs: TIGR01168; Ysirk_signal.1.
  DR PROSITE; PS50847; GRAM_POS_ANCHORING; 1.
  KW Cell wall, complete proteome; Peptidoglycan-anchor.
  SQ SEQUENCE 961 AA; 106010 MW; 364940F84EA4101 CRC64;
```

```
Query Match 90.7%; Score 107; DB 2; Length 961;
Best Local Similarity 90.5%; Pred. No. 1.1e-07;
Matches 19; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
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```
Qy 1 KPSYFGGHSVDFEPTLPK 21
Db 784 KPSYFGGHSVDFEPTLPK 804
```

```
RESULT 4
ID 06GDUS PRELIMINARY; PRT; 965 AA.
AC 06GDUS;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
```

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DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DE 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE Fibronectin-binding protein.
GN Name=fnbA; OrderedLocNames=SAR2580;
OS Staphylococcus aureus (strain MRSA252).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=282458;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed:1513324; DOI=10.1073/pnas.0402521101;
RA Holden M.T.G., Peil E.J., Lindsey J.A., Peacock S.J., Day N.P.J.,
RA Enright M.C., Foster T.J., Moore C.E., Hurst L., Atkin R., Barron A.,
RA Baeson N., Bentley S.D., Chillingworth C., Chillingworth T.,
RA Churcher C., Clark L., Cotton C., Cronin A., Doggett J., Dowd L.,
RA Feltwell T., Hance Z., Harris B., Hauser H., Holroyd S., Jagsle K.,
RA James K.D., Leonard N., Line A., Mayes R., Moulé S., Mungall K.,
RA Ormond D., Quail M.A., Rabinowitch E., Rutherford K.M., Sanders M.,
RA Sharp S., Simmonds M., Stevens K., Whitehead S., Barrett B.G.,
RA Spratt B.G., Parkhill J.;
RT "Complete genomes of two clinical Staphylococcus aureus strains:
RT evidence for the rapid evolution of virulence and drug resistance.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:9786-9791(2004).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC an amide bond (by similarity).
DR EMBL; BX571856; CAG41560.1; -.
DR GO; GO:0009986; C:cell surface; IEA.
DR GO; GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0007155; P:cell adhesion; IEA.
DR InterPro; IPR008966; Adhes_bact.
DR InterPro; IPR004237; Fn_bind.
DR InterPro; IPR005877; Gpos_YsIRK.
DR InterPro; IPR01899; Gram_pos_anchor.
DR Pfam; PF00746; Gram_pos_anchor; 1.
DR Pfam; PF04650; YsIRK_signal; 1.
DR TIGRFAMs; TIGR01167; LpxTG_anchor; 1.
DR TIGRFAMs; TIGR01168; YsIRK_signal; 1.
DR PROSITE; PS50847; GRAM_POS_ANCHORING; 1.
KW Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ SEQUENCE 965 AA; 105691 MW; 29828E3216400551 CRC64;

Query Match 90.7%; Score 107; DB 2; Length 965;
Best Local Similarity 90.5%; Pred. No. 1.1e-07;
Matches 19; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 KPSTQFGGNSVDPEPTLPK 21
DB 802 KPNYQFGGNSVDPEPTLPK 822

RESULT 5
OBNUT7 PRELIMINARY; PRT; 1015 AA.
ID Q8NUT7;
AC 01-OCT-2002 (TREMBlrel. 22, Created)
DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
DT 01-OCT-2002 (TREMBlrel. 25, Last annotation update)
DE Fnb protein.
GN Name=fnb; OrderedLocNames=MM2421;
OS Staphylococcus aureus (strain MM2).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=196620;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=MM2;
RX MEDLINE=22040717; PubMed=12044378; DOI=10.1016/S0140-6736(02)08713-5;
RA Baba T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Oguchi A.,
RA Nagai Y., Iwano K., Asano K., Naimi T., Kuroda H., Cui L.,
RA Yamamoto K., Hiratake K.;
RT "Genome and virulence determinants of high virulence community-
RT acquired MRSA.";
RL Lancet 359:1819-1827(2002).

```

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CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC an amide bond (by similarity).
DR EMBL; AP004830; BAB96286.1; -.
DR GO; GO:0009986; C:cell surface; IEA.
DR GO; GO:0005618; C:cell wall; IEA.
DR GO; GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0007155; P:cell adhesion; IEA.
DR InterPro; IPR008966; Adhes_bact.
DR InterPro; IPR004237; Fn_bind.
DR InterPro; IPR005877; Gpos_YsIRK.
DR InterPro; IPR01899; Gram_pos_anchor.
DR Pfam; PF00746; Gram_pos_anchor; 1.
DR Pfam; PF04650; YsIRK_signal; 1.
DR TIGRFAMs; TIGR01167; LpxTG_anchor; 1.
DR TIGRFAMs; TIGR01168; YsIRK_signal; 1.
DR PROSITE; PS50847; GRAM_POS_ANCHORING; 1.
KW Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ SEQUENCE 1015 AA; 111145 MW; D0F9281BB64D44D2 CRC64;

Query Match 90.7%; Score 107; DB 2; Length 1015;
Best Local Similarity 90.5%; Pred. No. 1.2e-07;
Matches 19; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 KPSTQFGGNSVDPEPTLPK 21
DB 838 KPNYQFGGNSVDPEPTLPK 858

RESULT 6
O6G6H3 PRELIMINARY; PRT; 1015 AA.
ID Q6G6H3;
AC 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE Fibronectin-binding protein.
GN OrderedLocNames=SAS2388;
OS Staphylococcus aureus (strain MSSA476).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=282459;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed:15213324; DOI=10.1073/pnas.0402521101;
RA Holden M.T.G., Peil E.J., Lindsey J.A., Peacock S.J., Day N.P.J.,
RA Enright M.C., Foster T.J., Moore C.E., Hurst L., Atkin R., Barron A.,
RA Baeson N., Bentley S.D., Chillingworth C., Chillingworth T.,
RA Churcher C., Clark L., Cotton C., Cronin A., Doggett J., Dowd L.,
RA Feltwell T., Hance Z., Harris B., Hauser H., Holroyd S., Jagsle K.,
RA James K.D., Leonard N., Line A., Mayes R., Moulé S., Mungall K.,
RA Ormond D., Quail M.A., Rabinowitch E., Rutherford K.M., Sanders M.,
RA Sharp S., Simmonds M., Stevens K., Whitehead S., Barrett B.G.,
RA Spratt B.G., Parkhill J.;
RT "Complete genomes of two clinical Staphylococcus aureus strains:
RT evidence for the rapid evolution of virulence and drug resistance.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:9786-9791(2004).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC an amide bond (by similarity).
DR EMBL; BX571857; CAG44202.1; -.
DR GO; GO:0009986; C:cell surface; IEA.
DR GO; GO:0005618; C:cell wall; IEA.
DR GO; GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0007155; P:cell adhesion; IEA.
DR InterPro; IPR008966; Adhes_bact.
DR InterPro; IPR004237; Fn_bind.
DR InterPro; IPR005877; Gpos_YsIRK.
DR InterPro; IPR01899; Gram_pos_anchor.
DR Pfam; PF00746; Gram_pos_anchor; 1.
DR Pfam; PF04650; YsIRK_signal; 1.
DR TIGRFAMs; TIGR01167; LpxTG_anchor; 1.

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DR TIGRFAMs: TIGR01168; YSIRK_signal: 1.
DR PROSITE; PS50847; GRAM_POS_ANCHORING; 1.
KW Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ SEQUENCE 1015 AA; 111145 MW; D0F9281BB64D4d2 CRC64;

Query Match 90.7%; Score 107; DB 2; Length 1015;
Best Local Similarity 90.5%; Pred. No. 1.2e-07;
Matches 19; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KPSYQFGGHSVDFEEDTLPK 21
Db 838 KPNYQFGGHSVDFEEDTLPK 858

RESULT 7
ID Q99RD2 PRELIMINARY; PRT; 1038 AA.
AC Q99RD2;
DT 01-JUN-2001 (TReMBLrel. 17, Last sequence update)
DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)
DE Fibronectin-binding protein homolog.
GN Name=fnb; OrderedLocustNames=SAV2503;
OS Staphylococcus aureus (strain Mu50 / ATCC 700699).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=158878;

RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21311952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2;
RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Iian J.-Q., Ito T.,
RA Kanamori M., Matsunaru H., Maruyama A., Murakami H., Hoshiyama A.,
RA Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
RA Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
RA Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
RA Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
RT "Whole genome sequencing of methicillin-resistant Staphylococcus
RT aureus.";
RL Lancet 357:1225-1240(2001).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC an amide bond (By similarity).
DR EMBL; AP003137; BAB5865.1; -.
DR PIR; H90053; H90053.
DR GO; GO:0009986; C:cell surface; IEA.
DR GO; GO:0005618; C:cell wall; IEA.
DR GO; GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0007155; P:cell adhesion; IEA.
DR InterPro; IPR008966; Adhes_bact.
DR InterPro; IPR004237; Fn_bind.
DR InterPro; IPR005877; Gpos_YSIRK.
DR InterPro; IPR001899; Gram_pos_anchor.
DR Pfam; PF02986; Fn_bind; 1.
DR Pfam; PF00746; Gram_pos_anchor; 1.
DR TIGRFAMs; TIGR01167; LPXTG_signal; 1.
DR TIGRFAMs; TIGR01167; LPXTG_anchor; 1.
DR TIGRFAMs; TIGR01168; YSIRK_signal; 1.
DR PROSITE; PS50847; GRAM_POS_ANCHORING; 1.
KW Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ SEQUENCE 1038 AA; 113618 MW; 666BF6BF2BFBB12 CRC64;

Query Match 90.7%; Score 107; DB 2; Length 1038;
Best Local Similarity 90.5%; Pred. No. 1.2e-07;
Matches 19; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KPSYQFGGHSVDFEEDTLPK 21
Db 833 KPNYQFGGHSVDFEEDTLPK 853

RESULT 8
ID Q7A3J7 PRELIMINARY; PRT; 1038 AA.
AC Q7A3J7;
DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TReMBLrel. 27, Last annotation update)
DE Fnb protein.
GN Name=fnb; OrderedLocustNames=SA2291;
OS Staphylococcus aureus (strain N315).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=158879;

RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21311952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2;
RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Iian J.-Q., Ito T.,
RA Kanamori M., Matsunaru H., Maruyama A., Murakami H., Hoshiyama A.,
RA Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
RA Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
RA Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
RA Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
RT "Whole genome sequencing of methicillin-resistant Staphylococcus
RT aureus.";
RL Lancet 357:1225-1240(2001).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC an amide bond (By similarity).
DR EMBL; AP003137; BAB43594.1; -.
DR GO; GO:0009986; C:cell surface; IEA.
DR GO; GO:0005618; C:cell wall; IEA.
DR GO; GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0007155; P:cell adhesion; IEA.
DR InterPro; IPR008966; Adhes_bact.
DR InterPro; IPR004237; Fn_bind.
DR InterPro; IPR005877; Gpos_YSIRK.
DR InterPro; IPR001899; Gram_pos_anchor.
DR Pfam; PF02986; Fn_bind; 1.
DR Pfam; PF00746; Gram_pos_anchor; 1.
DR TIGRFAMs; TIGR01167; LPXTG_signal; 1.
DR TIGRFAMs; TIGR01167; LPXTG_anchor; 1.
DR TIGRFAMs; TIGR01168; YSIRK_signal; 1.
DR PROSITE; PS50847; GRAM_POS_ANCHORING; 1.
KW Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ SEQUENCE 1038 AA; 113618 MW; 666BF6BF2BFBB12 CRC64;
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ID Q7A3J7 PRELIMINARY; PRT; 1038 AA.
AC Q7A3J7;
DT 05-JUL-2004 (TReMBLrel. 27, Created)
DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TReMBLrel. 27, Last annotation update)
DE Fnb protein.
GN Name=fnb; OrderedLocustNames=SA2291;
OS Staphylococcus aureus (strain N315).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=158879;

RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=8325-4;
RA Jonsson K., Sigmas C., Muller H.P., Lindberg M.;
RT "Two different genes encode fibronectin binding proteins in
RT Staphylococcus aureus. The complete nucleotide sequence and
RT characterization of the second gene."/;
```

RL Eur. J. Biochem. 202:1041-1048(1991).
 CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
 CC an amide bond (by similarity).
 DR EMBL: X62992; CAA44726.1; -.
 DR PIR: S19702; S19702.
 DR HSSP: Q53653; INE7.
 DR GO: GO:0009986; C:cell surface; IEA.
 DR GO: GO:0005618; C:cell wall; IEA.
 DR GO: GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
 DR GO: GO:0016020; C:membrane; IEA.
 DR GO: GO:0007155; P:cell adhesion; IEA.
 DR InterPro: IPR008966; Adhes_bact.
 DR InterPro: IPR004237; Fn_bind.
 DR InterPro: IPR005877; Gpos_YsIRK.
 DR InterPro: IPR001899; Gram_pos_anchor.
 DR Pfam: PF02986; Fn_bind_2.
 DR Pfam: PF00746; Gram_pos_anchor_1.
 DR Pfam: PF04650; YsIRK_signal; 1.
 DR TIGRfams: TIGR01167; LpxTG_anchor; 1.
 DR TIGRfams: TIGR01168; YsIRK_signal; 1.
 DR PROSITE: PS50847; GRAM_POS_ANCHORING; 1.
 DR Cell wall, peptidoglycan-anchor.
 KW SEQUENCE 940 AA; 10355 MW; E35FBBCA907AE345 CRC64;
 SQ
 Query Match 87.3%; Score 103; DB 2; Length 940;
 Best Local Similarity 85.7%; Pred. No. 4.5e-07;
 Matches 18; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 QY 1 KPSYQFGHNSVDPEEPTLPK 21
 DB 773 KPNYQFGHNSVDPEEDTLFQ 793
 RESULT 10
 Q8NTU8 PRELIMINARY; PRT; 943 AA.
 ID Q8NTU8;
 AC 01-OCT-2002 (TREMBLrel. 22, Created)
 DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update)
 DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
 CC FndB protein.
 DE Name=fndB; OrderedLocNames=MM2420;
 GN Staphylococcus aureus (strain MM2).
 OS Bacteria; Firmicutes; Bacillales; Staphylococcus.
 OC NCBI_Taxid=196620;
 OX [1]
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=MM2;
 RX MEDLINE=22040717; PubMed=12044378; DOI=10.1016/S0140-6736(02)08713-5;
 RA Baba T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Oguchi A.,
 RA Nagai Y., Iwama N., Asano K., Naimi T., Kuroda H., Cui L.,
 RA Yamamoto K., Hiramatsu K.;
 RT "Genome and virulence determinants of high virulence community-
 RT acquired MRSA.";
 RL Lancet 359:1819-1827(2002).
 CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
 CC an amide bond (by similarity).
 DR EMBL: AF004830; BAB96285.1; -.
 DR HSSP: Q53653; INE7.
 DR GO: GO:0009986; C:cell surface; IEA.
 DR GO: GO:0005618; C:cell wall; IEA.
 DR GO: GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
 DR GO: GO:0016020; C:membrane; IEA.
 DR GO: GO:0007155; P:cell adhesion; IEA.
 DR InterPro: IPR008966; Adhes_bact.
 DR InterPro: IPR004237; Fn_bind.
 DR InterPro: IPR005877; Gpos_YsIRK.
 DR InterPro: IPR001899; Gram_pos_anchor.
 DR Pfam: PF02986; Fn_bind_1.
 DR Pfam: PF00746; Gram_pos_anchor_1.
 DR Pfam: PF04650; YsIRK_signal; 1.
 DR TIGRfams: TIGR01167; LpxTG_anchor; 1.
 DR TIGRfams: TIGR01168; YsIRK_signal; 1.
 DR TIGRfams: TIGR01168; YsIRK_signal; 1.

DR PROSITE: PS50847; GRAM_POS_ANCHORING; 1.
 KW Cell wall, complete proteome; Peptidoglycan-anchor.
 SQ SEQUENCE 943 AA; 104537 MW; DAB5F31947E1B6A CRC64;
 SQ
 Query Match 87.3%; Score 103; DB 2; Length 943;
 Best Local Similarity 85.7%; Pred. No. 4.5e-07;
 Matches 18; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 QY 1 KPSYQFGHNSVDPEEPTLPK 21
 DB 780 KPNYQFGHNSVDPEEDTLFQ 800
 RESULT 11
 Q6G6H4 PRELIMINARY; PRT; 957 AA.
 ID Q6G6H4;
 AC Q6G6H4;
 DT 05-JUL-2004 (TREMBLrel. 27, Created)
 DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
 DE Fibronectin-binding protein.
 GN Name=fndB; OrderedLocNames=SA52387;
 OS Staphylococcus aureus (strain MSSA476).
 CC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 OC NCBI_Taxid=282459;
 OX [1]
 RN [1]
 RP SEQUENCE FROM N.A.
 RX PubMed=15213324; DOI=10.1073/pnas.0402521101;
 RA Holden M.T.G., Fell E.J., Lindsay J.A., Peacock S.J., Day N.P.J.,
 RA Enright M.C., Foster T.J., Moore C.B., Hurst R., Atkin R., Barron A.,
 RA Baeson N., Bentley S.D., Chillingworth C., Chillingworth T.,
 RA Churcher C., Clark L., Cronin A., Doggett J., Dowd L.,
 RA Felwell T., Hance Z., Harris B., Hauser H., Holtroyd S., Jagels K.,
 RA James K.D., Leonard N., Line A., Mayes R., Moutie S., Mungall K.,
 RA Ormond D., Quail M.A., Rabinowitch B., Rutherford K.M., Sanders M.,
 RA Sharp S., Simmonds M., Stevens K., Whitehead S., Barrall B.G.,
 RA Spratt B.G., Parkhill J.;
 RT "Complete genomes of two clinical Staphylococcus aureus strains:
 RT evidence for the rapid evolution of virulence and drug resistance.";
 RL Proc. Natl. Acad. Sci. U.S.A. 101:9786-9791(2004).
 CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
 CC an amide bond (by similarity).
 DR EMBL: BX571857; CAC44201.1; -.
 DR GO: GO:0009986; C:cell surface; IEA.
 DR GO: GO:0005618; C:cell wall; IEA.
 DR GO: GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
 DR GO: GO:0016020; C:membrane; IEA.
 DR GO: GO:0007155; P:cell adhesion; IEA.
 DR InterPro: IPR008966; Adhes_bact.
 DR InterPro: IPR004237; Fn_bind.
 DR InterPro: IPR005877; Gpos_YsIRK.
 DR InterPro: IPR001899; Gram_pos_anchor.
 DR Pfam: PF02986; Fn_bind_1.
 DR Pfam: PF00746; Gram_pos_anchor_1.
 DR Pfam: PF04650; YsIRK_signal; 1.
 DR TIGRfams: TIGR01167; LpxTG_anchor; 1.
 DR TIGRfams: TIGR01168; YsIRK_signal; 1.
 DR PROSITE: PS50847; GRAM_POS_ANCHORING; 1.
 KW Cell wall, complete proteome; Peptidoglycan-anchor.
 SQ SEQUENCE 957 AA; 105980 MW; 28F8BA7FFDF03EAF CRC64;
 SQ
 Query Match 87.3%; Score 103; DB 2; Length 957;
 Best Local Similarity 85.7%; Pred. No. 4.5e-07;
 Matches 18; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 QY 1 KPSYQFGHNSVDPEEPTLPK 21
 DB 780 KPNYQFGHNSVDPEEDTLFQ 800
 RESULT 12
 Q9AEP9 PRELIMINARY; PRT; 152 AA.
 ID Q9AEP9

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AC Q9AEP9;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DE 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Fibronectin-binding protein (Fragment).
GN Name=fnb:
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1280;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CMRSA-1;
RX MEDLINE=21246681; PubMed=11349044;
RX DOI=10.1128/IAI.69.6.3791-3799.2001;
RA Rice K., Huebner M., Vaz D., McGavin M.J.;
RT "Variance in fibronectin binding and fnb locus polymorphisms in
RT Staphylococcus aureus: identification of antigenic variation in a
RT fibronectin binding protein adhesion of the epidemic CMRSA-1 strain of
RT methicillin-resistant S. aureus.";
RL Invec. Immun. 69:3791-3799(2001).
DR EMBL; AY029184; AAK31588.1; -.
FT NON_TER
FT NON_TER
SQ SEQUENCE 152 AA; 17193 MW; CFA3913C2B11C025 CRC64;

Query Match 83.1%; Score 98; DB 2; Length 152;
Best Local Similarity 81.0%; Pred. No. 3.6e-07;
Matches 17; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Oy 1 KPSYFGGSHNSVDFEPTLPK 21
Db 130 KPSYFGGSHNSVDFEPTLPK 150

RESULT 13
O75HB3 PRELIMINARY; PRT; 467 AA.
AC O75HB3;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Expressed protein, 5'-partial (Fragment).
GN Name=OSJNB0056E06.1;
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaceae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
RP SEQUENCE FROM N.A.
RA Buehl C.R., Yuan Q., Ouyang S., Liu J., Ganeberger K., Jones K.M.,
RA Overton I.L., Taitlin T., Kim M.M., Bera J.J., Jin S.S.,
RA Padroch D.W., Tallon L.J., Koo H., Zismann V., Hsiao J., Blurt S.,
RA Vanaken S.S., Riedmiller S.B., Uteback T.T., Feldlyum T.V.,
RA Yang Q.Q., Haas B.J., Suh B.B., Peterson J.J., Quackenbush J.,
RA White O., Salzberg S.L., Fraser C.M.;
RL Submitted (OCT-2002) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Buehl R.;
RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC135792; AAR87180.1; -.
DR InterPro; IPR000697; EVH1.
DR InterPro; IPR011036; PH_related.
DR Pfam; PF00638; Ran_BP1; 1.
DR SMART; SM00160; RanBD; 1.
DR PROSITE; PS50196; RANBD1; 1.
FT NON_TER
FT NON_TER
SQ SEQUENCE 467 AA; 49994 MW; 416F8C54CC9EF2B7 CRC64;

Query Match 45.8%; Score 54; DB 2; Length 467;
Best Local Similarity 50.0%; Pred. No. 9.1;
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Matches 10; Conservative 4; Mismatches 4; Indels 2; Gaps 1;

Oy 1 KPSYFGGSHNSVDFEPTLPK 20
Db 264 KPSYFGGSHNSVDFEPTLPK 281

RESULT 14
O6L597 PRELIMINARY; PRT; 519 AA.
AC O6L597;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Putative beta-glucosidase.
GN Name=OU139_A07.1;
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaceae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
RP SEQUENCE FROM N.A.
RA Chow T.-Y., Hsing Y.-I.C., Chen C.-S., Chen H.-H., Liu S.-M.,
RA Chao Y.-T., Chang S.-J., Chen H.-C., Chen S.-K., Chen T.-R.,
RA Chen Y.-L., Cheng C.-H., Chung C.-I., Han S.-Y., Hsiao S.-H.,
RA Heung J.-N., Hsu C.-H., Huang J.-J., Kau P.-I., Lee M.-C., Leu H.-L.,
RA Li Y.-F., Lin S.-J., Lin Y.-C., Wu S.-W., Yu C.-X., Yu S.-W.,
RA Wu H.-P., Shaw J.-F.;
RL Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Belongs to family 1 of glycosyl hydrolases.
DR EMBL; AC104279; AAT38010.1; -.
DR GO; GO:0004553; F:hydrolase activity, hydrolyzing O-glycosyl . . .; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR InterPro; IPR001360; Glyco_hydro_1.
DR InterPro; IPR011580; Glyco_hydro_euk.
DR Pfam; PF00232; Glyco_hydro_1; 1.
DR PRINTS; PR00131; GLHYDRLASE1.
DR PRODOM; PD000650; Glyco_hydro_euk; 1.
KW Glycosidase; Hydrolase.
SQ SEQUENCE 519 AA; 58351 MW; 3C001A2F90461BFF CRC64;

Query Match 42.8%; Score 50.5; DB 2; Length 519;
Best Local Similarity 62.5%; Pred. No. 36;
Matches 10; Conservative 4; Mismatches 1; Indels 1; Gaps 1;

Oy 6 FGGHNSVDFEPTLPK 21
Db 469 FGLHH-VDFEPTLPK 483

RESULT 15
NUP2 YEAST STANDARD; PRT; 720 AA.
AC P32499; O06130;
DT 01-OCT-1993 (Rel. 27, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Nucleoporin NUP2 (nuclear pore protein NUP2) (p95).
GN Name=NUP2; Order=LOCUSNames=VLRJ35W; ORFNames=L8300.9;
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=S288C;
RX MEDLINE=93184405; PubMed=8443417;
RA Loeb J.D.J., Davis L.I., Fink G.R.;
RT "NUP2, a novel yeast nucleoporin, has functional overlap with other
RT proteins of the nuclear pore complex.";
RL Mol. Biol. Cell 4:209-222(1993).
RN [2]
```

SEQUENCE FROM N.A.
 STRAIN=S288c / AB972;
 MEDLINE=97313267; Pubmed=9169871; Albertmann K., Andre B., Ansgorge W.,
 RA Johnson M., Hillier L., Riles L., Dubois E., Duesterhoeft A.,
 RA Benes V., Brueckner M., Delius H., Hebling U., Heumann K.,
 RA Enrian K.-D., Floeth M., Goffeau A., Hebling U., Heumann K.,
 RA Heuss-Neitzel D., Hilbert H., Hilger F., Kleine K., Koetter P.,
 RA Louis E.U., Messenguy F., Mewes H.-W., Miosga T., Moestl D.,
 RA Mueller-Auer S., Nentwich U., Obermaler B., Piravandi E., Pohl T.M.,
 RA Portetelle D., Purnelle B., Reckmann S., Rieger M., Rinke M., Rose M.,
 RA Scharfe M., Scherens B., Scholler P., Schwager C., Schwarz S.,
 RA Underwood A.P., Urrestazu L.A., Vandenbol M., Verhaesselt P.,
 RA Vierendeels F., Voet M., Volckaert G., Voss H., Wambutt R., Wedler E.,
 RA Wedler H., Zimmermann F.K., Zollner A., Hant U., Honeisel J.D.,
 RT "The nucleotide sequence of Saccharomyces cerevisiae chromosome XII.",
 RL Nature 387:87-90(1997).
 [3]
 CHARACTERIZATION AND NPC SUBUNIT LOCATION.
 RA Pubmed=10684247; DOI=10.1083/jcb.148.4.635;
 RA Rout M.P., Altschson J.D., Suprapto A., Hjertaas K., Zhao Y.,
 RA Chait B.T.,
 RT "The yeast nuclear pore complex: composition, architecture, and
 RT transport mechanism.",
 RL J. Cell Biol. 148:635-651(2000).
 [4]
 FUNCTION, AND SRP1 RECYCLING.
 RA Pubmed=11046143; DOI=10.1128/MCB.20.22.8468-8479.2000;
 RA Solbacher J., Maurer P., Vogel F., Schlenstedt G.,
 RT "Nup2p, a yeast nucleoporin, functions in bidirectional transport of
 RT importin alpha.",
 RL Mol. Cell Biol. 20:8468-8479(2000).
 [5]
 FUNCTION, AND INTERACTIONS THROUGH FG REPEATS.
 RA Pubmed=11387327; DOI=10.1074/jbc.M102629200;
 RA Allen N.P., Huang L., Burlingame A., Rexach M.,
 RT "Proteomic analysis of nucleoporin interacting proteins.",
 RL J. Biol. Chem. 276:29268-29274(2001).
 [6]
 FUNCTION, AND ASSOCIATION WITH NPC.
 RA Pubmed=11425876; DOI=10.1083/jcb.153.7.1465;
 RA Dilworth D.J., Suprapto A., Padovan J.C., Chait B.T., Wozniak R.W.,
 RA Rout M.P., Altschson J.D.,
 RT "Nup2p dynamically associates with the distal regions of the yeast
 RT nuclear pore complex.",
 RL J. Cell Biol. 153:1465-1478(2001).
 [7]
 FUNCTION, AND GSP1-GTP-DEPENDENT INTERACTION WITH NUP60.
 RA Pubmed=11535617; DOI=10.1083/jcb.200101007;
 RA Denning D.P., Mykytka B., Allen N.P., Huang L., Burlingame A.,
 RA Rexach M.,
 RT "The nucleoporin Nup60p functions as a Gsp1p-GTP-sensitive tether for
 RT Nup2p at the nuclear pore complex.",
 RL J. Cell Biol. 154:937-950(2001).
 [8]
 FUNCTION, AND STRUCTURAL BASIS OF FG REPEAT INTERACTIONS.
 RA Pubmed=12372823; DOI=10.1074/jbc.M209037200;
 RA Bayliss R., Littlewood T., Strawn L.A., Wente S.R., Stewart M.,
 RT "Grg and Fxfg nucleoporins bind to overlapping sites on importin-
 RT beta.",
 RL J. Biol. Chem. 277:50597-50606(2002).
 [9]
 FUNCTION, AND INTERACTIONS WITH KARYOPHERINS THROUGH FG REPEATS.
 RA Pubmed=12543930; DOI=10.1074/mcp.T200012-MCP200;
 RA Allen N.P., Patel S.S., Huang L., Chalkley R.J., Burlingame A.,
 RA Lutzmann M., Hurt E.C., Rexach M.,
 RT "Disrupting networks of protein interactions at the nuclear pore
 RT complex.",
 RL Mol. Cell. Proteomics 1:930-946(2002).
 [10]
 FUNCTION, AND CHROMATIN BOUNDARY ACTIVITY.
 RA Pubmed=12062099; DOI=10.1016/S0092-8674(02)00756-0;
 RA Ishii K., Arrib G., Lin C., Van Houwe G., Laemmli U.K.,
 RT "Chromatin boundaries in budding yeast: the nuclear pore connection.",
 RL Cell 109:551-562(2002).
 [11]
 FUNCTION, AND SRP1-KAP95 NUCLEAR IMPORT COMPLEX DISASSEMBLY.
 RA Pubmed=11867631; DOI=10.1074/jbc.M112306200;
 RA Gilchrist D., Mykytka B., Rexach M.,
 RT "Accelerating the rate of disassembly of karyopherin-cargo
 RT complexes.",
 RL J. Biol. Chem. 277:18161-18172(2002).
 [12]
 FUNCTION, AND FG REPEAT AFFINITY GRADIENT FOR KARYOPHERIN KAP95.
 RA Pubmed=12917401; DOI=10.1074/jbc.M307135200;
 RA Pyhila B., Rexach M.,
 RT "A gradient of affinity for the karyopherin Kap95p along the yeast
 RT nuclear pore complex.",
 RL J. Biol. Chem. 278:42659-42709(2003).
 [13]
 FUNCTION, AND FG REPEAT STRUCTURE.
 RA Pubmed=12604785; DOI=10.1073/pnas.0437902100;
 RA Denning D.P., Patel S.S., Uversky V., Fink A.L., Rexach M.,
 RT "Disorder in the nuclear pore complex: the FG repeat regions of
 RT nucleoporins are natively unfolded.",
 RL Proc. Natl. Acad. Sci. U.S.A. 100:2450-2455(2003).
 [14]
 FUNCTION, AND INTERACTION WITH SRP1.
 RA Pubmed=14514698; DOI=10.1074/jbc.M307371200;
 RA Gilchrist D., Rexach M.,
 RT "Molecular basis for the rapid dissociation of nuclear localization
 RT signals from karyopherin alpha in the nucleoplasm.",
 RL J. Biol. Chem. 278:51937-51949(2003).
 [15]
 FUNCTION, AND FG REPEATS IN NPC TRANSPORT.
 RA Pubmed=15039779; DOI=10.1038/nrb1097;
 RA Strawn L.A., Shen T., Shulga N., Goldfarb D.S., Wente S.R.,
 RT "Minimal nuclear pore complexes define FG repeat domains essential for
 RT transport.",
 RL Nat. Cell Biol. 6:197-206(2004).
 [16]
 REVIEW.
 RA Pubmed=12791264; DOI=10.1016/S1534-5807(03)00162-X;
 RA Suntharalingam M., Wente S.R.,
 RT "Peering through the pore: nuclear pore complex structure, assembly,
 RT and function.",
 RL Dev. Cell 4:775-789(2003).
 [17]
 X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS) OF 36-50 IN COMPLEX WITH SRP1.
 RA Pubmed=14532109; DOI=10.1093/emboj/cdg358;
 RA Mateuwa Y., Lange A., Harreman M.T., Corbett A.H., Stewart M.,
 RT "Structural basis for Nup2p function in cargo release and karyopherin
 RT recycling in nuclear import.",
 RL EMBO J. 22:5358-5369(2003).
 -1- FUNCTION: Functions as a component of the nuclear pore complex
 (NPC). NPC components, collectively referred to as nucleoporins
 (NUPs), can play the role of both NPC structural components and of
 docking or interaction partners for transiently associated nuclear
 transport factors. Active directional transport is assured by
 both, a Phe-Gly (FG) repeat affinity gradient for these transport
 factors across the NPC and a transport cofactor concentration
 gradient across the nuclear envelope (GSP1 and GSP2 GTPases
 associated predominantly with GTP in the nucleus, with GDP in the
 cytoplasm). As one of the FG repeat nucleoporins NUP2 is involved
 in interactions with and guidance of nuclear transport receptors
 such as SRP1-KAP95 (importin alpha and beta) through the NPC. Like
 the closely related NUP1 it also plays an important role in
 disassembling and recycling SRP1-KAP95 to the cytoplasm after
 nuclear import. Upon entry of the heterotrimeric SRP1-KAP95-cargo
 complex in the nucleus, NUP2 binds through its N-terminus to the
 SRP1 nuclear localization signal (NLS) binding site, thus
 accelerating the release of the NLS-cargo. SRP1 in turn is
 released from NUP2 by binding of the NLS-GTP associated export
 factor CSE1. NUP2 may also have a chromatin boundary/insulator
 activity through indirect interaction with genomic DNA via CSE1
 and blocking of heterochromatin spreading.
 -1- SUBUNIT: The nuclear pore complex (NPC) constitutes the exclusive

CC streptococci, e.g. meningitis, otitis media, pneumonia, endocarditis,
 CC mastitis in cattle, abortion in horses and many others. Since the
 CC antibodies block binding of bacteria, they should be effective against
 CC antibiotic-resistant strains, and may replace antibiotic therapy or
 CC increase its effectiveness. Sequences AAW65670-90 represent a series of
 CC synthetic peptides based on the D3 repeat of *S. aureus* fibronectin
 CC binding protein A. They were synthesised to contain a proline residue at
 CC each position through the sequence (ie a proline scan)

XX
 SQ Sequence 21 AA;
 Query Match 100.0%; Score 119; DB 2; Length 21;
 Best Local Similarity 100.0%; Pred. No. 4.9e-11;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KPSYQFGGHSVDFEEDLPK 21
 DB 1 KPSYQFGGHSVDFEEDLPK 21

RESULT 2
 AAW65665
 ID AAW65665 standard; peptide; 21 AA.
 AC AAW65665;
 XX
 DT 16-OCT-1998 (first entry)
 XX
 DE Fibronectin binding protein-derived peptide #9.
 XX
 KM microbial surface components recognising adhesive matrix molecule;
 KM MSCRAMM; fibronectin; fibronectin-binding protein; antibody; epitope;
 KM antibiotic; bacterial infection; antibiotic-resistant strain.
 OS Synthetic.
 OS Staphylococcus aureus.
 XX
 PN MO9813389-A2.
 PD 23-JUL-1998.
 XX
 PF 21-JAN-1998; 98WO-US001222.
 XX
 PR 21-JAN-1997; 97US-0036139P.
 XX
 PA (TEXA) UNIV TEXAS A & M SYSTEM.
 PI Hoesek M, Patti JM, House-Pompeo KL, Speziale P, Joh D;
 PI McGavin MJ;
 XX
 DR WPI; 1998-413816/35.
 XX
 PT Antibody that binds to fibronectin-binding protein, preventing its
 PT binding to fibronectin - used to treat or prevent bacterial infection,
 PT especially by Staphylococci and Streptococci.
 XX
 PS Example 2; Page 92; 201pp; English.

XX The invention relates to antibodies that bind to a fibronectin-binding
 CC domain of a fibronectin-binding protein, and inhibit binding of the
 CC protein to fibronectin. Also claimed are: (1) isolated peptides of a
 CC fibronectin-binding protein that do not bind to fibronectin; (2) fusion
 CC protein containing at least one peptide of a fibronectin-binding protein
 CC linked to a second amino acid sequence; (3) nucleic acid encoding the
 CC isolated peptide of (1). Antibodies, the isolated peptides of (1) and the
 CC nucleic acids are all useful for immunisation (active or passive) and (by
 CC inhibiting binding of bacteria to fibronectin) for preventing or treating
 CC infection in humans or other animals, particularly by staphylococci or
 CC streptococci, e.g. meningitis, otitis media, pneumonia, endocarditis,
 CC mastitis in cattle, abortion in horses and many others. Since the
 CC antibodies block binding of bacteria, they should be effective against
 CC antibiotic-resistant strains, and may replace antibiotic therapy or
 CC increase its effectiveness. Sequences AAW65659-68 represent synthetic

CC epitopes from the fibronectin binding domains DU and D1-D4 of the S.
 CC aureus fbaA gene
 XX
 SQ Sequence 21 AA;
 Query Match 93.3%; Score 111; DB 2; Length 21;
 Best Local Similarity 95.2%; Pred. No. 8.2e-10;
 Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KPSYQFGGHSVDFEEDLPK 21
 DB 1 KPSYQFGGHSVDFEEDLPK 21

RESULT 3
 AAR21340
 ID AAR21340 standard; peptide; 22 AA.
 AC AAR21340;
 XX
 DT 25-MAR-2003 (revised)
 DT 15-JUN-1992 (first entry)
 XX
 DE Fibronectin binding protein.
 XX
 KM FbBP; wound infection reduction; vaccination; mastitis;
 KM Staphylococcal infections; D3.
 OS Synthetic.
 OS MO9202555-A.
 XX
 PD 20-FEB-1992.
 XX
 PF 10-AUG-1990; 90SE-00002617.
 XX
 PR 10-AUG-1990; 90SE-00002617.
 XX
 PA (ALFA) ALFA LAVAL AGRIC INT AB.
 XX
 PI Hook M, McGavin M, Rauczi G;
 XX
 DR WPI; 1992-080035/10.
 XX
 PT New fibronectin binding peptide - combines with fusion peptide to form
 PT large antigen, used in immunisation, diagnosis and for treating wounds.
 XX
 PS Claim 1; Page 22; 33pp; English.

XX The sequence comprises amino acids 17-33 of a tandem repeat, designated
 CC D3 of the fibronectin binding site of Staphylococcus aureus 8325-4 FbBP.
 CC The N-terminal DK may be replaced with H or K, and the C-terminal LKP may
 CC be replaced by either L, IP, or OH. The peptides were synthesised using
 CC standard methods and purified using reverse phase HPLC. The appropriate
 CC fractions were dialysed and lyophilised. Peptide sequencing was performed
 CC and the peptides digested and chemically modified by dihydroxypropylation
 CC of the amino side chain of lysine. The carboxylic side chains were
 CC converted to glycine methyl esters. The phenyl side chains of tyrosine
 CC residues were oxidised. Chemically modified peptide D3 was compared to
 CC unmodified D3. Lysine and tyrosine modifications only partially
 CC diminished its activity whereas modification of aspartic/glutamic
 CC residues resulted in reduction of activity. The peptide can be used
 CC for the prevention or reduction of the risk of wound infection. The
 CC peptide can be used to create a large antigen for vaccinating ruminants
 CC against mastitis caused by Staphylococcal infections. It can also be used
 CC to diagnose Staphylococcal infections using ELISA or DNA probes. (Updated
 CC on 25-MAR-2003 to correct PA field.)

XX
 SQ Sequence 22 AA;
 Query Match 93.3%; Score 111; DB 2; Length 22;
 Best Local Similarity 95.2%; Pred. No. 8.6e-10;
 Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 KPSYQFGHNSVDFEEDLPK 21
DB 2 KPSYQFGHNSVDFEEDLPK 22

RESULT 4
AAB91958
ID AAB91958 standard; peptide; 37 AA.

AC AAB91958;
DT 22-JUN-2001 (first entry)

DE Fibronectin fragment and fibrin related peptide SEQ ID NO:1134.

KW Protection; endogenous therapeutic peptide; peptidase; conjugation;
KM blood component; modification; succinimidyl; maleimido group; amino;
XX hydroxyl; thiol; hormone; growth factor; neurotransmitter.

OS Homo sapiens.
XX Synthetic.

PN WO200069900-A2.

PD 23-NOV-2000.

PF 17-MAY-2000; 2000WO-US013576.

PR 17-MAY-1999; 99US-0134406P.

PR 10-SEP-1999; 99US-0153406P.

PR 15-OCT-1999; 99US-0159783P.

PA (CONJ-) CONJUCHEM INC.

PI Bridon DP, Ezrin AM, Milner PG, Holmes DL, Thibaudau K;

DR WPI: 2001-112059/12.

PT Modifying and attaching therapeutic peptides to albumin prevents
XX peptidase degradation, useful for increasing length of in vivo activity.

XX Disclosure; Page 566; 733pp; English.

CC The present invention describes a modified therapeutic peptide (I)
CC comprising a therapeutically active amino acid region (III) and a
CC reactive group (II) (e.g. succinimidyl and maleimido groups) attached to
CC a less therapeutically active amino acid region (IV), which covalently
CC bonds with amino/hydroxyl/thiol groups on blood components to form a
CC peptidase stabilised therapeutic peptide composed of 3-50 amino acids.
CC (I) are useful for modifying therapeutic peptides e.g. hormones, growth
CC factors and neurotransmitters, to protect them from peptidase activity in
CC vivo for the treatment of various disorders. Endogenous therapeutic
CC peptides are not suitable as drug candidates as they require frequent
CC administration due to rapid degradation by peptidases in the body.
CC Modifying and attaching therapeutic peptides to albumin prevents or
CC reduces the action of peptidases to increase length of activity (half
CC life) and specificity as bonding to large molecules decreases
CC intracellular uptake and interference with physiological processes.
CC AAB90829 to AAB92441 represent peptides which can be used in the
CC exemplification of the present invention

XX Sequence 37 AA;

Query Match 93.3%; Score 111; DB 4; Length 37;

Best Local Similarity 95.2%; Pred. No. 1.5e-09;

Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 KPSYQFGHNSVDFEEDLPK 21
DB 16 KPSYQFGHNSVDFEEDLPK 36

RESULT 5
AAP80662
ID AAP80662 standard; protein; 38 AA.

AC AAP80662;

DT 25-MAR-2003 (revised)

DT 07-OCT-1990 (first entry)

DE Protein with fibronectin binding ability.

KW Hybrid DNA molecule; fibronectin binding; mastitis; ruminants;
KM wound infection.

XX Staphylococcus aureus.

PN EP294349-A.

PD 07-DEC-1988.

PF 30-MAY-1988; 88EP-00850188.

PR 01-JUN-1987; 87SE-00002272.

PA (ALFA) ALFA LAVAL AGRIC INT AB.

PI Lindberg MK, Signas LC, Wadstrom TM, Froman G;

DR WPI: 1988-347978/49.

DR N-PSDB; AAN81099.

PT Hybrid DNA encoding Staphylococcus aureus fibronectin binding protein -
XX useful for immunisation and topical application to prevent staphylococcal
XX infections.

PS Claim 11; Page 12; 23pp; English.

CC The peptide has fibronectin binding ability. It is useful for immunising
CC ruminants against staphylococcal mastitis, pret. when used at 0.5-5
CC micrograms/kg, using 3 doses given at 1-3 week intervals; for topical
CC application to prevent wound infection, using an isotonic saline soln. of
CC connon. 25-250 micrograms/ml; and, when immobilised on a carrier, for
CC diagnosing staphylococcal infections. (Updated on 25-MAR-2003 to correct
CC PF field.) (Updated on 25-MAR-2003 to correct PA field.)

XX Sequence 38 AA;

Query Match 93.3%; Score 111; DB 1; Length 38;

Best Local Similarity 95.2%; Pred. No. 1.5e-09;

Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 KPSYQFGHNSVDFEEDLPK 21
DB 17 KPSYQFGHNSVDFEEDLPK 37

RESULT 6
AAV29087

ID AAV29087 standard; protein; 134 AA.

AC AAV29087;

DT 28-SEP-1999 (first entry)

DE S. aureus fibronectin binding protein A (FnBA) binding domain.

KW Bovine herpes virus-2; BHV-2; cytokine; immune response; immunogen; IL;

KW Interleukin; colony stimulating factor; CSF; interferon; IFN; TNF;

KW tumour necrosis factor; recombinant virus; vaccine; mucosal disease;

KW mastitis; breast cancer; stress-induced disease; binding domain; FnBA;

XX fibronectin binding protein.

OS Staphylococcus aureus.

```

XX 09916892-A1.
XX 08-APR-1999.
XX 29-SEP-1998; 98WO-GB002927.
XX 29-SEP-1997; 97GB-00020633.
XX (UYBR-) UNIV BRISTOL.
XX Bradley AJ, Duffas WPJ;
XX WPI; 1999-255101/21.
XX N-PSDB; AAX91504.
XX New bovine herpes virus-2 vectors.
XX Example 2; Fig 8A-B; 130pp; English.
XX The invention provides bovine herpes virus-2 (BHV-2) based vectors that
XX comprise at least one cytokine-encoding DNA sequence. The expression of
XX cytokines in mammals can up-regulate immune responses to the immunogens.
XX The cytokine is selected from interleukins (IL), colony stimulating
XX factors (CSF), interferons (IFN) and tumour necrosis factors (TNF). The
XX BHV-2 based vector or recombinant virus can be used as vaccines. They can
XX be used for preventing or treating a mucosal disease in a subject, e.g.
XX ruminants, cattle, sheep, goats, dogs, cats, horses, or man, particularly
XX mastitis in cows or breast cancers in humans. They can also be used for
XX preventing or treating a stress-induced disease. The present sequence
XX represents the binding domain of a previously published S. aureus
XX fibronectin binding protein A (FnBA) sequence. The FnB binding domain
XX gene sequence FnBA, cloned for use in this invention has 97.8 percent
XX identity when compared to the previously published FnBA and fnbA gene
XX sequences
XX Sequence 134 AA:
XX
XX Query Match 93.3%; Score 111; DB 2; Length 134;
XX Best Local Similarity 95.2%; Pred. No. 5.8e-09;
XX Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX 1 KPSYFGGSHNSVDFEEDLPK 21
XX 93 KPSYFGGSHNSVDFEEDLPK 113
XX
XX RESULT 7
XX AAW31556
XX ID AAW31556 standard; protein; 139 AA.
XX
XX AAW31556;
XX
XX 27-AUG-2003 (revised)
XX DT 25-MAR-2003 (revised)
XX DT 21-MAY-1998 (first entry)
XX
XX Fibronectin-binding MSCRAMM derivative POD.
XX
XX Fibronectin; POD; collagen binding protein; sepsis; infectior;
XX microbial surface component recognising adhesive matrix molecule; MSCRAMM;
XX adhesin; vaccine; immunisation; diagnosis; therapy; mastitis.
XX
XX Staphylococcus aureus.
XX
XX Key Location/Qualifiers
XX Peptide 1..12
XX /note= "vector pQE30-derived peptide"
XX
XX W09743314-A2.
XX 20-NOV-1997.
XX

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PF 14-MAY-1997; 97WO-US008210.
XX 16-MAY-1996; 96US-0017678P.
XX (TEXA ) UNIV TEXAS A & M SYSTEM.
XX (UABR-) UAB RES FOUND.
XX
XX Hoeoek M, Patel JM, House-Pompeo K, Sthanam N, Symersky J;
XX WPI; 1998-008801/01.
XX
XX Antibody that interacts with collagen binding domain of Staphylococcal
XX cna gene product - useful to prevent bacterial sepsis in animal infected
XX with Staphylococcus aureus.
XX
XX Disclosure; Page 91; 143pp; English.
XX
XX This protein comprises Staphylococcus aureus fibronectin-binding
XX microbial surface component recognising adhesive matrix molecule (MSCRAMM)
XX derivative POD, plus a vector-derived N-terminal peptide. The invention
XX relates to claimed nucleic acid sequences (see AAT93436-38) encoding S.
XX aureus collagen binding protein (CBP) epitopes M17, M31 and M55 (see
XX AAW31552-54) that confer protection against S. aureus infection. CBP
XX protein and antigenic epitopes are contemplated for use in the treatment
XX of pathological infections, especially to prevent bacterial adhesion to
XX collagen. The epitopes are also contemplated for use in the preparation
XX of vaccines and as carrier proteins in vaccine formulations, as well as
XX in the formulation of compositions for the prevention of S. aureus
XX infection. pCF3 and POD (see AAW31556) were used to raise anti-MSCRAMM
XX polyclonal antibodies used in passive immunisation against bovine
XX mastitis. (Updated on 25-MAR-2003 to correct PI field.) (Updated on 27-
XX AUG-2003 to correct OS field.)
XX
XX Sequence 139 AA:
XX
XX Query Match 93.3%; Score 111; DB 2; Length 139;
XX Best Local Similarity 95.2%; Pred. No. 6.1e-09;
XX Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX 1 KPSYFGGSHNSVDFEEDLPK 21
XX 107 KPSYFGGSHNSVDFEEDLPK 127
XX
XX RESULT 8
XX AAP82115
XX ID AAP82115 standard; protein; 1018 AA.
XX
XX AAP82115;
XX
XX 25-MAR-2003 (revised)
XX DT 05-JAN-1990 (first entry)
XX
XX Fibronectin binding protein.
XX
XX Fibronectin binding protein; S. aureus; immunisation; mastitis; ruminants;
XX wound infection; diagnosis.
XX
XX Staphylococcus aureus.
XX
XX EP294349-A.
XX 07-DEC-1988.
XX
XX 30-MAY-1998; 88EP-00850188.
XX
XX 01-JUN-1987; 87SE-00002272.
XX
XX (ALFA ) ALFA LAVAL AGRIC INT AB.
XX
XX Lindberg MK, Signas LC, Wadstrom TM, Froman G;
XX WPI; 1988-347978/49.
XX

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DR P-PSDB; AAP82115.
 XX Hybrid DNA encoding Staphylococcus aureus fibronectin binding protein -
 PT useful for immunisation and topical application to prevent staphylococcal
 PT infections.
 XX
 XX Disclosure; Fig. 8A:1-8A:2; 23pp; English.
 CC The S. aureus fibronectin binding protein may be included in a hybrid
 CC protein. The protein may be used to immunise ruminants against
 CC staphylococcal mastitis; pref. when given at 0.5-5 microg/kg; using 3
 CC doses at 1-3 week intervals; and for topical applicn. to prevent wound
 CC infection; pref. using isotonic saline soln. of concn. 25-250 microg/mg.
 CC The DNA encoding the binding protein and the hybrid protein may be
 CC immobilised on a carrier and used to diagnose staphylococcal infections.
 CC (updated on 25-MAR-2003 to correct PA field.)
 CC
 SQ Sequence 1018 AA;
 Query Match 93.3%; Score 111; DB 1; Length 1018;
 Best Local Similarity 95.2%; Pred. No. 5e-08;
 Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Oy 1 KPSYQFGHNSVDFEEDLPK 21
 DB 837 KPSYQFGHNSVDFEEDLPK 857
 RESULT 9
 AAU37245
 ID AAU37245 standard; protein; 1018 AA.
 AC AAU37245;
 DT 14-FEB-2002 (first entry)
 DE Staphylococcus aureus cellular proliferation protein #1415.
 DE
 KW Antisense; prokaryotic cellular proliferation protein; antibiotic;
 KW antibacterial; drug design.
 OS Staphylococcus aureus.
 PN WO200170955-A2.
 PD 27-SEP-2001.
 PF 21-MAR-2001; 2001WO-US009180.
 PR 21-MAR-2000; 2000US-0191078P.
 PR 23-MAY-2000; 2000US-0206848P.
 PR 26-MAY-2000; 2000US-0207727P.
 PR 23-OCT-2000; 2000US-0242578P.
 PR 27-NOV-2000; 2000US-0253625P.
 PR 22-DEC-2000; 2000US-0257931P.
 PR 16-FEB-2001; 2001US-0269308P.
 PA (ELIT-) ELITRA PHARM INC.
 PI Haselbeck R, Ohlsen KL, Zyskind JW, Wall D, Trawick JD, Carr GJ;
 PI Yamamoto RT, Xu HH;
 DR N-PSDB; AAS55104.
 DR WPI; 2001-611495/70.
 PT New polynucleotides for the identification and development of
 PT antibiotics; comprise sequences of antisense nucleic acids.
 XX
 XX Example 3; SEQ ID NO 12838; 511pp; English.
 CC The invention relates to antisense inhibitors of genes essential to
 CC prokaryotic cellular proliferation, their use in identifying the genes,
 CC their use in the discovery of novel antibiotics, the essential genes

CC themselves and the encoded proteins. The prokaryotes used are Escherichia
 CC coli, Staphylococcus aureus, Salmonella typhi, Klebsiella pneumoniae,
 CC Pseudomonas aeruginosa and Enterococcus faecalis. The invention is also
 CC useful for the identification of potential new targets for antibiotic
 CC development. The antisense nucleic acids can also be used to identify
 CC proteins used in proliferation, to express these proteins, and to obtain
 CC antibodies capable of binding to the expressed proteins. The proteins can
 CC be used to screen compounds in rational drug discovery programmes. The
 CC antisense nucleic acid sequence is also useful to screen for homologous
 CC nucleic acids which are required for cell proliferation in a wide variety
 CC of organisms. The present sequence represents an essential prokaryotic
 CC cellular proliferation protein. Note: The sequence data for this patent
 CC did not form part of the printed specification, but was obtained in
 CC electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 CC
 SQ Sequence 1018 AA;
 Query Match 93.3%; Score 111; DB 4; Length 1018;
 Best Local Similarity 95.2%; Pred. No. 5e-08;
 Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Oy 1 KPSYQFGHNSVDFEEDLPK 21
 DB 837 KPSYQFGHNSVDFEEDLPK 857
 RESULT 10
 AAU34301
 ID AAU34301 standard; protein; 1018 AA.
 AC AAU34301;
 DT 14-FEB-2002 (first entry)
 DE Staphylococcus aureus cellular proliferation protein #577.
 DE
 KW Antisense; prokaryotic cellular proliferation protein; antibiotic;
 KW antibacterial; drug design.
 OS Staphylococcus aureus.
 PN WO200170955-A2.
 PD 27-SEP-2001.
 PF 21-MAR-2001; 2001WO-US009180.
 PR 21-MAR-2000; 2000US-0191078P.
 PR 23-MAY-2000; 2000US-0206848P.
 PR 26-MAY-2000; 2000US-0207727P.
 PR 23-OCT-2000; 2000US-0242578P.
 PR 27-NOV-2000; 2000US-0253625P.
 PR 22-DEC-2000; 2000US-0257931P.
 PR 16-FEB-2001; 2001US-0269308P.
 PA (ELIT-) ELITRA PHARM INC.
 PI Haselbeck R, Ohlsen KL, Zyskind JW, Wall D, Trawick JD, Carr GJ;
 PI Yamamoto RT, Xu HH;
 DR N-PSDB; AAS52160.
 DR WPI; 2001-611495/70.
 PT New polynucleotides for the identification and development of
 PT antibiotics; comprise sequences of antisense nucleic acids.
 XX
 XX Example 3; SEQ ID NO 5797; 511pp; English.
 CC The invention relates to antisense inhibitors of genes essential to
 CC prokaryotic cellular proliferation, their use in identifying the genes,
 CC their use in the discovery of novel antibiotics, the essential genes
 CC themselves and the encoded proteins. The prokaryotes used are Escherichia

CC coli, *Staphylococcus aureus*, *Salmonella typhi*, *Klebsiella pneumoniae*,
 CC *Pseudomonas aeruginosa* and *Enterococcus faecalis*. The invention is also
 CC useful for the identification of potential new targets for antibiotic
 CC development. The antisense nucleic acids can also be used to identify
 CC proteins used in proliferation, to express these proteins, and to obtain
 CC antibodies capable of binding to the expressed proteins. The proteins can
 CC be used to screen compounds in rational drug discovery programmes. The
 CC antisense nucleic acid sequence is also useful to screen for homologous
 CC nucleic acids which are required for cell proliferation in a wide variety
 CC of organisms. The present sequence represents an essential prokaryotic
 CC cellular proliferation protein. Note: The sequence data for this patent
 CC did not form part of the printed specification, but was obtained in
 CC electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences

XX Sequence 1018 AA;

Query Match 93.3%; Score 111; DB 4; Length 1018;
 Best Local Similarity 95.2%; Pred. No. 5e-08;
 Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 KPSYQFGGHSVDPEDPLPK 21
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 Db 837 KPSYQFGGHSVDPEDPLPK 857

RESULT 11

ABJ18922
 ID ABJ18922 standard; protein; 1018 AA.

XX ABJ18922;

XX 06-MAR-2003 (first entry)

XX Pathogen specific antigen related staphylococcal protein SEQ ID No 68.

XX Antibacterial; virucide; fungicide; protozoacide; cytostatic; anti-HIV;
 KW hyperimmune; serum-reactive; antigen; pathogen; tumour; allergen;
 KW auto-immunity; vaccine; staphylococcal infection; antibody; cancer;
 KW autoimmune disease; HIV; hepatitis.

XX *Staphylococcus* sp.

XX WO200259148-A2.

XX 01-AUG-2002.

XX 21-JAN-2002; 2002WO-EP000546.

XX 26-JAN-2001; 2001AT-00000130.

XX (CIST-) CISTEM BIOTECHNOLOGIES GMBH.

XX Weinke A, Nagy E, Von Ahsen U, Klade C, Henics T, Zauner W,
 PI Minh DB, Vytvytska O, Etz H, Dryla A, Weichart T, Hafner M;
 PI Tempelmeier B;

XX WPI: 2003-075410/07.

XX Identifying, isolating and producing hyperimmune serum-reactive antigens
 PT from a pathogen, for preparing vaccine or medicament for treating or
 PT preventing e.g. staphylococcal infections, comprises providing antibody
 PT preparation.

XX Example 7, Page 157; 252pp; English.

XX The invention relates to a novel method for identifying, isolating and
 CC producing hyperimmune serum-reactive antigens from a pathogen, tumour,
 CC allergen, a tissue or host prone to auto-immunity where the antigens are
 CC used in a vaccine, comprises providing antibody preparation from a plasma
 CC pool of a type of animal, or individual sera with antibodies against the
 CC specific pathogen, tumour, allergen, tissue or host prone to auto-
 CC immunity. The hyperimmune serum-reactive antigens comprising any of the

CC 62 sequences of 53-2261 amino acids fully defined in the specification,
 CC or their hyperimmune fragments are useful for the manufacture of a
 CC pharmaceutical preparation, particularly a vaccine against staphylococcal
 CC infections or colonisation against *S. aureus* or *S. epidermidis*. The
 CC preparation of antibodies is useful for the manufacture of a medicament
 CC for treating or preventing staphylococcal infections or colonisation
 CC against *S. aureus* or *S. epidermidis*. The antibody preparations may also
 CC be used for diagnostic and imaging purposes. Other conditions that can be
 CC treated include cancer, autoimmune diseases or infections caused by viral
 CC (e.g. HIV, hepatitis A, B or C), fungal or protozoan pathogens. This
 CC sequence represents a staphylococcal protein relating to the method for
 CC identifying and producing pathogen specific antigens of the invention

XX Sequence 1018 AA;

Query Match 93.3%; Score 111; DB 6; Length 1018;
 Best Local Similarity 95.2%; Pred. No. 5e-08;
 Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 KPSYQFGGHSVDPEDPLPK 21
 |||||
 Db 837 KPSYQFGGHSVDPEDPLPK 857

RESULT 12

ABM72537
 ID ABM72537 standard; protein; 1018 AA.

XX ABM72537;

XX 20-NOV-2003 (first entry)

XX *Staphylococcus aureus* protein #1777.

XX Antibacterial; vaccine; gene therapy; infection; sepsis; diagnosis;
 KW enzymatic assay; antibiotic target.

XX *Staphylococcus aureus*.

XX WO200294868-A2.

XX 28-NOV-2002.

XX 27-MAR-2002; 2002WO-IB002637.

XX 27-MAR-2001; 2001GB-00007661.

XX (CHIR-) CHIRON SPA.

XX Masignani V, Mora M, Scarselli M;

XX WPI: 2003-120786/11.
 DR N-PSDB; ACF74097.

XX New *Staphylococcus aureus* protein, useful as a vaccine for treating or
 PT preventing *Staphylococcal* infection, specifically an infection caused by
 PT *S. aureus*, e.g. sepsis.

XX Claim 1; SEQ ID NO 3554; 49pp; English.

XX The invention relates to novel genes and encoded proteins from
 CC *Staphylococcus aureus*. A composition comprising the *S. aureus* protein, a
 CC nucleic acid encoding the protein, or an antibody to the protein, is
 CC useful as a pharmaceutical, particularly as a vaccine for treating or
 CC preventing infection due to *Staphylococcus* bacteria, specifically an
 CC infection caused by *S. aureus*. The composition is particularly useful for
 CC treating or preventing sepsis in a patient. The composition can also be
 CC used for diagnostics. The protein is also used in an assay for enzymatic
 CC studies and as a target for antibiotics. This sequence represents one of
 CC the novel *S. aureus* proteins of the invention

XX Sequence 1018 AA;

Query Match 93.3%; Score 111; DB 6; Length 1018;
 Best Local Similarity 95.2%; Pred. No. 5e-08;
 Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KPSYQFGHNSVDFEEDLPK 21
 DB 837 KPSYQFGHNSVDFEEDLPK 857

RESULT 13

AAW89806
 ID AAW89806 standard; protein; 1027 AA.

AAW89806;
 16-MAR-1999 (first entry)

XX Staphylococcus aureus protein SEQ ID #5254.

XX Computer readable medium; vaccine; S.aureus infection; immunodetection;
 KW cellulitis; eyelid infection; food poisoning; osteomyelitis; therapy;
 KW skin infection; surgical wound infection; scalded skin syndrome;
 KW toxic shock syndrome.

XX Staphylococcus aureus.

OS EP786519-A2.

XX 30-JUL-1997.

XX 07-JAN-1997; 97EP-00100117.

XX 05-JAN-1996; 96US-0009861P.

XX (HUMA-) HUMAN GENOME SCI INC.

XX Kunesh CA, Choi GH, Barash SC, Dillon PJ, Fannon MR, Rosen CA;
 PI WPI; 1997-374922/35.

XX Polynucleotide(s) and proteins derived from Staphylococcus aureus -
 PT stored on computer readable medium and used in the production of anti-
 PT S.aureus vaccines.

XX Claim 23; Page 3263-3267; 3271pp; English.

XX This sequence represents a Staphylococcus aureus protein sequence of the
 CC invention. The DNA sequences encoding the S.aureus proteins are recorded
 CC on a computer readable medium, preferably selected from a floppy or hard
 CC disk, random access memory (RAM), read-only memory (ROM) or CD-ROM.
 CC Homology searches using the S.aureus DNA sequences allows putative
 CC functions to be assigned so that protein-encoding or regulatory regions
 CC of commercial, therapeutic or industrial importance can be obtained.
 CC Specifically, sequences which are likely to encode antigens have been
 CC identified and these polypeptides can be used in a vaccine composition
 CC against S.aureus infection. The polypeptides can also be used in a kit
 CC for the immunodetection of S.aureus in a sample. S.aureus is implicated
 CC in numerous human diseases, including cellulitis, eyelid infections, food
 CC poisoning, osteomyelitis, skin and surgical wound infections, scalded
 CC skin syndrome, toxic shock syndrome, etc. Organisms transformed with the
 CC DNA sequences can be used for recombinant production of the polypeptides.
 CC The new DNA sequences (and their fragments) are useful as primers or
 CC probes for isolating homologues of any of the 5191 S.aureus DNA sequences
 CC contained on the computer readable medium

XX Sequence 1027 AA;

Query Match 93.3%; Score 111; DB 2; Length 1027;
 Best Local Similarity 95.2%; Pred. No. 5e-08;
 Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KPSYQFGHNSVDFEEDLPK 21
 |||

DB 846 KPSYQFGHNSVDFEEDLPK 866

RESULT 14

ABU15854
 ID ABU15854 standard; protein; 961 AA.

XX ABU15854;
 19-JUN-2003 (first entry)

XX Protein encoded by Prokaryotic essential gene #1361.

XX Antisense; prokaryotic essential gene; cell proliferation; drug design.

XX Staphylococcus aureus.

XX WO20027183-A2.

XX 03-OCT-2002.

XX 21-MAR-2002; 2002WO-US009107.

XX 21-MAR-2001; 2001US-00815242.

XX 06-SEP-2001; 2001US-00948993.

XX 25-OCT-2001; 2001US-0342923P.

XX 08-FEB-2002; 2002US-00072851.

XX 06-MAR-2002; 2002US-0362699P.

XX (ELIT-) ELITRA PHARM INC.

XX Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zykkind JW;
 PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;
 XX N-PSDB; ACA19724.

XX WPI; 2003-029926/02.

XX New antisense nucleic acids, useful for identifying proteins or screening
 PT for homologous nucleic acids required for cellular proliferation to
 PT isolate candidate molecules for rational drug discovery programs.

XX Claim 25; SEQ ID NO 43778; 1766pp; English.

XX The invention relates to an isolated nucleic acid comprising any one of
 CC the 623 antisense sequences given in the specification where expression
 CC of the nucleic acid inhibits proliferation of a cell. Also included are:
 CC (1) a vector comprising a promoter operably linked to the nucleic acid
 CC encoding a polypeptide whose expression is inhibited by the antisense
 CC nucleic acid; (2) a host cell containing the vector; (3) an isolated
 CC polypeptide or its fragment whose expression is inhibited by the
 CC antisense nucleic acid; (4) an antibody capable of specifically binding
 CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular
 CC proliferation or the activity of a gene in an operon regulated for
 CC proliferation; (7) identifying a compound that influences the activity of
 CC the gene product or that has an activity against a biological pathway
 CC required for proliferation, or that inhibits cellular proliferation; (8)
 CC identifying a gene required for cellular proliferation or the biological
 CC pathway in which a proliferation-regulated gene or its gene product lies
 CC or a gene on which the test compound that inhibits proliferation of an
 CC organism acts; (9) manufacturing an antibiotic; (10) profiling a
 CC compound's activity; (11) a culture comprising strains in which the gene
 CC product is overexpressed or underexpressed; (12) determining the extent
 CC to which each of the strains is present in a culture or collection of
 CC strains; or (13) identifying the target of a compound that inhibits the
 CC proliferation of an organism. The antisense nucleic acids are useful for
 CC identifying proteins or screening for homologous nucleic acids required
 CC for cellular proliferation to isolate candidate molecules for rational
 CC drug discovery programs, or for screening homologous nucleic acids
 CC required for proliferation in cells other than S. aureus, S. typhimurium,
 CC K. pneumoniae or P. aeruginosa. The present sequence is encoded by one of
 CC the target prokaryotic essential genes. Note: The sequence data for this
 CC patent did not form part of the printed specification, but was obtained
 CC in electronic format directly from WIPO at

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CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 961 AA;
Query Match 90.8%; Score 108; DB 6; Length 961;
Best Local Similarity 90.5%; Pred. No. 1.3e-07;
Matches 19; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 KPSYQFGHNSVDFEEDLPK 21
DB 784 KPNYQFGHNSVDFEEDLPK 804

RESULT 15
AAU33960
ID AAU33960 standard; protein; 978 AA.
XX
AC AAU33960;
XX
DT 14-FEB-2002 (first entry)
XX
DE Staphylococcus aureus cellular proliferation protein #236.
XX
KM Antisense; prokaryotic cellular proliferation protein; antibiotic;
antibacterial; drug design.
XX
OS Staphylococcus aureus.
XX
WO200170955-A2.
XX
PD 27-SEP-2001.
XX
PI 21-MAR-2001; 2001WO-US009180.
XX
PR 21-MAR-2000; 2000US-0191078P.
PR 23-MAY-2000; 2000US-0206848P.
PR 26-MAY-2000; 2000US-0207227P.
PR 23-OCT-2000; 2000US-0242578P.
PR 27-NOV-2000; 2000US-0253625P.
PR 22-DEC-2000; 2000US-0257931P.
PR 16-FEB-2001; 2001US-0269308P.
XX
PA (ELIT-) ELITRA PHARM INC.
XX
PI Haselbeck R, Ohlsen KJ, Zyskind JW, Wall D, Trawick JD, Carr GJ;
PI Yamamoto RT, Xu HH;
XX
DR N-PSDB; AAS51819.
XX
WPI: 2001-611495/70.
XX
PT New polynucleotides for the identification and development of
antibiotics, comprise sequences of antisense nucleic acids.
XX
PS Example 3; SEQ ID NO 5456; 511pp; English.
XX
CC The invention relates to antisense inhibitors of genes essential to
prokaryotic cellular proliferation, their use in identifying the genes,
their use in the discovery of novel antibiotics, the essential genes
themselves and the encoded proteins. The prokaryotes used are Escherichia
coli, Staphylococcus aureus, Salmonella typhi, Klebsiella pneumoniae,
Pseudomonas aeruginosa and Enterococcus faecalis. The invention is also
useful for the identification of potential new targets for antibiotic
development. The antisense nucleic acids can also be used to identify
proteins used in proliferation, to express these proteins, and to obtain
antibodies capable of binding to the expressed proteins. The proteins can
be used to screen compounds in rational drug discovery programmes. The
antisense nucleic acid sequence is also useful to screen for homologous
nucleic acids which are required for cell proliferation in a wide variety
of organisms. The present sequence represents an essential prokaryotic
cellular proliferation protein. Note: The sequence data for this patent
did not form part of the printed specification, but was obtained in
electronic format directly from WIPO at
ftp.wipo.int/pub/published_pct_sequences

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XX
SQ Sequence 978 AA;
Query Match 90.8%; Score 108; DB 4; Length 978;
Best Local Similarity 90.5%; Pred. No. 1.4e-07;
Matches 19; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 KPSYQFGHNSVDFEEDLPK 21
DB 815 KPNYQFGHNSVDFEEDLPK 835

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 Job time : 60.1473 secs

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OM protein - protein search, using sw model

Run on: October 22, 2005, 02:23:36 ; Search time 15.9358 Seconds
(without alignments)
96.371 Million cell updates/sec

Title: US-10-731-238-30

Perfect score: 119

Sequence: 1 KPSYQFGHNSVDEEDPLPK 21

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Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- 4: /cgn2_6/ptodata/1/1aa/6B.COMB.pep:*
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- 6: /cgn2_6/ptodata/1/1aa/6D.COMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	111	93.3	21	4	US-09-010-317-9
3	111	93.3	37	1	US-08-234-622A-4
4	111	93.3	38	1	US-08-294-189-8
5	111	93.3	38	1	US-08-729-767-5
6	111	93.3	114	1	US-08-259-000-3
7	111	93.3	139	3	US-08-856-253-8
8	111	93.3	178	2	US-08-459-135A-12
9	111	93.3	178	3	US-08-495-559-12
10	111	93.3	1027	4	US-08-956-171E-5254
11	111	93.3	1027	4	US-08-781-986A-5254
12	106	89.1	21	4	US-09-010-317-14
13	106	89.1	21	4	US-09-010-317-16
14	106	89.1	21	4	US-09-010-317-23
15	106	89.1	21	4	US-09-010-317-33
16	105	88.2	21	4	US-09-010-317-18
17	105	88.2	21	4	US-09-010-317-24
18	105	88.2	21	4	US-09-010-317-27
19	105	88.2	21	4	US-09-010-317-28
20	104	87.4	21	4	US-09-010-317-25
21	104	87.4	21	4	US-09-010-317-29
22	104	87.4	21	4	US-09-010-317-31
23	104	87.4	130	2	US-08-459-135A-7
24	104	87.4	130	2	US-08-459-135A-8
25	104	87.4	130	3	US-08-495-559-7
26	104	87.4	130	3	US-08-495-559-8
27	104	87.4	174	2	US-08-459-135A-10

28	104	87.4	174	2	US-08-459-135A-13	Sequence 13, Appl
29	104	87.4	174	3	US-08-495-559-10	Sequence 10, Appl
30	104	87.4	174	3	US-08-495-559-13	Sequence 13, Appl
31	104	87.4	176	3	US-08-495-559-6	Sequence 6, Appl
32	104	87.4	181	2	US-08-459-135A-6	Sequence 6, Appl
33	104	87.4	559	4	US-08-956-171E-5251	Sequence 5251, Ap
34	104	87.4	559	4	US-08-781-986A-5251	Sequence 5251, Ap
35	103	86.6	21	4	US-09-010-317-10	Sequence 10, Appl
36	103	86.6	21	4	US-09-010-317-15	Sequence 15, Appl
37	103	86.6	21	4	US-09-010-317-20	Sequence 20, Appl
38	103	86.6	21	4	US-09-010-317-22	Sequence 22, Appl
39	103	86.6	21	4	US-09-010-317-32	Sequence 32, Appl
40	103	86.6	22	4	US-09-010-317-13	Sequence 13, Appl
41	101	84.9	21	4	US-09-010-317-17	Sequence 17, Appl
42	101	84.9	21	4	US-09-010-317-19	Sequence 19, Appl
43	101	84.9	21	4	US-09-010-317-21	Sequence 21, Appl
44	101	84.9	21	4	US-09-010-317-26	Sequence 26, Appl
45	91	76.5	19	1	US-08-234-622A-1	Sequence 1, Appl

ALIGNMENTS

RESULT 1
US-09-010-317-30
Sequence 30, Application US/09010317
Patent No. 6685943
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
APPLICANT: Patti, Joseph M.
APPLICANT: House-Pompeo, Karen L.
APPLICANT: Speziale, Pietro
APPLICANT: Joh, Danny
TITLE OF INVENTION: McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Arnold, White & Durkee
STREET: P. O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/010.317
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TANK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-09-010-317-30
Query Match 100.0%; Score 119; DB 4; Length 21;
Best Local Similarity 100.0%; Pred. No. 5.5e-12;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 KPSYFGGHSVDFEEDLPK 21
Db 1 KPSYFGGHSVDFEEDLPK 21

RESULT 2

US-09-010-317-9
Sequence 9, Application US/09010317
Patent No. 6685943
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
APPLICANT: Patli, Joseph M.
APPLICANT: House-Pompeo, Karen L.
APPLICANT: Speziale, Pietro
APPLICANT: McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
TITLE OF INVENTION: AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/010.317
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/036.139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibley, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAMK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-09-010-317-9

Query Match 93.3%; Score 111; DB 4; Length 21;
Best Local Similarity 95.2%; Pred. No. 9.8e-11;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 KPSYFGGHSVDFEEDLPK 21
Db 1 KPSYFGGHSVDFEEDLPK 21

RESULT 3
US-08-234-622A-4
Sequence 4, Application US/08234622A
Patent No. 5440014
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
APPLICANT: McGavin, Martin
APPLICANT: RAUCCI, Giuseppe
TITLE OF INVENTION: A FIBRONECTIN BINDING PEPTIDE

NUMBER OF SEQUENCES: 4

CORRESPONDENCE ADDRESS:

ADDRESSEE: Burns, Doane, Swecker & Mathis

STREET: P.O. Box 1404

CITY: Alexandria

STATE: Virginia

COUNTRY: United States

ZIP: 22313-1404

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/234.622A

FILING DATE: 28-APR-1994

CLASSIFICATION: 530

PRIOR APPLICATION DATA:

APPLICATION NUMBER: SE 9002617-0

FILING DATE: 10-AUG-1990

PRIOR APPLICATION DATA:

APPLICATION NUMBER: WO PCT/SE91/00534

FILING DATE: 09-AUG-1991

ATTORNEY/AGENT INFORMATION:

NAME: Meuth, Donna M

REGISTRATION NUMBER: 36,607

REFERENCE/DOCKET NUMBER: 012885-044

TELECOMMUNICATION INFORMATION:

TELEPHONE: (703) 836-6620

TELEFAX: (703) 836-2021

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 37 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-234-622A-4

Query Match 93.3%; Score 111; DB 1; Length 37;
Best Local Similarity 95.2%; Pred. No. 1.9e-10;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 KPSYFGGHSVDFEEDLPK 21
Db 16 KPSYFGGHSVDFEEDLPK 36

RESULT 4

US-08-294-189-8
Sequence 8, Application US/08294189
Patent No. 5707822
GENERAL INFORMATION:
APPLICANT: Fischetti, Vincent A.
APPLICANT: Rakonjac, Jasna
APPLICANT: Robbins, John
TITLE OF INVENTION: GENE SERUM OPACITY FACTOR
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Klauder & Jackson
STREET: 411 Hackensack Avenue
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/294.189
FILING DATE: 22-AUG-1994

CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-118
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 487-5800
TELEFAX: 201 343-1684
TELEX: 133521
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
ORGANISM: Streptococcus pyogenes
STRAIN: D734
INDIVIDUAL ISOLATE: 22
IMMEDIATE SOURCE:
CLONE: SAU3a
US-08-294-189-8

Query Match 93.3%; Score 111; DB 1; Length 38;
Best Local Similarity 95.2%; Pred. No. 1.9e-10;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KRSYQFGHNSVDFEEDLPK 21
Db 10 KRSYQFGHNSVDFEEDLPK 30

RESULT 5
US-08-729-767-5
Sequence 5, Application US/08729767
Patent No. 5770702
GENERAL INFORMATION:
APPLICANT: HOOK, Magnus
APPLICANT: LINDBERG, Martin Kjell
APPLICANT: SIGNAS, Lars Christer
APPLICANT: WADSTROM, Torkel Mikael
APPLICANT: FROMAN, Gunnar
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN AS WELL AS
TITLE OF INVENTION: ITS PREPARATION
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Burns, Doane, Swecker & Mathis, L.L.P.
STREET: P.O. Box 1404
CITY: Alexandria
STATE: Virginia
COUNTRY: United States
ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/729,767
FILING DATE: 07-OCT-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/259,000
FILING DATE: 13-JUN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/007,817
FILING DATE: 22-JAN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/201,028
FILING DATE: 01-JUN-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: SE 8702272-9

FILING DATE: 01-JUN-1987
ATTORNEY/AGENT INFORMATION:
NAME: McGowan, Malcolm K.
REGISTRATION NUMBER: 39,300
REFERENCE/DOCKET NUMBER: 012889-036
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-729-767-5

Query Match 93.3%; Score 111; DB 1; Length 38;
Best Local Similarity 95.2%; Pred. No. 1.9e-10;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KRSYQFGHNSVDFEEDLPK 21
Db 17 KRSYQFGHNSVDFEEDLPK 37

RESULT 6
US-08-259-000-3
Sequence 3, Application US/08259000
Patent No. 5571514
GENERAL INFORMATION:
APPLICANT: HOOK, Magnus
APPLICANT: LINDBERG, Martin Kjell
APPLICANT: SIGNAS, Lars Christer
APPLICANT: WADSTROM, Torkel Mikael
APPLICANT: FROMAN, Gunnar
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN AS WELL AS
TITLE OF INVENTION: ITS PREPARATION
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Burns, Doane, Swecker & Mathis
STREET: P.O. Box 1404
CITY: Alexandria
STATE: Virginia
COUNTRY: United States
ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/259,000
FILING DATE: 13-JUN-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: SE 8702272-9
FILING DATE: 01-JUN-1987
ATTORNEY/AGENT INFORMATION:
NAME: Meuth, Donna M.
REGISTRATION NUMBER: 36,607
REFERENCE/DOCKET NUMBER: 012885-062
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 114 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-259-000-3

Query Match 93.3%; Score 111; DB 1; Length 114;
Best Local Similarity 95.2%; Pred. No. 6.6e-10;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KPSYQFGHNSVDPEDPLPK 21
Db 93 KPSYQFGHNSVDPEDPLPK 113

RESULT 7

US-08-856-253-8
Sequence 8, Application US/08856253
Patent No. 6288214
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
APPLICANT: Patti, Joseph M.
APPLICANT: House-Pompeo, Karen
APPLICANT: Sthanam, Narayana
APPLICANT: Symersky, Jindrich
TITLE OF INVENTION: COLLAGEN BINDING PROTEIN COMPOSITIONS
NUMBER OF SEQUENCES: 8
METHODS OF USE
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: Texas
COUNTRY: U.S.
ZIP: 77210
TELEPHONE: 610-270-4478
TELEFAX: 610-270-5090
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/856,253
FILING DATE: Concurrently Herewith
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/017,678
FILING DATE: 16-MAY-1996
ATTORNEY/AGENT INFORMATION:
NAME: Kitchell, Barbara S.
REGISTRATION NUMBER: 33,928
REFERENCE/DOCKET NUMBER: TANK:193
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
TELEFAX: (512) 474-7577
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 139 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-08-856-253-8

Query Match 93.3%; Score 111; DB 3; Length 139;
Best Local Similarity 95.2%; Pred. No. 8.3e-10;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KPSYQFGHNSVDPEDPLPK 21
Db 107 KPSYQFGHNSVDPEDPLPK 127

RESULT 8

US-08-459-135A-12
Sequence 12, Application US/08459135A
Patent No. 5955078
GENERAL INFORMATION:
APPLICANT: BURHAM, Martin Karl Russel
APPLICANT: CHOPRA, Ian

APPLICANT: CRITCHLEY, Ian Alfred
APPLICANT: KNOWLES, David Justin Charles
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN: MONOCLONAL ANTIBODY AND THEIR US
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
STATE: PA

COUNTRY: U.S.A.

ZIP: 19406-0939

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FastSeq, Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/459,135A

FILING DATE: 02-JUN-1995

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/GB/94/00215

FILING DATE: 04-Feb-1994

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Gimmil, Edward R

REGISTRATION NUMBER: 38,891

REFERENCE/DOCKET NUMBER: P30591C2

TELECOMMUNICATION INFORMATION:

TELEPHONE: 610-270-4478

TELEFAX: 610-270-5090

TELEX:

INFORMATION FOR SEQ ID NO: 12:

SEQUENCE CHARACTERISTICS:

LENGTH: 178 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: Protein

US-08-459-135A-12
Query Match 93.3%; Score 111; DB 2; Length 178;
Best Local Similarity 95.2%; Pred. No. 1.1e-09;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KPSYQFGHNSVDPEDPLPK 21
Db 93 KPSYQFGHNSVDPEDPLPK 113

RESULT 9

US-08-495-559-12
Sequence 12, Application US/08495559A
Patent No. 6054572
GENERAL INFORMATION:
APPLICANT: BURHAM, Martin Karl Russel
APPLICANT: CHOPRA, Ian
APPLICANT: CRITCHLEY, Ian Alfred
APPLICANT: KNOWLES, David Justin Charles
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN: MONOCLONAL
TITLE OF INVENTION: ANTIBODY AND THEIR USE IN PREVENTING BACTERIAL ADHESION
FILE REFERENCE: P30591
CURRENT APPLICATION NUMBER: US/08/495,559A
CURRENT FILING DATE: 1995-08-03
EARLIER APPLICATION NUMBER: GB 9302289.5
EARLIER FILING DATE: 1993-02-05
EARLIER APPLICATION NUMBER: GB 9321592.9
EARLIER FILING DATE: 1993-10-20
NUMBER OF SEQ ID NOS: 13
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 12
LENGTH: 178
TYPE: PRT

ORGANISM: Staphylococcus aureus
US-08-495-559-12

Query Match 93.3%; Score 111; DB 3; Length 178;
Best Local Similarity 95.2%; Pred. No. 1.1e-09;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KPSYQFGHNSVDFEEDLPK 21
DB 93 KPSYQFGHNSVDFEEDLPK 113

RESULT 10
US-08-956-171E-5254

Sequence 5254, Application US/08956171E
Patent No. 6593114

GENERAL INFORMATION:

APPLICANT: Charles Kunach

Gill H. Choi

Patrick S. Dillon

Craig A. Rosen

Steven C. Barash

Michael R. Fannon

TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences

NUMBER OF SEQUENCES: 5256

CORRESPONDENCE ADDRESS:

ADDRESSEE: Human Genome Sciences, Inc.

STREET: 9410 Key West Avenue

CITY: Rockville

STATE: Maryland

COUNTRY: USA

ZIP: 20850

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4mb storage

COMPUTER: HP Vectra 486/33

OPERATING SYSTEM: MSDOS version 6.2

SOFTWARE: ASCII Text

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/956,171E

FILING DATE: 20-Oct-1997

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/009,861

FILING DATE: January 5, 1996

APPLICATION NUMBER: 08/781,986

FILING DATE: January 3, 1997

ATTORNEY/AGENT INFORMATION:

NAME: Mark J. Hyman

REGISTRATION NUMBER: 46,789

REFERENCE/DOCKET NUMBER: PB248P1

TELECOMMUNICATION INFORMATION:
TELEPHONE: (240) 314-1224

TELEFAX: (301) 309-8439

INFORMATION FOR SEQ ID NO: 5254:

SEQUENCE CHARACTERISTICS:

LENGTH: 1027 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 5254:

US-08-956-171E-5254

Query Match 93.3%; Score 111; DB 4; Length 1027;
Best Local Similarity 95.2%; Pred. No. 8e-09;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KPSYQFGHNSVDFEEDLPK 21
DB 846 KPSYQFGHNSVDFEEDLPK 866

RESULT 11

US-08-781-986A-5254
Sequence 5254, Application US/08781986A
Patent No. 6737248

GENERAL INFORMATION:

APPLICANT: Charles Kunach

TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences

NUMBER OF SEQUENCES: 5255

CORRESPONDENCE ADDRESS:

ADDRESSEE: Human Genome Sciences, Inc.

STREET: 9410 Key West Avenue

CITY: Rockville

STATE: Maryland

COUNTRY: USA

ZIP: 20850

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4mb storage

COMPUTER: HP Vectra 486/33

OPERATING SYSTEM: MSDOS version 6.2

SOFTWARE: ASCII Text

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/781,986A

FILING DATE:

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Benson, Bob

REGISTRATION NUMBER: 30,446

REFERENCE/DOCKET NUMBER: PB248PP

TELECOMMUNICATION INFORMATION:

TELEPHONE: (301) 309-8504

TELEFAX: (301) 309-8512

INFORMATION FOR SEQ ID NO: 5254:

SEQUENCE CHARACTERISTICS:

LENGTH: 1027 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-781-986A-5254

Query Match 93.3%; Score 111; DB 4; Length 1027;
Best Local Similarity 95.2%; Pred. No. 8e-09;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KPSYQFGHNSVDFEEDLPK 21
DB 846 KPSYQFGHNSVDFEEDLPK 866

RESULT 12

US-09-010-317-14

Sequence 14, Application US/09010317

Patent No. 6685943

GENERAL INFORMATION:

APPLICANT: Hook, Magnus

APPLICANT: Patti, Joseph M.

APPLICANT: House-Pompeo, Karen L.

APPLICANT: Speziale, Pietro

APPLICANT: John, Danny

APPLICANT: McGavin, Martin J.

TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS

NUMBER OF SEQUENCES: 105

CORRESPONDENCE ADDRESS:

ADDRESSEE: Arnold, White & Durkee

STREET: P.O. Box 4433

CITY: Houston

STATE: TX

COUNTRY: USA

ZIP: 77210-4433

COMPUTER READABLE FORM:

```

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/010.317
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-09-010-317-14

Query Match      89.1%; Score 106; DB 4; Length 21;
Best Local Similarity 95.0%; Pred. No. 5.9e-10;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy      2 PSYQFGHNSVDFEEDLPK 21
Db      2 PSYQFGHNSVDFEEDLPK 21

RESULT 13
US-09-010-317-16
Sequence 16, Application US/09010317
Patent No. 6685943
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
APPLICANT: Patti, Joseph M.
APPLICANT: House-Pompeo, Karen L.
APPLICANT: Speziale, Pietro
APPLICANT: Joh, Danny
APPLICANT: McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITION:
NUMBER OF SEQUENCES: 105
CURRENT APPLICATION DATA:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/010.317
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAMK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 105
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-09-010-317-23

Query Match      89.1%; Score 106; DB 4; Length 21;
Best Local Similarity 90.5%; Pred. No. 5.9e-10;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy      1 KPSYQFGHNSVDFEEDLPK 21
Db      1 KPSYQFGHNSVDFEEDLPK 21

RESULT 14
US-09-010-317-23
Sequence 23, Application US/09010317
Patent No. 6685943
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
APPLICANT: Patti, Joseph M.
APPLICANT: House-Pompeo, Karen L.
APPLICANT: Speziale, Pietro
APPLICANT: Joh, Danny
APPLICANT: McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
NUMBER OF SEQUENCES: 105
CURRENT APPLICATION DATA:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/010.317
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAMK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-09-010-317-23

Query Match      89.1%; Score 106; DB 4; Length 21;
Best Local Similarity 90.5%; Pred. No. 5.9e-10;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy      1 KPSYQFGHNSVDFEEDLPK 21
Db      1 KPSYQFGHNSVDFEEDLPK 21
```

```

TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-09-010-317-16

Query Match      89.1%; Score 106; DB 4; Length 21;
Best Local Similarity 90.5%; Pred. No. 5.9e-10;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy      1 KPSYQFGHNSVDFEEDLPK 21
Db      1 KPSYQFGHNSVDFEEDLPK 21

RESULT 14
US-09-010-317-23
Sequence 23, Application US/09010317
Patent No. 6685943
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
APPLICANT: Patti, Joseph M.
APPLICANT: House-Pompeo, Karen L.
APPLICANT: Speziale, Pietro
APPLICANT: Joh, Danny
APPLICANT: McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
NUMBER OF SEQUENCES: 105
CURRENT APPLICATION DATA:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/010.317
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAMK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-09-010-317-23

Query Match      89.1%; Score 106; DB 4; Length 21;
Best Local Similarity 90.5%; Pred. No. 5.9e-10;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy      1 KPSYQFGHNSVDFEEDLPK 21
Db      1 KPSYQFGHNSVDFEEDLPK 21
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Db 1 KPSYQFGHNPVDFEEDTLPK 21

RESULT 15

US-09-010-317-33

/ Sequence 33, Application US/09010317
/ Patent No. 6685943

/ GENERAL INFORMATION:

/ APPLICANT: Hook, Magnus

/ APPLICANT: Patti, Joseph M.

/ APPLICANT: House-Pompeo, Karen L.

/ APPLICANT: Speziale, Pietro

/ APPLICANT: Joh, Danny

/ APPLICANT: McGavin, Martin J.

/ TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS

/ TITLE OF INVENTION: AND METHODS OF USE

/ NUMBER OF SEQUENCES: 105

/ CORRESPONDENCE ADDRESS:

/ ADDRESSEE: Arnold, White & Durkee

/ STREET: P. O. Box 4433

/ CITY: Houston

/ STATE: TX

/ COUNTRY: USA

/ ZIP: 77210-4433

/ COMPUTER READABLE FORM:

/ MEDIUM TYPE: Floppy disk

/ COMPUTER: IBM PC compatible

/ OPERATING SYSTEM: PC-DOS/MS-DOS

/ SOFTWARE: Patentin Release #1.0, Version #1.30

/ CURRENT APPLICATION DATA:

/ APPLICATION NUMBER: US/09/010,317

/ FILING DATE:

/ CLASSIFICATION:

/ PRIOR APPLICATION DATA:

/ APPLICATION NUMBER: US 60/036,139

/ FILING DATE: 21-JAN-1997

/ ATTORNEY/AGENT INFORMATION:

/ NAME: Hibler, David W.

/ REGISTRATION NUMBER: 41, 071

/ REFERENCE/DOCKET NUMBER: TANK:189

/ TELECOMMUNICATION INFORMATION:

/ TELEPHONE: 512-418-3000

/ TELEFAX: 512-474-7577

/ INFORMATION FOR SEQ ID NO: 33:

/ SEQUENCE CHARACTERISTICS:

/ LENGTH: 21 amino acids

/ TYPE: amino acid

/ STRANDEDNESS:

/ TOPOLOGY: linear

US-09-010-317-33

Query Match 89.1%; Score 106; DB 4; Length 21;

Best Local Similarity 95.0%; Pred. No. 5.9e-10;

Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KPSYQFGHNSVDFEEDPLP 20

Db 1 KPSYQFGHNSVDFEEDTLPK 20

Search completed: October 22, 2005, 03:51:14
Job time : 15.9358 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 22, 2005, 10:49:15 ; Search time 59.2367 Seconds
(without alignments)
148.005 Million cell updates/sec

Title: US-10-731-238-30
Perfect score: 119
Sequence: 1 KPSYQFGHNSVDFEDPLPK 21

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1862951 seqs, 417491010 residues

Total number of hits satisfying chosen parameters: 1862951

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

Published Applications_AA:*

- 1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
- 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
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- 11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep:*
- 12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
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- 16: /cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pep:*
- 17: /cgn2_6/ptodata/2/pubpaa/US10E_PUBCOMB.pep:*
- 18: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
- 19: /cgn2_6/ptodata/2/pubpaa/US11A_PUBCOMB.pep:*
- 20: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep:*
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- 22: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	119	100.0	21	18	US-10-731-238-30
2	111	93.3	21	20	US-10-731-238-9
3	111	93.3	37	28	US-11-066-697-1134
4	111	93.3	139	9	US-09-813-820-8
5	111	93.3	1018	9	US-09-815-242-5797
6	111	93.3	1018	9	US-09-815-242-12838
7	111	93.3	1018	17	US-10-470-048B-68
8	111	93.3	1027	15	US-08-781-986A-5254
9	111	93.3	1027	15	US-10-329-62A-5254
10	108	90.8	961	15	US-10-282-122A-43778
11	108	90.8	978	9	US-09-815-242-5456

12	108	90.8	1001	9	US-09-815-242-12686	Sequence 12686, A
13	108	90.8	1038	15	US-10-282-122B-43827	Sequence 43827, A
14	106	89.1	21	18	US-10-731-238-14	Sequence 14, Appl
15	106	89.1	21	18	US-10-731-238-16	Sequence 16, Appl
16	106	89.1	21	18	US-10-731-238-23	Sequence 23, Appl
17	106	89.1	21	18	US-10-731-238-33	Sequence 33, Appl
18	105	88.2	21	18	US-10-731-238-18	Sequence 18, Appl
19	105	88.2	21	18	US-10-731-238-24	Sequence 24, Appl
20	105	88.2	21	18	US-10-731-238-27	Sequence 27, Appl
21	105	88.2	21	18	US-10-731-238-28	Sequence 28, Appl
22	104	87.4	21	18	US-10-731-238-25	Sequence 25, Appl
23	104	87.4	21	18	US-10-731-238-29	Sequence 29, Appl
24	104	87.4	21	18	US-10-731-238-31	Sequence 31, Appl
25	104	87.4	388	8	US-08-901-062-1	Sequence 1, Appl
26	104	87.4	559	8	US-08-781-986A-5251	Sequence 5251, Ap
27	104	87.4	559	15	US-10-329-62A-5251	Sequence 5251, Ap
28	104	87.4	940	17	US-10-470-048B-424	Sequence 424, App
29	104	87.4	948	17	US-10-470-048B-69	Sequence 69, Appl
30	103	86.6	21	18	US-10-731-238-10	Sequence 10, Appl
31	103	86.6	21	18	US-10-731-238-15	Sequence 15, Appl
32	103	86.6	21	18	US-10-731-238-20	Sequence 20, Appl
33	103	86.6	21	18	US-10-731-238-22	Sequence 22, Appl
34	103	86.6	21	18	US-10-731-238-32	Sequence 32, Appl
35	103	86.6	22	18	US-10-731-238-13	Sequence 13, Appl
36	101	84.9	21	18	US-10-731-238-17	Sequence 17, Appl
37	101	84.9	21	18	US-10-731-238-19	Sequence 19, Appl
38	101	84.9	21	18	US-10-731-238-21	Sequence 21, Appl
39	101	84.9	21	18	US-10-731-238-26	Sequence 26, Appl
40	83	69.7	21	18	US-10-731-238-34	Sequence 34, Appl
41	73	61.3	14	18	US-10-731-238-61	Sequence 61, Appl
42	59	49.6	10	18	US-10-731-238-96	Sequence 96, Appl
43	58	48.7	10	18	US-10-731-238-97	Sequence 97, Appl
44	57	47.9	10	18	US-10-731-238-98	Sequence 98, Appl
45	56	47.1	10	18	US-10-731-238-99	Sequence 99, Appl

ALIGNMENTS

RESULT 1
US-10-731-238-30
Sequence 30, Application US/10731238
Publication No. US20050123552A1
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
Patti, Joseph M.
House-Pompeo, Karen L.
Speziale, Pietro
Joh, Danny
McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/731,238
FILING DATE: 10-Dec-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE: 21-Jan-1998
APPLICATION NUMBER: US 60/036,139

FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TANK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 30:
US-10-731-238-30

Query Match 100.0%; Score 119; DB 18; Length 21;
Best Local Similarity 100.0%; Pred. No. 3.2e-11;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KPSYFGGHSVDPEDPLPK 21
Db 1 KPSYFGGHSVDPEDPLPK 21

RESULT 2
US-10-731-238-9
Sequence 9, Application US/10731238
Publication No. US20050123552A1
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
Patti, Joseph M.
House-Pompeo, Karen L.
Speziale, Pietro
Joh, Danny
McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/731,238
FILING DATE: 10-Dec-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE: 21-Jan-1998
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TANK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>

TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 9:
US-10-731-238-9

Query Match 93.3%; Score 111; DB 18; Length 21;
Best Local Similarity 95.2%; Pred. No. 5.5e-10;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KPSYFGGHSVDPEDPLPK 21
Db 1 KPSYFGGHSVDPEDTLPK 21

RESULT 3
US-11-066-697-1134
Sequence 1134, Application US/11066697
Publication No. US20050187159A1
GENERAL INFORMATION:
APPLICANT: Bridon, Dominique P.
APPLICANT: Ezrin, Alan M.
APPLICANT: Milner, Peter G.
APPLICANT: Holmes, Darren L.
APPLICANT: Thibaudau, Karen
TITLE OF INVENTION: PROTECTION OF ENDOGENOUS THERAPEUTIC PEPTIDES FROM
TITLE OF INVENTION: PEPTIDASE ACTIVITY THROUGH CONJUGATION TO BLOOD
FILE REFERENCE: 500862002301
CURRENT APPLICATION NUMBER: US/11/066,697
CURRENT FILING DATE: 2005-02-25
PRIOR APPLICATION NUMBER: 09/657,276
PRIOR FILING DATE: 2000-09-07
PRIOR APPLICATION NUMBER: 60/153,406
PRIOR FILING DATE: 1999-09-10
PRIOR APPLICATION NUMBER: 60/159,783
PRIOR FILING DATE: 1999-10-15
NUMBER OF SEQ ID NOS: 1617
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 1134
LENGTH: 37
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
OTHER INFORMATION: Peptide
US-11-066-697-1134

Query Match 93.3%; Score 111; DB 20; Length 37;
Best Local Similarity 95.2%; Pred. No. 1e-09; 1; Indels 0; Gaps 0;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KPSYFGGHSVDPEDPLPK 21
Db 16 KPSYFGGHSVDPEDTLPK 36

RESULT 4
US-09-813-820-8
Sequence 8, Application US/09813820
Patent No. US20020102262A1
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
Patti, Joseph M.
House-Pompeo, Karen
Sthanam, Narayana
Symeisky, Jindrich
TITLE OF INVENTION: COLLAGEN BINDING PROTEIN COMPOSITIONS
AND METHODS OF USE
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: Texas

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COUNTRY: U.S.
ZIP: 77720
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
  APPLICATION NUMBER: US/09/813,820
  FILING DATE: 22-Mar-2001
  CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
  APPLICATION NUMBER: 08/856,253
  FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
  NAME: Kitchell, Barbara S.
  REGISTRATION NUMBER: 33,928
  REFERENCE/DOCKET NUMBER: TANK:193
TELECOMMUNICATION INFORMATION:
  TELEPHONE: (512) 418-3000
  TELEFAX: (512) 474-7577
INFORMATION FOR SEQ ID NO: 8:
  SEQUENCE CHARACTERISTICS:
    LENGTH: 139 amino acids
    TYPE: amino acid
    STRANDEDNESS: <Unknown>
    TOPOLOGY: linear
  SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-09-813-820-8

Query Match      93.3%; Score 111; DB 9; Length 139;
Best Local Similarity 95.2%; Pred. NO. 4.2e-09;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0

Cy      1 KPSYQFGHNSVDFEEDLPK 21
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Db      107 KPSYQFGHNSVDFEEDLPK 127

RESULT 5
US-09-815-242-5797
Sequence 5797, Application US/09815242
Patent No. US20020061569A1
GENERAL INFORMATION:
  APPLICANT: Haselbeck, Robert
  APPLICANT: Ohlsen, Karl L.
  APPLICANT: Zyskind, Judith W.
  APPLICANT: Wall, Daniel
  APPLICANT: Twawick, John D.
  APPLICANT: Carr, Grant J.
  APPLICANT: Yamamoto, Robert T.
  TITLE OF INVENTION: Identification of Essential Genes in
  FILE REFERENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FastSeq for Windows Version 4.0

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; SEQ ID NO 5797
; LENGTH: 1018
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-09-815-242-5797

Query Match          93.3%; Score 111; DB 9; Length 1018;
Best Local Similarity 95.2%; Pred. No. 3.6e-08;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 KPSTYFGGHNVSVDPEEDTLPK 21
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Db       837 KPSTYFGGHNVSVDPEEDTLPK 857

RESULT 6
US-09-815-242-12838
; Sequence 12838, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haeselbeck, Robert
; APPLICANT: Ohlsen, Karl L.
; APPLICANT: Zyekind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; FILE OF INVENTION: Prokaryotes
; FILE REFERENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 12838
LENGTH: 1018
TYPE: PRT
ORGANISM: Staphylococcus aureus
US-09-815-242-12838

Query Match          93.3%; Score 111; DB 9; Length 1018;
Best Local Similarity 95.2%; Pred. No. 3.6e-08;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 KPSTYFGGHNVSVDPEEDTLPK 21
        |||
Db       837 KPSTYFGGHNVSVDPEEDTLPK 857

RESULT 7
US-10-470-048B-68
; Sequence 68, Application US/10470048B
; Publication No. US20050037444A1
; GENERAL INFORMATION:
; APPLICANT: MEINKE ET AL.
; TITLE OF INVENTION: A METHOD FOR IDENTIFICATION, ISOLATION AND PRODUCTION OF
; FILE OF INVENTION: ANTIGENS TO A SPECIFIC PATHOGEN
; FILE REFERENCE: SONN.0350S
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;; CURRENT APPLICATION NUMBER: US/10/470,048B
;; CURRENT FILING DATE: 2003-07-25
;; NUMBER OF SEQ ID NOS: 603
;; SOFTWARE: PatentIn version 3.1
;; SEQ ID NO 68
;; LENGTH: 1018
;; TYPE: PR
;; ORGANISM: Staphylococcus aureus
US-10-470-048B-68

Query Match 93.3%; Score 111; DB 17; Length 1018;
Best Local Similarity 95.2%; Pred. No. 3.6e-08;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 KPSYQFGHNSVDFEEDLPK 21
Db 837 KPSYQFGHNSVDFEEDLPK 857

RESULT 8
US-08-781-986A-5254
; Sequence 5254, Application US/08781986A
; Publication No. US20030054436A1
; GENERAL INFORMATION:
; APPLICANT: Charles Kunsch
; TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
; NUMBER OF SEQUENCES: 5255
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/781,986A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION NUMBER:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Benson, Bob
; REGISTRATION NUMBER: 30,446
; REFERENCE/DOCKET NUMBER: PB248PP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 5254:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1027 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-781-986A-5254

Query Match 93.3%; Score 111; DB 8; Length 1027;
Best Local Similarity 95.2%; Pred. No. 3.6e-08;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 KPSYQFGHNSVDFEEDLPK 21
Db 846 KPSYQFGHNSVDFEEDLPK 866

RESULT 9
US-10-329-624-5254

;; Sequence 5254, Application US/10329624
;; Publication No. US20040043037A1
;; GENERAL INFORMATION:
;; APPLICANT: Charles Kunsch
;; Gil H. Choi
;; Patrick S. Dillon
;; Craig A. Rosen
;; Steven C. Barash
;; Michael R. Fannon
;; TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
;; NUMBER OF SEQUENCES: 5256
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Human Genome Sciences, Inc.
;; STREET: 9410 Key West Avenue
;; CITY: Rockville
;; STATE: Maryland
;; COUNTRY: USA
;; ZIP: 20850
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
;; COMPUTER: HP Vectra 486/33
;; OPERATING SYSTEM: MSDOS version 6.2
;; SOFTWARE: ASCII Text
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/10/329,624
;; FILING DATE: 27-Dec-2002
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 08/956,171
;; FILING DATE: October 20, 1997
;; APPLICATION NUMBER: 60/009,861
;; FILING DATE: January 5, 1996
;; APPLICATION NUMBER: 08/781,986
;; FILING DATE: January 3, 1997
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Mark J. Hyman
;; REGISTRATION NUMBER: 46,789
;; REFERENCE/DOCKET NUMBER: PB248P1D1
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (240) 314-1224
;; TELEFAX: (301) 309-8439
;; INFORMATION FOR SEQ ID NO: 5254:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 1027 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; SEQUENCE DESCRIPTION: SEQ ID NO: 5254:
US-10-329-624-5254

Query Match 93.3%; Score 111; DB 15; Length 1027;
Best Local Similarity 95.2%; Pred. No. 3.6e-08;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 KPSYQFGHNSVDFEEDLPK 21
Db 846 KPSYQFGHNSVDFEEDLPK 866

RESULT 10
US-10-282-122A-43778
; Sequence 43778, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyckind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant

APPLICANT: Yamamoto, Robert
APPLICANT: Forsyth, R.
APPLICANT: Xu, H.
TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REFERENCE: ELITRA.01A
CURRENT FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/230,335
PRIOR FILING DATE: 2000-09-06
PRIOR APPLICATION NUMBER: 60/230,347
PRIOR FILING DATE: 2000-09-09
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2001-02-09
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 78614
SOFTWARE: PatentIn version 3.1
SEQ ID NO 43778
LENGTH: 961
TYPE: PRT
ORGANISM: Staphylococcus aureus
US-10-282-122A-43778

Query Match 90.8%; Score 108; DB 15; Length 961;
Best Local Similarity 90.5%; Pred. No. 9, 8e-08;
Matches 19; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 KPSYQFGHNSVDFEEDLPK 21
DB 784 KPNYQFGHNSVDFEEDLPK 804

RESULT 11
US-09-815-242-5456
Sequence 5456, Application US/09815242
Patent No. US20020061569A1
GENERAL INFORMATION:
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Karl L.
APPLICANT: Zyskind, Judith W.
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John D.
APPLICANT: Carr, Grant J.
APPLICANT: Yamamoto, Robert T.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in
FILE REFERENCE: ELITRA.01A
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27

PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 5456
LENGTH: 978
TYPE: PRT
ORGANISM: Staphylococcus aureus
US-09-815-242-5456

Query Match 90.8%; Score 108; DB 9; Length 978;
Best Local Similarity 90.5%; Pred. No. 1e-07;
Matches 19; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 KPSYQFGHNSVDFEEDLPK 21
DB 815 KPNYQFGHNSVDFEEDLPK 835

RESULT 12
US-09-815-242-12686
Sequence 12686, Application US/09815242
Patent No. US20020061569A1
GENERAL INFORMATION:
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Karl L.
APPLICANT: Zyskind, Judith W.
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John D.
APPLICANT: Carr, Grant J.
APPLICANT: Yamamoto, Robert T.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in
FILE REFERENCE: ELITRA.01A
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 12686
LENGTH: 1001
TYPE: PRT
ORGANISM: Staphylococcus aureus
US-09-815-242-12686

Query Match 90.8%; Score 108; DB 9; Length 1001;
Best Local Similarity 90.5%; Pred. No. 1e-07;
Matches 19; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 KPSYQFGHNSVDFEEDLPK 21
DB 838 KPNYQFGHNSVDFEEDLPK 858

RESULT 13
US-10-282-122A-43827
Sequence 43827, Application US/10282122A

```
Publication No. US20040029129A1
GENERAL INFORMATION:
APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haebebeck, Robert
APPLICANT: Ohlsen, Kari
APPLICANT: Zykend, Judith
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John
APPLICANT: Carr, Grant
APPLICANT: Yamamoto, Robert
APPLICANT: Forevych, R.
APPLICANT: Xu, H.
TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REFERENCE: ELITRA.034A
CURRENT APPLICATION NUMBER: US/10/282.122A
CURRENT FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/230,335
PRIOR FILING DATE: 2000-09-06
PRIOR APPLICATION NUMBER: 60/230,347
PRIOR FILING DATE: 2000-09-09
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/267,636
PRIOR FILING DATE: 2001-02-09
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 78614
SOFTWARE: PatentIn version 3.1
SEQ ID NO 43827
LENGTH: 1038
TYPE: PRT
ORGANISM: Staphylococcus aureus
US-10-282-122A-43827

Query Match          90.8%; Score 108; DB 15; Length 1038;
Best Local Similarity 90.5%; Pred. No. 1.1e-07;
Matches 19; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1 KPSYQFGGNSVDFEEDPLPK 21
Db      833 KPNYQFGGNSVDFEEDTLPK 853

RESULT 14
US-10-731-238-14
Sequence 14, Application US/10731238
Publication No. US20050123552A1
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
APPLICANT: Patti, Joseph M.
APPLICANT: House-Pompeo, Karen L.
APPLICANT: Speziale, Pietro
APPLICANT: Joh, Danny
APPLICANT: McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESS: Arnold, White & Durkee
STREET: P.O. Box 4433
```

```
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/731.238
FILING DATE: 10-Dec-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/010.317
FILING DATE: 21-Jan-1998
APPLICATION NUMBER: US 60/036.139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
TELECOMMUNICATION INFORMATION:
REFERENCE/DOCKET NUMBER: TMMK.189
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 14:
US-10-731-238-14

Query Match          89.1%; Score 106; DB 18; Length 21;
Best Local Similarity 95.0%; Pred. No. 3.3e-09;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2 PSYQFGGNSVDFEEDPLPK 21
Db      2 PSYQFGGNSVDFEEDTLPK 21

RESULT 15
US-10-731-238-16
Sequence 16, Application US/10731238
Publication No. US20050123552A1
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
APPLICANT: Patti, Joseph M.
APPLICANT: House-Pompeo, Karen L.
APPLICANT: Speziale, Pietro
APPLICANT: Joh, Danny
APPLICANT: McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESS: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/731.238
FILING DATE: 10-Dec-2003
CLASSIFICATION: <Unknown>
```

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE: 21-Jan-1998
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-Jan-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TANK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 16:
US-10-731-238-16

Query Match 89.1%; Score 106; DB 18; Length 21;
Best Local Similarity 90.5%; Pred. No. 3,3e-09;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 KPSYQFGGHSYDFEEDPLPK 21
|||
DB 1 KPSYQFGGHSYDFEEDPLPK 21

Search completed: October 22, 2005, 11:34:43
Job time : 59.2367 secs

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GenCore version 5.1.6
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OM protein - protein search, using SW model

Run on: October 22, 2005, 02:23:36 ; Search time 10.5465 Seconds
(without alignments)
191.586 Million cell updates/sec

Title: US-10-731-238-30
Perfect score: 119
Sequence: 1 KPSYQFGHNSVDFEDPLPK 21

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Length	DB	ID	Description
1	111	93.3	1018	2	A32192	fibronectin-binding
2	108	90.8	961	2	G90053	hypothetical prote
3	108	90.8	1038	2	H90053	hypothetical prote
4	104	87.4	940	2	S19702	fibronectin-binding
5	52.5	44.1	417	2	T34930	probable secreted
6	49	41.2	303	2	B75485	fructokinase - Del
7	49	41.2	474	2	B84357	serine-CRNA synth
8	49	41.2	660	2	T41580	probable dna-bind
9	49	41.2	739	2	T12864	subtilisin homolog
10	48	40.3	567	2	T49942	hypothetical prote
11	47	39.5	205	2	AH2714	lignin degradation
12	47	39.5	205	2	T49496	probable ligase [imp
13	47	39.5	445	2	F90562	hypothetical prote
14	46.5	39.1	757	2	C84120	subtilisin-type pr
15	46	38.7	453	2	H70333	conserved hypotet
16	46	38.7	468	2	T26081	hypothetical prote
17	45.5	38.2	871	2	T49354	hypothetical prote
18	45	37.8	216	2	A39926	hypothetical prote
19	45	37.8	241	1	HRNZPP	phosphoprotein P -
20	45	37.8	347	1	HPMS	haploglobin precu
21	45	37.8	427	1	ZFBG4	gene F protein - p
22	45	37.8	462	1	A39356	3-oxoacyl-lacyl-ca
23	45	37.8	459	2	T10061	3-oxoacyl-lacyl-ca
24	45	37.8	1332	2	A59288	myosin heavy chain
25	44	37.0	433	2	T01405	vesicle-associated
26	44	37.0	582	2	E84721	probable calcium-d
27	44	37.0	616	2	T07611	aconitate hydratase
28	43.5	36.6	439	2	C89890	hypothetical prote
29	43.5	36.6	692	2	T21722	hypothetical prote

30	43.5	36.6	1890	2	T04556	hypothetical prote
31	43	36.1	229	2	S13978	artemin - brine sh
32	43	36.1	288	2	T17395	probable 33.6K pro
33	43	36.1	288	2	A42518	A8r protein - vacc
34	43	36.1	347	2	E87369	transcription regu
35	43	36.1	394	2	T34708	hypothetical prote
36	43	36.1	448	2	E64407	hypothetical prote
37	43	36.1	542	1	S56651	calcium-dependent
38	43	36.1	591	1	S54788	calcium-stimulated
39	43	36.1	739	1	A34873	transcription fact
40	43	36.1	766	1	A47001	transcription fact
41	43	36.1	898	2	T10101	aconitate hydratase
42	43	36.1	1488	2	AH0615	cell division prot
43	43	36.1	2543	2	F69679	polyketide synthase
44	42.5	35.7	1373	2	I37463	acetylserotonin O-
45	42.5	35.3	163	2	H84488	hypothetical prote

ALIGNMENTS

RESULT 1

A32192
fibronectin-binding protein - Staphylococcus aureus
C/Species: Staphylococcus aureus
C/Date: 31-Jul-1989 #sequence_revision 31-Jul-1989 #text_change 16-Feb-1997
C/Accession: A32192
R/Signaes, C.; Rautci, G.; Jonsen, K.; Lindgren, P.E.; Anantharamiah, G.M.; Hoocek, M.
Proc. Natl. Acad. Sci. U.S.A. 86, 699-703, 1989
A>Title: Nucleotide sequence of the gene for a fibronectin-binding protein from Staphyloc
A/Reference number: A32192; MUID:89089898; PMID:2521391
A/Accession: A32192
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-1018 <SIG>
A/Cross-references: GB:J04151
C/Keywords: fibronectin binding

Query Match 93.3%; Score 111; DB 2; Length 1018;
Best Local Similarity 95.2%; Pred. No. 6.1e-09;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KPSYQFGHNSVDFEDPLPK 21
DB 837 KPSYQFGHNSVDFEDPLPK 857

RESULT 2

G90053
hypothetical protein fmbb [imported] - Staphylococcus aureus (strain N315)
C/Species: Staphylococcus aureus
C/Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
R/Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguc
ma, A.; Mizutani-U, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.
C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
A>Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.
A/Reference number: A89758; MUID:21311952; PMID:11418146
A/Accession: G90053
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-961 <KUR>
A/Cross-references: UNIPROT:Q99RD3; GB:BA000018; PID:G13702452; PIDN:BA843593.1; GSPDB:G
A/Experimental source: strain N315
C/Genetics:
A/Genes: fmbb

Query Match 90.8%; Score 108; DB 2; Length 961;
Best Local Similarity 90.5%; Pred. No. 1.7e-08;
Matches 19; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 KPSYQFGHNSVDFEDPLPK 21

Db 784 KPNYFGGHSVDFEEDLPK 804

RESULT 3
H90053
hypothetical protein fnb [imported] - Staphylococcus aureus (strain N315)

C/Species: Staphylococcus aureus
C/Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C/Accession: H90053
R/Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kito, C.; Sekimizu, K.; C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
A/Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.
A/Reference number: A89758; MUID:21311952; PMID:11418146

A/Accession: H90053
A/Status: Preliminary
A/Molecule type: DNA
A/Residues: 1-1038 <NR>
A/Cross-references: UNIPROT:Q99RD2; GB:BA000018; PID:g13702453; FIDN:BAB43594.1; GSPDB:C
A/Experimental source: strain N315
C/Genetics:
A/Gene: fnb

Query Match 90.8%; Score 108; DB 2; Length 1038;
Best Local Similarity 90.5%; Pred. No. 1.8e-08;
Matches 19; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KPSYFGGHSVDFEEDLPK 21
Db 833 KPNYFGGHSVDFEEDLPK 853

RESULT 4
S19702
fibronectin-binding protein B - Staphylococcus aureus

C/Species: Staphylococcus aureus
C/Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
C/Accession: S19702
R/Joensen, K.; Signaes, C.; Mueller, H.P.; Lindberg, M.
Eur. J. Biochem. 202, 1041-1048, 1991
A/Title: Two different genes encode fibronectin binding proteins in Staphylococcus aureus
A/Reference number: S19702; MUID:92111475; PMID:1837266
A/Accession: S19702
A/Status: Preliminary
A/Molecule type: DNA
A/Residues: 1-940 <JOB>
A/Cross-references: UNIPROT:Q53682; EMBL:X62992; NID:g49040; PIDN:CAA44726.1; PID:g58156
C/Keywords: fibronectin binding

Query Match 87.4%; Score 104; DB 2; Length 940;
Best Local Similarity 85.7%; Pred. No. 6.8e-08;
Matches 18; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KPSYFGGHSVDFEEDLPK 21
Db 773 KPNYFGGHSVDFEEDLPK 793

RESULT 5
T34930
Probable secreted protein - Streptomyces coelicolor

C/Species: Streptomyces coelicolor
C/Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 05-Jul-2004
C/Accession: T34930
R/Seeger, K.J.; Harris, D.; Parkhill, J.; Barrrell, B.G.; Rajandream, M.A.
submitted to the EMBL Data Library, June 1998
A/Reference number: Z21562

A/Accession: T34930
A/Status: Preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-417 <SBE>

A/Cross-references: UNIPROT:O69948; EMBL:AL023862; PIDN:CAA19631.1; GSPDB:GN00070; SCODEB
A/Experimental source: strain A3(2)

C/Genetics:
A/Gene: SCODEB:SC3F9.08
C/Superfamily: myo-inositol-1-phosphate synthase

Query Match 44.1%; Score 52.5; DB 2; Length 417;
Best Local Similarity 55.0%; Pred. No. 2.7;
Matches 11; Conservative 3; Mismatches 3; Indels 3; Gaps 1;

Qy 2 PSYFGGHSVDFEEDLPK 21
Db 62 PALVFGGHDIVDC---LPK 78

RESULT 6
B75485
fructokinase - Deinococcus radiodurans (strain R1)

C/Species: Deinococcus radiodurans
C/Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C/Accession: B75485
R/White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.; F.M.; Shen, M.; Vamathevan, J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; Mah
S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999

A/Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
A/Reference number: A75250; MUID:20036896; PMID:10567266

A/Accession: B75485
A/Status: Preliminary
A/Molecule type: DNA
A/Residues: 1-303 <WHI>
A/Cross-references: UNIPROT:Q9RWE1; GB:AE001928; GB:AE000513; NID:g6458421; PIDN:AAF10301
A/Experimental source: strain R1
C/Genetics:
A/Gene: DR0728
A/Map position: 1
C/Superfamily: ribokinase

Query Match 41.2%; Score 49; DB 2; Length 303;
Best Local Similarity 52.9%; Pred. No. 6.7;
Matches 9; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

Qy 2 PSYFGGHSVDFEEDLPK 18
Db 94 PQYRFLGNSADLHFP 110

RESULT 7
B84357
serine-tRNA synthetase [imported] - Halobacterium sp. NRC-1

C/Species: Halobacterium sp. NRC-1
C/Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
C/Accession: B84357
R/Ng, W.V.; Kennedy, S.P.; Mahiras, G.G.; Bergquist, B.; Pan, M.; Shukla, H.D.; Lasky, S.; Leithausen, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocke, D.G.; Jablor
Jung, K.H.; Alam, M.; Freitas, T.
Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000
A/Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ebnhardt, H.; Lowe, T.M.; Lie
A/Title: Genome sequence of Halobacterium species NRC-1.
A/Reference number: A84160; MUID:20504483; PMID:11016950

A/Accession: B84357
A/Status: Preliminary
A/Molecule type: DNA
A/Residues: 1-474 <STO>
A/Cross-references: UNIPROT:Q9HNU8; GB:AE004437; NID:g10581491; PIDN:AAG20222.1; GSPDB:G
C/Genetics:
A/Gene: serS
C/Superfamily: serine-tRNA ligase

Query Match 41.2%; Score 49; DB 2; Length 474;
Best Local Similarity 41.2%; Pred. No. 11;
Matches 7; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

Query Match 39.5%; Score 47; DB 2; Length 205;
Best Local Similarity 66.7%; Pred. No. 8.8;
Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 9 HNSVDFEEDPLP 20
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Db 6 HKGDPERPLP 17

RESULT 13

P90562
hypothetical protein MYPV_4060 [imported] - Mycoplasma pulmonis (strain UAB CTIP)
C/Species: Mycoplasma pulmonis
C/Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 09-Jul-2004
C/Accession: F90562
R/Chamoud, I.; Heilig, R.; Ferris, S.; Barbe, V.; Samson, D.; Gallison, F.; Moszer, I.;
Nucleic Acids Res. 29, 2145-2153, 2001
A/Title: The complete genome sequence of the murine respiratory pathogen Mycoplasma pulm
A/Reference number: A95512; MUID:21267165; PMID:11353084
A/Accession: F90562
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-445 <KUR>
A/Cross-references: UNIPROT:Q98G0; GB:AL445566; PID:g14089820; PIN:CA013579.1; GSPDB:G
A/Experimental source: strain UAB CTIP
C/Genetics:
A/Gene: MYPV_4060
A/Genetic code: GCC3

Query Match 39.5%; Score 47; DB 2; Length 445;
Best Local Similarity 43.8%; Pred. No. 21;
Matches 7; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 1 KPSYQFGHNSVDPEE 16
||:|||||
Db 334 KPDPVAGHNTYEHQE 349

RESULT 14

C84120
subtilisin-type proteinase (EC 3.4.21.-) BH3763 precursor [similarity] - Bacillus halodur
C/Species: Bacillus halodurans
C/Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004
C/Accession: C84120
R/Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masai, N.; Fujii, F.; Hira
Nucleic Acids Res. 28, 4317-4331, 2000
A/Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and
A/Reference number: A83650; MUID:20512582; PMID:11058132
A/Accession: C84120
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-757 <STO>
A/Cross-references: UNIPROT:Q9KGG6; GB:AP001519; GB:BA000004; NID:j10176109; PIN:BA074
A/Experimental source: strain C-125
C/Genetics:
A/Gene: BH3763
C/Superfamily: microbial serine proteinase vpr; subtilisin homolog/
C/Keywords: hydrolase; serine proteinase
F,1-20/Domain: signal sequence #status predicted <SIG>

Query Match 39.1%; Score 46.5; DB 2; Length 757;
Best Local Similarity 47.1%; Pred. No. 45;
Matches 8; Conservative 7; Mismatches 1; Indels 1; Gaps 1;

QY 3 SYQFGHNSVDPEEDPL 19
||:|||||
Db 154 SYK-GGYDFVDYDDPM 169

RESULT 15

H70333
conserved hypothetical protein aq_378 - Aquifex aeolicus
C/Species: Aquifex aeolicus

C/Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 09-Jul-2004
C/Accession: H70333
R/Dekert, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.; Ove
V.

Nature 392, 353-358, 1998
A/Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.
A/Reference number: A70300; MUID:98196666; PMID:9537320

A/Accession: H70333
A/Status: preliminary; nucleic acid sequence not shown; translation not shown
A/Molecule type: DNA
A/Residues: 1-453 <AGF>
A/Cross-references: UNIPROT:O66700; GB:AE000687; NID:g2983050; PIN:AA006670.1; PID:g298:
A/Experimental source: strain VF5
C/Genetics:
A/Gene: aq_378

Query Match 38.7%; Score 46; DB 2; Length 453;
Best Local Similarity 53.8%; Pred. No. 30;
Matches 7; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 3 SYQFGHNSVDPEE 15
||:|||||
Db 114 SYKGSYNTLEFE 126

Search completed: October 22, 2005, 04:13:58
Job time : 11.5465 secs


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FT REPEAT 545 574 B-1.
FT REPEAT 575 604 B-2.
FT DOMAIN 745 878 4 X approximate tandem repeats,
  fibronectin-binding domain.
FT REPEAT 745 782 D-1.
FT REPEAT 783 820 D-2.
FT REPEAT 821 859 D-3.
FT REPEAT 860 878 D-4 (incomplete).
FT DOMAIN 879 948 5 X tandem repeats, Pro-rich (KR).
FT REPEAT 879 892 WR 1.
FT REPEAT 893 906 WR 2.
FT REPEAT 907 920 WR 3.
FT REPEAT 921 934 WR 4.
FT REPEAT 935 948 WR 5.
FT SITE 982 986 LPXTG sorting signal (Potential).
FT MOD_RES 985 985 Pentaglycyl murein peptidoglycan amidated
  chreonine (Potential).
SQ SEQUENCE 1018 AA; 11780 MW; 58175E0020E81F1F CRC64;

Query Match 93.3%; Score 111; DB 1; Length 1018;
Best Local Similarity 95.2%; Pred. No. 1.1e-07;
Matches 20; Conservative 0; Mismatches 1; Indels 3; Gaps 0;

Oy 1 KPSYFGGHSVDFEEDLPK 21
Db 837 KPSYFGGHSVDFEEDLPK 857

RESULT 2
ID Q9GRD3 PRELIMINARY; PRT; 961 AA.
AC Q9GRD3;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Fibronectin-binding protein homolog.
DE Name=fnb3; OrderedLocusNames=SAV2502;
OS Staphylococcus aureus (strain Mu50 / ATCC 700699).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
NCBI_TaxID=158878;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Mu50 / ATCC 700699;
RX MEDLINE=21311952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2;
RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
  Cui L., Oguchi A., Aoki K.-I., Nagai Y., Iano J.-Q., Ito T.,
  Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hoshiyama A.,
  Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
  Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
  Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
  Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
RA "Whole genome sequencing of methicillin-resistant Staphylococcus
  aureus."
RT Lancel 357:1225-1240(2001).
RL -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
  an amide bond (By similarity).
CC EMBL; AP003365; BAB58664.1; -.
CC PIR; G90053; G90053.
DR HSSP; O53653; 1N67.
DR GO; GO:0009986; C:cell surface; IEA.
DR GO; GO:0005618; C:cell wall; IEA.
DR GO; GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:007155; P:cell adhesion; IEA.
DR InterPro; IPR008966; Adhes_bact.
DR InterPro; IPR004237; Fn_bind.
DR InterPro; IPR005877; Gpos_YsIRK.
DR Pfam; PF02986; Fn_bind; 1.
DR Pfam; PF02986; Fn_bind; 1.
DR Pfam; PF00746; Gram_pos_anchor; 1.
DR TIGRfams; TIGR01167; LPXTG_signal; 1.
DR TIGRfams; TIGR01167; LPXTG_signal; 1.
DR TIGRfams; TIGR01168; YsIRK_signal; 1.
DR TIGRfams; TIGR01168; YsIRK_signal; 1.
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DR PROSITE; PSS0847; GRAM_POS_ANCHORING; 1.
KW Cell wall; Complete proteome; Peptidoglycan anchor.
SQ SEQUENCE 961 AA; 106010 MW; 364940F884EA4101 CRC64;

Query Match 90.8%; Score 108; DB 2; Length 961;
Best Local Similarity 90.5%; Pred. No. 2.9e-07;
Matches 19; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Oy 1 KPSYFGGHSVDFEEDLPK 21
Db 784 KPSYFGGHSVDFEEDLPK 804

RESULT 3
ID Q7A3J8 PRELIMINARY; PRT; 961 AA.
AC Q7A3J8;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE FnB3 protein.
DE Name=fnb3; OrderedLocusNames=SA2290;
OS Staphylococcus aureus (strain N315).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
NCBI_TaxID=158879;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21311952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2;
RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
  Cui L., Oguchi A., Aoki K.-I., Nagai Y., Iano J.-Q., Ito T.,
  Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hoshiyama A.,
  Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
  Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
  Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
  Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
RA "Whole genome sequencing of methicillin-resistant Staphylococcus
  aureus."
RT Lancel 357:1225-1240(2001).
RL -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
  an amide bond (By similarity).
CC EMBL; AP003137; BAB3593.1; -.
CC GO; GO:0009986; C:cell surface; IEA.
CC GO; GO:0005618; C:cell wall; IEA.
CC GO; GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
CC GO; GO:0016020; C:membrane; IEA.
CC GO; GO:007155; P:cell adhesion; IEA.
CC InterPro; IPR008966; Adhes_bact.
CC InterPro; IPR004237; Fn_bind.
CC InterPro; IPR005877; Gpos_YsIRK.
CC InterPro; IPR001899; Gram_pos_anchor.
CC Pfam; PF02986; Fn_bind; 1.
CC Pfam; PF02986; Gram_pos_anchor; 1.
CC Pfam; PF00746; Gram_pos_anchor; 1.
CC TIGRfams; TIGR01167; LPXTG_signal; 1.
CC TIGRfams; TIGR01167; LPXTG_signal; 1.
CC TIGRfams; TIGR01168; YsIRK_signal; 1.
CC PROSITE; PSS0847; GRAM_POS_ANCHORING; 1.
KW Cell wall; Complete proteome; Peptidoglycan anchor.
SQ SEQUENCE 961 AA; 106010 MW; 364940F884EA4101 CRC64;

Query Match 90.8%; Score 108; DB 2; Length 961;
Best Local Similarity 90.5%; Pred. No. 2.9e-07;
Matches 19; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Oy 1 KPSYFGGHSVDFEEDLPK 21
Db 784 KPSYFGGHSVDFEEDLPK 804

RESULT 4
ID Q6GDUS PRELIMINARY; PRT; 965 AA.
AC Q6GDUS;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
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DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE Fibronectin-binding protein.
GN Name=fmbA; OrderedLocusNames=SR2580;
OS Staphylococcus aureus (strain MRS4252).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=282458;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=1523324; DOI=10.1073/pnas.0402521101;
RA Holden M.T.G., Fell E.J., Lindsay J.A., Peacock S.J., Day N.P.J.,
RA Enright M.C., Foster T.J., Moore C.E., Hurst L., Atkin R., Barron A.,
RA Bason N., Bentley S.D., Chillingworth C., Chillingworth T.,
RA Churcher C., Clark L., Cotton C., Cronin A., Doggett J., Dowd L.,
RA Felwell T., Hance Z., Harris B., Hauser H., Holroyd S., Jagsle K.,
RA James K.D., Leonard N., Line A., Mayes R., Moulé S., Mungall K.,
RA Ormond D., Quail M.A., Rabinowitch E., Rutherford K.M., Sanders M.,
RA Sharp S., Simmonds M., Stevens K., Whitehead S., Barrett B.G.,
RA Spratt B.G., Parkhill J.;
RT "Complete genomes of two clinical Staphylococcus aureus strains:
RT evidence for the rapid evolution of virulence and drug resistance.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:9786-9791(2004).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC an amide bond (By similarity).
CC EMBL: BX571856; CAC41560.1; -.
DR GO: GO:0009986; C:cell surface; IEA.
DR GO: GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO: GO:0016020; C:membrane; IEA.
DR GO: GO:0007155; P:cell adhesion; IEA.
DR InterPro: IPR008966; Adhes_bact.
DR InterPro: IPR004237; Fn_bind.
DR InterPro: IPR005877; Gpos_YsIRK.
DR InterPro: IPR001899; Gram_pos_anchor.
DR Pfam: PF00746; Gram_pos_anchor; 1.
DR Pfam: PF04650; YsIRK_signal; 1.
DR TIGRfams: TIGR01167; LpXTG_anchor; 1.
DR TIGRfams: TIGR01168; YsIRK_signal; 1.
DR PROSITE: PS00847; GRAM_POS_ANCHORING; 1.
KW Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ SEQUENCE 965 AA; 10561 MW; 2982B132164D0551 CRC64;

Query Match 90.8%; Score 108; DB 2; Length 965;
Best Local Similarity 90.5%; Pred. No. 2,9e-07;
Matches 19; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 KPSTYQFGHNSVDFEEDLPK 21
DB 802 KPSTYQFGHNSVDFEEDLPK 822

RESULT 5
Q6NTU7 PRELIMINARY; PRT; 1015 AA.
ID Q6NTU7;
AC Q6NTU7;
DT 01-OCT-2002 (TREMBlrel. 22, Created)
DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Fmb protein.
GN Name=fmb; OrderedLocusNames=NM2421;
OS Staphylococcus aureus (strain NM2).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=196620;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22040717; PubMed=12044378; DOI=10.1016/S0140-6736(02)08713-5;
RA Baba T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Oguchi A.,
RA Nagai Y., Iwano K., Amano K., Naimi T., Kuroda H., Cui L.,
RA Yamamoto K., Hiramatsu K.;
RT "Genome and virulence determinants of high virulence community-
RT acquired MRSA.";
RL Lancet 359:1819-1827(2002).

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CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC an amide bond (By similarity).
CC EMBL: AP004830; BAB96286.1; -.
DR GO: GO:0009986; C:cell surface; IEA.
DR GO: GO:0005618; C:cell wall; IEA.
DR GO: GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO: GO:0016020; C:membrane; IEA.
DR GO: GO:0007155; P:cell adhesion; IEA.
DR InterPro: IPR008966; Adhes_bact.
DR InterPro: IPR004237; Fn_bind.
DR InterPro: IPR005877; Gpos_YsIRK.
DR InterPro: IPR001899; Gram_pos_anchor.
DR Pfam: PF02986; Fn_bind; 1.
DR Pfam: PF00746; Gram_pos_anchor; 1.
DR TIGRfams: TIGR01167; LpXTG_anchor; 1.
DR TIGRfams: TIGR01168; YsIRK_signal; 1.
DR PROSITE: PS00847; GRAM_POS_ANCHORING; 1.
KW Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ SEQUENCE 1015 AA; 11145 MW; D0F9281BB64D44D2 CRC64;

Query Match 90.8%; Score 108; DB 2; Length 1015;
Best Local Similarity 90.5%; Pred. No. 3,1e-07;
Matches 19; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 KPSTYQFGHNSVDFEEDLPK 21
DB 838 KPSTYQFGHNSVDFEEDLPK 858

RESULT 6
Q6G6H3 PRELIMINARY; PRT; 1015 AA.
ID Q6G6H3;
AC Q6G6H3;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE Fibronectin-binding protein.
GN OrderedLocusNames=MSA2388;
OS Staphylococcus aureus (strain MSA476).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=282459;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=1523334; DOI=10.1073/pnas.0402521101;
RA Holden M.T.G., Fell E.J., Lindsay J.A., Peacock S.J., Day N.P.J.,
RA Enright M.C., Foster T.J., Moore C.E., Hurst L., Atkin R., Barron A.,
RA Bason N., Bentley S.D., Chillingworth C., Chillingworth T.,
RA Churcher C., Clark L., Cotton C., Cronin A., Doggett J., Dowd L.,
RA Felwell T., Hance Z., Harris B., Hauser H., Holroyd S., Jagsle K.,
RA James K.D., Leonard N., Line A., Mayes R., Moulé S., Mungall K.,
RA Ormond D., Quail M.A., Rabinowitch E., Rutherford K.M., Sanders M.,
RA Sharp S., Simmonds M., Stevens K., Whitehead S., Barrett B.G.,
RA Spratt B.G., Parkhill J.;
RT "Complete genomes of two clinical Staphylococcus aureus strains:
RT evidence for the rapid evolution of virulence and drug resistance.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:9786-9791(2004).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC an amide bond (By similarity).
CC EMBL: BX571857; CAC44202.1; -.
DR GO: GO:0009986; C:cell surface; IEA.
DR GO: GO:0005618; C:cell wall; IEA.
DR GO: GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO: GO:0016020; C:membrane; IEA.
DR GO: GO:0007155; P:cell adhesion; IEA.
DR InterPro: IPR008966; Adhes_bact.
DR InterPro: IPR004237; Fn_bind.
DR InterPro: IPR005877; Gpos_YsIRK.
DR InterPro: IPR001899; Gram_pos_anchor.
DR Pfam: PF00746; Gram_pos_anchor; 1.
DR Pfam: PF04650; YsIRK_signal; 1.
DR TIGRfams: TIGR01167; LpXTG_anchor; 1.

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DR TIGRFAMS; TIGR01168; YSIRK signal: 1.
 DR PROSITE; PS50847; GRAM_POS_ANCHORING; 1.
 KW Cell wall; Complete proteome; Peptidoglycan-anchor.
 SQ SEQUENCE 1015 AA; 111145 MW; D0F9281BB64D44D2 CRC64;

Query Match 90.8%; Score 108; DB 2; Length 1015;
 Best Local Similarity 90.5%; Pred. No. 3,1e-07;
 Matches 19; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KPSYQFGGHSVDFEEDLPK 21
 Db 838 KPNYQFGGHSVDFEEDLPK 858

RESULT 7
 Q99RD2 PRELIMINARY; PRT; 1038 AA.
 AC Q99RD2;
 DT 01-JUN-2001 (TIGR01168, 17, Last sequence update)
 DT 01-MAR-2004 (TIGR01168, 26, Last annotation update)
 DE Fibronectin-binding protein homolog.
 GN Name=fnb; OrderedLocustNames=SAV2503;
 OS Staphylococcus aureus (strain Mu50 / ATCC 700699).
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 NX NCBI_TaxID=158879;
 RX MEDLINE=21311952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2;
 RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
 Cui L., Oguchi A., Aoki K.-I., Nagai Y., Iino T.,
 Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hoshiyama A.,
 Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
 Sekimizu K., Hiraoka H., Kuhara S., Goto S., Yabuzaki J.,
 Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
 Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
 RT "Whole genome sequencing of methicillin-resistant Staphylococcus
 aureus.";
 RL Lancet 357:1225-1240(2001).
 CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
 an amide bond (By similarity).
 DR EMBL; AP003137; BAB3594.1; -;
 DR GO; GO:0009986; C:cell surface; IEA.
 DR GO; GO:0005618; C:cell wall; IEA.
 DR GO; GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0007155; P:cell adhesion; IEA.
 DR InterPro; IPR008966; Adhes_bact.
 DR InterPro; IPR004237; Fn_bind.
 DR InterPro; IPR005877; Gpos_YSIRK.
 DR InterPro; IPR001899; Gram_pos_anchor.
 DR Pfam; PF02986; Fn_bind; 1.
 DR Pfam; PF00746; Gram_pos_anchor; 1.
 DR Pfam; PF04650; YSIRK_signal; 1.
 DR TIGRFAMS; TIGR01167; LPXTG_anchor; 1.
 DR TIGRFAMS; TIGR01168; YSIRK_signal; 1.
 DR PROSITE; PS50847; GRAM_POS_ANCHORING; 1.
 KW Cell wall; Complete proteome; Peptidoglycan-anchor.
 SQ SEQUENCE 1038 AA; 113618 MW; 666BF6BF2BFBB12 CRC64;

Query Match 90.8%; Score 108; DB 2; Length 1038;
 Best Local Similarity 90.5%; Pred. No. 3,1e-07;
 Matches 19; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KPSYQFGGHSVDFEEDLPK 21
 Db 833 KPNYQFGGHSVDFEEDLPK 853

RESULT 8
 Q7A3J7

ID Q7A3J7 PRELIMINARY; PRT; 1038 AA.
 AC Q7A3J7;
 DT 05-JUL-2004 (TIGR01168, 27, Last sequence update)
 DT 05-JUL-2004 (TIGR01168, 27, Last annotation update)
 DE Fnb protein.
 GN Name=fnb; OrderedLocustNames=SA2291;
 OS Staphylococcus aureus (strain N315).
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 NX NCBI_TaxID=158879;
 RX MEDLINE=21311952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2;
 RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
 Cui L., Oguchi A., Aoki K.-I., Nagai Y., Iino T.,
 Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hoshiyama A.,
 Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
 Sekimizu K., Hiraoka H., Kuhara S., Goto S., Yabuzaki J.,
 Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
 Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
 RT "Whole genome sequencing of methicillin-resistant Staphylococcus
 aureus.";
 RL Lancet 357:1225-1240(2001).
 CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
 an amide bond (By similarity).
 DR EMBL; AP003137; BAB3594.1; -;
 DR GO; GO:0009986; C:cell surface; IEA.
 DR GO; GO:0005618; C:cell wall; IEA.
 DR GO; GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0007155; P:cell adhesion; IEA.
 DR InterPro; IPR008966; Adhes_bact.
 DR InterPro; IPR004237; Fn_bind.
 DR InterPro; IPR005877; Gpos_YSIRK.
 DR InterPro; IPR001899; Gram_pos_anchor.
 DR Pfam; PF02986; Fn_bind; 1.
 DR Pfam; PF00746; Gram_pos_anchor; 1.
 DR Pfam; PF04650; YSIRK_signal; 1.
 DR TIGRFAMS; TIGR01167; LPXTG_anchor; 1.
 DR TIGRFAMS; TIGR01168; YSIRK_signal; 1.
 DR PROSITE; PS50847; GRAM_POS_ANCHORING; 1.
 KW Cell wall; Complete proteome; Peptidoglycan-anchor.
 SQ SEQUENCE 1038 AA; 113618 MW; 666BF6BF2BFBB12 CRC64;

Query Match 90.8%; Score 108; DB 2; Length 1038;
 Best Local Similarity 90.5%; Pred. No. 3,1e-07;
 Matches 19; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KPSYQFGGHSVDFEEDLPK 21
 Db 833 KPNYQFGGHSVDFEEDLPK 853

RESULT 9
 Q53682 PRELIMINARY; PRT; 940 AA.
 ID Q53682;
 AC Q53682;
 DT 01-NOV-1996 (TIGR01168, 01, Last sequence update)
 DT 01-NOV-1996 (TIGR01168, 01, Last sequence update)
 DT 01-MAR-2004 (TIGR01168, 26, Last annotation update)
 DE Fibronectin binding protein B.
 GN Name=fnbB;
 OS Staphylococcus aureus.
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 NX NCBI_TaxID=1280;
 RX MEDLINE=92111475; PubMed=1837266;
 RA Jonsson K., Sigmas C., Muller H.P., Lindberg M.;
 RT "Two different genes encode fibronectin binding proteins in
 Staphylococcus aureus. The complete nucleotide sequence and
 characterization of the second gene.";

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RL Eur. J. Biochem. 202;1041-1048(1991).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC an amide bond (By similarity).
DR EMBL: X62992; CAA44726.1; -.
DR PIR: S19702; S19702.
DR HSPB; Q53653; 1N67.
DR GO: GO:0009986; C:cell surface; IEA.
DR GO: GO:0005618; C:cell wall; IEA.
DR GO: GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO: GO:0016020; C:membrane; IEA.
DR GO: GO:0007155; P:cell adhesion; IEA.
DR InterPro: IPR008966; Adhes_bact.
DR InterPro: IPR004237; Fn_bind.
DR InterPro: IPR005877; Gpos_YsIRK.
DR Pfam: PF02986; Fn_bind; 2.
DR Pfam: PF00746; Gram_pos_anchor; 1.
DR Pfam: PF04650; YsIRK_signal; 1.
DR TIGRfams: TIGR01167; LpxTG_anchor; 1.
DR TIGRfams: TIGR01168; YsIRK_signal; 1.
DR PROSITE: PS50847; GRAM_POS_ANCHORING; 1.
DR Cell wall; Peptidoglycan-anchor.
SQ SEQUENCE 940 AA, 10355 MW, E35FBBCA907AE345 CRC64;

Query Match 87.4%; Score 104; DB 2; Length 940;
Best Local Similarity 85.7%; Pred. No. 1.1e-06;
Matches 18; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 KPSYOGGCHNSVDFEDLPK 21
DB 773 KPNYOGGCHNSVDFEDTLPQ 793

RESULT 10
Q8NTU8 PRELIMINARY; PRT; 943 AA.
ID Q8NTU8
AC Q8NTU8;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE FndB protein.
GN Name=fndB; OrderedLocustNames=MM2420;
OS Staphylococcus aureus (strain MM2).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_Taxid=196620;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MM2;
RX MEDLINE=22040717; PubMed=12044378; DOI=10.1016/S0140-6736(02)08713-5;
RA Baba T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Oguchi A.,
RA Nagai Y., Iwano K., Asano K., Naito T., Kuroda H., Cui L.,
RA Yamamoto K., Hiramoto K.;
RT "Genome and virulence determinants of high virulence community-
RT acquired MRSA."
RL Lancet 359:1819-1827(2002).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC an amide bond (By similarity).
DR EMBL: AP004830; BAB96285.1; -.
DR HSPB; Q53653; 1N67.
DR GO: GO:0009986; C:cell surface; IEA.
DR GO: GO:0005618; C:cell wall; IEA.
DR GO: GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO: GO:0016020; C:membrane; IEA.
DR GO: GO:0007155; P:cell adhesion; IEA.
DR InterPro: IPR008966; Adhes_bact.
DR InterPro: IPR004237; Fn_bind.
DR InterPro: IPR005877; Gpos_YsIRK.
DR Pfam: PF02986; Fn_bind; 1.
DR Pfam: PF00746; Gram_pos_anchor; 1.
DR TIGRfams: TIGR01167; LpxTG_anchor; 1.
DR TIGRfams: TIGR01168; YsIRK_signal; 1.

```

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DR PROSITE: PS50847; GRAM_POS_ANCHORING; 1.
KW Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ SEQUENCE 943 AA, 104537 MW, DA8A5F31947B1B8A CRC64;

Query Match 87.4%; Score 104; DB 2; Length 943;
Best Local Similarity 85.7%; Pred. No. 1.1e-06;
Matches 18; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 KPSYOGGCHNSVDFEDLPK 21
DB 780 KPNYOGGCHNSVDFEDTLPQ 800

RESULT 11
Q6G6H4 PRELIMINARY; PRT; 957 AA.
ID Q6G6H4
AC Q6G6H4;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Fibronectin-binding protein.
GN Name=fndB; OrderedLocustNames=SAS2387;
OS Staphylococcus aureus (strain MSSA476).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_Taxid=282459;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=15213324; DOI=10.1073/pnas.0402521101;
RA Holden M.T.G., Fell E.J., Lindsay J.A., Peacock S.J., Day N.P.J.,
RA Enright M.C., Foster T.J., Moore C.E., Hurst L., Atkin R., Barron A.,
RA Baason N., Bentley S.D., Chillingworth C., Chillingworth T.,
RA Churcher C., Clark L., Corson C., Cronin A., Doggett J., Dowd L.,
RA Felwell T., Hance Z., Harris B., Hauser H., Holtroyd S., Jagels K.,
RA James K.D., Leonard N., Line A., Mayes R., Moule S., Mungall K.,
RA Ormond D., Quail M.A., Rabinowitch E., Rutherford K.M., Sanders M.,
RA Sharp S., Simmonds M., Stevens K., Whitehead S., Barrell B.G.,
RA Spratt B.G., Parkhill J.;
RT "Complete genomes of two clinical Staphylococcus aureus strains:
RT evidence for the rapid evolution of virulence and drug resistance."
RL Proc. Natl. Acad. Sci. U.S.A. 101:9786-9791(2004).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC an amide bond (By similarity).
DR EMBL: BX571857; CAG44201.1; -.
DR GO: GO:0009986; C:cell surface; IEA.
DR GO: GO:0005618; C:cell wall; IEA.
DR GO: GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO: GO:0016020; C:membrane; IEA.
DR GO: GO:0007155; P:cell adhesion; IEA.
DR InterPro: IPR008966; Adhes_bact.
DR InterPro: IPR004237; Fn_bind.
DR InterPro: IPR005877; Gpos_YsIRK.
DR InterPro: IPR001899; Gram_pos_anchor.
DR Pfam: PF02986; Fn_bind; 1.
DR Pfam: PF00746; Gram_pos_anchor; 1.
DR Pfam: PF04650; YsIRK_signal; 1.
DR TIGRfams: TIGR01167; LpxTG_anchor; 1.
DR TIGRfams: TIGR01168; YsIRK_signal; 1.
DR PROSITE: PS50847; GRAM_POS_ANCHORING; 1.
KW Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ SEQUENCE 957 AA, 105980 MW, 28F8BA7FDFD3EAF CRC64;

Query Match 87.4%; Score 104; DB 2; Length 957;
Best Local Similarity 85.7%; Pred. No. 1.1e-06;
Matches 18; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 KPSYOGGCHNSVDFEDLPK 21
DB 780 KPNYOGGCHNSVDFEDTLPQ 800

RESULT 12
Q9AEP9 PRELIMINARY; PRT; 152 AA.
ID Q9AEP9

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```
AC 09AEP9:
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Fibronectin-binding protein (Fragment).
GN Name=fnb;
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1280;
RN
RP
SEQUENCE FROM N.A.
RC STRAIN=CMRSA-1;
RX MEDLINE=21246681; PubMed=11349044;
RA DOI=10.1128/TAI.69.6.3791-3799.2001;
RA Rice K., Huesca M., Vaz D., McGavin M.J.;
RT "Variation in fibronectin binding and fnb locus polymorphisms in
RT Staphylococcus aureus: identification of antigenic variation in a
RT fibronectin binding protein adhesin of the epidemic CMRSA-1 strain of
RT methicillin-resistant S. aureus."
RL Infect. Immun. 69:3791-3799(2001).
DR EMBL, AY029184; AAK31588.1; -.
FT NON_TER
FT NON_TER
SQ SEQUENCE 152 AA; 17193 MW; CFA3913C2B11C025 CRC64;

Query Match 83.2%; Score 99; DB 2; Length 152;
Best Local Similarity 81.0%; Pred. No. 8.5e-07;
Matches 1; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 KPSYFGGSHNSVDEEDPLPK 21
Db 130 KPSYFGGSHNSVDEEDPLPK 150

RESULT 13
ID 069948 PRELIMINARY; PRT; 417 AA.
AC 069948:
DT 01-AUG-1998 (TrEMBLrel. 07, Created)
DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Putative secreted protein.
OR Names=SC3F9.08;
OS Streptomyces coelicolor.
OC Bacteria; Actinobacteriia; Actinobacteridae; Actinomycetales;
OC Streptomycinae; Streptomycetaceae; Streptomycetes.
OX NCBI_TaxID=1902;
RN [1]
RP
SEQUENCE FROM N.A.
RC STRAIN=A3(2) / M145;
RX MEDLINE=21996410; PubMed=12000953; DOI=10.1038/417141a;
RA Bentley S.D., Chater K.F., Cerdano-Tarraga A.-M., Challis G.L.,
RA Thomson N.R., James K.D., Harris D.B., Quail M.A., Kleiser H.,
RA Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
RA Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
RA Huang C.-H., Kleiser T., Larke L., Murphy L.D., Oliver K., O'Neill S.,
RA Rabinowitsch E., Rajandream M.A., Rutherford K.M., Rutter S.,
RA Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,
RA Warren T., Wietzorrek A., Woodward J.R., Barrett B.G., Parkhill J.,
RA Hopwood D.A.;
RT "Complete genome sequence of the model actinomycete Streptomyces
RT coelicolor A3(2).";
RL Nature 417:141-147(2002).
DR EMBL, AL939128; CAAL9631.1; -.
DR PIR, T34930; T34930.
DR GO; GO:0004512; F:inositol-3-phosphate synthase activity; IEA.
DR GO; GO:0006021; P:myo-inositol biosynthesis; IEA.
DR GO; GO:0008654; P:phospholipid biosynthesis; IEA.
DR InterPro; IPR002587; Inos-1_P_synth.
DR Pfam; PF01658; Inos-1_P_synth; 1.
KW Complete proteome.
SQ SEQUENCE 417 AA; 41769 MW; D38B6872PFA05E4 CRC64;
```

```
Query Match 44.1%; Score 52.5; DB 2; Length 417;
Best Local Similarity 55.0%; Pred. No. 23;
Matches 11; Conservative 3; Mismatches 3; Indels 3; Gaps 1;

Qy 2 PSYQFGGSHNSVDEEDPLPK 21
Db 62 PALVFGGSHNSVDEEDPLPK 78

RESULT 14
ID 06DH47 PRELIMINARY; PRT; 225 AA.
AC 06DH47:
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Zgc:92650.
GN Name=zgc:92650;
OS Brachydanio rerio (zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Osteichthyes; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP
SEQUENCE FROM N.A.
RC TISSUE=Eye;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strauberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Sherman C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diachenko L., Marusik K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Uedin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulik S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Hellon E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smallus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP
SEQUENCE FROM N.A.
RC TISSUE=Eye;
RA Strauberg R.;
RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
CC -1- BC076135; AAH76135.1; -.
DR EMBL, BC076135; AAH76135.1; -.
DR GO; GO:0004871; F:signal transducer activity; IEA.
DR InterPro; IPR000342; RGS.
DR Pfam; PF00615; RGS; 1.
DR PRINTS; PR01301; RGS-PROTEIN.
DR ProDom; PD001580; Reg1_Gproteins; 1.
DR SMART; SM00315; RGS; 1.
DR PROSITE; PS50132; RGS; 1.
SQ SEQUENCE 225 AA; 26016 MW; 1F453E91906DC8AC CRC64;

Query Match 41.2%; Score 49; DB 2; Length 225;
Best Local Similarity 45.0%; Pred. No. 39;
Matches 9; Conservative 1; Mismatches 10; Indels 0; Gaps 0;

Qy 1 KPSYFGGSHNSVDEEDPLPK 20
Db 68 RASTDFKADGDADPDESPKP 87

RESULT 15
```


CC streptococci, e.g. meningitis, otitis media, pneumonia, endocarditis,
 CC mastitis in cattle, abortion in horses and many others. Since the
 CC antibodies block binding of bacteria, they should be effective against
 CC antibiotic-resistant strains, and may replace antibiotic therapy or
 CC increase its effectiveness. Sequences AAW65670-90 represent a series of
 CC synthetic peptides based on the D3 repeat of *S. aureus* fibronectin
 CC binding protein A. They were synthesised to contain a proline residue at
 CC each position through the sequence (ie a proline scan)

XX
 SQ Sequence 21 AA;
 Query Match 100.0%; Score 120; DB 2; Length 21;
 Best Local Similarity 100.0%; Pred. No. 2.6e-11;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KPSYQFGGHSVPFEEDTPK 21
 |||||
 DB 1 KPSYQFGGHSVPFEEDTPK 21

RESULT 2
 AAW65665;
 ID AAW65665 standard; peptide; 21 AA.
 XX
 AC AAW65665;
 XX
 DT 16-OCT-1998 (first entry)
 XX
 DE Fibronectin binding protein-derived peptide #9.
 XX
 KM Microbial surface components recognising adhesive matrix molecule;
 KM MCRAMM; fibronectin; fibronectin-binding protein; antibody; epitope;
 KM antibiotic; bacterial infection; antibiotic-resistant strain
 XX
 OS Synthetic.
 OS *Staphylococcus aureus*.
 XX
 PN W09831389-A2.
 PD 23-JUL-1998.
 PF 21-JAN-1998; 98WO-US001222.
 XX
 PR 21-JAN-1997; 97US-0036139P.
 XX
 PA (TEXA) UNIV TEXAS A & M SYSTEM.
 PI Hoeoek M, Patti JM, House-Pompeo KL, Speziale P, Joh D;
 PI McGavin MJ;
 DR WPI; 1998-413816/35.
 XX
 PT Antibody that binds to fibronectin-binding protein, preventing its
 PT binding to fibronectin - used to treat or prevent bacterial infection,
 PT especially by *Staphylococci* and *Streptococci*.
 PS Example 2; Page 92; 201pp; English.

XX The invention relates to antibodies that bind to a fibronectin-binding
 CC domain of a fibronectin-binding protein, and inhibit binding of the
 CC protein to fibronectin. Also claimed are: (1) isolated peptides of a
 CC fibronectin-binding protein that do not bind to fibronectin; (2) fusion
 CC protein containing at least one peptide of a fibronectin-binding protein
 CC linked to a second amino acid sequence; (3) nucleic acid encoding the
 CC isolated peptide of (1). Antibodies, the isolated peptides of (1) and the
 CC nucleic acids are all useful for immunisation (active or passive) and (by
 CC inhibiting binding of bacteria to fibronectin) for preventing or treating
 CC infection in humans or other animals, particularly by *staphylococci* or
 CC *streptococci*, e.g. meningitis, otitis media, pneumonia, endocarditis,
 CC mastitis in cattle, abortion in horses and many others. Since the
 CC antibodies block binding of bacteria, they should be effective against
 CC antibiotic-resistant strains, and may replace antibiotic therapy or
 CC increase its effectiveness. Sequences AAW65659-68 represent synthetic

CC epitopes from the fibronectin binding domains DU and D1-D4 of the *S.*
 CC *aureus* fnbA gene
 XX
 SQ Sequence 21 AA;
 Query Match 91.7%; Score 110; DB 2; Length 21;
 Best Local Similarity 95.2%; Pred. No. 9.2e-10;
 Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KPSYQFGGHSVPFEEDTPK 21
 |||||
 DB 1 KPSYQFGGHSVPFEEDTPK 21

RESULT 3
 AAR21340
 ID AAR21340 standard; peptide; 22 AA.
 XX
 AC AAR21340;
 XX
 DT 25-MAR-2003 (revised)
 DT 15-JUN-1992 (first entry)
 XX
 DE Fibronectin binding protein.
 DE FNB; wound infection reduction; vaccination; mastitis;
 KM *Staphylococcal* infections; D3.
 KM
 XX Synthetic.
 OS
 PN W09202555-A.
 XX
 PD 20-FEB-1992.
 XX
 PF 10-AUG-1990; 90SE-00002617.
 XX
 PR 10-AUG-1990; 90SE-00002617.
 XX
 PA (ALFA) ALFA LAVAL AGRIC INT AB.
 XX
 PI Hook M, McGavin M, Raucsi G;
 PI WPI; 1992-080035/10.
 DR
 XX
 PT New fibronectin binding peptide - combines with fusion peptide to form
 PT large antigen, used in immunisation, diagnosis and for treating wounds.
 PS Claim 1; Page 22; 33pp; English.

XX The sequence comprises amino acids 17-33 of a tandem repeat, designated
 CC D3 of the fibronectin binding site of *Staphylococcus aureus* 8325-4 FNB.
 CC The N-terminal DK may be replaced with H or K, and the C-terminal LKP may
 CC be replaced by either L, LP, or OH. The peptides were synthesised using
 CC standard methods and purified using reverse phase HPLC. The appropriate
 CC fractions were dialysed and lyophilised. Peptide sequencing was performed
 CC and the peptides digested and chemically modified by dihydroxypropylation
 CC of the amino side chain of lysine. The carboxylic side chains were
 CC converted to glycine methyl esters. The phenyl side chains of tyrosine
 CC residues were oxidised. Chemically modified peptide D3 was compared to
 CC unmodified D3. Lysine and tyrosine modifications only partially
 CC diminished its activity whereas modification of aspartic/glutamic
 CC residues resulted in reduction of activity. The peptide can be used
 CC for the prevention or reduction of the risk of wound infection. The
 CC peptide can be used to create a large antigen for vaccinating ruminants
 CC against mastitis caused by *Staphylococcal* infections. It can also be used
 CC to diagnose *Staphylococcal* infections using ELISA or DNA probes. (Updated
 CC on 25-MAR-2003 to correct PA field.)

XX
 SQ Sequence 22 AA;
 Query Match 91.7%; Score 110; DB 2; Length 22;
 Best Local Similarity 95.2%; Pred. No. 9.7e-10;
 Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KPSYQFGHNSVDFEEDTPK 21
 |||||
 Db 2 KPSYQFGHNSVDFEEDTLPK 22

RESULT 4
 ID AAB91958 standard; peptide; 37 AA.
 XX AAB91958;

AC AAB91958;
 DT 22-JUN-2001 (first entry)

DE Fibrinectin fragment and fibrin related peptide SEQ ID NO:1134.

XX Protection; endogenous therapeutic peptide; peptidase; conjugation;
 KM blood component; modification; succinimidy; maleimido group; amino;
 KW hydroxyl; thiol; hormone; growth factor; neurotransmitter.

XX Homo sapiens.
 OS Synthetic.

XX MO200069900-A2.

XX 23-NOV-2000.

PF 17-MAY-2000; 2000MO-US013576.

PR 17-MAY-1999; 99US-0134406P.

PR 10-SEP-1999; 99US-0153406P.

PR 15-OCT-1999; 99US-0159783P.

XX (CONJ-) CONJUCHEM INC.

PI Bridon DP, Ezrin AM, Milner PG, Holmes DL, Thibaudau K;

DR WPI; 2001-112059/12.

PT Modifying and attaching therapeutic peptides to albumin prevents
 PT peptidase degradation, useful for increasing length of in vivo activity.

PS Disclosure; Page 566; 733pp; English.

XX The present invention describes a modified therapeutic peptide (I)
 CC comprising a therapeutically active amino acid region (III) and a
 CC reactive group (II) (e.g. succinimidy) and maleimido groups) attached to
 CC a less therapeutically active amino acid region (IV), which covalently
 CC bonds with amino/hydroxyl/thiol groups on blood components to form a
 CC peptidease stabilised therapeutic peptide composed of 3-50 amino acids.
 CC (I) are useful for modifying therapeutic peptides e.g. hormones, growth
 CC factors and neurotransmitters, to protect them from peptidase activity in
 CC vivo for the treatment of various disorders. Endogenous therapeutic
 CC peptides are not suitable as drug candidates as they require frequent
 CC administration due to rapid degradation by peptidases in the body.
 CC Modifying and attaching therapeutic peptides to albumin prevents or
 CC reduces the action of peptidases to increase length of activity (half
 CC life) and specificity as bonding to large molecules decreases
 CC intracellular uptake and interference with physiological processes.
 CC AAB90829 to AAB92441 represent peptides which can be used in the
 CC exemplification of the present invention

XX Sequence 37 AA;

Query Match 91.7%; Score 110; DB 4; Length 37;

Best Local Similarity 95.2%; Pred. No. 1.7e-09;

Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KPSYQFGHNSVDFEEDTPK 21
 |||||
 Db 16 KPSYQFGHNSVDFEEDTLPK 36

RESULT 5
 ID AAB90662 standard; protein; 38 AA.
 XX AAB90662;

AC AAB90662;

DT 25-MAR-2003 (revised)

DT 07-OCT-1990 (first entry)

DE Protein with fibronectin binding ability.

XX Hybrid DNA molecule; fibronectin binding; mastitis; ruminants;
 KW wound infection.

XX Staphylococcus aureus.

OS EP294349-A.

PN 07-DEC-1988.

XX 30-MAY-1988; 88EP-00850188.

XX 01-JUN-1987; 87SE-00002272.

XX (ALFA) ALFA LAVAL AGRIC INT AB.

PI Lindberg MK, Signas LC, Wadstrom TM, Froman G;

DR WPI; 1988-347978/49.

DR N-PSDB; AAN81099.

PT Hybrid DNA encoding Staphylococcus aureus fibronectin binding protein -
 PT useful for immunisation and topical application to prevent staphylococcal
 PT infections.

PS Claim 11; Page 12; 23pp; English.

XX The peptide has fibronectin binding ability. It is useful for immunising
 CC ruminants against staphylococcal mastitis, pref. when used at 0.5-5
 CC micrograms/kg, using 3 doses given at 1-3 week intervals; for topical
 CC application to prevent wound infection, using an isotonic saline soln. of
 CC concn. 25-250 micrograms/ml; and, when immobilised on a carrier, for
 CC diagnosing staphylococcal infections. (updated on 25-MAR-2003 to correct
 CC PF field.) (updated on 25-MAR-2003 to correct PA field.)

XX Sequence 38 AA;

Query Match 91.7%; Score 110; DB 1; Length 38;

Best Local Similarity 95.2%; Pred. No. 1.7e-09;

Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KPSYQFGHNSVDFEEDTPK 21
 |||||
 Db 17 KPSYQFGHNSVDFEEDTLPK 37

RESULT 6

ID AAY29087 standard; protein; 134 AA.

AC AAY29087;

DT 28-SEP-1999 (first entry)

DE S. aureus fibronectin binding protein A (FnBA) binding domain.

XX Bovine herpes virus-2; BHV-2; cytokine; immune response; immunogen; IL;

XX interleukin; colony stimulating factor; CSF; interferon; IFN; TNF;

XX tumour necrosis factor; recombinant virus; vaccine; mucosal disease;

XX mastitis; breast cancer; stress-induced disease; binding domain; FnBA;

XX fibronectin binding protein.

OS Staphylococcus aureus.

```
XX  NO9316892-A1.
XX
XX  08-APR-1999.
XX
XX  29-SEP-1998; 98MO-GB002927.
XX
XX  29-SEP-1997; 97GB-00020633.
XX
XX  (UYBR-) UNIV BRISTOL.
XX
XX  Bradley AJ, Duffas WPJ,
XX
XX  WPI; 1999-255101/21.
XX
XX  N-PSDB; AAK91504.
XX
XX  New bovine herpes virus-2 vectors.
XX
XX  Example 2; Fig 8A-B; 130pp; English.
XX
XX  The invention provides bovine herpes virus-2 (BHV-2) based vectors that
XX  comprise at least one cytokine-encoding DNA sequence. The expression of
XX  cytokines in mammals can up-regulate immune responses to the immunogens.
XX  The cytokine is selected from interleukins (IL), colony stimulating
XX  factors (CSF), interferons (IFN) and tumour necrosis factors (TNF). The
XX  BHV-2 based vector or recombinant virus can be used as vaccine. They can
XX  be used for preventing or treating a mucosal disease in a subject, e.g.
XX  ruminants, cattle, sheep, goats, dogs, cats, horses, or man, particularly
XX  mastitis in cows or breast cancers in humans. They can also be used for
XX  preventing or treating a stress-induced disease. The present sequence
XX  represents the binding domain of a previously published S. aureus
XX  fibronectin binding protein A (FnBA) sequence. The FnB binding domain
XX  gene sequence FnBAB, cloned for use in this invention has 97.1 percent
XX  identity when compared to the previously published FnBA and FnBB gene
XX  sequences
XX
XX  Sequence 134 AA:
XX
XX  Query Match 91.7%; Score 110; DB 2; Length 134;
XX  Best Local Similarity 95.2%; Pred. No. 6.6e-09;
XX  Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX  1 KPSYQFGHNSVDPEDTLPK 21
XX  93 KPSYQFGHNSVDPEDTLPK 113
XX
XX  RESULT 7
XX  AAM31556
XX  ID AAM31556 standard; protein; 139 AA.
XX
XX  AAM31556;
XX
XX  27-AUG-2003 (revised)
XX  25-MAR-2003 (revised)
XX  21-MAY-1998 (first entry)
XX
XX  Fibronectin-binding MSCRAMM derivative POD.
XX
XX  Fibronectin; POD; collagen binding protein; sepsis; infection;
XX  microbial surface component recognising adhesive matrix molecule; MSCRAMM;
XX  adhesin; vaccine; immunisation; diagnosis; therapy; mastitis.
XX
XX  Staphylococcus aureus.
XX
XX  Key Location/Qualifiers
XX  Peptide 1..12
XX  /note= "vector pQE30-derived peptide"
XX
XX  MO9743314-A2.
XX
XX  20-NOV-1997.
XX
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PF  14-MAY-1997; 97MO-US008210.
XX
XX  16-MAY-1996; 96US-0017678P.
XX
XX  (TEXA ) UNIV TEXAS A & M SYSTEM.
XX
XX  (UABR-) UAB RES FOUND.
XX
XX  Hoeoek M, Patci JM, House-Pompeo K, Stahanam N, Symersky J;
XX
XX  WPI; 1998-008801/01.
XX
XX  Antibody that interacts with collagen binding domain of Staphylococcal
XX  cna gene product - useful to prevent bacterial sepsis in animal infected
XX  with Staphylococcus aureus -
XX
XX  Disclosure; Page 91; 143pp; English.
XX
XX  This protein comprises Staphylococcus aureus fibronectin-binding
XX  microbial surface component recognising adhesive matrix molecule (MSCRAMM)
XX  derivative POD, plus a vector-derived N-terminal peptide. The invention
XX  relates to claimed nucleic acid sequences (see AAT93436-38) encoding S.
XX  aureus collagen binding protein (CBP) epitopes M17, M31 and M55 (see
XX  AAM31552-54) that confer protection against S. aureus infection. CBP
XX  protein and antigenic epitopes are contemplated for use in the treatment
XX  of pathological infections, especially to prevent bacterial adhesion to
XX  collagen. The epitopes are also contemplated for use in the preparation
XX  of vaccines and as carrier proteins in vaccine formulations, as well as
XX  in the formulation of compositions for the prevention of S. aureus
XX  infection. PCR33 and POD (see AAM31556) were used to raise anti-MSCRAMM
XX  polyclonal antibodies used in passive immunisation against bovine
XX  mastitis. (Updated on 25-MAR-2003 to correct PI field.) (Updated on 27-
XX  AUG-2003 to correct OS field.)
XX
XX  Sequence 139 AA:
XX
XX  Query Match 91.7%; Score 110; DB 2; Length 139;
XX  Best Local Similarity 95.2%; Pred. No. 6.6e-09;
XX  Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX  1 KPSYQFGHNSVDPEDTLPK 21
XX  107 KPSYQFGHNSVDPEDTLPK 127
XX
XX  RESULT 8
XX  AAP82115
XX  ID AAP82115 standard; protein; 1018 AA.
XX
XX  AAP82115;
XX
XX  25-MAR-2003 (revised)
XX  05-JAN-1990 (first entry)
XX
XX  Fibronectin binding protein.
XX
XX  Fibronectin binding protein; S. aureus; immunisation; mastitis; ruminants;
XX  wound infection; diagnosis.
XX
XX  Staphylococcus aureus.
XX
XX  EP294349-A.
XX
XX  07-DEC-1988.
XX
XX  30-MAY-1988; 88EP-00850188.
XX
XX  01-JUN-1987; 87SB-00002272.
XX
XX  (ALFA ) ALFA LAVAL AGRIC INT AB.
XX
XX  Lindberg MK, Signas LC, Wadstrom TM, Froman G;
XX
XX  WPI; 1988-347978/49.
XX
```


CC coli, *Staphylococcus aureus*, *Salmonella typhi*, *Klebsiella pneumoniae*,
CC *Pseudomonas aeruginosa* and *Enterococcus faecalis*. The invention is also
CC useful for the identification of potential new targets for antibiotic
CC development. The antisense nucleic acids can also be used to identify
CC proteins used in proliferation, to express these proteins, and to obtain
CC antibodies capable of binding to the expressed proteins. The proteins can
CC be used to screen compounds in rational drug discovery programmes. The
CC antisense nucleic acid sequence is also useful to screen for homologous
CC nucleic acids which are required for cell proliferation in a wide variety
CC of organisms. The present sequence represents an essential prokaryotic
CC cellular proliferation protein. Note: The sequence data for this patent
CC did not form part of the printed specification, but was obtained in
CC electronic format directly from WIPO at
CC [ftp.wipo.int/pub/published_pct_sequences](http://wipo.int/pub/published_pct_sequences)
CC
SQ Sequence 1018 AA;
Query Match 91.7%; Score 110; DB 4; Length 1018;
Best Local Similarity 95.2%; Pred. No. 5.6e-08;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 KPSYQFGGHSVDFEEDTPK 21
Db 837 KPSYQFGGHSVDFEEDTPK 857
RESULT 11
ABJ18922 ID ABJ18922 standard; protein: 1018 AA.
XX
AC ABJ18922;
DT 06-MAR-2003 (first entry)
XX
DE Pathogen specific antigen related staphylococcal protein SEQ ID No 68.
XX
XX Antibacterial; virucide; fungicide; protozoacide; cytostatic; anti-HIV;
KW hyperimmune; serum-reactive; antigen; pathogen; tumour; allergen;
KW auto-immunity; vaccine; staphylococcal infection; antibody; cancer;
KW autoimmune disease; HIV; hepatitis.
XX
OS *Staphylococcus* sp.
XX
PN WO200259148-A2.
PD 01-AUG-2002.
PF 21-JAN-2002; 2002WO-EP000546.
PR 26-JAN-2001; 2001AT-00000130.
PA (CIST-) CISTEM BIOTECHNOLOGIES GMBH.
PI Mejnke A, Nagy E, Von Ahnen U, Klade C, Henics T, Zauner W;
PI Muth DB, Vycvyscka O, Etz H, Dryla A, Weichart T, Hafner M;
PI Tempelmeier B;
XX
DR WPI; 2003-075410/07.
XX
PT Identifying, isolating and producing hyperimmune serum-reactive antigens
PT from a pathogen, for preparing vaccine or medicament for treating or
PT preventing e.g. staphylococcal infections, comprises providing antibody
PT preparation.
XX
PS Example 7; Page 157; 252pp; English.
XX
CC The invention relates to a novel method for identifying, isolating and
CC producing hyperimmune serum-reactive antigens from a pathogen, tumour,
CC allergen, a tissue or host prone to auto-immunity, where the antigens are
CC used in a vaccine, comprises providing antibody preparation from a plasma
CC pool of a type of animal, or individual sera with antibodies against the
CC specific pathogen, tumour, allergen, tissue or host prone to auto-
CC immunity. The hyperimmune serum-reactive antigens comprising any of the

CC 62 sequences of 53-2261 amino acids fully defined in the specification,
CC or their hyperimmune fragments are useful for the manufacture of a
CC pharmaceutical preparation, particularly a vaccine against staphylococcal
CC infections or colonisation against *S. aureus* or *S. epidermidis*. The
CC preparation of antibodies is useful for the manufacture of a medicament
CC for treating or preventing staphylococcal infections or colonisation
CC against *S. aureus* or *S. epidermidis*. The antibody preparations may also
CC be used for diagnostic and imaging purposes. Other conditions that can be
CC treated include cancer, autoimmune diseases or infections caused by viral
CC (e.g. HIV, hepatitis A, B or C), fungal or protozoan pathogens. This
CC sequence represents a staphylococcal protein relating to the method for
CC identifying and producing pathogen specific antigens of the invention
CC
SQ Sequence 1018 AA;
Query Match 91.7%; Score 110; DB 6; Length 1018;
Best Local Similarity 95.2%; Pred. No. 5.6e-08;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 KPSYQFGGHSVDFEEDTPK 21
Db 837 KPSYQFGGHSVDFEEDTPK 857
RESULT 12
ABM72537 ID ABM72537 standard; protein: 1018 AA.
XX
AC ABM72537;
DT 20-NOV-2003 (first entry)
XX
DE *Staphylococcus aureus* protein #1777.
XX
KW Antibacterial; vaccine; gene therapy; infection; sepsis; diagnosis;
KW enzymatic assay; antibiotic target.
XX
OS *Staphylococcus aureus*.
XX
PN WO200294868-A2.
PD 28-NOV-2002.
PF 27-MAR-2002; 2002WO-IB002637.
PR 27-MAR-2001; 2001GB-00007661.
PA (CHIR-) CHIRON SPA.
PI Masignani V, Mora M, Scarselli M;
PI N-PSDB; ACF74097.
XX
DR WPI; 2003-120786/11.
DR N-PSDB; ACF74097.
XX
PT New *Staphylococcus aureus* protein, useful as a vaccine for treating or
PT preventing *Staphylococcal* infection, specifically an infection caused by
PT *S. aureus*, e.g. sepsis.
XX
PS Claim 1; SEQ ID NO 3554; 49pp; English.
XX
CC The invention relates to novel genes and encoded proteins from
CC *Staphylococcus aureus*. A composition comprising the *S. aureus* protein, a
CC nucleic acid encoding the protein, or an antibody to the protein, is
CC useful as a pharmaceutical, particularly as a vaccine for treating or
CC preventing infection due to *Staphylococcus* bacteria, specifically an
CC infection caused by *S. aureus*. The composition is particularly useful for
CC treating or preventing sepsis in a patient. The composition can also be
CC used for diagnostics. The protein is also used in an assay for enzymatic
CC studies and as a target for antibiotics. This sequence represents one of
CC the novel *S. aureus* proteins of the invention
XX
SQ Sequence 1018 AA;

Query Match 91.7%; Score 110; DB 6; Length 1018;
 Best Local Similarity 95.2%; Pred. No. 5.6e-08;
 Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 KPSYQFGHNSVDFEEDTPK 21
 DB 837 KPSYQFGHNSVDFEEDTPK 857

RESULT 13

AAW89806
 ID AAW89806 standard; protein; 1027 AA.

AAW89806;

16-MAR-1999 (first entry)

Staphylococcus aureus protein SEQ ID #5254.

Computer readable medium; vaccine; S. aureus infection; immunodetection;
 cellulitis; eyelid infection; food poisoning; osteomyelitis; therapy;
 skin infection; surgical wound infection; scalded skin syndrome;
 toxic shock syndrome.

Staphylococcus aureus.

EP786519-A2.

30-JUL-1997.

07-JAN-1997; 97EP-00100117.

05-JAN-1996; 96US-0009861P.

(HUMA-) HUMAN GENOME SCI INC.

Kunesh CA, Choi GH, Barash SC, Dillon PJ, Fannon MR, Rosen CA;

WPI; 1997-374922/35.

Polynucleotide(s) and proteins derived from Staphylococcus aureus -
 stored on computer readable medium and used in the production of anti-
 S. aureus vaccines.

Claim 23; Page 3263-3267; 3271pp; English.

This sequence represents a Staphylococcus aureus protein sequence of the
 invention. The DNA sequences encoding the S. aureus proteins are recorded
 on a computer readable medium, preferably selected from a floppy or hard
 disk, random access memory (RAM), read-only memory (ROM) or CD-ROM.
 Homology searches using the S. aureus DNA sequences allows putative
 functions to be assigned so that protein-encoding or regulatory regions
 of commercial, therapeutic or industrial importance can be obtained.
 Specifically, sequences which are likely to encode antigens have been
 identified and these polypeptides can be used in a vaccine composition
 against S. aureus infection. The polypeptides can also be used in a kit
 for the immunodetection of S. aureus in a sample. S. aureus is implicated
 in numerous human diseases, including cellulitis, eyelid infections, food
 poisoning, osteomyelitis, skin and surgical wound infections, scalded
 skin syndrome, toxic shock syndrome, etc. Organisms transformed with the
 DNA sequences can be used for recombinant production of the polypeptides.
 The new DNA sequences (and their fragments) are useful as primers or
 probes for isolating homologues of any of the 5191 S. aureus DNA sequences
 contained on the computer readable medium

Sequence 1027 AA;

Query Match 91.7%; Score 110; DB 2; Length 1027;

Best Local Similarity 95.2%; Pred. No. 5.7e-08;
 Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 KPSYQFGHNSVDFEEDTPK 21
 |||||

DB 846 KPSYQFGHNSVDFEEDTPK 866

RESULT 14

ABU15854
 ID ABU15854 standard; protein; 961 AA.

ABU15854;

19-JUN-2003 (first entry)

Protein encoded by Prokaryotic essential gene #1381.

Antisense; prokaryotic essential gene; cell proliferation; drug design.

Staphylococcus aureus.

WO20027183-A2.

03-OCT-2002.

21-MAR-2002; 2002WO-US009107.

21-MAR-2001; 2001US-00815242.

06-SEP-2001; 2001US-00948993.

25-OCT-2001; 2001US-0342922P.

08-FEB-2002; 2002US-00072851.

06-MAR-2002; 2002US-0362699P.

(ELIT-) ELITRA PHARM INC.

Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zykkind JW;

Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;

WPI; 2003-029926/02.

N-PSDB; ACA19724.

New antisense nucleic acids, useful for identifying proteins or screening
 for homologous nucleic acids required for cellular proliferation to
 isolate candidate molecules for rational drug discovery programs.

Claim 25; SEQ ID NO 43778; 1766pp; English.

The invention relates to an isolated nucleic acid comprising any one of
 the 623 antisense sequences given in the specification where expression
 of the nucleic acid inhibits proliferation of a cell. Also included are:
 (1) a vector comprising a promoter operably linked to the nucleic acid
 encoding a polypeptide whose expression is inhibited by the antisense
 nucleic acid; (2) a host cell containing the vector; (3) an isolated
 polypeptide or its fragment whose expression is inhibited by the
 antisense nucleic acid; (4) an antibody capable of specifically binding
 the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular
 proliferation or the activity of a gene in an operon required for
 proliferation; (7) identifying a compound that influences the activity of
 the gene product or that has an activity against a biological pathway
 required for proliferation, or that inhibits cellular proliferation; (8)
 identifying a gene required for cellular proliferation or the biological
 pathway in which a proliferation-regulated gene or its gene product lies
 or a gene on which the test compound that inhibits proliferation of an
 organism acts; (9) manufacturing an antibiotic; (10) profiling a
 compound's activity; (11) a culture comprising strains in which the gene
 product is overexpressed or underexpressed; (12) determining the extent
 to which each of the strains is present in a culture or collection of
 strains; or (13) identifying the target of a compound that inhibits the
 proliferation of an organism. The antisense nucleic acids are useful for
 identifying proteins or screening for homologous nucleic acids required
 for cellular proliferation to isolate candidate molecules for rational
 drug discovery programs, or for screening homologous nucleic acids
 required for proliferation in cells other than S. aureus, S. typhimurium,
 K. pneumoniae or P. aeruginosa. The present sequence is encoded by one of
 the target prokaryotic essential genes. Note: The sequence data for this
 patent did not form part of the printed specification, but was obtained
 in electronic format directly from WIPO at

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CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 961 AA;
Query Match
Best Local Similarity 89.2%; Score 107; DB 6; Length 961;
Matches 19; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 KPSYQFGGHSVDPEDTTPK 21
DB 784 KPNYQFGGHSVDPEDTLPK 804

RESULT 15
AAU33960
ID AAU33960 standard; protein; 978 AA.
XX
AC AAU33960;
XX
DT 14-FEB-2002 (first entry)
XX
DE Staphylococcus aureus cellular proliferation protein #236.
XX
KM Antisense; prokaryotic cellular proliferation protein; antibiotic;
XX antibacterial; drug design.
XX
OS Staphylococcus aureus.
XX
MO200170955-A2.
XX
PN 27-SEP-2001.
XX
PD 27-SEP-2001.
XX
PE 21-MAR-2001; 2001WO-US009180.
XX
PR 21-MAR-2000; 2000US-0191078P.
XX PR 23-MAY-2000; 2000US-0206848P.
XX PR 26-MAY-2000; 2000US-0207727P.
XX PR 23-OCT-2000; 2000US-0242578P.
XX PR 27-NOV-2000; 2000US-0253625P.
XX PR 22-DEC-2000; 2000US-0257931P.
XX PR 16-FEB-2001; 2001US-0269308P.
XX
XX (ELIT-) ELITRA PHARM INC.
XX
PI Haaslbeck R, Ohlsen KU, Zyckind JW, Wall D, Trawick JD, Carr GJ;
PI Yamamoto RT, Xu HH;
XX
XX WPI; 2001-611495/70.
XX
DR N-PSDB; AAS51819.
XX
XX
XX New polynucleotides for the identification and development of
PT antibiotics, comprise sequences of antisense nucleic acids.
XX
XX Example 3; SEQ ID NO 5456; 511p; English.
XX
XX The invention relates to antisense inhibitors of genes essential to
CC prokaryotic cellular proliferation, their use in identifying the genes,
CC their use in the discovery of novel antibiotics, the essential genes
CC themselves and the encoded proteins. The prokaryotes used are Escherichia
CC coli, Staphylococcus aureus, Salmonella typhi, Klebsiella pneumoniae,
CC Pseudomonas aeruginosa and Enterococcus faecalis. The invention is also
CC useful for the identification of potential new targets for antibiotic
CC development. The antisense nucleic acids can also be used to identify
CC proteins used in proliferation, to express these proteins, and to obtain
CC antibodies capable of binding to the expressed proteins. The proteins can
CC be used to screen compounds in rational drug discovery programmes. The
CC antisense nucleic acid sequence is also useful to screen for homologous
CC nucleic acids which are required for cell proliferation in a wide variety
CC of organisms. The present sequence represents an essential prokaryotic
CC cellular proliferation protein. Note: The sequence data for this patent
CC did not form part of the printed specification, but was obtained in
CC electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
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XX
SQ Sequence 978 AA;
Query Match
Best Local Similarity 89.2%; Score 107; DB 4; Length 978;
Matches 19; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 KPSYQFGGHSVDPEDTTPK 21
DB 815 KPNYQFGGHSVDPEDTLPK 835

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Job time : 59.1473 secs
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 22, 2005, 02:23:36 / Search time 15.9358 seconds
(without alignments)
98.371 Million cell updates/sec

Title: US-10-731-238-31
Perfect score: 120
Sequence: 1 KPSYQFGHNSVDFEEDTPPK 21

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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4: /cgn2_6/prodata/1/1aa/6B_COMB.pep:*
5: /cgn2_6/prodata/1/1aa/ECTUS_COMB.pep:*
6: /cgn2_6/prodata/1/1aa/backfilest1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	120	100.0	21	4	US-09-010-317-31
2	110	91.7	21	4	US-09-010-317-9
3	110	91.7	37	1	US-08-234-622A-4
4	110	91.7	38	1	US-08-294-189-8
5	110	91.7	38	1	US-08-729-767-5
6	110	91.7	114	1	US-08-259-000-3
7	110	91.7	139	3	US-08-856-253-8
8	110	91.7	178	3	US-08-459-135A-12
9	110	91.7	178	3	US-08-495-559-12
10	110	91.7	1027	4	US-08-956-171B-5254
11	110	91.7	1027	4	US-08-781-986A-5254
12	105	87.5	21	4	US-09-010-317-14
13	105	87.5	21	4	US-09-010-317-16
14	105	87.5	21	4	US-09-010-317-23
15	105	87.5	21	4	US-09-010-317-33
16	104	86.7	21	4	US-09-010-317-18
17	104	86.7	21	4	US-09-010-317-24
18	104	86.7	21	4	US-09-010-317-27
19	104	86.7	21	4	US-09-010-317-28
20	104	86.7	21	4	US-09-010-317-30
21	103	85.8	21	4	US-09-010-317-25
22	103	85.8	21	4	US-09-010-317-29
23	103	85.8	130	2	US-08-459-135A-7
24	103	85.8	130	2	US-08-459-135A-8
25	103	85.8	130	3	US-08-495-559-7
26	103	85.8	130	3	US-08-495-559-8
27	103	85.8	174	2	US-08-459-135A-10

28	103	85.8	174	2	US-08-459-135A-13	Sequence 13, Appl
29	103	85.8	174	3	US-08-495-559-10	Sequence 10, Appl
30	103	85.8	174	3	US-08-495-559-13	Sequence 13, Appl
31	103	85.8	176	3	US-08-495-559-6	Sequence 6, Appl
32	103	85.8	181	2	US-08-459-135A-6	Sequence 6, Appl
33	103	85.8	559	4	US-08-956-171B-5251	Sequence 5251, Ap
34	103	85.8	559	4	US-08-781-986A-5251	Sequence 5251, Ap
35	102	85.0	21	4	US-09-010-317-10	Sequence 10, Appl
36	102	85.0	21	4	US-09-010-317-15	Sequence 15, Appl
37	102	85.0	21	4	US-09-010-317-20	Sequence 20, Appl
38	102	85.0	21	4	US-09-010-317-22	Sequence 22, Appl
39	102	85.0	21	4	US-09-010-317-32	Sequence 32, Appl
40	102	85.0	22	4	US-09-010-317-13	Sequence 13, Appl
41	100	83.3	21	4	US-09-010-317-17	Sequence 17, Appl
42	100	83.3	21	4	US-09-010-317-21	Sequence 21, Appl
43	100	83.3	21	4	US-09-010-317-21	Sequence 21, Appl
44	100	83.3	21	4	US-09-010-317-26	Sequence 26, Appl
45	96	80.0	19	1	US-08-234-622A-1	Sequence 1, Appl

ALIGNMENTS

```

RESULT 1
/ Sequence 31, Application US/09010317
/ Patent No. 6685943
/ GENERAL INFORMATION:
/ APPLICANT: Hook, Magnus
/ APPLICANT: Patti, Joseph M.
/ APPLICANT: House-Pompeo, Karen L.
/ APPLICANT: Speziale, Pietro
/ APPLICANT: Joh, Danny
/ APPLICANT: McGavin, Martin J.
/ TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
/ TITLE OF INVENTION: AND METHODS OF USE
/ NUMBER OF SEQUENCES: 105
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Arnold, White & Durkee
/ STREET: P.O. Box 4433
/ CITY: Houston
/ STATE: TX
/ COUNTRY: USA
/ ZIP: 77210-4433
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/010.317
/ FILING DATE:
/ CLASSIFICATION:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 60/036,139
/ FILING DATE: 21-JAN-1997
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Hibler, David W.
/ REGISTRATION NUMBER: 41,071
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 512-418-3000
/ TELEFAX: 512-474-7577
/ INFORMATION FOR SEQ ID NO: 31:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 21 amino acids
/ TYPE: amino acid
/ STRANDEDNESS:
/ TOPOLOGY: linear
/ US-09-010-317-31
/
Query Match      100.0%  Score 120; DB 4; Length 21;
Best Local Similarity 100.0%; Pred. No. 3,1e-12;

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Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KPSYQFGGHSVDPEDTTPK 21
Db 1 KPSYQFGGHSVDPEDTTPK 21

RESULT 2

US-09-010-317-9
Sequence 9, Application US/09010317
Patent No. 6685943
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
APPLICANT: Patil, Joseph M.
APPLICANT: House-Pompeo, Karen L.
APPLICANT: Speziale, Pietro
APPLICANT: McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITION;
TITLE OF INVENTION: AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hieber, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAWK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-09-010-317-9

Query Match 91.7%; Score 110; DB 4; Length 21;
Best Local Similarity 95.2%; Pred. No. 1.2e-10;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KPSYQFGGHSVDPEDTTPK 21
Db 1 KPSYQFGGHSVDPEDTTPK 21

RESULT 3

US-08-234-622A-4
Sequence 4, Application US/08234622A
Patent No. 5440014
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
APPLICANT: McGavin, Martin
APPLICANT: RAUCCI, Giuseppe
TITLE OF INVENTION: A FIBRONECTIN BINDING PEPTIDE

NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Burne, Doane, Swecker & Mathis
STREET: P.O. Box 1404
CITY: Alexandria
STATE: Virginia
COUNTRY: United States
ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/234,622A
FILING DATE: 28-APR-1994
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: SE 9002617-0
FILING DATE: 10-AUG-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/SE91/00534
FILING DATE: 09-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: Neuth, Donna M
REGISTRATION NUMBER: 36,607
REFERENCE/DOCKET NUMBER: 012885-044
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 37 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-234-622A-4

Query Match 91.7%; Score 110; DB 1; Length 37;
Best Local Similarity 95.2%; Pred. No. 2.2e-10;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KPSYQFGGHSVDPEDTTPK 21
Db 16 KPSYQFGGHSVDPEDTTPK 36

RESULT 4

US-08-294-189-8
Sequence 8, Application US/08294189
Patent No. 5707822
GENERAL INFORMATION:
APPLICANT: Fischetti, Vincent A.
APPLICANT: Rakonjac, Jasna
APPLICANT: Robbins, John
TITLE OF INVENTION: GENE SERUM OPACITY FACTOR
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauder & Jackson
STREET: 411 Hackensack Avenue
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/294,189
FILING DATE: 22-AUG-1994

CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-118
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 487-5800
TELEFAX: 201 343-1684
TELEX: 133521
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
ORGANISM: Streptococcus pyogenes
STRAIN: D734
INDIVIDUAL ISOLATE: 22
IMMEDIATE SOURCE:
CLONE: SAU3a
US-08-294-189-8

Query Match 91.7%; Score 110; DB 1; Length 38;
Best Local Similarity 95.2%; Pred. No. 2.2e-10;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KPSYQFGHNSVDFEETLPK 21
Db 10 KPSYQFGHNSVDFEETLPK 30

RESULT 5
US-08-729-767-5
Sequence 5, Application US/08729767
Patent No. 5770702
GENERAL INFORMATION:
APPLICANT: HOOK, Magnus
APPLICANT: LINDERBERG, Martin Kjell
APPLICANT: SIGNAS, Lars Christer
APPLICANT: WADSTROM, Torkel Mikael
APPLICANT: FROMAN, Gunnar
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN AS WELL AS
TITLE OF INVENTION: ITS PREPARATION
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Burns, Doane, Swecker & Mathis, L.L.P.
STREET: P.O. Box 1404
CITY: Alexandria
STATE: Virginia
COUNTRY: United States
ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/729,767
FILING DATE: 07-OCT-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/259,000
FILING DATE: 13-JUN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/007,817
FILING DATE: 22-JAN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/201,028
FILING DATE: 01-JUN-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: SE 8702272-9

FILING DATE: 01-JUN-1987
ATTORNEY/AGENT INFORMATION:
NAME: McGowan, Malcolm K.
REGISTRATION NUMBER: 39,300
REFERENCE/DOCKET NUMBER: 012889-036
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-729-767-5

Query Match 91.7%; Score 110; DB 1; Length 38;
Best Local Similarity 95.2%; Pred. No. 2.2e-10;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KPSYQFGHNSVDFEETLPK 21
Db 17 KPSYQFGHNSVDFEETLPK 37

RESULT 6
US-08-259-000-3
Sequence 3, Application US/08259000
Patent No. 5571514
GENERAL INFORMATION:
APPLICANT: HOOK, Magnus
APPLICANT: LINDERBERG, Martin Kjell
APPLICANT: SIGNAS, Lars Christer
APPLICANT: WADSTROM, Torkel Mikael
APPLICANT: FROMAN, Gunnar
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN AS WELL AS
TITLE OF INVENTION: ITS PREPARATION
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Burns, Doane, Swecker & Mathis
STREET: P.O. Box 1404
CITY: Alexandria
STATE: Virginia
COUNTRY: United States
ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/259,000
FILING DATE: 13-JUN-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: SE 8702272-9
FILING DATE: 01-JUN-1987
ATTORNEY/AGENT INFORMATION:
NAME: Meuth, Donna M
REGISTRATION NUMBER: 36,607
REFERENCE/DOCKET NUMBER: 012885-062
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 114 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-259-000-3

Query Match 91.7%; Score 110; DB 1; Length 114;
Best Local Similarity 95.2%; Pred. No. 7.7e-10;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KPSYQFGHNSVDFEEDTPK 21
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Db 93 KPSYQFGHNSVDFEEDTLPK 113

RESULT 7

US-08-856-253-8
; Sequence 8, Application US/08856253
; Patent No. 6288214
; GENERAL INFORMATION:
; APPLICANT: Hook, Magnus
; APPLICANT: Patti, Joseph M.
; APPLICANT: House-Pompeo, Karen
; APPLICANT: Sthanam, Narayana
; APPLICANT: Symersky, Jindrich
; TITLE OF INVENTION: COLLAGEN BINDING PROTEIN COMPOSITIONS
; NUMBER OF SEQUENCES: 8
; TITLE OF INVENTION: AND METHODS OF USE
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: U.S.
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/856,253
; FILING DATE: Concurrently Herewith
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/017,678
; FILING DATE: 16-MAY-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Kitchell, Barbara S.
; REGISTRATION NUMBER: 33,928
; REFERENCE/DOCKET NUMBER: TANK:193
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (512) 418-3000
; TELEFAX: (512) 474-7577
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 139 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
US-08-856-253-8

Query Match 91.7%; Score 110; DB 3; Length 139;
Best Local Similarity 95.2%; Pred. No. 9.7e-10;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KPSYQFGHNSVDFEEDTPK 21
|||
Db 107 KPSYQFGHNSVDFEEDTLPK 127

RESULT 8

US-08-459-135A-12
; Sequence 12, Application US/08459135A
; Patent No. 5955078
; GENERAL INFORMATION:
; APPLICANT: BURHAM, Martin Karl Russel
; APPLICANT: CHOPRA, Ian

APPLICANT: CRITCHLEY, Ian Alfred
; APPLICANT: KNOWLES, David Justin Charles
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN: MONOCLONAL ANTIBODY AND THEIR US
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corporation
; STREET: 709 Swedeland Road
; CITY: King of Prussia
; STATE: PA
; COUNTRY: U.S.A.
; ZIP: 19406-0939

COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: Fastseq, Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/459,135A
; FILING DATE: 02-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB/94/00215
; FILING DATE: 04-Feb-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Gimml, Edward R.
; REGISTRATION NUMBER: 38,891
; REFERENCE/DOCKET NUMBER: P30591C2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-270-4478
; TELEFAX: 610-270-5090
; TELEX:
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 178 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Protein
US-08-459-135A-12

Query Match 91.7%; Score 110; DB 2; Length 178;
Best Local Similarity 95.2%; Pred. No. 1.3e-09;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KPSYQFGHNSVDFEEDTPK 21
|||
Db 93 KPSYQFGHNSVDFEEDTLPK 113

RESULT 9

US-08-495-559-12
; Sequence 12, Application US/08495559A
; Patent No. 6054572
; GENERAL INFORMATION:
; APPLICANT: BURHAM, Martin Karl Russel
; APPLICANT: CHOPRA, Ian
; APPLICANT: CRITCHLEY, Ian Alfred
; APPLICANT: KNOWLES, David Justin Charles
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN: MONOCLONAL
; TITLE OF INVENTION: ANTIBODY AND THEIR USE IN PREVENTING BACTERIAL ADHESION
; FILE REFERENCE: P30591
; CURRENT APPLICATION NUMBER: US/08/495,559A
; CURRENT FILING DATE: 1995-08-03
; EARLIER APPLICATION NUMBER: GB 9302289.5
; EARLIER FILING DATE: 1993-02-05
; EARLIER APPLICATION NUMBER: GB 9321592.9
; EARLIER FILING DATE: 1993-10-20
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: Fastseq for Windows Version 3.0
; SEQ ID NO 12
; LENGTH: 178
; TYPE: PRT

ORGANISM: Staphylococcus aureus
US-08-495-559-12

Query Match 91.7%; Score 110; DB 3; Length 178;
Best Local Similarity 95.2%; Pred. No. 1.3e-09;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KPSYOGGHSVDFEEDTLPK 21
DB 93 KPSYOGGHSVDFEEDTLPK 113

RESULT 10
US-08-956-171E-5254

Sequence 5254, Application US/08956171E
Patent No. 6593114

GENERAL INFORMATION:

APPLICANT: Charles Kunach

Gil H. Choi

Patrick S. Dillon

Craig A. Rosen

Steven C. Barash

Michael R. Pannon

TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences

NUMBER OF SEQUENCES: 5256

CORRESPONDENCE ADDRESS:

ADDRESSEE: Human Genome Sciences, Inc.

STREET: 9410 Key West Avenue

CITY: Rockville

STATE: Maryland

COUNTRY: USA

ZIP: 20850

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.50 inch, 1.4mb storage

COMPUTER: HP Vectra 486/33

OPERATING SYSTEM: MSDOS version 6.2

SOFTWARE: ASCII Text

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/956,171E

FILING DATE: 20-Oct-1997

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 60/009,861

FILING DATE: January 5, 1996

APPLICATION NUMBER: 08/781,986

FILING DATE: January 3, 1997

ATTORNEY/AGENT INFORMATION:

NAME: Mark J. Hyman

REGISTRATION NUMBER: 46,789

REFERENCE/DOCKET NUMBER: PB248P1

TELECOMMUNICATION INFORMATION:

TELEPHONE: (240) 314-1224

TELEFAX: (301) 309-8439

INFORMATION FOR SEQ ID NO: 5254:

SEQUENCE CHARACTERISTICS:

LENGTH: 1027 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 5254:

US-08-956-171E-5254

Query Match 91.7%; Score 110; DB 4; Length 1027;
Best Local Similarity 95.2%; Pred. No. 9.1e-09;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KPSYOGGHSVDFEEDTLPK 21
DB 846 KPSYOGGHSVDFEEDTLPK 866

RESULT 11

US-08-781-986A-5254
Sequence 5254, Application US/08781986A
Patent No. 6737248

GENERAL INFORMATION:

APPLICANT: Charles Kunach

TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences

NUMBER OF SEQUENCES: 5255

CORRESPONDENCE ADDRESS:

ADDRESSEE: Human Genome Sciences, Inc.

STREET: 9410 Key West Avenue

CITY: Rockville

STATE: Maryland

COUNTRY: USA

ZIP: 20850

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.50 inch, 1.4mb storage

COMPUTER: HP Vectra 486/33

OPERATING SYSTEM: MSDOS version 6.2

SOFTWARE: ASCII Text

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/781,986A

FILING DATE:

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Benson, Bob

REGISTRATION NUMBER: 30,446

REFERENCE/DOCKET NUMBER: PB248BP

TELECOMMUNICATION INFORMATION:

TELEPHONE: (301) 309-8504

TELEFAX: (301) 309-8512

INFORMATION FOR SEQ ID NO: 5254:

SEQUENCE CHARACTERISTICS:

LENGTH: 1027 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-781-986A-5254

Query Match 91.7%; Score 110; DB 4; Length 1027;
Best Local Similarity 95.2%; Pred. No. 9.1e-09;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KPSYOGGHSVDFEEDTLPK 21
DB 846 KPSYOGGHSVDFEEDTLPK 866

RESULT 12
US-09-010-317-14
Sequence 14, Application US/09010317
Patent No. 6685943

GENERAL INFORMATION:

APPLICANT: Hook, Magnus

APPLICANT: Patti, Joseph M.

APPLICANT: House-Pompeo, Karen L.

APPLICANT: Speziale, Pietro

APPLICANT: Jon, Danny

APPLICANT: McGavin, Martin J.

TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS

NUMBER OF SEQUENCES: 105

CORRESPONDENCE ADDRESS:

ADDRESSEE: Arnold, White & Durkee

STREET: P.O. Box 4433

CITY: Houston

STATE: TX

COUNTRY: USA

ZIP: 77210-4433

COMPUTER READABLE FORM:


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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/010.317
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/036.139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-09-010-317-14

Query Match      87.5%; Score 105; DB 4; Length 21;
Best Local Similarity 95.0%; Pred. No. 7e-10;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy      2 PSYFGGHSVDFEEDTPK 21
Db      2 PSYFGGHSVDFEEDTPK 21

RESULT 13
US-09-010-317-16
Sequence 16, Application US/09010317
Patent No. 6685943
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
APPLICANT: Patti, Joseph M.
APPLICANT: House-Pompeo, Karen L.
APPLICANT: Speziale, Pietro
APPLICANT: Joh, Danny
APPLICANT: McGavin, Martin J.
TITLE OF INVENTION: FIBROECTIN BINDING PROTEIN COMPOSITIONS
NUMBER OF SEQUENCES: 105
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/010.317
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/036.139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-09-010-317-23

Query Match      87.5%; Score 105; DB 4; Length 21;
Best Local Similarity 90.5%; Pred. No. 7e-10;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy      1 KPSYFGGHSVDFEEDTPK 21
Db      1 KPSYFGGHSVDFEEDTPK 21

RESULT 14
US-09-010-317-23
Sequence 23, Application US/09010317
Patent No. 6685943
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
APPLICANT: Patti, Joseph M.
APPLICANT: House-Pompeo, Karen L.
APPLICANT: Speziale, Pietro
APPLICANT: Joh, Danny
APPLICANT: McGavin, Martin J.
TITLE OF INVENTION: FIBROECTIN BINDING PROTEIN COMPOSITIONS
NUMBER OF SEQUENCES: 105
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/010.317
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/036.139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-09-010-317-23

Query Match      87.5%; Score 105; DB 4; Length 21;
Best Local Similarity 90.5%; Pred. No. 7e-10;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy      1 KPSYFGGHSVDFEEDTPK 21
Db      1 KPSYFGGHSVDFEEDTPK 21
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```

TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-09-010-317-16

Query Match      87.5%; Score 105; DB 4; Length 21;
Best Local Similarity 90.5%; Pred. No. 7e-10;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy      1 KPSYFGGHSVDFEEDTPK 21
Db      1 KPSYFGGHSVDFEEDTPK 21

RESULT 14
US-09-010-317-23
Sequence 23, Application US/09010317
Patent No. 6685943
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
APPLICANT: Patti, Joseph M.
APPLICANT: House-Pompeo, Karen L.
APPLICANT: Speziale, Pietro
APPLICANT: Joh, Danny
APPLICANT: McGavin, Martin J.
TITLE OF INVENTION: FIBROECTIN BINDING PROTEIN COMPOSITIONS
NUMBER OF SEQUENCES: 105
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/010.317
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/036.139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-09-010-317-23

Query Match      87.5%; Score 105; DB 4; Length 21;
Best Local Similarity 90.5%; Pred. No. 7e-10;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy      1 KPSYFGGHSVDFEEDTPK 21
Db      1 KPSYFGGHSVDFEEDTPK 21
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OM protein - protein search, using sw model

Run on: October 22, 2005, 03:51:22 ; Search time 21.1723 Seconds
(without alignments)
133.980 Million cell updates/sec

Title: US-10-731-238-50

Perfect score: 218
Sequence: 1 QNKGNSFPDTEKDKPKYEHPPNIDIDPDSVPHHG 38

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA: *
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2: /cgn2_6/ptodata/1/1aa/5B.COMB.pep: *
3: /cgn2_6/ptodata/1/1aa/6A.COMB.pep: *
4: /cgn2_6/ptodata/1/1aa/6B.COMB.pep: *
5: /cgn2_6/ptodata/1/1aa/PC/COMB.COMB.pep: *
6: /cgn2_6/ptodata/1/1aa/backfile1.pep: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	218	100.0	38	4	US-09-010-317-50 Sequence 50, Appl
2	193	88.5	38	4	US-09-010-317-8 Sequence 8, Appl
3	193	88.5	38	4	US-09-010-317-49 Sequence 49, Appl
4	192	88.1	38	4	US-09-010-317-44 Sequence 44, Appl
5	192	88.1	38	4	US-09-010-317-46 Sequence 46, Appl
6	192	88.1	38	4	US-09-010-317-47 Sequence 47, Appl
7	184	84.4	38	1	US-08-234-622A-3 Sequence 3, Appl
8	184	84.4	38	1	US-09-010-317-7 Sequence 7, Appl
9	184	84.4	114	1	US-08-259-000-3 Sequence 3, Appl
10	184	84.4	139	3	US-08-856-253-8 Sequence 8, Appl
11	184	84.4	1027	4	US-08-956-171E-5254 Sequence 5254, Ap
12	184	84.4	1027	4	US-08-459-986A-5254 Sequence 5254, Ap
13	179	82.1	130	2	US-08-459-135A-8 Sequence 7, Appl
14	179	82.1	130	2	US-08-459-135A-8 Sequence 8, Appl
15	179	82.1	130	3	US-08-495-559-7 Sequence 7, Appl
16	179	82.1	130	3	US-08-495-559-8 Sequence 8, Appl
17	179	82.1	174	2	US-08-459-135A-10 Sequence 10, Appl
18	179	82.1	174	2	US-08-495-559-10 Sequence 10, Appl
19	179	82.1	176	3	US-08-495-559-6 Sequence 6, Appl
20	179	82.1	178	2	US-08-459-135A-12 Sequence 12, Appl
21	179	82.1	178	2	US-08-495-559-12 Sequence 12, Appl
22	179	82.1	181	2	US-08-459-135A-6 Sequence 6, Appl
23	178	81.7	38	1	US-08-729-767-4 Sequence 4, Appl
24	177	81.2	38	4	US-09-010-317-48 Sequence 48, Appl
25	174	79.8	38	4	US-09-010-317-45 Sequence 45, Appl
26	171	78.4	174	2	US-08-459-135A-13 Sequence 13, Appl
27	171	78.4	174	3	US-08-495-559-13 Sequence 13, Appl

28	171	78.4	559	4	US-08-956-171E-5251 Sequence 5251, Ap
29	171	78.4	559	4	US-08-781-986A-5251 Sequence 5251, Ap
30	170	78.0	36	4	US-09-010-317-59 Sequence 59, Appl
31	167	76.6	38	4	US-09-010-317-6 Sequence 6, Appl
32	167	76.6	38	4	US-09-010-317-43 Sequence 43, Appl
33	166	76.1	38	4	US-09-010-317-36 Sequence 36, Appl
34	166	76.1	38	4	US-09-010-317-37 Sequence 37, Appl
35	161	73.9	36	4	US-09-010-317-58 Sequence 58, Appl
36	158	72.5	38	1	US-08-234-622A-2 Sequence 2, Appl
37	158	72.5	38	4	US-09-010-317-5 Sequence 5, Appl
38	156.5	71.8	39	4	US-09-010-317-57 Sequence 57, Appl
39	156	71.6	38	4	US-09-010-317-41 Sequence 41, Appl
40	152	69.7	38	1	US-08-729-767-3 Sequence 3, Appl
41	152	69.7	38	4	US-09-010-317-39 Sequence 39, Appl
42	152	69.7	38	4	US-09-010-317-40 Sequence 40, Appl
43	151	69.3	38	4	US-09-010-317-38 Sequence 38, Appl
44	151	69.3	38	4	US-09-010-317-42 Sequence 42, Appl
45	148	67.9	38	4	US-09-010-317-35 Sequence 35, Appl

ALIGNMENTS

RESULT 1
US-09-010-317-50
Sequence 50, Application US/09010317
Patent No. 6685943
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
APPLICANT: Patti, Joseph M.
APPLICANT: House-Pompeo, Karen L.
APPLICANT: Speziale, Pietro
APPLICANT: Jon, Danny
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
TITLE OF INVENTION: AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
TELEPHONE: 512-418-3000
TELECOMMUNICATION INFORMATION:
REFERENCE/DOCKET NUMBER: TAMK:189
INFORMATION FOR SEQ ID NO: 50:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-09-010-317-50
Query Match 100.0%; Score 218; DB 4; Length 38;
Best local Similarity 100.0%; Pred. No. 1.6e-22;

Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QNKGNSFPDTEKDKRYEHPNIIIDPDSVPHNG 38
|||||

Db 1 QNKGNSFPDTEKDKRYEHPNIIIDPDSVPHNG 38

RESULT 2

US-09-010-317-8
; Sequence 8, Application US/09010317
; Patent No. 6685943
; GENERAL INFORMATION:
; APPLICANT: Hook, Magnus
; APPLICANT: Patli, Joseph M.
; APPLICANT: House-Pompeo, Karen L.
; APPLICANT: Speziale, Pietro
; APPLICANT: Joh, Danny
; APPLICANT: McGavin, Martin J.
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
; NUMBER OF SEQUENCES: 105
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: TX
; COUNTRY: USA
; ZIP: 77210-4433
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/010,317
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/036,139
; FILING DATE: 21-JAN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Hibler, David W.
; REGISTRATION NUMBER: 41,071
; REFERENCE/DOCKET NUMBER: TANK:189
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 512-418-3000
; TELEFAX: 512-474-7577
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 38 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; US-09-010-317-8

Query Match 88.5%; Score 193; DB 4; Length 38
Best Local Similarity 92.1%; Pred. No. 3,7e-19;
Matches 35; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 QNKGNSFPDTEKDKRYEHPNIIIDPDSVPHNG 38
|||||

Db 1 QNKGNSFPDTEKDKRYEHPNIIIDPDSVPHNG 38

RESULT 3

US-09-010-317-49
; Sequence 49, Application US/09010317
; Patent No. 6685943
; GENERAL INFORMATION:
; APPLICANT: Hook, Magnus
; APPLICANT: Patli, Joseph M.
; APPLICANT: House-Pompeo, Karen L.
; APPLICANT: Speziale, Pietro

APPLICANT: Joh, Danny
; APPLICANT: McGavin, Martin J.
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
; NUMBER OF SEQUENCES: 105
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: TX
; COUNTRY: USA
; ZIP: 77210-4433
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/010,317
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/036,139
; FILING DATE: 21-JAN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Hibler, David W.
; REGISTRATION NUMBER: 41,071
; REFERENCE/DOCKET NUMBER: TANK:189
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 512-418-3000
; TELEFAX: 512-474-7577
; INFORMATION FOR SEQ ID NO: 49:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 38 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; US-09-010-317-49

Query Match 88.5%; Score 193; DB 4; Length 38;
Best Local Similarity 92.1%; Pred. No. 3,7e-19;
Matches 35; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 QNKGNSFPDTEKDKRYEHPNIIIDPDSVPHNG 38
|||||

Db 1 QNKGNSFPDTEKDKRYEHPNIIIDPDSVPHNG 38

RESULT 4

US-09-010-317-44
; Sequence 44, Application US/09010317
; Patent No. 6685943
; GENERAL INFORMATION:
; APPLICANT: Hook, Magnus
; APPLICANT: Patli, Joseph M.
; APPLICANT: House-Pompeo, Karen L.
; APPLICANT: Speziale, Pietro
; APPLICANT: Joh, Danny
; APPLICANT: McGavin, Martin J.
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
; NUMBER OF SEQUENCES: 105
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: TX
; COUNTRY: USA
; ZIP: 77210-4433
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS

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; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/010,317
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/036,139
; FILING DATE: 21-JAN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Hibler, David W.
; REGISTRATION NUMBER: 41,071
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 512-418-3000
; TELEFAX: 512-474-7577
; INFORMATION FOR SEQ ID NO: 44:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 38 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
;
US-09-010-317-44
;
Query Match      88.1%; Score 192; DB 4; Length 38;
Best Local Similarity 86.8%; Pred. No. 5.1e-19;
Matches 33; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy
1 QNKGNSFPDTEKDKPKYEHHPNIIDIDFDSVPHNG 38
Db 1 QNKGNSFPDTEKDKPKYEHHPNIIDIDFDSVQING 38

RESULT 5
; Sequence 46, Application US/09010317
; Patent No. 6685943
; GENERAL INFORMATION:
; APPLICANT: Hook, Magnus
; APPLICANT: Patti, Joseph M.
; APPLICANT: House-Pompeo, Karen L.
; APPLICANT: Speziale, Pietro
; APPLICANT: John, Danny
; APPLICANT: McGavin, Martin J.
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
; NUMBER OF SEQUENCES: 105
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: TX
; COUNTRY: USA
; ZIP: 77210-4433
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/010,317
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/036,139
; FILING DATE: 21-JAN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Hibler, David W.
; REGISTRATION NUMBER: 41,071
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 512-418-3000
; TELEFAX: 512-474-7577
; INFORMATION FOR SEQ ID NO: 46:
; INFORMATION FOR SEQ ID NO: 46:

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```

; SEQUENCE CHARACTERISTICS:
; LENGTH: 38 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
;
US-09-010-317-46
;
Query Match      88.1%; Score 192; DB 4; Length 38;
Best Local Similarity 92.1%; Pred. No. 5.1e-19;
Matches 35; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy
1 QNKGNSFPDTEKDKPKYEHHPNIIDIDFDSVPHNG 38
Db 1 QNKGNSFPDTEKDKPKYEHGNIIDIDFDSVPHNG 38

RESULT 6
; Sequence 47, Application US/09010317
; Patent No. 6685943
; GENERAL INFORMATION:
; APPLICANT: Hook, Magnus
; APPLICANT: Patti, Joseph M.
; APPLICANT: House-Pompeo, Karen L.
; APPLICANT: Speziale, Pietro
; APPLICANT: John, Danny
; APPLICANT: McGavin, Martin J.
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
; NUMBER OF SEQUENCES: 105
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: TX
; COUNTRY: USA
; ZIP: 77210-4433
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/010,317
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/036,139
; FILING DATE: 21-JAN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Hibler, David W.
; REGISTRATION NUMBER: 41,071
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 512-418-3000
; TELEFAX: 512-474-7577
; INFORMATION FOR SEQ ID NO: 47:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 38 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
;
US-09-010-317-47
;
Query Match      88.1%; Score 192; DB 4; Length 38;
Best Local Similarity 92.1%; Pred. No. 5.1e-19;
Matches 35; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy
1 QNKGNSFPDTEKDKPKYEHHPNIIDIDFDSVPHNG 38
Db 1 QNKGNSFPDTEKDKPKYEHGNIIDIDFDSVPHNG 38

```

RESULT 7
US-08-234-622A-3
; Sequence 3, Application US/08234622A
; Patent No. 544014
; GENERAL INFORMATION:
; APPLICANT: HOOK, Magnus
; APPLICANT: MCGAVIN, Martin
; APPLICANT: RAUCCI, Giuseppe
; TITLE OF INVENTION: A FIBRONECTIN BINDING PEPTIDE
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Doane, Swecker & Mathis
; STREET: P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/234,622A
; FILING DATE: 28-APR-1994
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: SE 9002617-0
; FILING DATE: 10-AUG-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/SB91/00534
; FILING DATE: 09-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Meuth, Donna M
; REGISTRATION NUMBER: 36,607
; REFERENCE/DOCKET NUMBER: 012885-044
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 38 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-234-622A-3

Query Match 84.4%; Score 184; DB 1; Length 38;
Best Local Similarity 89.5%; Pred. No. 6,1e-18;
Matches 34; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 QNKGNSFPPTDKPKYEHPPNIIDIDFDSVPHHG 38
DB 1 QNKGNSFPPTDKPKYEHPPNIIDIDFDSVPHHG 38

RESULT 8
US-09-010-317-7
; Sequence 7, Application US/09010317
; Patent No. 6685943
; GENERAL INFORMATION:
; APPLICANT: Hook, Magnus
; APPLICANT: Patli, Joseph M.
; APPLICANT: House-Pompeo, Karen L.
; APPLICANT: Speziale, Pietro
; APPLICANT: Joh, Danny
; APPLICANT: McGavin, Martin J.
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
; TITLE OF INVENTION: AND METHODS OF USE
; NUMBER OF SEQUENCES: 105
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee

STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/010,317
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/036,139
; FILING DATE: 21-JAN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Hibler, David W.
; REGISTRATION NUMBER: 41,071
; REFERENCE/DOCKET NUMBER: TANK:189
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 512-418-3000
; TELEFAX: 512-474-7577
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 38 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; US-09-010-317-7

Query Match 84.4%; Score 184; DB 4; Length 38;
Best Local Similarity 89.5%; Pred. No. 6,1e-18;
Matches 34; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 QNKGNSFPPTDKPKYEHPPNIIDIDFDSVPHHG 38
DB 1 QNKGNSFPPTDKPKYEHPPNIIDIDFDSVPHHG 38

RESULT 9
US-08-259-000-3
; Sequence 3, Application US/08259000
; Patent No. 5571514
; GENERAL INFORMATION:
; APPLICANT: HOOK, Magnus
; APPLICANT: LINDBERG, Martin Kjell
; APPLICANT: SIGNAS, Lars Christer
; APPLICANT: MADSTROM, Torkei Mikael
; APPLICANT: FROMAN, Gunnar
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN AS WELL AS
; TITLE OF INVENTION: ITS PREPARATION
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Doane, Swecker & Mathis
; STREET: P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/259,000
; FILING DATE: 13-JUN-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: SE 8702272-9
; FILING DATE: 01-JUN-1987

ATTORNEY/AGENT INFORMATION:
NAME: Meuth, Donna M
REGISTRATION NUMBER: 36,607
REFERENCE/DOCKET NUMBER: 012885-062
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 114 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-259-000-3

Query Match 84.4%; Score 184; DB 1; Length 114;
Best Local Similarity 89.5%; Pred. No. 2.2e-17;
Matches 34; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 QNKGNSFPPTDKPKRYEHPNIIIDPDSVPHHG 38
Db 40 QNKGNSFPPTDKPKRYEHPNIIIDPDSVPHHG 77

RESULT 10
US-08-856-253-8
Sequence 8, Application US/08856253
Patent No. 6288214
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
APPLICANT: Patel, Joseph M.
APPLICANT: House-Pompeo, Karen
APPLICANT: Stnam, Narayana
APPLICANT: Symersky, Jindrich
TITLE OF INVENTION: COLLAGEN BINDING PROTEIN COMPOSITIONS
NUMBER OF SEQUENCES: 8
TITLE OF INVENTION: AND METHODS OF USE
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: Texas
COUNTRY: U.S.
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/856,253
FILING DATE: Concurrently Herewith
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/017,678
FILING DATE: 16-MAY-1996
ATTORNEY/AGENT INFORMATION:
NAME: Kitchell, Barbara S.
REGISTRATION NUMBER: 33,928
REFERENCE/DOCKET NUMBER: TAWK.193
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
TELEFAX: (512) 474-7577
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 139 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-08-856-253-8

Query Match 84.4%; Score 184; DB 3; Length 139;

Best Local Similarity 89.5%; Pred. No. 2.8e-17;
Matches 34; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 QNKGNSFPPTDKPKRYEHPNIIIDPDSVPHHG 38
Db 54 QNKGNSFPPTDKPKRYEHPNIIIDPDSVPHHG 91

RESULT 11
US-08-956-171E-5254
Sequence 5254, Application US/08956171E
Patent No. 6593114
GENERAL INFORMATION:
APPLICANT: Charles Kunsch
Gil H. Choi
Patrick S. Dillon
Craig A. Rosen
Steven C. Barash
Michael R. Fannon

TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
NUMBER OF SEQUENCES: 5256
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COUNTRY: USA
ZIP: 20850

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4mb storage
COMPUTER: HP Vectra 486/33

OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/956,171E
FILING DATE: 20-Oct-1997

CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/009,861
FILING DATE: January 5, 1996
APPLICATION NUMBER: 08/781,986
FILING DATE: January 3, 1997

ATTORNEY/AGENT INFORMATION:
NAME: Mark J. Hyman

REGISTRATION NUMBER: 46,789
REFERENCE/DOCKET NUMBER: PB248P1

TELECOMMUNICATION INFORMATION:
TELEPHONE: (240) 314-1224
TELEFAX: (301) 309-8439

INFORMATION FOR SEQ ID NO: 5254:
SEQUENCE CHARACTERISTICS:
LENGTH: 1027 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 5254:

US-08-956-171E-5254

Query Match 84.4%; Score 184; DB 4; Length 1027;
Best Local Similarity 89.5%; Pred. No. 3e-16;
Matches 34; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 QNKGNSFPPTDKPKRYEHPNIIIDPDSVPHHG 38
Db 793 QNKGNSFPPTDKPKRYEHPNIIIDPDSVPHHG 830

RESULT 12
US-08-781-986A-5254
Sequence 5254, Application US/08781986A
Patent No. 6737248
GENERAL INFORMATION:

APPLICANT: Charles Kunsch
TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
NUMBER OF SEQUENCES: 5255
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COUNTRY: USA
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4MB storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/781,986A
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
ATTORNEY/AGENT INFORMATION:
NAME: Benson, Bob
REGISTRATION NUMBER: 30,446
REFERENCE/DOCKET NUMBER: PB248PP
TELEPHONE: (301) 309-8504
TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 5254:
SEQUENCE CHARACTERISTICS:
LENGTH: 1027 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-781-986A-5254

Query Match 84.4%; Score 184; DB 4; Length 1027;
Best Local Similarity 89.5%; Pred. No. 3e-16;
Matches 34; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 ONKNGSPPTKDKPKYEHPPNIIDPDSVPHNG 38
DB 793 ONKNGSFEDTKDKPKYEHGNIIDPDSVPHNG 830

RESULT 13
US-08-459-135A-7
Sequence 7, Application US/08459135A
Patent No. 5955078
GENERAL INFORMATION:
APPLICANT: BURNHAM, Martin Karl Russel
APPLICANT: CHOPRA, Ian
APPLICANT: CRITCHLEY, Ian Alfred
APPLICANT: KNOWLES, David Justin Charles
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN: MONOCLONAL ANTIBODY AND THEIR US
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
STATE: PA
COUNTRY: U.S.A.
ZIP: 19406-0939
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: Fastseq, Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/459,135A
FILING DATE: 02-JUN-1995

CLASSIFICATION: 435
PRIOR APPLICATION DATA: PCT/GB/94/00215
APPLICATION NUMBER: PCT/GB/94/00215
FILING DATE: 04-Feb-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Gimm, Edward R
REGISTRATION NUMBER: 38,891
REFERENCE/DOCKET NUMBER: P30591C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-4478
TELEFAX: 610-270-5090
TELEX:
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 130 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-459-135A-7

Query Match 82.1%; Score 179; DB 2; Length 130;
Best Local Similarity 86.8%; Pred. No. 1.2e-16;
Matches 33; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 ONKNGSPPTKDKPKYEHPPNIIDPDSVPHNG 38
DB 40 ONKNGSFEDTKDKPKYEHGNIIDPDSVPHNG 77

RESULT 14
US-08-459-135A-8
Sequence 8, Application US/08459135A
Patent No. 5955078
GENERAL INFORMATION:
APPLICANT: BURNHAM, Martin Karl Russel
APPLICANT: CHOPRA, Ian
APPLICANT: CRITCHLEY, Ian Alfred
APPLICANT: KNOWLES, David Justin Charles
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN: MONOCLONAL ANTIBODY AND THEIR US
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
STATE: PA
COUNTRY: U.S.A.
ZIP: 19406-0939
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: Fastseq, Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/459,135A
FILING DATE: 02-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB/94/00215
FILING DATE: 04-Feb-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Gimm, Edward R
REGISTRATION NUMBER: 38,891
REFERENCE/DOCKET NUMBER: P30591C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-4478
TELEFAX: 610-270-5090
TELEX:
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 130 amino acids
TYPE: amino acid

TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-459-135A-8

Query Match 82.1%; Score 179; DB 2; Length 130;
Best local Similarity 86.8%; Pred. No. 1.2e-16;
Matches 33; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 QNKGNSFPPTKDKPKYEHHPNIIDIDFDSVPHIG 38
DB 40 QNKGDSFEDTEKDKPKYEHGNIIDIDFDSVPHIG 77

RESULT 15
US-08-495-559-7
Sequence 7, Application US/08495559A
Patent No. 6054572
GENERAL INFORMATION:
APPLICANT: BURMAN, Martin Karl Russel
APPLICANT: CHOPRA, Ian
APPLICANT: CRITCHLEY, Ian Alfred
APPLICANT: KNOWLES, David Justin Charles
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN: MONOCLONAL
TITLE OF INVENTION: ANTIBODY AND THEIR USE IN PREVENTING BACTERIAL ADHESION
FILE REFERENCE: P30591
CURRENT APPLICATION NUMBER: US/08/495,559A
CURRENT FILING DATE: 1995-08-03
EARLIER APPLICATION NUMBER: GB 9302289.5
EARLIER FILING DATE: 1993-02-05
EARLIER APPLICATION NUMBER: GB 9321592.9
EARLIER FILING DATE: 1993-10-20
NUMBER OF SEQ ID NOS: 13
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 7
LENGTH: 130
TYPE: PRT
ORGANISM: Staphylococcus aureus
US-08-495-559-7

Query Match 82.1%; Score 179; DB 3; Length 130;
Best local Similarity 86.8%; Pred. No. 1.2e-16;
Matches 33; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 QNKGNSFPPTKDKPKYEHHPNIIDIDFDSVPHIG 38
DB 40 QNKGDSFEDTEKDKPKYEHGNIIDIDFDSVPHIG 77

Search completed: October 22, 2005, 05:46:47
Job time : 21.2223 secs

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OM protein - protein search, using SW model

Run on: October 22, 2005, 11:35:03 ; Search time 70.1256 Seconds
(without alignments)
226.232 Million cell updates/sec

Title: US-10-731-238-50

Sequence: 1 QNKGNSFPPTREKDKYEHPPNIDIDFDSVPHIHG 38

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1862951 seqs, 417491010 residues

Total number of hits satisfying chosen parameters: 1862951

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

Published Applications_AA:*

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- 4: /cgn2_6/prodata/2/pubppaa/US06_PUBCOMB.pep:*
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- 10: /cgn2_6/prodata/2/pubppaa/US09_PUBCOMB.pep:*
- 11: /cgn2_6/prodata/2/pubppaa/US09C_PUBCOMB.pep:*
- 12: /cgn2_6/prodata/2/pubppaa/US09_NEW_PUB.pep:*
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- 15: /cgn2_6/prodata/2/pubppaa/US10C_PUBCOMB.pep:*
- 16: /cgn2_6/prodata/2/pubppaa/US10D_PUBCOMB.pep:*
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- 18: /cgn2_6/prodata/2/pubppaa/US10_NEW_PUB.pep:*
- 19: /cgn2_6/prodata/2/pubppaa/US11A_PUBCOMB.pep:*
- 20: /cgn2_6/prodata/2/pubppaa/US11_NEW_PUB.pep:*
- 21: /cgn2_6/prodata/2/pubppaa/US60_NEW_PUB.pep:*
- 22: /cgn2_6/prodata/2/pubppaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	218	100.0	38	18	US-10-731-238-50
2	193	88.5	38	18	US-10-731-238-8
3	193	88.5	38	18	US-10-731-238-49
4	192	88.1	38	18	US-10-731-238-44
5	192	88.1	38	18	US-10-731-238-46
6	192	88.1	38	18	US-10-731-238-47
7	184	84.4	38	18	US-10-731-238-7
8	184	84.4	139	9	US-09-813-820-8
9	184	84.4	1018	9	US-09-815-242-5797
10	184	84.4	1018	9	US-09-815-242-12838
11	184	84.4	1018	17	US-10-470-0488-68

12	184	84.4	1027	8	US-08-781-986A-5254	Sequence 5254, Ap
13	184	84.4	1027	15	US-10-329-624-5254	Sequence 5254, Ap
14	177	81.2	38	18	US-10-731-238-48	Sequence 48, Appl
15	174	79.8	38	18	US-10-731-238-45	Sequence 45, Appl
16	171	78.4	388	8	US-08-901-062-1	Sequence 1, Appl1
17	171	78.4	559	8	US-08-781-986A-5251	Sequence 5251, Ap
18	171	78.4	559	15	US-10-329-624-5251	Sequence 5251, Ap
19	171	78.4	767	9	US-09-815-242-5899	Sequence 5899, Ap
20	171	78.4	767	9	US-09-815-242-13140	Sequence 13140, A
21	171	78.4	940	17	US-10-470-048B-424	Sequence 424, App
22	171	78.4	948	17	US-10-470-048B-59	Sequence 69, Appl
23	171	78.4	1038	15	US-10-282-122A-43827	Sequence 43827, A
24	170	78.0	36	18	US-10-731-238-59	Sequence 59, Appl
25	167	76.6	38	18	US-10-731-238-6	Sequence 6, Appl1
26	167	76.6	38	18	US-10-731-238-43	Sequence 43, Appl
27	166	76.1	38	18	US-10-731-238-36	Sequence 36, Appl
28	166	76.1	38	18	US-10-731-238-37	Sequence 37, Appl
29	163	74.8	978	9	US-09-815-242-5456	Sequence 5456, Ap
30	163	74.8	1001	9	US-09-815-242-12686	Sequence 12686, A
31	161	73.9	36	18	US-10-731-238-58	Sequence 58, Appl
32	159	72.9	951	15	US-10-282-122A-43778	Sequence 43778, A
33	158	72.5	38	18	US-10-731-238-5	Sequence 5, Appl1
34	156.5	71.8	39	18	US-10-731-238-57	Sequence 57, Appl
35	156	71.6	38	18	US-10-731-238-41	Sequence 41, Appl
36	152	69.7	38	18	US-10-731-238-39	Sequence 39, Appl
37	152	69.7	38	18	US-10-731-238-40	Sequence 40, Appl
38	151	69.3	38	18	US-10-731-238-38	Sequence 38, Appl
39	151	69.3	38	18	US-10-731-238-42	Sequence 42, Appl
40	148	67.9	38	18	US-10-731-238-35	Sequence 35, Appl
41	147.5	67.7	39	18	US-10-731-238-56	Sequence 56, Appl
42	118	54.1	30	14	US-10-287-821-1	Sequence 2, Appl1
43	118	54.1	31	14	US-10-287-821-2	Sequence 1, Appl1
44	68.5	31.4	820	16	US-10-437-965-170477	Sequence 170477, A
45	64.5	29.6	37	20	US-11-066-697-1134	Sequence 1134, Ap

ALIGNMENTS

RESULT 1
US-10-731-238-50
Sequence 50, Application US/10731238
Publication No. US20050123552A1
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
Patli, Joseph M.
House-Pompeo, Karen L.
Speziale, Pietro
Joh, Danny
McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/731,238
FILING DATE: 10-Dec-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE: 21-Jan-1998
APPLICATION NUMBER: US 60/036,139

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; FILING DATE: 21-JAN-1997
; ATTORNEY/AGENT INFORMATION:
;   NAME: Hibler, David W.
;   REGISTRATION NUMBER: 41,071
;   REFERENCE/DOCKET NUMBER: TAMK:189
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE: 512-418-3000
;     TELEFAX: 512-474-7577
; INFORMATION FOR SEQ ID NO: 50:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH: 38 amino acids
;     TYPE: amino acid
;     STRANDEDNESS: <Unknown>
;     TOPOLOGY: linear
;   SEQUENCE DESCRIPTION: SEQ ID NO: 50:
US-10-731-238-50

Query Match      100.0%; Score 218; DB 18; Length 38;
Best Local Similarity 100.0%; Pred. No. 5, 9e-21;
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 QNKGNSFPDTEKDKPKYEHHPNIIDIDFDSVPHIHG 38
Db      1 QNKGNSFPDTEKDKPKYEHHPNIIDIDFDSVPHIHG 38

RESULT 2
US-10-731-238-8
; Sequence 8, Application US/10731238
; Publication No. US20050123552A1
; GENERAL INFORMATION:
;   APPLICANT: Hook, Magnus
;             Patti, Joseph M.
;             House-Pompeo, Karen L.
;             Speziale, Pietro
;             John, Danny
;             McGavin, Martin J.
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
; NUMBER OF SEQUENCES: 105
; CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Arnold, White & Durkee
;   STREET: P.O. Box 4433
;   CITY: Houston
;   STATE: TX
;   COUNTRY: USA
;   ZIP: 77210-4433
; COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/10/731,238
;   FILING DATE: 10-Dec-2003
;   CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US/09/010,317
;   FILING DATE: 21-Jan-1998
;   APPLICATION NUMBER: US 60/036,139
;   FILING DATE: 21-JAN-1997
; ATTORNEY/AGENT INFORMATION:
;   NAME: Hibler, David W.
;   REGISTRATION NUMBER: 41,071
;   REFERENCE/DOCKET NUMBER: TAMK:189
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE: 512-418-3000
;     TELEFAX: 512-474-7577
; INFORMATION FOR SEQ ID NO: 8:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH: 38 amino acids
;     TYPE: amino acid
;     STRANDEDNESS: <Unknown>

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; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-10-731-238-8

Query Match      88.5%; Score 193; DB 18; Length 38;
Best Local Similarity 92.1%; Pred. No. 1e-17;
Matches 35; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1 QNKGNSFPDTEKDKPKYEHHPNIIDIDFDSVPHIHG 38
Db      1 QNKGNSFPDTEKDKPKYEHHPNIIDIDFDSVPHIHG 38

RESULT 3
US-10-731-238-49
; Sequence 49, Application US/10731238
; Publication No. US20050123552A1
; GENERAL INFORMATION:
;   APPLICANT: Hook, Magnus
;             Patti, Joseph M.
;             House-Pompeo, Karen L.
;             Speziale, Pietro
;             John, Danny
;             McGavin, Martin J.
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
; AND METHODS OF USE
; NUMBER OF SEQUENCES: 105
; CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Arnold, White & Durkee
;   STREET: P.O. Box 4433
;   CITY: Houston
;   STATE: TX
;   COUNTRY: USA
;   ZIP: 77210-4433
; COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/10/731,238
;   FILING DATE: 10-Dec-2003
;   CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US/09/010,317
;   FILING DATE: 21-Jan-1998
;   APPLICATION NUMBER: US 60/036,139
;   FILING DATE: 21-JAN-1997
; ATTORNEY/AGENT INFORMATION:
;   NAME: Hibler, David W.
;   REGISTRATION NUMBER: 41,071
;   REFERENCE/DOCKET NUMBER: TAMK:189
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE: 512-418-3000
;     TELEFAX: 512-474-7577
; INFORMATION FOR SEQ ID NO: 49:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH: 38 amino acids
;     TYPE: amino acid
;     STRANDEDNESS: <Unknown>
;     TOPOLOGY: linear
;   SEQUENCE DESCRIPTION: SEQ ID NO: 49:
US-10-731-238-49

Query Match      88.5%; Score 193; DB 18; Length 38;
Best Local Similarity 92.1%; Pred. No. 1e-17;
Matches 35; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1 QNKGNSFPDTEKDKPKYEHHPNIIDIDFDSVPHIHG 38
Db      1 QNKGNSFPDTEKDKPKYEHHPNIIDIDFDSVPHIHG 38

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RESULT 4
US-10-731-238-44
; Sequence 44, Application US/10731238
; Publication No. US20050123552A1
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
Patti, Joseph M.
House-Pompeo, Karen L.
Speziale, Pietro
John, Danny
McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/731,238
FILING DATE: 10-Dec-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE: 21-Jan-1998
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-Jan-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAMK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 44:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 44:
US-10-731-238-44
Query Match 88.1%; Score 192; DB 18; Length 38;
Best Local Similarity 86.8%; Pred. No. 1,4e-17;
Matches 33; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
QY 1 QNKGNSFPDTEKDKPKYEHPPNIIDIDPSVPHNG 38
DB 1 QNKGNSFPDTEKDKPKYEHPPNIIDIDPSVPHNG 38
RESULT 5
US-10-731-238-46
; Sequence 46, Application US/10731238
; Publication No. US20050123552A1
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
Patti, Joseph M.
House-Pompeo, Karen L.
Speziale, Pietro
John, Danny
McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
AND METHODS OF USE

NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/731,238
FILING DATE: 10-Dec-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE: 21-Jan-1998
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-Jan-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAMK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 46:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 46:
US-10-731-238-46
Query Match 88.1%; Score 192; DB 18; Length 38;
Best Local Similarity 92.1%; Pred. No. 1,4e-17;
Matches 35; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 QNKGNSFPDTEKDKPKYEHPPNIIDIDPSVPHNG 38
DB 1 QNKGNSFPDTEKDKPKYEHGNIIDIDPSVPHNG 38
RESULT 6
US-10-731-238-47
; Sequence 47, Application US/10731238
; Publication No. US20050123552A1
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
Patti, Joseph M.
House-Pompeo, Karen L.
Speziale, Pietro
John, Danny
McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30

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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/731,238
; FILING DATE: 10-Dec-2003
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/010,317
; FILING DATE: 21-Jan-1998
; APPLICATION NUMBER: US 60/036,139
; FILING DATE: 21-JAN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Hibler, David W.
; REGISTRATION NUMBER: 41,071
; REFERENCE/DOCKET NUMBER: TAMK.189
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 512-418-3000
; TELEFAX: 512-474-7577
; INFORMATION FOR SEQ ID NO: 47:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 38 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 47:
US-10-731-238-47
;
; Query Match 88.1%; Score 192; DB 18; Length 38;
; Best Local Similarity 92.1%; Pred. No. 1,4e-17;
; Matches 35; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 ONKGNQSPPDTEKDKPKYEHPPNIIDIDPDSVPHIHG 38
DB 1 ONKGNQSPPDTEKDKPKYEHGNIIDIDPDSVPHIHG 38
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; RESULT 7
; US-10-731-238-7
; Sequence 7, Application US/10731238
; Publication No. US20050123552A1
; GENERAL INFORMATION:
; APPLICANT: Hook, Magnus
; Patti, Joseph M.
; House-Pompeo, Karen L.
; Speziale, Pietro
; John, Danny
; McGavin, Martin J.
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
; AND METHODS OF USE
; NUMBER OF SEQUENCES: 105
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: TX
; COUNTRY: USA
; ZIP: 77210-4433
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/731,238
; FILING DATE: 10-Dec-2003
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/010,317
; FILING DATE: 21-Jan-1998
; APPLICATION NUMBER: US 60/036,139
; FILING DATE: 21-JAN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Hibler, David W.
; REGISTRATION NUMBER: 41,071
; REFERENCE/DOCKET NUMBER: TAMK.189

;;
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 512-418-3000
; TELEFAX: 512-474-7577
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 38 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-10-731-238-7
;
; Query Match 84.4%; Score 184; DB 9; Length 139;
; Best Local Similarity 89.5%; Pred. No. 1.5e-16;
; Matches 34; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 1 ONKGNQSPPDTEKDKPKYEHPPNIIDIDPDSVPHIHG 38
DB 1 ONKGNQSPPDTEKDKPKYEHGNIIDIDPDSVPHIHG 38
;
; RESULT 8
; US-09-813-820-8
; Sequence 8, Application US/09813820
; Patent No. US20020102262A1
; GENERAL INFORMATION:
; APPLICANT: Hook, Magnus
; Patti, Joseph M.
; House-Pompeo, Karen
; Stnaman, Narayana
; Symeraky, Jindrich
; TITLE OF INVENTION: COLLAGEN BINDING PROTEIN COMPOSITIONS
; AND METHODS OF USE
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: U.S.
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/813,820
; FILING DATE: 22-Mar-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/856,253
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Kitchell, Barbara S.
; REGISTRATION NUMBER: 33,928
; REFERENCE/DOCKET NUMBER: TAMK.193
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (512) 418-3000
; TELEFAX: (512) 474-7577
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 139 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-09-813-820-8
;
; Query Match 84.4%; Score 184; DB 9; Length 139;
; Best Local Similarity 89.5%; Pred. No. 1.5e-16;
; Matches 34; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 QNKGNSFPDTEKDKPKYEHPPNIIDIDFDSVPHNG 38
Db 54 QNKGNSFEEDTEKDKPKYEHGNIIDIDFDSVPHNG 91

RESULT 9

US-09-815-242-5797
; Sequence 5797, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Karl L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; TITLE OF INVENTION: Identification of Essential Genes in
; FILE REFERENCE: ELITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5797
; LENGTH: 1018
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-09-815-242-5797

Query Match 84.4%; Score 184; DB 9; Length 1018;
Best Local Similarity 89.5%; Pred. No. 7e-15; Indels 4; Gaps 0;
Matches 34; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 QNKGNSFPDTEKDKPKYEHPPNIIDIDFDSVPHNG 38
Db 784 QNKGNSFEEDTEKDKPKYEHGNIIDIDFDSVPHNG 821

RESULT 10

US-09-815-242-12838
; Sequence 12838, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Karl L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; FILE REFERENCE: ELITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078

; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12838
; LENGTH: 1018
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-09-815-242-12838

Query Match 84.4%; Score 184; DB 9; Length 1018;
Best Local Similarity 89.5%; Pred. No. 7e-15; Indels 4; Gaps 0;
Matches 34; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 QNKGNSFPDTEKDKPKYEHPPNIIDIDFDSVPHNG 38
Db 784 QNKGNSFEEDTEKDKPKYEHGNIIDIDFDSVPHNG 821

RESULT 11

US-10-470-048B-68
; Sequence 68, Application US/10470048B
; Publication No. US2005003744A1
; GENERAL INFORMATION:
; APPLICANT: MEINKE ET AL.
; TITLE OF INVENTION: A METHOD FOR IDENTIFICATION, ISOLATION AND PRODUCTION OF
; FILE REFERENCE: SONN.035US
; CURRENT APPLICATION NUMBER: US/10/470,048B
; PRIOR FILING DATE: 2003-07-25
; NUMBER OF SEQ ID NOS: 603
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 68
; LENGTH: 1018
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-10-470-048B-68

Query Match 84.4%; Score 184; DB 17; Length 1018;
Best Local Similarity 89.5%; Pred. No. 7e-15; Indels 4; Gaps 0;
Matches 34; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 QNKGNSFPDTEKDKPKYEHPPNIIDIDFDSVPHNG 38
Db 784 QNKGNSFEEDTEKDKPKYEHGNIIDIDFDSVPHNG 821

RESULT 12

US-08-781-986A-5254
; Sequence 5254, Application US/08781986A
; Publication No. US2003005436A1
; GENERAL INFORMATION:
; APPLICANT: Charles Kunsch
; TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
; CORRESPONDENCE ADDRESS:
; ADDRESS: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/781,986A
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Benson, Bob
REGISTRATION NUMBER: 30,446
REFERENCE/DOCKET NUMBER: PB248PP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 5254:
SEQUENCE CHARACTERISTICS:
LENGTH: 1027 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-781-986A-5254

Query Match 84.4%; Score 184; DB 8; Length 1027;
Best Local Similarity 89.5%; Pred. No. 7e-15;
Matches 34; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 QNKGNSFPDTEKDKPKYEHHPNIIDIDFDSVPHHG 38
DB 793 QNKGNSFEDTEKDKPKYEHGNIIDIDFDSVPHHG 830

RESULT 13
US-10-329-624-5254
Sequence 5254, Application US/10329624
Publication No. US20040043037A1
GENERAL INFORMATION:
APPLICANT: Charles Kunsch
Gil H. Choi
Patrick S. Dillon
Craig A. Rosen
Steven C. Barash
Michael R. Fannon
TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
NUMBER OF SEQUENCES: 5256
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COUNTRY: USA
ZIP: 20850

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/329,624
FILING DATE: 27-Dec-2002
APPLICATION DATA:
FILING DATE: October 20, 1997
APPLICATION NUMBER: 60/009,861
FILING DATE: January 5, 1996
APPLICATION NUMBER: 08/781,986
FILING DATE: January 3, 1997
ATTORNEY/AGENT INFORMATION:

NAME: Mark J. Hyman
REGISTRATION NUMBER: 46,789
REFERENCE/DOCKET NUMBER: PB248P1D1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (240) 314-1224
TELEFAX: (301) 309-8439
INFORMATION FOR SEQ ID NO: 5254:
SEQUENCE CHARACTERISTICS:
LENGTH: 1027 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 5254:
US-10-329-624-5254

Query Match 84.4%; Score 184; DB 15; Length 1027;
Best Local Similarity 89.5%; Pred. No. 7e-15;
Matches 34; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 QNKGNSFPDTEKDKPKYEHHPNIIDIDFDSVPHHG 38
DB 793 QNKGNSFEDTEKDKPKYEHGNIIDIDFDSVPHHG 830

RESULT 14
US-10-731-238-48
Sequence 48, Application US/10731238
Publication No. US20050123552A1
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
Patti, Joseph M.
House-Pompeo, Karen L.
Speziale, Pietro
Jon, Danny
McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/731,238
FILING DATE: 10-Dec-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE: 21-Jan-1998
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-Jan-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAMK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 48:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear

SEQUENCE DESCRIPTION: SEQ ID NO: 48;
US-10-731-238-48

Job time : 71.1256 secs

Query Match 81.2%; Score 177; DB 18; Length 38;
Best Local Similarity 86.8%; Pred. No. 1.2e-15;
Matches 33; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 QNKGNSFPDTEKDKPKYEHHPNIIDIDFDSVPHIG 38
DB 1 QNKGNSFPDTEKDKPKYEHHPNIIDIDFDSVPHIG 38

RESULT 15

US-10-731-238-45
Sequence 45, Application US/10731238
Publication No. US20050123552A1

GENERAL INFORMATION:

APPLICANT: Hook, Magnus
Patti, Joseph M.
House-Pompeo, Karen L.
Speziale, Pietro
Joh, Danny
McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/731,238
FILING DATE: 10-Dec-2003
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/010,317
FILING DATE: 21-Jan-1998
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-Jan-1997

ATTORNEY/AGENT INFORMATION:

NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE//DOCKET NUMBER: TAWK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577

INFORMATION FOR SEQ ID NO: 45:

SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 45;
US-10-731-238-45

Query Match 79.8%; Score 174; DB 18; Length 38;

Best Local Similarity 86.8%; Pred. No. 3e-15;
Matches 33; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 QNKGNSFPDTEKDKPKYEHHPNIIDIDFDSVPHIG 38
DB 1 QNKGNSFPDTEKDKPKYEHHPNIIDIDFDSVPHIG 38

Search completed: October 22, 2005, 12:09:30

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 22, 2005, 04:14:19 ; Search time 13.8905 Seconds
(without alignments)
263.219 Million cell updates/sec

Title: US-10-731-238-50

Perfect score: 218
Sequence: 1 QNKGNSFPDTEKDKPKYEHPPNIIIDPDSVPHIHG 38

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR 79:.*
1: pirl:.*
2: pirl2:.*
3: pirl3:.*
4: pirl4:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	184	84.4	1018	2 A32192	fibronectin-binding
2	171	78.4	940	2 S19702	fibronectin-binding
3	171	78.4	1038	2 H90053	hypothetical prote
4	159	72.9	961	2 G90053	hypothetical prote
5	60	27.5	690	2 T01183	hypothetical prote
6	60	27.5	2647	2 T28161	hypothetical prote
7	59.5	27.3	223	1 KIHUW3	nucleoside-triphos
8	59	27.1	603	2 B64444	hypothetical prote
9	59	27.1	920	2 T18852	hypothetical prote
10	58	26.6	370	2 AB2578	membrane-bound lyp
11	58	26.6	370	2 A97360	outer membrane lip
12	58	26.6	606	1 S24758	catechol oxidase (
13	55	25.2	3433	1 S28381	urotholin - human
14	54.5	25.0	775	2 T45136	WD repeat protein
15	54	24.8	608	2 I53289	prolactin receptor
16	54	24.8	821	2 S76896	hypothetical prote
17	54	24.8	1122	2 B26427	period clock prote
18	54	24.8	1218	2 A26427	period clock prote
19	54	24.8	1464	2 T07050	hypothetical prote
20	53.5	24.5	610	2 A34631	lactogen receptor
21	53	24.3	170	2 A72638	hypothetical prote
22	53	24.3	330	2 S22140	nodulin Eno42 - Se
23	53	24.3	582	2 I38028	matrix metalloprot
24	53	24.3	808	2 AF1991	hypothetical prote
25	52.5	24.1	833	2 T22139	hypothetical prote
26	52	23.9	56	2 F86623	hypothetical prote
27	52	23.9	56	2 C72000	hypothetical prote
28	52	23.9	112	2 S10101	modulation protein
29	52	23.9	175	2 A84323	50S ribosomal prot

30	52	23.9	236	2 P00806	glycinin A3B4 - so
31	52	23.9	238	2 P00809	glycinin A3B4 (pla
32	52	23.9	243	2 P00807	glycinin A3B4 - so
33	52	23.9	251	2 P00808	glycinin A3B4 (pla
34	52	23.9	328	2 S51458	hypothetical prote
35	52	23.9	471	2 T48743	probable 26S ATP/u
36	52	23.9	516	1 FMSYG3	glycinin G5 precur
37	52	23.9	669	2 I38029	matrix metalloprot
38	52	23.9	920	2 F64697	isolectine-tRNA 11
39	52	23.9	984	2 C84781	hypothetical prote
40	52	23.9	1000	2 I46521	littin - rabbit (tr
41	52	23.9	6805	2 S20901	littin - rabbit (tr
42	52	23.9	26926	1 I38344	littin, cardiac mus
43	51.5	23.6	97	2 S04554	nodulin - alfalfa
44	51.5	23.6	169	2 B97562	peptidyl prollyl cl
45	51.5	23.6	169	2 A12782	peptidyl prollyl cl

ALIGNMENTS

RESULT 1

A32192

fibronectin-binding protein B - Staphylococcus aureus

C/Species: Staphylococcus aureus

C/Date: 31-Jul-1989 #sequence_revision 31-Jul-1989 #text_change 16-Feb-1997

C/Accession: A32192

R/Signaes, C.; Raucel, G.; Joensson, K.; Lindgren, P.E.; Anantharamaiah, G.M.; Hoeck, I

Proc. Natl. Acad. Sci. U.S.A. 86, 699-703, 1989

A/Title: Nucleotide sequence of the gene for a fibronectin-binding protein from Staphyl

A/Reference number: A32192; PMID:8908998; PMID:2521391

A/Accession: A32192

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-1018 <SIG>

A/Cross-references: GB:J04151

C/Keywords: fibronectin binding

Query Match 84.4%; Score 184; DB 2; Length 1018;
Best Local Similarity 89.5%; Pred. No. 1.4e-16;
Matches 34; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 QNKGNSFPDTEKDKPKYEHPPNIIIDPDSVPHIHG 38

DB 784 QNKGNSFPDTEKDKPKYEHPPNIIIDPDSVPHIHG 821

RESULT 2

S19702

fibronectin-binding protein B - Staphylococcus aureus

C/Species: Staphylococcus aureus

C/Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004

R/Joensson, K.; Signaes, C.; Mueller, H.P.; Lindberg, M.

Eur. J. Biochem. 202, 1041-1048, 1991

A/Title: Two different genes encode fibronectin binding proteins in Staphylococcus aure

A/Reference number: S19702; PMID:92111475; PMID:1837266

A/Accession: S19702

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-940 <JOB>

A/Cross-references: UNIPROT:Q53682; EMBL:X62992; NID:949040; PIDD:CAA44726.1; PID:95815

C/Keywords: fibronectin binding

Query Match 78.4%; Score 171; DB 2; Length 940;
Best Local Similarity 84.2%; Pred. No. 7.5e-15;
Matches 32; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 QNKGNSFPDTEKDKPKYEHPPNIIIDPDSVPHIHG 38

DB 720 QNKGNSFPDTEKDKPKYEHPPNIIIDPDSVPHIHG 757

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RESULT 3
H90053
hypothetical protein fnb [imported] - Staphylococcus aureus (strain N315)
C/Species: Staphylococcus aureus
C/Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change: 09-Jul-2004
C/Accession: H90053
R/Kuroda, M.; Ohita, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguc
ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, K.; Kaito, C.; Sekimizu, K.;
C.; Shiba, T.; Hatcori, M.; Ogasawara, N.; Hayashi, H.; Hirame tsu, K.
Lancet 357, 1225-1240, 2001
A/Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.
A/Reference number: A89758; PMID:21311952; PMID:11418146
A/Accession: H90053
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-1038 <KUR>
A/Cross-references: UNIPROT:Q99RD3; GB:BA000018; PID:g13702453; PIDN:BA843594.1; GSPDB:C
A/Experimental source: strain N315
C/Genetics:
A/Genes: fnb

Query Match          78.4%; Score 171; DB 2; Length 1038;
Best Local Similarity 84.2%; Pred. No. 8.4e-15;
Matches 32; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 QNKGNSFPDTEKDKPKYEHPPNIIDIDPDSVPHIHG 38
Db 780 QNKGDSFEDTEKDKPKYEHGNIIDIDPDSVPHIHG 817

RESULT 4
G90053
hypothetical protein fnb [imported] - Staphylococcus aureus (strain N315)
C/Species: Staphylococcus aureus
C/Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C/Accession: G90053
R/Kuroda, M.; Ohita, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguc
ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.;
C.; Shiba, T.; Hatcori, M.; Ogasawara, N.; Hayashi, H.; Hirame tsu, K.
Lancet 357, 1225-1240, 2001
A/Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.
A/Reference number: A89758; PMID:21311952; PMID:11418146
A/Accession: G90053
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-961 <KUR>
A/Cross-references: UNIPROT:Q99RD3; GB:BA000018; PID:g13702452; PIDN:BA843593.1; GSPDB:C
A/Experimental source: strain N315
C/Genetics:
A/Genes: fnb

Query Match          72.9%; Score 159; DB 2; Length 961;
Best Local Similarity 78.9%; Pred. No. 3.2e-13;
Matches 30; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

QY 1 QNKGNSFPDTEKDKPKYEHPPNIIDIDPDSVPHIHG 38
Db 731 QNKGNSFEDTEKDKPKYEHGNIIDIDPDSVPHIHG 768

RESULT 5
T01183
hypothetical protein T26D22.9 - Arabidopsis thaliana
C/Species: Arabidopsis thaliana (mouse-ear cress)
C/Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 16-Aug-2004
C/Accession: T01183
R/Becker, M.; Hinds, K.
submitted to the EMBL Data Library, April 1998
A/Description: The sequence of A. thaliana T26D22.
A/Reference number: Z14253
A/Accession: T01183
A/Status: translated from GB/EMBL/DBJ
A/Molecule type: DNA

A/Residues: 1-690 <BEC>
A/Cross-references: UNIPROT:Q65240; EMBL:AF058826; NID:g3047088; PID:g3047095
A/Experimental source: cultivar Columbia
C/Genetics:
A/Map position: 4
A/Introns: 62/1; 472/1
A/Note: T26D22.9
C/Superfamily: protein kinase homology

Query Match          27.5%; Score 60; DB 2; Length 690;
Best Local Similarity 54.5%; Pred. No. 5.6;
Matches 12; Conservative 1; Mismatches 9; Indels 0; Gaps 0;

QY 2 NKGNOSFPDTEKDKPKYEHPP 23
Db 250 NKGLYKPLETECDSPYIEHP 271

RESULT 6
T28161
hypothetical protein FC93-varT11-1 - malaria parasite (Plasmodium falciparum) (fragments
C/Species: Plasmodium falciparum
C/Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C/Accession: T28161
R/Hernandez-Rivas, R.; Mattei, D.; Sterkere, Y.; Peterson, D.S.; Wellems, T.E.; Scherf,
Mol. Cell. Biol. 17, 604-611, 1997
A/Title: Expressed var genes are found in Plasmodium falciparum subtelomeric regions.
A/Reference number: Z20483; PMID:97154495; PMID:9001213
A/Accession: T28161
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-2647 <HER>
A/Cross-references: UNIPROT:P90580; EMBL:U67959; NID:g1794255; PID:g1809295; PIDN:AA6474
A/Experimental source: strain FCQ27/PNG
C/Genetics:
A/Introns: 2158/3
A/Note: FC93-varT11-1

Query Match          27.5%; Score 60; DB 2; Length 2647;
Best Local Similarity 34.4%; Pred. No. 29;
Matches 11; Conservative 8; Mismatches 13; Indels 0; Gaps 0;

QY 4 GNOSFPDTEKDKPKYEHPPNIIDIDPDSVPH 35
Db 2268 GNNTTASDTQNDIPSTDPPTIDDEWNTLKH 2259

RESULT 7
K1HUA3
nucleoside-triphosphate-adenylate kinase (BC 2.7.4.10) 3 - human
N/Alternate names: adenylylate kinase 3
C/Species: Homo sapiens (man)
C/Date: 17-Apr-1993 #sequence_revision 23-Mar-1995 #text_change 09-Jul-2004
C/Accession: A42820; S16380; S16381
R/Xu, G.; O'Connell, P.; Stevens, J.; White, R.
Genomics 13, 537-542, 1992
A/Title: Characterization of human adenylylate kinase 3 (AK3) cDNA and mapping of the AK3
A/Reference number: A42820; PMID:92347846; PMID:1639383
A/Accession: A42820
A/Molecule type: mRNA
A/Residues: 1-223 <XUG>
A/Cross-references: UNIPROT:P27144; EMBL:X60673; NID:g28576; PIDN:CAA43088.1; PID:g28577.
A/Experimental source: frontal-cortex
A/Note: Sequence extracted from NCBI backbone (NCBI:109644, NCBI:109645)
C/Comment: This isozyme is found in the mitochondrial matrix.
C/Genetics:
A/Genes: GDB:AK3
A/Cross-references: GDB:118988; OMIM:103030
A/Map position: 9pter-9p13
A/Function: catalyzes the reversible phosphorylation of adenine monophosphate with m
A/Note: GMP is preferred to ATP as a substrate
C/Superfamily: adenylylate kinase
```

C;Keywords: ATP; mitochondrial matrix; mitochondrion; P-loop; phosphotransferase
 F/12-19/Region: nucleotide-binding motif A (P-loop) #status atypical
 F/58/Region: nucleotide-binding motif B #status atypical
 F/22,33,35,58/Active site: Cys, His, Ser, Asp #status predicted

Query Match 27.1%; Score 59.5; DB 1; Length 223;
 Best Local Similarity 36.1%; Pred. No. 1.7;
 Matches 13; Conservative 11; Mismatches 7; Indels 5; Gaps 3;
 7 SPFPDTEKDK-PKYEHPN-1IIDIDFDSVPHIG 38
 113 NIPETIKDRLSRWHPSPGRVYNDPFP-PRVHG 147

RESULT 8
 B64444
 hypothetical protein homolog MJ155 - Methanococcus jannaschii
 C;Species: Methanococcus jannaschii
 C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004
 C;Accession: B64444
 R;Bult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blake,
 R.; Bult, C.J.; Overbeek, R.; Kirschner, E.F.; Weissbrock, K.G.; Merrick, J.M.; Glodok, A.;
 rson, J.D.; Sadt, P.W.; Hanna, M.C.; Cocton, M.D.; Roberts, K.M.; Huret, M.A.
 Science 273, 1058-1073, 1996
 A;Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Frazer, C.M.; Smith, H.O.; Woese,
 A.; Title: Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschii
 A;Reference number: A64300; MUID:96337999; PMID:8688087
 A;Accession: B64444
 A;Status: preliminary; nucleic acid sequence not shown; translation not shown
 A;Molecule type: DNA
 A;Residues: 1-603 <BUL>
 A;Cross-references: UNIPROT:Q58555; GB:U67557; GB:L77117; NID:g1591777; PIDN:AA899152.1;
 C;Genetics:
 A;Map position: REV1093686-1091875

Query Match 27.1%; Score 59; DB 2; Length 603;
 Best Local Similarity 32.1%; Pred. No. 6.5;
 Matches 17; Conservative 4; Mismatches 14; Indels 18; Gaps 3;
 1 ONKNGO---SPFPD---TEKD-----PKYEHPNIIIDIDFDSVPH 35
 244 QKVGNOVLVQPPPIYLTKEMDIYEMPERKAPSYIVGIVVQPSVTH 296

RESULT 9
 T18852
 hypothetical protein CO1H6.9 - Caenorhabditis elegans
 C;Species: Caenorhabditis elegans
 C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
 C;Accession: T18852; T23974; T26002
 R;Berks, M.
 submitted to the EMBL Data Library, April 1996
 A;Reference number: Z19030
 A;Accession: T18852
 A;Status: preliminary; translated from GB/EMBL/DBJ
 A;Molecule type: DNA
 A;Residues: 1-920 <WIL>
 A;Cross-references: UNIPROT:O17985; EMBL:Z71258; PIDN:CAA95786.1; GSPDB:GN00019; CESP:CO1H6.9
 A;Experimental source: clone CO1H6
 R;Gardner, A.
 submitted to the EMBL Data Library, April 1996
 A;Reference number: Z19825
 A;Accession: T23974
 A;Status: preliminary; translated from GB/EMBL/DBJ
 A;Molecule type: DNA
 A;Residues: 1-920 <WIL>
 A;Cross-references: EMBL:Z71266; PIDN:CAA95847.1; GSPDB:GN00019; CESP:CO1H6.9
 A;Experimental source: clone R06C7
 R;Steward, C.
 submitted to the EMBL Data Library, August 1997
 A;Reference number: Z20124
 A;Accession: T26002
 A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA
 A;Residues: 1-920 <WIL>
 A;Cross-references: EMBL:Z98261; PIDN:CA10931.1; GSPDB:GN00019; CESP:CO1H6.9
 A;Experimental source: clone VC01H6R
 C;Genetics:
 A;Gene: CESP:CO1H6.9
 A;Map position: 1
 A;Introns: 63/2; 111/3; 154/1; 209/1; 226/1; 248/1; 296/1; 342/1; 490/1; 807/1; 841/2;

Query Match 27.1%; Score 59; DB 2; Length 920;
 Best Local Similarity 40.0%; Pred. No. 11;
 Matches 12; Conservative 5; Mismatches 11; Indels 2; Gaps 1;
 5 NOSFPDTEKDKPKYEHP--PNIIIDFDS 32
 58 NPEFKPSKKKKPKVPVPPSPVSDVEISS 87

RESULT 10
 AB2578
 membrane-bound lytic murein transglycosylase mlta (imported) - Agrobacterium tumefaciens
 C;Species: Agrobacterium tumefaciens
 C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 09-Jul-2004
 C;Accession: AB2578
 R;Wood, D.W.; Serubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo,
 erage, G.; Giller, W.; Grant, C.; Guenther, D.; Kutayavin, T.; Levy, R.; Li, M.; Mclel
 Karp, P.; Romero, P.; Zhang, S.
 Science 294, 2317-2323, 2001
 A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
 ster, B.W.
 A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
 A;Reference number: AB2577; MUID:21608550; PMID:11743193
 A;Accession: AB2578
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-370 <KUR>
 A;Cross-references: UNIPROT:Q8UJ9; GB:AE008688; PIDN:AL41040.1; PID:g17738325; GSPDB:
 A;Experimental source: strain C58 (Dupont)
 C;Genetics:
 A;Gene: mlta
 A;Map position: circular chromosome

Query Match 26.6%; Score 58; DB 2; Length 370;
 Best Local Similarity 42.9%; Pred. No. 4.9;
 Matches 12; Conservative 3; Mismatches 13; Indels 0; Gaps 0;
 7 SPFPDTEKDKPKYEHPNIIIDIDFDSV 34
 107 SATPDVWRKYPIRRREPVLVDINDNRP 134

RESULT 11
 A97360
 outer membrane lipoprotein gn33 (ecoli_mlta homolog) (AF226403) (imported) - Agrobacte
 C;Species: Agrobacterium tumefaciens
 C;Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 09-Jul-2004
 C;Accession: A97360
 R;Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Bianchard, M.; Qurollo, B.; Goldman
 A.; Liu, P.; Wollam, C.; Allinger, M.; Doughy, D.; Scott, C.; Lappas, C.; Markelz, B.
 Science 294, 2323-2328, 2001
 A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tu
 A;Reference number: A97359; MUID:21608551; PMID:11743194
 A;Accession: A97360
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-370 <KUR>
 A;Cross-references: UNIPROT:Q8UJ9; GB:AE007865; PIDN:AK85834.1; PID:g15154667; GSPDB:
 A;Gene: AGR_C_15
 A;Map position: circular chromosome

Query Match 26.6%; Score 58; DB 2; Length 370;
 Best Local Similarity 42.9%; Pred. No. 4.9;

Matches 12; Conservative 3; Mismatches 13; Indels 0; Gaps 0;

Qy 7 SPPDTEKDKPKYEHPPNIIDIDFDSVP 34

Db 107 SATPDDVWRYPYRPPPELVIDIDNDNR 134

RESULT 12

S24758

catechol oxidase (EC 1.10.3.1) precursor - fava bean
N:Alternate names: polyphenol oxidase

C:Species: *Vicia faba* (fava bean)

C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004

A:Accession: S24758; S19805

R:Carry, J.W.; Lax, A.R.; Flurkey, W.H.

Plant Mol. Biol. 20, 245-253, 1992

A>Title: Cloning and characterization of cDNAs coding for *Vicia faba* polyphenol oxidase.

A:Reference number: S24758; MUID:93004477; PMID:1391768

A:Accession: S24758

A:Molecule type: mRNA

A:Residues: 1-606 <CAR>

A:Cross-references: UNIPROT:Q06215; EMBL:Z11702

R:Carry, J.

submitted to the EMBL Data Library, February 1992

A:Reference number: S19805

A:Accession: S19805

A:Molecule type: mRNA

A:Residues: 1-247, 'T', 249-250, 'A', 252-278, 'IG', 281-283, 286, 'RN', 287-606 <CA2>

A:Cross-references: EMBL:Z11702; NID:923028; PIDN:CAA7764.1; PID:922029

C:Superfamily: catechol oxidase

C:Keyword: chloroplast; copper; metalloprotein; oxidoreductase

F:1-92/Domain: transit peptide (chloroplast) #status predicted <INP>

F:93-606/Product: catechol oxidase #status predicted <MAT>

F:202,211/Binding site: copper (His) #status predicted

F:333,337/Binding site: copper (His) #status predicted

Query Match 26.6%; Score 58; DB 1; Length 606;

Best Local Similarity 40.0%; Pred. No. 9;

Matches 14; Conservative 5; Mismatches 8; Indels 8; Gaps 2;

Qy 12 TEKDKPKYE-----HPPNIIDIDF-DSVPHIHG 38

Db 251 TDKASPLVDELRMAHQPFRLIDLNFCDSDDSIHG 285

RESULT 13

S28381

utrophin - human
N:Alternate names: dystrophin-related protein

C:Species: *Homo sapiens* (man)

C>Date: 17-Apr-1993 #sequence_revision 03-Oct-1995 #text_change 09-Jul-2004

C:Accession: S28381; S28914; S03966

R:Finley, J.M.

submitted to the EMBL Data Library, November 1992

A:Reference number: S28381

A:Accession: S28381

A:Molecule type: mRNA

A:Residues: 1-3433 <TIN1>

A:Cross-references: UNIPROT:P46939; EMBL:X69086; NID:934811; PIDN:CAA48829.1; PID:934812

R:Finley, J.M.; Blake, D.J.; Roche, A.; Fairbrother, U.; Ries, J.; Byth, B.C.; Knight, Nature 360, 591-593, 1992

A>Title: Primary structure of dystrophin-related protein.

A:Reference number: S28914; MUID:9306045; PMID:1461283

A:Accession: S28914

A:Molecule type: mRNA

A:Residues: 27-246; 2839-3343 <TIN2>

A:Cross-references: EMBL:X69086

R:Love, D.R.; Hill, D.F.; Dickson, G.; Spurr, N.K.; Byth, B.C.; Marsden, R.F.; Walsh, F. Nature 339, 55-58, 1989

A>Title: An autosomal transgenic in skeletal muscle with homology to dystrophin.

A:Reference number: S03966; MUID:89238543; PMID:2541343

A:Accession: S03966

A:Molecule type: mRNA

A:Residues: 2944-3433 <LOV>

A:Cross-references: EMBL:X1548; NID:930933; PIDN:CAA3351.1; PID:9930062

C:Comment: This protein is found primarily at the neuromuscular junctions in adult muscle d regenerating muscle.

C:Genetics:

A:Gene: GDB:UTRN; DMDL

A:Cross-references: GDB:119851; OMIM:128240

A:Map position: 6q24-6q24

C:Superfamily: dystrophin; alpha-actinin actin-binding domain homology; spectrin/dystrop

C:Keywords: actin binding; cytoskeleton; leucine zipper; membrane-associated protein; mu

F:30-248/Domain: alpha-actinin actin-binding domain homology <ACT>

F:308-417/Domain: spectrin/dystrophin repeat homology <SP01>

F:418-526/Domain: spectrin/dystrophin repeat homology <SP02>

F:528-637/Domain: spectrin/dystrophin repeat homology <SP03>

F:638-685/Region: hinge

F:686-796/Domain: spectrin/dystrophin repeat homology <SP04>

F:804-902/Domain: spectrin/dystrophin repeat homology <SP05>

F:906-1013/Domain: spectrin/dystrophin repeat homology <SP06>

F:1015-1122/Domain: spectrin/dystrophin repeat homology <SP07>

F:1124-1230/Domain: spectrin/dystrophin repeat homology <SP08>

F:1232-1334/Domain: spectrin/dystrophin repeat homology <SP10>

F:1339-1450/Domain: spectrin/dystrophin repeat homology <SP12>

F:1451-1541/Domain: spectrin/dystrophin repeat homology <SP13>

F:1543-1649/Domain: spectrin/dystrophin repeat homology <SP14>

F:1651-1755/Domain: spectrin/dystrophin repeat homology <SP15>

F:1756-1973/Domain: spectrin/dystrophin repeat homology <SP16>

F:1975-2081/Domain: spectrin/dystrophin repeat homology <SP17>

F:2083-2185/Domain: spectrin/dystrophin repeat homology <SP18>

F:2227-2333/Domain: spectrin/dystrophin repeat homology <SP19>

F:2335-2440/Domain: spectrin/dystrophin repeat homology <SP20>

F:2442-2556/Domain: spectrin/dystrophin repeat homology <SP21>

F:2558-2668/Domain: spectrin/dystrophin repeat homology <SP22>

F:2690-2797/Domain: spectrin/dystrophin repeat homology <SP23>

F:2798-2869/Region: hinge

F:2812-2849/Domain: WW repeat homology <WW1>

F:2837-3117/Region: cysteine-rich

F:3263-3284/Region: leucine zipper motif

F:3328-3349/Region: leucine zipper motif

Query Match 25.2%; Score 55; DB 1; Length 3433;

Best Local Similarity 34.6%; Pred. No. 1,9e+02;

Matches 9; Conservative 6; Mismatches 11; Indels 0; Gaps 0;

Qy 6 QSPDTEKDKPKYEHPPNIIDIDF 31

Db 285 QSTAPEEHESPRALPTSTVEVDMD 310

RESULT 14

T45136

WD repeat protein popl (imported) - fission yeast (*Schizosaccharomyces pombe*)

C:Species: *Schizosaccharomyces pombe*

C>Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 09-Jul-2004

C:Accession: T45136; T40157

R:Kominami, K.; Toda, T.

submitted to the EMBL Data Library, September 1996

A:Description: Fission yeast WD repeat protein Popl is involved in maintenance of ploidy

A:Reference number: Z22925

A:Accession: T45136

A:Molecule type: DNA

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Residues: 1-775 <KOW>

A:Cross-references: UNIPROT:P87060; EMBL:Y08391; PIDN:CAA69671.1

A:Experimental source: strain h- 972

R:Wood, V.; Rajandream, M.A.; Barrell, B.G.; Devlin, K.; Churcher, C.M.

submitted to the EMBL Data Library, March 1998

A:Reference number: Z21842

A:Accession: T40157

A:Molecule type: DNA

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Residues: 1-775 <KOW>

A:Cross-references: EMBL:AL022103; PIDN:CAA17898.1; GSPDB:GN00067; SPDB:SPBC2G2.18

A:Experimental source: strain 972h-, cosmid c2G2

C/Genetics:
A/Gene: SPBC262.18
A/Map position: 2
A/Note: pop1+

Query Match 25.0%; Score 54.5; DB 2; Length 775;
Best Local Similarity 36.1%; Pred. No. 36;
Matches 13; Conservative 4; Mismatches 18; Indels 1; Gaps 1;

QY 2 NKGNSFPPTTEKDKPKYEHPPNIIIDIPDSVPHIH 37
: | | | | | : | | | | | : | | | | |
DB 205 SKTRQSFPHSSSSSHNSLHEPVIYDPSSSEN-PSIH 239

RESULT 15

153269
Prolactin receptor, long form - mouse
C/Species: Mus musculus (house mouse)
C/Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 09-Jul-2004
C/Accession: 153269; J10671; S34356
R/Claude, D.L.; Linzer, D.I.H.
Endocrinology 133, 224-232, 1993
A/Title: Changes in prolactin receptor expression during pregnancy in the mouse ovary.
A/Reference number: 153269; MUID:93307149; PMID:8319571
A/Accession: 153269
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Residues: 1-608 <RES>
A/Molecule type: mRNA
A/Cross-references: UNIPROT:Q08501; GB:L14811; NID:G293769; PIDN:AAA02686.1; PID:G293770
R/Moore, R.C.; Oka, T.
Gene 134, 263-265, 1993
A/Title: Cloning and sequencing of the cDNA encoding the murine mammary gland long-form
A/Reference number: J10671; MUID:94085788; PMID:8262385
A/Accession: J10671
A/Molecule type: mRNA
A/Residues: 1-608 <MO>
A/Cross-references: GB:L13593; NID:G347398; PIDN:AA037641.1; PID:G347842
R/Edey, M.; Pezet, A.; Nandi, S.; Kelly, P.A.
submitted to the EMBL Data Library, June 1993
A/Description: Isolation and nucleotide sequence of a mouse CDNA prolactin receptor.
A/Reference number: S34356
A/Accession: S34356
A/Molecule type: mRNA
A/Residues: 1-557, 'F', 559-608 <EDE>
A/Cross-references: EMBL:X73372; NID:G312696; PIDN:CAA51789.1; PID:G312697
C/Comment: Prolactin receptor have long form and short form which are resulted from alternative splicing.
C/Keywords: prolactin receptor; transmembrane protein
F/31-216/Domain: cytokine receptor homology <CRS>
F/230-253/Domain: transmembrane #status predicted <TMM>

Query Match 24.8%; Score 54; DB 2; Length 608;
Best Local Similarity 40.7%; Pred. No. 31;
Matches 11; Conservative 5; Mismatches 11; Indels 0; Gaps 0;

QY 2 NKGNSFPPTTEKDKPKYEHPPNIIIDIPDSVPHIH 37
: | | | | | : | | | | | : | | | | |
DB 473 DKQNTSWPPLQEKGPYVAKRPPDYVEI 499

Search completed: October 22, 2005, 06:09:56
Job time : 14.8905 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 22, 2005, 04:10:49 ; Search time 69.6361 Seconds
(without alignments)
279.439 Million cell updates/sec

Title: US-10-731-238-50

Perfect score: 218

Sequence: 1 QNKGNSPPPTKDKPKYEHPPNIDIDPDSVPHIHG 38

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: UniProt_03:*

1: uniprot_sprot:*

2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	184	84.4	1018	1 FNBA_STNAU	P14738 staphylococ
2	179	82.1	943	2 Q8NU8	Q8NU8 staphylococ
3	179	82.1	957	2 Q6G6H4	Q6G6H4 staphylococ
4	176	80.7	152	2 Q9AEP9	Q9AEP9 staphylococ
5	171	78.4	940	2 Q53682	Q53682 staphylococ
6	171	78.4	1038	2 Q99RD2	Q99RD2 staphylococ
7	171	78.4	1038	2 Q7A3J7	Q7A3J7 staphylococ
8	163	74.8	1015	2 Q8NU07	Q8NU07 staphylococ
9	163	74.8	1015	2 Q6G6H3	Q6G6H3 staphylococ
10	159	72.9	961	2 Q99RD3	Q99RD3 staphylococ
11	159	72.9	961	2 Q7A3J8	Q7A3J8 staphylococ
12	159	72.9	961	2 Q6GDU5	Q6GDU5 staphylococ
13	159	72.9	961	2 Q69L72	Q69L72 oryza sativ
14	64	29.4	644	2 Q41940	Q41940 murid herpe
15	64	29.4	644	2 Q83342	Q83342 murid herpe
16	63.5	29.1	686	2 Q8N7Y8	Q8N7Y8 homo sapien
17	63.5	29.1	686	2 Q6P2C0	Q6P2C0 homo sapien
18	62.	28.4	746	2 Q6FTT2	Q6FTT2 candida gla
19	61	28.0	102	2 Q9SOP5	Q9SOP5 glycine max
20	61	28.0	1678	2 Q9BMP2	Q9BMP2 sterylomychia
21	60	27.5	690	2 Q65240	Q65240 arabidopsis
22	60	27.5	2647	2 P90580	P90580 plasmodium
23	59.5	27.3	223	1 QAD4 HUMAN	QAD4 homo sapien
24	59.5	27.3	223	1 Q8IUD9	Q8IUD9 homo sapien
25	59.5	27.3	223	2 Q6NXX5	Q6NXX5 homo sapien
26	59.5	27.3	223	2 Q6NXX5	Q6NXX5 homo sapien
27	59.5	27.3	223	2 Q6NXX5	Q6NXX5 homo sapien
28	59	27.1	603	1 Y855 METVA	Y855 METVA
29	59	27.1	920	2 Q17985	Q17985 caenorhabdi
30	58	26.6	370	2 Q8UJ89	Q8UJ89 agrobacteri
31	57.5	26.4	498	2 Q710D7	Q710D7 vulpes vulp
			894	2 P93237	P93237 lupinus lute

ALIGNMENTS

RESULT 1	FNBA_STNAU	STANDARD	PRT	1018 AA	
AC	P14738;				Q7Q2S6
DT	01-APR-1990 (Rel. 14, Created)				Q8KH7 erwina chr
DT	01-APR-1990 (Rel. 14, Last sequence update)				Q8IAS3 plasmodium
DT	25-OCT-2004 (Rel. 45, Last annotation update)				Q6C1J3 kluyveromyc
DE	Fibronectin-binding protein precursor (FNBP).				Q8DJN6 synechococ
GN	Name=fnba;				Q7TSG5 mus musculu
OS	Staphylococcus aureus.				Q96UQ5 aspergillus
OC	Bacteria; Firmicutes; Bacillales; Staphylococcus.				Q7RNJ1 plasmodium
OX	NCBI_TaxID=1280;				Q81521 plasmodium
RN	[1]				Q73Y17 mycobacteri
RP	SEQUENCE FROM N.A.				Q7N1X2 glieobacter
RC	STRAIN=NCTC 8325-4;				Q8M1E8 chaetosphe
RX	MEDLINE=89098998; PubMed=2521391;				Q6L1P4 photobacter
RA	Signaes C., Raucel G., Joensen K., Lindgren P.-E.,				Q9N4J9 caenorhabdi
RA	Anantharaman G.M., Hoeck M., Lindberg M.;				
RT	"Nucleotide sequence of the gene for a fibronectin-binding protein				
RT	from Staphylococcus aureus: use of this peptide sequence in the				
RT	synthesis of biologically active peptides."				
RL	Proc. Natl. Acad. Sci. U.S.A. 86:699-703(1989).				
CC	-1- FUNCTION: The ability of bacteria to bind fibronectin has been				
CC	proposed as a virulence factor enabling bacteria to colonize wound				
CC	tissues and blood clots. Binding of plasma fibronectin to the				
CC	bacterial surface might block adhesion receptors on S.aureus, thus				
CC	representing an important defense mechanism against tissue				
CC	invasion.				
CC	-1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by				
CC	an amide bond (Potential).				
CC	-----				
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration				
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -				
CC	the European Bioinformatics Institute. There are no restrictions on its				
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CC	entities requires a license agreement (See http://www.ebi.ac.uk/submit/				
CC	or send an email to license@ebi.ac.uk).				
CC	-----				
DR	EMBL: J04151; AAA26632.1; -				
DR	InterPro: IPR004237; Fp_bind.				
DR	InterPro: IPR005877; Gpos_YSTRK.				
DR	InterPro: IPR001899; Gram_pos_anchor.				
DR	Pfam: PF00746; Gram_pos_anchor; 1.				
DR	Pfam: PF04650; YSTRK_signal; 1.				
DR	TIGRFAMs: TIGR01167; LPTG_anchor; 1.				
DR	TIGRFAMs: TIGR01168; YSTRK_signal; 1.				
DR	PROSITE: PS50847; GRAM_POS_ANCHORING; 1.				
DR	Cell adhesion; Cell wall; Peptidoglycan-anchor; Repeat; Signal;				
KW	Virulence.				
FT	SIGNAL	1	36		
FT	CHAIN	37	985		
FT	PROPEP	986	1018		
					Fibronectin-binding protein.
					Removed by sortase (Potential).


```

FT REPEAT 545 574 B-1.
FT REPEAT 575 604 B-2.
FT DOMAIN 745 878 4 X approximate tandem repeats,
  fibronectin-binding domain.
FT REPEAT 745 782 D-1.
FT REPEAT 783 820 D-2.
FT REPEAT 821 859 D-3.
FT REPEAT 860 878 D-4 (incomplete).
FT DOMAIN 879 948 5 X tandem repeats, Pro-rich (WR).
FT REPEAT 879 892 WR 1.
FT REPEAT 893 906 WR 2.
FT REPEAT 907 920 WR 3.
FT REPEAT 921 934 WR 4.
FT REPEAT 935 948 WR 5.
FT SITE 982 986 LpxTG sorting signal (potential).
FT MOD_RES 985 985 Pentaglycyl murin peptidoglycan amidated
  threonine (Potential).
SQ SEQUENCE 1018 AA; 11780 MW; 58175E020E81F1F CRC64;

Query Match 84.4%; Score 184; DB 1; Length 1018;
Best Local Similarity 89.5%; Pred. No. 2e-14;
Matches 34; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 QNKGNSFPDTEKDKPKYEHHPNIIDIDFDSVPHHG 38
Db 784 QNKGNSFPDTEKDKPKYEHGNIIDIDFDSVPHHG 821

RESULT 2
Q8NUN8 PRELIMINARY; PRT; 943 AA.
ID 28NUN8;
AC 28NUN8;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE FmbB protein.
DE Name=fmbB; OrderedLocustNames=MM2420;
OS Staphylococcus aureus (strain MM2)
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=196620;
RN 1;
RP SEQUENCE FROM N.A.
RC STRAIN=MM2;
RA hada T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Oguchi A.,
  Yamaguchi Y., Iwama N., Amano K., Naito T., Kuroda H., Cui L.,
  Yamamoto K., Hiramatsu K.;
RT "Genome and virulence determinants of high virulence community-
  acquired MRSA.";
RL Lancet 359:1819-1827(2002).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
  an amide bond (By similarity).
DR EMBL; AP004830; BAB96285.1; -.
DR HSP; Q53653; IN67.
DR GO; GO:0009986; C:cell surface; IEA.
DR GO; GO:0005618; C:cell wall; IEA.
DR GO; GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0007155; P:cell adhesion; IEA.
DR InterPro; IPR008966; Adhes_bact.
DR InterPro; IPR004237; Fn_bind.
DR InterPro; IPR005877; Gpos_YsIRK.
DR InterPro; IPR001899; Gram_pos_anchor.
DR Pfam; PF02986; Fn_bind; 1.
DR Pfam; PF00746; Gram_pos_anchor; 1.
DR TIGRPFAMs; TIGR01167; LpxTG_signal; 1.
DR TIGRPFAMs; TIGR01168; YsIRK_signal; 1.
DR PROSITE; PS50847; GRAM_POS_ANCHORING; 1.
DR Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ SEQUENCE 943 AA; 104537 MW; DA8A5F31947E1B6A CRC64;

Query Match 82.1%; Score 179; DB 2; Length 943.

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Best Local Similarity 86.8%; Pred. No. 8e-14;
Matches 33; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 1 QNKGNSFPDTEKDKPKYEHHPNIIDIDFDSVPHHG 38
Db 727 QNKGDSFPDTEKDKPKYEHGNIIDIDFDSVPHHG 764

RESULT 3
Q6G6H4 PRELIMINARY; PRT; 957 AA.
ID Q6G6H4;
AC Q6G6H4;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Fibronectin-binding protein.
DE Name=fmbB; OrderedLocustNames=SAS2387;
OS Staphylococcus aureus (strain MSSA476).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=282459;
RN 1;
RP SEQUENCE FROM N.A.
RC PubMed=15213324; DOI=10.1073/pnas.0402521101;
RX Holden M.T.G., Fell E.J., Lindsay J.A., Peacock S.J., Day N.P.J.,
  Enright M.C., Foster T.J., Moore C.E., Hurst L., Atkin R., Barron A.,
  Bason N., Bentley S.D., Chillingworth C., Chillingworth T.,
  Churcher C., Clark L., Corton C., Cronin A., Doggett J., Dowd L.,
  Felwell T., Hance Z., Harris B., Hauser H., Holtroyd S., Jagels K.,
  James K.D., Lennard N., Line A., Mayes R., Moule S., Mungall K.,
  Ormond D., Quail M.A., Rabinowitch E., Rutherford K.M., Sanders M.,
  Sharp S., Simmonds M., Stevens K., Whitehead S., Barrett B.G.,
  RASart B.G., Parkhill J.;
RA "Complete genomes of two clinical Staphylococcus aureus strains:
  evidence for the rapid evolution of virulence and drug resistance.";
RT Proc. Natl. Acad. Sci. U.S.A. 101:9786-9791(2004).
RL -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
  an amide bond (By similarity).
CC EMBL; BX571857; CAG44201.1; -.
DR GO; GO:0009986; C:cell surface; IEA.
DR GO; GO:0005618; C:cell wall; IEA.
DR GO; GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0007155; P:cell adhesion; IEA.
DR InterPro; IPR008966; Adhes_bact.
DR InterPro; IPR004237; Fn_bind.
DR InterPro; IPR005877; Gpos_YsIRK.
DR InterPro; IPR001899; Gram_pos_anchor.
DR Pfam; PF02986; Fn_bind; 1.
DR Pfam; PF00746; Gram_pos_anchor; 1.
DR TIGRPFAMs; TIGR01167; LpxTG_signal; 1.
DR TIGRPFAMs; TIGR01168; YsIRK_signal; 1.
DR PROSITE; PS50847; GRAM_POS_ANCHORING; 1.
DR Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ SEQUENCE 957 AA; 105980 MW; 28F8BA7FFDFD3EAF CRC64;

Query Match 82.1%; Score 179; DB 2; Length 957;
Best Local Similarity 86.8%; Pred. No. 8.1e-14;
Matches 33; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 1 QNKGNSFPDTEKDKPKYEHHPNIIDIDFDSVPHHG 38
Db 727 QNKGDSFPDTEKDKPKYEHGNIIDIDFDSVPHHG 764

RESULT 4
Q9AEP9 PRELIMINARY; PRT; 152 AA.
ID Q9AEP9;
AC Q9AEP9;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Fibronectin-binding protein (Fragment).

```

GN Name=fnb;
 OS Staphylococcus aureus.
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 OX NCBI_TaxId=1280;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CMRSA-1;
 RX MEDLINE=21246681; PubMed=11349044;
 RI DOI=10.1128/JAI.69.6.3791-3799.2001;
 RA Rice K., Huesca M., Vaz D., McGavin M.J.;
 RT "variance in fibronectin binding and fnb locus polymorphisms in
 Staphylococcus aureus: identification of antigenic variation in a
 fibronectin binding protein adhesin of the epidemic CMRSA-1 strain of
 methicillin-resistant S. aureus.";
 RT Infect. Immun. 69:3791-3799 (2001).
 DR EMBL: AY029184; AAK31588.1; -
 FT NON_TER 1 152
 FT SEQUENCE 152 AA; 17193 MW; CFA3913C2B11C025 CRC64;
 SQ
 Query Match 80.7%; Score 176; DB 2; Length 152;
 Best Local Similarity 86.8%; Pred. No. 2.6e-14;
 Matches 33; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
 QY 1 ONKNGSFPPDTEKDKPKYHHPNIIIDIDFDSVPHIHG 38
 DB 77 ONKNGSFEDTEKDKPKYHGGNIIDIDFDSVPHIHG 114
 RESULT 5
 Q53682 ID Q53682 PRELIMINARY; PRT; 940 AA.
 AC Q53682;
 DT 01-NOV-1996 (TREMBlrel. 01, Created)
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
 DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
 DE Fibronectin binding protein B.
 GN Name=fnbB;
 OS Staphylococcus aureus.
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 OX NCBI_TaxId=1280;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=8325-4;
 RX MEDLINE=92111475; PubMed=1837266;
 RI Johnson K., Sigmas C., Muller H.P., Lindberg M.;
 RT "Two different genes encode fibronectin binding proteins in
 Staphylococcus aureus. The complete nucleotide sequence and
 RT characterization of the second gene.";
 RT Eur. J. Biochem. 202:1041-1048 (1991).
 CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
 an amide bond (By similarity).
 DR EMBL: X62992; CAA44726.1; -
 DR PIR: S19702; S19702.
 DR HSSP: Q53653; IN67.
 DR GO: GO:0009986; C:cell surface; IEA.
 DR GO: GO:0005618; C:cell wall; IEA.
 DR GO: GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
 DR GO: GO:0016020; C:membrane; IEA.
 DR GO: GO:0007155; P:cell adhesion; IEA.
 DR InterPro: IPR008966; Adhes_Bact.
 DR InterPro: IPR004237; Fn_bind.
 DR InterPro: IPR005877; Gpos_YsIRK.
 DR InterPro: IPR001899; Gram_pos_anchor.
 DR Pfam: PF02986; Fn_bind; 2.
 DR Pfam: PF00746; Gram_pos_anchor; 1.
 DR Pfam: PF04650; YsIRK_signal; 1.
 DR TIGRFAMs: TIGR01167; LPXTG_anchor; 1.
 DR TIGRFAMs: TIGR01168; YsIRK_signal; 1.
 DR PROSITE: PS50847; GRAM_POS_ANCHORING; 1.
 KM Cell wall; peptidoglycan-anchor.
 SQ SEQUENCE 940 AA; 10355 MW; E35FBBCA907AE345 CRC64;

Query Match 78.4%; Score 171; DB 2; Length 940;
 Best Local Similarity 84.2%; Pred. No. 8.2e-13;
 Matches 32; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
 QY 1 ONKNGSFPPDTEKDKPKYHHPNIIIDIDFDSVPHIHG 38
 DB 720 ONKNGSFEDTEKDKPKYHGGNIIDIDFDSVPHIHG 757
 RESULT 6
 Q099RD2 ID Q099RD2 PRELIMINARY; PRT; 1038 AA.
 AC Q099RD2;
 DT 01-JUN-2001 (TREMBlrel. 17, Created)
 DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
 DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
 DE Fibronectin-binding protein homolog.
 GN Name=fnb; OrderedLocNames=SAV2503;
 OS Staphylococcus aureus (strain Mu50 / ATCC 700699).
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 OX NCBI_TaxId=158878;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Mu50 / ATCC 700699;
 RX MEDLINE=21311952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2;
 RI Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
 RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Iian J.-Q., Ito T.,
 RA Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,
 RA Mizukami U. Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
 RA Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuuchi J.,
 RA Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
 RA Hatori M., Ogasawara N., Hayashi H., Hiratsuku K.;
 RT "Whole genome sequencing of methicillin-resistant Staphylococcus
 aureus.";
 RT Lancet 357:1225-1240 (2001).
 CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
 an amide bond (By similarity).
 DR EMBL: AP003365; BAB5665.1; -
 DR PIR: H90053; H90053.
 DR GO: GO:0009986; C:cell surface; IEA.
 DR GO: GO:0005618; C:cell wall; IEA.
 DR GO: GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
 DR GO: GO:0016020; C:membrane; IEA.
 DR GO: GO:0007155; P:cell adhesion; IEA.
 DR InterPro: IPR008966; Adhes_Bact.
 DR InterPro: IPR004237; Fn_bind.
 DR InterPro: IPR005877; Gpos_YsIRK.
 DR InterPro: IPR001899; Gram_pos_anchor.
 DR Pfam: PF02986; Fn_bind; 1.
 DR Pfam: PF00746; Gram_pos_anchor; 1.
 DR Pfam: PF04650; YsIRK_signal; 1.
 DR TIGRFAMs: TIGR01167; LPXTG_anchor; 1.
 DR TIGRFAMs: TIGR01168; YsIRK_signal; 1.
 DR PROSITE: PS50847; GRAM_POS_ANCHORING; 1.
 KM Cell wall; complete proteome; peptidoglycan-anchor.
 SQ SEQUENCE 1038 AA; 113618 MW; 66BFBFBFBFB12 CRC64;
 Query Match 78.4%; Score 171; DB 2; Length 1038;
 Best Local Similarity 84.2%; Pred. No. 9.1e-13;
 Matches 32; Conservative 1; Mismatches 5; Indels 0; Gaps 0;
 QY 1 ONKNGSFPPDTEKDKPKYHHPNIIIDIDFDSVPHIHG 38
 DB 780 ONKNGSFEDTEKDKPKYHGGNIIDIDFDSVPHIHG 817
 RESULT 7
 Q7A3J7 ID Q7A3J7 PRELIMINARY; PRT; 1038 AA.
 AC Q7A3J7;
 DT 05-JUL-2004 (TREMBlrel. 27, Created)
 DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
 DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)

```
DE Fnb protein.
GN Name=fnb; OrderedLocNames=SA2291;
OS Staphylococcus aureus (strain N15).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=158879;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21311952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2;
RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Iian J.-O., Ito T.,
RA Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,
RA Mizunuma-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
RA Sekizima K., Hirakawa H., Kohara S., Goto S., Yabuuchi J.,
RA Kanihisa M., Yamashita A., Ohshima K., Furuya K., Yoshino T., Shiba T.,
RA Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.,
RT "Whole genome sequencing of methicillin-resistant Staphylococcus
RT aureus".
RL Lancet 357:1225-1240(2001).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC an amide bond (By similarity).
CC EMBL: AP003137; BAB43594.1; -.
DR GO: GO:0009986; C:cell surface; IEA.
DR GO: GO:0005618; C:cell wall; IEA.
DR GO: GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO: GO:0016020; C:membrane; IEA.
DR GO: GO:0016020; C:membrane; IEA.
DR GO: GO:0007155; P:cell adhesion; IEA.
DR InterPro: IPR008966; Adhes_Dact.
DR InterPro: IPR004237; Fn_bind.
DR InterPro: IPR001899; Gram_pos_anchor.
DR Pfam: PF02986; Fnb_bind; 1.
DR Pfam: PF00746; Gram_pos_anchor; 1.
DR Pfam: PF04650; YSIRK_signal; 1.
DR TIGRPMAS: TIGR01167; LPXTG_anchor; 1.
DR TIGRPMAS: TIGR01168; YSIRK_signal; 1.
DR PROSITE: PS50847; GRAM_POS_ANCHORING; 1.
KM Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ SEQUENCE 1038 AA; 113618 MW; 666BF6B2BFB8B12 CRC64;

Query Match 78.4%; Score 171; DB 2; Length 1038;
Best Local Similarity 84.2%; Pred. No. 9,1e-13;
Matches 32; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 QNKGNSFPDTEKDKPKYEHPPNIIDIDFDSVPHIHG 38
DB 780 QNKGDSFEDTEKDKPKYEGGNIIDIDFDSVPOIHG 817

RESULT 8
Q8NDU7 PRELIMINARY; PRT; 1015 AA.
ID Q8NDU7;
AC Q8NDU7;
DT 01-OCT-2002 (TREMBlrel. 22, Created)
DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Fnb protein.
GN Name=fnb; OrderedLocNames=NM2421;
OS Staphylococcus aureus (strain MM2).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=196620;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=MM2;
RX MEDLINE=22040717; PubMed=12044378; DOI=10.1016/S0140-6736(02)08713-5;
RA Baba T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Oguchi A.,
RA Nagai Y., Iwama N., Asano K., Naimi T., Kuroda H., Cui L.,
RA Yamanoto K., Hiramatsu K.,
RT "Genome and virulence determinants of high virulence community-
RT acquired MRSA.".
RL Lancet 359:1819-1827(2002).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptid-glycan by
CC an amide bond (By similarity).
EMBL: AP004630; BAB96286.1; -.
```

```
DR GO: GO:0009986; C:cell surface; IEA.
DR GO: GO:0005618; C:cell wall; IEA.
DR GO: GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO: GO:0016020; C:membrane; IEA.
DR GO: GO:0007155; P:cell adhesion; IEA.
DR InterPro: IPR008966; Adhes_Dact.
DR InterPro: IPR004237; Fnb_bind.
DR InterPro: IPR001899; Gram_pos_anchor.
DR Pfam: PF02986; Fnb_bind; 1.
DR Pfam: PF00746; Gram_pos_anchor; 1.
DR Pfam: PF04650; YSIRK_signal; 1.
DR TIGRPMAS: TIGR01167; LPXTG_anchor; 1.
DR TIGRPMAS: TIGR01168; YSIRK_signal; 1.
DR PROSITE: PS50847; GRAM_POS_ANCHORING; 1.
KM Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ SEQUENCE 1015 AA; 111145 MW; D0F9281BB64D44D2 CRC64;

Query Match 74.8%; Score 163; DB 2; Length 1015;
Best Local Similarity 81.6%; Pred. No. 9,2e-12;
Matches 31; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 QNKGNSFPDTEKDKPKYEHPPNIIDIDFDSVPHIHG 38
DB 785 QNKGNSFEDTEKDKPKYEGGNIIDIDFDSVPOIHG 822

RESULT 9
Q6G6H3 PRELIMINARY; PRT; 1015 AA.
ID Q6G6H3;
AC Q6G6H3;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE Fibronectin-binding protein.
GN OrderedLocNames=SA62388;
OS Staphylococcus aureus (strain MSSA476).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=282459;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=15213324; DOI=10.1073/pnas.0402521101;
RA Holden M.T.G., Fell E.J., Lindsey J.A., Peacock S.J., Day N.P.J.,
RA Enright M.C., Foster T.J., Moore C.E., Hurst L., Atkin R., Barton A.,
RA Bason N., Bentley S.D., Chillingworth C., Chillingworth T.,
RA Churcher C., Clark L., Cotton C., Cronin A., Doggett J., Dowd L.,
RA Fellwell T., Hance Z., Harris B., Hauser H., Holtroyd S., Jagels K.,
RA James K.D., Lennard N., Line A., Mayes R., Moule S., Mungall K.,
RA Ormond D., Quail M.A., Rabinowitch B., Rutherford K.M., Sanders M.,
RA Sharp S., Simmonds M., Stevens K., Whitehead S., Barrett B.G.,
RA Spratt B.G., Parkhill J.,
RT "Complete genomes of two clinical Staphylococcus aureus strains:
RT evidence for the rapid evolution of virulence and drug resistance."
RL Proc. Natl. Acad. Sci. U.S.A. 101:9786-9791(2004).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC an amide bond (By similarity).
EMBL: BX571857; CAG44202.1; -.
DR GO: GO:0009986; C:cell surface; IEA.
DR GO: GO:0005618; C:cell wall; IEA.
DR GO: GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO: GO:0016020; C:membrane; IEA.
DR GO: GO:0007155; P:cell adhesion; IEA.
DR InterPro: IPR008966; Adhes_Dact.
DR InterPro: IPR004237; Fnb_bind.
DR InterPro: IPR001899; Gram_pos_anchor.
DR Pfam: PF02986; Fnb_bind; 1.
DR Pfam: PF00746; Gram_pos_anchor; 1.
DR Pfam: PF04650; YSIRK_signal; 1.
DR TIGRPMAS: TIGR01167; LPXTG_anchor; 1.
DR TIGRPMAS: TIGR01168; YSIRK_signal; 1.
DR PROSITE: PS50847; GRAM_POS_ANCHORING; 1.
KM Cell wall; Complete proteome; Peptidoglycan-anchor.
```

SQ SEQUENCE 1015 AA; 111145 MW; DOF9281BB64D44D2 CRC64;
 Query Match 74.8%; Score 163; DB 2; Length 1015;
 Best Local Similarity 81.6%; Pred. No. 9.2e-12;
 Matches 31; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
 QY 1 ONKGNOSFPPTDKPKRYEHPNIIIDIDFDSVPQIHG 38
 DB 785 ONKGNOSFPPTDKPKRYEHPNIIIDIDFDSVPQIHG 822
 RESULT 10
 ID Q99RD3 PRELIMINARY; PRT; 961 AA.
 AC Q99RD3
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
 DE F10necctin-24, Last annotation update)
 DE F10necctin-binding protein homolog.
 GN Name=fndb; OrderedlocusNames=SAV2502;
 OS Staphylococcus aureus (strain Mu50 / ATCC 700699).
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 NC NCBI_TaxID=158878;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Mu50 / ATCC 700699;
 RX MEDLINE=21311952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2;
 RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
 RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Iian J.-O., Ito T.,
 RA Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosooyama A.,
 RA Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
 RA Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
 RA Kanehisa M., Yamashta A., Oshima K., Furuya K., Yoshino C., Shiba T.,
 RA Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
 RT "whole genome sequencing of methicillin-resistant Staphylococcus
 aureus."
 RT Lancet 357:1225-1240(2001).
 RL -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
 CC an amide bond (By similarity).
 DR EMBL: AP003365; BAB58664.1; -.
 DR FTR; G90053; G90053.
 DR HSSP; Q53653; IN67.
 DR GO; GO:0009986; C:cell surface; IEA.
 DR GO; GO:0005618; C:cell wall; IEA.
 DR GO; GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0007155; P:cell adhesion; IEA.
 DR InterPro: IPR008966; Adhes_bact.
 DR InterPro: IPR004237; Fn_bind.
 DR InterPro: IPR005877; Gpos_YsIRK.
 DR InterPro: IPR001899; Gram_pos_anchor.
 DR Pfam; PF02986; Fn_bind; 1.
 DR Pfam; PF00746; Gram_pos_anchor; 1.
 DR Pfam; PF04650; YsIRK_signal; 1.
 DR TIGRFAMs; TIGR01167; LpxTG_anchor; 1.
 DR TIGRFAMs; TIGR01168; YsIRK_signal; 1.
 DR PROSITE; PS50847; GRAM_POS_ANCHORING; 1.
 KM Cell wall; Complete proteome; Peptidoglycan-anchor.
 SQ SEQUENCE 961 AA; 106010 MW; 364940F884EA4101 CRC64;
 Query Match 72.9%; Score 159; DB 2; Length 961;
 Best Local Similarity 78.9%; Pred. No. 2.8e-11;
 Matches 30; Conservative 1; Mismatches 7; Indels 0; Gaps 0;
 QY 1 ONKGNOSFPPTDKPKRYEHPNIIIDIDFDSVPQIHG 38
 DB 731 ONKGNOSFPPTDKPKRYEHPNIIIDIDFDSVPQIHG 768
 RESULT 11
 ID Q7A3J8 PRELIMINARY; PRT; 961 AA.
 AC Q7A3J8

DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DE Fndb protein.
 GN Name=fndb; OrderedlocusNames=SA2290;
 OS Staphylococcus aureus (strain N315).
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 NC NCBI_TaxID=158879;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC MEDLINE=21311952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2;
 RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
 RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Iian J.-O., Ito T.,
 RA Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosooyama A.,
 RA Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
 RA Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
 RA Kanehisa M., Yamashta A., Oshima K., Furuya K., Yoshino C., Shiba T.,
 RA Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
 RT "whole genome sequencing of methicillin-resistant Staphylococcus
 aureus."
 RT Lancet 357:1225-1240(2001).
 RL -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
 CC an amide bond (By similarity).
 DR EMBL: AP003365; BAB43593.1; -.
 DR GO; GO:0009986; C:cell surface; IEA.
 DR GO; GO:0005618; C:cell wall; IEA.
 DR GO; GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0007155; P:cell adhesion; IEA.
 DR InterPro: IPR008966; Adhes_bact.
 DR InterPro: IPR004237; Fn_bind.
 DR InterPro: IPR005877; Gpos_YsIRK.
 DR InterPro: IPR001899; Gram_pos_anchor.
 DR Pfam; PF02986; Fn_bind; 1.
 DR Pfam; PF00746; Gram_pos_anchor; 1.
 DR Pfam; PF04650; YsIRK_signal; 1.
 DR TIGRFAMs; TIGR01167; LpxTG_anchor; 1.
 DR TIGRFAMs; TIGR01168; YsIRK_signal; 1.
 DR PROSITE; PS50847; GRAM_POS_ANCHORING; 1.
 KM Cell wall; Complete proteome; Peptidoglycan-anchor.
 SQ SEQUENCE 961 AA; 106010 MW; 364940F884EA4101 CRC64;
 Query Match 72.9%; Score 159; DB 2; Length 961;
 Best Local Similarity 78.9%; Pred. No. 2.8e-11;
 Matches 30; Conservative 1; Mismatches 7; Indels 0; Gaps 0;
 QY 1 ONKGNOSFPPTDKPKRYEHPNIIIDIDFDSVPQIHG 38
 DB 731 ONKGNOSFPPTDKPKRYEHPNIIIDIDFDSVPQIHG 768
 RESULT 12
 ID Q6GDUS PRELIMINARY; PRT; 965 AA.
 AC Q6GDUS
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DE F10necctin-binding protein.
 GN Name=fndb; OrderedlocusNames=SA2580;
 OS Staphylococcus aureus (strain MRSA252).
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 NC NCBI_TaxID=282458;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC PubMed=15213324; DOI=10.1073/pnas.040251101;
 RA Holden M.T.G., Feil E.J., Lindsey J.A., Peacock S.J., Day N.P.J.,
 RA Enright M.C., Foster T.J., Moore C.E., Huret L., Atkin R., Barton A.,
 RA Bason N., Bentley S.D., Chillingworth C., Chillingworth T.,
 RA Churcher C., Clark L., Cotton C., Cronin A., Doggett J., Dowd L.,
 RA Feltham T., Hance Z., Harris B., Hauser H., Holtroyd J., Jagsle K.,
 RA James K.D., Leonard N., Line A., Mayes R., Mungall K.,
 RA Ormond D., Quail M.A., Rabinowitch E., Rutherford K.M., Sanders M.,

RA Sharp S., Simmonds M., Stevens K., Whitehead S., Barrell B G.,
 RA Spratt B.G., Parkhill J.,
 RT "Complete genomes of two clinical *Staphylococcus aureus* strains:
 evidence for the rapid evolution of virulence and drug resistance,"
 RL Proc. Natl. Acad. Sci. U.S.A. 101:9786-9791(2004).
 CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
 an amide bond (By similarity).
 DR EMBL: BX571856; CAC41560.1; -.
 DR GO: GO:0009986; C:cell surface; IEA.
 DR GO: GO:0009275; C:cell wall (sensu Gram-positive Bacteria) IEA.
 DR GO: GO:0016020; C:membrane; IEA.
 DR GO: GO:0007155; P:cell adhesion; IEA.
 DR InterPro: IPR008966; Adhes_bact.
 DR InterPro: IPR004237; Fn_bind.
 DR InterPro: IPR005877; Gpos_YsIRK.
 DR InterPro: IPR001899; Gram_pos_anchor.
 DR Pfam: PF02986; Fn_bind_1.
 DR Pfam: PF00746; Gram_pos_anchor_1.
 DR Pfam: PF04650; YsIRK_signal_1.
 DR TIGRfam: TIGR01167; LpxT_anchor_1.
 DR TIGRfam: TIGR01168; YsIRK_signal_1.
 DR PROSITE: PS50847; GRAM_POS_ANCHORING; 1.
 KM Cell wall; Complete proteome; Peptidoglycan-anchor.
 SQ SEQUENCE 965 AA; 105691 MW; 2982E132164D0551 CRC64;

Query Match 72.9%; Score 159; DB 2; Length 965
 Best Local Similarity 78.9%; Pred. No. 2.8e-11;
 Matches 30; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

Oy 1 QNKGNSFPPTDKPKYKHPNIIIDPDSVPHNG 38
 |||||
 Db 749 QNSGNSFEDTBDKPKYKQGNIIIDPDSVPHNG 786

RESULT 13
 069L72 PRELIMINARY; PRT; 923 AA.
 AC 069L72;
 DT 25-OCT-2004 (TrEMBLrel. 28, Created)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
 DE Putative PMS2 postmeiotic segregation increased 2.
 GN KmeOSJNBa0016810.12;
 OS Cryza sativa (japonica cultivar-group).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Ehrhartoideae; Oryzaceae; Oryza.
 OX NCBI_TaxID=39947;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Sasaki T., Matsumoto T., Katayose Y.;
 RT "Oryza sativa nipponbare (GA3) genomic DNA, chromosome 2, B/C
 RT clone:OSJNBa0016810.";
 RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL: APO05874; BAD34084.1; -.
 DR GO: GO:0005524; F:ATP binding; IEA.
 DR GO: GO:0006298; P:mismatch repair; IEA.
 DR InterPro: IPR003594; ATPbind_ATPase.
 DR InterPro: IPR002099; DNA_mis_repair.
 DR InterPro: IPR001002; MAP1B_neuraxin.
 DR Pfam: PF01119; DNA_mis_repair; 1.
 DR Pfam: PF02518; HATFase_C; 1.
 DR TIGRfam: TIGR00585; mutL_1.
 DR PROSITE: PS00058; DNA_MISMATCH_REPAIR_1; UNKNOWN_1.
 DR PROSITE: PS00230; MAP1B_NEURAXIN; UNKNOWN_1.
 SQ SEQUENCE 923 AA; 101237 MW; A5F02C047947191 CRC64;

Query Match 31.4%; Score 68.5; DB 2; Length 921;
 Best Local Similarity 41.9%; Pred. No. 7.3;
 Matches 13; Conservative 6; Mismatches 11; Indels 1; Gaps 1;

Oy 6 QSPPTDKPKYKHPNIIIDPDSVPHI 36
 |||||

Db 551 QSFVPEPDSPOHSEPPNIVS-HRDEVPOL 580

RESULT 14
 041940 PRELIMINARY; PRT; 644 AA.
 AC 041940;
 DT 01-JAN-1998 (TrEMBLrel. 05, Created)
 DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Thymidine kinase (21).
 GN NameGAMMAHV_ORF21;
 OS Murid herpesvirus 4 (MuHV-4) (murine gammaherpesvirus 68).
 OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
 OC Gammaherpesvirinae; Rhadinovirus.
 OX NCBI_TaxID=33708;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=MUMS, and 92.4;
 RX MEDLINE=97366649; PubMed=9223479;
 RA Virgin H.W. IV, Latrelle P., Mametley P., Hallsworth K., Weck K.E.,
 RA Dal Canto A.J., Speck S.H.;
 RT "Complete sequence and genomic analysis of murine gammaherpesvirus
 68.";
 RT J. Virol. 71:5894-5904(1997).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=92.4;
 RX MEDLINE=96213518; PubMed=8638414; DOI=10.1006/viro.1996.0274;
 RA Pepper S.D., Stewart J.P., Arrand J.R., Mackett M.;
 RT "Murine gammaherpesvirus-68 encodes homologues of thymidine kinase and
 RT glycoprotein H: sequence, expression, and characterization of
 RT pyrimidine kinase activity.";
 RL Virology 219:475-479(1996).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=92.4;
 RA Milligan S., Efethiou S., Stewart J.P., Naeh A.A., Davison A.J.;
 RL Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL: U97553; AAB66396.1; -.
 DR EMBL: AF105037; AAF19286.1; -.
 DR HSPB: P14344; IOSN.
 DR GO: GO:0005524; F:ATP binding; IEA.
 DR GO: GO:0016301; P:kinase activity; IEA.
 DR GO: GO:0004797; F:thymidine kinase activity; IEA.
 DR GO: GO:0006230; P:TMP biosynthesis; IEA.
 DR InterPro: IPR001889; Herpes_TK.
 DR Pfam: PF00693; Herpes_TK; 1.
 KM Kinase.
 SQ SEQUENCE 644 AA; 72269 MW; FD3CD1646FE5562 CRC64;

Query Match 29.4%; Score 64; DB 2; Length 644;
 Best Local Similarity 35.5%; Pred. No. 18;
 Matches 11; Conservative 6; Mismatches 14; Indels 0; Gaps 0;

Oy 3 KGNQSFPTDKPKYKHPNIIIDPDSV 33
 |||||
 Db 6 KNNPGFQPSDSDENHYAEPEEYVDNPFDM 36

RESULT 15
 083342 PRELIMINARY; PRT; 644 AA.
 AC 083342;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Thymidine kinase.
 OS Murid herpesvirus 4 (MuHV-4) (murine gammaherpesvirus 68).
 OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
 OC Gammaherpesvirinae; Rhadinovirus.
 OX NCBI_TaxID=33708;
 RN [1]

RP SEQUENCE FROM N.A.
RX MEDLINE=96213518; PubMed=8638414; DOI=10.1006/viro.1996.0274;
RA Pepper S.D., Stewart J.P., Arrand J.R., Mackelt M.;
RT "Murine gammaherpesvirus-68 encodes homologues of thymidine kinase and
RT glycoprotein H: sequence, expression, and characterization of
RT pyrimidine kinase activity.";
RL Virology 219:475-479 (1996).
RN [2]
RN SEQUENCE FROM N.A.
RA Pepper S.D.V.;
RL Submitted (NOV-1995) to the EMBL/GenBank/DBJ databases.
DR EMBL; X93468; CA63755.1; -.
DR HSSP; P14344; IOSN
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0016301; F:kinase activity; IEA.
DR GO; GO:0004797; F:thymidine kinase activity; IEA.
DR GO; GO:0006230; P:TMP biosynthesis; IEA.
DR InterPro; IPR001889; Herpes_TK.
DR Pfam; PF00693; Herpes_TK; 1.
KW Kinase.
SQ SEQUENCE 644 AA; 72255 MW; FDF782746EB557A9 CRC64;
Query Match 29.4%; Score 64; DB 2; Length 644;
Best Local Similarity 35.5%; Pred. No. 18;
Matches 11; Conservative 6; Mismatches 14; Indels 0; Gaps 0;
QY 3 KGNQSPPPDTEKDKPKYEHPPNIIIDPDSV 33
DB 6 KNNPGFQPDSDSDHVAEPPEVYDNPFDAM 36

Search completed: October 22, 2005, 06:06:13
Job time : 71.6361 secs

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OM protein - protein search, using SW model

Run on: October 25, 2005, 19:38:38 ; Search time 41.9163 Seconds
(without alignments)
175.313 Million cell updates/sec

Title: US-10-731-238-51

Perfect score: 104
Sequence: 1 GONEGQQTIEPDTTPPIVP 19

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

1: A_Geneseq_16Dec04:*
2: geneseqp1980s:*
3: geneseqp1990s:*
4: geneseqp2000s:*
5: geneseqp2001s:*
6: geneseqp2002s:*
7: geneseqp2003as:*
8: geneseqp2003bs:*
9: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	104	100.0	19	2	AAW65707
2	96	92.3	19	2	AAW65667
3	96	92.3	134	2	AAW29087
4	96	92.3	1018	1	AAW82115
5	96	92.3	1018	4	AAU37245
6	96	92.3	1018	4	AAU34301
7	96	92.3	1018	6	ABJ18922
8	96	92.3	1018	6	ABM72537
9	96	92.3	1027	2	AAW89806
10	91	87.5	134	2	AAW29089
11	91	87.5	134	2	AAW29088
12	91	87.5	559	2	AAW89803
13	91	87.5	940	2	AAW89803
14	91	87.5	940	6	AAW89803
15	91	87.5	948	6	AAW89803
16	91	87.5	948	6	AAW89803
17	91	87.5	948	6	AAW89803
18	90	86.5	19	2	AAW65668
19	89	85.6	19	2	AAW65709
20	89	85.6	19	2	AAW65708
21	85	81.7	961	6	AAU15854
22	85	81.7	978	4	AAU33960
23	85	81.7	1001	4	AAU37093
24	85	81.7	1038	6	AAU15803
25	80	76.9	101	2	AAW90939

26	80	76.9	124	2	AAW90940
27	80	76.9	128	2	AAW90941
28	80	76.9	162	2	AAW90942
29	80	76.9	164	2	AAW90938
30	80	76.9	174	2	AAW90938
31	80	76.9	174	2	AAW90938
32	80	76.9	181	2	AAW90938
33	80	76.9	181	2	AAW90938
34	80	76.9	181	2	AAW90938
35	69	66.3	130	2	AAW90937
36	69	66.3	130	2	AAW90937
37	62	59.6	130	2	AAW90937
38	62	59.6	130	2	AAW90937
39	51	49.0	686	4	AAW90937
40	50	48.1	181	6	AAW90937
41	50	48.1	181	6	AAW90937
42	50	48.1	212	7	AAW90937
43	50	48.1	3124	8	AAW90937
44	49	47.1	189	3	AAW90937
45	49	47.1	251	3	AAW90937

ALIGNMENTS

RESULT 1
ID AAW65707 standard; peptide; 19 AA.
AC AAW65707;
XX
XX
DT 16-OCT-1998 (first entry)
XX
XX
DE Fibronectin binding protein-derived peptide #51.
XX
XX
KW microbial surface components recognising adhesive matrix molecule;
KW MCRAMM; fibronectin; fibronectin-binding protein; antibody; epitope;
KW antibiotic; bacterial infection; antibiotic-resistant strain.
XX
XX
OS Synthetic.
OS Staphylococcus aureus.
XX
XX
PN W09831389-A2.
XX
XX
PD 23-JUL-1998.
XX
XX
PE 21-JAN-1998; 98WO-US001222.
XX
XX
PR 21-JAN-1997; 97US-0036139P.
XX
XX
PA (TEXA) UNIV TEXAS A & M SYSTEM.
XX
XX
PI Hoosok M, Patti JM, House-Pompeo KL, Speziale P, Joh D;
PI Mogavvin MJ;
PI WPI; 1998-413816/35.
DR
XX
XX
PT Antibody that binds to fibronectin-binding protein, preventing its
PT binding to fibronectin - used to treat or prevent bacterial infection,
PT especially by Staphylococci and Streptococci.
PT
XX
XX
PS Example 8; Page 102; 201p; English.
PS
XX
XX
CC The invention relates to antibodies that bind to a fibronectin-binding
CC domain of a fibronectin-binding protein, and inhibit binding of the
CC protein to fibronectin. Also claimed are: (1) isolated peptides of a
CC fibronectin-binding protein that do not bind to fibronectin; (2) fusion
CC protein containing at least one peptide of a fibronectin-binding protein
CC linked to a second amino acid sequence; (3) nucleic acid encoding the
CC isolated peptide of (1). Antibodies, the isolated peptides of (1) and the
CC nucleic acids are all useful for immunisation (active or passive) and (by
CC inhibiting binding of bacteria to fibronectin) for preventing or creating
CC infection in humans or other animals, particularly by staphylococci or

CC streptococci, e.g. meningitis, otitis media, pneumonia, endocarditis,
 CC mastitis in cattle, abortion in horses and many others. Since the
 CC antibodies block binding of bacteria, they should be effective against
 CC antibiotic-resistant strains, and may replace antibiotic therapy or
 CC increase its effectiveness. Sequences AAW65707-711 represent a series of
 CC synthetic peptides based on the DU region of *S. aureus* fibronectin
 CC binding protein A. They were synthesised to contain mutations
 XX
 SQ Sequence 19 AA;
 Query Match 100.0%; Score 104; DB 2; Length 19;
 Best Local Similarity 100.0%; Pred. No. 1.8e-08;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GONEGQQTIEPDTTPPIVP 19
 ID |||||
 DB 1 GONEGQQTIEPDTTPPIVP 19
 RESULT 2
 AAW65667
 ID AAW65667 standard; peptide; 19 AA.
 XX
 AC AAW65667;
 XX
 DT 16-OCT-1998 (first entry)
 XX
 DE Fibronectin binding protein-derived peptide #11.
 XX
 KM microbial surface components recognising adhesive matrix molecule;
 KM MSCRAMM; fibronectin; fibronectin-binding protein; antibody; epitope;
 KM antibiotic; bacterial infection; antibiotic-resistant strain.
 OS
 OS Synthetic.
 XX
 OS Staphylococcus aureus.
 XX
 PN WO9813389-A2.
 XX
 PD 23-JUL-1998.
 XX
 PF 21-JAN-1998; 98WO-US001222.
 XX
 PR 21-JAN-1997; 97US-0036139P.
 XX
 PA (TEXA) UNIV TEXAS A & M SYSTEM.
 XX
 PI Hoeek M, Patcl JM, House-Pompeo KL, Speziale P, Joh D;
 PI McGavin MJ;
 PI
 XX
 DR WPI; 1998-413816/35.
 XX
 PT Antibody that binds to fibronectin-binding protein, preventing its
 PT binding to fibronectin - used to treat or prevent bacterial infection,
 PT especially by Staphylococci and Streptococci.
 XX
 XX Example 2; Page 92; 201pp; English.
 CC The invention relates to antibodies that bind to a fibronectin-binding
 CC domain of a fibronectin-binding protein, and inhibit binding of the
 CC protein to fibronectin. Also claimed are: (1) isolated peptides of a
 CC fibronectin-binding protein that do not bind to fibronectin; (2) fusion
 CC protein containing at least one peptide of a fibronectin-binding protein
 CC linked to a second amino acid sequence; (3) nucleic acid encoding the
 CC isolated peptide of (1). Antibodies, the isolated peptides of (1) and the
 CC nucleic acids are all useful for immunisation (active or passive) and (by
 CC inhibiting binding of bacteria to fibronectin) for preventing or treating
 CC infection in humans or other animals, particularly by staphylococci or
 CC streptococci, e.g. meningitis, otitis media, pneumonia, endocarditis,
 CC mastitis in cattle, abortion in horses and many others. Since the
 CC antibodies block binding of bacteria, they should be effective against
 CC antibiotic-resistant strains, and may replace antibiotic therapy or
 CC increase its effectiveness. Sequences AAW65659-68 represent synthetic
 CC epitopes from the fibronectin binding domains DU and DL-D4 of the S.

CC aureus fnbA gene
 XX
 SQ Sequence 19 AA;
 Query Match 92.3%; Score 96; DB 2; Length 19;
 Best Local Similarity 94.7%; Pred. No. 2.8e-07;
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 GONEGQQTIEPDTTPPIVP 19
 ID |||||
 DB 1 GONEGQQTIEPDTTPPIVP 19
 RESULT 3
 AAY29087
 ID AAY29087 standard; protein; 134 AA.
 XX
 AC AAY29087;
 XX
 DT 28-SEP-1999 (first entry)
 XX
 DE S. aureus fibronectin binding protein A (FnBA) binding domain.
 XX
 XX Bovine herpes virus-2; BHV-2; cytokine; immune response; immunogen; IL;
 KM interleukin; colony stimulating factor; CSF; interferon; IFN; TNF;
 KM tumour necrosis factor; recombinant virus; vaccine; mucosal disease;
 KM mastitis; breast cancer; stress-induced disease; binding domain; FnBA;
 KM fibronectin binding protein.
 XX
 OS Staphylococcus aureus.
 XX
 PN WO9916892-A1.
 XX
 PD 08-APR-1999.
 XX
 PF 29-SEP-1998; 98WO-GB002927.
 XX
 PR 29-SEP-1997; 97GB-00020633.
 XX
 PA (UYBR-) UNIV BRISTOL.
 XX
 PI Bradley AJ, Duffas WP;
 PI
 XX
 DR WPI; 1999-255101/21.
 DR N-PSDB; AAX91504.
 XX
 PT New bovine herpes virus-2 vectors.
 PT
 XX
 PS Example 2; Fig 8A-B; 130pp; English.
 XX
 CC The invention provides bovine herpes virus-2 (BHV-2) based vectors that
 CC comprise at least one cytokine-encoding DNA sequence. The expression of
 CC cytokines in mammals can up-regulate immune responses to the immunogens.
 CC The cytokine is selected from interleukins (IL), colony stimulating
 CC factors (CSF), interferons (IFN) and tumour necrosis factors (TNF). The
 CC BHV-2 based vector or recombinant virus can be used as vaccines. They can
 CC be used for preventing or treating a mucosal disease in a subject, e.g.
 CC ruminants, cattle, sheep, goats, dogs, cats, horses, or man, particularly
 CC mastitis in cows or breast cancers in humans. They can also be used for
 CC preventing or treating a stress-induced disease. The present sequence
 CC represents the binding domain of a previously published *S. aureus*
 CC fibronectin binding protein A (FnBA) sequence. The FnB binding domain
 CC gene sequence FNBB, cloned for use in this invention has 97.8 percent
 CC identity when compared to the previously published FnBA and FnBB gene
 CC sequences
 XX
 SQ Sequence 134 AA;
 Query Match 92.3%; Score 96; DB 2; Length 134;
 Best Local Similarity 94.7%; Pred. No. 2.5e-06;
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 GONEGQQTIEPDTTPPIVP 19

Db 116 GONEGQOTIEEDTTPPIVP 134

RESULT 4
AAU82115
ID AAP82115 standard; protein; 1018 AA.

XX AAP82115;

XX 25-MAR-2003 (revised)

DT 05-JAN-1990 (first entry)

XX Fibronectin binding protein.

DE Fibronectin binding protein.

XX Fibronectin binding protein; S.aureus; immunisation; mastitis; ruminants;

KM wound infection; diagnosis.

XX Staphylococcus aureus.

OS EP294349-A.

XX 07-DEC-1988.

PD 30-MAY-1988; 88EP-00850188.

XX 01-JUN-1987; 87SE-00002272.

XX (ALFA) ALFA LAVAL AGRC INT AB.

XX Lindberg MK, Signas LC, Wadstrom TM, Froman G;

XX WPI; 1988-347978/49.

DR P-PSDB; AAP82115.

XX Hybrid DNA encoding Staphylococcus aureus fibronectin binding protein -

PT useful for immunisation and topical application to prevent staphylococcal

PT infections.

XX Disclosure; Fig. 8A:1-8A:2; 23pp; English.

XX The S.aureus fibronectin binding protein may be included in a hybrid

CC protein. The protein may be used to immunise ruminants against

CC staphylococcal mastitis, pref. when given at 0.5-5 mcg/kg, using 3

CC doses at 1-3 week intervals; and for topical applicn. to prevent wound

CC infection, pref. using isotonic saline soln. of concn. 25-250 mcg/mg.

CC The DNA encoding the binding protein and the hybrid protein may be

CC immobilised on a carrier and used to diagnose staphylococcal infections.

XX (Updated on 25-MAR-2003 to correct PA field.)

XX Sequence 1018 AA;

Query Match 92.3%; Score 96; DB 1; Length 1018;

Best Local Similarity 94.7%; Pred. No. 2.5e-05;

Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GONEGQOTIEEDTTPPIVP 19

Db 860 GONEGQOTIEEDTTPPIVP 878

RESULT 5

AAU37245

ID AU37245 standard; protein; 1018 AA.

XX AU37245;

XX 14-FEB-2002 (first entry)

DT Staphylococcus aureus cellular proliferation protein #1415.

DE Antisense; prokaryotic cellular proliferation protein; antibiotic;

KM antibacterial; drug design.

XX Staphylococcus aureus.

OS WO200170955-A2.

XX 27-SEP-2001.

XX 21-MAR-2001; 2001WO-US009180.

XX 21-MAR-2000; 2000US-0191078P.

XX 23-MAY-2000; 2000US-0206848P.

XX 26-MAY-2000; 2000US-0207727P.

XX 23-OCT-2000; 2000US-0242578P.

XX 27-NOV-2000; 2000US-0253625P.

XX 22-DEC-2000; 2000US-0257931P.

XX 16-FEB-2001; 2001US-0265308P.

XX (ELIT-) ELITRA PHARM INC.

XX Haselbeck R, Ohlsen KL, Zyskind JW, Wall D, Trawick JD, Carr GJ;

XX Yamamoto RT, Xu HH;

XX WPI; 2001-611495/70.

XX N-PSDB; AAS55104.

XX New polynucleotides for the identification and development of

XX antibiotics, comprise sequences of antisense nucleic acids.

XX Example 3; SEQ ID NO 12838; 511pp; English.

XX The invention relates to antisense inhibitors of genes essential to

CC prokaryotic cellular proliferation, their use in identifying the genes,

CC their use in the discovery of novel antibiotics, the essential genes

CC themselves and the encoded proteins. The prokaryotes used are Escherichia

CC coli, Staphylococcus aureus, Salmonella typhi, Klebsiella pneumoniae,

CC Pseudomonas aeruginosa and Enterococcus faecalis. The invention is also

CC useful for the identification of potential new targets for antibiotic

CC development. The antisense nucleic acids can also be used to identify

CC proteins used in proliferation, to express these proteins, and to obtain

CC antibodies capable of binding to the expressed proteins. The proteins can

CC be used to screen compounds in rational drug discovery programmes. The

CC antisense nucleic acid sequence is also useful to screen for homologous

CC nucleic acids which are required for cell proliferation in a wide variety

CC of organisms. The present sequence represents an essential prokaryotic

CC cellular proliferation protein. Note: The sequence data for this patent

CC did not form part of the printed specification, but was obtained in

CC electronic format directly from WIPO at

CC fep.wipo.int/pub/published_pct_sequences

XX Sequence 1018 AA;

Query Match 92.3%; Score 96; DB 4; Length 1018;

Best Local Similarity 94.7%; Pred. No. 2.5e-05;

Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GONEGQOTIEEDTTPPIVP 19

Db 860 GONEGQOTIEEDTTPPIVP 878

RESULT 6

AAU34301

ID AU34301 standard; protein; 1018 AA.

XX AU34301;

XX 14-FEB-2002 (first entry)

DT Staphylococcus aureus cellular proliferation protein #577.

DE Antisense; prokaryotic cellular proliferation protein; antibiotic;

KM antibacterial; drug design.

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OS Staphylococcus aureus.
XX
XX WO200170955-A2.
XX
XX 27-SEP-2001.
XX
XX 21-MAR-2001; 2001WO-US009180.
XX
XX 21-MAR-2000; 2000US-0191078P.
XX
XX 23-MAY-2000; 2000US-0206848P.
XX
XX 26-MAY-2000; 2000US-0207727P.
XX
XX 23-OCT-2000; 2000US-0242578P.
XX
XX 27-NOV-2000; 2000US-0253625P.
XX
XX 22-DEC-2000; 2000US-0257931P.
XX
XX 16-FEB-2001; 2001US-0269308P.
XX
XX (ELITRA) ELITRA PHARM INC.
XX
XX Haselbeck R, Ohlsen KL, Zykkind JW, Wall D, Trawick JD, Carr GJ;
PI Yamamoto RT, Xu HH;
XX
XX WPI; 2001-611495/70.
XX
XX N-PSDB; AAS52160.
XX
XX New polynucleotides for the identification and development of
PT antibiotics, comprise sequences of antisense nucleic acids.
XX
XX
XX Example 3; SEQ ID NO 5797; 511pp; English.
XX
XX The invention relates to antisense inhibitors of genes essential to
CC prokaryotic cellular proliferation, their use in identifying the genes,
CC their use in the discovery of novel antibiotics, the essential genes,
CC themselves and the encoded proteins. The prokaryotes used are Escherichia
CC coli, Staphylococcus aureus, Salmonella typhi, Klebsiella pneumoniae,
CC Pseudomonas aeruginosa and Enterococcus faecalis. The invention is also
CC useful for the identification of potential new targets for antibiotic
CC development. The antisense nucleic acids can also be used to identify
CC proteins used in proliferation, to express these proteins, and to obtain
CC antibodies capable of binding to the expressed proteins. The proteins can
CC be used to screen compounds in rational drug discovery programmes. The
CC antisense nucleic acid sequence is also useful to screen for homologous
CC nucleic acids which are required for cell proliferation in a wide variety
CC of organisms. The present sequence represents an essential prokaryotic
CC cellular proliferation protein. Note: The sequence data for this patent
CC did not form part of the printed specification, but was obtained in
CC electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 1018 AA;
SQ
Query Match 92.3%; Score 96; DB 4; Length 1018;
Best Local Similarity 94.7%; Pred. No. 2.5e-05;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 1 GONEGQQTIEPTTPPIVP 19
Db 860 GONEGQQTIEPTTPPIVP 878

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XX
XX Staphylococcus sp.
OS
XX
XX WO200259148-A2.
XX
XX 01-AUG-2002.
XX
XX 21-JAN-2002; 2002WO-EP000546.
XX
XX 26-JAN-2001; 2001AT-00000130.
XX
XX (CISTEM) CISTEM BIOTECHNOLOGIES GMBH.
XX
XX Meinke A, Nagy E, Von Ahnen U, Klade C, Henics T, Zauner W;
PI Minh DB, Vytvytska O, Etz H, Dryla A, Weichardt T, Hafner M;
PI Tempelmeier B;
XX
XX WPI; 2003-075410/07.
XX
XX Identifying, isolating and producing hyperimmune serum-reactive antigens
PT from a pathogen, for preparing vaccine or medicament for treating or
PT preventing e.g. staphylococcal infections, comprises providing antibody
PT preparation.
XX
XX Example 7; Page 157; 252pp; English.
XX
XX The invention relates to a novel method for identifying, isolating and
CC producing hyperimmune serum-reactive antigens from a pathogen, tumour,
CC allergen, a tissue or host prone to auto-immunity, where the antigens are
CC used in a vaccine, comprises providing antibody preparation from a plasma
CC pool of a type of animal, or individual sera with antibodies against the
CC specific pathogen, tumour, allergen, tissue or host prone to auto-
CC immunity. The hyperimmune serum-reactive antigens comprising any of the
CC 62 sequences of 53-2261 amino acids fully defined in the specification,
CC or their hyperimmune fragments are useful for the manufacture of a
CC pharmaceutical preparation, particularly a vaccine against staphylococcal
CC infections or colonisation against S. aureus or S. epidermidis. The
CC preparation of antibodies is useful for the manufacture of a medicament
CC for treating or preventing staphylococcal infections or colonisation
CC against S. aureus or S. epidermidis. The antibody preparations may also
CC be used for diagnostic and imaging purposes. Other conditions that can be
CC treated include cancer, autoimmune diseases or infections caused by viral
CC (e.g. HIV, hepatitis A, B or C), fungal or protozoan pathogens. This
CC sequence represents a staphylococcal protein relating to the method for
CC identifying and producing pathogen specific antigens of the invention
XX
XX Sequence 1018 AA;
SQ
Query Match 92.3%; Score 96; DB 6; Length 1018;
Best Local Similarity 94.7%; Pred. No. 2.5e-05;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 1 GONEGQQTIEPTTPPIVP 19
Db 860 GONEGQQTIEPTTPPIVP 878

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RESULT 7
ABJ18922
ID ABJ18922 standard; protein; 1018 AA.
XX
XX ABJ18922;
AC
XX
XX 06-MAR-2003 (first entry)
DT
XX
XX Pathogen specific antigen related staphylococcal protein S10 ID No 68.
XX
XX Antibacterial; virucide; fungicide; protozoacide; cytostatic; anti-HIV;
XX hyperimmune; serum-reactive; antigen; pathogen; tumour; allergen;
XX auto-immunity; vaccine; staphylococcal infection; antibody; cancer;
XX autoimmune disease; HIV; hepatitis.
KM

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RESULT 8
ABM72537
ID ABM72537 standard; protein; 1018 AA.
XX
XX ABM72537;
AC
XX
XX 20-NOV-2003 (first entry)
DT
XX
XX Staphylococcus aureus protein #1777.
XX
XX Antibacterial; vaccine; gene therapy; infection; sepsis; diagnosis;
XX enzymatic assay; antibiotic target.
XX
XX Staphylococcus aureus.
OS
XX
XX WO200294868-A2.
PN

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XX 28-NOV-2002.
PD 27-MAR-2002; 2002MO-1B002637.
XX 27-MAR-2001; 2001GB-00007661.
XX (CHIR-) CHIRON SPA.
XX Masignani V, Mora M, Scarselli M;
XX WPI: 2003-120786/11.
DR N-PSDB; ACF74097.
XX New Staphylococcus aureus protein, useful as a vaccine for treating or
PT preventing Staphylococcal infection, specifically an infection caused by
PT S. aureus, e.g. sepsis.
XX Claim 1; SEQ ID NO 3554; 49pp; English.
XX The invention relates to novel genes and encoded proteins from
CC Staphylococcus aureus. A composition comprising the S. aureus protein, a
CC nucleic acid encoding the protein, or an antibody to the protein, is
CC useful as a pharmaceutical, particularly as a vaccine for treating or
CC preventing infection due to Staphylococcus bacteria, specifically an
CC infection caused by S. aureus. The composition is particularly useful for
CC treating or preventing sepsis in a patient. The composition can also be
CC used for diagnostics. The protein is also used in an assay for enzymatic
CC studies and as a target for antibiotics. This sequence represents one of
CC the novel S. aureus proteins of the invention
XX
SQ Sequence 1018 AA;
Query Match 92.3%; Score 96; DB 6; Length 1018;
Best Local Similarity 94.7%; Pred. No. 2.5e-05;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 GONEGQQTIEPDTTPPIV 19
DB 860 GONEGQQTIEPDTTPPIV 878
RESULT 9
AAW89806
ID AAW89806 standard; protein; 1027 AA.
XX
XX AAW89806;
AC
XX 16-MAR-1999 (first entry)
DT
XX
XX Staphylococcus aureus protein SEQ ID #5254.
DE
XX
XX Computer readable medium; vaccine; S aureus infection; immunodetection;
KM cellulitis; eyelid infection; food poisoning; osteomyelitis; therapy;
KM skin infection; surgical wound infection; scalded skin syndrome;
KM toxic shock syndrome.
XX
XX Staphylococcus aureus.
XX OS
XX EP786519-A2.
XX 30-JUL-1997.
PD
XX
XX 07-JAN-1997; 97EP-00100117.
PF
XX 05-JAN-1996; 96US-0009861P.
PR
XX (HUMA-) HUMAN GENOME SCI INC.
PA
XX Kunsch CA, Choi GH, Barash SC, Dillon PJ, Fannon MR, Rosen CA;
XX WPI: 1997-374922/35.
XX
```

```
PT Polynucleotide(s) and proteins derived from Staphylococcus aureus -
PT stored on computer readable medium and used in the production of anti-
PT S. aureus vaccines.
XX Claim 23; Page 3263-3267; 3271pp; English.
XX
XX This sequence represents a Staphylococcus aureus protein sequence of the
CC invention. The DNA sequences encoding the S. aureus proteins are recorded
CC on a computer readable medium, preferably selected from a floppy or hard
CC disk, random access memory (RAM), read-only memory (ROM) or CD-ROM.
CC Homology searches using the S. aureus DNA sequences allows putative
CC functions to be assigned so that protein-encoding or regulatory regions
CC of commercial, therapeutic or industrial importance can be obtained.
CC Specifically, sequences which are likely to encode antigens have been
CC identified and these polypeptides can be used in a vaccine composition
CC against S. aureus infection. The polypeptides can also be used in a kit
CC for the immunodetection of S. aureus in a sample. S. aureus is implicated
CC in numerous human diseases, including cellulitis, eyelid infections, food
CC poisoning, osteomyelitis, skin and surgical wound infections, scalded
CC skin syndrome, toxic shock syndrome, etc. Organisms transformed with the
CC DNA sequences can be used for recombinant production of the polypeptides.
CC The new DNA sequences (and their fragments) are useful as primers or
CC probes for isolating homologues of any of the 5191 S. aureus DNA sequences
CC contained on the computer readable medium
XX
SQ Sequence 1027 AA;
Query Match 92.3%; Score 96; DB 2; Length 1027;
Best Local Similarity 94.7%; Pred. No. 2.5e-05;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 GONEGQQTIEPDTTPPIV 19
DB 869 GONEGQQTIEPDTTPPIV 887
RESULT 10
AAV29089
ID AAV29089 standard; protein; 134 AA.
XX
XX AAV29089;
AC
XX 28-SEP-1999 (first entry)
DT
XX
XX Cloned fibronectin binding protein binding domain (FnBAB) sequence.
DE
XX
XX Bovine herpes virus-2; BHV-2; cytokine; immune response; immunogen; IL;
KM interleukin; colony stimulating factor; CSF; interferon; IFN; TNF;
KM tumour necrosis factor; recombinant virus; vaccine; mucosal disease;
KM mastitis; breast cancer; stress-induced disease; binding domain; FnBAB;
KM fibronectin binding protein.
XX
XX Staphylococcus aureus.
XX OS
XX W09916892-A1.
XX 08-APR-1999.
PD
XX
XX 29-SEP-1998; 98WO-GS002927.
PF
XX 29-SEP-1997; 97GB-00020633.
PR
XX (UYBR-) UNIV BRISTOL.
XX
XX Bradley AJ, Duffas WP;
XX WPI: 1999-255101/21.
XX N-PSDB; AAX91506.
XX
XX New bovine herpes virus-2 vectors.
XX Example 2; Fig 8A-B, 130pp; English.
XX
```

CC The invention provides bovine herpes virus-2 (BHV-2) based vectors that
CC comprise at least one cytokine-encoding DNA sequence. The expression of
CC cytokines in mammals can up-regulate immune responses to the immunogens.
CC The cytokine is selected from interleukins (IL), colony stimulating
CC factors (CSF), interferons (IFN) and tumour necrosis factors (TNF). The
CC BHV-2 based vector or recombinant virus can be used as vaccines. They can
CC be used for preventing or treating a mucosal disease in a subject, e.g.
CC ruminants, cattle, sheep, goats, dogs, cats, horses, or man, particularly
CC mastitis in cows or breast cancers in humans. They can also be used for
CC preventing or treating a stress-induced disease. The present sequence

Query Match 87.5%; Score 91; DB 2; Length 134;
Best Local Similarity 89.5%; Pred. No. 1.4e-05;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

1 GONEGQQTIEPDTTPPIVP 19
116 GHNEGQQTIEEDTTPPIVP 134

RESULT 11
AAV29088
ID AAV29088 standard; protein; 134 AA.
XX
AC AAV29088;
XX
DT 28-SEP-1999 (first entry)
XX
XX S. aureus fibronectin binding protein B (FnBB) binding domain.
DE
XX
XX Bovine herpes virus-2; BHV-2; cytokine; immune response; immunogen; IL;
XX Interleukin; colony stimulating factor; CSF; interferon; IFN; TNF;
XX tumour necrosis factor; recombinant virus; vaccine; mucosa. disease;
XX mastitis; breast cancer; stress-induced disease; binding domain; FnBB;
XX fibronectin binding protein.
XX
XX Staphylococcus aureus.
OS
XX
XX WO9916892-A1.
PN
XX
XX C8-APR-1999.
PD
XX
XX 29-SEP-1998; 98WO-GB002927.
PF
XX
XX 29-SEP-1997; 97GB-00020633.
PR
XX
XX (UYBR-) UNIV BRISTOL.
PA
XX
XX Etardley AJ, Duffas WP;
PI
XX WPI; 1999-255101/21.
DR
XX N-PSDB; AAX91505.
XX
XX New bovine herpes virus-2 vectors.
PT
XX
XX Example 2; Fig 8A-B; 130pp; English.
XX
XX The invention provides bovine herpes virus-2 (BHV-2) based vectors that
CC comprise at least one cytokine-encoding DNA sequence. The expression of
CC cytokines in mammals can up-regulate immune responses to the immunogens.
CC The cytokine is selected from interleukins (IL), colony stimulating
CC factors (CSF), interferons (IFN) and tumour necrosis factors (TNF). The
CC BHV-2 based vector or recombinant virus can be used as vaccines. They can
CC be used for preventing or treating a mucosal disease in a subject, e.g.
CC ruminants, cattle, sheep, goats, dogs, cats, horses, or man, particularly
CC mastitis in cows or breast cancers in humans. They can also be used for
CC preventing or treating a stress-induced disease. The present sequence

CC represents the binding domain of a previously published S. aureus
CC fibronectin binding protein B (FnBB) sequence. The FnB binding domain
CC gene sequence FnBBB, cloned for use in this invention has 97.8 percent
CC identity when compared to the previously published FnBB and FnBB gene
CC sequences
XX
SQ Sequence 134 AA;
Query Match 87.5%; Score 91; DB 2; Length 134;
Best Local Similarity 89.5%; Pred. No. 1.4e-05;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

1 GONEGQQTIEPDTTPPIVP 19
116 GHNEGQQTIEEDTTPPIVP 134

RESULT 12
AAW89803
ID AAW89803 standard; protein; 559 AA.
XX
XX AAW89803;
XX
DT 16-MAR-1999 (first entry)
XX
XX Staphylococcus aureus protein SEQ ID #5251.
DE
XX
XX Computer readable medium; vaccine; S. aureus infection; immunodetection;
XX cellulitis; eyelid infection; food poisoning; osteomyelitis; therapy;
XX skin infection; surgical wound infection; scalded skin syndrome;
XX toxic shock syndrome.
XX
XX Staphylococcus aureus.
OS
XX
XX EP786519-A2.
PN
XX
XX 30-JUL-1997.
PD
XX
XX 07-JAN-1997; 97EP-00100117.
PF
XX
XX 05-JAN-1996; 96US-0009861P.
PR
XX
XX (HUMA-) HUMAN GENOME SCI INC.
PA
XX
XX Kunesch CA, Choi GH, Barash SC, Dillon PJ, Fannon MR, Rosen CA;
PI
XX WPI; 1997-374922/35.
DR
XX
XX Polynucleotide(s) and proteins derived from Staphylococcus aureus -
PT stored on computer readable medium and used in the production of anti-
PT S. aureus vaccines.
XX
XX
XX Claim 23; Page 3259-3261; 3271pp; English.
XX
XX This sequence represents a Staphylococcus aureus protein sequence of the
CC invention. The DNA sequences encoding the S. aureus proteins are recorded
CC on a computer readable medium, preferably selected from a floppy or hard
CC disk, random access memory (RAM), read-only memory (ROM) or CD-ROM.
CC Homology searches using the S. aureus DNA sequences allows putative
CC functions to be assigned so that protein-encoding or regulatory regions
CC of commercial, therapeutic or industrial importance can be obtained.
CC Specifically, sequences which are likely to encode antigens have been
CC identified and these polypeptides can be used in a vaccine composition
CC against S. aureus infection. The polypeptides can also be used in a kit
CC for the immunodetection of S. aureus in a sample. S. aureus is implicated
CC in numerous human diseases, including cellulitis, eyelid infections, food
CC poisoning, osteomyelitis, skin and surgical wound infections, scalded
CC skin syndrome, toxic shock syndrome, etc. Organisms transformed with the
CC DNA sequences can be used for recombinant production of the polypeptides.
CC The new DNA sequences (and their fragments) are useful as primers or
CC probes for isolating homologues of any of the 5191 S. aureus DNA sequences
CC contained on the computer readable medium

SQ Sequence 559 AA:

Query Match 87.5%; Score 91; DB 2; Length 559;
 Best Local Similarity 89.5%; Pred. No. 7e-05;
 Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GONEGQOTIEPTTPIVP 19
 DB 415 GHNEGQOTIEPTTPIVP 433

RESULT 13

ID AAR07070 standard; protein; 940 AA.

AC AAR07070;

XX 25-MAR-2003 (revised)

DT 21-FEB-1991 (first entry)

DE Fibronectin-binding protein encoded by gene 2, fnbB.

KM Wound healing; immunisation; mastitis; fnbA; ss.

OS Staphylococcus aureus.

XX Key Location/Qualifiers

FH Peptide 1..36

FT /label= signal peptide

XX EP397633-A.

XX 14-NOV-1990.

XX 04-MAY-1990; 90EP-00850166.

XX 11-MAY-1989; 89SE-00001687.

XX (ALFA) ALFA LAVAL AGRIC INT AB.

XX Hook M, Jonsson K, Lindberg KM, Signas LC;

XX WPI; 1990-343563/46.

XX N-PSDB; AAQ06550.

XX Fibronectin binding protein gene - isolated from S. aureus and used for

XX producing protein for wound healing, immunisation or diagnosis.

XX Claim 11; Page 17; 24pp; English.

XX The sequence is deduced from a gene, designated gene 2 (fnbB), localised

XX downstream of that disclosed in SE8702272 (gene 1; fnbA) encoding a

XX fibronectin binding protein, fnbB in S. aureus. Gene 2 encodes fnbB.

XX (95%). Downstream is a stretch of 66 AAs with 75% homology to the same

XX stretch in fnbB. The following 44 AAs have only 40% homology and the B

XX repeats in fnbB are absent. However the rest of the peptide (394 AAs is

XX nearly identical to fnbB, the main difference being a deletion of 14 AAs.

XX This highly homologous region contains the same repeat (D1-D4 and W1-5)

XX found in fnbB with the exception that W1 is missing. The WC region and

XX the hydrophobic M domain as well as the C-terminal end are conserved.

XX (Updated on 25-MAR-2003 to correct PR field.) (Updated on 25-MAR-2003 to

XX correct PA field.)

RESULT 14

ID ABJ19111 standard; protein; 940 AA.

AC ABJ19111;

XX 06-MAR-2003 (first entry)

DE Pathogen specific antigen related staphylococcal protein SEQ ID No 424.

KM Antibacterial; virucide; fungicide; protozoacide; cytostatic; anti-HIV;

KM hyperimmune; serum-reactive; antigen; pathogen; tumour; allergen;

KM auto-immunity; vaccine; staphylococcal infection; antibody; cancer;

XX auto-immune disease; HIV; hepatitis.

XX Staphylococcus sp.

XX W0200259148-A2.

XX 01-AUG-2002.

XX 21-JAN-2002; 2002WC-EP000546.

XX 26-JAN-2001; 2001AT-00000130.

XX (CIST-) CISTEM BIOTECHNOLOGIES GMBH.

XX Meinke A, Nagy E, Von Ahnen U, Klade C, Henics T, Zauner W;

XX Minn DB, Vytvytska O, Etz H, Dryla A, Weichart T, Hafner M;

XX Tempelmeier B;

XX WPI; 2003-075410/07.

XX Identifying, isolating and producing hyperimmune serum-reactive antigens

XX from a pathogen, for preparing vaccine or medicament for treating or

XX preventing e.g. staphylococcal infections, comprises providing antibody

XX preparation.

XX Example 7; Page 223; 252pp; English.

XX The invention relates to a novel method for identifying, isolating and

XX producing hyperimmune serum-reactive antigens from a pathogen, tumour,

XX allergen, a tissue or host prone to auto-immunity, where the antigens are

XX used in a vaccine, comprises providing antibody preparation from a plasma

XX pool of a type of animal, or individual sera with antibodies against the

XX specific pathogen, tumour, allergen, tissue or host prone to auto-

XX immunity. The hyperimmune serum-reactive antigens comprising any of the

XX 62 sequences of 53-2261 amino acids fully defined in the specification,

XX or their hyperimmune fragments are useful for the manufacture of a

XX pharmaceutical preparation, particularly a vaccine against staphylococcal

XX infections or colonisation against S. aureus or S. epidermidis. The

XX preparation of antibodies is useful for the manufacture of a medicament

XX for treating or preventing staphylococcal infections or colonisation

XX against S. aureus or S. epidermidis. The antibody preparations may also

XX be used for diagnostic and imaging purposes. Other conditions that can be

XX treated include cancer, autoimmune diseases or infections caused by viral

XX (e.g. HIV, hepatitis A, B or C), fungal or protozoan pathogens. This

XX sequence represents a staphylococcal protein relating to the method for

XX identifying and producing pathogen specific antigens of the invention

SQ Sequence 940 AA:

Query Match 87.5%; Score 91; DB 6; Length 940;
 Best Local Similarity 89.5%; Pred. No. 0.00013;
 Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GONEGQOTIEPTTPIVP 19
 DB 796 GHNEGQOTIEPTTPIVP 814

RESULT 15
 ADA89470
 ID ADA89470 standard; protein; 948 AA.
 AC ADA89470;
 XX
 DT 20-NOV-2003 (first entry)
 DE Staphylococcus aureus antigenic protein #9.
 XX
 KW antigenic protein; vaccine; Staphylococcus aureus; pathogenic organism;
 KW antibacterial; neuroprotective; immunosuppressive; antineoplastic;
 KW antitumor; immunostimulant; ophthalmological; pathogenic microbe;
 KW bacteraemia; septic shock; organ infection; skin infection;
 KW bacterial basal colonisation; bacterial eye infection; septicaemia;
 KW tuberculosis; food poisoning; blood infection; peritonitis; endocarditis;
 KW sepsis; meningitis; pneumonia; stomach ulcer; gonorrhoea; toxic shock;
 KW necrotising fasciitis; impetigo; histoplasmosis; Lyme disease;
 KW gastro-enteritis; dysentery; shigellosis; skin disorder.
 XX
 OS Staphylococcus aureus.
 XX
 PN MO2003011899-A2.
 XX
 PD 13-FEB-2003.
 XX
 PF 02-AUG-2002; 2002MO-GB003606.
 XX
 PR 02-AUG-2001; 2001GB-00018825.
 PR 03-JAN-2002; 2002GB-00000349.
 XX
 PA (UYSH-) UNIV SHEPFIELD.
 PA (3IOS-) BIOSYNEXUS INC.
 XX
 PI Foster S, Mond J, Clarke S, McDowell P, Brummel K;
 DR WPI; 2003-256434/25.
 XX
 PT New antigenic polypeptides from Staphylococcus aureus or S. epidermidis,
 PT useful as a vaccine for immunizing humans against e.g. bacteraemia, septic
 PT shock, septicaemia, tuberculosis, meningitis, pneumonia, gonorrhoea or
 PT impetigo.
 XX
 PS Claim 4; Page 124-125; 189pp; English.
 XX
 CC The present invention describes an antigenic protein or its part, which
 CC is for use as a vaccine. The antigenic protein is encoded by an isolated
 CC DNA molecule of Staphylococcus aureus or S. epidermidis partial gene
 CC sequences (designated dnash and dna SE, respectively) and which encodes a
 CC protein expressed by a pathogenic organism. Also described: (1) a vaccine
 CC composition comprising at least one antigenic protein; (2) a method of
 CC immunising an animal against a disease or condition caused by a
 CC pathogenic microbe by administering the antigenic protein or the vaccine;
 CC (3) an antibody or its binding part obtainable by the method above; (4)
 CC preparing a hybridoma cell line producing monoclonal antibodies; (5) a
 CC hybridoma cell line produced by the method of (4); and (6) identifying
 CC epsonic antigens expressed by a pathogenic microbe. The antigenic
 CC proteins have antibacterial, neuroprotective, immunosuppressive,
 CC antiinflammatory, antitumor, immunostimulant and ophthalmological
 CC activities, and can be used in vaccines. The antigenic proteins or
 CC vaccines can be used for immunising an animal (specifically, a human)
 CC against a disease or condition caused by a pathogenic microbe, e.g.
 CC bacteraemia, septic shock, organ infection, skin infection bacterial
 CC basal colonisation, bacterial eye infections, septicaemia, tuberculosis,
 CC bacteria-associated food poisoning, blood infections, peritonitis,
 CC endocarditis, sepsis, meningitis, pneumonia, stomach ulcer, gonorrhoea,
 CC strep throat, streptococcal-associated toxic shock, necrotising
 CC fasciitis, impetigo, histoplasmosis, Lyme disease, gastro-intestitis,
 CC dysentery, shigellosis, S. aureus-associated septicaemia, food-poisoning,
 CC skin disorders, S. epidermidis-associated septicaemia, peritonitis or
 CC endocarditis. The present sequence represents a S. aureus antigenic
 CC protein sequence from the present invention.
 CC

SQ Sequence 948 AA;
 Query Match 87.5%; Score 91; DB 6; Length 948;
 Best Local Similarity 89.5%; Pred. No. 0.00013;
 Matches 17; Conservative 0; Mismatches 2; Indels 0;
 Gaps 0;

QY 1 GNEGQQTIEPTTPIVP 19
 | ||||| ||||| |||||
 DB 804 GNEGQQTIEPTTPIVP 822

Search completed: October 25, 2005, 20:21:07
 Job time : 42.9663 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 22, 2005, 03:51:22; Search time 10.5862 Seconds
(without alignments)
133.980 Million cell updates/sec

Title: US-10-731-238-51

Perfect score: 104

Sequence: 1 GQNEGGQGTTPPTTPV 19

Scoring table:

BIOSUM62
Gapop 10.0, Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database:

Issued Patents AA:*

- 1: /cgn2_6/ptodata/1/1aa/5A.COMB.pep:*
- 2: /cgn2_6/ptodata/1/1aa/5B.COMB.pep:*
- 3: /cgn2_6/ptodata/1/1aa/6A.COMB.pep:*
- 4: /cgn2_6/ptodata/1/1aa/6B.COMB.pep:*
- 5: /cgn2_6/ptodata/1/1aa/PTCTUS.COMB.pep:*
- 6: /cgn2_6/ptodata/1/1aa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	104	100.0	19	4	US-09-010-317-51
2	96	92.3	19	4	US-09-010-317-11
3	96	92.3	178	3	US-08-459-135A-12
4	96	92.3	178	3	US-08-495-559-12
5	96	92.3	1027	4	US-08-956-171E-5254
6	96	92.3	1027	4	US-08-956-171E-5254
7	91	87.5	174	2	US-08-459-135A-13
8	91	87.5	174	2	US-08-459-135A-13
9	91	87.5	174	2	US-08-459-135A-13
10	91	87.5	559	4	US-08-956-171E-5251
11	90	86.5	19	4	US-09-010-317-12
12	89	85.6	19	4	US-09-010-317-52
13	89	85.6	19	4	US-09-010-317-52
14	89	85.6	19	4	US-09-010-317-52
15	80	76.9	174	2	US-08-459-135A-10
16	80	76.9	174	2	US-08-459-135A-10
17	80	76.9	176	3	US-08-495-559-6
18	80	76.9	181	2	US-08-459-135A-6
19	69	66.3	130	2	US-08-459-135A-8
20	69	66.3	130	2	US-08-459-135A-8
21	62	59.6	130	2	US-08-459-135A-7
22	53	51.0	90	4	US-09-248-796A-21460
23	53	51.0	401	4	US-09-248-796A-25547
24	48	46.2	134	3	US-09-415-522-12
25	47	45.2	38	4	US-09-010-317-47
26	47	45.2	1619	4	US-09-328-352-7347
27	46	44.2	38	4	US-09-010-317-37

28	46	44.2	366	4	US-09-377-285B-20	Sequence 20, Appl
29	46	44.2	476	3	US-09-189-035-1	Sequence 1, Appl
30	46	44.2	476	3	US-09-382-086-1	Sequence 1, Appl
31	46	44.2	943	3	US-09-056-556-204	Sequence 204, App
32	46	44.2	943	4	US-09-072-596-199	Sequence 199, App
33	46	44.2	943	4	US-09-477-135A-131	Sequence 131, App
34	46	44.2	943	4	US-09-072-967-204	Sequence 204, App
35	46	44.2	2736	4	US-09-252-991A-30227	Sequence 30227, A
36	45	43.3	38	1	US-08-729-767-4	Sequence 4, Appl
37	45	43.3	114	1	US-08-259-000-3	Sequence 3, Appl
38	45	43.3	139	3	US-08-856-253-8	Sequence 8, Appl
39	45	43.3	158	4	US-08-826-134-11	Sequence 11, Appl
40	45	43.3	158	4	US-08-826-134-22	Sequence 22, Appl
41	45	43.3	302	4	US-09-248-796A-25270	Sequence 25270, A
42	45	43.3	356	6	5223606-7	Patent No. 5223606
43	45	43.3	356	6	5223606-7	Patent No. 5223606
44	45	43.3	667	4	US-09-125-491C-4	Sequence 4, Appl
45	45	43.3	777	3	US-08-764-870-13	Sequence 13, Appl

ALIGNMENTS

RESULT 1
US-09-010-317-51
Sequence 51, Application US/09010317
Patent No. 6685943
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
APPLICANT: Patti, Joseph M.
APPLICANT: House-Pompeo, Karen L.
APPLICANT: Speziale, Pietro
APPLICANT: Jon, Danny
APPLICANT: McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
TITLE OF INVENTION: AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/010.317
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/036.139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAMK.189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 51:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-09-010-317-51
Query Match 100.0%; Score 104; DB 4; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.7e-08;


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Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GONEGQOTIEBPTTPPIV 19
   |||||
Db 1 GONEGQOTIEBPTTPPIV 19

RESULT 2
US-09-010-317-11
; Sequence 11, Application US/09010317
; Patent No. 6685943
; GENERAL INFORMATION:
; APPLICANT: Hook, Magnus
; APPLICANT: Patti, Joseph M.
; APPLICANT: House-Pompeo, Karen L.
; APPLICANT: Speziale, Pietro
; APPLICANT: McGavin, Martin J.
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
; NUMBER OF SEQUENCES: 105
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: TX
; COUNTRY: USA
; ZIP: 77210-4433
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/010,317
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/036,139
; FILING DATE: 21-JAN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Hibler, David W.
; REGISTRATION NUMBER: 41,071
; REFERENCE/DOCKET NUMBER: TAMK:189
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 512-418-3000
; TELEFAX: 512-474-7577
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 19 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; US-09-010-317-11

Query Match 92.3%; Score 96; DB 4; Length 19;
Best Local Similarity 94.7%; Pred. No. 2.3e-07;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GONEGQOTIEBPTTPPIV 19
   |||||
Db 1 GONEGQOTIEBPTTPPIV 19

RESULT 3
US-08-459-135A-12
; Sequence 12, Application US/08459135A
; Patent No. 5955078
; GENERAL INFORMATION:
; APPLICANT: BURHAM, Martin Karl Russel
; APPLICANT: CHOPRA, Ian
; APPLICANT: CRITCHLEY, Ian Alfred
; APPLICANT: KNOWLES, David Justin Charles
; SEQ ID NO 12
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
; US-08-459-559-12

TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN: MONOCLONAL ANTIBODY AND THEIR US
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
STATE: PA
COUNTRY: U.S.A.
ZIP: 19406-0939
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq, Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/459,135A
; FILING DATE: 02-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB/94/00215
; FILING DATE: 04-Feb-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Gimmil, Edward R.
; REGISTRATION NUMBER: 38,891
; REFERENCE/DOCKET NUMBER: P30591C2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-270-4478
; TELEFAX: 610-270-5090
; TELEX:
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 178 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Protein
; US-08-459-135A-12

Query Match 92.3%; Score 96; DB 2; Length 178;
Best Local Similarity 94.7%; Pred. No. 2.5e-06;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GONEGQOTIEBPTTPPIV 19
   |||||
Db 116 GONEGQOTIEBPTTPPIV 134

RESULT 4
US-08-495-559-12
; Sequence 12, Application US/08495559A
; Patent No. 6054572
; GENERAL INFORMATION:
; APPLICANT: BURHAM, Martin Karl Russel
; APPLICANT: CHOPRA, Ian
; APPLICANT: CRITCHLEY, Ian Alfred
; APPLICANT: KNOWLES, David Justin Charles
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN: MONOCLONAL
; TITLE OF INVENTION: ANTIBODY AND THEIR USE IN PREVENTING BACTERIAL ADHESION
; FILE REFERENCE: P30591
; CURRENT APPLICATION NUMBER: US/08/495,559A
; CURRENT FILING DATE: 1995-08-03
; EARLIER APPLICATION NUMBER: GB 9302289.5
; EARLIER FILING DATE: 1993-02-05
; EARLIER APPLICATION NUMBER: GB 9321592.9
; EARLIER FILING DATE: 1993-10-20
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 12
; LENGTH: 178
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
; US-08-495-559-12
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; APPLICATION NUMBER: US/08/459, 135A
; FILING DATE: 02-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB/94/00215
; FILING DATE: 04-Feb-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Gimm, Edward R
; REGISTRATION NUMBER: 38,891
; REFERENCE/DOCKET NUMBER: P30591C2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-270-4478
; TELEFAX: 610-270-5090
;
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 174 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
;
US-08-459-135A-13

Query Match 87.5%; Score 91; DB 3; Length 174;
Best Local Similarity 89.5%; Pred. No. 1.3e-05;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 GONEGQQTIEPTTPPIVP 19
| | | | | | | | | | | | | | | | | | | |
Db 116 GHNEGQQTIEEDTTPPIVP 134

RESULT 8
US-08-495-559-13
; Sequence 13, Application US/08495559A
; Patent No. 6054572
; GENERAL INFORMATION:
; APPLICANT: BURMAN, Martin Karl Russel
; APPLICANT: CHOPRA, Ian
; APPLICANT: CRITCHLEY, Ian Alfred
; APPLICANT: KNOWLES, David Justin Charles
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN: MONOCLONAL
; FILE REFERENCE: P30591
; CURRENT APPLICATION NUMBER: US/08/495,559A
; CURRENT FILING DATE: 1995-08-03
; EARLIER FILING DATE: 1993-02-05
; EARLIER APPLICATION NUMBER: GB 9302289.5
; EARLIER FILING DATE: 1993-10-20
; EARLIER APPLICATION NUMBER: GB 9321592.9
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 13
; LENGTH: 174
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-08-495-559-13

Query Match 87.5%; Score 91; DB 3; Length 174;
Best Local Similarity 89.5%; Pred. No. 1.3e-05;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 GONEGQQTIEPTTPPIVP 19
| | | | | | | | | | | | | | | | | | | |
Db 116 GHNEGQQTIEEDTTPPIVP 134

RESULT 9
US-08-956-171E-5251
; Sequence 5251, Application US/08956171E
; Patent No. 6593114
; GENERAL INFORMATION:

```

```

APPLICANT: Charles Kunsch
          Gil H. Choi
          Patrick S. Dillon
          Craig A. Rosen
          Steven C. Barash
          Michael R. Fannon
TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
NUMBER OF SEQUENCES: 5256
CORRESPONDENCE ADDRESS:
ADDRESSSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COUNTRY: USA
ZIP: 20850

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/956,171E
FILING DATE: 20-Oct-1997
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/009,861
FILING DATE: January 5, 1996
APPLICATION NUMBER: 08/781,986
FILING DATE: January 3, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Mark J. Hyman
REGISTRATION NUMBER: 46,789
REFERENCE/DOCKET NUMBER: PB248P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (240) 314-1224
TELEFAX: (301) 309-8439
INFORMATION FOR SEQ ID NO: 5251:
SEQUENCE CHARACTERISTICS:
LENGTH: 559 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 5251:
US-08-956-171E-5251

Query Match      87.5%; Score 91; DB 4; Length 559;
Best Local Similarity 89.5%; Pred. No. 4,4e-05;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY      1 GONEGQQTIEPDTPPIVP 19
        | ||||| |||||
Db      415 GHNEGQQTIEDTPIVP 433

RESULT 10
US-08-781-986A-5251
Sequence 5251, Application US/08781986A
Patent No. 6737248
GENERAL INFORMATION:
APPLICANT: Charles Kunsch
TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
NUMBER OF SEQUENCES: 5255
CORRESPONDENCE ADDRESS:
ADDRESSSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COUNTRY: USA
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4mb storage
COMPUTER: HP Vectra 486/33

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; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/781,986A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Benson, Bob
; REGISTRATION NUMBER: 30,446
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 5251:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 559 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
;
US-08-781-986A-5251

Query Match      87.5%; Score 91; DB 4; Length 559;
Best Local Similarity 89.5%; Pred. No. 4,4e-05;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 GONEGQOTIEPDTTPPIVP 19
Db      415 GHNEGQOTIEPDTTPPIVP 433

RESULT 11
US-09-010-317-12
; Sequence 12, Application US/09010317
; Patent No. 6685943
; GENERAL INFORMATION:
; APPLICANT: Hook, Magnus
; APPLICANT: Patti, Joseph M.
; APPLICANT: House-Pompeo, Karen L.
; APPLICANT: Speziale, Pietro
; APPLICANT: Joh, Danny
; APPLICANT: McGavin, Martin J.
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
; NUMBER OF SEQUENCES: 105
; TITLE OF INVENTION: AND METHODS OF USE
; CLASSIFICATION:
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: TX
; COUNTRY: USA
; ZIP: 77210-4433
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/010,317
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/036,139
; FILING DATE: 21-JAN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Hibler, David W.
; REGISTRATION NUMBER: 41,071
; REFERENCE/DOCKET NUMBER: TAMK.189
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 512-418-3000
```

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; TELEFAX: 512-474-7577
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 19 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
;
US-09-010-317-12

Query Match      86.5%; Score 90; DB 4; Length 19;
Best Local Similarity 89.5%; Pred. No. 1,6e-06;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 GONEGQOTIEPDTTPPIVP 19
Db      1 GONEGQOTIEPDTTPPIVP 19

RESULT 12
US-09-010-317-52
; Sequence 52, Application US/09010317
; Patent No. 6685943
; GENERAL INFORMATION:
; APPLICANT: Hook, Magnus
; APPLICANT: Patti, Joseph M.
; APPLICANT: House-Pompeo, Karen L.
; APPLICANT: Speziale, Pietro
; APPLICANT: Joh, Danny
; APPLICANT: McGavin, Martin J.
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
; NUMBER OF SEQUENCES: 105
; TITLE OF INVENTION: AND METHODS OF USE
; CLASSIFICATION:
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: TX
; COUNTRY: USA
; ZIP: 77210-4433
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/010,317
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/036,139
; FILING DATE: 21-JAN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Hibler, David W.
; REGISTRATION NUMBER: 41,071
; REFERENCE/DOCKET NUMBER: TAMK.189
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 512-418-3000
; TELEFAX: 512-474-7577
; INFORMATION FOR SEQ ID NO: 52:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 19 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
;
US-09-010-317-52

Query Match      85.6%; Score 89; DB 4; Length 19;
Best Local Similarity 89.5%; Pred. No. 2,3e-06;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 GONEGQOTIEPDTTPPIVP 19
Db      1 GONEGQOTIEPDTTPPIVP 19
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RESULT 13
US-09-010-317-53
Sequence 53, Application US/09010317
Patent No. 6685943
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
APPLICANT: Patti, Joseph M.
APPLICANT: House-Pompeo, Karen L.
APPLICANT: Speziale, Pietro
APPLICANT: John, Danny
APPLICANT: McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
TITLE OF INVENTION: AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAMK:169
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 53:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-09-010-317-53

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Best Local Similarity 89.5%; Pred. No. 2.3e-06;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GONEGQOTIEPTTPPIVP 19
DB 1 GONEGQOTIEPTTPPIVP 19

RESULT 14
US-08-459-135A-10
Sequence 10, Application US/08459135A
Patent No. 5955078
GENERAL INFORMATION:
APPLICANT: BURHAM, Martin Karl Russel
APPLICANT: CHOPRA, Ian
APPLICANT: CRITCHLEY, Ian Alfred
APPLICANT: KNOWLES, David Justin Charles
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN: MONOCLONAL ANTIBODY AND THEIR USE
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road

CITY: King of Prussia
STATE: PA
COUNTRY: U.S.A.
ZIP: 19406-0939
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: Fastseq, Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/459,135A
FILING DATE: 02-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB/94/00215
FILING DATE: 04-Feb-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Gimm, Edward R.
REGISTRATION NUMBER: 38,891
REFERENCE/DOCKET NUMBER: P30591C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-4478
TELEFAX: 610-270-5090
TELEX:
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 174 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: Protein
US-08-459-135A-10

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Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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DB 116 GONEGQOTIEPTTPPIVP 134

RESULT 15
US-08-495-559-10
Sequence 10, Application US/08495559A
Patent No. 6054572
GENERAL INFORMATION:
APPLICANT: BURHAM, Martin Karl Russel
APPLICANT: CHOPRA, Ian
APPLICANT: CRITCHLEY, Ian Alfred
APPLICANT: KNOWLES, David Justin Charles
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN: MONOCLONAL ANTIBODY AND THEIR USE IN PREVENTING BACTERIAL ADHESION
FILE REFERENCE: P30591
CURRENT APPLICATION NUMBER: US/08/495,559A
CURRENT FILING DATE: 1995-08-03
EARLIER APPLICATION NUMBER: GB 9302289.5
EARLIER FILING DATE: 1993-02-05
EARLIER APPLICATION NUMBER: GB 9321592.9
EARLIER FILING DATE: 1993-10-20
NUMBER OF SEQ ID NOS: 13
SOFTWARE: Fastseq for Windows Version 3.0
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LENGTH: 174
TYPE: PRT
ORGANISM: Staphylococcus aureus
US-08-495-559-10

Query Match 76.9%; Score 80; DB 3; Length 174;
Best Local Similarity 78.9%; Pred. No. 0.00046;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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GenCore version 5.1.6
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OM protein - protein search, using SW model

Run on: October 22, 2005, 11:35:03 ; Search time 35.0628 Seconds
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Title: US-10-731-238-51

Perfect score: 104
Sequence: 1 GONEGQTEPPPTPIPV 19

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Gapop 10.0 , Gapext 0.5

Searched: 1862951 seqs, 417491010 residues

Total number of hits satisfying chosen parameters: 1862951

Minimum DB seq length: 0

Maximum DB seq length: 200000000

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Maximum Match 100%
Listing first 45 summaries

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22: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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2	96	92.3	18	US-10-731-238-51
3	96	92.3	19	US-10-731-238-51
4	96	92.3	1018	US-09-815-242-5797
5	96	92.3	1018	US-09-815-242-5797
6	96	92.3	1018	US-10-470-0488-68
7	96	92.3	1027	US-08-781-986A-5254
8	96	92.3	1027	US-10-329-624-5254
9	91	87.5	559	US-08-781-986A-5251
10	91	87.5	559	US-10-329-624-5251
11	91	87.5	940	US-10-470-0488-424
12	91	87.5	948	US-10-470-0488-69

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13	89	85.6 <td>19</td> <td>18<th>US-10-731-238-52</th><th>Sequence 52, Appl</th></td>	19	18 <th>US-10-731-238-52</th> <th>Sequence 52, Appl</th>	US-10-731-238-52	Sequence 52, Appl
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17	85	81.7 <td>1001</td> <td>9<th>US-09-815-242-12686</th><th>Sequence 12686, A</th></td>	1001	9 <th>US-09-815-242-12686</th> <th>Sequence 12686, A</th>	US-09-815-242-12686	Sequence 12686, A
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21	50	48.1 <td>824</td> <td>15<th>US-10-108-260A-3650</th><th>Sequence 3650, Ap</th></td>	824	15 <th>US-10-108-260A-3650</th> <th>Sequence 3650, Ap</th>	US-10-108-260A-3650	Sequence 3650, Ap
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23	50	48.1 <td>2999</td> <td>17<th>US-10-732-923-8107</th><th>Sequence 8107, Ap</th></td>	2999	17 <th>US-10-732-923-8107</th> <th>Sequence 8107, Ap</th>	US-10-732-923-8107	Sequence 8107, Ap
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25	50	48.1 <td>3124</td> <td>17<th>US-10-732-923-8854</th><th>Sequence 8854, Ap</th></td>	3124	17 <th>US-10-732-923-8854</th> <th>Sequence 8854, Ap</th>	US-10-732-923-8854	Sequence 8854, Ap
26	49	47.1 <td>156</td> <td>15<th>US-10-425-114-41165</th><th>Sequence 41165, A</th></td>	156	15 <th>US-10-425-114-41165</th> <th>Sequence 41165, A</th>	US-10-425-114-41165	Sequence 41165, A
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ALIGNMENTS

RESULT 1
US-10-731-238-51
Sequence 51, Application US/10731238
Publication No. US20050123552A1
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
Patli, Joseph M.
House-Pompeo, Karen L.
Speziale, Pietro
Joh. Danny
McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSER: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/731.238
FILING DATE: 10-Dec-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/010.317
FILING DATE: 21-Jan-1998
APPLICATION NUMBER: US 60/036,139


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; FILING DATE: 21-JAN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Hibler, David W.
; REGISTRATION NUMBER: 41,071
; REFERENCE/DOCKET NUMBER: TAMK.189
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 512-418-3000
; TELEFAX: 512-474-7577
; INFORMATION FOR SEQ ID NO: 51:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 19 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 51:
US-10-731-238-51

Query Match      100.0%; Score 104; DB 18; Length 19;
Best Local Similarity 100.0%; Pred. No. 8.6e-08;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 2
US-10-731-238-11
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; Publication No. US20050123552A1
; GENERAL INFORMATION:
; APPLICANT: Hook, Magnus
;             Patli, Joseph M.
;             Hoube-Pompeo, Karen L.
;             Speziale, Pietro
;             Jch, Danny
;             McGavin, Martin J.
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
; NUMBER OF SEQUENCES: 105.
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: TX
; COUNTRY: USA
; ZIP: 77210-4433
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/731.238
; FILING DATE: 10-Dec-2003
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/010.317
; FILING DATE: 21-Jan-1998
; APPLICATION NUMBER: US 60/036.139
; FILING DATE: 21-JAN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Hibler, David W.
; REGISTRATION NUMBER: 41,071
; REFERENCE/DOCKET NUMBER: TAMK.189
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 512-418-3000
; TELEFAX: 512-474-7577
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 19 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
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; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 11:
US-10-731-238-11

Query Match      92.3%; Score 96; DB 18; Length 19;
Best Local Similarity 94.7%; Pred. No. 1.2e-06;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Db      1 GONEGQQTIEPDTTPPIV 19

RESULT 3
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; Sequence 5797, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Karl L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
;             Prokaryotes
; FILE REFERENCE: ELITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815.242
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for windows Version 4.0
; SEQ ID NO 5797
; LENGTH: 1018
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-09-815-242-5797

Query Match      92.3%; Score 96; DB 9; Length 1018;
Best Local Similarity 94.7%; Pred. No. 8.3e-05;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 GONEGQQTIEPDTTPPIV 19
        |||||||
Db      860 GONEGQQTIEPDTTPPIV 878

RESULT 4
US-09-815-242-12838
; Sequence 12838, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Karl L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
```

```

; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; FILE REFERENCE: ELITRA.01A
; CURRENT APPLICATION NUMBER: US/09/815,242
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 1410
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12838
; LENGTH: 1018
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-09-815-242-12838

Query Match      92.3%: Score 96; DB 9; Length 1018;
Best Local Similarity 94.7%: Pred. No. 8.3e-05;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 GONEGQQTIEBDDTTPPIVP 19
Db      860 GONEGQQTIEBDDTTPPIVP 878

RESULT 5
US-10-470-048B-68
; Sequence 68: Application US/10470048B
; Publication No. US20050037444A1
; GENERAL INFORMATION:
; APPLICANT: MEINKE ET AL.
; TITLE OF INVENTION: A METHOD FOR IDENTIFICATION, ISOLATION AND PRODUCTION OF
; FILE REFERENCE: SONN.035US
; CURRENT APPLICATION NUMBER: US/10/470,048B
; CURRENT FILING DATE: 2003-07-25
; NUMBER OF SEQ ID NOS: 603
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 68
; LENGTH: 1018
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-10-470-048B-68

Query Match      92.3%: Score 96; DB 17; Length 1018;
Best Local Similarity 94.7%: Pred. No. 8.3e-05;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 GONEGQQTIEBDDTTPPIVP 19
Db      860 GONEGQQTIEBDDTTPPIVP 878

RESULT 6
US-08-781-986A-5254
; Sequence 5254: Application US/08781986A
; Publication No. US20030054436A1
; GENERAL INFORMATION:
; APPLICANT: Charles Kunsch
; TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
```

```

; NUMBER OF SEQUENCES: 5255
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/781,986A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Benson, Bob
; REGISTRATION NUMBER: 30,446
; REFERENCE/DOCKET NUMBER: PB248PP
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 5254:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1027 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-781-986A-5254

Query Match      92.3%: Score 96; DB 8; Length 1027;
Best Local Similarity 94.7%: Pred. No. 8.4e-05;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 GONEGQQTIEBDDTTPPIVP 19
Db      869 GONEGQQTIEBDDTTPPIVP 887

RESULT 7
US-10-329-624-5254
; Sequence 5254: Application US/10329624
; Publication No. US20040043037A1
; GENERAL INFORMATION:
; APPLICANT: Charles Kunsch
; Gil H. Choi
; Patrick S. Dillon
; Craig A. Rosen
; Steven C. Barash
; Michael R. Fannon
; TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
; NUMBER OF SEQUENCES: 5256
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/329,624
; FILING DATE: 27-Dec-2002
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```

      PRIOR APPLICATION DATA:
      APPLICATION NUMBER: 08/956,171
      FILING DATE: October 20, 1997
      APPLICATION NUMBER: 60/009,861
      FILING DATE: January 5, 1996
      APPLICATION NUMBER: 08/781,986
      FILING DATE: January 3, 1997
      ATTORNEY/AGENT INFORMATION:
      NAME: Mark J. Hyman
      REGISTRATION NUMBER: 46,789
      REFERENCE/DOCKET NUMBER: PB248P1D1
      TELECOMMUNICATION INFORMATION:
      TELEPHONE: (240) 314-1224
      TELEFAX: (301) 309-8439
      INFORMATION FOR SEQ ID NO: 5254:
      SEQUENCE CHARACTERISTICS:
      LENGTH: 1027 amino acids
      TYPE: amino acid
      STRANDEDNESS: single
      TOPOLOGY: linear
      MOLECULE TYPE: protein
      SEQUENCE DESCRIPTION: SEQ ID NO: 5254:
      US-10-329-624-5254

      Query Match      92.3% Score 96; DB 15; Length 1027;
      Best Local Similarity 94.7%; Pred. No. 8.4e-05;
      Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps

      Oy      1 GQNEGQQTIEPDTTPPIV 19
      |||||
      Db      869 GQNEGQQTIEPDTTPPIV 887

      RESULT 8
      US-08-781-986A-5251
      Sequence 5251, Application US/08781986A
      Publication No. US20030054436A1
      GENERAL INFORMATION:
      APPLICANT: Charles Kunach
      TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
      NUMBER OF SEQUENCES: 5255
      CORRESPONDENCE ADDRESS:
      ADDRESSEE: Human Genome Sciences, Inc.
      STREET: 9410 Key West Avenue
      CITY: Rockville
      STATE: Maryland
      COUNTRY: USA
      ZIP: 20850
      COMPUTER READABLE FORM:
      MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
      COMPUTER: HP Vectra 486/33
      OPERATING SYSTEM: MSDOS version 6.2
      SOFTWARE: ASCII Text
      CURRENT APPLICATION DATA:
      APPLICATION NUMBER: US/08/781,986A
      FILING DATE:
      CLASSIFICATION: 435
      PRIOR APPLICATION DATA:
      APPLICATION NUMBER:
      FILING DATE:
      ATTORNEY/AGENT INFORMATION:
      NAME: Benson, Bob
      REGISTRATION NUMBER: 30,446
      REFERENCE/DOCKET NUMBER: PB248BP
      TELECOMMUNICATION INFORMATION:
      TELEPHONE: (301) 309-8504
      TELEFAX: (301) 309-8512
      INFORMATION FOR SEQ ID NO: 5251:
      SEQUENCE CHARACTERISTICS:
      LENGTH: 559 amino acids
      TYPE: amino acid
      STRANDEDNESS: single
      TOPOLOGY: linear

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; MOLECULE TYPE: protein
US-08-781-986A-5251

Query Match      87.5%; Score 91; DB 8; Length 559;
Best Local Similarity 89.5%; Pred. No. 0.00022;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY      1 GONEGQOTIEPTTPPIVP 19
      |||||||
Db      415 GHNEGQOTIEPTTPPIVP 433

RESULT 9
US-10-329-624-5251
; Sequence 5251, Application US/10329624
; Publication No. US20040043037A1
; GENERAL INFORMATION:
; APPLICANT: Charles Kunsch
; Gil H. Choi
; Patrick S. Dillon
; Craig A. Rosen
; Steven C. Barash
; Michael R. Fannon
TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
NUMBER OF SEQUENCES: 5256
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COUNTRY: USA
ZIP: 20850

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4MB storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/329,624
FILING DATE: 27-Dec-2002

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/956,171
FILING DATE: October 20, 1997
APPLICATION NUMBER: 60/009,861
FILING DATE: January 5, 1996
APPLICATION NUMBER: 08/781,986
FILING DATE: January 3, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Mark J. Hyman
REGISTRATION NUMBER: 46,769
REFERENCE/DOCKET NUMBER: PB248PDI1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (240) 314-1224
TELEFAX: (301) 309-8439
INFORMATION FOR SEQ ID NO: 5251:
SEQUENCE CHARACTERISTICS:
LENGTH: 559 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 5251:
US-10-329-624-5251

Query Match      87.5%; Score 91; DB 15; Length 559;
Best Local Similarity 89.5%; Pred. No. 0.00022;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY      1 GONEGQOTIEPTTPPIVP 19
      |||||||
Db      415 GHNEGQOTIEPTTPPIVP 433

```

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RESULT 10
US-10-470-048B-424
; Sequence 424, Application US/10470048B
; Publication No. US20050037444A1
; GENERAL INFORMATION:
; APPLICANT: MEINKE ET AL.
; TITLE OF INVENTION: A METHOD FOR IDENTIFICATION, ISOLATION AND PRODUCTION OF
; FILE REFERENCE: SONN:035US
; CURRENT APPLICATION NUMBER: US/10/470,048B
; CURRENT FILING DATE: 2003-07-25
; NUMBER OF SEQ ID NOS: 603
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 424
; LENGTH: 940
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-10-470-048B-424

Query Match      87.5%; Score 91; DB 17; Length 940;
Best Local Similarity 89.5%; Pred. No. 0.00039;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 GONEGQQTIEPDTTPPIVP 19
Db      796 GNEGQQTIEPDTTPPIVP 814

RESULT 11
US-10-470-048B-69
; Sequence 69, Application US/10470048B
; Publication No. US20050037444A1
; GENERAL INFORMATION:
; APPLICANT: MEINKE ET AL.
; TITLE OF INVENTION: A METHOD FOR IDENTIFICATION, ISOLATION AND PRODUCTION OF
; FILE REFERENCE: SONN:035US
; CURRENT APPLICATION NUMBER: US/10/470,048B
; CURRENT FILING DATE: 2003-07-25
; NUMBER OF SEQ ID NOS: 603
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 69
; LENGTH: 948
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-10-470-048B-69

Query Match      87.5%; Score 91; DB 17; Length 948;
Best Local Similarity 89.5%; Pred. No. 0.00039;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 GONEGQQTIEPDTTPPIVP 19
Db      804 GNEGQQTIEPDTTPPIVP 822

RESULT 12
US-10-731-238-12
; Sequence 12, Application US/10731238
; Publication No. US20050123552A1
; GENERAL INFORMATION:
; APPLICANT: Hook, Magnus
;             Patil, Joseph M.
;             House-Pompeo, Karen L.
;             Speziale, Pietro
;             Joh, Danny
;             McGavin, Martin J.
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
; AND METHODS OF USE
; NUMBER OF SEQUENCES: 105
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P. O. Box 4433
```

```

; CITY: Houston
; STATE: TX
; COUNTRY: USA
; ZIP: 77210-4433
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/731,238
; FILING DATE: 10-Dec-2003
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/010,317
; FILING DATE: 21-Jan-1998
; APPLICATION NUMBER: US 60/036,139
; FILING DATE: 21-JAN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Hibler, David W.
; REGISTRATION NUMBER: 41,071
; REFERENCE/DOCKET NUMBER: TAMK:189
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 512-418-3000
; TELEFAX: 512-474-7577
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 19 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 12:
US-10-731-238-12

Query Match      86.5%; Score 90; DB 18; Length 19;
Best Local Similarity 89.5%; Pred. No. 8.2e-06;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 GONEGQQTIEPDTTPPIVP 19
Db      1 GONEGQQTIEPDTTPPIVP 19

RESULT 13
US-10-731-238-52
; Sequence 52, Application US/10731238
; Publication No. US20050123552A1
; GENERAL INFORMATION:
; APPLICANT: Hook, Magnus
;             Patil, Joseph M.
;             House-Pompeo, Karen L.
;             Speziale, Pietro
;             Joh, Danny
;             McGavin, Martin J.
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
; AND METHODS OF USE
; NUMBER OF SEQUENCES: 105
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P. O. Box 4433
; CITY: Houston
; STATE: TX
; COUNTRY: USA
; ZIP: 77210-4433
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/731,238
; FILING DATE: 10-Dec-2003
; CLASSIFICATION: <Unknown>
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;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/010.317
; FILING DATE: 21-Jan-1998
; APPLICATION NUMBER: US 60/036.139
; FILING DATE: 21-JAN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Hibler, David W.
; REGISTRATION NUMBER: 41,071
; REFERENCE/DOCKET NUMBER: TAMK:189
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 512-418-3000
; TELEFAX: 512-474-7577
;
; INFORMATION FOR SEQ ID NO: 52:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 19 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
;
; SEQUENCE DESCRIPTION: SEQ ID NO: 52:
US-10-731-238-52

Query Match      85.6%; Score 89; DB 18; Length 19;
Best Local Similarity 89.5%; Pred. No. 1.1e-05;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 GONEGQQTIEPTTPPIVP 19
DB      1 GONEGQQTIEPTTPPIVP 19

RESULT 14
US-10-731-238-53
; Sequence 53, Application US/10731238
; Publication No. US20050123552A1
; GENERAL INFORMATION:
; APPLICANT: Hook, Magnus
; Partti, Joseph M.
; House-Pompeo, Karen L.
; Speziale, Pietro
; Joh, Danny
; McGavin, Martin J.
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
; NUMBER OF SEQUENCES: 105
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: TX
; COUNTRY: USA
; ZIP: 77210-4433
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/731.238
; FILING DATE: 10-Dec-2003
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/010.317
; FILING DATE: 21-Jan-1998
; APPLICATION NUMBER: US 60/036.139
; FILING DATE: 21-JAN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Hibler, David W.
; REGISTRATION NUMBER: 41,071
; REFERENCE/DOCKET NUMBER: TAMK:189
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 512-418-3000
; TELEFAX: 512-474-7577
; INFORMATION FOR SEQ ID NO: 53:

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;
; SEQUENCE CHARACTERISTICS:
; LENGTH: 19 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
;
; SEQUENCE DESCRIPTION: SEQ ID NO: 53:
US-10-731-238-53

Query Match      85.6%; Score 89; DB 18; Length 19;
Best Local Similarity 89.5%; Pred. No. 1.1e-05;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 GONEGQQTIEPTTPPIVP 19
DB      1 GONEGQQTIEPTTPPIVP 19

RESULT 15
US-10-282-122A-43778
; Sequence 43778, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyckind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282.122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See file Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 43778
; LENGTH: 961
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-10-282-122A-43778

Query Match      81.7%; Score 85; DB 15; Length 961;
Best Local Similarity 84.2%; Pred. No. 0.0028;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1 GONEGQQTIEPTTPPIVP 19

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Db 807 GONEGQTIIBDTPPP 825

Search completed: October 22, 2005, 12:09:31
Job time : 36.0628 secs

This Page Blank (uspto)

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 22, 2005, 04:14:19 ; Search time 6.94525 Seconds
(without alignments)
263.219 Million cell updates/sec

Title: US-10-731-238-51

Perfect score: 104

Sequence: 1 GONEGQQTIEPDTPPIVP 19

Scoring table: BL0SUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	96	92.3	1018	2 A32192	fibronectin-binding
2	91	87.5	940	2 S19702	fibronectin-binding
3	85	81.7	961	2 G90053	hypothetical prote
4	85	81.7	1038	2 H90053	hypothetical prote
5	57	54.8	488	2 A41961	chitinase (Ec 3.2.
6	49	47.1	120	2 F72586	hypothetical prote
7	49	47.1	485	2 F70464	hypothetical prote
8	49	47.1	741	2 I51657	suppressor of yeas
9	48	46.2	218	2 T17259	hypothetical prote
10	48	46.2	576	2 T16385	hypothetical prote
11	48	46.2	1575	2 S68448	synaptojanin, 170K
12	47	45.2	283	2 E71310	conserved hypotet
13	47	45.2	370	1 S68187	choleine-phosphate
14	46	44.2	308	2 H96827	protein F20817.12
15	46	44.2	613	2 S75976	hypothetical prote
16	46	44.2	2468	2 A83412	hypothetical prote
17	46	44.2	3300	2 D70575	probable PPE prote
18	45	43.3	367	2 A13319	choleylglycine hyd
19	45	43.3	480	2 C86357	hypothetical prote
20	45	43.3	490	2 T02545	probable MYB fam11
21	45	43.3	742	1 Q8HUB8	glucocorticoid rec
22	45	43.3	777	1 Q8HUGA	glucocorticoid rec
23	45	43.3	900	2 A42024	transcription fact
24	45	43.3	933	2 S17233	transcription fact
25	45	43.3	1381	2 T31083	paranodin - rat
26	45	43.3	1385	2 T14158	neurexin IV - mous
27	44.5	42.8	868	2 AF3204	autotransporter pr
28	44.5	42.8	1468	2 P96610	probable polypote
29	44	42.3	497	2 T41468	hypothetical prote

30	44	42.3	855	2 S47533	glucose-6-phosphat
31	44	42.3	910	2 S40259	glucose-6-phosphat
32	44	42.3	1086	2 JC7736	C3g protein, long
33	44	42.3	1200	2 T17404	hyalin - sea urchi
34	44	42.3	1262	2 T13353	protein gtn-B - fr
35	43	41.3	135	2 G81107	hypothetical prote
36	43	41.3	135	2 A81908	probable membrane
37	43	41.3	179	2 C86292	F7H2.13 protein -
38	43	41.3	206	2 B48441	antigen (C-termi
39	43	41.3	224	2 D72861	antigen (C-termi
40	43	41.3	231	2 JU0061	beta-casein precu
41	43	41.3	311	2 A48441	antigen (C-termi
42	43	41.3	318	2 T29479	hypothetical prote
43	43	41.3	333	2 C48423	homeotic protein e
44	43	41.3	376	2 AB0116	probable oxygen-in
45	43	41.3	393	2 S06259	major outer membra

ALIGNMENTS

RESULT 1

A32192
Fibronectin-binding protein - Staphylococcus aureus
C:Species: Staphylococcus aureus
C>Date: 31-Jul-1989 #sequence_revision 31-Jul-1989 #text_change 16-Feb-1997
C:Accession: A32192
R:Signaes, C.; Raucet, G.; Joensen, K.; Lindgren, P.E.; Anantharamaiah, G.M.; Heoek,
Proc. Natl. Acad. Sci. U.S.A. 86, 699-703, 1989
A:Title: Nucleotide sequence of the gene for a fibronectin-binding protein from Staphy1
A:Reference number: A32192; MUID:8908998; PMID:2521391
A:Accession: A32192
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1018 <SIG>
A:Cross-references: GB:J04151
C:Keywords: fibronectin binding

Query Match 92.3%; Score 96; DB 2; Length 1018;
Best Local Similarity 94.7%; Pred. No. 1.9e-06;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GONEGQQTIEPDTPPIVP 19
Db 860 GONEGQQTIEPDTPPIVP 878

RESULT 2

S19702
Fibronectin-binding protein B - Staphylococcus aureus
C:Species: Staphylococcus aureus
C>Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
C:Accession: S19702
R:Joensen, K.; Signaes, C.; Mueller, H.P.; Lindberg, M.
Eur. J. Biochem. 202, 1041-1048, 1991
A:Title: Two different genes encode fibronectin binding proteins in Staphylococcus aure
A:Reference number: S19702; MUID:92111475; PMID:1857266
A:Accession: S19702
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-940 <JOB>
A:Cross-references: UNIPROT:Q53682; EMBL:X62992; NID:949040; PIDD:CAA44726.1; PID:G5015
C:Keywords: fibronectin binding

Query Match 87.5%; Score 91; DB 2; Length 940;
Best Local Similarity 89.5%; Pred. No. 1e-05;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GONEGQQTIEPDTPPIVP 19
Db 796 GONEGQQTIEPDTPPIVP 814

RESULT 8

151657
suppressor of yeast mitotic catastrophe - African clawed frog
C/Species: Xenopus laevis (African clawed frog)
C/Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004
C/Accession: 151657
R/Su, U.; Muller, J.L.
Gene 145, 155-156, 1994
A/Title: Identification of a Xenopus cDNA clone preventing mitotic catastrophe in the f
C/Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 05-Nov-1999
A/Reference number: 151657; MUID:94320781; PMID:8045419
C/Accession: 151657
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-741 <SU>
A/Cross-references: UNIPROT:Q91552; EMBL:U07608; NID:9464002; PID:AAA20939.1; PID:94640

Query Match 47.1%; Score 49; DB 2; Length 741;
Best Local Similarity 44.4%; Pred. No. 19;
Matches 8; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 2 QNEGGQTIETPTPIVP 19
DB 488 RNSSQPNKADTSPVP 505

RESULT 9

117259
hypothetical protein DKFZp727C091.1 - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C/Accession: 117259
R/Pouska, A.; Klein, M.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.
submitted to the Protein Sequence Database, September 1999
A/Reference number: 218723
A/Accession: 117259
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-218 <PO>
A/Cross-references: UNIPROT:Q9UFT0; EMBL:AL117476
A/Experimental source: adult breast cancer; clone DKFZp727C091
A/Genetics:
A/Note: DKFZp727C091.1

Query Match 46.2%; Score 48; DB 2; Length 218;
Best Local Similarity 47.4%; Pred. No. 7;
Matches 9; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

QY 1 GONEGGQTIETPTPIVP 19
DB 182 GSKTGRETAAPTPPIVP 200

RESULT 10

146385
hypothetical protein DKFZp434K031.1 - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 09-Jul-2004
C/Accession: 146385
R/Pouska, A.; Klein, M.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.
submitted to the Protein Sequence Database, January 2000
A/Reference number: 223029
A/Accession: 146385
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-576 <AA>
A/Cross-references: UNIPROT:Q9NTE7; EMBL:AL137317
A/Experimental source: adult testis; clone DKFZp434K031
C/Genetics:
A/Note: DKFZp434K031.1

Query Match 46.2%; Score 48; DB 2; Length 576;
Best Local Similarity 47.4%; Pred. No. 21;

Matches 9; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

QY 1 GONEGGQTIETPTPIVP 19
DB 540 GSKTGRETAAPTPPIVP 558

RESULT 11

S68448
synaptojanin, 170K - rat
C/Species: Rattus norvegicus (Norway rat)
C/Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 05-Nov-1999
C/Accession: S68448; S78547; S78527
R/McPherson, P.S.; Garcia, E.P.; Slepnev, V.I.; David, C.; Zhang, X.; Grabs, D.; Soesin
Nature 379, 353-357, 1996
A/Title: A presynaptic inositol-5-phosphatase.
A/Reference number: A58183; MUID:96149250; PMID:8552192
A/Accession: S68448
A/Status: nucleic acid sequence not shown

A/Molecule type: mRNA
A/Residues: 1-1575 <MC>
A/Cross-references: EMBL:U45479; NID:91166574; PID:AA60525.1; PID:91166575; PID:91166
A/Experimental source: brain
A/Accession: S78547

A/Molecule type: protein
A/Residues: 1075-1093;1173-1199;1290-1308 <MC>
A/Experimental source: brain
R/de Camilli, P.
submitted to the EMBL Data Library, January 1996
A/Reference number: S78527

A/Accession: S78527
A/Molecule type: mRNA
A/Residues: 1-587;1'p, 589-1575 <DEC>
A/Cross-references: EMBL:U45479

A/Function:
A/Description: binds the SH3 domain of amphiphysin
A/Keywords: alternative splicing; alternative termination; synaptic vesicle
F;1-1575/Product: synaptojanin, long form b #status predicted <MAT>
F;1-1139,1156-1575/Product: synaptojanin, long form a #status predicted <MAT>
F;1-113,1156-1308/Product: synaptojanin, short form #status predicted <MAT>

Query Match 46.2%; Score 48; DB 2; Length 1575;
Best Local Similarity 55.6%; Pred. No. 64;
Matches 10; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 2 QNEGGQTIETPTPIVP 19
DB 1093 QKSSQTIETPTPIVP 1110

RESULT 12

E71310
conserved hypothetical protein TP0561 - syphilis spirochete
C/Species: Treponema pallidum subsp. pallidum (syphilis spirochete)
C/Date: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 09-Jul-2004
C/Accession: E71310
R/Fraser, C.M.; Norris, S.J.; Weinstock, G.M.; White, O.; Sutton, G.G.; Dodson, R.; Gwi
rson, J.; Khalak, H.; Richardson, D.; Howell, J.K.; Chidambaram, M.; Uetzerback, T.; McD
they, L.; Weidman, J.; Smith, H.O.; Venter, J.C.
Science 281, 375-388, 1998
A/Title: Complete genome sequence of Treponema pallidum, the syphilis spirochete.
A/Reference number: A71250; MUID:98332770; PMID:9665876
A/Accession: E71310
A/Status: preliminary; nucleic acid sequence not shown; translation not shown
A/Molecule type: DNA
A/Residues: 1-283 <CO>
A/Cross-references: UNIPROT:O83572; GB:AE001231; GB:AE000520; NID:93322846; PID:AA6265
A/Experimental source: strain Nichols
C/Genetics:
A/Genes: TP0561

Query Match 45.2%; Score 47; DB 2; Length 283;
Best Local Similarity 47.4%; Pred. No. 13;

Matches 9; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 1 GQNEGQQTIEPDTTPPIVP 19
||:||||:|
Db 184 GQHEVQGFQMPRSVGPAPV 202

RESULT 13

S68187
choleine-phosphate cytidyltransferase (EC 2.7.7.15) - malaria parasite (Plasmodium falciparum)
N:Alternate names: CTP:choleine-phosphate cytidyltransferase; phosphorylcholine transferase
C:Species: Plasmodium falciparum
C:Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
A:Accession: S68187
R:Yeo, H.J.; Sri Widadu, J.; Mercereau-Pujalon, O.; Vial, H.J.
Eur. J. Biochem. 233, 62-72, 1995
A:Title: Molecular cloning of CTP:phosphocholine cytidyltransferase from Plasmodium falciparum
A:Reference number: S68187; PMID:96061933; PMID:7588775

A:Accession: S68187
A:Molecule type: DNA
A:Residues: 1-370 <YEO>
A:Cross-references: UNIPROT:P49587; EMBL:X84041; NID:G1054826; ITDN:CAA58860.1; PID:G1054826
C:Genetics:
A:Gene: CTP

A:introns: #status absent
C:Function:
A:Description: catalyzes the formation of cytidinediphosphate cline and pyrophosphate
A:Pathway: phospholipid biosynthesis
C:Superfamily: choline-phosphate cytidyltransferase
C:Keyword: membrane-associated protein; nucleotidyltransferase, phospholipid biosynthesis
F:274-294/Domain: amphipathic helix #status predicted <AH1>
F:308-324/Domain: amphipathic helix #status predicted <AH2>

Query Match 45.2%; Score 47; DB 1; Length 370;
Best Local Similarity 47.1%; Pred. No. 18;
Matches 8; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

QY 3 NSEQQTIEPDTTPPIVP 19
|:|||||
Db 40 NSEQQVDDPDTNDAVP 56

RESULT 14

H96827
protein F20B17.12 [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C:Accession: H96827
R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kau, S.; White, O.; Alonso, J.; Chiu, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; Hansen, N.F.; Hughes, B.; Hultz, L.
Nature 408, 816-820, 2000
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.A.; Li, J.H.; Li, Y.; Loh, X.; Liu, S.X.; Liu, Z.A.; Lueros, J.S.; Maitl, R.; Marziani, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shim, P.; Southwick, A.M.; Sun, H.; Tallon, Ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A:Reference number: A86141; PMID:21016719; PMID:11130712

A:Accession: H96827
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-308 <STO>
A:Cross-references: UNIPROT:Q9WA06; GB:AE005173; NID:G7715603; ITDN:AAF68121.1; GSPDB:GN
C:Genetics:
A:Gene: F20B17.12
A:Map position: 1

Query Match 44.2%; Score 46; DB 2; Length 308;
Best Local Similarity 37.5%; Pred. No. 21;
Matches 6; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

QY 4 EGQQTIEPDTTPPIVP 19

Db 245 KSEVIEPSTSPSEVIP 260
:|:||||:|:|:|

RESULT 15

S75976
hypothetical protein - Synechocystis sp. (strain PCC 6803)
C:Species: Synechocystis sp.
A:Variety: PCC 6803
C:Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004
A:Accession: S75976
R:Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.; O, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda
DNA Res. 3, 109-136, 1996
A:Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis sp.
A:Reference number: S74322; PMID:97061201; PMID:8905231
A:Accession: S75976
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-613 <KAN>
A:Cross-references: UNIPROT:Q55477; EMBL:D64006; GB:AB001339; NID:G1001291; PIDN:BAAL082
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
F:139-361/Domain: subtilisin homology <SBT>

Query Match 44.2%; Score 46; DB 2; Length 613;
Best Local Similarity 37.5%; Pred. No. 45;
Matches 9; Conservative 5; Mismatches 4; Indels 6; Gaps 1;

QY 1 GQNEG-----QQTIEPDTTPPIVP 18
|:|:|:|:|:|:|:|
Db 317 GSTDGKDKILQETIDPDTREPVL 340

Search completed: October 22, 2005, 06:09:57
Job time : 7.94525 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 22, 2005, 04:10:49 ; Search time 34.818 Seconds
(without alignments)
279.439 Million cell updates/sec

Title: US-10-731-238-51
Perfect score: 104
Sequence: 1 GONEGQOTIEPDTTPPIVP 19

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_03:.*
1: uniprot_sprot:.*
2: uniprot_trembl:.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	96	92.3	1018	1 FNBA_STAAU	P14738 staphylococ
2	91	87.5	940	2 Q53682	Q53682 staphylococ
3	85	81.7	961	2 Q99R3	Q99R3 staphylococ
4	85	81.7	961	2 Q7A338	Q7A338 staphylococ
5	85	81.7	965	2 Q6GDUS	Q6GDUS staphylococ
6	85	81.7	1015	2 Q8NUV7	Q8NUV7 staphylococ
7	85	81.7	1015	2 Q6G6H3	Q6G6H3 staphylococ
8	85	81.7	1038	2 Q99RD2	Q99RD2 staphylococ
9	85	81.7	1038	2 Q7A3J7	Q7A3J7 staphylococ
10	80	76.9	957	2 Q6G6H4	Q6G6H4 staphylococ
11	70	67.3	943	2 Q8NUU8	Q8NUU8 staphylococ
12	57	54.8	524	1 CHID_BACCI	P27050 bacillus c1
13	52	50.0	546	2 Q8D5G8	Q8D5G8 vibrio vuln
14	51	49.0	462	2 Q9L1N4	Q9L1N4 streptomyce
15	51	49.0	686	2 Q9V550	Q9V550 dirosophila
16	51	49.0	1025	2 Q7A1N7	Q7A1N7 neurospora
17	50.5	48.6	148	2 Q7Q8G9	Q7Q8G9 giardia lam
18	50	48.1	130	2 Q7R6Q8	Q7R6Q8 giardia lam
19	50	48.1	181	2 Q96MM1	Q96MM1 homo sapien
20	50	48.1	311	2 Q9DAS4	Q9DAS4 mus musculu
21	50	48.1	649	2 Q641K9	Q641K9 mus musculu
22	50	48.1	886	2 Q8C0P6	Q8C0P6 mus musculu
23	50	48.1	822	2 Q8BYW3	Q8BYW3 mus musculu
24	50	48.1	824	2 Q8N8Q7	Q8N8Q7 homo sapien
25	50	48.1	826	2 Q6B2F5	Q6B2F5 homo sapien
26	50	48.1	985	2 Q8N8O5	Q8N8O5 homo sapien
27	50	48.1	1731	2 Q9P230	Q9P230 homo sapien
28	50	48.1	2999	2 Q8CH17	Q8CH17 mus musculu
29	50	48.1	3035	2 Q8CH18	Q8CH18 mus musculu
30	50	48.1	3124	2 Q96L91	Q96L91 homo sapien
31	49	47.1	120	2 Q9YCU9	Q9YCU9 aeropyrum p

32	49	47.1	236	2 Q7PIW4	Q7PIW4 anopheles g
33	49	47.1	251	2 Q84V67	Q84V67 zea mays (m
34	49	47.1	468	2 Q91WQ1	Q91WQ1 mus musculu
35	49	47.1	485	2 Q67746	Q67746 aquifex aeo
36	49	47.1	709	2 Q8CCB7	Q8CCB7 mus musculu
37	49	47.1	709	2 Q9CYA6	Q9CYA6 mus musculu
38	49	47.1	741	2 Q91552	Q91552 xenopus lae
39	49	47.1	812	2 Q6NRN7	Q6NRN7 xenopus lae
40	49	47.1	1406	2 Q7Q4U2	Q7Q4U2 anopheles g
41	49	47.1	1427	1 ZFH2_HUMAN	Q9C0A1 homo sapien
42	49	47.1	1603	2 Q8G499	Q8G499 bifidobacte
43	49	47.1	2722	2 Q8GJN0	Q8GJN0 dictyostell
44	49	46.2	162	2 Q7NN16	Q7NN16 gloeobacter
45	48	46.2	218	2 Q9UFT0	Q9UFT0 homo sapien

ALIGNMENTS

RESULT 1
FNBA_STAAU STANDARD; PRT; 1018 AA.
ID FNBA_STAAU STANDARD; PRT; 1018 AA.
AC P14738;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Fibronectin-binding protein precursor (FNBP).
GN Name=fnba;
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1280;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NCITC 8325-4;
RX MEDLINE=69098998; PubMed=2521391;
RA Signas C., Raucsi G., Joensson K., Lindgren P.-E.,
RA Mantzarakis G.M., Hoeck M., Lindberg M.;
RA "Nucleotide sequence of the gene for a fibronectin-binding protein
RT from Staphylococcus aureus: use of this peptide sequence in the
RT synthesis of biologically active peptides."
RL Proc. Natl. Acad. Sci. U.S.A. 86:699-703(1989).
CC -!- FUNCTION: The ability of bacteria to bind fibronectin has been
CC proposed as a virulence factor enabling bacteria to colonize wound
CC tissues and blood clots. Binding of plasma fibronectin to the
CC bacterial surface might block adhesion receptors on S.aureus, thus
CC representing an important defense mechanism against tissue
CC invasion.
CC -!- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC an amide bond (Potential).
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC or send an email to license@sib-sib.ch).
CC -----
CC EMBL: J04151; AAA26632.1; -;
CC InterPro: IPR004237; Fn_bind.
CC InterPro: IPR005877; Gpos_Y5IRK.
CC InterPro: IPR001899; Gram_pos_anchor.
CC Pfam: PF02986; Fn_bind; 1.
CC Pfam: PF00746; Gram_pos_anchor; 1.
CC Pfam: PF04650; Y5IRK_signal; 1.
CC TIGRFAMs: TIGR01167; LpxTG_anchor; 1.
CC TIGRFAMs: TIGR01168; Y5IRK_signal; 1.
CC PROSITE: PS50847; GRAM_POS_ANCHORING; 1.
CC Cell adhesion; Cell wall; Peptidoglycan-anchor; Repeat; Signal;
CC Virulence.
CC SIGNAL 1 36
CC CHAIN 37 985 Fibronectin-binding protein.
CC PROPEP 986 1018 Removed by sortase (Potential).
FT

```
FT REPEAT 545 574 B-1.
FT REPEAT 575 604 B-2.
FT DOMAIN 745 878 4 X approximate tandem repeats,
  fibronectin-binding domain.
FT REPEAT 745 782 D-1.
FT REPEAT 783 820 D-2.
FT REPEAT 821 859 D-3.
FT DOMAIN 860 878 D-4 (incomplete).
FT REPEAT 879 948 5 X tandem repeats, Pro-rich (WR).
FT REPEAT 879 892 WR 1.
FT REPEAT 893 906 WR 2.
FT REPEAT 907 920 WR 3.
FT REPEAT 921 934 WR 4.
FT REPEAT 935 948 WR 5.
FT SITE 982 986 LpXTG sorting signal (Potential).
FT MOD_RES 985 985 Pentaglycyl murein peptidoglycan amidated
  chreonine (Potential).
SO SEQUENCE 1018 AA; 111780 MW; 58175E0020E81F1F CRC64;

Query Match 92.3%; Score 96; DB 1; Length 1018;
Best Local Similarity 94.7%; Pred. No. 1.2e-05;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GONEGQOTIEBDDTTPPIV 19
Db 860 GONEGQOTIEBDDTTPPIV 878

RESULT 2
Q53682 PRELIMINARY; PRT; 940 AA.
AC Q53682;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Fibronectin binding protein B.
GN Name=fnb3;
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1280;
[1]
RN SEQUENCE FROM N.A.
RC STRAIN=8325-4;
RX MEDLINE=92111475; PubMed=1837266;
RA Jonsson K., Signas C., Muller H.P., Lindberg M.;
RT "Two different genes encode fibronectin binding proteins in
  Staphylococcus aureus. The complete nucleotide sequence and
  characterization of the second gene."
RL Bur. J. Biochem. 202;1041-1048(1991).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
  an amide bond (By similarity).
CD HMBL; X62992; CAA44726.1; -.
DR PIR; S19702; S19702.
DR HSSP; Q53653; 1N67.
DR GO; GO:0009986; C:cell surface; IEA.
DR GO; GO:0005618; C:cell wall; IEA.
DR GO; GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0007155; P:cell adhesion; IEA.
DR InterPro; IPR008966; Adhes_bact.
DR InterPro; IPR004237; Fn_bind.
DR InterPro; IPR005877; Gpos_YsIRK.
DR InterPro; IPR001899; Gram_pos_anchor.
DR Pfam; PF02986; Fn_bind_2.
DR Pfam; PF00746; Gram_pos_anchor; 1.
DR TIGRfam; TIGR01167; LpXTG_anchor; 1.
DR TIGRfam; TIGR01168; YsIRK_signal; 1.
DR PROSITE; PS50847; GRAM_POS_ANCHORING; 1.
KM Cell wall; Peptidoglycan-anchor.
SO SEQUENCE 940 AA; 103555 MW; E35FBBCA907AE345 CRC64;

Query Match 87.5%; Score 91; DB 2; Length 940;
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Best Local Similarity 89.5%; Pred. No. 6.5e-05;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GONEGQOTIEBDDTTPPIV 19
Db 796 GONEGQOTIEBDDTTPPIV 814

RESULT 3
Q59RD3 PRELIMINARY; PRT; 961 AA.
AC Q59RD3;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Fibronectin-binding protein homolog.
GN Name=fnb3; Ordered locus names=SAV2502;
OS Staphylococcus aureus (strain Mu50 / ATCC 700699).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=158878;
[1]
RN SEQUENCE FROM N.A.
RC STRAIN=Mu50 / ATCC 700699;
RX MEDLINE=21311952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2;
RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
  Cui L., Oguchi A., Aoki K.-I., Nagai Y., Iino T.,
  Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,
  Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
  Sekimizu K., Hiraoka H., Kohara S., Goto S., Yabuaki J.,
  RA Kaneshita M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
  RA Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
RT "Whole genome sequencing of methicillin-resistant Staphylococcus
  aureus."
RL Lancet 357;1225-1240(2001).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
  an amide bond (By similarity).
CD EMBL; AP003365; BAB58664.1; -.
DR PIR; G90053; G90053.
DR HSSP; Q53653; 1N67.
DR GO; GO:0009986; C:cell surface; IEA.
DR GO; GO:0005618; C:cell wall; IEA.
DR GO; GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0007155; P:cell adhesion; IEA.
DR InterPro; IPR008966; Adhes_bact.
DR InterPro; IPR004237; Fn_bind.
DR InterPro; IPR005877; Gpos_YsIRK.
DR InterPro; IPR001899; Gram_pos_anchor.
DR Pfam; PF02986; Fn_bind_1.
DR Pfam; PF00746; Gram_pos_anchor; 1.
DR TIGRfam; TIGR01167; LpXTG_anchor; 1.
DR TIGRfam; TIGR01168; YsIRK_signal; 1.
DR PROSITE; PS50847; GRAM_POS_ANCHORING; 1.
KM Cell wall; Complete proteome; Peptidoglycan-anchor.
SO SEQUENCE 961 AA; 106010 MW; 364940F884EA4101 CRC64;

Query Match 81.7%; Score 85; DB 2; Length 961;
Best Local Similarity 84.2%; Pred. No. 0.00054;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GONEGQOTIEBDDTTPPIV 19
Db 807 GONEGQOTIEBDDTTPPIV 825

RESULT 4
Q7A3J8 PRELIMINARY; PRT; 961 AA.
AC Q7A3J8;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
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DE FndB protein.
GN Name=fndB; OrderedLocustNames=SA2290;
OS Staphylococcus aureus (strain N315).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=158879;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21311952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2;
RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Iian J.-Q., Ito T.,
RA Kanamori M., Matsunaru H., Maruyama A., Murakami H., Hoshoyama A.,
RA Mizutani U. Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
RA Sekimizu K., Hirakawa H., Kunara S., Goto S., Yabuzaki J.,
RA Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
RA Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
RT "Whole genome sequencing of methicillin-resistant Staphylococcus
aureus".
RL Lancer 357:1225-1240(2001).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC an amide bond (By similarity).
DR EMBL; AP003137; BAB43593.1; -.
DR GO; GO:0009986; C:cell surface; IEA.
DR GO; GO:0005618; C:cell wall; IEA.
DR GO; GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0007155; P:cell adhesion; IEA.
DR InterPro; IPR008966; Adhes_bact.
DR InterPro; IPR004237; Fn_bind.
DR InterPro; IPR005877; Gpos_YsIRK.
DR InterPro; IPR001899; Gram_pos_anchor.
DR Pfam; PF02986; Fn_bind; 1.
DR Pfam; PF00746; Gram_pos_anchor; 1.
DR Pfam; PF04650; YsIRK_signal; 1.
DR TIGRFAMs; TIGR01167; LPXTG_anchor; 1.
DR TIGRFAMs; TIGR01168; YsIRK_signal; 1.
DR PROSITE; PS50847; GRAM_POS_ANCHORING; 1.
DR Cell wall; Complete proteome; Peptidoglycan-anchor.
KW SEQUENCE 961 AA; 106010 MW; 364940F84EA4101 CRC64;
SQ
Query Match 81.7%; Score 85; DB 2; Length 961;
Best Local Similarity 84.2%; Pred. No. 0.00054;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 GONEGQQTIEPTTPPIVP 19
DB 807 GONEGQQTIEPTTPPP 825
RESULT 5
Q6GDUS PRELIMINARY; PRT; 965 AA.
AC O6GDUS;
ID O6GDUS;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Fibronectin-binding protein.
GN Name=fnbA; OrderedLocustNames=SA2580;
OS Staphylococcus aureus (strain MRSA252).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=282458;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=15213324; DOI=10.1073/pnas.0402521101;
RA Hoiden M.T.G., Fell E.J., Lindsay J.A., Peacock S.J., Day N.P.J.,
RA Enright M.C., Foster T.J., Moore C.E., Hurst L., Atkin R., Barton A.,
RA Baeson N., Bentley S.D., Chillingworth C., Chillingworth T.,
RA Churcher C., Clark L., Cotton C., Cronin A., Doggett J., Dowd L.,
RA Feltwell T., Hance Z., Harris B., Hauser H., Holtroyd S., Jagels K.,
RA James K.D., Leonard N., Line A., Mayes R., Moule S., Mungall K.,
RA Ormond D., Quail M.A., Rabinovitch E., Rutherford K.M., Sanders M.,
RA Sharp S., Simmonds M., Stevens K., Whitehead S., Barrall B.G.,
RA Spratt B.G., Fairhill J.;
RT "Complete genomes of two clinical Staphylococcus aureus strains:

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RT evidence for the rapid evolution of virulence and drug resistance."
RL Proc Natl Acad Sci U S A. 101:9786-9791(2004).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC an amide bond (By similarity).
DR EMBL; BX571856; CAG41560.1; -.
DR GO; GO:0009986; C:cell surface; IEA.
DR GO; GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0007155; P:cell adhesion; IEA.
DR InterPro; IPR008966; Adhes_bact.
DR InterPro; IPR004237; Fn_bind.
DR InterPro; IPR005877; Gpos_YsIRK.
DR InterPro; IPR001899; Gram_pos_anchor.
DR Pfam; PF02986; Fn_bind; 1.
DR Pfam; PF00746; Gram_pos_anchor; 1.
DR Pfam; PF04650; YsIRK_signal; 1.
DR TIGRFAMs; TIGR01167; LPXTG_anchor; 1.
DR TIGRFAMs; TIGR01168; YsIRK_signal; 1.
DR PROSITE; PS50847; GRAM_POS_ANCHORING; 1.
DR Cell wall; Complete proteome; Peptidoglycan-anchor.
KW SEQUENCE 965 AA; 105691 MW; 2982E132164D0551 CRC64;
SQ
Query Match 81.7%; Score 85; DB 2; Length 965;
Best Local Similarity 84.2%; Pred. No. 0.00054;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 GONEGQQTIEPTTPPIVP 19
DB 825 GONEGQQTIEPTTPPP 843
RESULT 6
Q8NUU7 PRELIMINARY; PRT; 1015 AA.
AC Q8NUU7;
ID Q8NUU7;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE FndB protein.
GN Name=fnb; OrderedLocustNames=MM2421;
OS Staphylococcus aureus (strain MM2).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=196620;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=MM2;
RA Baba T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Oguchi A.,
RA Nagai Y., Iwano N., Asano K., Naimi T., Kuroda H., Cui L.,
RA Yamamoto K., Hiramatsu K.;
RT "Genome and virulence determinants of high virulence community-
acquired MRSA."
RL Lancer 359:1819-1827(2002).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC an amide bond (By similarity).
DR EMBL; AP004830; BAB96286.1; -.
DR GO; GO:0009986; C:cell surface; IEA.
DR GO; GO:0005618; C:cell wall; IEA.
DR GO; GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0007155; P:cell adhesion; IEA.
DR InterPro; IPR008966; Adhes_bact.
DR InterPro; IPR004237; Fn_bind.
DR InterPro; IPR005877; Gpos_YsIRK.
DR InterPro; IPR001899; Gram_pos_anchor.
DR Pfam; PF02986; Fn_bind; 1.
DR Pfam; PF00746; Gram_pos_anchor; 1.
DR Pfam; PF04650; YsIRK_signal; 1.
DR TIGRFAMs; TIGR01167; LPXTG_anchor; 1.
DR TIGRFAMs; TIGR01168; YsIRK_signal; 1.
DR PROSITE; PS50847; GRAM_POS_ANCHORING; 1.
DR Cell wall; Complete proteome; Peptidoglycan-anchor.
KW SEQUENCE 1015 AA; 111145 MW; D0F9281B864D4D2 CRC64;
SQ

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Query Match	Similarity	84.2%	Score 85;	DB 2;	Length 1015;
Best Local	Similarity	84.2%	Pred. No. 0.00058;		
Matches 16;	Conservative	0;	Mismatches 3;	Indels 0;	Gaps 0;
QY	1 GONEGQQTIEPTTPPIP 19				
DB	861 GONEGQQTIEPTTPPIP 879				
RESULT 7					
06G6H3	PRELIMINARY;		PRT;	1015 AA.	
AC	06G6H3;				
DT	05-JUL-2004 (TREMBlrel. 27, Created)				
DT	05-JUL-2004 (TREMBlrel. 27, Last sequence update)				
DE	05-JUL-2004 (TREMBlrel. 27, Last annotation update)				
GN	Fibronectin-binding protein.				
OS	OrderedLocNames=5A82388;				
OC	Staphylococcus aureus (strain MSSA476).				
OK	Bacteria; Firmicutes; Bacillales; Staphylococcus.				
NCBI	_TaxID=282459;				
SEQUENCE FROM N.A.					
RP	Pubmed=1523324; DOI=10.1073/pnas.040221101;				
RX	Holden M.T.G., Fell E.J., Lindstedt J.A., Peacock S.J., Day N.P.U.,				
RA	Bright M.C., Foster T.J., Moore C.E., Hirst L., Atkin R., Barton A.,				
RA	Baeson N., Bentley S.D., Chillingworth C., Chillingworth T.,				
RA	Churcher C., Clark L., Cotton C., Cronin A., Doggett J., Dowd L.,				
RA	Feltwell T., Hance Z., Harris B., Hauser H., Holroyd S., Jagsle K.,				
RA	James K.D., Lennard N., Line A., Mayes R., Moule S., Mungall K.,				
RA	Ormond D., Quail M.A., Rabinovitch E., Rutherford K.M., Sanders M.,				
RA	Sharp S., Simmonds M., Stevens K., Whitehead S., Barrall E.G.,				
RT	Sprate B.G., Parkhill J.;				
RT	"Complete genomes of two clinical Staphylococcus aureus strains:				
RT	evolution for the rapid evolution of virulence and drug resistance.";				
Proc. Natl. Acad. Sci. U.S.A.	101:9786-9791(2004).				
-1- SUBCELLULAR LOCATION:	Attached to the cell wall peptidoglycan by				
an amide bond (by similarity).					
EMBL	EX571857; CAG44202.1; -;				
DR	GO; GO:0009986; C:cell surface; IEA.				
DR	GO; GO:0009986; C:cell wall; IEA.				
DR	GO; GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.				
DR	GO; GO:0016020; C:membrane; IEA.				
DR	GO; GO:0007155; P:cell adhesion; IEA.				
DR	InterPro; IPR008966; Adhes_bact.				
DR	InterPro; IPR004237; Fn_bind.				
DR	InterPro; IPR005877; Gpos_Y5IRK.				
DR	InterPro; IPR01899; Gram_pos_anchor.				
DR	pfam; PF02986; Fn_bind; 1.				
DR	pfam; PF00746; Gram_pos_anchor; 1.				
DR	pfam; PF04550; Y5IRK_signal; 1.				
DR	TIGRFAMs; TIGR01167; LpxTG_anchor; 1.				
DR	TIGRFAMs; TIGR01168; Y5IRK_signal; 1.				
DR	PROSITE; PS50847; GRAM_POS_ANCHORING; 1.				
KW	Cell wall; Complete proteome; Peptidoglycan-anchor.				
SEQUENCE	1015 AA; 111145 MW; DQF92818B64D44D2 CRC64;				
Query Match		81.7%;	Score 85;	DB 2;	Length 1015;
Best Local Similarity	84.2%;	Pred. No. 0.00058;			
Matches 16;	Conservative 0;	Mismatches 3;	Indels 0;	Gaps 0;	
QY	1 GONEGQQTIEPTTPPIP 19				
DB	861 GONEGQQTIEPTTPPIP 879				
RESULT 8					
099RD2	PRELIMINARY;		PRT;	1038 AA.	
AC	099RD2;				
DT	01-JUN-2001 (TREMBlrel. 17, Created)				
DT	01-JUN-2001 (TREMBlrel. 17, Last sequence update)				

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DT 01-MAR-2004 (TREMblrel. 26, last annotation update)
DE Fibronectin-binding protein homolog.
GN Name=fnb; OrderedLocusNames=SAV2503;
OS Staphylococcus aureus (strain Mu50 / ATCC 700699) .
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
ON NCBI_TaxId=158878;
RX MEDLINE=21311952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2;
RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Iian J.-Q., Ito T.,
RA Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,
RA Mizutani-Ui Y., Takahashi N., Kuhara S., Goto S., Yabuzaki J.,
RA Sekimizu K., Hatakewa H., Kohara S., Goto S., Furuya K., Yoshino C., Shiba T.,
RA Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
RT "Whole genome sequencing of methicillin-resistant Staphylococcus
RT aureus."
RL Lancet.357:1225-1240(2001).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC an amide bond (By similarity) .
DR EMBL; AP003365; BAB58665.1; -.
DR PIR; H90053; H90053.
DR GO; GO:0009986; C:cell surface; IEA.
DR GO; GO:0005618; C:cell wall; IEA.
DR GO; GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0007155; P:cell adhesion; IEA.
DR InterPro; IPR008966; Adhes_bact.
DR InterPro; IPR004237; Fn_bind.
DR InterPro; IPR005877; GPos_YSTRK.
DR InterPro; IPR001899; Gram_pos_anchor.
DR Pfam; PF02986; Fn_bind.1.
DR Pfam; PF00746; Gram_pos_anchor.1.
DR Pfam; PF04650; YSTRK_signal.1.
DR TIGRFAMs; TIGR01167; LpxK_anchor.1.
DR TIGRFAMs; TIGR01168; YSTRK_signal.1.
DR PROSITE; PS50847; GRAM_POS_ANCHORING.1.
DR Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ SEQUENCE 1038 AA; 6668BFB2BFBEB12 CRC64;

Query Match 81.7%; Score 85; DB 2; Length 1038;
Best Local Similarity 84.2%; Pred. No. 0.00059;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps

Oy 1 GONEGOTIEPTTPPIVP 19
Db 856 GONEGOTIEPTTPPP 874

RESULT 9
07A3J7 PRELIMINARY; PRT; 1038 AA.
AC 07A3J7;
DT 05-JUL-2004 (TREMblrel. 27, Created)
DT 05-JUL-2004 (TREMblrel. 27, last sequence update)
DT 05-JUL-2004 (TREMblrel. 27, last annotation update)
DE Fnb protein.
GN Name=fnb; OrderedLocusNames=SA2291;
OS Staphylococcus aureus (strain N315).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxId=158879;
RX MEDLINE=21311952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2;
RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Iian J.-Q., Ito T.,
RA Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,
RA Mizutani-Ui Y., Takahashi N., Kuhara S., Goto S., Furuya K., Yoshino C., Shiba T.,
RA Sekimizu K., Hatakewa H., Kohara S., Goto S., Furuya K., Yoshino C., Shiba T.,
RA Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;

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RT "Whole genome sequencing of methicillin-resistant *Staphylococcus aureus*."
RT Lancet 357:1225-1240(2001).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by an amide bond (By similarity).
DR EMBL:AB003337; BAB43594.1; -.
DR GO: GO:0009986; C:cell surface; IEA.
DR GO: GO:0005618; C:cell wall; IEA.
DR GO: GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO: GO:0016020; C:membrane; IEA.
DR GO: GO:0007155; P:cell adhesion; IEA.
DR InterPro: IPR008966; Adhes_bact.
DR InterPro: IPR004237; Fn_bind.
DR InterPro: IPR005877; Gpos_YsIRK.
DR InterPro: IPR001899; Gram_pos_anchor.
DR Pfam: PF02986; Fn_bind. 1.
DR Pfam: PF00746; Gram_pos_anchor; 1.
DR TIGRFAMs: TIGR01167; LPXTG_anchor; 1.
DR TIGRFAMs: TIGR01168; YsIRK_signal; 1.
DR PROSITE: PS50847; GRAM_POS_ANCHORING; 1.
KM Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ SEQUENCE 1038 AA; 113618 MW; 666BF6BF2BFBEB12 CRC64;

Query Match 81.7%; Score 85; DB 2; Length 1038;
Best Local Similarity 84.2%; Pred. No. 0.00059;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GONEGQOTIEPTTPTTP 19
Db 856 GONEGQOTIEPTTPTTP 874

RESULT 10
O6G6H4 PRELIMINARY; PRT; 957 AA.
AC O6G6H4;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Fibronectin-binding protein.
GN Name=fnbB; OrderedLocustNames=SA62387;
OS *Staphylococcus aureus* (strain MSSA476).
OC Bacteria; Firmicutes; Bacillales; *Staphylococcus*.
OX NCBI_TaxID=282459;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=15213324; DOI=10.1073/pnas.0402521101;
RA Holden M.T.G., Fell E.J., Lindsay J.A., Peacock S.J., Day N.P.J., Barrington M.C., Foster T.J., Moore C.E., Hurst L., Atkin R., Barton A., Bason N., Bentley S.D., Chillingworth C., Chillingworth T., Churcher C., Clark L., Cotton C., Cronin A., Doggett J., Dowd L., Feltwell T., Hance Z., Harris B., Hauser H., Holtroyd S., Jasele K., James K.D., Lennard N., Line A., Mayes R., Moule S., Mungall K., Omond D., Quail M.A., Rabinowitsch E., Rutherford K.M., Sanders M., Sharp S., Simmonds M., Stevens K., Whitehead S., Barrett B.G., Serrat B.G., Parkhill J.;
RT "Complete genomes of two clinical *Staphylococcus aureus* strains: evidence for the rapid evolution of virulence and drug resistance.";
RT Proc. Natl. Acad. Sci. U.S.A. 101:9786-9791(2004).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by an amide bond (By similarity).
DR EMBL:BX571857; CAG44201.1; -.
DR GO: GO:0009986; C:cell surface; IEA.
DR GO: GO:0005618; C:cell wall; IEA.
DR GO: GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO: GO:0016020; C:membrane; IEA.
DR GO: GO:0007155; P:cell adhesion; IEA.
DR InterPro: IPR008966; Adhes_bact.
DR InterPro: IPR004237; Fn_bind.
DR InterPro: IPR005877; Gpos_YsIRK.
DR InterPro: IPR001899; Gram_pos_anchor.
DR Pfam: PF02986; Fn_bind. 1.
DR Pfam: PF00746; Gram_pos_anchor; 1.
DR TIGRFAMs: TIGR01167; LPXTG_anchor; 1.
DR TIGRFAMs: TIGR01168; YsIRK_signal; 1.
DR PROSITE: PS50847; GRAM_POS_ANCHORING; 1.
KM Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ SEQUENCE 943 AA; 104537 MW; DA8A5F1947E1B6A CRC64;

DR Pfam: PF00746; Gram_pos_anchor; 1.
DR Pfam: PF04650; YsIRK_signal; 1.
DR TIGRFAMs: TIGR01167; LPXTG_anchor; 1.
DR TIGRFAMs: TIGR01168; YsIRK_signal; 1.
DR PROSITE: PS50847; GRAM_POS_ANCHORING; 1.
KM Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ SEQUENCE 957 AA; 105980 MW; 28F8BA7FFDFD3EAF CRC64;

Query Match 76.9%; Score 80; DB 2; Length 957;
Best Local Similarity 78.9%; Pred. No. 0.0031;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GONEGQOTIEPTTPTTP 19
Db 803 GONEGQOTIEPTTPTTP 821

RESULT 11
O8NNU8 PRELIMINARY; PRT; 943 AA.
AC O8NNU8;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE FnbB protein.
GN Name=fnbB; OrderedLocustNames=NM2420;
OS *Staphylococcus aureus* (strain MW2).
OC Bacteria; Firmicutes; Bacillales; *Staphylococcus*.
OX NCBI_TaxID=196620;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22040717; PubMed=12044378; DOI=10.1016/S0140-6736(02)08713-5;
RA Baba T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Oguchi A., Nagai Y., Iwama N., Asano K., Naimi T., Kuroda H., Cui L., Yamamoto K., Hiramatsu K.;
RT "Genome and virulence determinants of high virulence community-acquired MRSA.";
RT Lancet 359:1819-1827(2002).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by an amide bond (By similarity).
DR EMBL:AP004830; BAB96285.1; -.
DR HSSP: Q51653; 1N67.
DR GO: GO:0009986; C:cell surface; IEA.
DR GO: GO:0005618; C:cell wall; IEA.
DR GO: GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO: GO:0016020; C:membrane; IEA.
DR GO: GO:0007155; P:cell adhesion; IEA.
DR InterPro: IPR008966; Adhes_bact.
DR InterPro: IPR004237; Fn_bind.
DR InterPro: IPR005877; Gpos_YsIRK.
DR InterPro: IPR001899; Gram_pos_anchor.
DR Pfam: PF02986; Fn_bind. 1.
DR Pfam: PF00746; Gram_pos_anchor; 1.
DR TIGRFAMs: TIGR01167; LPXTG_anchor; 1.
DR TIGRFAMs: TIGR01168; YsIRK_signal; 1.
DR PROSITE: PS50847; GRAM_POS_ANCHORING; 1.
KM Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ SEQUENCE 943 AA; 104537 MW; DA8A5F1947E1B6A CRC64;

Query Match 67.3%; Score 70; DB 2; Length 943;
Best Local Similarity 73.7%; Pred. No. 0.1;
Matches 14; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 GONEGQOTIEPTTPTTP 19
Db 803 GONEGQOTIEPTTPTTP 821

RESULT 12
CHID_BACCI STANDARD; PRT; 524 AA.
ID CHID_BACCI

Db 420 GCGGQWOTPTTTPP 435

RESULT 15

ID 09V550 PRELIMINARY; PRT; 686 AA.

AC 09V550, 09V550, 13, Created)

DT 01-MAY-2000 (TEMBLrel. 13, last sequence update)

DT 01-MAR-2004 (TEMBLrel. 26, last annotation update)

DE CG8024-BB.

OS Name-Rab-RP1, ORFNames=CG8024;

ON Drosophila melanogaster (fruit fly).

OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

OC Ephydroidea; Drosophilidae; Drosophila.

NCBI_TaxID=7227;

RA [1]

RA MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;

RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,

RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,

RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,

RA Branton R.C., Rogers Y.H., Blazer R.G., Champe M., Pfeiffer B.D.,

RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Gaber G.L.,

RA Abril J.F., Agbayani A., An H.J., Andrews-Pfannkoch C., Baldwin D.,

RA Ballou R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,

RA Beeson K.Y., Berno P.V., Berman B.P., Bhandari D., Bolshakov S.,

RA Borokova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,

RA Burris K.C., Busam D.A., Butler H., Cadiou E., Center A., Chandra I.,

RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,

RA de Pablo B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,

RA Dodson K., Dou P.L., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,

RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriere S., Fleischmann W.,

RA Foster C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,

RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,

RA Hostin D., Houston K.A., Howland T.J., Wei M.H., Ibegwam C.,

RA Jalili M., Kalush F., Karpen G.H., Ke Z., Kenison J.A., Ketchum K.A.,

RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,

RA Laeko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,

RA Liu X., Matei B., McIntosh T.C., McLeod W.P., McPherson D.,

RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,

RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,

RA Nelson D.R., Nelson K.A., Nixon K., Nuskern D.R., Paclet J.M.,

RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,

RA Reinert K., Remington K., Saunders R.D., Scheeler F., Shen H.,

RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,

RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,

RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,

RA Wang Z.Y., Wasserman D.A., Weinstein G.M., Weissbach J.,

RA Williams S.M., Woodrager, Worley K.C., Wu D., Yang S., Yao Q.A., Ye J.,

RA Yeh R.F., Zaveri J.S., Zhao W., Zhang Q., Zhao Q., Zheng L.,

RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu H.O.,

RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.,

RT "The genome sequence of Drosophila melanogaster.";

RT Science 287:2185-2195(2000).

RA [2]

RA MEDLINE=22426065; PubMed=12537573;

RA Celniker S.E., Wheeler D.A., Krommiller B., Carlson J.W., Halpern A.,

RA Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A.,

RA George R.A., Hoskins R.A., Laverly T., Muzny D.M., Nelson C.R.,

RA Paclet J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,

RA Svirskas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,

RA Weinstein G., Scher S.E., Myers E.W., Gibbs R.A., Rubin G.M.,

RT "Finishing a whole-genome shotgun: Release 3 of the Drosophila

RX MEDLINE=22426070; PubMed=12537573;

RA Kaminker J.S., Bergman C.M., Krommiller B., Carlson J., Svirskas R.,

RA Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,

RA Ashburner M., Celniker S.E.,

RT "The transposable elements of the Drosophila melanogaster euchromatin:

RT a genomics perspective.";

RL Genome Biol. 3:RESEARCH0084-RESEARCH0084(2002).

RA [4]

RA MEDLINE=22426069; PubMed=12537572;

RA Mista S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,

RA Hradecky P., Huang Y., Kaminker J.S., Milburn G.H., Prochuk S.E.,

RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,

RA Bettencourt B.R., Celniker S.E., de Grey A.D., Drysdale R.A.,

RA Harris N.L., Richter C., Russo S., Schroeder A.J., Shu S.Q.,

RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,

RA Lewis S.E.,

RT "Annotation of the Drosophila melanogaster euchromatic genome: a

RT systematic review.";

RL Genome Biol. 3:RESEARCH0083-RESEARCH0083(2002).

RA [5]

RA MEDLINE=22426069; PubMed=12537572;

RA Mista S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,

RA Hradecky P., Huang Y., Kaminker J.S., Milburn G.H., Prochuk S.E.,

RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,

RA Bettencourt B.R., Celniker S.E., de Grey A.D., Drysdale R.A.,

RA Harris N.L., Richter C., Russo S., Schroeder A.J., Shu S.Q.,

RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,

RA Lewis S.E.,

RT "Annotation of the Drosophila melanogaster euchromatic genome: a

RT systematic review.";

RL Genome Biol. 3:RESEARCH0083-RESEARCH0083(2002).

RA [6]

RA MEDLINE=22426069; PubMed=12537572;

RA Mista S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,

RA Hradecky P., Huang Y., Kaminker J.S., Milburn G.H., Prochuk S.E.,

RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,

RA Bettencourt B.R., Celniker S.E., de Grey A.D., Drysdale R.A.,

RA Harris N.L., Richter C., Russo S., Schroeder A.J., Shu S.Q.,

RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,

RA Lewis S.E.,

RT "Annotation of the Drosophila melanogaster euchromatic genome: a

RT systematic review.";

RL Genome Biol. 3:RESEARCH0083-RESEARCH0083(2002).

RA [7]

RA MEDLINE=22426069; PubMed=12537572;

RA Mista S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,

RA Hradecky P., Huang Y., Kaminker J.S., Milburn G.H., Prochuk S.E.,

RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,

RA Bettencourt B.R., Celniker S.E., de Grey A.D., Drysdale R.A.,

RA Harris N.L., Richter C., Russo S., Schroeder A.J., Shu S.Q.,

RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,

RA Lewis S.E.,

RT "Annotation of the Drosophila melanogaster euchromatic genome: a

RT systematic review.";

RL Genome Biol. 3:RESEARCH0083-RESEARCH0083(2002).

RA [8]

RA MEDLINE=22426069; PubMed=12537572;

RA Mista S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,

RA Hradecky P., Huang Y., Kaminker J.S., Milburn G.H., Prochuk S.E.,

RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,

RA Bettencourt B.R., Celniker S.E., de Grey A.D., Drysdale R.A.,

RA Harris N.L., Richter C., Russo S., Schroeder A.J., Shu S.Q.,

RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,

Search completed: October 22, 2005, 06:06:16
Job time : 37.818 secs

Query Match 49.0%; Score 51; DB 2; Length 686;
Best Local Similarity 53.3%; Pred. No. 55;
Matches 8; Conservative 4; Mismatches 3; Indels 0; Gaps 0;
QY 2 QNCGQQTTPPTTTPP 16
Db 322 QPQGQGLDSTSP 336

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CC streptococci, e.g. meningitis, otitis media, pneumonia, endocarditis,
 CC mastitis in cattle, abortion in horses and many others. Since the
 CC antibodies block binding of bacteria, they should be effective against
 CC antibiotic-resistant strains, and may replace antibiotic therapy or
 CC increase its effectiveness. Sequences AAW65707-711 represent a series of
 CC synthetic peptides based on the DU region of *S. aureus* fibronectin
 CC binding protein A. They were synthesised to contain mutations
 XX
 SQ Sequence 19 AA:
 Query Match 100.0%; Score 103; DB 2; Length 19;
 Best Local Similarity 100.0%; Pred. No. 9.8e-08;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GONEGQQTIEPTPIVP 19
 DB 1 GONEGQQTIEPTPIVP 19
 RESULT 2
 ID AAW65667 standard; peptide; 19 AA.
 XX
 AC AAW65667;
 XX
 DT 16-OCT-1998 (first entry)
 XX
 DE Fibronectin binding protein-derived peptide #11.
 XX
 KW microbial surface components recognising adhesive matrix molecule;
 KW MSCRAMM; fibronectin; fibronectin-binding protein; antibody; epitope;
 KW antibiotic; bacterial infection; antibiotic-resistant strain.
 XX
 OS Synthetic.
 OS Staphylococcus aureus.
 XX
 PN WO9811389-A2.
 XX
 PD 23-JUL-1998.
 XX
 PF 21-JAN-1998; 98WO-US001222.
 XX
 PR 21-JAN-1997; 97US-0036139P.
 XX
 PA (TEXA) UNIV TEXAS A & M SYSTEM.
 XX
 PI Hoeoek M, Patli JM, House-Pompeo KL, Speciale P, Joh D:
 PI McGavin MJ;
 XX
 DR WPI; 1998-413816/35.
 XX
 PT Antibody that binds to fibronectin-binding protein, preventing its
 PT binding to fibronectin - used to treat or prevent bacteria infection,
 PT especially by Staphylococci and Streptococci.
 XX
 PS Example 2; Page 92; 201pp; English.
 XX
 CC The invention relates to antibodies that bind to a fibronectin-binding
 CC domain of a fibronectin-binding protein, and inhibit binding of the
 CC protein to fibronectin. Also claimed are: (1) isolated peptides of a
 CC fibronectin-binding protein that do not bind to fibronectin; (2) fusion
 CC protein containing at least one peptide of a fibronectin-binding protein
 CC linked to a second amino acid sequence; (3) nucleic acid encoding the
 CC isolated peptide of (1). Antibodies, the isolated peptides of (1) and the
 CC nucleic acids are all useful for immunisation (active or passive) and (by
 CC inhibiting binding of bacteria to fibronectin) for preventing or treating
 CC infection in humans or other animals, particularly by staphylococci or
 CC streptococci, e.g. meningitis, otitis media, pneumonia, endocarditis,
 CC mastitis in cattle, abortion in horses and many others. Since the
 CC antibodies block binding of bacteria, they should be effective against
 CC antibiotic-resistant strains, and may replace antibiotic therapy or
 CC increase its effectiveness. Sequences AAW65659-68 represent synthetic
 CC epitopes from the fibronectin binding domain DU and DI-D4 of the S.

CC aureus fnba gene
 XX
 SQ Sequence 19 AA:
 Query Match 92.2%; Score 95; DB 2; Length 19;
 Best Local Similarity 94.7%; Pred. No. 1.4e-06;
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 GONEGQQTIEPTPIVP 19
 DB 1 GONEGQQTIEPTPIVP 19
 RESULT 3
 ID AAY29087 standard; protein; 134 AA.
 XX
 AC AAY29087;
 XX
 DT 28-SEP-1999 (first entry)
 XX
 DE *S. aureus* fibronectin binding protein A (FnBA) binding domain.
 XX
 KW Bovine herpes virus-2; BHV-2; cytokine; immune response; immunogen; IL;
 KW interleukin; colony stimulating factor; CSF; interferon; IFN; TNF;
 KW tumour necrosis factor; recombinant virus; vaccine; mucosal disease;
 KW mastitis; breast cancer; stress-induced disease; binding domain; FnBA;
 KW fibronectin binding protein.
 XX
 OS Staphylococcus aureus.
 XX
 PN WO9916892-A1.
 XX
 PD 08-APR-1999.
 XX
 PF 29-SEP-1998; 98WO-GB002927.
 XX
 PR 29-SEP-1997; 97GB-00020633.
 XX
 PA (UYBR-) UNIV BRISTOL.
 XX
 PI Bradley AJ, Duffas WP;
 XX
 DR WPI; 1999-255101/21.
 XX
 DR N-PSDB; AAX91504.
 XX
 PT New bovine herpes virus-2 vectors.
 XX
 PS Example 2; Fig 8A-B; 130pp; English.
 XX
 CC The invention provides bovine herpes virus-2 (BHV-2) based vectors that
 CC comprise at least one cytokine-encoding DNA sequence. The expression of
 CC cytokines in mammals can up-regulate immune responses to the immunogens.
 CC The cytokine is selected from interleukins (IL), colony stimulating
 CC factors (CSF), interferons (IFN) and tumour necrosis factors (TNF). The
 CC BHV-2 based vector or recombinant virus can be used as vaccines. They can
 CC be used for preventing or treating a mucosal disease in a subject, e.g.
 CC ruminants, cattle, sheep, goats, dogs, cats, horses, or man, particularly
 CC mastitis in cows or breast cancers in humans. They can also be used for
 CC preventing or treating a stress-induced disease. The present sequence
 CC represents the binding domain of a previously published *S. aureus*
 CC fibronectin binding protein A (FnBA) sequence. The FnB binding domain
 CC gene sequence FNMB, cloned for use in this invention has 97.8 percent
 CC identity when compared to the previously published Fnba and Fnab gene
 CC sequences
 XX
 SQ Sequence 134 AA:
 Query Match 92.2%; Score 95; DB 2; Length 134;
 Best Local Similarity 94.7%; Pred. No. 1.1e-05;
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 GONEGQQTIEPTPIVP 19

Db 116 GONEGQOTIEBTPPIVP 134

RESULT 4
AAP82115 standard; protein; 1018 AA.

XX AAP82115;
XX
XX 25-MAR-2003 (revised)
DT 05-JAN-1990 (first entry)
XX
XX Fibronectin binding protein.
DE
XX Fibronectin binding protein; S. aureus; immunisation; mastitis; ruminants;
KM wound infection; diagnosis.
XX

OS Staphylococcus aureus.

PN EP294349-A.

XX 07-DEC-1986.

XX 30-MAY-1988; 88BP-00850188.

XX 01-JUN-1987; 87SE-00002272.

XX (ALFA) ALFA LIVAL AGRIC INT AB.

PI Lindberg MK, Signas LC, Madstrom TM, Froman G;

XX WPI; 1988-347978/49.

DR P-PSDB; AAP82115.

PT Hybrid DNA encoding Staphylococcus aureus fibronectin binding protein -
PT useful for immunisation and topical application to prevent staphylococcal
PT infections.

XX Disclosure; Fig. 8A:1-8A:2; 23pp; English.

XX The S. aureus fibronectin binding protein may be included in a hybrid
CC protein. The protein may be used to immunise ruminants against
CC staphylococcal mastitis, pref. when given at 0.5-5 microg/kg, using 3
CC doses at 1-3 week intervals; and for topical applicn. to prevent wound
CC infection, pref. using isotonic saline soln. of concn. 25-250 microg/mg.
CC The DNA encoding the binding protein and the hybrid protein may be
CC immobilised on a carrier and used to diagnose staphylococcal infections.
CC (Updated on 25-MAR-2003 to correct PA field.)
XX

SQ Sequence 1018 AA;

Query Match 92.2%; Score 95; DB 1; Length 1018;

Best Local Similarity 94.7%; Pred. No. 0.0001; Mismatches 1; Indels 0; Gaps 0;

QY 1 GONEGQOTIEBTPPIVP 19
Db 860 GONEGQOTIEBTPPIVP 878

RESULT 5

AAU37245 standard; protein; 1018 AA.

XX AAU37245;

XX 14-FEB-2002 (first entry)

DE Staphylococcus aureus cellular proliferation protein #1415.

XX Antisense; prokaryotic cellular proliferation protein; antibiotic;
KM antibacterial; drug design.

XX Staphylococcus aureus.

XX WO200170955-A2.

XX 27-SEP-2001.

XX 21-MAR-2001; 2001WO-US009180.

XX 21-MAR-2000; 2000US-0191078P.

XX 23-MAY-2000; 2000US-0206848P.

XX 26-MAY-2000; 2000US-0207727P.

XX 23-OCT-2000; 2000US-0242578P.

XX 27-NOV-2000; 2000US-0253625P.

XX 22-DEC-2000; 2000US-0257931P.

XX 16-FEB-2001; 2001US-0269308P.

XX (ELIT-) ELITRA PHARM INC.

XX Haselbeck R, Ohlsen KL, Zyskind JW, Wall D, Trawick JD, Carr GJ;

XX Yamamoto RT, Xu HH;

XX WPI; 2001-611495/70.

XX N-PSDB; AAS55104.

XX New polynucleotides for the identification and development of

XX antibiotics, comprise sequences of antisense nucleic acids.

XX Example 3; SEQ ID NO 12838; 511pp; English.

XX The invention relates to antisense inhibitors of genes essential to
CC prokaryotic cellular proliferation, their use in identifying the genes,
CC their use in the discovery of novel antibiotics, the essential genes
CC themselves and the encoded proteins. The prokaryotes used are Escherichia
CC coli, Staphylococcus aureus, Salmonella typhi, Klebsiella pneumoniae,
CC Pseudomonas aeruginosa and Enterococcus faecalis. The invention is also
CC useful for the identification of potential new targets for antibiotic
CC development. The antisense nucleic acids can also be used to identify
CC proteins used in proliferation, to express these proteins. The proteins can
CC antibodies capable of binding to the expressed proteins. The proteins can
CC be used to screen compounds in rational drug discovery programmes. The
CC antisense nucleic acid sequence is also useful to screen for homologous
CC nucleic acids which are required for cell proliferation in a wide variety
CC of organisms. The present sequence represents an essential prokaryotic
CC cellular proliferation protein. Note: The sequence data for this patent
CC did not form part of the printed specification, but was obtained in
CC electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX

SQ Sequence 1018 AA;

Query Match 92.2%; Score 95; DB 4; Length 1018;

Best Local Similarity 94.7%; Pred. No. 0.0001; Mismatches 1; Indels 0; Gaps 0;

QY 1 GONEGQOTIEBTPPIVP 19
Db 860 GONEGQOTIEBTPPIVP 878

RESULT 6

AAU34301 standard; protein; 1018 AA.

XX AAU34301;

XX 14-FEB-2002 (first entry)

DE Staphylococcus aureus cellular proliferation protein #577.

XX Antisense; prokaryotic cellular proliferation protein; antibiotic;
KM antibacterial; drug design.

```

OS Staphylococcus aureus.
XX WO200170955-A2.
XX PD
XX 27-SEP-2001.
XX 21-MAR-2001; 2001WO-US009180.
XX 21-MAR-2000; 2000US-0191078P.
PR 23-MAY-2000; 2000US-0206848P.
PR 26-MAY-2000; 2000US-0207727P.
PR 23-OCT-2000; 2000US-0242578P.
PR 27-NOV-2000; 2000US-0253625P.
PR 22-DEC-2000; 2000US-0257931P.
PR 16-FEB-2001; 2001US-0269308P.
XX (ELIT-) ELITRA PHARM INC.
XX PA
XX Haselbeck R, Ohlsen KL, Zyckind JW, Wall D, Trawick JD, Carr GJ;
PI Yamamoto RT, Xu HH;
XX MPI; 2001-611495/70.
DR N-PSTDB; AAS52160.
XX
PT New polynucleotides for the identification and development of
PT antibiotics, comprise sequences of antisense nucleic acids.
XX
PS Example 3; SEQ ID NO 5797; 51pp; English.
XX
CC The invention relates to antisense inhibitors of genes essential to
CC prokaryotic cellular proliferation, their use in identifying the genes,
CC their use in the discovery of novel antibiotics, the essential genes,
CC themselves and the encoded proteins. The prokaryotes used are Escherichia
CC coli, Staphylococcus aureus, Salmonella typhi, Klebsiella pneumoniae,
CC Pseudomonas aeruginosa and Enterococcus faecalis. The invention is also
CC useful for the identification of potential new targets for antibiotic
CC development. The antisense nucleic acids can also be used to identify
CC proteins used in proliferation, to express these proteins, and to obtain
CC antibodies capable of binding to the expressed proteins. The proteins can
CC be used to screen compounds in rational drug discovery programmes. The
CC antisense nucleic acid sequence is also useful to screen for homologous
CC nucleic acids which are required for cell proliferation in a wide variety
CC of organisms. The present sequence represents an essential prokaryotic
CC cellular proliferation protein. Note: The sequence data to this patent
CC did not form part of the printed specification, but was obtained in
CC electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 1018 AA:
Query Match 92.2%; Score 95; DB 4; Length 1018
Best Local Similarity 94.7%; Pred. No. 0.0001;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0.
QY 1 GONEGQQTIEPTTPVIP 19
DB 860 GONEGQQTIEDTTPVIP 878
RESULT 7
ABJ18922
ID ABJ18922 standard; protein, 1018 AA.
XX
XX ABJ18922;
AC
AC 06-MAR-2003 (first entry)
DE Pathogen specific antigen related staphylococcal protein Stp ID No 68.
XX
XX Antibacterial; virucide; fungicide; protozoacide; cytostatic; anti-HIV;
KM hyperimmune; serum-reactive; antigen; pathogen; tumour; allergen;
KM auto-immunity; vaccine; staphylococcal infection; antibody; cancer;
KM autoimmune disease; HIV; hepatitis.

```

```

OS   Staphylococcus sp.
XX
XX   WO200259148-A2.
XX
XX   01-AUG-2002.
XX
XX   21-JAN-2002; 2002WO-EP000546.
XX
XX   26-JAN-2001; 2001AT-00000130.
XX
XX   (CIST-) CISTEM BIOTECHNOLOGIES GMBH.
XX
XX   Meinke A, Nagy E, Von Ahnen U, Klade C, Henics T, Zanner W;
PI   Minh DB, Vyrvytska O, Ecz H, Dryla A, Weichart T, Hafner M;
PI   Tempelmaier B;
XX
XX   WPI; 2003-075410/07.
XX
XX   Identifying, isolating and producing hyperimmune serum-reactive antigens
PT   from a pathogen, for preparing vaccine or medicament for treating or
PT   preventing e.g. staphylococcal infections, comprises providing antibody
PT   preparation.
XX
XX   Example 7; Page 157; 252pp; English.
XX
XX   The invention relates to a novel method for identifying, isolating and
CC   producing hyperimmune serum-reactive antigens from a pathogen, tumour,
CC   allergen, a tissue or host prone to auto-immunity, where the antigens are
CC   used in a vaccine, comprises providing antibody preparation from a plasma
CC   pool of a type of animal, or individual sera with antibodies against the
CC   specific pathogen, tumour, allergen, tissue or host prone to auto-
CC   immunity. The hyperimmune serum-reactive antigens comprising any of the
CC   62 sequences of 53-2261 amino acids fully defined in the specification,
CC   or their hyperimmune fragments are useful for the manufacture of a
CC   pharmaceutical preparation, particularly a vaccine against staphylococcal
CC   infections or colonisation against S. aureus or S. epidermidis. The
CC   preparation of antibodies is useful for the manufacture of a medicament
CC   for treating or preventing staphylococcal infections or colonisation
CC   against S. aureus or S. epidermidis. The antibody preparations may also
CC   be used for diagnostic and imaging purposes. Other conditions that can be
CC   treated include cancer, autoimmune diseases or infections caused by viral
CC   (e.g. HIV, hepatitis A, B or C), fungal or protozoan pathogens. This
CC   sequence represents a staphylococcal protein relating to the method for
CC   identifying and producing pathogen specific antigens of the invention
XX
XX   SQ   Sequence 1018 AA:
XX
XX   Query Match          92.2%; Score 95; DB 6; Length 1018;
XX   Best Local Similarity 94.7%; Pred. No. 0.0001;
XX   Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX   QY   1 GONEGQQTIEEPTPIVP 19
XX       ||||| ||||| |||||
XX   DB   860 GONEGQTIEDTTPPIVP 878
XX
XX   RESULT 8
XX   ABM72537
XX   ID   ABM72537 standard; protein; 1018 AA.
XX
XX   AC   ABM72537;
XX
XX   DT   20-NOV-2003 (first entry)
XX
XX   DE   Staphylococcus aureus protein #1777.
XX
XX   KW   Antibacterial; vaccine; gene therapy; infection; sepsis; diagnosis;
XX   enzymatic assay; antibiotic target.
XX
XX   OS   Staphylococcus aureus.
XX
XX   PN   WO200294868-A2.

```

XX 28-NOV-2002.
 PD 27-MAR-2002; 2002MO-IB002637.
 XX PF 27-MAR-2001; 2001GB-00007661.
 XX PR (CHIR-) CHIRON SPA.
 XX PA Masignani V, Mora M, Scarselli M;
 XX PI Masignani V, Mora M, Scarselli M;
 XX DR WPI: 2003-120786/11.
 XX DR N-PSDB; ACF74097.
 XX PT New Staphylococcus aureus protein, useful as a vaccine for treating or
 PT preventing Staphylococcal infection, specifically an infection caused by
 PT S. aureus, e.g. sepsis.
 PS Claim 1; SEQ ID NO 3554; 49pp; English.
 XX The invention relates to novel genes and encoded proteins from
 CC Staphylococcus aureus. A composition comprising the S. aureus protein, a
 CC nucleic acid encoding the protein, or an antibody to the protein, is
 CC useful as a pharmaceutical, particularly as a vaccine for treating or
 CC preventing infection due to Staphylococcus bacteria, specifically an
 CC infection caused by S. aureus. The composition is particularly useful for
 CC treating or preventing sepsis in a patient. The composition can also be
 CC used for diagnostics. The protein is also used in an assay for enzymatic
 CC studies and as a target for antibiotics. This sequence represents one of
 CC the novel S. aureus proteins of the invention
 XX SQ Sequence 1018 AA;
 SQ Query Match 92.2%; Score 95; DB 6; Length 1018;
 Best Local Similarity 94.7%; Pred. No. 0.0001;
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 GONEGQOTIEPTPIVP 19
 DB 860 GONEGQOTIEPTPIVP 878
 RESULT 9
 AAW89806
 ID AAW89806 standard; protein; 1027 AA.
 XX AAW89806;
 AC 16-MAR-1999 (first entry)
 DT Staphylococcus aureus protein SEQ ID #5254.
 DE Staphylococcus aureus protein SEQ ID #5254.
 XX Computer readable medium; vaccine; S.aureus infection; immunodetection;
 KM cellulitis; eyelid infection; food poisoning; osteomyelitis; therapy;
 KM skin infection; surgical wound infection; scalded skin syndrome;
 KM toxic shock syndrome.
 XX Staphylococcus aureus.
 OS EP786519-A2.
 XX EP786519-A2.
 PN 30-JUL-1997.
 PD 07-JAN-1997; 97EP-00100117.
 PF 05-JAN-1996; 96US-0009861P.
 PR (HUMA-) HUMAN GENOME SCI INC.
 XX Kunsch CA, Choi GH, Barash SC, Dillon PJ, Fannon MR, Rosen CA;
 XX WPI: 1997-374922/35.
 XX

PT Polynucleotide(s) and proteins derived from Staphylococcus aureus -
 PT stored on computer readable medium and used in the production of anti-
 PT S. aureus vaccines.
 XX Claim 23; Page 3263-3267; 3271pp; English.
 XX This sequence represents a Staphylococcus aureus protein sequence of the
 CC invention. The DNA sequences encoding the S. aureus proteins are recorded
 CC on a computer readable medium, preferably selected from a floppy or hard
 CC disk, random access memory (RAM), read-only memory (ROM) or CD-ROM.
 CC Homology searches using the S. aureus DNA sequences allows putative
 CC functions to be assigned so that protein-encoding or regulatory regions
 CC of commercial, therapeutic or industrial importance can be obtained.
 CC Specifically, sequences which are likely to encode antigens have been
 CC identified and these polypeptides can be used in a vaccine composition
 CC against S. aureus infection. The polypeptides can also be used in a kit
 CC for the immunodetection of S. aureus in a sample. S. aureus is implicated
 CC in numerous human diseases, including cellulitis, eyelid infections, food
 CC poisoning, osteomyelitis, skin and surgical wound infections, scalded
 CC skin syndrome, toxic shock syndrome, etc. Organisms transformed with the
 CC DNA sequences can be used for recombinant production of the polypeptides.
 CC The new DNA sequences (and their fragments) are useful as primers or
 CC probes for isolating homologues of any of the 5191 S. aureus DNA sequences
 CC contained on the computer readable medium
 XX SQ Sequence 1027 AA;
 SQ Query Match 92.2%; Score 95; DB 2; Length 1027;
 Best Local Similarity 94.7%; Pred. No. 0.0001;
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 GONEGQOTIEPTPIVP 19
 DB 869 GONEGQOTIEPTPIVP 887
 RESULT 10
 AAY29089
 ID AAY29089 standard; protein; 134 AA.
 XX AAY29089;
 AC 28-SEP-1999 (first entry)
 DT Cloned fibronectin binding protein binding domain (FnBAB) sequence.
 DE Bovine herpes virus-2; BHV-2; cytokine; immune response; immunogen; IL;
 XX interleukin; colony stimulating factor; CSF; interferon; IFN; TNF;
 KM tumour necrosis factor; recombinant virus; vaccine; mucosal disease;
 KM mastitis; breast cancer; stress-induced disease; binding domain; FnBAB;
 KM fibronectin binding protein.
 XX Staphylococcus aureus.
 OS W09916892-A1.
 XX W09916892-A1.
 PN 08-APR-1999.
 PD 29-SEP-1998; 98WO-GB002927.
 PF 29-SEP-1997; 97GB-00020633.
 PR (UYBR-) UNIV BRISTOL.
 XX Bradley AJ, Duffas WP;
 XX WPI: 1999-255101/21.
 XX N-PSDB; AAX91506.
 XX New bovine herpes virus-2 vectors.
 XX Example 2; Fig 8A-B, 130pp; English.
 XX

CC The invention provides bovine herpes virus-2 (BHV-2) based vectors that
CC comprise at least one cytokine-encoding DNA sequence. The expression of
CC cytokines in mammals can up-regulate immune responses to the immunogens.
CC The cytokine is selected from interleukins (IL), colony stimulating
CC factors (CSF), interferons (IFN) and tumor necrosis factors (TNF). The
CC BHV-2 based vector or recombinant virus can be used as vaccines. They can
CC be used for preventing or treating a mucosal disease in a subject, e.g.
CC ruminants, cattle, sheep, goats, dogs, cats, horses, or man, particularly
CC mastitis in cows or breast cancers in humans. They can also be used for
CC preventing or treating a stress-induced disease. The present sequence
CC represents a S. aureus fibronectin binding protein binding domain
CC sequence FNAB, the gene cloned for use in this invention. The gene has
CC 97.8 percent identity when compared to the previously published sequences
CC FNBA and FNBB
CC
SQ Sequence 134 AA;

Query Match 87.4%; Score 90; DB 2; Length 134;
Best Local Similarity 89.5%; Pred. No. 5.9e-05;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GONEGQQTIEPTPIVP 19
| | | | | | | | | | | | | | | | | | | | | |
DB 116 GHNEGQQTIEBTPPIVP 134

RESULT 11
AAV29088
ID AAV29088 standard; protein; 134 AA.

AC AAV29088;

DT 28-SEP-1999 (first entry)

DE S. aureus fibronectin binding protein B (FnBB) binding domain.

XX Bovine herpes virus-2; BHV-2; cytokine; immune response; immunogen; IL;
XX Interleukin; colony stimulating factor; CSF; interferon; IFN; TNF;
XX tumour necrosis factor; recombinant virus; vaccine; mucosal disease;
XX mastitis; breast cancer; stress-induced disease; binding domain; FNBB;
XX fibronectin binding protein.
XX

OS Staphylococcus aureus.

PN WO9116892-A1.

PD 08-APR-1999.

PF 29-SEP-1998; 98WO-GB002927.

PR 29-SEP-1997; 97GB-00020633.

PA (UYBR-) UNITV BRISTOL.

PI Bradley AJ, Duffas WPJ;

XX WPI; 1999-255101/21.

DR N-PSDB; AAX91505.

XX New bovine herpes virus-2 vectors.

PT Example 2; Fig 8A-B; 130pp; English.

XX The invention provides bovine herpes virus-2 (BHV-2) based vectors that
XX comprise at least one cytokine-encoding DNA sequence. The expression of
XX cytokines in mammals can up-regulate immune responses to the immunogens.
XX The cytokine is selected from interleukins (IL), colony stimulating
XX factors (CSF), interferons (IFN) and tumour necrosis factors (TNF). The
XX BHV-2 based vector or recombinant virus can be used as vaccines. They can
XX be used for preventing or treating a mucosal disease in a subject, e.g.
XX ruminants, cattle, sheep, goats, dogs, cats, horses, or man, particularly
XX mastitis in cows or breast cancers in humans. They can also be used for
XX preventing or treating a stress-induced disease. The present sequence

CC represents the binding domain of a previously published S. aureus
CC fibronectin binding protein B (FnBB) sequence. The FnB binding domain
CC gene sequence FNAB, cloned for use in this invention has 97.8 percent
CC identity when compared to the previously published FNBA and FNBB gene
CC sequences
CC
SQ Sequence 134 AA;

Query Match 87.4%; Score 90; DB 2; Length 134;
Best Local Similarity 89.5%; Pred. No. 5.9e-05;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GONEGQQTIEPTPIVP 19
| | | | | | | | | | | | | | | | | | | | | |
DB 116 GHNEGQQTIEBTPPIVP 134

RESULT 12
AAW89803
ID AAW89803 standard; protein; 559 AA.

AC AAW89803;

DT 16-MAR-1999 (first entry)

DE Staphylococcus aureus protein SEQ ID #5251.

XX Computer readable medium; vaccine; S. aureus infection; immunodetection;
XX cellulitis; eyelid infection; food poisoning; osteomyelitis; therapy;
XX skin infection; surgical wound infection; scalded skin syndrome;
XX toxic shock syndrome.
XX

OS Staphylococcus aureus.

PN EP786519-A2.

PD 30-JUL-1997.

PF 07-JAN-1997; 97EP-00100117.

PR 05-JAN-1996; 96US-0009861P.

PA (HUMA-) HUMAN GENOME SCI INC.

PI Kunesh CA, Choi GH, Barash SC, Dillon RJ, Fannon MR, Rosen CA;

XX WPI; 1997-374922/35.

PT Polynucleotide(s) and proteins derived from Staphylococcus aureus -
PT stored on computer readable medium and used in the production of anti-
PT S. aureus vaccines.
PT

XX Claim 23; Page 3259-3261; 3271pp; English.

XX This sequence represents a Staphylococcus aureus protein sequence of the
XX invention. The DNA sequences encoding the S. aureus proteins are recorded
XX on a computer readable medium, preferably selected from a floppy or hard
XX disk, random access memory (RAM), read-only memory (ROM) or CD-ROM.
XX Homology searches using the S. aureus DNA sequences allows putative
XX functions to be assigned so that protein-encoding or regulatory regions
XX of commercial, therapeutic or industrial importance can be obtained.
XX Specifically, sequences which are likely to encode antigens have been
XX identified and these polypeptides can be used in a vaccine composition
XX against S. aureus infection. The polypeptides can also be used in a kit
XX for the immunodetection of S. aureus in a sample. S. aureus is implicated
XX in numerous human diseases, including cellulitis, eyelid infections, food
XX poisoning, osteomyelitis, skin and surgical wound infections, scalded
XX skin syndrome, toxic shock syndrome, etc. Organisms transformed with the
XX DNA sequences can be used for recombinant production of the polypeptides.
XX The new DNA sequences (and their fragments) are useful as primers or
XX probes for isolating homologues of any of the 5191 S. aureus DNA sequences
XX contained on the computer readable medium

RESULT 15
 ADA89470
 ID ADA89470 standard, protein, 948 AA.
 AC
 ADA89470;
 XX
 DT 20-NOV-2003 (first entry)
 XX
 DE Staphylococcus aureus antigenic protein #9.
 XX
 KM antigenic protein; vaccine; Staphylococcus aureus; pathogenic organism;
 KM antibacterial; neuroprotective; immunosuppressive; antiinflammatory;
 KM antifungal; immunostimulant; ophthalmological; pathogenic microbe;
 KM bacteremia; septic shock; organ infection; skin infection;
 KM bacterial basal colonisation; bacterial eye infection; septicaemia;
 KM tuberculosis; food poisoning; blood infection; peritonitis; endocarditis;
 KM sepsis; meningitis; pneumonia; stomach ulcer; gonorrhoea; toxic shock;
 KM necrotising fasciitis; impetigo; histoplasmosis; Lyme disease;
 KM gastro-enteritis; dysentery; shigellosis; skin disorder.
 XX
 OS Staphylococcus aureus.
 XX
 PN WO2003011899-A2.
 XX
 PD 13-FEB-2003.
 XX
 PF 02-AUG-2002; 2002WO-GB003606.
 XX
 PR 02-AUG-2001; 2001GB-00018825.
 PR 09-JAN-2002; 2002GB-0000349.
 XX
 PA (UVSH-) UNIV SHEFFIELD.
 PA (BIOS-) BIOSYNEXUS INC.
 XX
 PI Foster S, Mond J, Clarke S, McDowell P, Brummett K;
 XX
 DR WPI: 2003-256434/25.
 XX
 PT New antigenic polypeptides from Staphylococcus aureus or S. epidermidis,
 PT useful as a vaccine for immunizing humans against e.g. bacteraemia, septic
 PT shock, septicemia, tuberculosis, meningitis, pneumonia, gonorrhea or
 PT impetigo.
 XX
 PS Claim 4; Page 124-125; 189pp; English.
 CC
 CC The present invention describes an antigenic protein or its part, which
 CC is for use as a vaccine. The antigenic protein is encoded by an isolated
 CC DNA molecule of Staphylococcus aureus or S. epidermidis partial gene
 CC sequences (designated dnaSA and dna SE, respectively; and which encodes a
 CC protein expressed by a pathogenic organism. Also described: (1) a vaccine
 CC composition comprising at least one antigenic protein; (2) a method of
 CC immunising an animal against a disease or condition caused by a
 CC pathogenic microbe by administering the antigenic protein or the vaccine;
 CC (3) an antibody or its binding part obtainable by the method above; (4)
 CC preparing a hybridoma cell line producing monoclonal antibodies; (5) a
 CC hybridoma cell line produced by the method of (4); and (6) identifying
 CC opsonic antigens expressed by a pathogenic microbe. The antigenic
 CC proteins have antibacterial, neuroprotective, immunosuppressive,
 CC antiinflammatory, antifungal, immunostimulant and ophthalmological
 CC activities, and can be used in vaccines. The antigenic proteins or
 CC vaccines can be used for immunising an animal (specifically a human)
 CC against a disease or condition caused by a pathogenic microbe, e.g.
 CC bacteraemia, septic shock, organ infection, skin infection, bacterial
 CC basal colonisation, bacterial eye infections, septicaemia, tuberculosis,
 CC bacteria-associated food poisoning, blood infections, peritonitis,
 CC endocarditis, sepsis, meningitis, pneumonia, stomach ulcer, gonorrhoea,
 CC strep throat, streptococcal-associated toxic shock, necrotising
 CC fasciitis, impetigo, histoplasmosis, Lyme disease, gastro-enteritis,
 CC dysentery, shigellosis, S. aureus-associated septicaemia, food-poisoning,
 CC skin disorders, S. epidermidis-associated septicaemia, peritonitis or
 CC endocarditis. The present sequence represents a S. aureus antigenic
 CC protein sequence from the present invention.

SQ Sequence 948 AA;
 Query Match 87.4%; Score 90; DB 6; Length 948;
 Best Local Similarity 89.5%; Pred. No. 0.0005;
 Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 GNEGQQTIEPTTPPIVP 19
 | ||||| |||||
 DP 804 GNEGQQTIEPTTPPIVP 822

Search completed: October 25, 2005, 20:21:08
 Job time : 42.9663 secs

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OM protein - protein search, using SW model

Run on: October 22, 2005, 03:51:22 ; Search time 10.5862 Seconds
(without alignments)
133.980 Million cell updates/sec

Title: US-10-731-238-52

Sequence: 1 GONEGQQTIEEPTPIVP 19

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA: *
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2: /cgn2_6/ptodata/1/iaa/5B COMB.pep: *
3: /cgn2_6/ptodata/1/iaa/6A COMB.pep: *
4: /cgn2_6/ptodata/1/iaa/6B COMB.pep: *
5: /cgn2_6/ptodata/1/iaa/PCTUS COMB.pep: *
6: /cgn2_6/ptodata/1/iaa/backfile1.pep: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	103	100.0	19	4	US-09-010-317-52
2	95	92.2	19	4	US-09-010-317-11
3	95	92.2	178	2	US-08-459-135A-12
4	95	92.2	178	3	US-08-495-559-12
5	95	92.2	1027	4	US-08-956-171E-5254
6	95	92.2	1027	4	US-08-781-986A-5254
7	90	87.4	174	2	US-08-459-135A-13
8	90	87.4	174	3	US-08-495-559-13
9	90	87.4	559	4	US-08-956-171E-5251
10	89	86.4	19	4	US-09-010-317-12
11	89	86.4	19	4	US-09-010-317-51
12	89	86.4	19	4	US-09-010-317-53
13	88	85.4	19	4	US-08-459-135A-10
14	88	85.4	174	3	US-08-495-559-10
15	79	76.7	174	3	US-08-495-559-6
16	79	76.7	174	3	US-08-459-135A-8
17	79	76.7	181	2	US-08-459-135A-6
18	68	66.0	130	3	US-08-495-559-8
19	68	66.0	130	3	US-08-459-135A-7
20	61	59.2	130	3	US-08-495-559-7
21	61	59.2	130	3	US-10-142-231-92
22	55	45.6	150	4	US-09-270-767-48050
23	47	45.6	150	4	US-09-270-767-48050
24	47	45.6	212	4	US-10-380-105-6
25	47	45.6	212	4	US-09-010-317-48
26	46	44.7	38	4	US-09-543-681A-4756
27	46	44.7	206	4	US-09-543-681A-4756

28	46	44.7	365	4	US-09-270-767-42927	Sequence 42927, A
29	45	43.7	38	4	US-09-010-317-38	Sequence 38, Appl
30	45	43.7	466	2	US-08-836-791-9	Sequence 318, Appl
31	45	43.7	466	4	US-09-919-039-318	Sequence 2, Appl
32	45	43.7	899	1	US-08-365-689-2	Sequence 2, Appl
33	45	43.7	899	1	US-08-145-138A-2	Sequence 2, Appl
34	45	43.7	933	1	US-07-747-781-2	Sequence 2, Appl
35	45	43.7	933	5	PCT-US92-06888-2	Sequence 204, App
36	45	43.7	943	3	US-09-056-556-204	Sequence 199, App
37	45	43.7	943	4	US-09-072-596-199	Sequence 131, App
38	45	43.7	943	4	US-09-477-135A-131	Sequence 204, App
39	45	43.7	943	4	US-09-072-967-204	Sequence 4, Appl
40	44	42.7	38	1	US-08-729-767-4	Sequence 17, Appl
41	44	42.7	73	3	US-08-963-851-17	Sequence 3, Appl
42	44	42.7	114	1	US-08-259-000-3	Sequence 8, Appl
43	44	42.7	139	3	US-08-856-253-8	Sequence 8705, Ap
44	44	42.7	410	4	US-09-949-016-8705	Sequence 32, Appl
45	44	42.7	411	4	US-09-886-319A-32	

ALIGNMENTS

RESULT 1
US-09-010-317-52
Sequence 52, Application US/09010317
Patent No. 6685943
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
APPLICANT: Patti, Joseph M.
APPLICANT: House-Pompeo, Karen L.
APPLICANT: Speziale, Pietro
APPLICANT: Job, Danny
APPLICANT: Mcgavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
TITLE OF INVENTION: AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAMK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 52:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-09-010-317-52
Query Match 100.0%; Score 103; DB 4; Length 19;
Best Local Similarity 100.0%; Pred. No. 5.2e-06;

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Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GONEGQOTIEPTPIVP 19
| | | | | | | | | | | | | | | | | | | | |
Db 1 GONEGQOTIEPTPIVP 19

RESULT 2
US-09-010-317-11
; Sequence 11, Application US/09010317
; Patent No. 6685943
; GENERAL INFORMATION:
; APPLICANT: Hook, Magnus
; APPLICANT: Patti, Joseph M.
; APPLICANT: House-Pompeo, Karen L.
; APPLICANT: Speciale, Pietro
; APPLICANT: Joh, Danny
; APPLICANT: McGavin, Martin J.
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
; NUMBER OF SEQUENCES: 105
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Arnold, White & Durkee
; CITY: Houston
; STATE: TX
; COUNTRY: USA
; ZIP: 77210-4433
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/010,317
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/036,139
; FILING DATE: 21-JAN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Hibley, David W.
; REGISTRATION NUMBER: 41,071
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 512-418-3000
; TELEFAX: 512-474-7577
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 19 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
US-09-010-317-11

Query Match 92.2%; Score 95; DB 4; Length 19;
Best Local Similarity 94.7%; Pred. No. 6,7e-07;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 GONEGQOTIEPTPIVP 19
| | | | | | | | | | | | | | | | | | | | |
Db 1 GONEGQOTIEPTPIVP 19

RESULT 3
US-08-459-135A-12
; Sequence 12, Application US/08459135A
; Patent No. 5955078
; GENERAL INFORMATION:
; APPLICANT: BURHAM, Martin Karl Russel
; APPLICANT: CHOPRA, Ian
; APPLICANT: CRITCHLEY, Ian Alfred
; APPLICANT: KNOWLES, David Justin Charles

; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN: MONOCLONAL ANTIBODY AND THEIR USE
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corporation
; STREET: 709 Swedeland Road
; CITY: King of Prussia
; STATE: PA
; COUNTRY: U.S.A.
; ZIP: 19406-0939
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: DOS
; SOFTWARE: Fastseq, Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/459,135A
; FILING DATE: 02-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB/94/00215
; FILING DATE: 04-Feb-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Gimmil, Edward R
; REGISTRATION NUMBER: 38,891
; REFERENCE/DOCKET NUMBER: P30591C2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-270-4478
; TELEFAX: 610-270-5090
; TELEX:
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 178 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Protein
US-08-459-135A-12

Query Match 92.2%; Score 95; DB 2; Length 178;
Best Local Similarity 94.7%; Pred. No. 7e-06;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 GONEGQOTIEPTPIVP 19
| | | | | | | | | | | | | | | | | | | | |
Db 116 GONEGQOTIEPTPIVP 134

RESULT 4
US-08-495-559-12
; Sequence 12, Application US/08495559A
; Patent No. 6054572
; GENERAL INFORMATION:
; APPLICANT: BURHAM, Martin Karl Russel
; APPLICANT: CHOPRA, Ian
; APPLICANT: CRITCHLEY, Ian Alfred
; APPLICANT: KNOWLES, David Justin Charles
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN: MONOCLONAL ANTIBODY AND THEIR USE IN PREVENTING BACTERIAL ADHESION
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corporation
; STREET: 709 Swedeland Road
; CITY: King of Prussia
; STATE: PA
; COUNTRY: U.S.A.
; ZIP: 19406-0939
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: DOS
; SOFTWARE: Fastseq, Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/495,559A
; FILING DATE: 1995-08-03
; EARLIER FILING DATE: 1993-02-05
; EARLIER APPLICATION NUMBER: GB 9302289.5
; EARLIER FILING DATE: 1993-02-05
; EARLIER APPLICATION NUMBER: GB 9321592.9
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 12
; LENGTH: 178
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-08-495-559-12
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APPLICATION NUMBER: US/08/459,135A
FILING DATE: 02-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB/94/00215
FILING DATE: 04-Feb-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Gimmil, Edward R.
REGISTRATION NUMBER: 38,891
REFERENCE/DOCKET NUMBER: P30591C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-4478
TELEFAX: 610-270-5090
TELEX:
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 174 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-459-135A-13

Query Match 87.4%; Score 90; DB 2; Length 174;
Best Local Similarity 89.5%; Pred. No. 3.4e-05;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GONEGOOTIEPTTPIVP 19
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Db 116 GHNCGOQTIEEDTTPPIVP 134

RESULT 8
US-08-495-559-13
Sequence 13, Application US/08495559A
Patent No. 6054572
GENERAL INFORMATION:
APPLICANT: BURNAM, Martin Karl Russel
APPLICANT: CHOPRA, Ian
APPLICANT: CRITCHLEY, Ian Alfred
APPLICANT: KNOWLES, David Justin Charles
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN: MONOCLONAL
TITLE OF INVENTION: ANTIBODY AND THEIR USE IN PREVENTING BACTERIAL ADHESION
FILE REFERENCE: P30591
CURRENT APPLICATION NUMBER: US/08/495,559A
CURRENT FILING DATE: 1995-08-03
EARLIER APPLICATION NUMBER: GB 9302289.5
EARLIER FILING DATE: 1993-02-05
EARLIER APPLICATION NUMBER: GB 9321592.9
NUMBER OF SEQ ID NOS: 13
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 13
LENGTH: 174
TYPE: PRT
ORGANISM: Staphylococcus aureus
US-08-495-559-13

Query Match 87.4%; Score 90; DB 3; Length 174;
Best Local Similarity 89.5%; Pred. No. 3.4e-05;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GONEGOOTIEPTTPIVP 19
| | | | | | | | | | | | | | | | | | | | | |
Db 116 GHNCGOQTIEEDTTPPIVP 134

RESULT 9
US-08-956-171E-5251
Sequence 5251, Application US/08956171E
Patent No. 6593114
GENERAL INFORMATION:

APPLICANT: Charles Kunsch
Gil H. Choi
Patrick S. Dillon
Craig A. Rosen
Steven C. Barash
Michael R. Fannon
TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
NUMBER OF SEQUENCES: 5256
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COUNTRY: USA
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4MB storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/956,171E
FILING DATE: 20-Oct-1997
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/009,861
FILING DATE: January 5, 1996
APPLICATION NUMBER: 08/781,986
FILING DATE: January 3, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Mark J. Hyman
REGISTRATION NUMBER: 46,789
REFERENCE/DOCKET NUMBER: PB248P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (240) 314-1224
TELEFAX: (301) 309-8439
INFORMATION FOR SEQ ID NO: 5251:
SEQUENCE CHARACTERISTICS:
LENGTH: 559 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 5251:
US-08-956-171E-5251

Query Match 87.4%; Score 90; DB 4; Length 559;
Best Local Similarity 89.5%; Pred. No. 0.00011;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GONEGOOTIEPTTPIVP 19
| | | | | | | | | | | | | | | | | | | | | |
Db 415 GHNCGOQTIEEDTTPPIVP 433

RESULT 10
US-08-781-986A-5251
Sequence 5251, Application US/08781986A
Patent No. 6737248
GENERAL INFORMATION:
APPLICANT: Charles Kunsch
TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
NUMBER OF SEQUENCES: 5255
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COUNTRY: USA
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4MB storage
COMPUTER: HP Vectra 486/33

OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/781,986A
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Benson, Bob
REGISTRATION NUMBER: 30,446
REFERENCE/DOCKET NUMBER: PB248PP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 5251:
SEQUENCE CHARACTERISTICS:
LENGTH: 559 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-781-986A-5251

Query Match 87.4%; Score 90; DB 4; Length 559;
Best Local Similarity 89.5%; Pred. No. 0.00011;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GONEGQOTIEPTPIVP 19
Db 415 GNEGQOTIEPTPIVP 433

RESULT 11
US-09-010-317-12
Sequence 12, Application US/09010317
Patent No. 6685943
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
APPLICANT: Patti, Joseph M.
APPLICANT: House-Pompeo, Karen L.
APPLICANT: Speziale, Pietro
APPLICANT: Job, Danny
APPLICANT: McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
TITLE OF INVENTION: AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAMK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000

TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-09-010-317-12

Query Match 86.4%; Score 89; DB 4; Length 19;
Best Local Similarity 89.5%; Pred. No. 4.5e-06;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GONEGQOTIEPTPIVP 19
Db 1 GONEGQOTIEPTPIVP 19

RESULT 12
US-09-010-317-51
Sequence 51, Application US/09010317
Patent No. 6685943
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
APPLICANT: Patti, Joseph M.
APPLICANT: House-Pompeo, Karen L.
APPLICANT: Speziale, Pietro
APPLICANT: Job, Danny
APPLICANT: McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
TITLE OF INVENTION: AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAMK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 51:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-09-010-317-51

Query Match 86.4%; Score 89; DB 4; Length 19;
Best Local Similarity 89.5%; Pred. No. 4.5e-06;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GONEGQOTIEPTPIVP 19
Db 1 GONEGQOTIEPTPIVP 19

RESULT 13
US-09-010-317-53
Sequence 53, Application US/09010317
Patent No. 6685943
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
APPLICANT: Patli, Joseph M.
APPLICANT: House-Pompeo, Karen L.
APPLICANT: Speciale, Pietro
APPLICANT: Joh, Danny
APPLICANT: McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
TITLE OF INVENTION: AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAMK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 53:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-09-010-317-53

Query Match 85.4%; Score 88; DB 4; Length 19;
Best Local Similarity 89.5%; Pred. No. 6,2e-06;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GONEGQOTIEPTPIVP 19
DB 1 GONEGQOTIEPTPIVP 19

RESULT 14
US-08-459-135A-10
Sequence 10, Application US/08459135A
Patent No. 5955078
GENERAL INFORMATION:
APPLICANT: BURHAM, Martin Karl Russel
APPLICANT: CHOPRA, Ian
APPLICANT: CRITCHLEY, Ian Alfred
APPLICANT: KNOWLES, David Justin Charles
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN: MONOCLONAL ANTIBODY AND THEIR US
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road

CITY: King of Prussia
STATE: PA
COUNTRY: U.S.A.
ZIP: 19406-0939
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: Fastseq, Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/459,135A
FILING DATE: 02-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB/94/00215
FILING DATE: 04-Feb-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Gimm1, Edward R
REGISTRATION NUMBER: 38,891
REFERENCE/DOCKET NUMBER: P30591C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-4478
TELEFAX: 610-270-5090
TELEX:
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 174 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: Protein
US-08-459-135A-10

Query Match 76.7%; Score 79; DB 2; Length 174;
Best Local Similarity 78.9%; Pred. No. 0.0011;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GONEGQOTIEPTPIVP 19
DB 116 GONEGQOTIEPTPIVP 134

RESULT 15
US-08-495-559-10
Sequence 10, Application US/08495559A
Patent No. 6054572
GENERAL INFORMATION:
APPLICANT: BURHAM, Martin Karl Russel
APPLICANT: CHOPRA, Ian
APPLICANT: CRITCHLEY, Ian Alfred
APPLICANT: KNOWLES, David Justin Charles
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN: MONOCLONAL
TITLE OF INVENTION: ANTIBODY AND THEIR USE IN PREVENTING BACTERIAL ADHESION
FILE REFERENCE: P30591
CURRENT APPLICATION NUMBER: US/08/495,559A
CURRENT FILING DATE: 1995-08-03
EARLIER APPLICATION NUMBER: GB 9302289.5
EARLIER FILING DATE: 1993-02-05
EARLIER APPLICATION NUMBER: GB 9321592.9
NUMBER OF SEQ ID NOS: 13
NUMBER OF FILING DATE: 1993-10-20
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 10
LENGTH: 174
TYPE: PRT
ORGANISM: *Staphylococcus aureus*
US-08-495-559-10

Query Match 76.7%; Score 79; DB 3; Length 174;
Best Local Similarity 78.9%; Pred. No. 0.0011;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GONEGQOTIEPTPIVP 19

Db 116 GHNCGOQTIBEDTTPPTPP 134

Search completed: October 22, 2005, 05:46:49
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 22, 2005, 11:35:03 ; Search time 35.0628 Seconds
(without alignments)
226.232 Million cell updates/sec

Title: US-10-731-238-52

Perfect score: 1 GQNEGGQGTBEPTTPPIVP 19

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1862951 seqs, 417491010 residues

Total number of hits satisfying chosen parameters: 1862951

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Published Applications_AA:*

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	103	100.0	19	US-10-731-238-52	Sequence 52, Appl
2	95	92.2	19	US-10-731-238-11	Sequence 11, Appl
3	95	92.2	1018	US-09-815-242-5797	Sequence 5797, A
4	95	92.2	1018	US-09-815-242-12838	Sequence 12838, A
5	95	92.2	1018	US-10-470-0488-68	Sequence 68, Appl
6	95	92.2	1027	US-08-781-986A-5254	Sequence 5254, Ap
7	95	92.2	1027	US-10-329-624-5254	Sequence 5254, Ap
8	90	87.4	559	US-08-781-986A-5251	Sequence 5251, Ap
9	90	87.4	559	US-10-329-624-5251	Sequence 5251, Ap
10	90	87.4	940	US-10-470-0488-424	Sequence 424, Appl
11	90	87.4	948	US-10-470-0488-69	Sequence 69, Appl

12	89	86.4	19	US-10-731-238-12	Sequence 12, Appl
13	89	86.4	19	US-10-731-238-51	Sequence 51, Appl
14	88	85.4	19	US-10-731-238-53	Sequence 53, Appl
15	84	81.6	961	US-10-282-122A-43778	Sequence 43778, A
16	84	81.6	978	US-09-815-242-5456	Sequence 5456, Ap
17	84	81.6	1001	US-09-815-242-12686	Sequence 12686, A
18	84	81.6	1038	US-10-282-122A-43827	Sequence 43827, A
19	84	81.6	1038	US-10-282-122A-43827	Sequence 43827, A
20	56	54.4	661	US-10-450-763-38821	Sequence 38821, A
21	56	54.4	661	US-10-450-763-38822	Sequence 38822, A
22	55	53.4	1042	US-10-473-576-10	Sequence 10, Appl
23	55	53.4	486	US-10-142-231-92	Sequence 92, Appl
24	55	53.4	486	US-10-356-153-92	Sequence 92, Appl
25	51	49.5	373	US-10-884-115-92	Sequence 92, Appl
26	50	48.5	373	US-10-108-260A-2882	Sequence 2882, Ap
27	50	48.5	64	US-10-424-599-279670	Sequence 279670, A
28	49.5	48.1	1905	US-11-097-143-21567	Sequence 21567, A
29	49.5	48.1	181	US-10-094-749-2746	Sequence 2746, Ap
30	49	47.6	1427	US-10-408-765A-2873	Sequence 2873, Ap
31	49	47.6	1460	US-10-408-765A-1400	Sequence 1400, Ap
32	47	45.6	212	US-10-380-105-6	Sequence 6, Appl
33	47	45.6	1086	US-11-097-143-9150	Sequence 9150, Ap
34	47	45.6	1379	US-11-097-143-33612	Sequence 33612, A
35	47	45.6	1552	US-11-097-143-42084	Sequence 42084, A
36	46	44.7	1564	US-10-292-798-1354	Sequence 1254, Appl
37	46	44.7	38	US-10-731-238-48	Sequence 48, Appl
38	46	44.7	88	US-10-425-115-330245	Sequence 330245, A
39	46	44.7	16	US-10-425-115-284579	Sequence 284579, A
40	46	44.7	16	US-10-425-115-330872	Sequence 330872, A
41	46	44.7	263	US-10-425-115-330872	Sequence 330872, A
42	46	44.7	325	US-11-097-143-4875	Sequence 4875, Ap
43	46	44.7	413	US-10-425-115-274419	Sequence 274419, A
44	46	44.7	872	US-10-092-900A-72	Sequence 72, Appl
45	46	44.7	9	US-09-950-370-2	Sequence 2, Appl
			15	US-10-433-579-3	Sequence 3, Appl
			16	US-10-391-364-2	Sequence 2, Appl

ALIGNMENTS

RESULT 1
US-10-731-238-52
Sequence 52, Application US/10731238
Publication No. US20050123552A1
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
Patli, Joseph M.
House-Pompeo, Karen L.
Speziale, Pietro
Joh, Danny
McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/731,238
FILING DATE: 10-Dec-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE: 21-Jan-1998
APPLICATION NUMBER: US 60/036,139

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; FILING DATE: 21-JAN-1997
; ATTORNEY/AGENT INFORMATION:
;   NAME: Hibler, David W.
;   REGISTRATION NUMBER: 41,071
;   REFERENCE/DOCKET NUMBER: TAMK:189
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE: 512-418-3000
;     TELEFAX: 512-474-7577
; INFORMATION FOR SEQ ID NO: 52:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH: 19 amino acids
;     TYPE: amino acid
;     STRANDEDNESS: <Unknown>
;   TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 52:
US-10-731-238-52

Query Match      100.0%; Score 103; DB 18; Length 19;
Best Local Similarity 100.0%; Pred. No. 2, 1e-07;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GONEGQQTIEEPTPIVP 19
        |||
        1 GONEGQQTIEEPTPIVP 19

RESULT 2
US-10-731-238-11
; Sequence 11, Application US/1071238
; Publication No. US20050123552A1
; GENERAL INFORMATION:
;   APPLICANT: Hook, Magnus
;             Patli, Joseph M.
;             House-Pompeo, Karen L.
;             Speziale, Pietro
;             Joh, Danny
;             McGavin, Martin J.
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
; AND METHODS OF USE
; NUMBER OF SEQUENCES: 105
; CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Arnold, White & Durkee
;   STREET: P.O. Box 4433
;   CITY: Houston
;   STATE: TX
;   COUNTRY: USA
;   ZIP: 77210-4433
; COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION NUMBER: US/10/731,238
; APPLICATION NUMBER: US/10/731,238
; FILING DATE: 10-Dec-2003
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US/09/010,317
;   FILING DATE: 21-Jan-1998
;   APPLICATION NUMBER: US 60/036,139
;   FILING DATE: 21-JAN-1997
; ATTORNEY/AGENT INFORMATION:
;   NAME: Hibler, David W.
;   REGISTRATION NUMBER: 41,071
;   REFERENCE/DOCKET NUMBER: TAMK:189
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE: 512-418-3000
;     TELEFAX: 512-474-7577
; INFORMATION FOR SEQ ID NO: 11:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH: 19 amino acids
;     TYPE: amino acid
;     STRANDEDNESS: <Unknown>
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; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 11:
US-10-731-238-11

Query Match      92.2%; Score 95; DB 18; Length 19;
Best Local Similarity 94.7%; Pred. No. 2, 7e-06;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 GONEGQQTIEEPTPIVP 19
        |||
        1 GONEGQQTIEEPTPIVP 19
        |||

Db      1 GONEGQQTIEEPTPIVP 19
        |||
        1 GONEGQQTIEEPTPIVP 19
        |||

RESULT 3
US-09-815-242-5797
; Sequence 5797, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
;   APPLICANT: Haselbeck, Robert
;   APPLICANT: Ohlsen, Karl L.
;   APPLICANT: Zyskind, Judith W.
;   APPLICANT: Wall, Daniel
;   APPLICANT: Trawick, John D.
;   APPLICANT: Carr, Grant J.
;   APPLICANT: Yamamoto, Robert T.
;   APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; PROKARYOTES
; FILE REFERENCE: ELITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR FILING DATE: 2000-05-23
; PRIOR FILING DATE: 2000-05-23
; PRIOR FILING DATE: 2000-05-23
; PRIOR FILING DATE: 2000-05-26
; PRIOR FILING DATE: 2000-07,727
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for windows Version 4.0
; SEQ ID NO 5797
; LENGTH: 1018
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-09-815-242-5797

Query Match      92.2%; Score 95; DB 9; Length 1018;
Best Local Similarity 94.7%; Pred. No. 0,00019;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 GONEGQQTIEEPTPIVP 19
        |||
        1 GONEGQQTIEEPTPIVP 19
        |||

Db      860 GONEGQQTIEEPTPIVP 878
        |||
        1 GONEGQQTIEEPTPIVP 19
        |||

RESULT 4
US-09-815-242-12838
; Sequence 12838, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
;   APPLICANT: Haselbeck, Robert
;   APPLICANT: Ohlsen, Karl L.
;   APPLICANT: Zyskind, Judith W.
;   APPLICANT: Wall, Daniel
;   APPLICANT: Trawick, John D.
;   APPLICANT: Carr, Grant J.
```

```

; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; FILE REFERENCE: ELITRA 011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12838
; LENGTH: 1018
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-09-815-242-12838

Query Match          92.2%; Score 95; DB 9; Length 1018;
Best Local Similarity 94.7%; Pred. No. 0.00019;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GONEGQOTIEPTPIVP 19
    |||||
Db 860 GONEGQOTIEPTPIVP 878

RESULT 5
US-10-470-048B-68
; Sequence 68, Application US/10470048B
; Publication No. US2005003744A1
; GENERAL INFORMATION:
; APPLICANT: MEINKE ET AL.
; TITLE OF INVENTION: A METHOD FOR IDENTIFICATION, ISOLATION AND PRODUCTION OF
; FILE REFERENCE: SONN-035US
; CURRENT APPLICATION NUMBER: US/10/470,048B
; CURRENT FILING DATE: 2003-07-25
; NUMBER OF SEQ ID NOS: 603
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 68
; LENGTH: 1018
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-10-470-048B-68

Query Match          92.2%; Score 95; DB 17; Length 1018;
Best Local Similarity 94.7%; Pred. No. 0.00019;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GONEGQOTIEPTPIVP 19
    |||||
Db 860 GONEGQOTIEPTPIVP 878

RESULT 6
US-08-781-986A-5254
; Sequence 5254, Application US/08781986A
; Publication No. US20030054436A1
; GENERAL INFORMATION:
; APPLICANT: Charles Kunesh
; TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
```

```

; NUMBER OF SEQUENCES: 5255
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/781,986A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Benson, Bob
; REGISTRATION NUMBER: 30,446
; REFERENCE/DOCKET NUMBER: PB248PP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 5254:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1027 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-781-986A-5254

Query Match          92.2%; Score 95; DB 8; Length 1027;
Best Local Similarity 94.7%; Pred. No. 0.00019;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GONEGQOTIEPTPIVP 19
    |||||
Db 869 GONEGQOTIEPTPIVP 887

RESULT 7
US-10-329-624-5254
; Sequence 5254, Application US/10329624
; Publication No. US20040043037A1
; GENERAL INFORMATION:
; APPLICANT: Charles Kunesh
; TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
; NUMBER OF SEQUENCES: 5256
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/329,624
; FILING DATE: 27-Dec-2002
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/956,171
FILING DATE: October 20, 1997
APPLICATION NUMBER: 60/009,861
FILING DATE: January 5, 1996
APPLICATION NUMBER: 08/781,986
FILING DATE: January 3, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Mark J. Hyman
REGISTRATION NUMBER: 46,789
REFERENCE/DOCKET NUMBER: PB248PID1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (240) 314-1224
TELEFAX: (301) 309-8439
INFORMATION FOR SEQ ID NO: 5254:
SEQUENCE CHARACTERISTICS:
LENGTH: 1027 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: Protein
SEQUENCE DESCRIPTION: SEQ ID NO: 5254:
US-10-329-624-5254

Query Match          92.2%  Score 95;  DB 15;  Length 1027;
Best Local Similarity 94.7%  Pred No. 0.00019;
Matches 18;  Conservative 0;  Mismatches 1;  Indels 0;  Gaps 0.

QY      1  GQNEGQTIETETPTPIVP 19
      |||||
Db      869  GQNEGQTIETETPTPIVP 887

RESULT 8
US-08-781-986A-5251
Sequence 5251, Application US/08781986A
Publication No. US20030054436A1
GENERAL INFORMATION:
APPLICANT: Charles Kunsch
TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
NUMBER OF SEQUENCES: 5255
CORRESPONDENCE ADDRESS:
ADDRESSER: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COUNTRY: USA
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/781,986A
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Benson, Bob
REGISTRATION NUMBER: 30,446
REFERENCE/DOCKET NUMBER: PB248PP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 5251:
SEQUENCE CHARACTERISTICS:
LENGTH: 559 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear

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; MOLECULE TYPE: protein
US-08-781-986A-5251

Query Match      87.4%; Score 90; DB 8; Length 559;
Best Local Similarity 89.5%; Pred. No. 0.00049;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY      1 GONEGQOTIEPTPIVP 19
      |||||||
Db      415 GHNEGQOTIEDTTPIVP 433

RESULT 9
US-10-329-624-5251
; Sequence 5251, Application US/10329624
; Publication No. US20040043037A1
; GENERAL INFORMATION:
; APPLICANT: Charles Kunsch
;      Gil H. Choi
;      Patrick S. Dillon
;      Craig A. Rosen
;      Steven C. Barash
;      Michael R. Fannon
; TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
; NUMBER OF SEQUENCES: 5256
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 Inch, 1.4MB storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/329,624
; FILING DATE: 27-Dec-2002
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/956,171
; FILING DATE: October 20, 1997
; APPLICATION NUMBER: 60/009,861
; FILING DATE: January 5, 1996
; APPLICATION NUMBER: 08/781,986
; FILING DATE: January 3, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Mark J. Hyman
; REGISTRATION NUMBER: 46,789
; REFERENCE/DOCKET NUMBER: PB246PID1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (240) 314-1224
; TELEFAX: (301) 309-8439
; INFORMATION FOR SEQ ID NO: 5251:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 559 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 5251:
US-10-329-624-5251

Query Match      87.4%; Score 90; DB 15; Length 559;
Best Local Similarity 89.5%; Pred. No. 0.00049;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY      1 GONEGQOTIEPTPIVP 19
      |||||||
Db      415 GHNEGQOTIEDTTPIVP 433

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;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/010,317
; FILING DATE: 21-Jan-1998
; APPLICATION NUMBER: US 60/036,139
; FILING DATE: 21-JAN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Hibler, David W.
; REGISTRATION NUMBER: 41,071
; REFERENCE/DOCKET NUMBER: TAMK:189
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 512-418-3000
; TELEFAX: 512-474-7577
;
; INFORMATION FOR SEQ ID NO: 51:
;
; SEQUENCE CHARACTERISTICS:
; LENGTH: 19 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
;
; SEQUENCE DESCRIPTION: SEQ ID NO: 51:
US-10-731-238-51

Query Match      86.4%; Score 89; DB 18; Length 19;
Best Local Similarity 89.5%; Pred. No. 1.8e-05;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 GONEGQQTIEPTPIVP 19
DB      1 GONEGQQTIEPTPIVP 19

RESULT 14
US-10-731-238-53
; Sequence 53, Application US/10731238
; Publication No. US20050123552A1
; GENERAL INFORMATION:
; APPLICANT: Hook, Magnus
; Patti, Joseph M.
; House-Pompeo, Karen L.
; Speziale, Pietro
; John, Danny
; McGavin, Martin J.
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
;
; NUMBER OF SEQUENCES: 105
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: TX
; COUNTRY: USA
; ZIP: 77210-4433
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/731,238
; FILING DATE: 10-Dec-2003
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/010,317
; FILING DATE: 21-Jan-1998
; APPLICATION NUMBER: US 60/036,139
; FILING DATE: 21-JAN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Hibler, David W.
; REGISTRATION NUMBER: 41,071
; REFERENCE/DOCKET NUMBER: TAMK:189
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 512-418-3000
; TELEFAX: 512-474-7577
;
; INFORMATION FOR SEQ ID NO: 53:

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;
; SEQUENCE CHARACTERISTICS:
; LENGTH: 19 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
;
; SEQUENCE DESCRIPTION: SEQ ID NO: 53:
US-10-731-238-53

Query Match      85.4%; Score 88; DB 18; Length 19;
Best Local Similarity 89.5%; Pred. No. 2.5e-05;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 GONEGQQTIEPTPIVP 19
DB      1 GONEGQQTIEPTPIVP 19

RESULT 15
US-10-282-122A-43778
; Sequence 43778, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zykkind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See file wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 43778
; LENGTH: 961
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-10-282-122A-43778

Query Match      81.6%; Score 84; DB 15; Length 961;
Best Local Similarity 84.2%; Pred. No. 0.0059;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1 GONEGQQTIEPTPIVP 19

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Wed Oct 26 15:02:37 2005

us-10-731-238-52.rapb

Page 7

Db 807 GONEGQTIEDTTPPTPP 825

Search completed: October 22, 2005, 12:09:32
Job time : 36.0628 secs

7
This Page Blank (28/01/19)

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 22, 2005, 04:14:19 ; Search time 6.94525 Seconds
(without alignments)
263.219 Million cell updates/sec

Title: US-10-731-238-52

Perfect score: 103
Sequence: 1 GONEGQQTIEEDTTPPIVP 19

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : PIR_79:*

1: p1r1:*

2: p1r2:*

3: p1r3:*

4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	95	92.2	1018	2 A32192	fibronectin-binding
2	90	87.4	940	2 S19702	fibronectin-binding
3	84	81.6	961	2 G90053	hypothetical prote
4	84	81.6	1038	2 H90053	hypothetical prote
5	56	54.4	218	2 T17259	hypothetical prote
6	56	54.4	576	2 T46385	hypothetical prote
7	51	49.5	318	2 T29479	hypothetical prote
8	50.5	49.0	341	2 T17502	hypothetical prote
9	46	44.7	239	2 T36995	hypothetical prote
10	46	44.7	331	2 A61046	ecdysone-induced m
11	46	44.7	1695	2 T19823	hypothetical prote
12	45	43.7	150	2 B72705	hypothetical prote
13	45	43.7	315	2 J01250	coat protein - chr
14	45	43.7	479	1 B69652	lincomycin-resista
15	45	43.7	490	2 T02545	probable MYB fami
16	45	43.7	574	2 T01131	hypothetical prote
17	45	43.7	900	2 A42024	transcription fact
18	45	43.7	933	2 S17233	transcription fact
19	45	43.7	1272	2 T49313	copla-type reverse
20	45	43.7	1320	2 F96614	hypothetical prote
21	45	43.7	1352	2 F86246	hypothetical prote
22	45	43.7	1352	2 T47925	chromatin structur
23	45	43.7	1726	2 T30810	probable PPS prote
24	45	43.7	3300	2 D70575	hypothetical membr
25	44	42.7	138	2 A95913	protein gp17 (Bact
26	44	42.7	272	2 A71360	hypothetical prote
27	44	42.7	275	2 B70576	hypothetical prote
28	44	42.7	330	2 A86355	hypothetical prote
29	44	42.7	500	2 T26078	hypothetical prote

30	44	42.7	758	2 S60586	glucocorticoid rec
31	44	42.7	1086	2 J07736	C3G protein, long
32	44	42.7	1122	2 T14180	exit protein - Myc
33	44	42.7	1483	2 E86143	F6f3.12 protein -
34	44	42.7	1962	2 A32634	lactocarpin (EC 3.4
35	43	41.7	156	2 F88175	protein T24H7.3 (l
36	43	41.7	209	2 F90261	conserved hypothet
37	43	41.7	224	2 D72861	Acortf-91 protein -
38	43	41.7	267	2 F97741	cell division prot
39	43	41.7	460	2 T31587	hypothetical prote
40	43	41.7	478	2 D97682	hypothetical prote
41	43	41.7	478	2 AD2907	cell division part
42	43	41.7	679	2 B75262	conserved hypothet
43	43	41.7	782	2 J07284	phospholipase A2 (
44	43	41.7	801	2 A37353	membrane protein 4
45	43	41.7	858	2 A57513	heat shock protein

ALIGNMENTS

RESULT 1

A32192
Fibronectin-binding protein - Staphylococcus aureus
C:Species: Staphylococcus aureus
C>Date: 31-Jul-1989 #sequence_revision 31-Jul-1989 #text_change 16-Feb-1997
C:Accession: A32192
R:Signaes, C.; Raucel, G.; Joensen, K.; Lindgren, P.E.; Anantharamaiah, G.M.; Hoeck, Proc. Natl. Acad. Sci. U.S.A. 86, 699-703, 1989
A:Title: Nucleotide sequence of the gene for a fibronectin-binding protein from Staphyl
A:Reference number: A32192; MUID:8908998; PMID:2521391
A:Accession: A32192
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1018 <SIG>
A:Cross-references: GB:J04151
C:Keywords: fibronectin binding

Query Match 92.2%; Score 95; DB 2; Length 1018;
Best Local Similarity 94.7%; Pred. No. 4.9e-06;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GONEGQQTIEEDTTPPIVP 19
DB 860 GONEGQQTIEEDTTPPIVP 878

RESULT 2

S19702
Fibronectin-binding protein B - Staphylococcus aureus
C:Species: Staphylococcus aureus
C>Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
C:Accession: S19702
R:Joensen, K.; Signaes, C.; Mueller, H.P.; Lindberg, M. Eur. J. Biochem. 202, 1041-1048, 1991
A:Title: Two different gene encode fibronectin binding proteins in Staphylococcus aure
A:Reference number: S19702; MUID:92111475; PMID:1857286
A:Accession: S19702
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-940 <JOB>
A:Cross-references: UNIPROT:Q53682; EMBL:X62992; NID:g49040; PIDD:CAA44726.1; PID:g5615
C:Keywords: fibronectin binding

Query Match 87.4%; Score 90; DB 2; Length 940;
Best Local Similarity 89.5%; Pred. No. 2.5e-05;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GONEGQQTIEEDTTPPIVP 19
DB 796 GONEGQQTIEEDTTPPIVP 814

RESULT 3

hypothetical protein fnbB [imported] - Staphylococcus aureus (strain N315)
 G90053
 C/Species: Staphylococcus aureus
 C/Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
 C/Accession: G90053
 R/Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguc
 ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kato, C.; Sekimizu, K.;
 C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
 Lancet 357, 1225-1240, 2001
 A/Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.
 A/Reference number: A89758; PMID:21311952; PMID:11418146
 A/Accession: G90053
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-961 <RUR>
 A/Cross-references: UNIPROT:Q99RD3; GB:BA000018; PID:G13702452; PIDN:BABA3593.1; GSPDB:G
 A/Experimental source: strain N315
 C/Genetics:
 A/Gene: fnbB

Query Match 81.6%; Score 84; DB 2; Length 961;
 Best Local Similarity 84.2%; Pred. No. 0.0002;
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GONEGQOTIEPTTPPIV 19
 |||||
 DB 807 GONEGQOTIEPTTPPIV 825

RESULT 4

hypothetical protein fnb [imported] - Staphylococcus aureus (strain N315)
 H90053
 C/Species: Staphylococcus aureus
 C/Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
 C/Accession: H90053
 R/Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguc
 ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kato, C.; Sekimizu, K.;
 C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
 Lancet 357, 1225-1240, 2001
 A/Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.
 A/Reference number: A89758; PMID:21311952; PMID:11418146
 A/Accession: H90053
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-1038 <KUR>
 A/Cross-references: UNIPROT:Q99RD2; GB:BA000018; PID:G13702453; PIDN:BABA3594.1; GSPDB:G
 A/Experimental source: strain N315
 C/Genetics:
 A/Gene: fnb

Query Match 81.6%; Score 84; DB 2; Length 1038;
 Best Local Similarity 84.2%; Pred. No. 0.0002;
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GONEGQOTIEPTTPPIV 19
 |||||
 DB 856 GONEGQOTIEPTTPPIV 874

RESULT 5

hypothetical protein DKFZP727C091.1 - human (fragment)
 T17259
 C/Species: Homo sapiens (man)
 C/Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
 C/Accession: T17259
 R/Pouetka, A.; Klein, M.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.
 submitted to the Protein Sequence Database, September 1999
 A/Reference number: Z18723
 A/Accession: T17259
 A/Status: preliminary
 A/Molecule type: mRNA
 A/Residues: 1-218 <POU>

A/Cross-references: UNIPROT:Q9UFT0; EMBL:AL117476
 A/Experimental source: adult breast cancer; clone DKFZP727C091
 C/Genetics:
 A/Note: DKFZP727C091.1

Query Match 54.4%; Score 56; DB 2; Length 218;
 Best Local Similarity 52.6%; Pred. No. 0.58;
 Matches 10; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 1 GONEGQOTIEPTTPPIV 19
 |||||
 DB 182 GSKTGTEPAAPSPPIV 200

RESULT 6

hypothetical protein DKFZP434K031.1 - human (fragment)
 T46385
 C/Species: Homo sapiens (man)
 C/Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 09-Jul-2004
 C/Accession: T46385
 R/Pouetka, A.; Klein, M.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.
 submitted to the Protein Sequence Database, January 2000
 A/Reference number: Z23029
 A/Accession: T46385
 A/Status: preliminary
 A/Molecule type: mRNA
 A/Residues: 1-576 <RAA>
 A/Cross-references: UNIPROT:Q9NTE7; EMBL:AL137317
 A/Experimental source: adult testis; clone DKFZP434K031
 C/Genetics:
 A/Note: DKFZP434K031.1

Query Match 54.4%; Score 56; DB 2; Length 576;
 Best Local Similarity 52.6%; Pred. No. 1.7;
 Matches 10; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 1 GONEGQOTIEPTTPPIV 19
 |||||
 DB 540 GSKTGTEPAAPSPPIV 558

RESULT 7

hypothetical protein ZC487.4 - Caenorhabditis elegans
 T29479
 C/Species: Caenorhabditis elegans
 C/Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
 C/Accession: T29479
 R/Pauley, A.; Gattung, S.
 submitted to the EMBL Data Library, February 1996
 A/Description: The sequence of C. elegans cosmid ZC487.
 A/Reference number: Z20624
 A/Accession: T29479
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: DNA
 A/Residues: 1-318 <PAU>
 A/Cross-references: UNIPROT:Q23352; EMBL:U50310; PIDN:AAA92541.1; CESP:ZC487.4
 A/Experimental source: strain Bristol N2
 C/Genetics:
 A/Gene: CESP:ZC487.4
 A/Introns: 31/1; 71/3; 175/2; 228/1

Query Match 49.5%; Score 51; DB 2; Length 318;
 Best Local Similarity 55.6%; Pred. No. 4.9;
 Matches 10; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

QY 2 GONEGQOTIEPTTPPIV 19
 |||||
 DB 124 QNKGQPYIEAPPPSPPIV 141

RESULT 8

hypothetical protein SPAC10F6.08c - fission yeast (Schizosaccharomyces pombe)

C:Species: Schizosaccharomyces pombe
 C>Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
 C:Accession: T37502
 R:Conor, R.; Churcher, C.M.; Barrall, B.G.; Rajandream, M.A.; Wood, V.
 submitted to the EMBL Data Library, November 1997
 A:Reference number: Z21719
 A:Accession: T37502
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-341 <CON>
 A:Cross-references: UNIPROT:O42648; EMBL:AL009197; PIDN:CAA15721.1; GSPDB:GN00066; SPDB:
 A:Experimental source: strain 972h-; cosmid c10F6
 C:Genetics:
 A:Gene: SPDB:SPAC10F6.08c
 A:Map position: 1
 A:Introns: 15/1; 84/3

Query Match 49.0%; Score 50.5; DB 2; Length 341;
 Best Local Similarity 50.0%; Pred. No. 6.3;
 Matches 10; Conservative 4; Mismatches 5; Indels 1; Gaps 1;

QY 1 GONE-GQOTIEPTTPIVP 19
 ||| :|: ||| ||| :|:
 Db 301 GQKEVDEPSPPTSPILP 320

RESULT 9
 T36995
 hypothetical protein SCJ11.24C - Streptomyces coelicolor
 C:Species: Streptomyces coelicolor
 C>Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
 C:Accession: T36995
 R:Oliver, K.; Harris, D.; Bentley, S.D.; Parkhill, J.; Barrall, B.G.; Rajandream, M.A.
 submitted to the EMBL Data Library, August 1999
 A:Reference number: Z21618
 A:Accession: T36995
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-239 <OLI>
 A:Cross-references: UNIPROT:Q9R181; EMBL:AL109949; PIDN:CA52909.1; GSPDB:GN00070; SCOE
 A:Experimental source: strain A3(2)
 C:Genetics:
 A:Gene: SCOE:SCJ11.24c

Query Match 44.7%; Score 46; DB 2; Length 239;
 Best Local Similarity 47.4%; Pred. No. 20;
 Matches 9; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

QY 1 GONEGQOTIEPTTPIVP 19
 ||| :|: ||| ||| :|:
 Db 178 GQIEGPRTATSPPLPPLP 196

RESULT 10
 A61046
 ecdysone-induced membrane protein IMP-E3 - fruit fly (Drosophila melanogaster)
 C:Species: Drosophila melanogaster
 C>Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004
 C:Accession: A61046
 R:Moore, U.T.; Fristrom, D.; Hammonds, A.S.; Fristrom, J.W.
 Dev. Genet. 11, 299-309, 1990
 A:Title: Characterization of IMP-E3, a gene active during imaginal disc morphogenesis in
 A:Reference number: A61046; MUID:9121865; PMID:2128624
 A:Accession: A61046
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-331 <MOO>
 A:Cross-references: UNIPROT:Q9VHM8
 C:Genetics:
 A:Gene: FlyBase:IMP-E3
 A:Cross-references: FlyBase:FBgn0001255
 C:Keywords: membrane protein

Query Match 44.7%; Score 46; DB 2; Length 331;
 Best Local Similarity 66.7%; Pred. No. 28;
 Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 8 TIEPTTPIVP 19
 ||| :|: ||| ||| :|:
 Db 123 TTERPTSPPTVP 134

RESULT 11
 T19823
 hypothetical protein C38D4.3 - Caenorhabditis elegans
 C:Species: Caenorhabditis elegans
 C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
 C:Accession: T19823
 R:Colles, L.
 submitted to the EMBL Data Library, October 1994
 A:Reference number: Z19183
 A:Accession: T19823
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-1695 <WIL>
 A:Cross-references: UNIPROT:Q18508; EMBL:Z46241; PIDN:CAA86316.1; GSPDB:GN00021; CESP:C
 A:Experimental source: clone C38D4
 C:Genetics:
 A:Gene: CESP:C38D4.3
 A:Map position: 3
 A:Introns: 31/1; 77/1; 160/1; 196/1; 501/3; 541/3; 703/2; 875/1; 989/3; 1352/3; 1383/3;

Query Match 44.7%; Score 46; DB 2; Length 1695;
 Best Local Similarity 80.0%; Pred. No. 1.7e+02;
 Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 6 QOTIEPTTP 15
 ||| :|: ||| ||| :|:
 Db 1647 QQEVETPTTP 1656

RESULT 12
 B72705
 hypothetical protein APE1057 - Aeropyrum pernix (strain K1)
 C:Species: Aeropyrum pernix
 C>Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004
 C:Accession: B72705
 R:Kawarabayashi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Hatake, Y.; Jin-no, K.; Takai
 awa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kodon, Y.; Yamazaki, J.;
 DNA Res. 6, 83-101, 1999
 A:Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropy
 A:Reference number: A72450; MUID:99310339; PMID:10382966
 A:Accession: B72705
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-150 <KAW>
 A:Cross-references: UNIPROT:Q9YD55; DBJ:AP000060; NID:95104188; PIDN:BA80042.1; PID:d
 A:Experimental source: strain K1
 C:Genetics:
 A:Gene: APE1057

Query Match 43.7%; Score 45; DB 2; Length 150;
 Best Local Similarity 42.1%; Pred. No. 17;
 Matches 8; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

QY 1 GONEGQOTIEPTTPIVP 19
 ||| :|: ||| ||| :|:
 Db 56 GLHQGDPRDPNPTTPPLP 74

RESULT 13
 JQ1250
 coat protein - chrysanthemum virus B
 N:Alternate names: 35K protein
 C:Species: Chrysanthemum virus B
 C>Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 22, 2005, 04:10:49 ; Search time 34,818 Seconds
(without alignments)
279,439 Million cell updates/sec

Title: US-10-731-238-52

Perfect score: 103
Sequence: 1 GQNEGQQTIEPTPIPV 19

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_03:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	95	92.2	1018	1	FNBA_STA4U	P14738 staphylococ
2	90	87.4	940	2	Q53682	Q53682 staphylococ
3	84	81.6	961	2	Q99RD3	Q99RD3 staphylococ
4	84	81.6	961	2	Q7A378	Q7A378 staphylococ
5	84	81.6	965	2	Q6GDU5	Q6GDU5 staphylococ
6	84	81.6	1015	2	Q8NU77	Q8NU77 staphylococ
7	84	81.6	1015	2	Q6G6H3	Q6G6H3 staphylococ
8	84	81.6	1038	2	Q99RD2	Q99RD2 staphylococ
9	84	81.6	1038	2	Q7A377	Q7A377 staphylococ
10	79	76.7	957	2	Q6G6H4	Q6G6H4 staphylococ
11	69	67.0	943	2	Q8NU78	Q8NU78 staphylococ
12	56	54.4	218	2	Q9U7T0	Q9U7T0 homo sapien
13	56	54.4	432	2	Q6AW85	Q6AW85 homo sapien
14	56	54.4	531	2	Q81YH1	Q81YH1 homo sapien
15	56	54.4	576	2	Q9NTE7	Q9NTE7 homo sapien
16	56	54.4	1105	2	Q723B3	Q723B3 homo sapien
17	56	54.4	1105	2	Q9U7R3	Q9U7R3 homo sapien
18	54	52.4	582	2	Q6CDJ8	Q6CDJ8 varrowia li
19	51	49.5	182	2	Q7MSR5	Q7MSR5 porcine ade
20	51	49.5	195	2	Q7MSR4	Q7MSR4 porcine ade
21	51	49.5	219	2	Q99AD5	Q99AD5 porcine ade
22	51	49.5	318	2	Q23352	Q23352 caenorhabdi
23	51	49.5	1603	2	Q8G499	Q8G499 biffidobacte
24	50.5	49.0	341	2	Q62668	Q62668 schizosacch
25	50	48.5	933	2	Q8T4F9	Q8T4F9 drosophila
26	50	48.5	2072	2	Q9VCH1	Q9VCH1 drosophila
27	49.5	48.1	181	2	Q96MM1	Q96MM1 homo sapien
28	49	47.6	213	2	Q8R3L6	Q8R3L6 mus musculu
29	49	47.6	236	2	Q7PIW4	Q7PIW4 anopheles g
30	49	47.6	266	2	Q9D9C0	Q9D9C0 mus musculu
31	49	47.6	379	2	Q7UT64	Q7UT64 rhodospirell

32	49	47.6	497	2	Q9EWG7	Q9EWG7 streptomyce
33	49	47.6	1036	2	Q80XP7	Q80XP7 mus musculu
34	49	47.6	1036	2	Q80TGL	Q80TGL mus musculu
35	49	47.6	1066	2	Q7Q4U2	Q7Q4U2 anopheles g
36	49	47.6	1427	1	ZFH2_HUMAN	ZFH2_HUMAN homo sapien
37	49	47.6	4998	2	Q8CG65	Q8CG65 mus musculu
38	48	46.6	468	2	Q8JKN0	Q8JKN0 heliothis z
39	48	46.6	1255	2	Q7S1N7	Q7S1N7 neurospora
40	47	45.6	190	2	Q9Y187	Q9Y187 cynops pyrr
41	47	45.6	269	2	Q8MYR3	Q8MYR3 drosophila
42	47	45.6	276	1	DX2B_BRARE	DX2B_BRARE brachydanio
43	47	45.6	508	2	Q6FP67	Q6FP67 candida gla
44	47	45.6	816	2	Q8ITZ3	Q8ITZ3 caenorhabdi
45	47	45.6	848	2	O16796	O16796 caenorhabdi

ALIGNMENTS

```

RESULT 1
FNBA_STA4U STANDARD; PRT; 1018 AA.
ID FNBA_STA4U
AC P14738;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Fibronectin-binding protein precursor (FNBP).
GN Name=fnbp;
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1280;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NCTC 8325-4;
RX MEDLINE=89098998; PubMed=2521391;
RA Signaes C., Raucel G., Joensson K., Lindgren P.-E.,
  Anantharamiah G.M., Hoeck M., Lindberg M.;
RT "Nucleotide sequence of the gene for a fibronectin-binding protein
  from Staphylococcus aureus: use of this peptide sequence in the
  synthesis of biologically active peptides."
RL Proc. Natl. Acad. Sci. U.S.A. 86:699-703(1989).
CC -!- FUNCTION: The ability of bacteria to bind fibronectin has been
  proposed as a virulence factor enabling bacteria to colonize wound
  tissues and blood clots. Binding of plasma fibronectin to the
  bacterial surface might block adhesion receptors on S.aureus, thus
  representing an important defense mechanism against tissue
  invasion.
CC -!- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
  an amide bond (Potential).
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
  or send an email to license@isb-sib.ch).
CC -----
CC EMBL; J04151; AAA26632.1; -
  InterPro: IPR004237; Fn bind.
  InterPro: IPR005877; Gpos_Y5IRK.
  InterPro: IPR001899; Gram_pos_anchor.
  Pfam; PF02986; Fn_bind; 1.
  Pfam; PF00746; Gram_pos_anchor; 1.
  Pfam; PF04650; Y5IRK signal; 1.
  DR TIGRPFAMs; TIGR01167; LPXTG anchor; 1.
  DR TIGRPFAMs; TIGR01168; Y5IRK signal; 1.
  DR PROSITE; PSS0847; GRAM_POS_ANCHORING; 1.
  Cell adhesion; Cell wall; Peptidoglycan-anchor; Repeat; Signal;
  virulence.
  FT SIGNAL 1 36
  FT CHAIN 37 985 Fibronectin-binding protein.
  FT PROPEP 986 1018 Removed by sortase (Potential).

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FT REPEAT 545 574 B-1.
FT REPEAT 575 604 B-2.
FT DOMAIN 745 878 4 X approximate tandem repeats,
  fibronectin-binding domain.
FT REPEAT 745 782 D-1.
FT REPEAT 783 820 D-2.
FT REPEAT 821 859 D-3.
FT REPEAT 860 878 D-4 (incomplete).
FT DOMAIN 879 948 5 X tandem repeats, Pro-rich (WR).
FT REPEAT 879 892 WR 1.
FT REPEAT 893 906 WR 2.
FT REPEAT 907 920 WR 3.
FT REPEAT 921 934 WR 4.
FT REPEAT 935 948 WR 5.
FT MOD_RES 982 986 LpXTG sorting signal (potential).
FT SITE 985 985 Pentaglycyl murein peptidoglycan amidated
  chreonine (potential).
SQ SEQUENCE 1018 AA; 11780 MW; 58175E020E81F1F CRC64;

Query Match 92.2%; Score 95; DB 1; Length 1018;
Best Local Similarity 94.7%; Pred. No. 4.6e-05;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GONEGOQTEBPTTPVP 19
DB 860 GONEGOQTEBPTTPVP 878

RESULT 2
Q53682 PRELIMINARY; PRT; 940 AA.
AC Q53682;
AT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Fibronectin binding protein B.
GN Name=fnbB;
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1280;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=8325-4;
RX MEDLINE=92111475; PubMed=1837266;
RA Jonsson K., Sigmas C., Muller H.P., Lindberg M.;
RT "Two different genes encode fibronectin binding proteins in
  Staphylococcus aureus. The complete nucleotide sequence and
  characterization of the second gene."
RL Eur. J. Biochem. 202;1041-1048(1991).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
  an amide bond (By similarity).
CC EMBL; X62992; CAA44726.1; -.
DR PIR; S19702; S19702.
DR HSSP; O53653; 1N67.
DR GO; GO:0009986; C:cell surface; IEA.
DR GO; GO:0005618; C:cell wall; IEA.
DR GO; GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0007155; P:cell adhesion; IEA.
DR InterPro; IPR008966; Adhes_bact.
DR InterPro; IPR004237; Fn_bind.
DR InterPro; IPR005877; Gpos_YsIRK.
DR InterPro; IPR001899; Gram_pos_anchor.
DR Pfam; PF02986; Fn_bind_2.
DR Pfam; PF04650; YsIRK_signal; 1.
DR TIGRPFAMs; TIGR01167; LpXTG_anchor; 1.
DR TIGRPFAMs; TIGR01168; YsIRK_signal; 1.
DR PROSITE; PS50847; GRAM_POS_ANCHORING; 1.
KW Cell wall; Peptidoglycan-anchor.
SQ SEQUENCE 940 AA; 10355 MW; E35FBBCA907AE345 CRC64;

Query Match 87.4%; Score 90; DB 2; Length 940;

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Best Local Similarity 89.5%; Pred. No. 0.00023;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GONEGOQTEBPTTPVP 19
DB 796 GNEGOQTEBPTTPVP 814

RESULT 3
Q99RD3 PRELIMINARY; PRT; 961 AA.
AC Q99RD3;
AT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Fibronectin-binding protein homolog.
GN Name=fnbB; OrderedLocustNames=SAV2502;
OS Staphylococcus aureus (strain Mu50 / ATCC 700699).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=158878;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MU50 / ATCC 700699;
RX MEDLINE=21311952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2;
RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
  Cui L., Oguchi A., Aoki K.-I., Nagai Y., Iian J.-Q., Ito T.,
  Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,
  Mizutani-Ul Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
  Sekimizu K., Hirakawa H., Kuhara S., Goto S., Tabuaki J.,
  Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
  Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
RT "Whole genome sequencing of methicillin-resistant Staphylococcus
  aureus."
RL Lancet 357;1225-1240(2001).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
  an amide bond (By similarity).
CC EMBL; AP003365; BAB58664.1; -.
DR PIR; G90053; G90053.
DR HSSP; O53653; 1N67.
DR GO; GO:0009986; C:cell surface; IEA.
DR GO; GO:0005618; C:cell wall; IEA.
DR GO; GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0007155; P:cell adhesion; IEA.
DR InterPro; IPR008966; Adhes_bact.
DR InterPro; IPR004237; Fn_bind.
DR InterPro; IPR005877; Gpos_YsIRK.
DR InterPro; IPR001899; Gram_pos_anchor.
DR Pfam; PF02986; Fn_bind_1.
DR Pfam; PF00746; Gram_pos_anchor; 1.
DR Pfam; PF04650; YsIRK_signal; 1.
DR TIGRPFAMs; TIGR01167; LpXTG_anchor; 1.
DR TIGRPFAMs; TIGR01168; YsIRK_signal; 1.
DR PROSITE; PS50847; GRAM_POS_ANCHORING; 1.
KW Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ SEQUENCE 961 AA; 106010 MW; 364940F884EA4101 CRC64;

Query Match 81.6%; Score 84; DB 2; Length 961;
Best Local Similarity 84.2%; Pred. No. 0.0018;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GONEGOQTEBPTTPVP 19
DB 807 GONEGOQTEBPTTPVP 825

RESULT 4
Q7A3J8 PRELIMINARY; PRT; 961 AA.
AC Q7A3J8;
AT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)

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DE  FndB protein.
GN  Name=fndB; OrderedLocustNames=SA2290;
OS  Staphylococcus aureus (strain N315).
OC  Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX  NCBI_TaxID=158879;
RN  [1]
RP  SEQUENCE FROM N.A.
RX  MEDLINE=2111952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2;
RA  Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
RA  Cui L., Oguchi A., Aoki K.-I., Nagai Y., Ito T.,
RA  Kanemori M., Matsunari H., Maruyama A., Murakami H., Hosoyama A.,
RA  Mizutani-Uji Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
RA  Sekizima K., Hatakeyama H., Kihara S., Goto S., Yabuuchi J.,
RA  Kashiwa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
RA  Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
RT  "Whole genome sequencing of methicillin-resistant Staphylococcus
RT  aureus."
RL  Lancet 357:1225-1240(2001).
CC  -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC  an amide bond (By similarity).
CC  EMBL: AP003137; BAB43593.1; -.
DR  GO: GO:0009986; C:cell surface; IEA.
DR  GO: GO:0005618; C:cell wall; IEA.
DR  GO: GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR  GO: GO:0016020; C:membrane; IEA.
DR  GO: GO:0007155; P:cell adhesion; IEA.
DR  InterPro: IPR008966; Adhes_bact.
DR  InterPro: IPR004237; Fn_bind.
DR  InterPro: IPR005877; Gpos_YsIRK.
DR  InterPro: IPR001899; Gram_pos_anchor.
DR  Pfam: PF02986; Fn_bind. 1.
DR  Pfam: PF00746; Gram_pos_anchor; 1.
DR  Pfam: PF04650; YsIRK_signal; 1.
DR  TIGRPFAM: TIGR01167; LPXTG_anchor; 1.
DR  TIGRPFAM: TIGR01168; YsIRK_signal; 1.
DR  PROSITE: PS50847; GRAM_POS_ANCHORING; 1.
SQ  Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ  SEQUENCE 961 AA; 106010 MW; 364940F84EA4101 CRC64;

Query Match      81.6%; Score 84; DB 2; Length 961;
Best Local Similarity 84.2%; Pred. No. 0.0018;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY  1 GONEGQQTIEPTTPPV 19
DB  807 GONEGQQTIEPTTPPV 825

RESULT 5
Q6GDUS PRELIMINARY; PRT; 965 AA.
ID 06GDUS;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Fibronectin-binding protein.
GN Name=fndB; OrderedLocustNames=SA2580;
OS Staphylococcus aureus (strain MRSA252).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=282458;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=1521324; DOI=10.1073/pnas.0402521101;
RA Holden M.T.G., Felt E.J., Lindsey J.A., Peacock S.J., Day N.P.J.,
RA Enright M.C., Foster T.J., Moore C.B., Hurst L., Atkin R., Barron A.,
RA Bason N., Bentley S.D., Chillingworth C., Chillingworth T.,
RA Churcher C., Clark L., Corton C., Cronin A., Doggett J., Dowd L.,
RA Felwell T., Hance Z., Harris B., Hauser R., Holtroyd S., Jagsels K.,
RA James K.D., Lennard N., Line A., Mayes R., Moule S., Mungall K.,
RA Ormond D., Quail M.A., Rabinowitch E., Rutherford K.M., Sanders M.,
RA Sharp S., Simmonds M., Stevens K., Whitehead S., Barrell B.G.,
RA Spratt B.G., Parkhill J.;
RT "Complete genomes of two clinical Staphylococcus aureus strains:

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RT evidence for the rapid evolution of virulence and drug resistance."
RL Proc. Natl. Acad. Sci. U.S.A. 101:9786-9791(2004).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC an amide bond (By similarity).
CC EMBL: BX571856; CAG41560.1; -.
DR GO: GO:0009986; C:cell surface; IEA.
DR GO: GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO: GO:0016020; C:membrane; IEA.
DR GO: GO:0007155; P:cell adhesion; IEA.
DR InterPro: IPR008966; Adhes_bact.
DR InterPro: IPR004237; Fn_bind.
DR InterPro: IPR005877; Gpos_YsIRK.
DR InterPro: IPR001899; Gram_pos_anchor.
DR Pfam: PF02986; Fn_bind; 1.
DR Pfam: PF00746; Gram_pos_anchor; 1.
DR Pfam: PF04650; YsIRK_signal; 1.
DR TIGRPFAM: TIGR01167; LPXTG_anchor; 1.
DR TIGRPFAM: TIGR01168; YsIRK_signal; 1.
DR PROSITE: PS50847; GRAM_POS_ANCHORING; 1.
SQ Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ SEQUENCE 965 AA; 105691 MW; 2982E132164D0551 CRC64;

Query Match      81.6%; Score 84; DB 2; Length 965;
Best Local Similarity 84.2%; Pred. No. 0.0018;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY  1 GONEGQQTIEPTTPPV 19
DB  825 GONEGQQTIEPTTPPV 843

RESULT 6
Q8NUU7 PRELIMINARY; PRT; 1015 AA.
ID 08NUU7;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE FndB protein.
GN Name=fndB; OrderedLocustNames=MW2421;
OS Staphylococcus aureus (strain MW2).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=196620;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=MW2;
RX MEDLINE=22040717; PubMed=12044378; DOI=10.1016/S0140-6736(02)08713-5;
RA Baba T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Oguchi A.,
RA Nagai Y., Iwano N., Asano K., Naimi T., Kuroda H., Cui L.,
RA Yamamoto K., Hiramatsu K.;
RT "Genome and virulence determinants of high virulence community-
RT acquired MRSA."
RL Lancet 359:1819-1827(2002).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC an amide bond (By similarity).
CC EMBL: AP004830; BAB96286.1; -.
DR GO: GO:0009986; C:cell surface; IEA.
DR GO: GO:0005618; C:cell wall; IEA.
DR GO: GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO: GO:0016020; C:membrane; IEA.
DR GO: GO:0007155; P:cell adhesion; IEA.
DR InterPro: IPR008966; Adhes_bact.
DR InterPro: IPR004237; Fn_bind.
DR InterPro: IPR005877; Gpos_YsIRK.
DR InterPro: IPR001899; Gram_pos_anchor.
DR Pfam: PF02986; Fn_bind; 1.
DR Pfam: PF00746; Gram_pos_anchor; 1.
DR Pfam: PF04650; YsIRK_signal; 1.
DR TIGRPFAM: TIGR01167; LPXTG_anchor; 1.
DR TIGRPFAM: TIGR01168; YsIRK_signal; 1.
DR PROSITE: PS50847; GRAM_POS_ANCHORING; 1.
SQ Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ SEQUENCE 1015 AA; 111145 MW; D0F9281BB64D44D2 CRC64;

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Query Match      81.6%; Score 84; DB 2; Length 1015;
Best Local Similarity 84.2%; Pred. No. 0.0019;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1 GONEGQQTIEEDTTPPTPP 19
      |||||
Db      861 GONEGQQTIEEDTTPPTPP 879

RESULT 7
ID 066H3 PRELIMINARY; PRT; 1015 AA.
AC 066H3;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DE Fibronectin-binding protein.
GN OrderedLocuNames=SA52388;
OS Staphylococcus aureus (strain MSSA476).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=282459;
RP SEQUENCE FROM N.A.
RX PubMed=15213324; DOI=10.1073/pnas.0402521101;
RA Holden M.T.G., Fell E.J., Lindsay J.A., Peacock S.J., Day J.P.J.,
RA Enright M.C., Foster T.J., Moore C.E., Hurst L., Atkin R., Barron A.,
RA Bason N., Bentley S.D., Chillingworth C., Chillingworth T.,
RA Churchill C., Clark L., Corton C., Cronin A., Duggett J., Dowd L.,
RA Felwell T., Hance Z., Harris B., Hauser H., Holroyd S., Jigels K.,
RA James K.D., Leonard N., Line A., Mayes R., Moule S., Mungall K.,
RA Ormond D., Quail M.A., Rabinovitch E., Rutherford K.M., Sanders M.,
RA Sharp S., Simmonds M., Stevens K., Whitehead S., Barrett B.G.,
RA Spratt B.G., Parkhill J.;
RT "Complete genomes of two clinical Staphylococcus aureus strains:
RT evidence for the rapid evolution of virulence and drug resistance.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:9786-9791(2004).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC an amide bond (By similarity).
DR EMBL: BX571857; CAG44202.1; -
DR GO: GO:0009986; C:cell surface; IEA.
DR GO: GO:0005618; C:cell wall; IEA.
DR GO: GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO: GO:0016020; C:membrane; IEA.
DR GO: GO:007153; P:cell adhesion; IEA.
DR InterPro: IPR008966; Adhes_bact.
DR InterPro: IPR004237; Fn_bind.
DR InterPro: IPR005877; Gpos_YsIRK.
DR InterPro: IPR001899; Gram_pos_anchor.
DR Pfam: PF02986; Fn_bind; 1.
DR Pfam: PF00746; Gram_pos_anchor; 1.
DR Pfam: PF04650; YsIRK_signal; 1.
DR TIGRFAMs: TIGR01167; LPXTG_anchor; 1.
DR TIGRFAMs: TIGR01168; YsIRK_signal; 1.
DR PROSITE: PS50847; GRAM_POS_ANCHORING; 1.
KW Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ SEQUENCE 1015 AA; 111145 MW; DOF9281BB6444D2 CRC64;

Query Match      81.6%; Score 84; DB 2; Length 1015.
Best Local Similarity 84.2%; Pred. No. 0.0019;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1 GONEGQQTIEEDTTPPTPP 19
      |||||
Db      861 GONEGQQTIEEDTTPPTPP 879

RESULT 8
ID 099RD2 PRELIMINARY; PRT; 1038 AA.
AC 099RD2;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)

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DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE Fibronectin-binding protein homolog.
GN Name=fnb; OrderedLocuNames=SAV2503;
OS Staphylococcus aureus (strain Mu50 / ATCC 700699).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=158878;
RP SEQUENCE FROM N.A.
RX STRAIN=Mu50 / ATCC 700699;
RX MEDLINE=21311952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2;
RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Iian J.-Q., Ito T.,
RA Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hoshoyama A.,
RA Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
RA Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
RA Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
RA Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
RT "Whole genome sequencing of methicillin-resistant Staphylococcus
RT aureus.";
RL Lancet 357:1225-1240(2001).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC an amide bond (By similarity).
DR EMBL: AP003365; BAB58665.1; -
DR PIR: H90053; H90053.
DR GO: GO:0009986; C:cell surface; IEA.
DR GO: GO:0005618; C:cell wall; IEA.
DR GO: GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO: GO:0016020; C:membrane; IEA.
DR GO: GO:007155; P:cell adhesion; IEA.
DR InterPro: IPR008966; Adhes_bact.
DR InterPro: IPR004237; Fn_bind.
DR InterPro: IPR005877; Gpos_YsIRK.
DR InterPro: IPR001899; Gram_pos_anchor.
DR Pfam: PF02986; Fn_bind; 1.
DR Pfam: PF00746; Gram_pos_anchor; 1.
DR Pfam: PF04650; YsIRK_signal; 1.
DR TIGRFAMs: TIGR01167; LPXTG_anchor; 1.
DR TIGRFAMs: TIGR01168; YsIRK_signal; 1.
DR PROSITE: PS50847; GRAM_POS_ANCHORING; 1.
KW Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ SEQUENCE 1038 AA; 113618 MW; 666BF6B2B8BB12 CRC64;

Query Match      81.6%; Score 84; DB 2; Length 1038;
Best Local Similarity 84.2%; Pred. No. 0.0019;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1 GONEGQQTIEEDTTPPTPP 19
      |||||
Db      866 GONEGQQTIEEDTTPPTPP 874

RESULT 9
ID 07A3J7 PRELIMINARY; PRT; 1038 AA.
AC 07A3J7;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DE Fnb protein.
GN Name=fnb; OrderedLocuNames=SA2291;
OS Staphylococcus aureus (strain N315).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=158879;
RP SEQUENCE FROM N.A.
RX MEDLINE=21311952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2;
RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Iian J.-Q., Ito T.,
RA Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hoshoyama A.,
RA Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
RA Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
RA Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
RA Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;

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"Whole genome sequencing of methicillin-resistant *Staphylococcus aureus*." Lancet 357:1225-1240(2001).
 CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by an amide bond (By similarity).
 DR EMBL: AP003137; BAB43594.1; -;
 DR GO: GO:0009986; C:cell surface; IEA.
 DR GO: GO:0005618; C:cell wall; IEA.
 DR GO: GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
 DR GO: GO:0016020; C:membrane; IEA.
 DR GO: GO:0007155; P:cell adhesion; IEA.
 DR InterPro: IPR008966; Adhes_bact.
 DR InterPro: IPR004237; Fn_bind.
 DR InterPro: IPR005877; Gpos_Ysirk.
 DR InterPro: IPR001899; Gram_pos_anchor.
 DR Pfam: PF02986; Fn_bind.1.
 DR Pfam: PF00746; Gram_pos_anchor.1.
 DR Pfam: PF04650; Ysirk_signal.1.
 DR TIGRfam: TIGR01167; LPXTG_anchor.1.
 DR TIGRfam: TIGR01168; Ysirk_signal.1.
 DR PROSITE: PS50847; GRAM_POS_ANCHORING.1.
 DR Cell wall; Complete proteome; Peptidoglycan-anchor.
 SO SEQUENCE 1038 AA; 113618 MW; 666BF6BF2FBEB12 CRC64;

Query Match 81.6%; Score 84; DB 2; Length 1038;
 Best Local Similarity 84.2%; Pred. No. 0.0019;
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GONEGQOTIEPTTPP 19
 Db 856 GONEGQOTIEPTTPP 874

RESULT 10
 OGG6H4 PRELIMINARY; PRT; 957 AA.
 AC QGG6H4;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Fibronectin-binding protein.
 GN Name=fnb3; OrderedLocustNames=SA52387;
 OS *Staphylococcus aureus* (strain MSSA476).
 OC Bacteria; Firmicutes; Bacillales; *Staphylococcus*.
 OC NCBI_TaxID=282459;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX PubMed=15213324; DOI=10.1073/pnas.0402521101;
 RA Holden M.T.G., Fell E.J., Lindsay J.A., Peacock S.J., Day N.P.J.,
 RA Enright M.C., Foster T.J., Moore C.E., Hurst L., Atkin R., Barron A.,
 RA Bason N., Bentley S.D., Chillingworth C., Chillingworth T.,
 RA Churcher C., Clark L., Cotton C., Cronin A., Doggett J., Dowd L.,
 RA Felwell T., Hance Z., Harris B., Hauser H., Holtroyd S., Jorgensen K.,
 RA James K.D., Lennard N., Line A., Mayes R., Moule S., Mungall K.,
 RA Ormond D., Quail M.A., Rabinowitsch E., Rutherford K.M., Sanders M.,
 RA Sharp S., Simmonds M., Stevens K., Whitehead S., Barrett B.G.,
 RA Spratt B.G., Parkhill J.;
 RT "Complete genomes of two clinical *Staphylococcus aureus* strains: evidence for the rapid evolution of virulence and drug resistance." Proc. Natl. Acad. Sci. U.S.A. 101:9786-9791(2004).
 RL CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by an amide bond (By similarity).
 DR EMBL: BX571857; CAC44201.1; -;
 DR GO: GO:0009986; C:cell surface; IEA.
 DR GO: GO:0005618; C:cell wall; IEA.
 DR GO: GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
 DR GO: GO:0016020; C:membrane; IEA.
 DR GO: GO:0007155; P:cell adhesion; IEA.
 DR InterPro: IPR008966; Adhes_bact.
 DR InterPro: IPR004237; Fn_bind.
 DR InterPro: IPR005877; Gpos_Ysirk.
 DR InterPro: IPR001899; Gram_pos_anchor.
 DR Pfam: PF02986; Fn_bind.1.

DR Pfam: PF00746; Gram_pos_anchor.1.
 DR Pfam: PF04650; Ysirk_signal.1.
 DR TIGRfam: TIGR01167; LPXTG_anchor.1.
 DR TIGRfam: TIGR01168; Ysirk_signal.1.
 DR PROSITE: PS50847; GRAM_POS_ANCHORING.1.
 DR Cell wall; Complete proteome; Peptidoglycan-anchor.
 SO SEQUENCE 957 AA; 105980 MW; 28F8BA7FFDFD3EAF CRC64;

Query Match 76.7%; Score 79; DB 2; Length 957;
 Best Local Similarity 78.9%; Pred. No. 0.0095;
 Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 GONEGQOTIEPTTPP 19
 Db 803 GONEGQOTIEPTTPP 821

RESULT 11
 Q8NUU8 PRELIMINARY; PRT; 943 AA.
 AC Q8NUU8;
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE FnbB protein.
 GN Name=fnbB; OrderedLocustNames=MM2420;
 OS *Staphylococcus aureus* (strain MM2).
 OC Bacteria; Firmicutes; Bacillales; *Staphylococcus*.
 OC NCBI_TaxID=196620;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=MM2;
 RX MEDLINE=22040717; PubMed=12044378; DOI=10.1016/S0140-6736(02)08713-5;
 RA Baba T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Oguchi A.,
 RA Nagai Y., Iwama N., Asano K., Naimi T., Kuroda H., Cui L.,
 RA Yamanoto K., Hiramatsu K.;
 RT "Genome and virulence determinants of high virulence community-acquired MRSA." Lancet 359:1819-1827(2002).
 RL Lancet 359:1819-1827(2002).
 CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by an amide bond (By similarity).
 DR EMBL: AP004830; BAB96285.1; -;
 DR HSSP: Q53653; 1N67.
 DR GO: GO:0009986; C:cell surface; IEA.
 DR GO: GO:0005618; C:cell wall; IEA.
 DR GO: GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
 DR GO: GO:0016020; C:membrane; IEA.
 DR GO: GO:0007155; P:cell adhesion; IEA.
 DR InterPro: IPR008966; Adhes_bact.
 DR InterPro: IPR004237; Fn_bind.
 DR InterPro: IPR005877; Gpos_Ysirk.
 DR InterPro: IPR001899; Gram_pos_anchor.
 DR Pfam: PF02986; Fn_bind.1.
 DR Pfam: PF00746; Gram_pos_anchor.1.
 DR Pfam: PF04650; Ysirk_signal.1.
 DR TIGRfam: TIGR01167; LPXTG_anchor.1.
 DR TIGRfam: TIGR01168; Ysirk_signal.1.
 DR PROSITE: PS50847; GRAM_POS_ANCHORING.1.
 DR Cell wall; Complete proteome; Peptidoglycan-anchor.
 SO SEQUENCE 943 AA; 104537 MW; DA8A5F31947E1B6A CRC64;

Query Match 67.0%; Score 69; DB 2; Length 943;
 Best Local Similarity 73.7%; Pred. No. 0.27;
 Matches 14; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 GONEGQOTIEPTTPP 19
 Db 803 GONEGQOTIEPTTPP 821

RESULT 12
 Q9UFT0 PRELIMINARY; PRT; 218 AA.

```

AC Q9UT0;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Hypothetical protein DKFZp727C091 (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Breast cancer;
RG The German CDNA Consortium;
RA Pouska A., Albert R., Moosmayer P., Schupp I., Wellenreuther R.,
RA Mewes H.W., Weill B., Amid C., Oanger A., Fobo G., Han M., Wiemann S.;
RL Submitted (SEP-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; A117476; CAB55949.1; -.
DR PIR; T17259; T17259.
KW Hypothetical protein.
FT NON_TER
SQ SEQUENCE 218 AA; 24001 MW; 3F831E0E5D83CEDE CRC64;

Query Match 54.4%; Score 56; DB 2; Length 218;
Best Local Similarity 52.6%; Pred. No. 4.4;
Matches 10; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 1 GONEGQOTIEPTPIVP 19
| : : : | : : |
182 GSKTGRETEAAPTSPPIVP 200

RESULT 13
ID Q6AM85 PRELIMINARY; PRT; 432 AA.
AC Q6AM85;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DE Hypothetical protein DKFZp686P06109 (Fragment).
GN Name=DKFZp686P06109;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Fetal kidney;
RG The German CDNA Consortium;
RA Bahr A., Lauber J., Mewes H.W., Weill B., Amid C., Oanger A., Fobo G.,
RA Han M., Wiemann S.;
RL Submitted (SEP-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BX648760; CAH10565.1; -.
KW Hypothetical protein.
FT NON_TER
SQ SEQUENCE 432 AA; 47968 MW; 3BAB47807DABE124 CRC64;

Query Match 54.4%; Score 56; DB 2; Length 432;
Best Local Similarity 52.6%; Pred. No. 9.3;
Matches 10; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 1 GONEGQOTIEPTPIVP 19
| : : : | : : |
396 GSKTGRETEAAPTSPPIVP 414

RESULT 14
ID Q81YH1 PRELIMINARY; PRT; 531 AA.
AC Q81YH1;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)

```

```

DE LOC284058 protein (Fragment).
GN Name=LOC284058;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Blood;
RX MEDLINE=22389257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Mang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ushed T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulik S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Buterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smalls D.E., Scherch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Blood;
RA Strausberg R.;
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC035892; AAH35892.1; -.
FT NON_TER
SQ SEQUENCE 531 AA; 58743 MW; 5BE29C31A2B334B4 CRC64;

Query Match 54.4%; Score 56; DB 2; Length 531;
Best Local Similarity 52.6%; Pred. No. 12;
Matches 10; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 1 GONEGQOTIEPTPIVP 19
| : : : | : : |
495 GSKTGRETEAAPTSPPIVP 513

RESULT 15
ID Q9NTE7 PRELIMINARY; PRT; 576 AA.
AC Q9NTE7;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Hypothetical protein DKFZp434K031 (Fragment).
GN Name=DKFZp434K031;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Testis;
RA Pouska A., Klein M., Mewes H.W., Gassenhuber J., Wiemann S.;
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; A1137317; CAB70694.1; -.
DR PIR; T46385; T46385.
KW Hypothetical protein.
FT NON_TER
SQ SEQUENCE 576 AA; 63516 MW; 559EC6FB4B19595C CRC64;

Query Match 54.4%; Score 56; DB 2; Length 576;

```

Best Local Similarity 52.6%; Pred. No. 13;
Matches 10; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

Qy 1 GONEGQQTIEEPTTPPIVP 19
Db 540 GSKTGRETBAAPTSPPIVP 558

Search completed: October 22, 2005, 06:06:17
Job time : 35.818 secs

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OM protein - protein search, using SW model

Run on: October 25, 2005, 19:38:38 ; Search time 41.9163 Seconds
(without alignments)
175.313 Million cell updates/sec

Title: US-10-731-238-53

Perfect score: 105
Sequence: 1 GQNEGQGPEDPTPIPV 19

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: Geneseq_16Dec04:.*
2: geneseqp1980s:.*
3: geneseqp1990s:.*
4: geneseqp2000s:.*
5: geneseqp2001s:.*
6: geneseqp2002s:.*
7: geneseqp2003as:.*
8: geneseqp2003bs:.*
9: geneseqp2004s:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	105	100.0	19	2 AAW65709	AAW65709 Fibronect
2	95	90.5	19	2 AAW65667	AAW65667 Fibronect
3	95	90.5	134	2 AAY29087	AAY29087 S. aureus
4	95	90.5	1018	1 AAP82115	AAP82115 Fibronect
5	95	90.5	1018	4 AAU37245	AAU37245 Staphyloc
6	95	90.5	1018	4 AAU34301	AAU34301 Staphyloc
7	95	90.5	1018	6 ABU18922	ABU18922 Pathogen
8	95	90.5	1018	6 ABM72537	ABM72537 Staphyloc
9	95	90.5	1027	2 AAW89806	AAW89806 Staphyloc
10	90	85.7	134	2 AAY29089	AAY29089 Cloned fi
11	90	85.7	134	2 AAY29088	AAY29088 S. aureus
12	90	85.7	559	2 AAW89803	AAW89803 Staphyloc
13	90	85.7	940	2 AAR07070	AAR07070 Fibronect
14	90	85.7	940	6 ABU19111	ABU19111 Pathogen
15	90	85.7	948	6 ADA89470	ADA89470 Staphyloc
16	90	85.7	948	6 ABU18923	ABU18923 Pathogen
17	90	85.7	948	6 ABM72536	ABM72536 Staphyloc
18	89	84.8	19	2 AAW65668	AAW65668 Fibronect
19	89	84.8	19	2 AAW65707	AAW65707 Fibronect
20	88	83.0	19	2 AAW65708	AAW65708 Fibronect
21	84	80.0	961	6 ABU15854	ABU15854 Protein e
22	84	80.0	978	4 AAU33960	AAU33960 Staphyloc
23	84	80.0	1001	4 AAU37093	AAU37093 Staphyloc
24	84	80.0	1038	6 ABU15903	ABU15903 Protein e
25	79	75.2	101	2 AAR90939	AAR90939 D3d4 poly

ALIGNMENTS

RESULT 1	26	79	75.2	124	2	AAR90940	AAR90940 D3d4 poly
AAW65709	27	79	75.2	128	2	AAR90941	AAR90941 D3d4 poly
ID	28	79	75.2	162	2	AAR90942	AAR90942 D3d4 poly
XX	29	79	75.2	164	2	AAR90938	AAR90938 D3d4 poly
XX	30	79	75.2	174	2	AAR58808	AAR58808 Fdp fibro
XX	31	79	75.2	174	2	AAR91203	AAR91203 D1-D4 fib
XX	32	79	75.2	181	2	AAR58805	AAR58805 Fibronect
XX	33	79	75.2	181	2	AAR91200	AAR91200 D1-D4 fib
XX	34	68	64.8	130	2	AAR58807	AAR58807 Fibronect
XX	35	68	64.8	130	2	AAR91202	AAR91202 D1-D4 fib
XX	36	61	58.1	113	2	AAR90937	AAR90937 D3d4 poly
XX	37	61	58.1	130	2	AAR58806	AAR58806 Fibronect
XX	38	61	58.1	130	2	AAR91201	AAR91201 D1-D4 fib
XX	39	56	53.3	1022	4	ABM62978	ABM62978 Drosophila
XX	40	54	51.4	336	4	ABM67940	ABM67940 Drosophila
XX	41	53	50.5	1603	5	ABP66158	ABP66158 Bifidobac
XX	42	52	49.5	38	2	AAW65701	AAW65701 Fibronect
XX	43	51	48.6	38	2	AAW65691	AAW65691 Fibronect
XX	44	50.5	48.1	1449	4	AAE02535	AAE02535 Porcine a
XX	45	50	47.6	218	4	ABG08462	ABG08462 Novel hum

AAW65709 standard; peptide; 19 AA.
16-OCT-1998 (first entry)
Fibronectin binding protein-derived peptide #53.
microbial surface components recognising adhesive matrix molecule;
MEMGRAM; fibronectin; fibronectin-binding protein; antibody; epitope;
antibiotic; bacterial infection; antibiotic-resistant strain.
Synthetic.
Staphylococcus aureus.
WO9831389-A2.
23-JUL-1998.
21-JAN-1998; 98WO-US001222.
21-JAN-1997; 97US-0036139P.
(TEXA) UNIV TEXAS A & M SYSTEM.
Hosook M, Patil JM, House-Pompeo KL, Speziale P, Joh D;
Megavir MJ;
WPI; 1998-413816/35.
Antibody that binds to fibronectin-binding protein, preventing its
binding to fibronectin - used to treat or prevent bacterial infection,
especially by Staphylococci and Streptococci.
Example 8; Page 102; 201p; English.
The invention relates to antibodies that bind to a fibronectin-binding
domain of a fibronectin-binding protein, and inhibit binding of the
protein to fibronectin. Also claimed are: (1) isolated peptides of a
fibronectin-binding protein that do not bind to fibronectin; (2) fusion
protein containing at least one peptide of a fibronectin-binding protein
linked to a second amino acid sequence; (3) nucleic acid encoding the
isolated peptide of (1). Antibodies, the isolated peptides of (1) and the
nucleic acids are all useful for immunisation (active or passive) and (by
inhibiting binding of bacteria to fibronectin) for preventing or treating
infection in humans or other animals, particularly by staphylococci or

CC streptococci, e.g. meningitis, otitis media, pneumonia, endocarditis,
 CC mastitis in cattle, abortion in horses and many others. Since the
 CC antibodies block binding of bacteria, they should be effective against
 CC antibiotic-resistant strains, and may replace antibiotic therapy or
 CC increase its effectiveness. Sequences AAW65707-711 represent a series of
 CC synthetic peptides based on the DU region of *S. aureus* fibronectin
 CC binding protein A. They were synthesized to contain mutations
 XX
 SQ Sequence 19 AA;
 Query Match 100.0%; Score 105; DB 2; Length 15;
 Best Local Similarity 100.0%; Pred. No. 1.4e-07;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GONEGGQTPEEDTTPPIVP 19
 DB 1 GONEGGQTPEEDTTPPIVP 19
 RESULT 2
 AAW65667
 ID AAW65667 standard; peptide; 19 AA.
 XX
 AC AAW65667;
 XX
 DT 16-OCT-1998 (first entry)
 XX
 DE Fibronectin binding protein-derived peptide #11.
 XX
 KM microbial surface components recognising adhesive matrix molecule;
 KM MSCRAM; fibronectin; fibronectin-binding protein; antibody; epitope;
 KM antibiotic; bacterial infection; antibiotic-resistant strain.
 XX
 OS Synthetic.
 OS Staphylococcus aureus.
 XX
 PN WO9811389-A2.
 XX
 PD 23-JUL-1998.
 XX
 PF 21-JAN-1998; 98WO-US001222.
 XX
 PR 21-JAN-1997; 97US-0036139P.
 XX
 PA (TEXA) UNIV TEXAS A & M SYSTEM.
 XX
 PI Hoeck M, Patti JM, House-Pompeo KL, Speciale P, Joh E;
 PI McGavin MJ;
 XX
 DR WPI; 1998-413816/35.
 XX
 PT Antibody that binds to fibronectin-binding protein, preventing its
 PT binding to fibronectin - used to treat or prevent bacterial infection,
 PT especially by Staphylococci and Streptococci.
 XX
 PS Example 2; Page 92; 201pp; English.
 XX
 CC The invention relates to antibodies that bind to a fibronectin-binding
 CC domain of a fibronectin-binding protein, and inhibit binding of the
 CC protein to fibronectin. Also claimed are: (1) isolated peptides of a
 CC fibronectin-binding protein that do not bind to fibronectin; (2) fusion
 CC protein containing at least one peptide of a fibronectin-binding protein
 CC linked to a second amino acid sequence; (3) nucleic acid encoding the
 CC isolated peptide of (1). Antibodies, the isolated peptides of (1) and the
 CC nucleic acids are all useful for immunisation (active or passive) and (by
 CC inhibiting binding of bacteria to fibronectin) for preventing or treating
 CC infection in humans or other animals, particularly by staphylococci or
 CC streptococci, e.g. meningitis, otitis media, pneumonia, endocarditis,
 CC mastitis in cattle, abortion in horses and many others. Since the
 CC antibodies block binding of bacteria, they should be effective against
 CC antibiotic-resistant strains, and may replace antibiotic therapy or
 CC increase its effectiveness. Sequences AAW65659-68 represent synthetic
 CC epitopes from the fibronectin binding domains DU and DI-D4 of the S.

CC aureus fnbA gene
 XX
 SQ Sequence 19 AA;
 Query Match 90.5%; Score 95; DB 2; Length 19;
 Best Local Similarity 94.7%; Pred. No. 3.3e-06;
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 GONEGGQTPEEDTTPPIVP 19
 DB 1 GONEGGQTPEEDTTPPIVP 19
 RESULT 3
 AAY29087
 ID AAY29087 standard; protein; 134 AA.
 XX
 AC AAY29087;
 XX
 DT 28-SEP-1999 (first entry)
 XX
 DE S. aureus fibronectin binding protein A (FnBA) binding domain.
 XX
 KM Bovine herpes virus-2; BHV-2; cytokine; immune response; immunogen; IL;
 KM interleukin; colony stimulating factor; CSF; interferon; IFN; TNF;
 KM tumor necrosis factor; recombinant virus; vaccine; mucosal disease;
 KM mastitis; breast cancer; stress-induced disease; binding domain; FnBA;
 KM fibronectin binding protein.
 XX
 OS Staphylococcus aureus.
 XX
 PN WO9916892-A1.
 XX
 PD 08-APR-1999.
 XX
 PF 29-SEP-1998; 98WO-GB002927.
 XX
 PR 29-SEP-1997; 97GB-00020633.
 XX
 PA (UYBR-) UNIV BRISTOL.
 XX
 PI Bradley AJ, Duffas WP;
 XX
 DR WPI; 1999-255101/21.
 XX
 DR N-PSDB; AAX91504.
 XX
 PT New bovine herpes virus-2 vectors.
 XX
 PS Example 2; Fig 8A-B; 130pp; English.
 XX
 CC The invention provides bovine herpes virus-2 (BHV-2) based vectors that
 CC comprise at least one cytokine-encoding DNA sequence. The expression of
 CC cytokines in mammals can up-regulate immune responses to the immunogens.
 CC The cytokine is selected from interleukins (IL), colony stimulating
 CC factors (CSF), interferons (IFN) and tumor necrosis factors (TNF). The
 CC BHV-2 based vector or recombinant virus can be used as vaccines. They can
 CC be used for preventing or treating a mucosal disease in a subject, e.g.
 CC ruminants, cattle, sheep, goats, dogs, cats, horses, or man, particularly
 CC mastitis in cows or breast cancers in humans. They can also be used for
 CC preventing or treating a stress-induced disease. The present sequence
 CC represents the binding domain of a previously published S. aureus
 CC fibronectin binding protein A (FnBA) sequence. The FnB binding domain
 CC gene sequence FNMB, cloned for use in this invention has 97.8 percent
 CC identity when compared to the previously published FnBA and FnBB gene
 CC sequences
 XX
 SQ Sequence 134 AA;
 Query Match 90.5%; Score 95; DB 2; Length 134;
 Best Local Similarity 94.7%; Pred. No. 2.6e-05;
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 GONEGGQTPEEDTTPPIVP 19

Db 116 GONEGQOTIEEDTTPPIVP 134

RESULT 4
AAP82115 standard; protein; 1018 AA.

AC AAP82115;
XX
XX 25-MAR-2003 (revised)
DT 05-JUN-1990 (first entry)
XX
XX Fibronectin binding protein.
DE Fibronectin binding protein.
XX
XX Fibronectin binding protein; S.aureus; immunisation; mastitis; ruminants;
KM wound infection; diagnosis.
XX
XX Staphylococcus aureus.

OS Staphylococcus aureus.
XX
XX EP294349-A.

PN 07-DEC-1988.

XX 30-MAY-1988; 88EP-00850188.

XX 01-JUN-1987; 87SE-00002272.

XX (ALFA) ALFA LAVAL AGRIC INT AB.

XX Lindberg MK, Signas LC, Wadstrom TM, Froman G;

XX WPI: 1988-347978/49.

DR P-PSDB; AAP82115.

XX Hybrid DNA encoding Staphylococcus aureus fibronectin binding protein -
PT useful for immunisation and topical application to prevent staphylococcal
PT infections.

XX Disclousure; Fig. 8A:1-8A:2; 23pp; English.

XX The S.aureus fibronectin binding protein may be included in a hybrid
CC protein. The protein may be used to immunise ruminants against
CC staphylococcal mastitis, pref. when given at 0.5-5 microg/Kg, using 3
CC doses at 1-3 week intervals; and for topical applicn. to prevent wound
CC infection, pref. using isotonic saline soln. of concn. 25-250 microg/mg.
CC The DNA encoding the binding protein and the hybrid protein may be
CC immobilised on a carrier and used to diagnose staphylococcal infections.
CC (Updated on 25-MAR-2003 to correct PA field.)
XX

SQ Sequence 1018 AA;

Query Match 90.5%; Score 95; DB 1; Length 1018;
Best Local Similarity 94.7%; Pred. No. 0.00022;

Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GONEGQOTPEEDTTPPIVP 19
Db 860 GONEGQOTIEEDTTPPIVP 878

RESULT 5
AAU37245
ID AAU37245 standard; protein; 1018 AA.

XX AAU37245;

XX 14-FEB-2002 (first entry)

XX Staphylococcus aureus cellular proliferation protein #1415.

XX Antisense; prokaryotic cellular proliferation protein; antibiotic;
KW antibacterial; drug design.

XX Staphylococcus aureus.

OS WO200170955-A2.

XX 27-SEP-2001.

XX 21-MAR-2001; 2001WO-US009180.

XX 21-MAR-2000; 2000US-0191078P.

XX 23-MAY-2000; 2000US-0206848P.

XX 26-MAY-2000; 2000US-0207727P.

XX 23-OCT-2000; 2000US-0242578P.

XX 27-NOV-2000; 2000US-0253625P.

XX 22-DEC-2000; 2000US-0257931P.

XX 16-FEB-2001; 2001US-0269308P.

XX (ELIT-) ELITRA PHARM INC.

XX Haselbeck R, Ohlsen KL, Zyskind JW, Wall D, Trawick JD, Carr GJ;

XX Yamamoto RT, Xu HH;

XX WPI: 2001-611495/70.

XX N-PSDB; AAS55104.

XX New polynucleotides for the identification and development of

XX antibiotics, comprise sequences of antisense nucleic acids.

XX Example 3; SEQ ID NO 12838; 511pp; English.

XX The invention relates to antisense inhibitors of genes essential to
CC prokaryotic cellular proliferation, their use in identifying the genes,
CC their use in the discovery of novel antibiotics, the essential genes
CC themselves and the encoded proteins. The prokaryotes used are Escherichia
CC coli, Staphylococcus aureus, Salmonella typhi, Klebsiella pneumoniae,
CC Pseudomonas aeruginosa and Enterococcus faecalis. The invention is also
CC useful for the identification of potential new targets for antibiotic
CC development. The antisense nucleic acids can also be used to identify
CC proteins used in proliferation, to express these proteins, and to obtain
CC antibodies capable of binding to the expressed proteins. The proteins can
CC be used to screen compounds in rational drug discovery programmes. The
CC antisense nucleic acid sequence is also useful to screen for homologous
CC nucleic acids which are required for cell proliferation in a wide variety
CC of organisms. The present sequence represents an essential prokaryotic
CC cellular proliferation protein. Note: The sequence data for this patent
CC did not form part of the printed specification, but was obtained in
CC electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX

SQ Sequence 1018 AA;

Query Match 90.5%; Score 95; DB 4; Length 1018;
Best Local Similarity 94.7%; Pred. No. 0.00022;

Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GONEGQOTPEEDTTPPIVP 19
Db 860 GONEGQOTIEEDTTPPIVP 878

RESULT 6
AAU34301
ID AAU34301 standard; protein; 1018 AA.

XX AAU34301;

XX 14-FEB-2002 (first entry)

XX Staphylococcus aureus cellular proliferation protein #577.

XX Antisense; prokaryotic cellular proliferation protein; antibiotic;
KW antibacterial; drug design.

```

OS Staphylococcus aureus.
XX
XX WO200170955-A2.
XX
XX PD 27-SEP-2001.
XX
XX PF 21-MAR-2001; 2001WO-US009180.
XX
XX PR 21-MAR-2000; 2000US-0191078P.
XX PR 23-MAY-2000; 2000US-0206848P.
XX PR 26-MAY-2000; 2000US-0207727P.
XX PR 23-OCT-2000; 2000US-0242578P.
XX PR 27-NOV-2000; 2000US-0253625P.
XX PR 22-DEC-2000; 2000US-0257931P.
XX PR 16-FEB-2001; 2001US-0269308P.
XX
XX PA (ELIT-) ELITRA PHARM INC.
XX
XX PI Haeselbeck R, Ohlsen KL, Zyskind JW, Wall D, Traxwick JL, Carr GJ,
XX P1 Yamamoto RT, Xu HH;
XX
XX DR WPI, 2001-611495/70.
XX
XX DR N-Psdb; AAS52160.
XX
XX PT New polynucleotides for the identification and development of
XX PT antibiotics, comprise sequences of antisense nucleic acids.
XX
XX PS Example 3; SEQ ID NO 5797; 511pp; English.
XX
XX CC The invention relates to antisense inhibitors of genes essential to
XX CC prokaryotic cellular proliferation, their use in identifying the genes,
XX CC their use in the discovery of novel antibiotics, the essential genes
XX CC themselves and the encoded proteins. The prokaryotes used are Escherichia
XX CC coli, Staphylococcus aureus, Salmonella typhi, Klebsiella pneumoniae,
XX CC Pseudomonas aeruginosa and Enterococcus faecalis. The invention is also
XX CC useful for the identification of potential new targets for antibiotic
XX CC development. The antisense nucleic acids can also be used to identify
XX CC proteins used in proliferation, to express these proteins, and to obtain
XX CC antibodies capable of binding to the expressed proteins. The proteins can
XX CC be used to screen compounds in rational drug discovery programmes. The
XX CC antisense nucleic acid sequence is also useful to screen for homologous
XX CC nucleic acids which are required for cell proliferation in a wide variety
XX CC of organisms. The present sequence represents an essential prokaryotic
XX CC cellular proliferation protein. Note: The sequence data for this patent
XX CC did not form part of the printed specification, but was obtained in
XX CC electronic format directly from WIPO at
XX CC ftp.wipo.int/pub/published_pct_sequences
XX
XX SQ Sequence 1018 AA;
XX
XX Query Match 90.5%; Score 95; DB 4; Length 101f;
XX Best Local Similarity 94.7%; Pred. No. 0.00022;
XX Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX QY 1 GONEGQQTPEEDTTPPIVP 19
XX ||||| |
XX DB 860 GONEGQQTPEEDTTPPIVP 878
XX
XX RESULT 7
XX ABU18922
XX ID ABU18922 standard; protein; 1018 AA.
XX
XX AC ABU18922;
XX
XX DT 06-MAR-2003 (first entry)
XX
XX DE Pathogen specific antigen related staphylococcal protein (EQ ID No 68.
XX
XX KW Antibacterial; virucide; fungicide; protozoacide; cytostatic; anti-HIV;
XX KW hyperimmune; serum-reactive; antigen; pathogen; tumour; allergen;
XX KW auto-immune; vaccine; staphylococcal infection; antibody; cancer;
XX KW autoimmune disease; HIV; hepatitis.

```

```

XX Staphylococcus sp.
OS
XX WO200259148-A2.
XX
XX 01-AUG-2002.
XX
XX 21-JAN-2002; 2002WO-EP000546.
XX
XX 26-JAN-2001; 2001AT-00000130.
XX
XX (CIST-) CISTEM BIOECHOLOGIES GMBH.
XX
XX Meinke A, Nagy E, Von Ahnen U, Klade C, Henics T, Zauner W;
XX Mihh DB, Vyryvcska O, Ecz H, Dryla A, Weichhart T, Hafner M;
XX Tempelmaier B;
XX
XX WPI; 2003-075410/07.
XX
XX Identifying, isolating and producing hyperimmune serum-reactive antigens
XX from a pathogen, for preparing vaccine or medicament for treating or
XX preventing e.g. staphylococcal infections, comprises providing antibody
XX preparation.
XX
XX Example 7; Page 157; 252pp; English.
XX
XX The invention relates to a novel method for identifying, isolating and
XX producing hyperimmune serum-reactive antigens from a pathogen, tumour,
XX allergen, a tissue or host prone to auto-immunity, where the antigens are
XX used in a vaccine, comprises providing antibody preparation from a plasma
XX pool of a type of animal, or individual sera with antibodies against the
XX specific pathogen, tumour, allergen, tissue or host prone to auto-
XX immunity. The hyperimmune serum-reactive antigens comprising any of the
XX 62 sequences of 53-2261 amino acids fully defined in the specification,
XX or their hyperimmune fragments are useful for the manufacture of a
XX pharmaceutical preparation, particularly a vaccine against staphylococcal
XX infections or colonisation against S. aureus or S. epidermidis. The
XX preparation of antibodies is useful for the manufacture of a medicament
XX for treating or preventing staphylococcal infections or colonisation
XX against S. aureus or S. epidermidis. The antibody preparations may also
XX be used for diagnostic and imaging purposes. Other conditions that can be
XX treated include cancer, autoimmune diseases or infections caused by viral
XX (e.g. HIV, hepatitis A, B or C), fungal or protozoan pathogens. This
XX sequence represents a staphylococcal protein relating to the method for
XX identifying and producing pathogen specific antigens of the invention
XX
XX SQ Sequence 1018 AA:
XX
XX Query Match 90.5%; Score 95; DB 6; Length 1018;
XX Best Local Similarity 94.7%; Pred. No. 0.00022;
XX Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX 1 GONEGQQTPEEDTTPPIVP 19
XX ||||| ||||| |||||
XX Db 860 GONEGQRTIEDTTPPIVP 878
XX
XX RESULT 8
XX ABM72537
XX ID ABM72537 standard; protein; 1018 AA.
XX
XX ABM72537;
XX
XX 20-NOV-2003 (first entry)
XX
XX Staphylococcus aureus protein #1177.
XX
XX Antibacterial; vaccine; gene therapy; infection; sepsis; diagnosis;
XX enzymatic assay; antibiotic target.
XX
XX Staphylococcus aureus.
XX
XX WO200294868-A2.
XX

```

```

XX 28-NOV-2002.
PD
XX
XX 27-MAR-2002; 2002WO-IB002637.
PF
XX 27-MAR-2001; 2001GB-00007661.
PR
XX (CHIR-) CHIRON SPA.
PA
XX
XX Masignani V, Mora M, Scarselli M;
PI
XX WPI: 2003-120786/11.
DR
XX N-PSDB; ACF74097.
XX
XX New Staphylococcus aureus protein, useful as a vaccine for treating or
PT preventing Staphylococcal infection, specifically an infection caused by
PT S. aureus, e.g. sepsis.
XX
PS Claim 1; SEQ ID NO 3554; 49pp; English.
XX
XX The invention relates to novel genes and encoded proteins from
CC Staphylococcus aureus. A composition comprising the S. aureus protein, a
CC nucleic acid encoding the protein, or an antibody to the protein, is
CC useful as a pharmaceutical, particularly as a vaccine for treating or
CC preventing infection due to Staphylococcus bacteria, specifically an
CC infection caused by S. aureus. The composition is particularly useful for
CC treating or preventing sepsis in a patient. The composition can also be
CC used for diagnostics. The protein is also used in an assay for enzymatic
CC studies and as a target for antibiotics. This sequence represents one of
CC the novel S. aureus proteins of the invention
XX
SQ Sequence 1018 AA;
XX
Query Match 90.5%; Score 95; DB 6; Length 1018;
Best Local Similarity 94.7%; Pred. No. 0.00022;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 GONEGQQTPEEDTTPPIVP 19
DB 860 GONEGQQTPEEDTTPPIVP 878
AAW89806
ID AAW89806 standard; protein; 1027 AA.
XX
XX AAW89806;
AC
XX 16-MAR-1999 (first entry)
DT
XX
XX Staphylococcus aureus protein SEQ ID #5254.
DE
XX
XX Computer readable medium; vaccine; S.aureus infection; immunodetection;
KM cellulitis; eyelid infection; food poisoning; osteomyelitis; therapy;
KM skin infection; surgical wound infection; scalded skin syndrome;
XX toxic shock syndrome.
XX
XX Staphylococcus aureus.
OS
XX EP786519-A2.
PN
XX
XX 30-JUL-1997.
PD
XX
XX 07-JAN-1997; 97EP-00100117.
PF
XX 05-JAN-1996; 96US-0009861P.
PR
XX (HUMA-) HUMAN GENOME SCI INC.
PA
XX
XX Kunusch CA, Choi GH, Barash SC, Dillon PJ, Fannon MR, Rosen CA;
PI
XX WPI: 1997-374922/35.
DR
XX

```

```

PT Polynucleotide(s) and proteins derived from Staphylococcus aureus -
PT stored on computer readable medium and used in the production of anti-
PT S.aureus vaccines.
XX
XX Claim 23; Page 3263-3267; 3271pp; English.
PS
XX
XX This sequence represents a Staphylococcus aureus protein sequence of the
CC invention. The DNA sequences encoding the S.aureus proteins are recorded
CC on a computer readable medium, preferably selected from a floppy or hard
CC disk, random access memory (RAM), read-only memory (ROM) or CD-ROM.
CC Homology searches using the S.aureus DNA sequences allows putative
CC functions to be assigned so that protein-encoding or regulatory regions
CC of commercial, therapeutic or industrial importance can be obtained.
CC Specifically, sequences which are likely to encode antigens have been
CC identified and these polypeptides can be used in a vaccine composition
CC against S.aureus infection. The polypeptides can also be used in a kit
CC for the immunodetection of S.aureus in a sample. S.aureus is implicated
CC in numerous human diseases, including cellulitis, eyelid infections, food
CC poisoning, osteomyelitis, skin and surgical wound infections, scalded
CC skin syndrome, toxic shock syndrome, etc. Organisms transformed with the
CC DNA sequences can be used for recombinant production of the polypeptides.
CC The new DNA sequences (and their fragments) are useful as primers or
CC probes for isolating homologues of any of the 5191 S.aureus DNA sequences
CC contained on the computer readable medium
XX
SQ Sequence 1027 AA;
XX
Query Match 90.5%; Score 95; DB 2; Length 1027;
Best Local Similarity 94.7%; Pred. No. 0.00023;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 GONEGQQTPEEDTTPPIVP 19
DB 869 GONEGQQTPEEDTTPPIVP 887
AAV29089
ID AAV29089 standard; protein; 134 AA.
XX
XX AAV29089;
AC
XX 28-SEP-1999 (first entry)
DT
XX
XX Cloned fibronectin binding protein binding domain (FnBAB) sequence.
DE
XX
XX Bovine herpes virus-2; BHV-2; cytokine; immune response; immunogen; IL;
KM interleukin; colony stimulating factor; CSF; interferon; IFN; TNF;
KM tumour necrosis factor; recombinant virus; vaccine; mucosal disease;
KM mastitis; breast cancer; stress-induced disease; binding domain; FnBAB;
KM fibronectin binding protein.
XX
XX Staphylococcus aureus.
OS
XX W09916892-A1.
PN
XX
XX 08-APR-1999.
PD
XX
XX 29-SEP-1998; 98WO-GB002927.
PF
XX 29-SEP-1997; 97GB-00020633.
PR
XX (UYBR-) UNIV BRISTOL.
PA
XX
XX Bradley AJ, Duffas WP;
PI
XX WPI: 1999-255101/21.
DR
XX N-PSDB; AAX91506.
DR
XX New bovine herpes virus-2 vectors.
PT
XX
XX Example 2; Fig 8A-B; 130pp; English.
PS
XX

```


SQ Sequence 559 AA:
 Query Match 85.7%; Score 90; DB 2; Length 559;
 Best Local Similarity 89.5%; Pred. No. 0.00058;
 Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 GONEGQQTPEEDTTPPIVP 19
 DB 415 GHNKGQQTIEEDTTPPIVP 433
 RESULT 13
 AAR07070 standard; protein; 940 AA.
 XX AAR07070;
 AC AAR07070;
 XX 25-MAR-2003 (revised)
 DT 21-FEB-1991 (first entry)
 XX Fibronectin-binding protein encoded by gene 2, fnbB.
 DE Fibronectin-binding protein encoded by gene 2, fnbB.
 XX Wound healing; immunisation; mastitis; fnbA; ss.
 KM Staphylococcus aureus.
 OS Staphylococcus aureus.
 FH Key Location/Qualifiers
 FT Peptide 1..36
 /label= signal peptide
 XX BP397633-A.
 XX 14-NOV-1990.
 PD 04-MAY-1990; 90EP-00850166.
 XX 11-MAY-1989; 89SE-00001687.
 PR (ALFA) ALFA LAVAL AGRIC INT AB.
 PA Hook M, Jonsson K, Lindberg KM, Sigmas LC;
 PI WPI; 1990-343563/46.
 DR N-PSDB; AAQ06550.
 XX Fibronectin binding protein gene - isolated from S. aureus and used for
 PT producing protein for wound healing, immunisation or diagnosis.
 PS Claim 11; Page 17; 24pp; English.
 XX The sequence is deduced from a gene, designated gene 2 (fnbB), localised
 CC downstream of that disclosed in SE8702272 (gene 1; fnbA) encoding a
 CC fibronectin binding protein, fnbA in S. aureus. Gene 2 encodes fnbB.
 CC The two proteins show considerable homology, esp. in the signal sequence
 CC (95%). Downstream is a stretch of 66 AAs with 75% homology to the same
 CC stretch in fnbPA. The following 444 AAs have only 40% homology and the B
 CC repeats of fnbPA are absent. However the rest of the peptide (394 AAs) is
 CC nearly identical to fnbPA, the main difference being a deletion of 14 AAs.
 CC This highly homologous region contains the same repeat (D1-D4 and W1-5)
 CC found in fnbPA with the exception that W1 is missing. The Wc region and
 CC the hydrophobic M domain as well as the C-terminal end are conserved.
 CC (Updated on 25-MAR-2003 to correct PR field.) (Updated on 25-MAR-2003 to
 CC correct PA field.)
 XX Sequence 940 AA;
 SQ Query Match 85.7%; Score 90; DB 2; Length 940;
 Best Local Similarity 89.5%; Pred. No. 0.001;
 Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 GONEGQQTPEEDTTPPIVP 19
 DB 796 GHNKGQQTIEEDTTPPIVP 814

RESULT 14
 ABJ19111 standard; protein; 940 AA.
 XX ABJ19111;
 AC ABJ19111;
 XX 06-MAR-2003 (first entry)
 DT Pathogen specific antigen related staphylococcal protein SEQ ID No 424.
 DE Antibacterial; virucide; fungicide; protozoacide; cytostatic; anti-HIV;
 XX hyperimmune; serum-reactive; antigen; pathogen; tumour; allergen;
 KM auto-immunity; vaccine; staphylococcal infection; antibody; cancer;
 KM autoimmune disease; HIV; hepatitis.
 XX Staphylococcus sp.
 OS Staphylococcus sp.
 XX W0200259148-A2.
 PN 01-AUG-2002.
 XX 21-JAN-2002; 2002MO-EP000546.
 PF 26-JAN-2001; 2001AT-00000130.
 PR (CIST-) CISTEM BIOTECHNOLOGIES GMBH.
 XX Meinke A, Nagy E, Von Absen U, Klade C, Henkes T, Zauner W;
 PI Minh DB, Vytvytska O, Etz H, Dryla A, Welchhart T, Hafner M;
 PI Tempelmeier B;
 XX WPI; 2003-075410/07.
 DR Identifying, isolating and producing hyperimmune serum-reactive antigens
 PT from a pathogen, for preparing vaccine or medicament for treating or
 PT preventing e.g. staphylococcal infections, comprises providing antibody
 PT preparation.
 PS Example 7; Page 223; 252pp; English.
 XX The invention relates to a novel method for identifying, isolating and
 CC producing hyperimmune serum-reactive antigens from a pathogen, tumour,
 CC allergen, a tissue or host prone to auto-immunity, where the antigens are
 CC used in a vaccine, comprises providing antibody preparation from a plasma
 CC pool of a type of animal, or individual sera with antibodies against the
 CC specific pathogen, tumour, allergen, tissue or host prone to auto-
 CC immunity. The hyperimmune serum-reactive antigens comprising any of the
 CC 62 sequences of 53-2261 amino acids fully defined in the specification,
 CC or their hyperimmune fragments are useful for the manufacture of a
 CC pharmaceutical preparation, particularly a vaccine against staphylococcal
 CC infections or colonisation against S. aureus or S. epidermidis. The
 CC preparation of antibodies is useful for the manufacture of a medicament
 CC for treating or preventing staphylococcal infections or colonisation
 CC against S. aureus or S. epidermidis. The antibody preparations may also
 CC be used for diagnostic and imaging purposes. Other conditions that can be
 CC treated include cancer, autoimmune diseases or infections caused by viral
 CC (e.g. HIV, hepatitis A, B or C), fungal or protozoan pathogens. This
 CC sequence represents a staphylococcal protein relating to the method for
 CC identifying and producing pathogen specific antigens of the invention
 CC
 XX Sequence 940 AA;
 SQ Query Match 85.7%; Score 90; DB 6; Length 940;
 Best Local Similarity 89.5%; Pred. No. 0.001;
 Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 GONEGQQTPEEDTTPPIVP 19
 DB 796 GHNKGQQTIEEDTTPPIVP 814

RESULT 15
 ADA89470
 ID ADA89470 standard; protein; 948 AA.
 AC
 ADADA89470;
 DT 20-NOV-2003 (first entry)
 DE Staphylococcus aureus antigenic protein #9.
 XX
 XX antigenic protein; vaccine; Staphylococcus aureus; pathogenic organism;
 KW antibacterial; neuroprotective; immunosuppressive; antiinflammatory;
 KW antitumor; immunostimulant; ophthalmological; pathogenic microbe;
 KW bacteremia; septic shock; organ infection; skin infection; septicemia;
 KW bacterial basal colonisation; bacterial eye infection; bacteremia;
 KW tuberculosis; food poisoning; blood infection; peritonitis; endocarditis;
 KW sepsis; meningitis; pneumonia; stomach ulcer; gonorrhoea; toxic shock;
 KW necrotising fasciitis; impetigo; histoplasmosis; Lyme disease;
 KW gastro-enteritis; dysentery; shigellosis; skin disorder.
 XX
 OS Staphylococcus aureus.
 XX
 PN WO2003011899-A2.
 XX
 PD 13-FEB-2003.
 XX
 PF 02-AUG-2002; 2002WO-GB003606.
 XX
 PR 02-AUG-2001; 2001GB-00018825.
 PR 09-JAN-2002; 2002GB-00000349.
 XX
 PA (UYSH-) UNIV SHEPHERD.
 PA (BIOS-) BIOSYNEXUS INC.
 XX
 PI Foster S, Mond J, Clarke S, McDowell P, Brummel K;
 XX
 DR WPI; 2003-256434/25.
 XX
 PT New antigenic polypeptides from Staphylococcus aureus or S. epidermidis,
 PT useful as a vaccine for immunizing humans against e.g. bacteraemia, septic
 PT shock, septicemia, tuberculosis, meningitis, pneumonia, gonorrhoea or
 PT impetigo.
 XX
 PS Claim 4; Page 124-125; 189pp; English.
 XX
 CC The present invention describes an antigenic protein or its part, which
 CC is for use as a vaccine. The antigenic protein is encoded by an isolated
 CC DNA molecule of Staphylococcus aureus or S. epidermidis partial gene
 CC sequences (designated dnaSA and dna SE, respectively; and which encodes a
 CC protein expressed by a pathogenic organism. Also described: (1) a vaccine
 CC composition comprising at least one antigenic protein; (2) a method of
 CC immunising an animal against a disease or condition caused by a
 CC pathogenic microbe by administering the antigenic protein or the vaccine;
 CC (3) an antibody or its binding part obtainable by the method above; (4)
 CC preparing a hybridoma cell line producing monoclonal antibodies; (5) a
 CC hybridoma cell line produced by the method of (4); and (6) identifying
 CC opsonic antigens expressed by a pathogenic microbe. The antigenic
 CC proteins have antibacterial, neuroprotective, immunosuppressive,
 CC antiinflammatory, antitumor, immunostimulant and ophthalmological
 CC activities, and can be used in vaccines. The antigenic proteins or
 CC vaccines can be used for immunising an animal (specifically a human)
 CC against a disease or condition caused by a pathogenic microbe, e.g.
 CC bacteraemia, septic shock, organ infection, skin infection, bacterial
 CC basal colonisation, bacterial eye infections, septicemia, tuberculosis,
 CC bacteria-associated food poisoning, blood infections, peritonitis,
 CC endocarditis, sepsis, meningitis, pneumonia, stomach ulcers, gonorrhoea,
 CC strep throat, streptococcal-associated toxic shock, necrotising
 CC fasciitis, impetigo, histoplasmosis, Lyme disease, gastro-enteritis,
 CC dysentery, shigellosis, S. aureus-associated septicemia, food-poisoning,
 CC skin disorders, S. epidermidis-associated septicemia, peritonitis or
 CC endocarditis. The present sequence represents a S. aureus antigenic
 CC protein sequence from the present invention.

SQ Sequence 948 AA;
 Query Match 85.7%; Score 90; DB 6; Length 948;
 Best Local Similarity 89.5%; Pred No. 0.001;
 Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 GONEGQQTPEEDTTPPIV 19
 | | | | | | | | | | | | | | | | | | | | | |
 Db 804 GHNEGQQTIEDTTPPIV 822

Search completed: October 25, 2005, 20:21:09
 Job time : 42.9663 secs

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OM protein - protein search, using SW model

Run on: October 22, 2005, 03:51:22 ; Search time 10.5862 Seconds
(without alignments)
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Title: US-10-731-238-53

Sequence: 1 GONEGQGTPEEDTTPPIV 19

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Total number of hits satisfying chosen parameters: 513545

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Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	95	90.5	19	4	US-09-010-317-11 Sequence 11, Appl
3	95	90.5	178	2	US-08-459-155A-12 Sequence 12, Appl
4	95	90.5	178	3	US-08-495-559-12 Sequence 12, Appl
5	95	90.5	1027	4	US-08-956-171E-5254 Sequence 5254, Ap
6	95	90.5	1027	4	US-08-781-986A-5254 Sequence 5254, Ap
7	90	85.7	174	2	US-08-459-135A-13 Sequence 13, Appl
8	90	85.7	174	2	US-08-459-559-13 Sequence 13, Appl
9	90	85.7	559	4	US-08-956-171E-5251 Sequence 5251, Ap
10	89	84.8	19	4	US-09-010-317-12 Sequence 12, Appl
11	89	84.8	19	4	US-09-010-317-51 Sequence 51, Appl
12	88	83.8	19	4	US-09-010-317-52 Sequence 52, Appl
13	88	83.8	174	2	US-08-459-155A-10 Sequence 10, Appl
14	79	75.2	174	3	US-08-495-559-10 Sequence 10, Appl
15	79	75.2	176	3	US-08-495-559-6 Sequence 6, Appl
16	79	75.2	181	2	US-08-459-135A-6 Sequence 6, Appl
17	79	75.2	181	2	US-08-459-135A-6 Sequence 6, Appl
18	68	64.8	130	2	US-08-495-559-8 Sequence 8, Appl
19	68	64.8	130	3	US-08-459-135A-7 Sequence 7, Appl
20	61	58.1	130	2	US-08-495-559-7 Sequence 7, Appl
21	61	58.1	130	3	US-08-495-559-7 Sequence 7, Appl
22	56	53.3	205	4	US-09-270-767-43520 Sequence 43520, A
23	52	49.5	38	4	US-09-010-317-45 Sequence 35, Appl
24	51	48.6	38	4	US-09-010-317-35 Sequence 35, Appl
25	47	44.8	38	1	US-08-729-767-4 Sequence 3, Appl
26	47	44.8	114	1	US-08-259-000-3 Sequence 3, Appl
27	47	44.8	139	3	US-08-856-253-8 Sequence 8, Appl

28	47	44.8	412	2	US-08-741-134-2 Sequence 2, Appl
29	47	44.8	847	4	US-09-949-016-11002 Sequence 11002, A
30	46	43.8	38	1	US-08-729-767-3 Sequence 3, Appl
31	46	43.8	38	4	US-09-010-317-41 Sequence 41, Appl
32	45.5	43.3	630	4	US-09-602-787A-548 Sequence 548, App
33	45	42.9	38	4	US-09-010-317-42 Sequence 42, Appl
34	45	42.9	141	4	US-09-828-995B-29 Sequence 29, Appl
35	45	42.9	150	4	US-09-270-767-32833 Sequence 32833, A
36	45	42.9	150	4	US-09-270-767-48050 Sequence 48050, A
37	45	42.9	200	4	US-09-248-796A-27101 Sequence 27101, A
38	45	42.9	215	4	US-10-101-464A-483 Sequence 483, App
39	45	42.9	334	2	US-08-646-981-16 Sequence 16, Appl
40	45	42.9	375	4	US-09-828-995B-32 Sequence 32, Appl
41	45	42.9	473	4	US-09-828-995B-20 Sequence 20, Appl
42	45	42.9	565	4	US-09-828-995B-75 Sequence 75, Appl
43	45	42.9	1109	4	US-09-949-016-10771 Sequence 10771, A
44	45	42.9	1203	4	US-09-949-016-6615 Sequence 6615, Ap
45	44	41.9	134	4	US-09-328-352-4247 Sequence 4247, Ap

ALIGNMENTS

RESULT 1
US-09-010-317-53
Sequence 53, Application US/09010317
Patent No. 6685943
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
APPLICANT: Patti, Joseph M.
APPLICANT: House-Pompeo, Karen L.
APPLICANT: Speziale, Pietro
APPLICANT: John, Danny
APPLICANT: McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
TITLE OF INVENTION: AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAMK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-5000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 53:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-09-010-317-53
Query Match 100.0%; Score 105; DB 4; Length 19;
Best Local Similarity 100.0%; Pred. No. 7.8e-08;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GONEGQOTPEEDTTPPIV 19
 |||||
 DB 1 GONEGQOTPEEDTTPPIV 19

RESULT 2

US-09-010-317-11
 ; Sequence 11, Application US/09010317
 ; Patent No. 6685943
 ; GENERAL INFORMATION:
 ; APPLICANT: Hook, Magnus
 ; APPLICANT: Patli, Joseph M.
 ; APPLICANT: House-Pompeo, Karen L.
 ; APPLICANT: Speziale, Pietro
 ; APPLICANT: Joh, Danny
 ; APPLICANT: McGavin, Martin J.
 ; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
 ; TITLE OF INVENTION: AND METHODS OF USE
 ; NUMBER OF SEQUENCES: 105
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Arnold, White & Durkee
 ; STREET: P.O. Box 4433
 ; CITY: Houston
 ; STATE: TX
 ; COUNTRY: USA
 ; ZIP: 77210-4433
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patentin Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/010,317
 ; FILING DATE:
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 60/036,139
 ; FILING DATE: 21-JAN-1997
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Hibler, David W.
 ; REGISTRATION NUMBER: 41,071
 ; REFERENCE/DOCKET NUMBER: TAMK:189
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 512-418-3000
 ; TELEFAX: 512-474-7577
 ; INFORMATION FOR SEQ ID NO: 11:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 19 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS:
 ; TOPOLOGY: linear
 ; US-09-010-317-11

Query Match 90.5%; Score 95; DB 4; Length 19;
 Best Local Similarity 94.7%; Pred. No. 1,7e-06;
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GONEGQOTPEEDTTPPIV 19
 |||||
 DB 1 GONEGQOTPEEDTTPPIV 19

RESULT 3

US-08-459-135A-12
 ; Sequence 12, Application US/08459135A
 ; Patent No. 5955078
 ; GENERAL INFORMATION:
 ; APPLICANT: BURHAM, Martin Karl Russel
 ; APPLICANT: CHOPRA, Ian
 ; APPLICANT: CRITCHLEY, Ian Alfred
 ; APPLICANT: KNOWLES, David Justin Charles

; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN: MONOCLONAL ANTIBODY AND THEIR US

; NUMBER OF SEQUENCES: 15

; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: SmithKline Beecham Corporation

; STREET: 709 Swedeland Road
 ; CITY: King of Prussia

; STATE: PA

; COUNTRY: U.S.A.

; ZIP: 19406-0939

; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: DOS

; SOFTWARE: Fastseq, Version 2.0

; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/459,135A

; FILING DATE: 02-JUN-1995

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: PCT/GB/94/00215

; FILING DATE: 04-Feb-1994

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:
 ; NAME: Gimm, Edward R

; REGISTRATION NUMBER: 38,891

; REFERENCE/DOCKET NUMBER: P30591C2

; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 610-270-4478

; TELEFAX: 610-270-5090

; TELEX:
 ; INFORMATION FOR SEQ ID NO: 12:

; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 178 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: Protein

US-08-459-135A-12

Query Match 90.5%; Score 95; DB 2; Length 178;
 Best Local Similarity 94.7%; Pred. No. 1.6e-05;
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GONEGQOTPEEDTTPPIV 19
 |||||
 DB 116 GONEGQOTPEEDTTPPIV 134

RESULT 4

US-08-495-559-12
 ; Sequence 12, Application US/08495559A
 ; Patent No. 6054572
 ; GENERAL INFORMATION:
 ; APPLICANT: BURHAM, Martin Karl Russel
 ; APPLICANT: CHOPRA, Ian
 ; APPLICANT: CRITCHLEY, Ian Alfred
 ; APPLICANT: KNOWLES, David Justin Charles
 ; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN: MONOCLONAL
 ; TITLE OF INVENTION: ANTIBODY AND THEIR USE IN PREVENTING BACTERIAL ADHESION
 ; FILE REFERENCE: P30591
 ; CURRENT APPLICATION NUMBER: US/08/495,559A
 ; CURRENT FILING DATE: 1995-08-03
 ; EARLIER APPLICATION NUMBER: GB 9302289.5
 ; EARLIER FILING DATE: 1993-02-05
 ; EARLIER APPLICATION NUMBER: GB 9321592.9
 ; EARLIER FILING DATE: 1993-10-20
 ; NUMBER OF SEQ ID NOS: 13
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 12
 ; LENGTH: 178
 ; TYPE: PRT
 ; ORGANISM: Staphylococcus aureus
 ; US-08-495-559-12

Query Match 90.5%; Score 95; DB 3; Length 178;
Best Local Similarity 94.7%; Pred. No. 1.6e-05;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GONEGQOTPEEDTTPPIVP 19
|||||
DB 116 GONEGQOTPEEDTTPPIVP 134

RESULT 5

US-08-956-171E-5254
; Sequence 5254, Application US/08956171E
; Patent No. 6593114
; GENERAL INFORMATION:
; APPLICANT: Charles Kunsch

Patent No. 6737248
; APPLICANT: Charles Kunsch
; TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
; NUMBER OF SEQUENCES: 5255
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA

ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/956,171E
; FILING DATE: 20-Oct-1997
; CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/009,861
; FILING DATE: January 5, 1996
; APPLICATION NUMBER: 08/781,986
; FILING DATE: January 3, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Mark J. Hyman
; REGISTRATION NUMBER: 46,789
; REFERENCE/DOCKET NUMBER: PB248P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (240) 314-1224
; TELEFAX: (301) 309-8439

INFORMATION FOR SEQ ID NO: 5254:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1027 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 5254:
US-08-956-171E-5254

Query Match 90.5%; Score 95; DB 4; Length 1027;
Best Local Similarity 94.7%; Pred. No. 9.7e-05;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GONEGQOTPEEDTTPPIVP 19
|||||
DB 869 GONEGQOTPEEDTTPPIVP 887

US-08-459-135A-13
; Sequence 13, Application US/08459135A
; Patent No. 5955078
; GENERAL INFORMATION:
; APPLICANT: BURHAM, Martin Karl Russel
; APPLICANT: CHOPRA, Ian
; APPLICANT: CRITCHLEY, Ian Alfred
; APPLICANT: KNOWLES, David Justin Charles
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN: MONOCLONAL ANTIBODY AND THEIR US

NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corporation
; STREET: 709 Swedeland Road
; CITY: King of Prussia
; STATE: PA
; COUNTRY: U.S.A.
; ZIP: 19406-0939
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: Fastseq, Version 2.0
; CURRENT APPLICATION DATA:

Query Match 90.5%; Score 95; DB 3; Length 178;
Best Local Similarity 94.7%; Pred. No. 1.6e-05;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GONEGQOTPEEDTTPPIVP 19
|||||
DB 869 GONEGQOTPEEDTTPPIVP 887

US-08-956-171E-5254
; Sequence 5254, Application US/08781986A

Query Match 90.5%; Score 95; DB 4; Length 1027;
Best Local Similarity 94.7%; Pred. No. 9.7e-05;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GONEGQOTPEEDTTPPIVP 19
|||||
DB 869 GONEGQOTPEEDTTPPIVP 887

RESULT 6
US-08-781-986A-5254
; Sequence 5254, Application US/08781986A

Patent No. 6737248
; GENERAL INFORMATION:
; APPLICANT: Charles Kunsch
; TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
; NUMBER OF SEQUENCES: 5255
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA

ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/781,986A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Benson, Bob
; REGISTRATION NUMBER: 30,446
; REFERENCE/DOCKET NUMBER: PB248PP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512

INFORMATION FOR SEQ ID NO: 5254:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1027 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-781-986A-5254

Query Match 90.5%; Score 95; DB 4; Length 1027;
Best Local Similarity 94.7%; Pred. No. 9.7e-05;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GONEGQOTPEEDTTPPIVP 19
|||||
DB 869 GONEGQOTPEEDTTPPIVP 887

US-08-459-135A-13
; Sequence 13, Application US/08459135A
; Patent No. 5955078
; GENERAL INFORMATION:
; APPLICANT: BURHAM, Martin Karl Russel
; APPLICANT: CHOPRA, Ian
; APPLICANT: CRITCHLEY, Ian Alfred
; APPLICANT: KNOWLES, David Justin Charles
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN: MONOCLONAL ANTIBODY AND THEIR US

NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corporation
; STREET: 709 Swedeland Road
; CITY: King of Prussia
; STATE: PA
; COUNTRY: U.S.A.
; ZIP: 19406-0939
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: Fastseq, Version 2.0
; CURRENT APPLICATION DATA:

Query Match 90.5%; Score 95; DB 3; Length 178;
Best Local Similarity 94.7%; Pred. No. 1.6e-05;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GONEGQOTPEEDTTPPIVP 19
|||||
DB 869 GONEGQOTPEEDTTPPIVP 887

US-08-956-171E-5254
; Sequence 5254, Application US/08781986A

Query Match 90.5%; Score 95; DB 4; Length 1027;
Best Local Similarity 94.7%; Pred. No. 9.7e-05;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GONEGQOTPEEDTTPPIVP 19
|||||
DB 869 GONEGQOTPEEDTTPPIVP 887

US-08-781-986A-5254
; Sequence 5254, Application US/08781986A

Query Match 90.5%; Score 95; DB 3; Length 178;
Best Local Similarity 94.7%; Pred. No. 1.6e-05;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GONEGQOTPEEDTTPPIVP 19
|||||
DB 869 GONEGQOTPEEDTTPPIVP 887

US-08-956-171E-5254
; Sequence 5254, Application US/08956171E

Query Match 90.5%; Score 95; DB 4; Length 1027;
Best Local Similarity 94.7%; Pred. No. 9.7e-05;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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; APPLICATION NUMBER: US/08/459,135A
; FILING DATE: 02-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB/94/00215
; FILING DATE: 04-Feb-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Gimmil, Edward R.
; REGISTRATION NUMBER: 38,891
; REFERENCE/DOCKET NUMBER: P30591C2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-270-4478
; TELEFAX: 610-270-5090
; TELEX:
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 174 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-459-135A-13

Query Match      85.7%; Score 90; DB 2; Length 174;
Best Local Similarity 89.5%; Pred. No. 7.4e-05;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 GONEGQQTPEEDTTPPIVP 19
Db      116 GHNEGQQTIEDTTPPIVP 134

RESULT 8
; US-08-495-559-13
; Sequence 13, Application US/08495559A
; Patent No. 6054572
; GENERAL INFORMATION:
; APPLICANT: BURNAM, Martin Karl Russel
; APPLICANT: CHOPRA, Ian
; APPLICANT: CRITCHLEY, Ian Alfred
; APPLICANT: KNOWLES, David Justin Charles
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN: MONOCLONAL
; TITLE OF INVENTION: ANTIBODY AND THEIR USE IN PREVENTING BACTERIAL ADHESION
; FILE REFERENCE: P30591
; CURRENT APPLICATION NUMBER: US/08/495,559A
; CURRENT FILING DATE: 1995-08-03
; EARLIER APPLICATION NUMBER: GB 9302289.5
; EARLIER FILING DATE: 1993-02-05
; EARLIER APPLICATION NUMBER: GB 9321592.9
; EARLIER FILING DATE: 1993-10-20
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 13
; LENGTH: 174
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
; US-08-495-559-13

Query Match      85.7%; Score 90; DB 3; Length 174;
Best Local Similarity 89.5%; Pred. No. 7.4e-05;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 GONEGQQTPEEDTTPPIVP 19
Db      116 GHNEGQQTIEDTTPPIVP 134

RESULT 9
; US-08-956-171E-5251
; Sequence 5251, Application US/08956171E
; Patent No. 6593114
; GENERAL INFORMATION:
```

```

; APPLICANT: Charles Kunsch
;           Gil H. Choi
;           Patrick S. Dillon
;           Craig A. Rosen
;           Steven C. Barash
;           Michael R. Fannon
; TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
; NUMBER OF SEQUENCES: 5256
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/956,171E
; FILING DATE: 20-Oct-1997
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/009,861
; FILING DATE: January 5, 1996
; APPLICATION NUMBER: 08/781,986
; FILING DATE: January 3, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Mark J. Hyman
; REGISTRATION NUMBER: 46,789
; REFERENCE/DOCKET NUMBER: PB248P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (240) 314-1224
; TELEFAX: (301) 309-8439
; INFORMATION FOR SEQ ID NO: 5251:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 559 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 5251:
; US-08-956-171E-5251

Query Match      85.7%; Score 90; DB 4; Length 559;
Best Local Similarity 89.5%; Pred. No. 0.00024;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 GONEGQQTPEEDTTPPIVP 19
Db      415 GHNEGQQTIEDTTPPIVP 433

RESULT 10
; US-08-781-986A-5251
; Sequence 5251, Application US/08781986A
; Patent No. 6737248
; GENERAL INFORMATION:
; APPLICANT: Charles Kunsch
; TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
; NUMBER OF SEQUENCES: 5255
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
; COMPUTER: HP Vectra 486/33
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OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/781,986A
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Benson, Bob
REGISTRATION NUMBER: 30,446
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 5251:
SEQUENCE CHARACTERISTICS:
LENGTH: 559 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-781-986A-5251

Query Match 85.7%; Score 90; DB 4; Length 559;
Best Local Similarity 89.5%; Pred. No. 0.00024;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GONEGQOTPEEDTTPPIV 19
DB 415 GHNEGQOTIEEDTTPPIV 433

RESULT 11
US-09-010-317-12
Sequence 12, Application US/09010317
Patent No. 6685943
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
APPLICANT: Patti, Joseph M.
APPLICANT: House-Pompeo, Karen L.
APPLICANT: Speziale, Pietro
APPLICANT: McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
TITLE OF INVENTION: AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hilder, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAMK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000

TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-09-010-317-12

Query Match 84.8%; Score 89; DB 4; Length 19;
Best Local Similarity 89.5%; Pred. No. 1.1e-05;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GONEGQOTPEEDTTPPIV 19
DB 1 GONEGQOTIEEDTTPPIV 19

RESULT 12
US-09-010-317-51
Sequence 51, Application US/09010317
Patent No. 6685943
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
APPLICANT: Patti, Joseph M.
APPLICANT: House-Pompeo, Karen L.
APPLICANT: Speziale, Pietro
APPLICANT: McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
TITLE OF INVENTION: AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hilder, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAMK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 51:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-09-010-317-51

Query Match 84.8%; Score 89; DB 4; Length 19;
Best Local Similarity 89.5%; Pred. No. 1.1e-05;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GONEGQOTPEEDTTPPIV 19
DB 1 GONEGQOTIEEDTTPPIV 19

RESULT 13
US-09-010-317-52
Sequence 52, Application US/09010317
Patent No. 6685943
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
APPLICANT: Patti, Joseph M.
APPLICANT: House-Pompeo, Karen L.
APPLICANT: Speziale, Pietro
APPLICANT: Joh, Danny
APPLICANT: Mcgavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAMK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 52:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-09-010-317-52

Query Match 83.8%; Score 88; DB 4; Length 19;
Best Local Similarity 89.5%; Pred. No. 1,4e-05;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GONEGQOTPEEDTTPPIV 19
DB 1 GONEGQOTIEBPTTPPIV 19

RESULT 14
US-08-459-135A-10
Sequence 10, Application US/08459135A
Patent No. 5955078
GENERAL INFORMATION:
APPLICANT: BURHAM, Martin Karl Russel
APPLICANT: CHOPRA, Ian
APPLICANT: CRITCHLEY, Ian Alfred
APPLICANT: KNOWLES, David Justin Charles
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN: MONOCLONAL ANTIBODY AND THEIR US
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road

CITY: King of Prussia
STATE: PA
COUNTRY: U.S.A.
ZIP: 19406-0939
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: Fastseq, Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/459,135A
FILING DATE: 02-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB/94/00215
FILING DATE: 04-Feb-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Gimm, Edward R
REGISTRATION NUMBER: 38,891
REFERENCE/DOCKET NUMBER: P30591C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-4478
TELEFAX: 610-270-5090
TELEX:
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 174 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: Protein
US-08-459-135A-10

Query Match 75.2%; Score 79; DB 2; Length 174;
Best Local Similarity 78.9%; Pred. No. 0.0022;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GONEGQOTPEEDTTPPIV 19
DB 116 GNEGQOTIEBPTTPPP 134

RESULT 15
US-08-495-559-10
Sequence 10, Application US/08495559A
Patent No. 6054572
GENERAL INFORMATION:
APPLICANT: BURHAM, Martin Karl Russel
APPLICANT: CHOPRA, Ian
APPLICANT: CRITCHLEY, Ian Alfred
APPLICANT: KNOWLES, David Justin Charles
TITLE OF INVENTION: ANTIBODY AND THEIR USE IN PREVENTING BACTERIAL ADHESION
FILE REFERENCE: P30591
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/495,559A
FILING DATE: 1995-08-03
EARLIER APPLICATION NUMBER: GB 9302289.5
EARLIER FILING DATE: 1993-02-05
EARLIER APPLICATION NUMBER: GB 9321592.9
EARLIER FILING DATE: 1993-10-20
NUMBER OF SEQ ID NOS: 13
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 10
LENGTH: 174
TYPE: PRT
ORGANISM: Staphylococcus aureus
US-08-495-559-10

Query Match 75.2%; Score 79; DB 3; Length 174;
Best Local Similarity 78.9%; Pred. No. 0.0022;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GONEGQOTPEEDTTPPIV 19

Wed Oct 26 15:02:38 2005

us-10-731-238-53.ral

Page 7

Db 116 GHNEGQOTIEEDTTPTPP 134

Search completed: October 22, 2005, 05:46:50
Job time : 11.6362 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 22, 2005, 11:35:03 ; Search time 35.0628 Seconds
(without alignments)
226.232 Million cell updates/sec

Title: US-10-731-238-53

Perfect score: 105

Sequence: 1 GQNEGGQQTPEEDTTPPIV 19

Scoring table: BLOSUM62

Searched: 1862951 seqs, 417491010 residues

Total number of hits satisfying chosen parameters: 1862951

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database: Published Applications AA:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	105	100.0	19	US-10-731-238-53	Sequence 53, Appl
2	95	90.5	19	US-10-731-238-11	Sequence 51, Appl
3	95	90.5	1018	US-09-815-242-5797	Sequence 5797, Ap
4	95	90.5	1018	US-09-815-242-12838	Sequence 12838, A
5	95	90.5	1018	US-10-470-0488-68	Sequence 68, Appl
6	95	90.5	1027	US-08-781-986A-5254	Sequence 5254, Ap
7	95	90.5	1027	US-10-329-624-5254	Sequence 5254, Ap
8	90	85.7	559	US-08-781-986A-5251	Sequence 5251, Ap
9	90	85.7	559	US-10-329-624-5251	Sequence 5251, Ap
10	90	85.7	940	US-10-470-0488-424	Sequence 424, Appl
11	90	85.7	948	US-10-470-0488-69	Sequence 69, Appl

12	89	84.8	19	US-10-731-238-12	Sequence 12, Appl
13	88	84.8 <td>19</td> <td>US-10-731-238-51</td> <td>Sequence 51, Appl</td>	19	US-10-731-238-51	Sequence 51, Appl
14	88	83.8 <td>19</td> <td>US-10-731-238-52</td> <td>Sequence 52, Appl</td>	19	US-10-731-238-52	Sequence 52, Appl
15	84	80.0 <td>961</td> <td>US-10-282-122A-43778</td> <td>Sequence 43778, A</td>	961	US-10-282-122A-43778	Sequence 43778, A
16	84	80.0 <td>978</td> <td>US-09-815-242-5456</td> <td>Sequence 5456, Ap</td>	978	US-09-815-242-5456	Sequence 5456, Ap
17	84	80.0 <td>1001</td> <td>US-09-815-242-12686</td> <td>Sequence 12686, A</td>	1001	US-09-815-242-12686	Sequence 12686, A
18	84	80.0 <td>1038</td> <td>US-10-282-122A-43827</td> <td>Sequence 43827, A</td>	1038	US-10-282-122A-43827	Sequence 43827, A
19	84	80.0 <td>1038</td> <td>US-11-097-143-15726</td> <td>Sequence 15726, A</td>	1038	US-11-097-143-15726	Sequence 15726, A
20	56	53.3	336	US-11-097-143-30612	Sequence 30612, A
21	54	51.4	336	US-10-731-238-45	Sequence 45, Appl
22	52	49.5	38	US-10-731-238-35	Sequence 35, Appl
23	50.5	48.1	1449	US-10-402-089-8	Sequence 8, Appl1
24	50.5	48.1	1449	US-10-402-072A-8	Sequence 8, Appl1
25	50	47.6	218	US-10-450-763-38821	Sequence 38821, A
26	50	47.6	661	US-10-450-763-38822	Sequence 38822, A
27	50	47.6	1042	US-10-473-576-10	Sequence 10, Appl
28	50	47.6	1463	US-10-402-089-2	Sequence 2, Appl1
29	50	47.6	1463	US-10-402-072A-2	Sequence 2, Appl1
30	49	46.7	168	US-10-108-260A-4405	Sequence 4405, Ap
31	49	46.7	419	US-10-104-047-3514	Sequence 3514, Ap
32	49	46.7	752	US-09-764-853-641	Sequence 641, Appl
33	49	46.7	776	US-10-367-057-2	Sequence 2, Appl1
34	48	45.7	114	US-10-425-115-349268	Sequence 349268, A
35	48	45.7	319	US-10-425-114-72305	Sequence 72305, A
36	48	45.7	495	US-10-425-115-364526	Sequence 364526, A
37	48	45.7	1520	US-10-437-963-150499	Sequence 150499, A
38	47	44.8	139	US-09-813-820-8	Sequence 8, Appl1
39	47	44.8	253	US-10-485-710-111	Sequence 111, Appl
40	47	44.8	495	US-10-198-070-48	Sequence 48, Appl
41	47	44.8	495	US-10-408-765A-1628	Sequence 1628, Ap
42	47	44.8	563	US-11-097-143-5277	Sequence 5277, Ap
43	47	44.8	772	US-10-450-763-31797	Sequence 31797, A
44	47	44.8	833	US-10-303-683-17	Sequence 17, Appl
45	47	44.8	836	US-10-425-114-39187	Sequence 39187, A

ALIGNMENTS

RESULT 1
US-10-731-238-53
Sequence 53, Application US/10731238
Publication No. US20050123552A1
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
Patel, Joseph M.
House-Pompeo, Karen L.
Speziale, Pietro
Joh, Danny
McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/731.238
FILING DATE: 10-Dec-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/010.317
FILING DATE: 21-Jan-1998
APPLICATION NUMBER: US 60/036.139


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; FILING DATE: 21-JAN-1997
; ATTORNEY/AGENT INFORMATION:
;   NAME: Hibler, David W.
;   REGISTRATION NUMBER: 41,071
;   REFERENCE/DOCKET NUMBER: TAMK:189
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE: 512-418-3000
;     TELEFAX: 512-474-7577
; INFORMATION FOR SEQ ID NO: 53:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH: 19 amino acids
;     TYPE: amino acid
;     STRANDEDNESS: <Unknown>
;   TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 53:
US-10-731-238-53

Query Match      100.0%; Score 105; DB 18; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.7e-07;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GONEGQQTPEEDTTPPIVP 19
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DB      1 GONEGQQTPEEDTTPPIVP 19

RESULT 2
US-10-731-238-11
; Sequence 11, Application US/10731238
; Publication No. US20050123552A1
; GENERAL INFORMATION:
;   APPLICANT: Hook, Magnus
;             Patti, Joseph M.
;             House-Pompeo, Karen L.
;             Speziale, Pietro
;             Job, Danny
;             McGavin, Martin J.
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
; AND METHODS OF USE
; NUMBER OF SEQUENCES: 105
; CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Arnold, White & Durkee
;   STREET: P.O. Box 4433
;   CITY: Houston
;   STATE: TX
;   COUNTRY: USA
;   ZIP: 77210-4433
; COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/10/731,238
;   FILING DATE: 10-Dec-2003
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US/09/010,317
;   FILING DATE: 21-Jan-1998
;   APPLICATION NUMBER: US 60/036,139
;   FILING DATE: 21-JAN-1997
; ATTORNEY/AGENT INFORMATION:
;   NAME: Hibler, David W.
;   REGISTRATION NUMBER: 41,071
;   REFERENCE/DOCKET NUMBER: TAMK:189
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE: 512-418-3000
;     TELEFAX: 512-474-7577
; INFORMATION FOR SEQ ID NO: 11:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH: 19 amino acids
;     TYPE: amino acid
;     STRANDEDNESS: <Unknown>

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; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 11:
US-10-731-238-11

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Best Local Similarity 94.7%; Pred. No. 6e-06;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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DB      1 GONEGQQTPEEDTTPPIVP 19

RESULT 3
US-09-815-242-5797
; Sequence 5797, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
;   APPLICANT: Haselbeck, Robert
;             Ohlsen, Karl L.
;             Zyskind, Judith W.
;             Wall, Daniel
;             Trawick, John D.
;             Carr, Grant J.
;             Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; Prokaryotes
; FILE REFERENCE: ELITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5797
; LENGTH: 1018
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-09-815-242-5797

Query Match      90.5%; Score 95; DB 9; Length 1018;
Best Local Similarity 94.7%; Pred. No. 0.0004;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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      |||||
DB      860 GONEGQQTPEEDTTPPIVP 878

RESULT 4
US-09-815-242-12838
; Sequence 12838, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
;   APPLICANT: Haselbeck, Robert
;             Ohlsen, Karl L.
;             Zyskind, Judith W.
;             Wall, Daniel
;             Trawick, John D.
;             Carr, Grant J.

```

```

; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; FILE REFERENCE: ELITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12838
; LENGTH: 1018
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-09-815-242-12838

Query Match          90.5%; Score 95; DB 9; Length 1018;
Best Local Similarity 94.7%; Pred. No. 0.0004;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GONEGOOTPEEDTTPPIV 19
Db 860 GONEGOOTIEEDTTPPIV 878

RESULT 5
US-10-470-048B-68
; Sequence 68, Application US/10470048B
; Publication No. US20050037444A1
; GENERAL INFORMATION:
; APPLICANT: MEINKE ET AL.
; TITLE OF INVENTION: A METHOD FOR IDENTIFICATION, ISOLATION AND PRODUCTION OF
; FILE REFERENCE: SONN.035US
; CURRENT APPLICATION NUMBER: US/10/470,048B
; CURRENT FILING DATE: 2003-07-25
; NUMBER OF SEQ ID NOS: 603
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 68
; LENGTH: 1018
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-10-470-048B-68

Query Match          90.5%; Score 95; DB 17; Length 1018;
Best Local Similarity 94.7%; Pred. No. 0.0004;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GONEGOOTPEEDTTPPIV 19
Db 860 GONEGOOTIEEDTTPPIV 878

RESULT 6
US-08-781-986A-5254
; Sequence 5254, Application US/08781986A
; Publication No. US20030054436A1
; GENERAL INFORMATION:
; APPLICANT: Charles Kunsch
; TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences

```

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; NUMBER OF SEQUENCES: 5255
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4mb storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/781,986A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Benson, Bob
; REGISTRATION NUMBER: 30,446
; REFERENCE/DOCKET NUMBER: PB248PP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 5254:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1027 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-781-986A-5254

Query Match          90.5%; Score 95; DB 8; Length 1027;
Best Local Similarity 94.7%; Pred. No. 0.0004;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GONEGOOTPEEDTTPPIV 19
Db 869 GONEGOOTIEEDTTPPIV 887

RESULT 7
US-10-329-624-5254
; Sequence 5254, Application US/10329624
; Publication No. US20040043037A1
; GENERAL INFORMATION:
; APPLICANT: Charles Kunsch
; Gil H. Choi
; Patrick S. Dillon
; Craig A. Rosen
; Steven C. Barash
; Michael R. Fannon
; TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
; NUMBER OF SEQUENCES: 5256
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4mb storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/329,624
; FILING DATE: 27-Dec-2002

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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/956,171
FILING DATE: October 20, 1997
APPLICATION NUMBER: 60/009,861
FILING DATE: January 5, 1996
APPLICATION NUMBER: 08/781,986
FILING DATE: January 3, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Mark J. Hyman
REGISTRATION NUMBER: 46,789
REFERENCE/DOCKET NUMBER: PB248P1D1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (240) 314-1224
TELEFAX: (301) 309-8439
INFORMATION FOR SEQ ID NO: 5254:
SEQUENCE CHARACTERISTICS:
LENGTH: 1027 amino acids
TYPE: amino acid
STRANDEDNESS: single
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 5254:
US-10-329-624-5254
Query Match 90.5%; Score 95; DB 15; Length 1027;
Best Local Similarity 94.7%; Pred. No. 0.0004;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 GONEGQQTPEEDTTPPIVP 19
DB 869 GONEGQQTPEEDTTPPIVP 897
RESULT 8
US-08-781-986A-5251
Sequence 5251, Application US/08781986A
Publication No. US20030054436A1
GENERAL INFORMATION:
APPLICANT: Charles Kunesh
TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
NUMBER OF SEQUENCES: 5255
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COUNTRY: USA
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/781,986A
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Benson, Bob
REGISTRATION NUMBER: 30,446
REFERENCE/DOCKET NUMBER: PB248PP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 5251:
SEQUENCE CHARACTERISTICS:
LENGTH: 559 amino acids
TYPE: amino acid
STRANDEDNESS: single
MOLECULE TYPE: protein
TOPOLOGY: linear

MOLECULE TYPE: protein
US-08-781-986A-5251
Query Match 85.7%; Score 90; DB 8; Length 559;
Best Local Similarity 89.5%; Pred. No. 0.00099;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 GONEGQQTPEEDTTPPIVP 19
DB 415 GNEGQQTPEEDTTPPIVP 433
RESULT 9
US-10-329-624-5251
Sequence 5251, Application US/10329624
Publication No. US20040043037A1
GENERAL INFORMATION:
APPLICANT: Charles Kunesh
Gail H. Choi
Patrick S. Dillon
Craig A. Rosen
Steven C. Barash
Michael R. Fannon
TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
NUMBER OF SEQUENCES: 5256
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COUNTRY: USA
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/329,624
FILING DATE: 27-Dec-2002
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/956,171
FILING DATE: October 20, 1997
APPLICATION NUMBER: 60/009,861
FILING DATE: January 5, 1996
APPLICATION NUMBER: 08/781,986
FILING DATE: January 3, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Mark J. Hyman
REGISTRATION NUMBER: 46,789
REFERENCE/DOCKET NUMBER: PB248P1D1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (240) 314-1224
TELEFAX: (301) 309-8439
INFORMATION FOR SEQ ID NO: 5251:
SEQUENCE CHARACTERISTICS:
LENGTH: 559 amino acids
TYPE: amino acid
STRANDEDNESS: single
MOLECULE TYPE: protein
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 5251:
US-10-329-624-5251
Query Match 85.7%; Score 90; DB 15; Length 559;
Best Local Similarity 89.5%; Pred. No. 0.00099;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 GONEGQQTPEEDTTPPIVP 19
DB 415 GNEGQQTPEEDTTPPIVP 433


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;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/010,317
; FILING DATE: 21-Jan-1998
; APPLICATION NUMBER: US 60/036,139
; FILING DATE: 21-JAN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Hibler, David W.
; REGISTRATION NUMBER: 41,071
; REFERENCE/DOCKET NUMBER: TAMK:189
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 512-418-3000
; TELEFAX: 512-474-7577
; INFORMATION FOR SEQ ID NO: 51:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 19 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 51:
US-10-731-238-51

Query Match      84.8%; Score 89; DB 18; Length 19;
Best Local Similarity 89.5%; Pred. No. 3.8e-05;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 GONEGQOTPEEDTTPPIVP 19
DB      1 GONEGQOTPEEDTTPPIVP 19

RESULT 14
US-10-731-238-52
; Sequence 52, Application US/10731238
; Publication No. US20050123552A1
; GENERAL INFORMATION:
; APPLICANT: Hook, Magnus
;             Patti, Joseph M.
;             House-Pompeo, Karen L.
;             Speziale, Pietro
;             John, Danny
;             McGavin, Martin J.
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
; NUMBER OF SEQUENCES: 105
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: TX
; COUNTRY: USA
; ZIP: 77210-4433
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/731,238
; FILING DATE: 10-Dec-2003
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/010,317
; FILING DATE: 21-Jan-1998
; APPLICATION NUMBER: US 60/036,139
; FILING DATE: 21-JAN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Hibler, David W.
; REGISTRATION NUMBER: 41,071
; REFERENCE/DOCKET NUMBER: TAMK:189
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 512-418-3000
; TELEFAX: 512-474-7577
; INFORMATION FOR SEQ ID NO: 52:
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```

;
; SEQUENCE CHARACTERISTICS:
; LENGTH: 19 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 52:
US-10-731-238-52

Query Match      83.8%; Score 88; DB 18; Length 19;
Best Local Similarity 89.5%; Pred. No. 5.2e-05;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 GONEGQOTPEEDTTPPIVP 19
DB      1 GONEGQOTPEEDTTPPIVP 19

RESULT 15
US-10-282-122A-43778
; Sequence 43778, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zykkind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See file wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: Patent version 3.1
; SEQ ID NO 43778
; LENGTH: 961
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-10-282-122A-43778

Query Match      80.0%; Score 84; DB 15; Length 961;
Best Local Similarity 84.2%; Pred. No. 0.011;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1 GONEGQOTPEEDTTPPIVP 19
          ||||||| |||||||
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Db 807 GONEGQTIEDTTPPP 825

Search completed: October 22, 2005, 12:09:33
Job time : 36.0628 secs

This Page Blank (uspto)

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 22, 2005, 04:14:19 : Search time 6.94525 Seconds
(without alignments)
263.219 Million cell updates/sec

Title: US-10-731-238-53

Perfect score: 105

Sequence: 1 GQNEGGQTPBEDTTPRIPV 19

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR 79: *
1: PIR1: *
2: PIR2: *
3: PIR3: *
4: PIR4: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	95	90.5	1018	2 A32192	fibronectin-bindin
2	90	85.7	940	2 S19702	fibronectin-bindin
3	84	80.0	961	2 G90053	hypothetical prote
4	84	80.0	1038	2 H90053	hypothetical prote
5	59	56.2	488	2 A41961	chitinase (EC 3.2.
6	50	47.6	218	2 T17259	hypothetical prote
7	48	45.7	576	2 T46385	hypothetical prote
8	45	47.6	286	2 C84857	hypothetical prote
9	48	45.7	307	2 S50586	hypothetical prote
10	48	45.7	400	1 A28172	spasmolysin precu
11	48	45.7	537	2 B46535	interleukin 2 rece
12	48	45.7	748	2 D84595	PEARL 4 protein [
13	47.5	45.2	412	2 E88736	protein F33D4.6a
14	47.5	45.2	672	2 T32557	hypothetical prote
15	47	44.8	150	2 B2705	hypothetical prote
16	47	44.8	179	2 C86282	FH2.13 protein -
17	47	44.8	412	2 A55320	immunophilin FKBP4
18	47	44.8	681	2 T01469	hypothetical prote
19	46	43.8	3624	2 AD0835	large repetitive p
20	45	42.9	293	2 G82525	RNA polymerase sig
21	45	42.9	307	2 B2677	hypothetical prote
22	45	42.9	731	2 B86369	hypothetical prote
23	45	42.9	865	2 A47282	calcium-binding pr
24	45	42.9	873	2 A47283	calphostin - fruit
25	45	42.9	1301	1 A41622	protein-tyrosine-P
26	45	42.9	1490	2 T20513	hypothetical prote
27	45	42.9	2924	2 T18378	variant-specific s
28	44	41.9	75	2 T23357	hypothetical prote
29	44	41.9	205	2 C88712	protein CT7H12.11

30	44	41.9	247	2 D87304	transcription regu
31	44	41.9	485	2 F70464	hypothetical prote
32	44	41.9	873	2 T25442	hypothetical prote
33	44	41.9	897	2 T43628	phosphatidylinosit
34	44	41.9	1039	2 B71342	hypothetical prote
35	44	41.9	1086	2 JC7736	C3G protein, long
36	44	41.9	1356	2 T09107	DNA (cytosine-5-)-
37	44	41.9	1464	2 CGH015	collagen alpha 1(I
38	43.5	41.4	892	2 B46203	matrig type A alph
39	43	41.0	119	2 B27201	hypothetical prote
40	43	41.0	137	2 AF2790	conserved hypochet
41	43	41.0	173	2 E97569	hypothetical prote
42	43	41.0	188	2 T37183	hypothetical prote
43	43	41.0	380	2 AH2232	hypothetical prote
44	43	41.0	416	1 OKBYRC	protein kinase (EC
45	43	41.0	416	2 S27198	homeotic protein H

ALIGNMENTS

RESULT 1

A32192
fibronectin-binding protein B - Staphylococcus aureus
C/Species: Staphylococcus aureus
C/Date: 31-Jul-1989 #sequence_revision 31-Jul-1989 #text_change 16-Feb-1997
C/Accession: A32192
R/Sigmaes, C.; Raucsi, G.; Joensson, K.; Lindgren, P.E.; Anantharamaiah, G.M.; Hoeoek,
Proc. Natl. Acad. Sci. U.S.A. 86, 699-703, 1989
A/Title: Nucleotide sequence of the gene for a fibronectin-binding protein from Staphy1
A/Reference number: A32192, PMID:8908998; PMID:2521391
A/Accession: A32192
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-1018 <SIG>
A/Cross-references: GB:J04151
C/Keywords: fibronectin binding

Query Match 90.5%; Score 95; DB 2; Length 1018;
Best Local Similarity 94.7%; Pred. No. 8.9e-06;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GQNEGGQTPBEDTTPRIPV 19
DB 860 GQNEGGQTPBEDTTPRIPV 878

RESULT 2

S19702
fibronectin-binding protein B - Staphylococcus aureus
C/Species: Staphylococcus aureus
C/Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
C/Accession: S19702
R/Joensson, K.; Sigmaes, C.; Mueller, H.P.; Linderberg, M.
Eur. J. Biochem. 202, 1041-1048, 1991
A/Title: Two different genes encode fibronectin binding proteins in Staphylococcus aure
A/Reference number: S19702, PMID:9211475; PMID:1837266
A/Accession: S19702
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-940 <JOB>
A/Cross-references: UNIPROT:Q53682; EMBL:X62992; NID:G49040; PIDD:CAA44726.1; PID:G5815
C/Keywords: fibronectin binding

Query Match 85.7%; Score 90; DB 2; Length 940;
Best Local Similarity 89.5%; Pred. No. 4.3e-05;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GQNEGGQTPBEDTTPRIPV 19
DB 796 GQNEGGQTPBEDTTPRIPV 814


```
RESULT 3
G90053
Hypothetical protein fnbB [imported] - Staphylococcus aureus (strain N315)
C:Species: Staphylococcus aureus
C>Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C:Accession: G90053
R:Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguc
ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Gaito, C.; Sekimizu, K.;
C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hirama-su, K.
Lancet 357, 1225-1240, 2001
A>Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.
A:Reference number: A89758; PMID:21311952; PMID:11418146
A:Accession: G90053
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-961 <KUR>
A:Cross-references: UNIPROT:Q99RD3; GB:BA000018; PID:G13702452; PIDN:BAB43593.1; GSPDB:G
A:Experimental source: strain N315
C:Genetics:
A:Gene: fnbB

Query Match          80.0%; Score 84; DB 2; Length 961;
Best Local Similarity 84.2%; Pred. No. 0.00033;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GONEGQOTPEEDTPTPIV 19
DB 807 GONEGQOTIEEDTPTPTP 825

RESULT 4
H90053
Hypothetical protein fnb [imported] - Staphylococcus aureus (strain N315)
C:Species: Staphylococcus aureus
C>Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C:Accession: H90053
R:Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguc
ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Gaito, C.; Sekimizu, K.;
C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramaetsu, K.
Lancet 357, 1225-1240, 2001
A>Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.
A:Reference number: A89758; PMID:21311952; PMID:11418146
A:Accession: H90053
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1038 <KUR>
A:Cross-references: UNIPROT:Q99RD2; GB:BA000018; PID:G13702453; PIDN:BAB43594.1; GSPDB:G
A:Experimental source: strain N315
C:Genetics:
A:Gene: fnb

Query Match          80.0%; Score 84; DB 2; Length 1038;
Best Local Similarity 84.2%; Pred. No. 0.00036;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GONEGQOTPEEDTPTPIV 19
DB 856 GONEGQOTIEEDTPTPTP 874

RESULT 5
A41961
Chitinase (EC 3.2.1.14) D - Bacillus circulans
C:Species: Bacillus circulans
C>Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C:Accession: A41961
R:Matnabe, T.; Oyanagi, W.; Suzuki, K.; Onishi, K.; Tanaka, I.
J. Bacteriol. 174, 408-414, 1992
A>Title: Structure of the gene encoding chitinase D of Bacillus circulans WL-12 and pose
A:Reference number: A41961; PMID:92105006; PMID:1729234
A:Accession: A41961
A:Status: preliminary; not compared with conceptual translation.
A:Molecule type: nucleic acid; protein
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A:Residues: 1-488 <MAT>
A:Cross-references: UNIPROT:P27050
A:Experimental source: WL-12
A>Note: sequence extracted from NCBI backbone (NCBI:P27050)
C:Superfamily: Streptomyces chitinase chIA
C:Keywords: glycosidase; hydrolase; polysaccharide degradation

Query Match          56.2%; Score 59; DB 2; Length 488;
Best Local Similarity 57.9%; Pred. No. 0.67;
Matches 11; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

QY 1 GONEGQOTPEEDTPTPIV 19
DB 78 GEGTGAGTPTPTPTPTPTP 96

RESULT 6
T17259
Hypothetical protein DKFZp272C091.1 - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T17259
R:Poulet, A.; Klein, M.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.
submitted to the Protein Sequence Database, September 1999
A:Reference number: Z18723
A:Accession: T17259
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-218 <POU>
A:Cross-references: UNIPROT:Q9UFT0; EMBL:AL117476
A:Experimental source: adult breast cancer; clone DKFZp272C091
C:Genetics:
A>Note: DKFZp272C091.1

Query Match          47.6%; Score 50; DB 2; Length 218;
Best Local Similarity 47.4%; Pred. No. 5.7;
Matches 9; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

QY 1 GONEGQOTPEEDTPTPIV 19
DB 182 GSKTGRETEAAPTSPPIV 200

RESULT 7
T46385
Hypothetical protein DKFZp434K031.1 - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 09-Jul-2004
C:Accession: T46385
R:Poulet, A.; Klein, M.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.
submitted to the Protein Sequence Database, January 2000
A:Reference number: Z23029
A:Accession: T46385
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-576 <AAA>
A:Cross-references: UNIPROT:Q9NTE7; EMBL:AL137317
A:Experimental source: adult testis; clone DKFZp434K031
C:Genetics:
A>Note: DKFZp434K031.1

Query Match          47.6%; Score 50; DB 2; Length 576;
Best Local Similarity 47.4%; Pred. No. 16;
Matches 9; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

QY 1 GONEGQOTPEEDTPTPIV 19
DB 540 GSKTGRETEAAPTSPPIV 558

RESULT 8
C84857
Hypothetical protein At2g42710 [imported] - Arabidopsis thaliana
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C/Species: Arabidopsis thaliana (mouse-ear cress)
 C/Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
 C/Accession: CB4857
 R/Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
 M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.;
 Neus, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.
 Nature 402, 761-768, 1999
 A/Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
 A/Reference number: AB4420; MUID:20083487; PMID:10617197
 A/Accession: CB4857
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1286 <STO>
 A/Cross-references: UNIPROT:Q95UJ5; GB:AE002093; NID:94512681; PIDN:AD21735.1; GSPDB:GN
 C/Genetics:
 A/Gene: AT2G42710
 A/Map position: 2
 C/Superfamily: ribosomal protein L1p/L10e

Query Match 45.7%; Score 48; DB 2; Length 286;
 Best Local Similarity 72.7%; Pred. No. 15;
 Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 1 GONEGQOTPEEDTPPIV 11
 DB 129 GENEGRTPPE 139

RESULT 9
 B45086
 hypothetical protein YER083c - yeast (Saccharomyces cerevisiae)
 C/Species: Saccharomyces cerevisiae
 C/Date: 28-May-1993 #sequence_revision 24-Feb-1995 #text_change 09-Jul-2004
 C/Accession: S50586
 R/Dietrich, F.S.
 submitted to the EMBL Data Library, December 1994
 A/Description: The sequence of S. cerevisiae cosmids 9747, 8198, 9781, and lambda clones
 A/Reference number: S50436
 A/Accession: S50586
 A/Molecule type: DNA
 A/Residues: 1-307 <DIE>
 A/Cross-references: UNIPROT:P40056; EMBL:U18839; NID:9603313; PID:9603321; GSPDB:GN00005
 C/Genetics:
 A/Gene: MIPS:YER083c
 A/Cross-references: SGD:S0000885
 A/Map position: 5R

Query Match 45.7%; Score 48; DB 2; Length 307;
 Best Local Similarity 38.9%; Pred. No. 16;
 Matches 7; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

OY 1 GONEGQOTPEEDTPPIV 18
 DB 111 GQGTGKSTPQDSSTPDL 128

RESULT 10
 A28172
 spasmolysin precursor - African clawed frog
 N/Alternate names: Prospsmolysin
 C/Species: Xenopus laevis (African clawed frog)
 C/Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
 C/Accession: A28172
 R/Hoffmann, W.
 J. Biol. Chem. 263, 7686-7690, 1988
 A/Title: A new repetitive protein from Xenopus laevis skin highly homologous to pancreat
 A/Reference number: A28172; MUID:88227968; PMID:3372504
 A/Accession: A28172
 A/Molecule type: mRNA
 A/Residues: 1-400 <HOP>
 A/Cross-references: UNIPROT:P10667; GB:M19971; NID:9214791; PIDN:AAA49960.1; GSPDB:G
 C/Superfamily: spasmolysin; trefol homology
 C/Keywords: duplication; glycoprotein; skin; tandem repeat

F/1-20/Domain: signal sequence #status predicted <SIG>
 F/21-400/Product: spasmolysin #status predicted <ANT>
 F/21-65/Product: spasmolysin I #status predicted <SPI>
 F/22-65/Domain: trefol homology <TRF1>
 F/72-348/Product: spasmolysin-glycopeptide #status predicted <SPG>
 F/74-114/Domain: trefol homology <TRF2>
 F/115-309/Region: PST sequence
 F/123-131,231-229/Region: 9-residue repeats (D/E-T-T-A-S-T-T-A)
 F/132-230,240-248/Region: 9-residue repeats (E-T-T-T-V-P-T-T-P)
 F/249-252,276-299/Region: 4-residue repeats (E-T-T-T)
 F/305-342/Domain: trefol homology <TRF3>
 F/351-400/Product: spasmolysin II #status predicted <SP2>
 F/353-393/Domain: trefol homology <TRF4>
 F/22-43,33-48,43-60,74-100,84-99,94-111,312-327,332-339,353-379,363-378,373-390/Disulf
 F/63/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 45.7%; Score 48; DB 1; Length 400;
 Best Local Similarity 56.2%; Pred. No. 21;
 Matches 9; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

OY 4 EGQOTPEEDTPPIV 19
 DB 253 EPTTPTTDTTPTPLP 268

RESULT 11
 B46535
 interleukin 2 receptor beta chain - rat
 C/Species: Rattus norvegicus (Norway rat)
 C/Date: 18-Jun-1993 #sequence_revision 18-Nov-1994 #text_change 02-Aug-2002
 C/Accession: B46535
 R/Page, T.H.; Dallman, M.J.
 Eur. J. Immunol. 21, 2133-2138, 1991
 A/Title: Molecular cloning of cDNAs for the rat interleukin 2 receptor alpha and beta c
 A/Reference number: B46535; MUID:91364784; PMID:1889461
 A/Accession: B46535
 A/Status: preliminary
 A/Molecule type: mRNA
 A/Residues: 1-537 <PAG>
 A/Note: sequence inconsistent with the nucleotide translation
 A/Note: sequence extracted from NCBI backbone (NCBI:60818, NCBI:60819)
 C/Superfamily: interleukin-2 receptor beta chain; fibronectin type III repeat homology
 C/Keywords: cytokine receptor

Query Match 45.7%; Score 48; DB 2; Length 537;
 Best Local Similarity 38.9%; Pred. No. 29;
 Matches 7; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

OY 2 QNEGQOTPEEDTPPIV 19
 DB 395 EEDGPRLPESPPPLP 412

RESULT 12
 D84595
 PEARL1 4 protein [imported] - Arabidopsis thaliana
 C/Species: Arabidopsis thaliana (mouse-ear cress)
 C/Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
 C/Accession: D84595
 R/Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
 M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.
 eus, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.
 Nature 402, 761-768, 1999
 A/Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
 A/Reference number: AB4420; MUID:20083487; PMID:10617197
 A/Accession: D84595
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-748 <STO>
 A/Cross-references: UNIPROT:Q95KR5; GB:AE002093; NID:94803947; PIDN:AD29820.1; GSPDB:G
 C/Genetics:
 A/Gene: AT2G20960
 A/Map position: 2

Query Match 45.7%; Score 48; DB 2; Length 748;
 Best Local Similarity 53.3%; Pred. No. 42;
 Matches 8; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 5 GQTPBEDTPPIVP 19
 ||||| |||||
 Db 46 GKRTSRDQTPPASP 60

RESULT 13
 E88736
 Protein F33D4.6a [imported] - Caenorhabditis elegans
 C:Species: Caenorhabditis elegans
 C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
 C:Accession: E88736
 R:Anonymous, The C. elegans Sequencing Consortium.
 Science 282, 2012-2018, 1998
 A:Title: Genome sequence of the nematode C. elegans: a platform for investigating biolog
 A:Reference number: A75000; PMID:99069613; PMID:9851916
 A:Note: see websites genome.wustl.edu/gsc/C.elegans/ and www.sanger.ac.uk/Projects/C_ele
 A:Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and
 A:Accession: E88736
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-412 <STO>
 A:Cross-references: UNIPROT:Q44190; GB:chr_IV; PIDN:AAB88378.1; PID:G262622; GSPDB:GN00
 C:Genetics:
 A:Gene: F33D4.6a
 A:Map position: 4

Query Match 45.2%; Score 47.5; DB 2; Length 41;;
 Best Local Similarity 52.9%; Pred. No. 26;
 Matches 9; Conservative 4; Mismatches 1; Indels 3; Gaps 1;

QY 6 QQTPEED---TTPPIVP 19
 |||||:|:|:|:|
 Db 186 QQTPEEDPMITLPLVP 202

RESULT 14

T32557
 hypothetical protein F33D4.6b - Caenorhabditis elegans
 C:Species: Caenorhabditis elegans
 C:Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
 C:Accession: T32557; T32558
 R:Johnson, D.; Stellyes, L.
 submitted to the EMBL Data Library, December 1997
 A:Description: The sequence of C. elegans cosmid F33D4.
 A:Reference number: Z21190
 A:Accession: T32557
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-672 <JOH>
 A:Cross-references: UNIPROT:Q44189; EMBL:AF036702; PIDN:AAB88379.1; GSPDB:GN00022; CESP:
 A:Experimental source: strain Bristol N2; clone F33D4
 A:Accession: T32558
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-404, 'VTFCFMHF' <JO2>
 A:Cross-references: EMBL:AF036702; PIDN:AAB88378.1; GSPDB:GN00022; CESP:F33D4.6a
 A:Experimental source: strain Bristol N2; clone F33D4
 C:Genetics:
 A:Gene: CESP:F33D4.6b; CESP:F33D4.6a
 A:Map position: 4
 A:Introns: 131/3; 164/2; 215/2; 237/2; 276/3; 293/3; 380/3; 404/3

Query Match 45.2%; Score 47.5; DB 2; Length 672;
 Best Local Similarity 52.9%; Pred. No. 44;
 Matches 9; Conservative 4; Mismatches 1; Indels 3; Gaps 1;

Db 186 QQTPEEDPMITLPLVP 202

RESULT 15
 B72705
 hypothetical protein APE1057 - Aeropyrum pernix (strain K1)
 C:Species: Aeropyrum pernix
 C:Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004
 C:Accession: B72705
 R:Kawarayashi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Takei
 awa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudo, Y.; Yamazaki, J.; K
 DNA Res. 6, 83-101, 1999
 A:Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropyr
 A:Reference number: A72450; PMID:99310339; PMID:10382966
 A:Accession: B72705
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-150 <KAW>
 A:Cross-references: UNIPROT:Q9YD55; DBJ:AP000060; NID:G5104188; PIDN:BAA80042.1; PID:di
 C:Genetics:
 A:Experimental source: strain K1
 A:Gene: APE1057

Query Match 44.8%; Score 47; DB 2; Length 150;
 Best Local Similarity 42.1%; Pred. No. 10;
 Matches 8; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

QY 1 GONEGQQTPEEDTPPIVP 19
 |:|:|:|:|:|:|:|
 Db 56 GJHGGQDRPDNPTPELP 74

Search completed: October 22, 2005, 06:09:59
 Job time : 7.94525 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 22, 2005, 04:10:49 ; Search time 34.818 Seconds
(without alignments)
279.439 Million cell updates/sec

Title: US-10-731-238-53

Perfect score: 105
Sequence: 1 GQNEGQGTPEEDTTPPIVP 19

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_03 : *
1: uniprot_sprot : *
2: uniprot_trembl : *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	95	90.5	1018	1 FNBA_STAUV	P14738 staphylococ
2	90	85.7	940	2 Q53682	Q53682 staphylococ
3	84	80.0	961	2 Q99RD3	Q99RD3 staphylococ
4	84	80.0	961	2 Q7A3J8	Q7A3J8 staphylococ
5	84	80.0	965	2 Q6GDU5	Q6GDU5 staphylococ
6	84	80.0	1015	2 Q8NUU7	Q8NUU7 staphylococ
7	84	80.0	1015	2 Q6G6H3	Q6G6H3 staphylococ
8	84	80.0	1038	2 Q99RD2	Q99RD2 staphylococ
9	84	80.0	1038	2 Q7A3J7	Q7A3J7 staphylococ
10	79	75.2	957	2 Q6G6H4	Q6G6H4 staphylococ
11	69	65.7	943	2 Q8NUU8	Q8NUU8 staphylococ
12	59	56.2	524	2 CHID_BACCI	CHID_BACCI
13	56	53.3	561	2 Q960U5	Q960U5
14	56	53.3	1117	2 Q9V7A9	Q9V7A9
15	54	51.4	384	2 Q8T9J3	Q8T9J3
16	54	51.4	384	2 Q9VPC4	Q9VPC4
17	53	50.5	833	2 Q9DEB7	Q9DEB7
18	53	50.5	1603	2 Q8G4S9	Q8G4S9
19	50.5	48.1	126	2 Q9T7B6	Q9T7B6
20	50	47.6	157	2 Q95ND9	Q95ND9
21	50	47.6	218	2 Q9UFW0	Q9UFW0
22	50	47.6	219	2 Q9MZK3	Q9MZK3
23	50	47.6	432	2 Q6A8S5	Q6A8S5
24	50	47.6	531	2 Q8YH1	Q8YH1
25	50	47.6	576	2 Q9NTE7	Q9NTE7
26	50	47.6	608	2 Q9AXR6	Q9AXR6
27	50	47.6	714	2 Q7TUM4	Q7TUM4
28	50	47.6	1105	2 Q7Z3B3	Q7Z3B3
29	50	47.6	1105	2 Q9UFR3	Q9UFR3
30	50	47.6	1171	2 Q96U77	Q96U77
31	49.5	47.1	290	2 Q93CK9	Q93CK9

ALIGNMENTS

RESULT 1	FNBA_STAUV	STANDARD;	PRT;	1018 AA.
AC	P14738;			
DT	01-APR-1990 (Rel. 14, Created)			
DT	01-APR-1990 (Rel. 14, Last sequence update)			
DT	25-OCT-2004 (Rel. 45, Last annotation update)			
DE	Fibronectin-binding protein precursor (FNBP).			
GN	Name=fnbp;			
OS	Staphylococcus aureus.			
OC	Bacteria; Firmicutes; Bacillales; Staphylococcus.			
OX	NCBI_TaxID=1280;			
RN	(1)			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=NCCTC 8325-4;			
RX	MEDLINE=89098998; PubMed=2521391;			
RA	Singnes C., Raucel G., Joensen K., Lindgren P.-E.,			
RA	Anantharamiah G.M., Hoeck M., Lindberg M.;			
RT	"Nucleotide sequence of the gene for a fibronectin-binding protein from Staphylococcus aureus: use of this peptide sequence in the synthesis of biologically active peptides."			
RT	Proc. Natl. Acad. Sci. U.S.A. 86:699-703(1989).			
CC	- FUNCTION: The ability of bacteria to bind fibronectin has been proposed as a virulence factor enabling bacteria to colonize wound tissues and blood clots. Binding of plasma fibronectin to the bacterial surface might block adhesion receptors on S.aureus, thus representing an important defense mechanism against tissue invasion.			
CC	- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by an amide bond (Potential).			
CC	-----			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL Outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).			
CC	-----			
DR	EMBL; J04151; AAA26632.1; -			
DR	InterPro; IPR004237; Fn_bind.			
DR	InterPro; IPR005877; Gpos_YsIRK.			
DR	InterPro; IPR001899; Gram_pos_anchor.			
DR	Pfam; PF02986; Fn_bind.1.			
DR	Pfam; PF00746; Gram_pos_anchor.1.			
DR	Pfam; PF04650; YsIRK_signal.1.			
DR	TIGRFAMs; TIGR01167; LPXTG_anchor.1.			
DR	TIGRFAMs; TIGR01168; YsIRK_signal.1.			
DR	PROSITE; PS50847; GRAM_POS_ANCHORING.1.			
KW	Cell adhesion; Cell wall; Peptidoglycan-anchor; Repeat; Signal; Virulence.			
FT	SIGNAL	1	36	
FT	CHAIN	37	985	Fibronectin-binding protein.
FT	PROPEP	986	1018	Removed by sortase (Potential).

32	49	46.7	168	2	Q8N7Z4	Q8N7Z4 homo sapien
33	49	46.7	279	2	Q6NSJ2	Q6NSJ2 homo sapien
34	49	46.7	401	2	Q8MK45	Q8MK45 taptus ter
35	49	46.7	416	2	Q9NKG9	Q9NKG9 homo sapien
36	49	46.7	711	2	Q6LWF5	Q6LWF5 lactobacill
37	49	46.7	748	2	Q7L621	Q7L621 homo sapien
38	49	46.7	776	2	Q8TEA5	Q8TEA5 homo sapien
39	49	46.7	1097	1	KPID_RAT	KPID_RAT
40	48	45.7	286	2	Q9SJT5	Q9SJT5
41	48	45.7	307	1	YERJ_YEAST	YERJ_YEAST
42	48	45.7	400	1	MUAI_XENLA	MUAI_XENLA
43	48	45.7	415	2	Q8RWT4	Q8RWT4
44	48	45.7	537	1	IL2B_RAT	IL2B_RAT
45	48	45.7	583	2	Q7UYM6	Q7UYM6 rhodoptrell

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FT REPEAT 545 574 B-1.
FT REPEAT 575 604 B-2.
FT DOMAIN 745 878 4 X approximate tandem repeats,
  fibronectin-binding domain.
FT REPEAT 745 782 D-1.
FT REPEAT 783 820 D-2.
FT REPEAT 821 859 D-3.
FT REPEAT 860 878 D-4 (incomplete).
FT DOMAIN 879 948 5 X tandem repeats, Pro-rich (WR).
FT REPEAT 879 892 WR 1.
FT REPEAT 893 906 WR 2.
FT REPEAT 907 920 WR 3.
FT REPEAT 921 934 WR 4.
FT REPEAT 935 948 WR 5.
FT SITE 982 986 LpXTG sorting signal (potential).
FT MOD_RES 985 985 PentaglycyI murein peptidoglycan amidated
  threonine (Potential).
SQ SEQUENCE 1018 AA; 111780 MW; 58175E020E81F1F CRC64;

Query Match 90.5%; Score 95; DB 1; Length 1016;
Best Local Similarity 94.7%; Pred. No. 5.6e-05;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GONEGOQTPEDTTPPIV 19
DB 860 GONEGOQTEEDTTPPIV 878

RESULT 2
QY 053682; PRELIMINARY; PRT; 940 AA.
ID 053682;
AC 053682;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DE 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Fibronectin binding protein B.
GN Name=fnbB;
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1280;
[1]
RP SEQUENCE FROM N.A.
RC STRAIN=8325-4;
RX MEDLINE=92111475; PubMed=1837266;
RA Joneson K., Signas C., Muller H.P., Lindberg M.;
RT "Two different genes encode fibronectin binding proteins in
  Staphylococcus aureus. The complete nucleotide sequence and
  characterization of the second gene."
RT Eur. J. Biochem. 202;1041-1048(1991).
RL -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
  an amide bond (By similarity).
CC EMBL; X62992; CAA44726.1; -.
CC PIR; S19702; S19702.
DR HSSP; 053653; 1N67.
DR GO; GO:0009986; C:cell surface; IEA.
DR GO; GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0007155; P:cell adhesion; IEA.
DR InterPro; IPR008966; Adhes_bact.
DR InterPro; IPR004237; Fn_bind.
DR InterPro; IPR005877; Gpos_YsIRK.
DR InterPro; IPR001899; Gram_pos_anchor.
DR Pfam; PF02986; Fn_bind; 2.
DR Pfam; PF00746; Gram_pos_anchor; 1.
DR TIGRfams; TIGR01167; LpXTG_signal; 1.
DR TIGRfams; TIGR01168; YsIRK_signal; 1.
DR PROSITE; PS50847; GRAM_POS_ANCHORING; 1.
KW Cell wall; Peptidoglycan-anchor.
SQ SEQUENCE 940 AA; 103555 MW; E35FBBCA907AE345 CRC64;

Query Match 85.7%; Score 90; DB 2; Length 940;

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Best Local Similarity 89.5%; Pred. No. 0.00027;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GONEGOQTPEDTTPPIV 19
DB 796 GNEGOQTEEDTTPPIV 814

RESULT 3
QY 099RD3; PRELIMINARY; PRT; 961 AA.
ID 099RD3;
AC 099RD3;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Fibronectin-binding protein homolog.
DE Name=fnbB; OrderedLocustNames=SAV2502;
OS Staphylococcus aureus (strain Mu50 / ATCC 700699).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=158878;
[1]
RP SEQUENCE FROM N.A.
RC STRAIN=MU50 / ATCC 700699;
RX MEDLINE=21311952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2;
RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
  Cui L., Oguchi A., Aoki K.-I., Nagai Y., Iino U.-O., Ito T.,
  Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,
  Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
  RA Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
  RA Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
  RA Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
RT "Whole genome sequencing of methicillin-resistant Staphylococcus
  aureus."
RL Lancet 357;1225-1240(2001).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
  an amide bond (By similarity).
CC EMBL; AP003365; BAB58664.1; -.
DR PIR; G90053; G90053.
DR HSSP; 053653; 1N67.
DR GO; GO:0009986; C:cell surface; IEA.
DR GO; GO:0005618; C:cell wall; IEA.
DR GO; GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0007155; P:cell adhesion; IEA.
DR InterPro; IPR008966; Adhes_bact.
DR InterPro; IPR004237; Fn_bind.
DR InterPro; IPR005877; Gpos_YsIRK.
DR InterPro; IPR001899; Gram_pos_anchor.
DR Pfam; PF02986; Fn_bind; 1.
DR Pfam; PF00746; Gram_pos_anchor; 1.
DR TIGRfams; TIGR01167; LpXTG_signal; 1.
DR TIGRfams; TIGR01168; YsIRK_signal; 1.
DR PROSITE; PS50847; GRAM_POS_ANCHORING; 1.
KW Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ SEQUENCE 961 AA; 106010 MW; 364940F884EA4101 CRC64;

Query Match 80.0%; Score 84; DB 2; Length 961;
Best Local Similarity 84.2%; Pred. No. 0.0021;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GONEGOQTEEDTTPPIV 19
DB 807 GNEGOQTEEDTTPPIV 825

RESULT 4
QY 07A3J8; PRELIMINARY; PRT; 961 AA.
ID 07A3J8;
AC 07A3J8;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)

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DE FndB protein.
GN Name=fndB; OrderedLocusNames=SA2290;
OS Staphylococcus aureus (strain N315).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=158879;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=21311952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2;
RX Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Iian J.-Q., Ito T.,
RA Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyma A.,
RA Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
RA Sekizawa K., Hirakawa H., Ohnaka K., Furuya K., Yoshino C., Shiba T.,
RA Kanetsu M., Yamashita A., Ohnaka K., Furuya K., Yoshino C., Shiba T.,
RA Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.,
RT "Whole genome sequencing of methicillin-resistant Staphylococcus
RT aureus".
RL Lancet 357:1225-1240(2001).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC an amide bond (By similarity).
DR EMBL; AP003137; BAB43593.1; -.
DR GO; GO:0009986; C:cell surface; IEA.
DR GO; GO:0005618; C:cell wall; IEA.
DR GO; GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0007155; P:cell adhesion; IEA.
DR InterPro; IPR008966; Adhes_Bact.
DR InterPro; IPR004237; Fn_bind.
DR InterPro; IPR005877; Gpos_YsIRK.
DR InterPro; IPR001899; Gram_pos_anchor.
DR Pfam; PF02986; Fn_bind; 1.
DR Pfam; PF00746; Gram_pos_anchor; 1.
DR Pfam; PF04650; YsIRK_signal; 1.
DR TIGRFAMs; TIGR01167; LPXTG_anchor; 1.
DR TIGRFAMs; TIGR01168; YsIRK_signal; 1.
DR PROSITE; PSS0847; GRAM_POS_ANCHORING; 1.
DR Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ SEQUENCE 961 AA; 106010 MW; 364940F84EA4101 CRC64;

Query Match 80.0%; Score 84; DB 2; Length 961;
Best Local Similarity 84.2%; Pred. No. 0.0021;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GQNEGQQTPEEDTTPPTP 19
DB 807 GQNEGQQTPEEDTTPPTP 825

RESULT 5
Q6GDU5 PRELIMINARY; PRT; 965 AA.
ID O6GDU5;
AC O6GDU5;
DT 05-JUN-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Fibrinectin-binding protein.
GN Name=fndB; OrderedLocusNames=SA2580;
OS Staphylococcus aureus (strain MRSA252).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=282458;
RN [1]
RP SEQUENCE FROM N.A.
RA PubMed=15213324; DOI=10.1073/pnas.0402521101;
RX Holden M.T.G., Feil E.J., Lindsay J.A., Peacock S.J., Day N.P.J.,
RA Barron A., Burrows L., Moore C.E., Hurst L., Atkin R., Barron A.,
RA Barron A., Bentley S.D., Chillingworth C., Chillingworth T.,
RA Churcher C., Clark L., Cotton C., Cronin A., Doggett J., Dowd L.,
RA Feltwell T., Hance Z., Harris B., Hauser R., Holtroyd S., Jagels K.,
RA James K.D., Lennard N., Line A., Mayes R., Mould S., Mungall K.,
RA Omond D., Quail M.A., Rabinowitsch E., Rutherford K.M., Sanders M.,
RA Sharp S., Simmonds M., Stevens K., Whitehead S., Barrall B.G.,
RA Spratt B.G., Parkhill J.,
RT "Complete genomes of two clinical Staphylococcus aureus strains:

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RT evidence for the rapid evolution of virulence and drug resistance.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:9786-9791(2004).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC an amide bond (By similarity).
DR EMBL; BX571856; CAG41560.1; -.
DR GO; GO:0009986; C:cell surface; IEA.
DR GO; GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0007155; P:cell adhesion; IEA.
DR InterPro; IPR008966; Adhes_Bact.
DR InterPro; IPR004237; Fn_bind.
DR InterPro; IPR005877; Gpos_YsIRK.
DR InterPro; IPR001899; Gram_pos_anchor.
DR Pfam; PF02986; Fn_bind; 1.
DR Pfam; PF00746; Gram_pos_anchor; 1.
DR Pfam; PF04650; YsIRK_signal; 1.
DR TIGRFAMs; TIGR01167; LPXTG_anchor; 1.
DR TIGRFAMs; TIGR01168; YsIRK_signal; 1.
DR PROSITE; PSS0847; GRAM_POS_ANCHORING; 1.
DR Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ SEQUENCE 965 AA; 105691 MW; 2982E132164D0551 CRC64;

Query Match 80.0%; Score 84; DB 2; Length 965;
Best Local Similarity 84.2%; Pred. No. 0.0021;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GQNEGQQTPEEDTTPPTP 19
DB 825 GQNEGQQTPEEDTTPPTP 843

RESULT 6
Q8NUU7 PRELIMINARY; PRT; 1015 AA.
ID Q8NUU7;
AC Q8NUU7;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE FndB protein.
GN Name=fndB; OrderedLocusNames=NM2421;
OS Staphylococcus aureus (strain NM2).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=196620;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=NM2;
RX PubMed=12040717; PubMed=1204378; DOI=10.1016/S0140-6736(02)08713-5;
RA Baba T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Oguchi A.,
RA Nagai Y., Ikawa N., Asano K., Naimi T., Kuroda H., Cui L.,
RA Yamamoto K., Hiramatsu K.,
RT "Genome and virulence determinants of high virulence community-
RT acquired MRSA.".
RL Lancet 359:1819-1827(2002).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC an amide bond (By similarity).
DR EMBL; AP004630; BAB96286.1; -.
DR GO; GO:0009986; C:cell surface; IEA.
DR GO; GO:0005618; C:cell wall; IEA.
DR GO; GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0007155; P:cell adhesion; IEA.
DR InterPro; IPR008966; Adhes_Bact.
DR InterPro; IPR004237; Fn_bind.
DR InterPro; IPR005877; Gpos_YsIRK.
DR InterPro; IPR001899; Gram_pos_anchor.
DR Pfam; PF02986; Fn_bind; 1.
DR Pfam; PF00746; Gram_pos_anchor; 1.
DR Pfam; PF04650; YsIRK_signal; 1.
DR TIGRFAMs; TIGR01167; LPXTG_anchor; 1.
DR TIGRFAMs; TIGR01168; YsIRK_signal; 1.
DR PROSITE; PSS0847; GRAM_POS_ANCHORING; 1.
DR Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ SEQUENCE 1015 AA; 111145 MW; D0F9281BB64D44D2 CRC64;

```

Query Match 80.0%; Score 84; DB 2; Length 1015
 Best Local Similarity 84.2%; Pred. No. 0.0022;
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GONEGQOTPEEDTTPPIVP 19
 Db 861 GONEGQOTPEEDTTPPIVP 879

RESULT 7

Q6G6H3 PRELIMINARY; PRT; 1015 AA.
 AC Q6G6H3;
 DT 05-JUL-2004 (TREMBlrel. 27, Created)
 DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
 DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
 DE Fibronectin-binding protein.
 GN OrderedLocustNames=SA52388;
 OS Staphylococcus aureus (strain MSSA476).
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 OX NCBI_TaxID=282459;
 RN [1]

SEQUENCE FROM N.A.
 RP PubMed=15213324; DOI=10.1073/pnas.0402521101.
 RX Holden M.T.G., Fell E.J., Lindsey J.A., Peacock S.J., Day V.P.J.,
 RA Enright M.C., Foster T.J., Moore C.E., Hurst L., Atkin R., Barron A.,
 RA Bason N., Bentley S.D., Chillingworth C., Chillingworth T.,
 RA Churcher C., Clark L., Corton C., Cronin A., Doggett J., Dowd L.,
 RA Fellwell T., Hance Z., Harris B., Hauser H., Holroyd S., Jagsels K.,
 RA James K.D., Lennard N., Line A., Mayes R., Moule S., Mungall K.,
 RA Omond D., Quail M.A., Rabbittowitch E., Rutherford K.M., Sanders M.,
 RA Sharp S., Simmonds M., Stevens K., Whitehead S., Barrett B.G.,
 RA Spratt B.G., Parkhill J.;
 RT "Complete genomes of two clinical Staphylococcus aureus strains:
 RT evidence for the rapid evolution of virulence and drug resistance."
 RL Proc. Natl. Acad. Sci. U.S.A. 101:9786-9791(2004).
 CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
 CC an amide bond (By similarity).
 DR EMBL: BX571857; CAG44202.1; -;
 DR GO: GO:0009986; C:cell surface; IEA.
 DR GO: GO:0005618; C:cell wall; IEA.
 DR GO: GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
 DR GO: GO:0016020; C:membrane; IEA.
 DR GO: GO:0007155; P:cell adhesion; IEA.
 DR InterPro: IPR008966; Adhes_bact.
 DR InterPro: IPR004237; Fn_bind.
 DR InterPro: IPR005877; Gpos_YsIRK.
 DR InterPro: IPR001899; Gram_pos_anchor.
 DR Pfam: PF02986; Fn_bind; 1.
 DR Pfam: PF00746; Gram_pos_anchor; 1.
 DR TIGRPFAM: TIGR01167; LPXTG_anchor; 1.
 DR TIGRPFAM: TIGR01168; YsIRK_signal; 1.
 DR PROSITE: PS50847; GRAM_POS_ANCHORING; 1.
 DR Cell wall; Complete proteome; Peptidoglycan-anchor.
 KW Cell wall; Complete proteome; Peptidoglycan-anchor.
 SQ SEQUENCE 1015 AA; 111145 MW; D0F9281BB64D44D2 CRC64;

Query Match 80.0%; Score 84; DB 2; Length 1015;
 Best Local Similarity 84.2%; Pred. No. 0.0022;
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GONEGQOTPEEDTTPPIVP 19
 Db 861 GONEGQOTPEEDTTPPIVP 879

RESULT 8

Q99RD2 PRELIMINARY; PRT; 1038 AA.
 AC Q99RD2;
 DT 01-JUN-2001 (TREMBlrel. 17, Created)
 DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)

DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
 DE Fibronectin-binding protein homolog.
 GN Name=fnb; OrderedLocustNames=SAV2503;
 OS Staphylococcus aureus (strain Mu50 / ATCC 700699).
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 OX NCBI_TaxID=158878;
 RN [1]

SEQUENCE FROM N.A.
 RP STRAIN=Mu50 / ATCC 700699;
 RX MEDLINE=21311952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2;
 RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
 RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Iano J.-Q., Ito T.,
 RA Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hotoyama A.,
 RA Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
 RA Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
 RA Kanahisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
 RA Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
 RT "Whole genome sequencing of methicillin-resistant Staphylococcus
 RT aureus."
 RL Lancet 357:1225-1240(2001).
 CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
 CC an amide bond (By similarity).
 DR EMBL: AP003365; BAB58665.1; -;
 DR PIR: H90053; H90053.
 DR GO: GO:0009986; C:cell surface; IEA.
 DR GO: GO:0005618; C:cell wall; IEA.
 DR GO: GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
 DR GO: GO:0016020; C:membrane; IEA.
 DR GO: GO:0007155; P:cell adhesion; IEA.
 DR InterPro: IPR008966; Adhes_bact.
 DR InterPro: IPR004237; Fn_bind.
 DR InterPro: IPR005877; Gpos_YsIRK.
 DR InterPro: IPR001899; Gram_pos_anchor.
 DR Pfam: PF02986; Fn_bind; 1.
 DR Pfam: PF00746; Gram_pos_anchor; 1.
 DR Pfam: PF04650; YsIRK_signal; 1.
 DR TIGRPFAM: TIGR01167; LPXTG_anchor; 1.
 DR TIGRPFAM: TIGR01168; YsIRK_signal; 1.
 DR PROSITE: PS50847; GRAM_POS_ANCHORING; 1.
 DR Cell wall; Complete proteome; Peptidoglycan-anchor.
 KW Cell wall; Complete proteome; Peptidoglycan-anchor.
 SQ SEQUENCE 1038 AA; 113618 MW; 666BFB62BFBEB12 CRC64;

Query Match 80.0%; Score 84; DB 2; Length 1038;
 Best Local Similarity 84.2%; Pred. No. 0.0023;
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GONEGQOTPEEDTTPPIVP 19
 Db 856 GONEGQOTPEEDTTPPIVP 874

RESULT 9

Q7A3J7 PRELIMINARY; PRT; 1038 AA.
 ID Q7A3J7;
 AC Q7A3J7;
 DT 05-JUL-2004 (TREMBlrel. 27, Created)
 DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
 DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
 DE Fnb protein.
 GN Name=fnb; OrderedLocustNames=SA2291;
 OS Staphylococcus aureus (strain N315).
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 OX NCBI_TaxID=158879;
 RN [1]

SEQUENCE FROM N.A.
 RP MEDLINE=21311952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2;
 RX Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
 RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Iano J.-Q., Ito T.,
 RA Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hotoyama A.,
 RA Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
 RA Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
 RA Kanahisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
 RA Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;

RT "Whole genome sequencing of methicillin-resistant *Staphylococcus aureus*." Lancet 357:1225-1240(2001).
 RL -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by an amide bond (By similarity).
 CC EMBL: AP003137; BAB43594.1; -;
 DR GO: GO:0009986; C:cell surface; IEA.
 DR GO: GO:0005618; C:cell wall; IEA.
 DR GO: GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
 DR GO: GO:0016020; C:membrane; IEA.
 DR GO: GO:0007155; P:cell adhesion; IEA.
 DR InterPro: IPR008966; Adhes_bact.
 DR InterPro: IPR004237; Fn_bind.
 DR InterPro: IPR005877; Gpob_YsIRK.
 DR InterPro: IPR001899; Gram_pos_anchor.
 DR Pfam: PF02986; Fn_bind; 1.
 DR Pfam: PF00746; Gram_pos_anchor; 1.
 DR TIGRfams: TIGR01167; LPXTG_anchor; 1.
 DR TIGRfams: TIGR01168; YsIRK_signal; 1.
 DR PROSITE: PS50847; GRAM_POS_ANCHORING; 1.
 DR Cell wall; Complete proteome; Peptidoglycan-anchor.
 SO SEQUENCE 1038 AA; 113618 MW; 666BF6BFBB12 CRC64;

Query Match 80.0%; Score 84; DB 2; Length 1038;
 Best Local Similarity 84.2%; Pred. No. 0.0023;
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GONEGOOTPEEDTTPPIV 19
 Db 856 GONEGOOTPEEDTTPPIV 874

RESULT 10
 Q6G6H4 PRELIMINARY; PRT; 957 AA.
 AC Q6G6H4;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Fibronectin-binding protein.
 GN Name=fnb3; Ordered locus names=SA93387;
 OS *Staphylococcus aureus* (strain MSSA476).
 OC Bacteria; Firmicutes; Bacillales; *Staphylococcus*.
 NCBI_TaxID=282459;
 RX PubMed=15213324; DOI=10.1073/pnas.040521101;
 RA Holden M.T.G., Fell E.J., Lindsay J.A., Peacock S.J., Day N.P.J., Barton A., Barrington M.C., Foster T.J., Moore C.E., Hurst L., Atkin R., Bason N., Bentley S.D., Chillingworth C., Chillingworth T., Churcher C., Clark L., Cotton C., Cronin A., Doggett J., Dowd L., Peltwell T., Hance Z., Harris B., Hauser H., Holtroyd S., Jørgensen K., James K.D., Lennard N., Line A., Mayes R., Moule S., Murgall K., Ormond D., Quail M.A., Rabinowitsch E., Rutherford K.W., Sanders M., Sharp S., Simmonds M., Stevens K., Whitehead S., Barrall B.G., Spratt B.G., Parkhill J.;
 RA "Complete genomes of two clinical *Staphylococcus aureus* strains: evidence for the rapid evolution of virulence and drug resistance." Proc. Natl. Acad. Sci. U.S.A. 101:9786-9791(2004).
 RL -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by an amide bond (By similarity).
 CC EMBL: BX571857; CAG44201.1; -;
 DR GO: GO:0009986; C:cell surface; IEA.
 DR GO: GO:0005618; C:cell wall; IEA.
 DR GO: GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
 DR GO: GO:0016020; C:membrane; IEA.
 DR InterPro: IPR008966; Adhes_bact.
 DR InterPro: IPR004237; Fn_bind.
 DR InterPro: IPR005877; Gpob_YsIRK.
 DR InterPro: IPR001899; Gram_pos_anchor.
 DR Pfam: PF02986; Fn_bind; 1.

DR Pfam: PF00746; Gram_pos_anchor; 1.
 DR Pfam: PF04650; YsIRK_signal; 1.
 DR TIGRfams: TIGR01167; LPXTG_anchor; 1.
 DR TIGRfams: TIGR01168; YsIRK_signal; 1.
 DR PROSITE: PS50847; GRAM_POS_ANCHORING; 1.
 DR Cell wall; Complete proteome; Peptidoglycan-anchor.
 SO SEQUENCE 957 AA; 105980 MW; 28F8BA7FFDFD3EAF CRC64;

Query Match 75.2%; Score 79; DB 2; Length 957;
 Best Local Similarity 78.9%; Pred. No. 0.011;
 Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GONEGOOTPEEDTTPPIV 19
 Db 803 GANEGOOTPEEDTTPPIV 821

RESULT 11
 Q8NUU8 PRELIMINARY; PRT; 943 AA.
 AC Q8NUU8;
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Fnb3 protein.
 GN Name=fnb3; Ordered locus names=NM2420;
 OS *Staphylococcus aureus* (strain MW2).
 OC Bacteria; Firmicutes; Bacillales; *Staphylococcus*.
 NCBI_TaxID=196620;
 RX PubMed=12044378; DOI=10.1016/S0140-6736(02)08713-5;
 RA Baba T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Oguchi A., Nagai Y., Iwama N., Asano K., Naimi T., Kuroda H., Cui L., Yamamoto K., Hiramatsu K.;
 RA "Genome and virulence determinants of high virulence community-acquired MRSA." Lancet 359:1819-1827(2002).
 RL Lancet 359:1819-1827(2002).
 CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by an amide bond (By similarity).
 CC EMBL: AP004830; BAB96285.1; -;
 DR HSP: Q51653; 1N67.
 DR GO: GO:0009986; C:cell surface; IEA.
 DR GO: GO:0005618; C:cell wall; IEA.
 DR GO: GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
 DR GO: GO:0016020; C:membrane; IEA.
 DR GO: GO:0007155; P:cell adhesion; IEA.
 DR InterPro: IPR008966; Adhes_bact.
 DR InterPro: IPR004237; Fn_bind.
 DR InterPro: IPR005877; Gpob_YsIRK.
 DR InterPro: IPR001899; Gram_pos_anchor.
 DR Pfam: PF02986; Fn_bind; 1.
 DR Pfam: PF00746; Gram_pos_anchor; 1.
 DR Pfam: PF04650; YsIRK_signal; 1.
 DR TIGRfams: TIGR01167; LPXTG_anchor; 1.
 DR TIGRfams: TIGR01168; YsIRK_signal; 1.
 DR PROSITE: PS50847; GRAM_POS_ANCHORING; 1.
 DR Cell wall; Complete proteome; Peptidoglycan-anchor.
 SO SEQUENCE 943 AA; 104537 MW; DA8A5F1947E1B6A CRC64;

Query Match 65.7%; Score 69; DB 2; Length 943;
 Best Local Similarity 73.7%; Pred. No. 0.31;
 Matches 14; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 GONEGOOTPEEDTTPPIV 19
 Db 803 GANEGOOTPEEDTTPPIV 821

RESULT 12
 CHID_BACCI STANDARD; PRT; 524 AA.

AC P27050.1992 (Rel. 23, Created)
 DT 01-AUG-1992 (Rel. 23, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Chitinase D precursor (EC 3.2.1.14).
 DB Chitinase D precursor (EC 3.2.1.14).
 GN Name-chid:
 OS Bacillus circulans.
 CC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
 OX NCBI_TaxID=1397;
 RN (1)
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 31-42.
 RC STRAIN=WL-12;
 RX MEDLINE=92105006; PubMed=1729234;
 RA Watanabe T., Oyanagi W., Suzuki K., Ohnishi K., Tanaka H.;
 RT "Structure of the gene encoding chitinase D of *Bacillus circulans* WL-
 RT 12 and possible homology of the enzyme to other prokaryotic chitinases
 RT and class III plant chitinases.";
 RL J. Bacteriol. 174:408-414(1992).
 RN (2)
 RP REVISIONS.
 RC STRAIN=WL-12;
 RA Watanabe T.;
 RL Submitted (NOV-1998) to the EMBL/Genbank/DBJ databases.
 CC -1- CATALYTIC ACTIVITY: Hydrolysis of the 1,4-beta-linkages of N-
 CC acetyl-D-glucosamine polymers of chitin.
 CC -1- SIMILARITY: Belongs to the glycosyl hydrolase 18 family. Chitinase
 CC class II subfamily.
 CC -1- SIMILARITY: Contains 1 fibronectin type III domain.
 CC -----
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 CC or send an email to license@isb-ebi.ch).
 CC -----
 DR EMBL, D10594; BAA34114.1; -.
 DR PIR, A41961; A41961.
 DR HSSP, P20533; 1ED7.
 DR InterPro: IPR003610; CSM_5_12.
 DR InterPro: IPR003961; FN_III.
 DR InterPro: IPR008957; FN_III-like.
 DR InterPro: IPR001223; Glyco_hydro_18.
 DR InterPro: IPR001579; Glyco_hydro_18AS.
 DR Pfam: PF02839; CSM_5_12; 1.
 DR Pfam: PF00041; fn3_1.
 DR Pfam: PF00704; Glyco_hydro_18; 1.
 DR PRINTS, PR00014; FNTYPEIII.
 DR SMART, SMO0495; ChtdB3; 1.
 DR SMART, SMO0060; FN3; 1.
 DR PROSITE, PS01095; CHITINASE_18; 1.
 DR PROSITE, PS50853; FN3; 1.
 DR Chitin degradation; Direct protein sequencing; Glycosidase; Hydrolase;
 KW Signal.
 KM 1 30
 FT SIGNAL. 1 30
 FT CHAIN 1 524 Chitinase D.
 FT DOMAIN 92 177 Fibronectin type-III.
 FT DOMAIN 180 524 Catalytic.
 FT ACT_SITE 303 303 Proton donor (by similarity).
 SQ SEQUENCE 524 AA, 55760 MW, 208DJ74902A741B6 CRC64;
 Query Match 56.2%; Score 59; DB 1; Length 524;
 Best Local Similarity 57.9%; Pred. No. 4.5;
 Matches 11; Conservative 1; Mismatches 7; Indels 0; Gaps 0;
 QY 1 GONEGQOTPEEDTTPPIVP 19
 | : | | | | | | | | | |
 DB GEGTGCGTPTPTTPTTPVP 96

ID	096005				
AC	096005	PRELIMINARY;	PRT;	561	AA.
DT	01-DEC-2001	(T'REMBL-rel, 19,	Created)		
DT	01-DEC-2001	(T'REMBL-rel, 19,	Last sequence update)		
DT	01-MAR-2002	(T'REMBL-rel, 20,	Last annotation update)		
DE	LD34444P.				
GN	ORENames=CG8155;				
OS	Drosophila melanogaster (Fruit fly).				
OC	Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;				
OC	Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;				
OX	Ephydroidea; Drosophilidae; Drosophila.				
OX	NCBI_TaxID=7227;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=Berkley;				
RA	Stapleton M., Broketein P., Hong L., Agbayani A., Carlson J.,				
RA	Champe M., Chavez C., Dorsett V., Farián D., Fries E., George R.,				
RA	González M., Guérin H., Li P., Liao G., Miranda A., Mungall C.J.,				
RA	Munro J., Paolel J., Paragas V., Park S., Phouanetavong S., Wan K.,				
RA	Yu C., Lewis S.E., Rubin G.M., Gelniker S.,				
RL	Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.				
DR	EMBL; AY051840; AAK93264.1; -				
DR	FLYbase; FBgn0034009; CG8155.				
DR	InterPro; IPR000195; RABGAP_TBC.				
QO	SEQUENCE 561 AA; 62030 MW; 315A866C42D48785D CRC64;				

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Query Match Similarity 53.3% Score 56 DB 2 Length 561;
Best Local 44.4% Pred. No. 13;
Matches 8; Conservative 6; Mismatches 4; Indels 0; Gaps 0;
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RESULT	14			
Q9V7A9				
ID	Q9V7A9	PRELIMINARY;	PRT;	1117 AA.
AC	Q9V7A9;			
DT	01-MAY-2000	(TREMBLrel. 13, Created)		
DT	01-OCT-2002	(TREMBLrel. 22, Last sequence update)		
DT	01-MAR-2003	(TREMBLrel. 23, Last annotation update)		
DE	CG8155-PA.			
GN	ORFNames=CG8155;			
OS	Drosophila melanogaster ('Fruit fly').			
OC	Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;			
OC	Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;			
OC	Ephydriodea; Drosophilidae; Drosophila.			
OX	NCBI_TaxId=7227;			
OX	[1]			
RN	SEQUENCE FROM N.A.			
RP	MEDLINE=20196006; PubMed=10731133; DOI=10.1126/science.287.5461.2185;			
RA	Adams M.D., Celisner S.E., Holt R.A., Evans C.A., Gocayne J.D.,			
RA	Amanatides P.G., Scherer S.E., Li P.W., Hopkins R.A., Galle R.F.,			
RA	George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,			
RA	Sutten G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,			
RA	Brandon R.C., Rogers Y.H., Blazel R.G., Champe M., Pfeiffer B.D.,			
RA	Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Gabor G.L.,			
RA	Abtill J.F., Agbayani A., An H.J., Andrews-Pfannkoch C., Baldwin D.,			
RA	Ballew R.M., Baau A., Bakendate J., Bayraktaroglu L., Beasley E.M.,			
RA	Beeson K.Y., Benos P.V., Bernan B.P., Bhandari D., Bolshakov S.,			
RA	Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotilier P.,			
RA	Buttis K.C., Busam D.A., Butler H., Cadieu E., Center A.J., Chandra I.,			
RA	Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,			
RA	de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,			
RA	Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,			
RA	Dubin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,			
RA	Foster C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,			
RA	Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,			
RA	Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,			
RA	Hoeft D., Houston K.A., Howland T.J., Wei M.H., Idegam C.,			
RA	Jalali M., Kalush F., Karpen G.H., Ke Z., Kennish J.A., Ketchum K.A.,			

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OM protein - protein search, using sw model

Run on: October 22, 2005, 03:51:22 ; Search time 21.1723 Seconds
(without alignments)
133.980 Million cell updates/sec

Title: US-10-731-238-45
Perfect score: 213
Sequence: 1 ONKGNQSPEDTEKDKPKYHGNIGNIDIDFDSVPHIG 38

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: Issued Patents AA:*
2: /cgn2_6/prodata/1/iaa/5A_COMB.pep:*
3: /cgn2_6/prodata/1/iaa/5B_COMB.pep:*
4: /cgn2_6/prodata/1/iaa/6A_COMB.pep:*
5: /cgn2_6/prodata/1/iaa/6B_COMB.pep:*
6: /cgn2_6/prodata/1/iaa/PORTUS_COMB.pep:*
7: /cgn2_6/prodata/1/iaa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysts of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	213	100.0	38	4	US-09-010-317-45 Sequence 45, Appl
2	202	94.8	38	1	US-08-234-622A-3 Sequence 3, Appl
3	202	94.8	38	4	US-09-010-317-7 Sequence 7, Appl
4	202	94.8	114	1	US-08-259-000-3 Sequence 3, Appl
5	202	94.8	139	3	US-08-856-253-8 Sequence 8, Appl
6	202	94.8	1027	4	US-08-956-171E-5254 Sequence 5254, Ap
7	202	94.8	1027	4	US-08-781-986A-5254 Sequence 7, Appl
8	197	92.5	130	2	US-08-459-135A-7 Sequence 8, Appl
9	197	92.5	130	2	US-08-459-135A-8 Sequence 8, Appl
10	197	92.5	130	3	US-08-495-559-7 Sequence 7, Appl
11	197	92.5	130	3	US-08-495-559-8 Sequence 8, Appl
12	197	92.5	174	2	US-08-459-135A-10 Sequence 10, Appl
13	197	92.5	174	3	US-08-495-559-10 Sequence 10, Appl
14	197	92.5	176	3	US-08-495-559-6 Sequence 6, Appl
15	197	92.5	178	2	US-08-459-135A-12 Sequence 12, Appl
16	197	92.5	178	3	US-08-495-559-12 Sequence 12, Appl
17	197	92.5	181	2	US-08-459-135A-6 Sequence 6, Appl
18	196	92.0	38	1	US-08-729-767-4 Sequence 4, Appl
19	196	92.0	38	4	US-09-010-317-46 Sequence 46, Appl
20	196	92.0	38	4	US-09-010-317-47 Sequence 47, Appl
21	195	91.5	38	4	US-09-010-317-48 Sequence 48, Appl
22	194	91.1	38	4	US-09-010-317-8 Sequence 8, Appl
23	194	91.1	38	4	US-09-010-317-49 Sequence 9, Appl
24	189	88.7	174	3	US-08-459-135A-13 Sequence 13, Appl
25	189	88.7	174	2	US-08-495-559-13 Sequence 5251, Ap
26	189	88.7	559	4	US-08-956-171E-5251 Sequence 5251, Ap
27	189	88.7	559	4	US-08-781-986A-5251 Sequence 5251, Ap

ALIGNMENTS

28	187	87.8	38	4	US-09-010-317-35	Sequence 35, Appl
29	179	84.0	36	4	US-09-010-317-58	Sequence 58, Appl
30	176	82.6	38	1	US-08-234-622A-2	Sequence 2, Appl
31	176	82.6	38	4	US-09-010-317-5	Sequence 5, Appl
32	174	81.7	38	4	US-09-010-317-41	Sequence 41, Appl
33	174	81.7	38	4	US-09-010-317-50	Sequence 50, Appl
34	171	80.3	36	4	US-09-010-317-59	Sequence 59, Appl
35	170	79.8	38	1	US-08-729-767-3	Sequence 3, Appl
36	170	79.8	38	4	US-09-010-317-36	Sequence 36, Appl
37	170	79.8	38	4	US-09-010-317-37	Sequence 37, Appl
38	170	79.8	38	4	US-09-010-317-39	Sequence 39, Appl
39	170	79.8	38	4	US-09-010-317-40	Sequence 40, Appl
40	169	79.3	38	4	US-09-010-317-38	Sequence 38, Appl
41	169	79.3	38	4	US-09-010-317-42	Sequence 42, Appl
42	168	78.9	38	4	US-09-010-317-43	Sequence 43, Appl
43	168	78.9	38	4	US-09-010-317-56	Sequence 56, Appl
44	165.5	77.7	39	4	US-09-010-317-57	Sequence 57, Appl
45	157.5	73.9	39	4	US-09-010-317-57	Sequence 57, Appl

RESULT 1
US-09-010-317-45
Sequence 45, Application US/09010317
Patent No. 6685943
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
APPLICANT: Patti, Joseph M.
APPLICANT: House-Pompeo, Karen L.
APPLICANT: Speziale, Pietro
APPLICANT: John, Danny
APPLICANT: McQuinn, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
TITLE OF INVENTION: AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSER: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 45:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-09-010-317-45
Query Match 100.0%; Score 213; DB 4; Length 38;
Best Local Similarity 100.0%; Pred. No. 3.7e-23;

Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ONKGNQSPEDTEKDKPKYEHGNIIDIDFDSVPHIHG 38
DB 1 ONKGNQSPEDTEKDKPKYEHGNIIDIDFDSVPHIHG 38

RESULT 2

US-08-234-622A-3
; Sequence 3, Application US/08234622A
; Patent No. 5440014
; GENERAL INFORMATION:
; APPLICANT: HOOK, Magnus
; APPLICANT: MCGAVIN, Martin
; APPLICANT: RAUCCI, Giuseppe
; TITLE OF INVENTION: A FIBRONECTIN BINDING PEPTIDE
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Doane, Swecker & Mathis
; STREET: P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 2213-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/234,622A
; FILING DATE: 28-APR-1994
; CLASSIFICATION: 530
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: SE 9002617-0
; FILING DATE: 10-AUG-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/SE91/00534
; FILING DATE: 09-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Meuth, Donna M.
; REGISTRATION NUMBER: 36,607
; REFERENCE/DOCKET NUMBER: 012885-044
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 38 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-234-622A-3

Query Match 94.8%; Score 202; DB 1; Length 38;
Best Local Similarity 97.4%; Pred. No. 1.3e-21;

Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ONKGNQSPEDTEKDKPKYEHGNIIDIDFDSVPHIHG 38
DB 1 ONKGNQSPEDTEKDKPKYEHGNIIDIDFDSVPHIHG 38

RESULT 3

US-09-010-317-7
; Sequence 7, Application US/09010317
; Patent No. 6685943
; GENERAL INFORMATION:
; APPLICANT: Hook, Magnus
; APPLICANT: Patti, Joseph M.
; APPLICANT: House-Pompeo, Karen L.
; APPLICANT: Speziale, Pietro

APPLICANT: Joh, Danny
; APPLICANT: McGavin, Martin J.
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
; TITLE OF INVENTION: AND METHODS OF USE
; NUMBER OF SEQUENCES: 105
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: TX
; COUNTRY: USA
; ZIP: 77210-4433
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/010,317
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/036,139
; FILING DATE: 21-JAN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Hilder, David W.
; REGISTRATION NUMBER: 41,071
; REFERENCE/DOCKET NUMBER: TAMK-189
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 512-474-7577
; TELEFAX: 512-418-3000
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 38 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; US-09-010-317-7

Query Match 94.8%; Score 202; DB 4; Length 38;
Best Local Similarity 97.4%; Pred. No. 1.3e-21;

Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ONKGNQSPEDTEKDKPKYEHGNIIDIDFDSVPHIHG 38
DB 1 ONKGNQSPEDTEKDKPKYEHGNIIDIDFDSVPHIHG 38

RESULT 4

US-08-259-000-3
; Sequence 3, Application US/08259000
; Patent No. 5571514
; GENERAL INFORMATION:
; APPLICANT: HOOK, Magnus
; APPLICANT: LINDBERG, Martin Kjell
; APPLICANT: SIGNAS, Lars Christer
; APPLICANT: WADSTROM, Torkel Mikael
; APPLICANT: ROMAN, Gunnar
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN AS WELL AS
; TITLE OF INVENTION: ITS PREPARATION
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Doane, Swecker & Mathis
; STREET: P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 2213-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/259,000
FILING DATE: 13-JUN-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: SE 8702272-9
FILING DATE: 01-JUN-1987
ATTORNEY/AGENT INFORMATION:
NAME: Meuth, Donna M
REGISTRATION NUMBER: 36,607
REFERENCE/DOCKET NUMBER: 012885-062
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-2021
TELEFAX: (703) 836-6620
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 114 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-259-000-3

Query Match 94.8%; Score 202; DB 1; Length 114;
Best Local Similarity 97.4%; Pred. No. 5,1e-21;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QNKGNSPEEDTEKDKPKYEHGNIIDIDPDSVPHIHG 38
DB 40 QNKGNSPEEDTEKDKPKYEHGNIIDIDPDSVPHIHG 77

RESULT 5
US-08-856-253-8
Sequence 8, Application US/08856253
Patent No. 6288214
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
APPLICANT: Patti, Joseph M.
APPLICANT: House-Pompeo, Karen
APPLICANT: Schanam, Narayana
APPLICANT: Symersky, Jindrich
TITLE OF INVENTION: COLLAGEN BINDING PROTEIN COMPOSITIONS
TITLE OF INVENTION: AND METHODS OF USE
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: Texas
COUNTRY: U.S.
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/856,253
FILING DATE: Concurrently Herewith
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/017,678
FILING DATE: 16-MAY-1996
ATTORNEY/AGENT INFORMATION:
NAME: Kitchell, Barbara S.
REGISTRATION NUMBER: 33,928
REFERENCE/DOCKET NUMBER: TAMK.193
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
TELEFAX: (512) 474-7577
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:

LENGTH: 139 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-08-856-253-8

Query Match 94.8%; Score 202; DB 3; Length 139;
Best Local Similarity 97.4%; Pred. No. 6,5e-21;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QNKGNSPEEDTEKDKPKYEHGNIIDIDPDSVPHIHG 38
DB 54 QNKGNSPEEDTEKDKPKYEHGNIIDIDPDSVPHIHG 91

RESULT 6
US-08-956-171E-5254
Sequence 5254, Application US/08956171E
Patent No. 6593114
GENERAL INFORMATION:
APPLICANT: Charles Kunach
Gail H. Choi
Patrick S. Dillon
Craig A. Rosen
Steven C. Barash
Michael R. Rannon
TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
NUMBER OF SEQUENCES: 5256
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COUNTRY: USA
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4MB storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/956,171E
FILING DATE: 20-Oct-1997
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/009,861
FILING DATE: January 5, 1996
APPLICATION NUMBER: 08/781,986
FILING DATE: January 3, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Mark J. Hyman
REGISTRATION NUMBER: 46,789
REFERENCE/DOCKET NUMBER: PB248P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (240) 314-1224
TELEFAX: (301) 309-8439
INFORMATION FOR SEQ ID NO: 5254:
SEQUENCE CHARACTERISTICS:
LENGTH: 1027 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 5254:
US-08-956-171E-5254

Query Match 94.8%; Score 202; DB 4; Length 1027;
Best Local Similarity 97.4%; Pred. No. 7,7e-20;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QNKGNSPEEDTEKDKPKYEHGNIIDIDPDSVPHIHG 38
DB 793 QNKGNSPEEDTEKDKPKYEHGNIIDIDPDSVPHIHG 830

RESULT 7
US-08-781-986A-5254
Sequence 5254, Application US/08781986A
Patent No. 6737248
GENERAL INFORMATION:
APPLICANT: Charles Kunach
TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
NUMBER OF SEQUENCES: 5255
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COUNTRY: USA
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/781,986A
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Benson, Bob
REGISTRATION NUMBER: 30,446
REFERENCE/DOCKET NUMBER: PB248PP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 5254:
SEQUENCE CHARACTERISTICS:
LENGTH: 1027 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-781-986A-5254
Query Match 94.8%; Score 202; DB 4; Length 1027;
Best Local Similarity 97.4%; Pred. No. 7.7e-20;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 1 QNKGNSPEEDTEKDKPKYEHGNIIDIDFDSVPHIHG 38
DB 793 QNKGNSPEEDTEKDKPKYEHGNIIDIDFDSVPHIHG 830
RESULT 8
US-08-459-135A-7
Sequence 7, Application US/08459135A
Patent No. 5955078
GENERAL INFORMATION:
APPLICANT: BURNHAM, Martin Karl Russel
APPLICANT: CHOPRA, Ian
APPLICANT: CRITCHLEY, Ian Alfred
APPLICANT: KNOWLES, David Justin Charles
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN: MONOCLONAL ANTIBODY AND THEIR US
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
STATE: PA
COUNTRY: U.S.A.
ZIP: 19406-0939
COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: Pastseq, Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/459,135A
FILING DATE: 02-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB/94/00215
FILING DATE: 04-Feb-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Gimm, Edward R
REGISTRATION NUMBER: 38,891
REFERENCE/DOCKET NUMBER: P30591C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-4478
TELEFAX: 610-270-5090
TELEX:
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 130 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-459-135A-7
Query Match 92.5%; Score 197; DB 2; Length 130;
Best Local Similarity 94.7%; Pred. No. 3.1e-20;
Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
OY 1 QNKGNSPEEDTEKDKPKYEHGNIIDIDFDSVPHIHG 38
DB 40 QNKGNSPEEDTEKDKPKYEHGNIIDIDFDSVPHIHG 77
RESULT 9
US-08-459-135A-8
Sequence 8, Application US/08459135A
Patent No. 5955078
GENERAL INFORMATION:
APPLICANT: BURNHAM, Martin Karl Russel
APPLICANT: CHOPRA, Ian
APPLICANT: CRITCHLEY, Ian Alfred
APPLICANT: KNOWLES, David Justin Charles
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN: MONOCLONAL ANTIBODY AND THEIR US
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
STATE: PA
COUNTRY: U.S.A.
ZIP: 19406-0939
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: Pastseq, Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/459,135A
FILING DATE: 02-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB/94/00215
FILING DATE: 04-Feb-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Gimm, Edward R
REGISTRATION NUMBER: 38,891
REFERENCE/DOCKET NUMBER: P30591C2
TELECOMMUNICATION INFORMATION:

TELEPHONE: 610-270-4478
TELEFAX: 610-270-5090
TELEX:
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 130 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-459-135A-8

Query Match 92.5%; Score 197; DB 2; Length 130;
Best Local Similarity 94.7%; Pred. No. 3.1e-20;
Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 QNKGNSPEEDTEKDKPKYEHGNIIDIDPDSVPHING 38
DB 40 QNKGDSFEEDTEKDKPKYEHGNIIDIDPDSVPHING 77

RESULT 10
US-08-495-559-7
Sequence 7, Application US/08495559A
Patent No. 6054572
GENERAL INFORMATION:
APPLICANT: BURNHAM, Martin Karl Russel
APPLICANT: CHOPRA, Ian
APPLICANT: CRITCHLEY, Ian Alfred
APPLICANT: KNOWLES, David Justin Charles
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN: MONOCLONAL
TITLE OF INVENTION: ANTIBODY AND THEIR USE IN PREVENTING BACTERIAL ADHESION
FILE REFERENCE: P30591
CURRENT APPLICATION NUMBER: US/08/495,559A
CURRENT FILING DATE: 1995-08-03
EARLIER APPLICATION NUMBER: GB 9302289.5
EARLIER FILING DATE: 1993-02-05
EARLIER APPLICATION NUMBER: GB 9321592.9
EARLIER FILING DATE: 1993-10-20
NUMBER OF SEQ ID NOS: 13
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 7
LENGTH: 130
TYPE: PRT
ORGANISM: Staphylococcus aureus
US-08-495-559-7

Query Match 92.5%; Score 197; DB 3; Length 130;
Best Local Similarity 94.7%; Pred. No. 3.1e-20;
Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 QNKGNSPEEDTEKDKPKYEHGNIIDIDPDSVPHING 38
DB 40 QNKGDSFEEDTEKDKPKYEHGNIIDIDPDSVPHING 77

RESULT 11
US-08-495-559-8
Sequence 8, Application US/08495559A
Patent No. 6054572
GENERAL INFORMATION:
APPLICANT: BURNHAM, Martin Karl Russel
APPLICANT: CHOPRA, Ian
APPLICANT: CRITCHLEY, Ian Alfred
APPLICANT: KNOWLES, David Justin Charles
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN: MONOCLONAL
TITLE OF INVENTION: ANTIBODY AND THEIR USE IN PREVENTING BACTERIAL ADHESION
FILE REFERENCE: P30591
CURRENT APPLICATION NUMBER: US/08/495,559A
CURRENT FILING DATE: 1995-08-03
EARLIER APPLICATION NUMBER: GB 9302289.5
EARLIER FILING DATE: 1993-02-05
EARLIER APPLICATION NUMBER: GB 9321592.9
EARLIER FILING DATE: 1993-10-20

NUMBER OF SEQ ID NOS: 13
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 8
LENGTH: 130
TYPE: PRT
ORGANISM: Staphylococcus aureus
US-08-495-559-8

Query Match 92.5%; Score 197; DB 3; Length 130;
Best Local Similarity 94.7%; Pred. No. 3.1e-20;
Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 QNKGNSPEEDTEKDKPKYEHGNIIDIDPDSVPHING 38
DB 40 QNKGDSFEEDTEKDKPKYEHGNIIDIDPDSVPHING 77

RESULT 12
US-08-459-135A-10
Sequence 10, Application US/08459135A
Patent No. 5955078
GENERAL INFORMATION:
APPLICANT: BURNHAM, Martin Karl Russel
APPLICANT: CHOPRA, Ian
APPLICANT: CRITCHLEY, Ian Alfred
APPLICANT: KNOWLES, David Justin Charles
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN: MONOCLONAL ANTIBODY AND THEIR USE
CORRESPONDENCE ADDRESS:
ADDRESSER: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
STATE: PA
COUNTRY: U.S.A.
ZIP: 19406-0939
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq, Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/459,135A
FILING DATE: 02-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB/94/00215
FILING DATE: 04-Feb-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Gimmil, Edward R
REGISTRATION NUMBER: 38,891
REFERENCE/DOCKET NUMBER: P30591C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-4478
TELEFAX: 610-270-5090
TELEX:
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 174 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-459-135A-10

Query Match 92.5%; Score 197; DB 2; Length 174;
Best Local Similarity 94.7%; Pred. No. 4.4e-20;
Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 QNKGNSPEEDTEKDKPKYEHGNIIDIDPDSVPHING 38
DB 40 QNKGDSFEEDTEKDKPKYEHGNIIDIDPDSVPHING 77


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RESULT 13
US-08-495-559-10
; Sequence 10, Application US/08495559A
; Patent No. 6054572
; GENERAL INFORMATION:
; APPLICANT: BURHAM, Martin Karl Russel
; APPLICANT: CHOPRA, Ian
; APPLICANT: CRITCHLEY, Ian Alfred
; APPLICANT: KNOWLES, David Justin Charles
; TITLE OF INVENTION: FIBROBLAST BINDING PROTEIN: MONOCLONAL
; FILE REFERENCE: P30591
; CURRENT FILING DATE: 1995-08-03
; EARLIER FILING DATE: 1993-02-05
; EARLIER APPLICATION NUMBER: GB 9321592.9
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 10
; LENGTH: 174
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-08-495-559-10

Query Match      92.5%; Score 197; DB 3; Length 174;
Best Local Similarity 94.7%; Pred. No. 4.4e-20;
Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 ONKGNQSPEDTEKDKPKYEHGNIIDIDFDSVPHIHG 38
DB 40 ONKGDQSPEDTEKDKPKYEHGNIIDIDFDSVPHIHG 77

RESULT 14
US-08-495-559-6
; Sequence 6, Application US/08495559A
; Patent No. 6054572
; GENERAL INFORMATION:
; APPLICANT: BURHAM, Martin Karl Russel
; APPLICANT: CHOPRA, Ian
; APPLICANT: CRITCHLEY, Ian Alfred
; APPLICANT: KNOWLES, David Justin Charles
; TITLE OF INVENTION: FIBROBLAST BINDING PROTEIN: MONOCLONAL
; FILE REFERENCE: P30591
; CURRENT FILING DATE: 1995-08-03
; EARLIER FILING DATE: 1993-02-05
; EARLIER APPLICATION NUMBER: GB 9321592.9
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 176
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-08-495-559-6

Query Match      92.5%; Score 197; DB 3; Length 176;
Best Local Similarity 94.7%; Pred. No. 4.4e-20;
Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
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; Patent No. 595078
; GENERAL INFORMATION:
; APPLICANT: BURHAM, Martin Karl Russel
; APPLICANT: CHOPRA, Ian
; APPLICANT: CRITCHLEY, Ian Alfred
; APPLICANT: KNOWLES, David Justin Charles
; TITLE OF INVENTION: FIBROBLAST BINDING PROTEIN: MONOCLONAL ANTIBODY AND THEIR US
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESS: Smithkline Beecham Corporation
; STREET: 709 Swedeland Road
; CITY: King of Prussia
; STATE: PA
; COUNTRY: U.S.A.
; ZIP: 19406-0939
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq, Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/459,135A
; FILING DATE: 02-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB/94/00215
; FILING DATE: 04-Feb-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Gimmil, Edward R
; REGISTRATION NUMBER: 38,891
; REFERENCE/DOCKET NUMBER: P30591C2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-270-4478
; TELEFAX: 610-270-5090
;
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 178 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Protein
US-08-459-135A-12

Query Match      92.5%; Score 197; DB 2; Length 178;
Best Local Similarity 94.7%; Pred. No. 4.5e-20;
Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 ONKGNQSPEDTEKDKPKYEHGNIIDIDFDSVPHIHG 38
DB 40 ONKGDQSPEDTEKDKPKYEHGNIIDIDFDSVPHIHG 77
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Search completed: October 22, 2005, 05:46:46
Job time : 22.2223 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: October 22, 2005, 11:35:03 ; Search time 70.1256 Seconds
(without alignments)
226.232 Million cell updates/sec

Title: US-10-731-238-45
Perfect score: 213
Sequence: 1 ONKGNQSPEDTEKDKPKYEHGNIIDIDFDSVPHIHG 38

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1862951 seqs, 417491010 residues

Total number of hits satisfying chosen parameters: 1862951

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
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9: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep.*
10: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep.*
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13: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep.*
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15: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep.*
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18: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep.*
19: /cgn2_6/ptodata/2/pubpaa/US11_PUBCOMB.pep.*
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22: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	213	100.0	38	18	US-10-731-238-45
2	202	94.8	38	18	US-10-731-238-45
3	202	94.8	139	9	US-09-813-820-8
4	202	94.8	1018	9	US-09-815-242-5797
5	202	94.8	1018	9	US-09-815-242-12838
6	202	94.8	1018	17	US-10-470-048B-68
7	202	94.8	1027	8	US-08-781-986A-5254
8	202	94.8	1027	15	US-10-329-624-5254
9	196	92.0	38	18	US-10-731-238-45
10	196	92.0	38	18	US-10-731-238-47
11	195	91.5	38	18	US-10-731-238-48

12	194	91.1	38	18	US-10-731-238-8	Sequence 8, Appli
13	194	91.1	38	18	US-10-731-238-49	Sequence 49, Appli
14	189	88.7	388	8	US-08-901-062-1	Sequence 1, Appli
15	189	88.7	559	8	US-08-781-986A-5251	Sequence 5251, Ap
16	189	88.7	559	15	US-10-329-624-5251	Sequence 5899, Ap
17	189	88.7	767	9	US-09-815-242-5899	Sequence 13140, A
18	189	88.7	767	9	US-09-815-242-13140	Sequence 424, App
19	189	88.7	940	17	US-10-470-048B-424	Sequence 69, Appli
20	189	88.7	948	17	US-10-470-048B-69	Sequence 43827, A
21	189	88.7	1038	15	US-10-282-122A-43827	Sequence 35, Appli
22	187	87.8	38	18	US-10-731-238-35	Sequence 5455, Ap
23	181	85.0	978	9	US-09-815-242-5456	Sequence 12686, A
24	181	85.0	1001	9	US-09-815-242-12686	Sequence 58, Appli
25	179	84.0	36	18	US-10-731-238-58	Sequence 43778, A
26	177	83.1	961	15	US-10-282-122A-43778	Sequence 5, Appli
27	176	82.6	38	18	US-10-731-238-5	Sequence 41, Appli
28	174	81.7	38	18	US-10-731-238-41	Sequence 59, Appli
29	174	81.7	38	18	US-10-731-238-59	Sequence 36, Appli
30	171	80.3	36	18	US-10-731-238-36	Sequence 37, Appli
31	170	79.8	38	18	US-10-731-238-37	Sequence 39, Appli
32	170	79.8	38	18	US-10-731-238-39	Sequence 40, Appli
33	170	79.8	38	18	US-10-731-238-40	Sequence 38, Appli
34	170	79.8	38	18	US-10-731-238-38	Sequence 42, Appli
35	169	79.3	38	18	US-10-731-238-42	Sequence 6, Appli
36	169	79.3	38	18	US-10-731-238-6	Sequence 43, Appli
37	168	78.9	38	18	US-10-731-238-43	Sequence 56, Appli
38	168	78.9	38	18	US-10-731-238-56	Sequence 44, Appli
39	165.5	77.7	39	18	US-10-731-238-57	Sequence 1, Appli
40	157.5	73.9	39	18	US-10-731-238-44	Sequence 2, Appli
41	148	69.5	38	14	US-10-287-821-1	Sequence 114, Ap
42	136	63.8	31	14	US-10-287-821-2	Sequence 103, App
43	136	63.8	31	14	US-10-287-821-2	
44	88.5	41.5	37	20	US-11-066-657-1134	
45	77	36.2	14	18	US-10-731-238-103	

ALIGNMENTS

RESULT 1
US-10-731-238-45
Sequence 45, Application US/10731238
Publication No. US20050123552A1
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
Patti, Joseph M.
House-Pompeo, Karen L.
Speziale, Pietro
John, Danny
McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSER: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version. #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/731,238
FILING DATE: 10-Dec-2003
CLASSIFICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE: 21-Jan-1998
APPLICATION NUMBER: US 60/036,139

FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TANK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 45:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 45:
US-10-731-238-45

Query Match 100.0%; Score 213; DB 18; Length 38;
Best Local Similarity 100.0%; Pred. No. 1,1e-20;
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ONKGNQSPEDTEKDKPKYEHGNGNIIDIDFDSVPHIHG 38
DB 1 ONKGNQSPEDTEKDKPKYEHGNGNIIDIDFDSVPHIHG 38

RESULT 2
US-10-731-238-7
Sequence 7, Application US/10731238
Publication No. US20050123552A1
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
Pattl, Joseph M.
House-Pompeo, Karen L.
Speziale, Pietro
Joh, Danny
McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/731,238
FILING DATE: 10-Dec-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE: 21-Jan-1998
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TANK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>

TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-10-731-238-7

Query Match 94.8%; Score 202; DB 18; Length 38;
Best Local Similarity 97.4%; Pred. No. 3,2e-19;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ONKGNQSPEDTEKDKPKYEHGNGNIIDIDFDSVPHIHG 38
DB 1 ONKGNQSPEDTEKDKPKYEHGNGNIIDIDFDSVPHIHG 38

RESULT 3
US-09-813-820-8
Sequence 8, Application US/09813820
Patent No. US20020102262A1
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
Pattl, Joseph M.
House-Pompeo, Karen
Shanam, Narayana
Symerky, Jindrich
TITLE OF INVENTION: COLLAGEN BINDING PROTEIN COMPOSITIONS
AND METHODS OF USE
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: Texas
COUNTRY: U.S.
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/813,820
FILING DATE: 22-Mar-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/856,253
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Kitchenell, Barbara S.
REGISTRATION NUMBER: 33,928
REFERENCE/DOCKET NUMBER: TANK:193
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
TELEFAX: (512) 474-7577
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 139 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-09-813-820-8

Query Match 94.8%; Score 202; DB 9; Length 139;
Best Local Similarity 97.4%; Pred. No. 1,5e-18;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ONKGNQSPEDTEKDKPKYEHGNGNIIDIDFDSVPHIHG 38
DB 54 ONKGNQSPEDTEKDKPKYEHGNGNIIDIDFDSVPHIHG 91

RESULT 4
US-09-815-242-5797
Sequence 5797, Application US/09815242

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; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari L.
; APPLICANT: Zykkind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; FILE OF INVENTION: Prokaryotes
; FILE REFERENCE: ELITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5797
; LENGTH: 1018
; TYPE: PRF
; ORGANISM: Staphylococcus aureus
; US-09-815-242-5797

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Query Match          94.8%; Score 202; DB 9; Length 1018;
Best Local Similarity 97.4%; Pred. No. 1,5e-17;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy 1 ONKGNQSPEDTEKDKPKYEHGNIIDIDFDSVPHIHG 38
Db 784 ONKGNQSPEDTEKDKPKYEHGNIIDIDFDSVPHIHG 821

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RESULT 5
US-09-815-242-12838
; Sequence 12838, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari L.
; APPLICANT: Zykkind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; FILE OF INVENTION: Prokaryotes
; FILE REFERENCE: ELITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625

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; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12838
; LENGTH: 1018
; TYPE: PRF
; ORGANISM: Staphylococcus aureus
; US-09-815-242-12838

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Query Match          94.8%; Score 202; DB 9; Length 1018;
Best Local Similarity 97.4%; Pred. No. 1,5e-17;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy 1 ONKGNQSPEDTEKDKPKYEHGNIIDIDFDSVPHIHG 38
Db 784 ONKGNQSPEDTEKDKPKYEHGNIIDIDFDSVPHIHG 821

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RESULT 6
US-10-470-048B-68
; Sequence 68, Application US/10470048B
; Publication No. US2005003744A1
; GENERAL INFORMATION:
; APPLICANT: MEINKE ET AL.
; TITLE OF INVENTION: A METHOD FOR IDENTIFICATION, ISOLATION AND PRODUCTION OF
; FILE OF INVENTION: ANTIGENS TO A SPECIFIC PATHOGEN
; FILE REFERENCE: SONN-035US
; CURRENT APPLICATION NUMBER: US/10/470,048B
; CURRENT FILING DATE: 2003-07-25
; NUMBER OF SEQ ID NOS: 603
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 68
; LENGTH: 1018
; TYPE: PRF
; ORGANISM: Staphylococcus aureus
; US-10-470-048B-68

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Query Match          94.8%; Score 202; DB 17; Length 1018;
Best Local Similarity 97.4%; Pred. No. 1,5e-17;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy 1 ONKGNQSPEDTEKDKPKYEHGNIIDIDFDSVPHIHG 38
Db 784 ONKGNQSPEDTEKDKPKYEHGNIIDIDFDSVPHIHG 821

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RESULT 7
US-08-781-986A-5254
; Sequence 5254, Application US/08781986A
; Publication No. US20030054436A1
; GENERAL INFORMATION:
; APPLICANT: Charles Kunesh
; TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
; NUMBER OF SEQUENCES: 5255
; CORRESPONDENCE ADDRESSES:
; ADDRESSER: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4mb storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/781,986A
; FILING DATE:

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CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Benson, Bob
REGISTRATION NUMBER: 30,446
REFERENCE/DOCKET NUMBER: PB248PP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 5254:
SEQUENCE CHARACTERISTICS:
LENGTH: 1027 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-781-986A-5254

Query Match 94.8%; Score 202; DB 8; Length 1027;
Best Local Similarity 97.4%; Pred. No. 1,5e-17;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ONKGNQSPEDTEKDKPKYEHGNIIDIDFDSVPHING 38
Db 793 ONKGNQSPEDTEKDKPKYEHGNIIDIDFDSVPHING 830

RESULT 8
US-10-329-624-5254
Sequence 5254, Application US/10329624
Publication No. US20040043037A1
GENERAL INFORMATION:
APPLICANT: Charles Kunach
Gill H. Choi
Patrick S. Dillon
Craig A. Rosen
Steven C. Barash
Michael R. Fannin
TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
NUMBER OF SEQUENCES: 5256
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COUNTRY: USA
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/329,624
FILING DATE: 27-Dec-2002
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/956,171
FILING DATE: October 20, 1997
APPLICATION NUMBER: 60/009,861
FILING DATE: January 5, 1996
APPLICATION NUMBER: 08/781,986
FILING DATE: January 3, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Mark J. Hyman
REGISTRATION NUMBER: 46,789
REFERENCE/DOCKET NUMBER: PB248P1D1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (240) 314-1224
TELEFAX: (301) 309-8439
INFORMATION FOR SEQ ID NO: 5254:
SEQUENCE CHARACTERISTICS:

LENGTH: 1027 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 5254:
US-10-329-624-5254

Query Match 94.8%; Score 202; DB 15; Length 1027;
Best Local Similarity 97.4%; Pred. No. 1,5e-17;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ONKGNQSPEDTEKDKPKYEHGNIIDIDFDSVPHING 38
Db 793 ONKGNQSPEDTEKDKPKYEHGNIIDIDFDSVPHING 830

RESULT 9
US-10-731-238-46
Sequence 46, Application US/10731238
Publication No. US20050123552A1
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
Patti, Joseph M.
House-Pompeo, Karen L.
Speziale, Pietro
Joh, Danny
McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/731,238
FILING DATE: 10-Dec-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE: 21-Jan-1998
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-Jan-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAWK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 46:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 46:
US-10-731-238-46

Query Match 92.0%; Score 196; DB 18; Length 38;
Best Local Similarity 94.7%; Pred. No. 2e-18;
Matches 36; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ONKGNQSPEDTEKDKPKYEHGNIIDIDFDSVPHING 38

Db 1 ONKGNQSPEDTEKDKPKYEHGNIIDIDFDSVPHIHG 38

RESULT 10
US-10-731-238-47

Sequence 47, Application US/10731238
Publication No. US20050123552A1
GENERAL INFORMATION:

APPLICANT: Hook, Magnus

Parti, Joseph M.
House-Pompeo, Karen L.
Speziale, Pietro

Joh, Danny

McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
AND METHODS OF USE

NUMBER OF SEQUENCES: 105

CORRESPONDENCE ADDRESS:

ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX

COUNTRY: USA
ZIP: 77210-4433

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/731,238
FILING DATE: 10-Dec-2003
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE: 21-Jan-1998
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997

ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAMK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577

INFORMATION FOR SEQ ID NO: 47:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear

US-10-731-238-47
SEQUENCE DESCRIPTION: SEQ ID NO: 47:
Query Match 92.0%; Score 196; DB 18; Length 38;
Best Local Similarity 94.7%; Pred. No. 2e-18; 2; Indels 0; Gaps 0;
Matches 36; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ONKGNQSPEDTEKDKPKYEHGNIIDIDFDSVPHIHG 38
Db 1 ONKGNQSPEDTEKDKPKYEHGNIIDIDFDSVPHIHG 38

RESULT 11
US-10-731-238-48

Sequence 48, Application US/10731238
Publication No. US20050123552A1
GENERAL INFORMATION:

APPLICANT: Hook, Magnus

Parti, Joseph M.
House-Pompeo, Karen L.
Speziale, Pietro

Joh, Danny
McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
AND METHODS OF USE

NUMBER OF SEQUENCES: 105

CORRESPONDENCE ADDRESS:

ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX

COUNTRY: USA
ZIP: 77210-4433

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/731,238

FILING DATE: 10-Dec-2003
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317

FILING DATE: 21-Jan-1998
APPLICATION NUMBER: US 60/036,139

FILING DATE: 21-JAN-1997

ATTORNEY/AGENT INFORMATION:

NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAMK:189

TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577

INFORMATION FOR SEQ ID NO: 48:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear

US-10-731-238-48
SEQUENCE DESCRIPTION: SEQ ID NO: 48:
Query Match 91.5%; Score 195; DB 18; Length 38;
Best Local Similarity 94.7%; Pred. No. 2.7e-18;
Matches 36; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ONKGNQSPEDTEKDKPKYEHGNIIDIDFDSVPHIHG 38
Db 1 ONKGNQSPEDTEKDKPKYEHGNIIDIDFDSVPHIHG 38

RESULT 12
US-10-731-238-8

Sequence 8, Application US/10731238
Publication No. US20050123552A1
GENERAL INFORMATION:

APPLICANT: Hook, Magnus

Parti, Joseph M.
House-Pompeo, Karen L.
Speziale, Pietro

Joh, Danny

McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
AND METHODS OF USE

NUMBER OF SEQUENCES: 105

CORRESPONDENCE ADDRESS:

ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX

COUNTRY: USA
ZIP: 77210-4433

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/731,238
FILING DATE: 10-Dec-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE: 21-Jan-1998
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TANK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-10-731-238-8

Query Match 91.1%; Score 194; DB 18; Length 38;
Best Local Similarity 94.7%; Pred. No. 3,6e-18;
Matches 36; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ONKGNQSPEDTEKDKPKYEHGNIIDIDFDSVPHHG 38
Db 1 ONKGNQSPEDTEKDKPKYEHGNIIDIDFDSVPHHG 38

RESULT 13
US-10-731-238-49
Sequence 49, Application US/10731238
Publication No. US20050123552A1
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
Patti, Joseph M.
House-Pompeo, Karen L.
Speziale, Pietro
Joh, Danny
McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/731,238
FILING DATE: 10-Dec-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE: 21-Jan-1998
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997

ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TANK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 49:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 49:
US-10-731-238-49

Query Match 91.1%; Score 194; DB 18; Length 38;
Best Local Similarity 94.7%; Pred. No. 3,6e-18;
Matches 36; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ONKGNQSPEDTEKDKPKYEHGNIIDIDFDSVPHHG 38
Db 1 ONKGNQSPEDTEKDKPKYEHGNIIDIDFDSVPHHG 38

RESULT 14
US-08-901-062-1
Sequence 1, Application US/08901062
Publication No. US20020025324A1
GENERAL INFORMATION:
APPLICANT: SEALS, JONATHAN R.
TITLE OF INVENTION: RECOMBINANT BIVALENT BACTERIAL VACCINE
TITLE OF INVENTION: FOR THE PREVENTION OF MASTITIS
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: HALE AND DORR LLP
STREET: 60 State Street
CITY: Boston
STATE: MA
COUNTRY: United States Of America
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/901,062
FILING DATE: 25-JUL-1997
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Baker, Hollie L.
REGISTRATION NUMBER: 31,321
REFERENCE/DOCKET NUMBER: 106941.153
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 526-6000
TELEFAX: (617)526-5000
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 388 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-901-062-1

Query Match 88.7%; Score 189; DB 8; Length 388;
Best Local Similarity 92.1%; Pred. No. 2,5e-16;
Matches 35; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 ONKGNQSPEDTEKDKPKYEHGNIIDIDFDSVPHHG 38

Db 303 QNNGNQFEEDTEKDKPKYEGGNIIDIDFDSVPHIHG 340

RESULT 15
US-08-781-986A-5251

```

Sequence 551. Application US/08781986A
Publication No. US20030054435A1
GENERAL INFORMATION:
APPLICANT: Charles Kunsch
TITLE OF INVENTION: Staphylococcus aureus Polymucl[ei]otides and Sequences
NUMBER OF SEQUENCES: 5255
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COUNTRY: USA
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/781,986A
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Benson, Bob
REGISTRATION NUMBER: 30,446
REFERENCE/DOCKET NUMBER: P2248PP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 5251:
SEQUENCE CHARACTERISTICS:
LENGTH: 559 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-781-986A-5251

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Query Match	88.7%	Score 189;	DB 8;	Length 559;
Best Local Similarity	92.1%	Pred. No. 3.9e-16;		
Matches 35; Conservative	0;	Mismatches 3;	Indels 0;	Gaps 0

Oy 1 QNKGNSPEEDTEKPKYEHGNNIIDIDPDSVPHHG 38
 |||||
Db 339 QNKGNSFEEDTEKPKYEAGNIIDIDPDSVPHHG 376

Search completed: October 22, 2005, 12:09:28
Job time : 71.1256 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 22, 2005, 04:14:19 ; Search time 13.8905 Seconds
(without alignments)
263.219 Million cell updates/sec

Title: US-10-731-238-45

Perfect score: 213

Sequence: 1 QNKGNSPEEDTEKDKPKYEHGNIIDIDPDSVPHING 38

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing filter 45 summaries

Database: PIR_79:*

1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	202	94.8	1018	2	A32192 fibronectin-binding
2	189	88.7	940	2	S19702 fibronectin-binding
3	189	88.7	1038	2	H90053 fibronectin-binding
4	177	83.1	961	2	G90053 fibronectin-binding
5	60.5	28.4	214	2	A89895 fibronectin-binding
6	57	26.8	442	2	H72266 fibronectin-binding
7	56.5	26.3	788	2	T30510 fibronectin-binding
8	56	26.3	264	2	C87605 fibronectin-binding
9	55	25.8	345	2	T33966 fibronectin-binding
10	54.5	25.6	603	2	S34130 fibronectin-binding
11	54.5	25.6	786	2	A35466 fibronectin-binding
12	54	25.4	400	2	S67062 fibronectin-binding
13	54	25.4	400	2	T41569 fibronectin-binding
14	54	25.4	1817	2	T34249 fibronectin-binding
15	53	24.9	218	2	A95232 fibronectin-binding
16	53	24.9	218	2	G98096 fibronectin-binding
17	53	24.9	391	1	S15617 fibronectin-binding
18	53	24.9	427	1	S38002 fibronectin-binding
19	53	24.9	481	2	T15657 fibronectin-binding
20	53	24.9	683	2	S34961 fibronectin-binding
21	53	24.9	790	2	T7959 fibronectin-binding
22	52.5	24.6	511	1	S1308 fibronectin-binding
23	52	24.4	155	2	H97849 fibronectin-binding
24	52	24.4	428	2	T32952 fibronectin-binding
25	52	24.4	558	2	C71609 fibronectin-binding
26	52	24.4	606	1	S24758 fibronectin-binding
27	52	24.4	658	2	B85024 fibronectin-binding
28	52	24.4	841	2	B82755 fibronectin-binding
29	52	24.4	1157	2	T19187 fibronectin-binding

30	52	24.4	2910	2	T28156
31	52	24.4	5138	2	B96695
32	51.5	24.2	381	2	E95142
33	51.5	24.2	391	2	C98010
34	51.5	24.2	952	2	AG1209
35	51.5	24.2	1010	1	PK282P
36	51.5	24.2	1339	2	JC5508
37	51	23.9	436	2	F82354
38	51	23.9	653	2	T32320
39	50.5	23.7	333	2	F90014
40	50.5	23.7	361	2	T51078
41	50.5	23.7	511	2	E84685
42	50.5	23.7	1273	1	TDRLT
43	50.5	23.7	1291	1	A28334
44	50	23.5	265	2	A43738
45	50	23.5	398	2	D83956

ALIGNMENTS

DNA-directed RNA p
hypothetical prote
A/G-specific aden
A/G-specific aden
B. subtilis Yfho p
H+-exporting ATPas
DNA-directed DNA p
hypothetical prote
hypothetical prote
hypothetical prote
related to homeoti
probable seed stor
leucocyte common a
protein-tyrosine-p
Endo16 protein - s
hypothetical prote

RESULT 1
A32192
fibronectin-binding protein - Staphylococcus aureus
C/Species: Staphylococcus aureus
C/Date: 31-Jul-1989 #sequence_revision 31-Jul-1989 #text_change 16-Feb-1997
C/Accession: A32192
R/Sigmaes, C.; Raucel, G.; Joenson, K.; Lindgren, P.E.; Anantharamaiah, G.M.; Hoeck,
Proc. Natl. Acad. Sci. U.S.A. 86, 699-703, 1989
A/Title: Nucleotide sequence of the gene for a fibronectin-binding protein from Staphy
A/Reference number: A32192; MUID:8908998; PMID:2521391
A/Accession: A32192
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-1018 <SIG>
A/Cross-references: GB:J04151
C/Keywords: fibronectin binding

Query Match 94.8%; Score 202; DB 2; Length 1018;
Best Local Similarity 97.4%; Pred. No. 1.1e-17;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QNKGNSPEEDTEKDKPKYEHGNIIDIDPDSVPHING 38
DB 784 QNKGNSPEEDTEKDKPKYEHGNIIDIDPDSVPHING 821

RESULT 2

S19702
fibronectin-binding protein B - Staphylococcus aureus
C/Species: Staphylococcus aureus
C/Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
C/Accession: S19702
R/Joenson, K.; Sigmaes, C.; Mueller, H.P.; Lindberg, M.
Eur. J. Biochem. 202, 1041-1048, 1991
A/Title: Two different genes encode fibronectin binding proteins in Staphylococcus aure
A/Reference number: S19702; MUID:9211475; PMID:1857286
A/Accession: S19702
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-940 <JOB>
A/Cross-references: UNIPROT:Q51682; EMBL:X62992; NID:949040; PIDD:CAA44726.1; PID:95815
C/Keywords: fibronectin binding

Query Match 88.7%; Score 189; DB 2; Length 940;
Best Local Similarity 92.1%; Pred. No. 4.8e-16;
Matches 35; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 QNKGNSPEEDTEKDKPKYEHGNIIDIDPDSVPHING 38
DB 720 QNKGNSPEEDTEKDKPKYEHGNIIDIDPDSVPHING 757

```
RESULT 3
H90053
Hypothetical protein fnb [imported] - Staphylococcus aureus (strain N315)
C/Species: Staphylococcus aureus
C/Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C/Accession: H90053
R/Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguc
ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kato, C.; Sekimizu, K.;
C.; Shibba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
A/Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.
A/Reference number: A89758; PMID:21311952; PMID:11418146
A/Accession: H90053
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-1038 <KUR>
A/Cross-references: UNIPROT:Q99RD2; GB:BA000018; PID:g13702453; PIDN:BA843594.1; GSPDB:G
A/Experimental source: strain N315
C/Genetics:
A/Gene: fnb

Query Match      88.7%; Score 189; DB 2; Length 1038;
Best Local Similarity 92.1%; Pred. No. 5.3e-16;
Matches 35; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      1 QNKGNSPEDTEKDKPKYEHGNIIDIDPDSVPHIHG 38
DB      780 QNKGNSPEDTEKDKPKYEHGNIIDIDPDSVPHIHG 817

RESULT 4
G90053
Hypothetical protein fnb [imported] - Staphylococcus aureus (strain N315)
C/Species: Staphylococcus aureus
C/Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C/Accession: G90053
R/Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguc
ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kato, C.; Sekimizu, K.;
C.; Shibba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
A/Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.
A/Reference number: A89758; PMID:21311952; PMID:11418146
A/Accession: G90053
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-961 <KUR>
A/Cross-references: UNIPROT:Q99RD3; GB:BA000018; PID:g13702452; PIDN:BA843593.1; GSPDB:G
A/Experimental source: strain N315
C/Genetics:
A/Gene: fnb

Query Match      83.1%; Score 177; DB 2; Length 961;
Best Local Similarity 86.8%; Pred. No. 1.7e-14;
Matches 33; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY      1 QNKGNSPEDTEKDKPKYEHGNIIDIDPDSVPHIHG 38
DB      731 QNKGNSPEDTEKDKPKYEHGNIIDIDPDSVPHIHG 768

RESULT 5
A89895
Hypothetical protein cfxe [imported] - Staphylococcus aureus (strain N315)
C/Species: Staphylococcus aureus
C/Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C/Accession: A89895
R/Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguc
ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kato, C.; Sekimizu, K.;
C.; Shibba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
A/Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.
A/Reference number: A89758; PMID:21311952; PMID:11418146
A/Accession: A89895
```

```
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-214 <KUR>
A/Cross-references: UNIPROT:Q99UP6; GB:BA000018; PID:g13701022; PIDN:BA842317.1; GSPDB:G
A/Experimental source: strain N315
C/Genetics:
A/Gene: cfxe
C/Superfamily: yeast ribulose-5-phosphate-epimerase

Query Match      28.4%; Score 60.5; DB 2; Length 214;
Best Local Similarity 44.8%; Pred. No. 2.5;
Matches 13; Conservative 5; Mismatches 10; Indels 1; Gaps 1;

QY      10 EDTKDKPKY-EHGGNIIDIDPDSVPHIH 37
DB      69 EKPETIASFAEHGADMISIHVESTPHIH 97

RESULT 6
H72266
aseB/chuR-related protein - Thermotoga maritima (strain MSB8)
C/Species: Thermotoga maritima
C/Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
C/Accession: H72266
R/Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwin, M.L.; Dodson, R.J.; Haft, D.H.; Hickey
Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.;
C.M.
Nature 399, 323-329, 1999
A/Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome seq
A/Reference number: A72200; PMID:99287316; PMID:10360571
A/Accession: H72266
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-442 <ARN>
A/Cross-references: UNIPROT:Q9X147; GB:AE001787; GB:AE000512; NID:g4981882; PIDN:AA03639
A/Experimental source: strain MSB8
C/Genetics:
A/Gene: TM1324

Query Match      26.8%; Score 57; DB 2; Length 442;
Best Local Similarity 31.4%; Pred. No. 16;
Matches 11; Conservative 9; Mismatches 11; Indels 4; Gaps 1;

QY      6 QSPEDTEKD---KPKYEHGNIIDIDPDSVPHI 36
DB      43 KPDEIRIPBEMSLIKDILYGGYIVDBPDEIEHL 77

RESULT 7
T30510
viral enhancing factor 2 - Lymantria dispar nuclear polyhedrosis virus
C/Species: Lymantria dispar nuclear polyhedrosis virus, LdMNPV
C/Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
C/Accession: T30510
R/Kuzio, J.; Pearson, M.N.; Harwood, S.H.; Funk, C.J.; Evans, J.T.; Slavicek, J.M.; Rohr
Virology 253, 17-34, 1999
A/Title: Sequence and analysis of the genome of a baculovirus pathogenic for Lymantria d
A/Reference number: Z20836; PMID:99124785; PMID:9887315
A/Accession: T30510
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-788 <KUZ>
A/Cross-references: UNIPROT:Q9YMG8; EMBL:AF081810; PIDN:AACT0346.1

Query Match      26.5%; Score 56.5; DB 2; Length 788;
Best Local Similarity 54.5%; Pred. No. 36;
Matches 12; Conservative 1; Mismatches 4; Indels 5; Gaps 1;

QY      17 PKYEHGNIIDIDF-----DSV 33
DB      114 PYEHGNAVAPDFKRSRDSV 135
```

RESULT 10
S34130
serine/threonine-specific protein kinase PLK (EC 2.7.1.-) - human
N:Alternate names: polo-like protein kinase; protein kinase plk-1
C:Species: Homo sapiens (man)
C>Date: 06-Jan-1995 #sequence revision 06-Jan-1995 #text_change 16-Aug-2004
C:Accession: S34130, I18123, S61543
R:Golsteyn, R.M.; Schaller, S.J.; Bartek, J.; Ziemiecki, A.; Ried, T.; Nigg, E.A.
submitted to the EMBL data library, June 1993
A:Description: Cloning and characterization of a novel human protein kinase plk-1 a potential
through mitosis.
A:Reference number: S34130
A:Accession: S34130
A:Molecule type: mRNA

A:Molecule type: DNA
A:Residues: 1-786 <GRO>
A:Cross-references: EMBL:Y00092; NID:G63744; PIDN:CAA68282.1; PID:963745
R:Comely, O.M.; Dobson, A.D.W.; Tsai, M.-J.; Beattie, W.G.; Toft, D.O.; Huckaby, C.S.;
Mol. Endocrinol. 1, 517-525, 1987
A>Title: Sequence and expression of a functional chicken progesterone receptor.
A:Reference number: A40903; MUID:91042592; PMID:3153474
A:Accession: A40903
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-64, 'E', 65-786 <CON>
A:Cross-references: GB:M37518

RESULT 15

A95232

ribulose-phosphate 3-epimerase [imported] - Streptococcus pneumoniae (strain TIGR4)

C:Species: Streptococcus pneumoniae

C:Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 09-Jul-2004

C:Accession: A95232

R;Retelien, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Heid
on, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtapple,
nson, T.; Hickey, E.K.; Holt, I.E.

Science 293, 498-506, 2001

A:Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison,

A:Title: Complete Genome Sequence of a virulent isolate of Streptococcus pneumoniae.

A:Reference number: A95000; MUID:21357209; PMID:11463916

A:Accession: A95232

A:Status: Preliminary

A:Molecule type: DNA

A:Residues: 1218 <RUR>

A:Cross-references: UNIPROT:Q97NN7; GB:AE005672; PIDD:AAK76050.1; PIDD:G14973490; GSPDB:G

A:Experimental source: strain TIGR4

C:Genetics:

A:Gene: SP1983

C:superfamily: yeast ribulose-5-phosphate-epimerase

Query Match 24.9%; Score 53; DB 2; Length 218;

Best Local Similarity 52.9%; Pred. No. 24;

Matches 9; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 22 GGNIDIDPDSVPHHG 38

DB 84 GADISIHVEATPHHG 100

Search completed: October 22, 2005, 06:09:52
Job time : 15.8905 secs

This is my dream (copy)

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 22, 2005, 04:10:49 ; Search time 69.6361 Seconds
(without alignments)
279.439 Million cell updates/sec

Title: US-10-731-238-45

Perfect score: 213
Sequence: 1 QNKGNSPEEDTEKDKPKYEHGNGNIDIDPDSVPHING 38

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: UniProt_03: *
1: uniprot_sprot: *
2: uniprot_trembl: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	202.	94.8	1018	1	FNBA_STAU
2	197	92.5	943	2	Q8NU08
3	197	92.5	957	2	Q6G6H4
4	194	91.1	152	2	Q9AEP9
5	189	88.7	940	2	Q536R2
6	189	88.7	1038	2	Q99RD2
7	189	88.7	1038	2	Q7A3J7
8	181	85.0	1015	2	Q8NU07
9	181	85.0	1015	2	Q6G6H3
10	177	83.1	961	2	Q99RD3
11	177	83.1	961	2	Q7A3J8
12	177	83.1	965	2	Q6GDU5
13	66	31.0	716	2	Q7RBE0
14	64	30.0	367	1	COBD_THRTN
15	62	29.1	1182	2	Q7RC73
16	61	28.6	265	2	Q6Z4K4
17	60.5	28.4	214	2	Q99UP6
18	60.5	28.4	214	2	Q7A126
19	60.5	28.4	214	2	Q7A527
20	60.5	28.4	214	2	Q6G921
21	60.5	28.4	214	2	Q6GHL3
22	60.5	28.4	889	2	Q6CBW0
23	60	28.2	979	2	Q7R3N1
24	59	27.7	457	2	Q9GDV3
25	59	27.7	552	2	Q81BB4
26	59	27.7	1858	2	Q8MSU5
27	59	27.7	2145	2	Q9W003
28	58	27.2	574	2	Q7YZ15
29	58	27.2	673	2	Q7R912
30	58	27.2	1259	2	Q8S5Z6
31	58	27.2	1265	2	Q8S768

ALIGNMENTS

RESULT 1	FNBA_STAU	STANDARD;	PRT;	1018	AA.
AC	P14738;				
DT	01-APR-1990 (Rel. 14, Created)				
DT	01-APR-1990 (Rel. 14, Last sequence update)				
DT	25-OCT-2004 (Rel. 45, Last annotation update)				
DE	Fibronectin-binding protein precursor (FNBP).				
GN	Name=fnba;				
OS	Staphylococcus aureus.				
OC	Bacteria; Firmicutes; Bacillales; Staphylococcus.				
OX	NCBI_TaxID=1280;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=NCTC 8325-4;				
RX	MEDLINE=89098998; PubMed=2521391;				
RA	Sigman C., Raucsi G., Joenson K., Lindgren P.-E.,				
RA	Anantharaman G. M., Hoeck M., Lindberg M.;				
RT	"Nucleotide sequence of the gene for a fibronectin-binding protein				
RT	from Staphylococcus aureus: use of this peptide sequence in the				
RT	synthesis of biologically active peptides."				
RL	Proc. Natl. Acad. Sci. U.S.A. 86:699-703(1989).				
CC	-1- FUNCTION: The ability of bacteria to bind fibronectin has been				
CC	proposed as a virulence factor enabling bacteria to colonize wound				
CC	tissues and blood clots. Binding of plasma fibronectin to the				
CC	bacterial surface might block adhesion receptors on S.aureus, thus				
CC	representing an important defense mechanism against tissue				
CC	invasion.				
CC	-1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by				
CC	an amide bond (Potential).				
CC	-----				
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration				
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -				
CC	the European Bioinformatics Institute. There are no restrictions on its				
CC	use by non-profit institutions as long as its content is in no way				
CC	modified and this statement is not removed. Usage by and for commercial				
CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/				
CC	or send an email to license@isb-sib.ch).				
CC	-----				
DR	EMBL: J04151; AAA26632.1; -				Q7XFR2
DR	InterPro: IPR004237; Fn_bind.				Q6BYE3
DR	InterPro: IPR005877; Gpos_YsIRK.				Q9CS87
DR	InterPro: IPR001899; Gram_pos_anchor.				Q9CS10
DR	Pfam: PF02986; Fn_bind_1.				Q8BK20
DR	Pfam: PF04650; Gram_pos_anchor; 1.				Q8BK21
DR	Pfam: PF04650; YsIRK_signal; 1.				Q810A4
DR	TIGRFAMS: TIGR01167; LpxTG_anchor; 1.				Q6ZPL9
DR	TIGRFAMS: TIGR01168; YsIRK_signal; 1.				Q6MEU6
DR	TIGRFAMS: TIGR01168; YsIRK_signal; 1.				Q9X147
DR	PROSITE: PS50847; GRAM_POS_ANCHORING; 1.				Q6BP33
KW	Cell adhesion; Cell wall; Peptidoglycan-anchor; Repeat; Signal;				Q6FY67
KW	Virulence.				Q9VHR2
FT	SIGNAL	1	36		Q6BMZ3
FT	CHAIN	37	985		
FT	PROPEP	986	1018		
					Fibronectin-binding protein.
					Removed by sortase (Potential).

FT REPEAT 545 574 B-1.
FT REPEAT 575 604 B-2.
FT DOMAIN 745 878 4 X approximate tandem repeats,
fibronectin-binding domain.
FT REPEAT 745 782 D-1.
FT REPEAT 821 859 D-2.
FT REPEAT 860 878 D-3.
FT DOMAIN 879 948 D-4 (incomplete).
FT REPEAT 893 906 5 X tandem repeats, Pro-rich (WR).
FT REPEAT 907 920 WR 1.
FT REPEAT 921 934 WR 2.
FT REPEAT 935 948 WR 3.
FT SITE 982 985 WR 4.
FT MOD_RES 985 985 WR 5.
SQ SEQUENCE 1018 AA; 111780 MW; 58175E0020E81F1F CRC64;
LpXtg sorting signal (potential).
Pentaglycyl murein peptidoglycan amidated
threonine (potential).
Query Match 94.8%; Score 202; DB 1; Length 1018;
Best Local Similarity 97.4%; Pred. No. 5.7e-16;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 ONKGNQSPEDTEKDKPKYEHGNIIDIDFDSVPHIHG 38
DB 784 QNKGDSFEEDTEKDKPKYEHGNIIDIDFDSVPHIHG 821
RESULT 2
Q8NUT8 PRELIMINARY; PRT; 943 AA.
ID Q8NUT8
AC Q8NUT8; 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE FnBb protein.
DE Name=fnbB; OrderedLocusNames=MMW2420;
OS Staphylococcus aureus (strain MM2).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=196620;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MM2;
RX MEDLINE=22040717; PubMed=12044378; DOI=10.1016/S0140-6736(02)08713-5;
RA Baba T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Oguchi A.,
Nagai Y., Iwano N., Asano K., Naito T., Kuroda H., Cui L.,
Yamamoto K., Hiramatsu K.;
RA "Genome and virulence determinants of high virulence community-
RT acquired MRSA";
RL Lancet 359:1819-1827(2002).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
an amide bond (By similarity).
DR EMBL; AP004830; BAB96285.1; -;
DR HSSP; O53653; IN67.
DR GO; GO:0009986; C:cell surface; IEA.
DR GO; GO:0005618; C:cell wall; IEA.
DR GO; GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0007155; P:cell adhesion; IEA.
DR InterPro; IPR008966; Adhes_bact.
DR InterPro; IPR004237; Fn_bind.
DR InterPro; IPR005877; Gpos_YsIRK.
DR InterPro; IPR001899; Gram_pos_anchor.
DR Pfam; PF02986; Fn_bind; 1.
DR Pfam; PF00746; Gram_pos_anchor; 1.
DR TIGRfams; TIGR01167; LpXtg_anchor; 1.
DR TIGRfams; TIGR01168; YsIRK_signal; 1.
DR PROSITE; PS50847; GRAM_POS_ANCHORING; 1.
KW Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ SEQUENCE 943 AA; 104537 MW; DA8A5F31947E1B6A CRC64;
Query Match 92.5%; Score 197; DB 2; Length 943

Best Local Similarity 94.7%; Pred. No. 2.1e-15;
Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 ONKGNQSPEDTEKDKPKYEHGNIIDIDFDSVPHIHG 38
DB 727 QNKGDSFEEDTEKDKPKYEHGNIIDIDFDSVPHIHG 764
RESULT 3
Q6G6H4 PRELIMINARY; PRT; 957 AA.
ID Q6G6H4
AC Q6G6H4; 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Fibronectin-binding protein.
DE Name=fnbB; OrderedLocusNames=SAS2387;
OS Staphylococcus aureus (strain MSSA476).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=282459;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=15213324; DOI=10.1073/pnas.0402521101;
RA Holden M.T.G., Fell E.J., Lindsay J.A., Peacock S.J., Day N.P.J.,
RA Enright M.C., Foster T.J., Moore C.E., Hurst L., Atkin R., Barton A.,
RA Bason N., Bentley S.D., Chillingworth C., Chillingworth T.,
RA Churcher C., Clark L., Cronin A., Doggett J., Dowd L.,
RA Felwell T., Hance Z., Harris B., Hauser H., Holroyd S., Jagels K.,
RA James K.D., Lennard N., Line A., Mayer R., Moule S., Mungall K.,
RA Ormond D., Quail M.A., Rabinowitch E., Rutherford K.M., Sanders M.,
RA Sharp S., Simmonds M., Stevens K., Whitehead S., Barrall B.G.,
RA Spratt B.G., Parkhill J.;
RT "Complete genomes of two clinical Staphylococcus aureus strains:
RT evidence for the rapid evolution of virulence and drug resistance";
RL Proc. Natl. Acad. Sci. U.S.A. 101:9786-9791(2004).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
an amide bond (By similarity).
DR EMBL; BX571857; CAG44201.1; -;
DR GO; GO:0009986; C:cell surface; IEA.
DR GO; GO:0005618; C:cell wall; IEA.
DR GO; GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0007155; P:cell adhesion; IEA.
DR InterPro; IPR008966; Adhes_bact.
DR InterPro; IPR004237; Fn_bind.
DR InterPro; IPR005877; Gpos_YsIRK.
DR InterPro; IPR001899; Gram_pos_anchor.
DR Pfam; PF02986; Fn_bind; 1.
DR Pfam; PF00746; Gram_pos_anchor; 1.
DR TIGRfams; TIGR01167; LpXtg_anchor; 1.
DR TIGRfams; TIGR01168; YsIRK_signal; 1.
DR PROSITE; PS50847; GRAM_POS_ANCHORING; 1.
KW Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ SEQUENCE 957 AA; 105980 MW; 28F8BA7FFDFD3EAF CRC64;
Query Match 92.5%; Score 197; DB 2; Length 957;
Best Local Similarity 94.7%; Pred. No. 2.2e-15;
Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 ONKGNQSPEDTEKDKPKYEHGNIIDIDFDSVPHIHG 38
DB 727 QNKGDSFEEDTEKDKPKYEHGNIIDIDFDSVPHIHG 764
RESULT 4
Q9AEP9 PRELIMINARY; PRT; 152 AA.
ID Q9AEP9
AC Q9AEP9; 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Fibronectin-binding protein (Fragment).

GN Name=fnb;
 OS Staphylococcus aureus.
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 OX NCBI_TaxId=1280;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CMRSA-1;
 RX MEDLINE=21246681; PubMed=11349044;
 RI DOI=10.1128/IAI.69.6.3791-3799.2001;
 RA Rice K., Huesca M., Vaz D., McGavin M.J.;
 RT "Variance in fibronectin binding and fnb locus polymorphisms in
 RT Staphylococcus aureus: identification of antigenic variation in a
 RT fibronectin binding protein adhesin of the epidemic CMRSA-1 strain of
 RT methicillin-resistant S. aureus.";
 RL Infect. Immun. 69:3791-3799(2001).
 DR EMBL; AY029184; AAK31588.1; -.
 FT NON_TER 1
 FT 152 152
 SQ SEQUENCE 152 AA; 17193 MW; CFA3913C2B11C025 CRC64;

Query Match 91.1%; Score 194; DB 2; Length 152;
 Best Local Similarity 94.7%; Pred. No. 6,4e-16;
 Matches 36; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 QNKGNSPEEDTEKDKPKYEHGNIIDIDPDSVPHHG 38
 DB 77 QNKGNSPEEDTEKDKPKYEHGNIIDIDPDSVPHHG 114

RESULT 5
 ID Q53682 PRELIMINARY; PRT; 940 AA.
 AC Q53682;
 DT 01-NOV-1996 (TREMBlrel. 01, Created)
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
 DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
 DE Fibronectin binding protein B.
 GN Name=fnbB;
 OS Staphylococcus aureus.
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 OX NCBI_TaxId=1280;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=8325-4;
 RX MEDLINE=92111475; PubMed=1837266;
 RA Jonsson K., Sigmas C., Muller H.P., Lindberg M.;
 RT "Two different genes encode fibronectin binding proteins in
 RT Staphylococcus aureus. The complete nucleotide sequence and
 RT characterization of the second gene.";
 RL Eur. J. Biochem. 202:1041-1048(1991).
 CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
 CC an amide bond (By similarity).
 DR EMBL; X62992; CAA44726.1; -.
 DR FTR; S19702; S19702.
 DR HSSP; Q53653; IN67.
 DR GO; GO:0009986; C:cell surface; IEA.
 DR GO; GO:0005618; C:cell wall; IEA.
 DR GO; GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:007155; P:cell adhesion; IEA.
 DR InterPro; IPR008966; Adhes_bact.
 DR InterPro; IPR004237; Fn_bind.
 DR InterPro; IPR001899; Gram_pos_anchor.
 DR Pfam; PF02986; Fn_bind_2.
 DR Pfam; PF00746; Gram_pos_anchor; 1.
 DR Pfam; PF04650; YSIRK_signal; 1.
 DR TIGRFAMs; TIGR01167; LPXTG_anchor; 1.
 DR TIGRFAMs; TIGR01168; YSIRK_signal; 1.
 DR PROSITE; PSS0847; GRAM_POS_ANCHORING; 1.
 KW Cell wall; peptidoglycan-anchor.
 SQ SEQUENCE 940 AA; 10355 MW; E35FBBCA907AE345 CRC64;

Query Match 88.7%; Score 189; DB 2; Length 940;
 Best Local Similarity 92.1%; Pred. No. 2e-14;
 Matches 35; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 QNKGNSPEEDTEKDKPKYEHGNIIDIDPDSVPHHG 38
 DB 720 QNKGNSPEEDTEKDKPKYEHGNIIDIDPDSVPHHG 757

RESULT 6
 ID Q99RD2 PRELIMINARY; PRT; 1038 AA.
 AC Q99RD2;
 DT 01-JUN-2001 (TREMBlrel. 17, Created)
 DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
 DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
 DE Fibronectin-binding protein homolog.
 GN Name=fnb; Order:locusNames=SAV2503;
 OS Staphylococcus aureus (strain Mu50 / ATCC 700699).
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 OX NCBI_TaxId=158878;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Mu50 / ATCC 700699;
 RX MEDLINE=21311952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2;
 RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
 RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Iian J.-Q., Ito T.,
 RA Kanamori M., Matsumaru H., Maruyama A., Murakami A.,
 RA Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
 RA Sekimizu K., Hirakawa H., Kohara S., Goto S., Yabuuchi J.,
 RA Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
 RA Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
 RT "Whole genome sequencing of methicillin-resistant Staphylococcus
 RT aureus.";
 RL Lancet 357:1225-1240(2001).
 CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
 CC an amide bond (By similarity).
 DR EMBL; AP003365; BAB58665.1; -.
 DR FTR; H90053; H90053.
 DR GO; GO:0009986; C:cell surface; IEA.
 DR GO; GO:0005618; C:cell wall; IEA.
 DR GO; GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:007155; P:cell adhesion; IEA.
 DR InterPro; IPR008966; Adhes_bact.
 DR InterPro; IPR004237; Fn_bind.
 DR InterPro; IPR005877; Gpos_YSIRK.
 DR InterPro; IPR001899; Gram_pos_anchor.
 DR Pfam; PF02986; Fn_bind_1.
 DR Pfam; PF00746; Gram_pos_anchor; 1.
 DR Pfam; PF04650; YSIRK_signal; 1.
 DR TIGRFAMs; TIGR01167; LPXTG_anchor; 1.
 DR TIGRFAMs; TIGR01168; YSIRK_signal; 1.
 DR PROSITE; PSS0847; GRAM_POS_ANCHORING; 1.
 KW Cell wall; complete proteome; peptidoglycan-anchor.
 SQ SEQUENCE 1038 AA; 113618 MW; 666BFBFBFB12 CRC64;

Query Match 92.1%; Score 189; DB 2; Length 1038;
 Best Local Similarity 92.1%; Pred. No. 2,3e-14;
 Matches 35; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 QNKGNSPEEDTEKDKPKYEHGNIIDIDPDSVPHHG 38
 DB 780 QNKGNSPEEDTEKDKPKYEHGNIIDIDPDSVPHHG 817

RESULT 7
 ID Q7A3J7 PRELIMINARY; PRT; 1038 AA.
 AC Q7A3J7;
 DT 05-JUL-2004 (TREMBlrel. 27, Created)
 DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
 DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)

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DE  fnb protein.
CN  Name=fnb; OrderedlocusNames=SA2291;
OS  Staphylococcus aureus (strain N315);
OC  Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX  NCBI_TaxID=158879;
RN  [1]
RP  SEQUENCE FROM N.A.
RX  MEDLINE=2111952; PubMed=11418146; DOI=10.1016/S0140-6736(01)04403-2;
RA  Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
RA  Cui L., Oguchi A., Aoki K.-I., Nagai Y., Lian J.-Q., Ito T.,
RA  Kanamori M., Matsunari H., Maruyama A., Murakami H., Hosoyama A.,
RA  Mizutani-Uji Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
RA  Sekizima K., Hirakawa H., Kohara S., Goto S., Yabuuchi J.,
RA  Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
RA  Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.,
RT  "Whole genome sequencing of methicillin-resistant Staphylococcus
RT  aureus.";
RL  Lancet 357:1225-1240(2001).
CC  -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC  an amide bond (By similarity).
DR  EMBL; AP003137; BAB43594.1; -.
DR  GO; GO:0009986; C:cell surface; IEA.
DR  GO; GO:0005618; C:cell wall; IEA.
DR  GO; GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR  GO; GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR  GO; GO:0016020; C:membrane; IEA.
DR  GO; GO:007155; P:cell adhesion; IEA.
DR  InterPro; IPR008966; Adhes_bact.
DR  InterPro; IPR004237; Fn_bind.
DR  InterPro; IPR005877; Gpos_YsIRK.
DR  InterPro; IPR001899; Gram_pos_anchor.
DR  Pfam; PF02986; Fn_bind; 1.
DR  Pfam; PF00746; Gram_pos_anchor; 1.
DR  TIGRfams; TIGR01167; LpXTG_anchor; 1.
DR  TIGRfams; TIGR01168; YsIRK_signal; 1.
DR  PROSITE; PS50847; GRAM_POS_ANCHORING; 1.
KW  Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ  SEQUENCE 1038 AA; 113518 MW; 666BFBFB2BFB2B12 CRC64;

Query Match      88.7%; Score 189; DB 2; Length 1038;
Best Local Similarity 92.1%; Pred. No. 2.3e-14;
Matches 35; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY  1 ONKGNQSPEDTEKDKPKYEHCNIIIDIDFDSVPFHIG 38
DB  780 ONKGNQSPEDTEKDKPKYEHCNIIIDIDFDSVPFHIG 817

RESULT 8
Q8NUU7 PRELIMINARY; PRT; 1015 AA.
AC Q8NUU7;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Fnb protein.
GN Name=fnb; OrderedlocusNames=MM2421;
OS Staphylococcus aureus (strain MM2).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=196620;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=MM2;
RX MEDLINE=22040717; PubMed=12044378; DOI=10.1016/S0140-6736(02)08713-5;
RA Baba T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Oguchi A.,
RA Nagai Y., Iwama N., Amano K., Naimi T., Kuroda H., Cui L.,
RA Yamamoto K., Hiramatsu K.;
RT "Genome and virulence determinants of high virulence community-
RT acquired MRSA.";
RL Lancet 359:1819-1827(2002).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC an amide bond (By similarity).
EMBL; AP004830; BAB96286.1; -.

```

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DR  GO; GO:0009986; C:cell surface; IEA.
DR  GO; GO:0005618; C:cell wall; IEA.
DR  GO; GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR  GO; GO:0016020; C:membrane; IEA.
DR  GO; GO:007155; P:cell adhesion; IEA.
DR  InterPro; IPR008966; Adhes_bact.
DR  InterPro; IPR005877; Gpos_YsIRK.
DR  InterPro; IPR001899; Gram_pos_anchor.
DR  Pfam; PF02986; Fn_bind; 1.
DR  Pfam; PF00746; Gram_pos_anchor; 1.
DR  TIGRfams; TIGR01167; LpXTG_anchor; 1.
DR  TIGRfams; TIGR01168; YsIRK_signal; 1.
DR  PROSITE; PS50847; GRAM_POS_ANCHORING; 1.
KW  Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ  SEQUENCE 1015 AA; 111145 MW; D0F281B864D4D2 CRC64;

Query Match      85.0%; Score 181; DB 2; Length 1015;
Best Local Similarity 89.5%; Pred. No. 2.1e-13;
Matches 34; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY  1 ONKGNQSPEDTEKDKPKYEHCNIIIDIDFDSVPFHIG 38
DB  785 ONKGNQSPEDTEKDKPKYEHCNIIIDIDFDSVPFHIG 822

RESULT 9
Q6G6H3 PRELIMINARY; PRT; 1015 AA.
AC Q6G6H3;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Fibronectin-binding protein.
GN OrderedlocusNames=SA52388;
OS Staphylococcus aureus (strain MSSA476).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=282459;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=15213324; DOI=10.1073/pnas.0402521101;
RA Holden M.T.G., Fell E.J., Lindsey J.A., Peacock S.J., Day N.P.J.,
RA Enright M.C., Foster T.J., Moore C.E., Hurst L., Atkin R., Barron A.,
RA Bason N., Bentley S.D., Chillingworth C., Chillingworth T.,
RA Churcher C., Clark L., Cotton C., Cronin A., Doggett J., Dowd L.,
RA Fellwell T., Hance Z., Harris B., Hauser H., Holroyd S., Jagels K.,
RA James K.D., Lennard N., Line A., Mayes R., Moutle S., Mungall K.,
RA Ormond D., Quail M.A., Rabinowitch E., Rutherford K.M., Sanders M.,
RA Sharp S., Simmonds M., Stevens K., Whitehead S., Barrett B.G.,
RA Spratt B.G., Parkhill J.;
RT "Complete genomes of two clinical Staphylococcus aureus strains:
RT evidence for the rapid evolution of virulence and drug resistance.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:9786-9791(2004).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC an amide bond (By similarity).
EMBL; BX571857; CAG44202.1; -.
DR  GO; GO:0009986; C:cell surface; IEA.
DR  GO; GO:0005618; C:cell wall; IEA.
DR  GO; GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR  GO; GO:0016020; C:membrane; IEA.
DR  GO; GO:007155; P:cell adhesion; IEA.
DR  InterPro; IPR008966; Adhes_bact.
DR  InterPro; IPR004237; Fn_bind.
DR  InterPro; IPR005877; Gpos_YsIRK.
DR  InterPro; IPR001899; Gram_pos_anchor.
DR  Pfam; PF02986; Fn_bind; 1.
DR  Pfam; PF00746; Gram_pos_anchor; 1.
DR  TIGRfams; TIGR01167; LpXTG_anchor; 1.
DR  TIGRfams; TIGR01168; YsIRK_signal; 1.
DR  PROSITE; PS50847; GRAM_POS_ANCHORING; 1.
KW  Cell wall; Complete proteome; Peptidoglycan-anchor.

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SQ SEQUENCE 1015 AA; 111145 MW; DOF9281BB64D44D2 CRC64;
 Query Match 85.0%; Score 181; DB 2; Length 1015;
 Best Local Similarity 89.5%; Pred. No. 2.1e-13;
 Matches 34; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 QNKGNSPEEDTEKDKPKYEGHGNIIIDIDPDSVPHIHG 38
 DB 785 QNKGNSPEEDTEKDKPKYEGHGNIIIDIDPDSVPHIHG 822

RESULT 10
 ID Q99RD3 PRELIMINARY; PRT; 961 AA.
 AC Q99RD3;
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Fibronectin-binding protein homolog.
 GN Name=fnb8; OrderedLocustNames=SAV2502;
 OS Staphylococcus aureus (strain Mu50 / ATCC 700699).
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 NC NCBI_TaxID=158878;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Mu50 / ATCC 700699;
 RX MEDLINE=21311952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2;
 RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
 RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Iano J.-O., Ito T.,
 RA Kanamori M., Matsunaru H., Maruyama A., Murakami H., Hosoyama A.,
 RA Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
 RA Sekintzu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
 RA Kanehisa M., Yamaashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
 RA Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
 RT "Whole genome sequencing of methicillin-resistant Staphylococcus
 aureus.";
 RL Lancet 357:1225-1240(2001).
 CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
 an amide bond (By similarity).
 DR EMBL: AP003365; BAB58664.1; -;
 DR PIR: G90053; G90053.
 DR HSSP: Q53653; IN67.
 DR GO: GO:0009986; C:cell surface; IEA.
 DR GO: GO:0005618; C:cell wall; IEA.
 DR GO: GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
 DR GO: GO:0016020; C:membrane; IEA.
 DR GO: GO:0007155; P:cell adhesion; IEA.
 DR InterPro: IPR008966; Adhes_bact.
 DR InterPro: IPR004237; Fn_bind.
 DR InterPro: IPR005877; Gpos_YsIRK.
 DR InterPro: IPR001899; Gram_pos_anchor.
 DR Pfam: PF02986; Fn_bind; 1.
 DR Pfam: PF00746; Gram_pos_anchor; 1.
 DR Pfam: PF04650; YsIRK_signal; 1.
 DR TIGRfams: TIGR01167; LPXTG_anchor; 1.
 DR TIGRfams: TIGR01168; YsIRK_signal; 1.
 DR PROSITE: PS50847; GRAM_POS_ANCHORING; 1.
 KM Cell wall, Complete proteome; Peptidoglycan-anchor.
 SQ SEQUENCE 961 AA; 106010 MW; 364940F884EA4101 CRC64;

Query Match 83.1%; Score 177; DB 2; Length 961;
 Best Local Similarity 86.8%; Pred. No. 6.2e-13;
 Matches 33; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 QNKGNSPEEDTEKDKPKYEGHGNIIIDIDPDSVPHIHG 38
 DB 731 QNKGNSPEEDTEKDKPKYEGHGNIIIDIDPDSVPHIHG 768

RESULT 11
 ID Q7A3J8 PRELIMINARY; PRT; 961 AA.
 AC Q7A3J8;

DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DE FnbB protein.
 GN Name=fnb8; OrderedLocustNames=SA2290;
 OS Staphylococcus aureus (strain N315).
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 NC NCBI_TaxID=158879;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21311952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2;
 RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
 RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Iano J.-O., Ito T.,
 RA Kanamori M., Matsunaru H., Maruyama A., Murakami H., Hosoyama A.,
 RA Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
 RA Sekintzu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
 RA Kanehisa M., Yamaashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
 RA Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
 RT "Whole genome sequencing of methicillin-resistant Staphylococcus
 aureus.";
 RL Lancet 357:1225-1240(2001).
 CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
 an amide bond (By similarity).
 DR EMBL: AP003337; BAB43593.1; -;
 DR GO: GO:0009986; C:cell surface; IEA.
 DR GO: GO:0005618; C:cell wall; IEA.
 DR GO: GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
 DR GO: GO:0016020; C:membrane; IEA.
 DR GO: GO:0007155; P:cell adhesion; IEA.
 DR InterPro: IPR008966; Adhes_bact.
 DR InterPro: IPR004237; Fn_bind.
 DR InterPro: IPR005877; Gpos_YsIRK.
 DR InterPro: IPR001899; Gram_pos_anchor.
 DR Pfam: PF02986; Fn_bind; 1.
 DR Pfam: PF00746; Gram_pos_anchor; 1.
 DR Pfam: PF04650; YsIRK_signal; 1.
 DR TIGRfams: TIGR01167; LPXTG_anchor; 1.
 DR TIGRfams: TIGR01168; YsIRK_signal; 1.
 DR PROSITE: PS50847; GRAM_POS_ANCHORING; 1.
 KM Cell wall, Complete proteome; Peptidoglycan-anchor.
 SQ SEQUENCE 961 AA; 106010 MW; 364940F884EA4101 CRC64;

Query Match 83.1%; Score 177; DB 2; Length 961;
 Best Local Similarity 86.8%; Pred. No. 6.2e-13;
 Matches 33; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 QNKGNSPEEDTEKDKPKYEGHGNIIIDIDPDSVPHIHG 38
 DB 731 QNKGNSPEEDTEKDKPKYEGHGNIIIDIDPDSVPHIHG 768

RESULT 12
 ID Q6GDUS PRELIMINARY; PRT; 965 AA.
 AC Q6GDUS;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Fibronectin-binding protein.
 GN Name=fnb8; OrderedLocustNames=SA2580;
 OS Staphylococcus aureus (strain MSA252).
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 NC NCBI_TaxID=282458;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX PubMed=15213324; DOI=10.1073/pnas.0402521101;
 RA Holden M.T.G., Fell E.J., Lindsay J.A., Peacock S.J., Day N.P.J.,
 RA Enright M.C., Foster T.J., Moore C.B., Hurst L., Atkin R., Barron A.,
 RA Baeson N., Bentley S.D., Chillingworth C., Chillingworth T.,
 RA Churcher C., Clark L., Corton C., Cronin A., Doggett J., Dowd L.,
 RA Feltwell T., Hance Z., Harris B., Hauser H., Holtroyd S., Jørgensen K.,
 RA James K.D., Lennard N., Line A., Mayes R., Moule S., Mungall K.,
 RA Ormond D., Quail M.A., Rabinowitsch E., Rutherford K.M., Sanders M.,

RA Sharp S., Simmonds M., Stevens K., Whitehead S., Barrell B.G.,
 RA Spratt B.G., Parkhill J.:
 RT "Complete genomes of two clinical *Staphylococcus aureus* strains:
 RT evidence for the rapid evolution of virulence and drug resistance.";
 RL Proc. Natl. Acad. Sci. U.S.A. 101:9786-9791(2004).
 CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
 CC an amide bond (By similarity).
 DB EMBL: BX571856; CAG41560.1; -.
 DR GO: GO:0009986; C:cell surface; IEA.
 DR GO: GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
 DR GO: GO:0016020; C:membrane; IEA.
 DR GO: GO:0007155; P:cell adhesion; IEA.
 DR InterPro: IPR008966; A:Adhes_bact.
 DR InterPro: IPR004237; F:Fn_bind.
 DR InterPro: IPR005877; G:Gos_YsIRK.
 DR InterPro: IPR001899; G:Gram_pos_anchor.
 DR Pfam: PF02986; F:Fn_bind; 1.
 DR Pfam: PF00746; G:Gram_pos_anchor; 1.
 DR TIGRfam: TIGR01167; L:LPXG_anchor; 1.
 DR TIGRfam: TIGR01168; YsIRK_signal; 1.
 DR PROSITE: PS50847; G:RAM_POS_ANCHORING; 1.
 KW Cell wall; Complete proteome; Peptidoglycan-anchor.
 SQ SEQUENCE 965 AA; 105691 MW; 2982E132164D0551 CRC64;
 Query Match 83.1%; Score 177; DB 2; Length 965;
 Best Local Similarity 86.8%; Pred. No. 6,3e-13;
 Matches 33; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
 QY 1 QNKGNSPEEDTEKDKPKYEHGNIIDIDPDSVPHNG 38
 DB 749 QNKGNSPEEDTEKDKPKYEGSNIIDIDPDSVPHNG 786
 RESULT 13
 Q7RB60 PRELIMINARY; PRT; 716 AA.
 AC Q7RB60;
 DT 01-MAR-2004 (TrEMBLrel. 26, Created)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Hypothetical protein.
 GN Name=PY06288;
 OS Plasmodium yoelii yoelii.
 OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
 OX NCBI_TaxID=73239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=17XNL;
 RX PubMed=1236865; DOI=10.1038/nature01099;
 RA Carlson J.M., Angluoli S.V., Suh B.B., Kooij T.W., Perce A.,
 RA Silva J.C., Ermolaeva M.D., Allen J.E., Selenut J.D., Koo H.L.,
 RA Peterson J.D., Pop M., Kosack D.S., Shumway M.F., Bidwell J.L.,
 RA Stallom S.J., Van Aken S.B., Riedmiller S.B., Feldblum T.T.,
 RA Cho J.K., Quackenbush J., Sedegah M., Shoaibi A., Cummings L.M.,
 RA Florens L., Yates F.R., III, Raine J.D., Sinden R.E., Harris M.A.,
 RA Cunningham D.A., Preiser P.R., Bergman L.W., Vaitya A.B.,
 RA van Lin L.H., Janse C.J., Waters A.P., Smith H.O., White O.R.,
 RA Salzberg S.L., Venter J.C., Fraser C.M., Hoffman S.L., Gartner M.J.,
 RA Carucci D.J.;
 RT "Genome sequence and comparative analysis of the model rodent malaria
 RT parasite *Plasmodium yoelii yoelii*.";
 RL Nature 419:512-519(2002).
 CC -1- CAUTION: The sequence shown here is derived from an
 CC preliminary data.
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.
 DR EMBL: AABL01002106; EAA18479.1; -.
 DR InterPro: IPR008941; TPR-like.
 KW Hypothetical protein.
 SQ SEQUENCE 716 AA; 86599 MW; E11BE234A397B6F7 CRC64;
 Query Match 31.0%; Score 66; DB 2; Length 716;
 Best Local Similarity 34.3%; Pred. No. 19;

Matches 12; Conservative 7; Mismatches 16; Indels 0; Gaps 0;
 QY 2 NKGNSPEEDTEKDKPKYEHGNIIDIDPDSVPHI 36
 DB 109 NNYHEHTWEKKQKSKFPNNNIIDVDSYEQYRKI 143
 RESULT 14
 COBD_THETN STANDARD; PRT; 367 AA.
 ID COBD_THETN
 AC Q8R504;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Putative threonine-phosphate decarboxylase (EC 4.1.1.81) (L-threonine-
 DE O-3-phosphate decarboxylase).
 GN Name=COBD; Ordered locus names=TTB0380;
 OS Thermoanaerobacter tengcongensis.
 OC Bacteria; Firmicutes; Clostridia; Thermoanaerobacteriales;
 OC Thermoanaerobacteriaceae; Thermoanaerobacter.
 OX NCBI_TaxID=119072;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=MB4 / JCM 11007;
 RX MEDLINE=21992816; PubMed=11997336; DOI=10.1101/gr.219302;
 RA Bao Q., Tian Y., Li W., Xu Z., Hu S., Dong W., Yang J.,
 RA Chen Y., Xue Y., Xu Y., Lai X., Huang L., Dong X., Ma Y., Ling L.,
 RA Tan H., Chen R., Wang J., Yu J., Yang H.;
 RT "A complete sequence of the *T. tengcongensis* genome.";
 RL Genome Res. 12:689-700(2002).
 CC -1- FUNCTION: Decarboxylates L-threonine-O-3-phosphate to yield (R)-1-
 CC amino-2-propanol O-2-phosphate, the precursor for the linkage
 CC between the nucleotide loop and the corrin ring in cobalamin (by
 CC similarity).
 CC -1- CATALYTIC ACTIVITY: L-threonine O-3-phosphate = (R)-1-aminopropan-
 CC 2-yl phosphate + CO(2).
 CC -1- COFACTOR: Pyridoxal phosphate (By similarity).
 CC -1- PATHWAY: Adenosylcobalamin biosynthesis; conversion of
 CC adenosylcobyrinic acid to adenosylcobinamide.
 CC -1- SIMILARITY: Belongs to the class-II pyridoxal-phosphate-dependent
 CC aminotransferase family.
 CC
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 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC
 DR EMBL: AE013011; AM23667.1; -.
 DR HSSP: P97084; ILCS.
 DR InterPro: IPR001176; ACC_synthase.
 DR InterPro: IPR004839; Aminotransf_1/II.
 DR InterPro: IPR001917; Aminotransf_II.
 DR InterPro: IPR005860; COBD.
 DR Pfam: PF00155; Aminotransf_1_2; 1.
 DR PRINTS: PR00753; ACCSYNTHASE.
 DR TIGRfam: TIGR01140; COBD; 1.
 DR PROSITE: PS00599; AA_TRANSFERS_CLASS_2; FALSE_NEG.
 KW Cobalamin biosynthesis; Complete proteome; Lyase; Pyridoxal phosphate.
 FT BINDING 213 213 Pyridoxal phosphate (By similarity).
 SQ SEQUENCE 367 AA; 42396 MW; 292512F7E1F6835 CRC64;
 Query Match 30.0%; Score 64; DB 1; Length 367;
 Best Local Similarity 57.1%; Pred. No. 16;
 Matches 16; Conservative 2; Mismatches 4; Indels 6; Gaps 2;
 QY 10 EDTKDKPKYEHGNIIDIDPDS 32
 DB 2 KEGEKKPKP-YEHGNIYDQGNLIDPSS 28

RESULT 15

07RC73 PRELIMINARY; PRT; 1182 AA.
 ID 07RC73;
 AC 07RC73;
 DT 01-MAR-2004 (TEMBLrel. 26, Created)
 DT 01-MAR-2004 (TEMBLrel. 26, Last sequence update)
 DT 01-MAR-2004 (TEMBLrel. 26, Last annotation update)
 DE Hypothetical protein.
 GN Name=PY05911;
 OS Plasmodium yoelii yoelii.
 OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
 OX NCBI_TaxID=73239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=17XNL;
 RX PubMed=1236865; DOI=10.1038/nature01099;
 RA Carlton J.M., Angiuoli S.V., Suh B.B., Kooij T.W., Perera M.,
 RA Silva J.C., Ermolaeva M.D., Allen J.E., Selengut J.D., Koo H.L.,
 RA Peterson J.D., Pop M., Kosack D.S., Shumway M.F., Bidwell S.L.,
 RA Shallom S.J., van Aken S.E., Riedmiller S.B., Feldblyum T.V.,
 RA Cho J.K., Quackenbush J., Sedegah M., Shoaihi A., Cummings L.M.,
 RA Florens L., Yates F.R. III, Raine J.D., Sinden R.E., Harris M.A.,
 RA Cunningham D.A., Preiser P.R., Bergman L.W., Valdya A.B.,
 RA van Lin L.H., Janse C.J., Waters A.P., Smith H.O., White O.R.,
 RA Salzberg S.L., Venter J.C., Fraser C.M., Hoffman S.L., Gardner M.J.,
 RA Carucci D.J.;
 RT "Genome sequence and comparative analysis of the model rodent malaria
 parasite Plasmodium yoelii yoelii.";
 RL Nature 419:512-519(2002).
 CC -!- CAUTION: The sequence shown here is derived from an
 EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 preliminary data.
 CC EMBL; AABL01001939; EAA18016.1; -.
 DR InterPro: IPR001990; Granin.
 DR InterPro: IPR011046; WD40 like.
 DR PROSITE, PS00422; GRANINS_1; UNKNOWN_1.
 KW Hypothetical protein.
 SQ SEQUENCE 1182 AA; 139875 MW; 97519E22F96A071B CRC64;

Query Match 29.1%; Score 62; DB 2; Length 1182;
 Best Local Similarity 38.1%; Pred. No. 1e+02;
 Matches 16; Conservative 7; Mismatches 11; Indels 8; Gaps 2;
 QY 1 QNKGNSPEEDTEKPKRYHGNI---DIDFDSVPHITG 38
 DB 946 QNKLNDDEEBDEENENEKY---NITVVKININYKNTPIING 983

Search completed: October 22, 2005, 06:06:07
 Job time : 72.6361 secs

GenCore version 5.1.6
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OM protein - protein search, using SW model

Run on: October 25, 2005, 19:38:38 ; Search time 83.8325 Seconds
(without alignments)
175.313 Million cell updates/sec

Title: US-10-731-238-46

Perfect score: 214 1 QNKGNSPDETEKDKPKYEHGQNIIDFDVSYPHIG 38

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database: A_Geneseq_16Dec04:*

1: geneseqp1980s:.*
2: geneseqp1990s:.*
3: geneseqp2000s:.*
4: geneseqp2001s:.*
5: geneseqp2002s:.*
6: geneseqp2003as:.*
7: geneseqp2003bs:.*
8: geneseqp2004s:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	214	100.0	38	2	AAW65702 Fibronec
2	206	96.3	38	2	AAW65663 Fibronec
3	206	96.3	134	2	AAW29087 S. aureus
4	206	96.3	139	2	AAW31556 Fibronec
5	206	96.3	1018	1	AAW82115 Fibronec
6	206	96.3	1018	4	AAU37245 Staphyloc
7	206	96.3	1018	4	AAU34301 Staphyloc
8	206	96.3	1018	6	ABM18922 Staphyloc
9	206	96.3	1018	6	ABM18922 Staphyloc
10	206	96.3	1027	2	AAW89806 Staphyloc
11	201	93.9	77	2	AAW88749 S. aureus
12	201	93.9	113	2	AAW90937 D3D4 poly
13	201	93.9	130	2	AAW58806 Fibronec
14	201	93.9	130	2	AAW58807 Fibronec
15	201	93.9	130	2	AAW91202 D1-D4 fib
16	201	93.9	130	2	AAW91201 D1-D4 fib
17	201	93.9	162	2	AAW90942 D3D4 poly
18	201	93.9	164	2	AAW90938 D3D4 poly
19	201	93.9	174	2	AAW58808 Fbp fibro
20	201	93.9	174	2	AAW91203 D1-D4 fib
21	201	93.9	181	2	AAW58805 Fibronec
22	201	93.9	181	2	AAW91200 D1-D4 fib
23	200	93.5	38	1	AAW80661 Protein w
24	200	93.5	38	1	AAW82117 Fibronec
25	200	93.5	38	2	AAW65703 Fibronec

ALIGNMENTS

RESULT 1
AAW65702 standard; peptide; 38 AA.

AAW65702:

16-OCT-1998 (first entry)

Fibronecin binding protein-derived peptide #46.

mCGRAMM; fibronecin; fibronecin-binding protein; antibody; epitope;

antibiotic; bacterial infection; antibiotic-resistant strain.

Synthetic.

Staphylococcus aureus.

W09831389-A2.

21-JUN-1998; 98WO-US001222.

21-JAN-1997; 97US-0036139P.

(TEXA) UNIV TEXAS A & M SYSTEM.

Hoecek M, Patil JM, House-Pompeo KL, Speziale P, Joh D;

Mogavin MJ;

WPI; 1998-413816/35.

Antibody that binds to fibronecin-binding protein, preventing its

binding to fibronecin - used to treat or prevent bacterial infection,

especially by Staphylococci and Streptococci.

Example 8; Page 102; 201pp; English.

The invention relates to antibodies that bind to a fibronecin-binding domain of a fibronecin-binding protein, and inhibit binding of the protein to a fibronecin. Also claimed are: (1) isolated peptides of a fibronecin-binding protein that do not bind to fibronecin; (2) fusion protein containing at least one peptide of a fibronecin-binding protein linked to a second amino acid sequence; (3) nucleic acid encoding the isolated peptide of (1). Antibodies, the isolated peptides of (1) and the nucleic acids are all useful for immunisation (active or passive) and (by inhibiting binding of bacteria to fibronecin) for preventing or treating infection in humans or other animals, particularly by staphylococci or

CC streptococci, e.g. meningitis, otitis media, pneumonia, endocarditis,
 CC mastitis in cattle, abortion in horses and many others. Since the
 CC antibodies block binding of bacteria, they should be effective against
 CC antibiotic-resistant strains, and may replace antibiotic therapy or
 CC increase its effectiveness. Sequences AAW65701-706 represent a series of
 CC synthetic peptides based on the D2 region of *S. aureus* fibronectin
 CC binding protein A. They were synthesised to contain mutations
 XX
 SQ Sequence 38 AA;
 Query Match 100.0%; Score 214; DB 2; Length 38;
 Best Local Similarity 100.0%; Pred. No. 5e-23;
 Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 QNKGNSFPEDTEKDKPKYEHGNGNIIDIDFDSVPHIHG 38
 DB 1 QNKGNSFPEDTEKDKPKYEHGNGNIIDIDFDSVPHIHG 38
 RESULT 2
 ID AAW65663 standard; peptide; 38 AA.
 XX AAW65663;
 AC AAW65663;
 XX
 DT 16-OCT-1998 (first entry)
 XX
 DE Fibronectin binding protein-derived peptide #7.
 XX
 KM microbial surface components recognising adhesive matrix molecule;
 KM MSCRAMM; fibronectin; fibronectin-binding protein; antibody; epitope;
 KM antibiotic; bacterial infection; antibiotic-resistant strain.
 XX
 OS Synthetic.
 OS Staphylococcus aureus.
 XX
 PN MO9831389-A2.
 XX
 PD 23-UTL-1998.
 XX
 PF 21-JAN-1998; 98MO-US001222.
 XX
 PR 21-JAN-1997; 97US-0036139P.
 XX
 PA (TEXA) UNIV TEXAS A & M SYSTEM.
 XX
 PI Hoeck M, Patli JM, House-Pompeo KL, Speciale P, Joh D;
 PI McGavin MJ;
 PI
 XX
 DR WPI; 1998-413816/35.
 XX
 PT Antibody that binds to fibronectin-binding protein, preventing its
 PT binding to fibronectin - used to treat or prevent bacterial infection,
 PT especially by Staphylococci and Streptococci.
 XX
 PS Example 2; Page 92; 201pp; English.
 XX
 CC The invention relates to antibodies that bind to a fibronectin-binding
 CC domain of a fibronectin-binding protein, and inhibit binding of the
 CC protein to fibronectin. Also claimed are: (1) isolated peptides of a
 CC fibronectin-binding protein that do not bind to fibronectin; (2) fusion
 CC protein containing at least one peptide of a fibronectin-binding protein
 CC linked to a second amino acid sequence; (3) nucleic acid encoding the
 CC isolated peptide of (1). Antibodies, the isolated peptides of (1) and the
 CC nucleic acids are all useful for immunisation (active or passive) and (by
 CC inhibiting binding of bacteria to fibronectin) for preventing or treating
 CC infection in humans or other animals, particularly by staphylococci or
 CC streptococci, e.g. meningitis, otitis media, pneumonia, endocarditis,
 CC mastitis in cattle, abortion in horses and many others. Since the
 CC antibodies block binding of bacteria, they should be effective against
 CC antibiotic-resistant strains, and may replace antibiotic therapy or
 CC increase its effectiveness. Sequences AAW65659-68 represent synthetic
 CC epitopes from the fibronectin binding domains DU and D1-D4 of the S.

CC aureus fnbA gene
 XX
 SQ Sequence 38 AA;
 Query Match 96.3%; Score 206; DB 2; Length 38;
 Best Local Similarity 97.4%; Pred. No. 7e-22;
 Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 QNKGNSFPEDTEKDKPKYEHGNGNIIDIDFDSVPHIHG 38
 DB 1 QNKGNSFPEDTEKDKPKYEHGNGNIIDIDFDSVPHIHG 38
 RESULT 3
 ID AAY29087 standard; protein; 134 AA.
 XX AAY29087;
 AC AAY29087;
 XX
 DT 28-SEP-1999 (first entry)
 XX
 DE *S. aureus* fibronectin binding protein A (FnBA) binding domain.
 XX
 KM Bovine herpes virus-2; BHV-2; cytokine; immune response; immunogen; IL;
 KM interleukin; colony stimulating factor; CSF; interferon; IFN; TNF;
 KM tumour necrosis factor; recombinant virus; vaccine; mucosal disease;
 KM mastitis; breast cancer; stress-induced disease; binding domain; FnBA;
 KM fibronectin binding protein.
 XX
 OS Staphylococcus aureus.
 OS
 PN MO9916892-A1.
 XX
 PD 08-APR-1999.
 XX
 PF 29-SEP-1998; 98MO-GB002927.
 XX
 PR 29-SEP-1997; 97GB-00020633.
 XX
 PA (UYBR-) UNIV BRISTOL.
 XX
 PI Bradley AJ, Duffas WP;
 PI
 XX
 DR WPI; 1999-255101/21.
 XX
 DR N-PSDB; AAX91504.
 XX
 PT New bovine herpes virus-2 vectors.
 PT
 PS Example 2; Fig 8A-B; 130pp; English.
 XX
 CC The invention provides bovine herpes virus-2 (BHV-2) based vectors that
 CC comprise at least one cytokine-encoding DNA sequence. The expression of
 CC cytokines in mammals can up-regulate immune responses to the immunogens.
 CC The cytokine is selected from interleukins (IL), colony stimulating
 CC factors (CSF), interferons (IFN) and tumour necrosis factors (TNF). The
 CC BHV-2 based vector or recombinant virus can be used as vaccines. They can
 CC be used for preventing or treating a mucosal disease in a subject, e.g.
 CC ruminants, cattle, sheep, goats, dogs, cats, horses, or man, particularly
 CC mastitis in cows or breast cancers in humans. They can also be used for
 CC preventing or treating a stress-induced disease. The present sequence
 CC represents the binding domain of a previously published *S. aureus*
 CC fibronectin binding protein A (FnBA) sequence. The FnB binding domain
 CC gene sequence FNBA-B, cloned for use in this invention has 97.8 percent
 CC identity when compared to the previously published FnBA and FnBB gene
 CC sequences
 XX
 SQ Sequence 134 AA;
 Query Match 96.3%; Score 206; DB 2; Length 134;
 Best Local Similarity 97.4%; Pred. No. 3.3e-21;
 Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 QNKGNSFPEDTEKDKPKYEHGNGNIIDIDFDSVPHIHG 38

DB 40 QNKGNSFEEDTEKDKPKYEHGNNIIDIDFDSVPHING 77

RESULT 4

AAW31556 standard; protein: 139 AA.

AAW31556;

27-AUG-2003 (revised)

25-MAR-2003 (revised)

21-MAY-1998 (first entry)

Fibronectin-binding MSCRAMM derivative pOD.

Fibronectin; pOD: collagen binding protein; sepsis; infection; microbial surface component; regonising adhesive matrix molecule; MSCRAMM; adhesin; vaccine; immunisation; diagnosis; therapy; mastitis.

Staphylococcus aureus.

Key Location/Qualifiers

Peptide 1..12 /note= "vector POE30-derived peptide"

MO9743314-A2.

20-NOV-1997.

14-MAY-1997; 97MO-US008210.

16-MAY-1996; 96US-0017678P.

(TEXA) UNIV TEXAS A & M SYSTEM.

(UABR-) UAB RES FOUND.

Hoeek M, Patil JM, House-Pompeo K, Sthanam N, Symersky J;

WPI; 1998-008801/01.

Antibody that interacts with collagen binding domain of Staphylococcal pT cna gene product - useful to prevent bacterial sepsis in animal infected with Staphylococcus aureus.

PS Disclosure; Page 91; 143pp; English.

XX This protein comprises Staphylococcus aureus fibronectin-binding
CC microbial surface component regonising adhesive matrix molecule (MSCRAMM)
CC derivative pOD, plus a vector-derived N-terminal peptide. The invention
CC relates to claimed nucleic acid sequences (see AAT93436-38) encoding S.
CC aureus collagen binding protein (CBP) epitopes M1, M31 and M55 (see
CC AAM31552-54) that confer protection against S. aureus infection. CBP
CC protein and antigenic epitopes are contemplated for use in the treatment
CC of pathological infections, especially to prevent bacterial adhesion to
CC collagen. The epitopes are also contemplated for use in the preparation
CC of vaccines and as carrier proteins in vaccine formulations, as well as
CC in the formulation of compositions for the prevention of S. aureus
CC infection. pCP33 and pOD (see AAM31556) were used to raise anti-MSCRAMM
CC polyclonal antibodies used in passive immunisation against bovine
CC mastitis. (Updated on 25-MAR-2003 to correct PI field.) (Updated on 27-
CC AUG-2003 to correct OS field.)

XX Sequence 139 AA;

Query Match 96.3%; Score 206; DB 2; Length 139;

Best Local Similarity 97.4%; Pred. No. 3.4e-21;

Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QNKGNSFEEDTEKDKPKYEHGNNIIDIDFDSVPHING 38

DB 54 QNKGNSFEEDTEKDKPKYEHGNNIIDIDFDSVPHING 91

RESULT 5
ID AAP82115 standard; protein: 1018 AA.

AAP82115;

25-MAR-2003 (revised)

05-JUN-1990 (first entry)

Fibronectin binding protein.

Fibronectin binding protein; S. aureus; immunisation; mastitis; ruminants;

wound infection; diagnosis.

Staphylococcus aureus.

EP294349-A.

07-DEC-1988.

30-MAY-1988; 88EP-00850188.

01-JUN-1987; 87SE-00002272.

(ALFA) ALFA LAVAL AGRIC INT AB.

Lindberg MK, Signas LC, Wadstrom TM, Froman G;

WPI; 1988-347978/49.

Hybrid DNA encoding Staphylococcus aureus fibronectin binding protein -

useful for immunisation and topical application to prevent staphylococcal

infections.

PS Disclosure; Fig. 8A:1-8A:2; 23pp; English.

XX The S. aureus fibronectin binding protein may be included in a hybrid
CC protein. The protein may be used to immunise ruminants against
CC staphylococcal mastitis, pref. when given at 0.5-5 microg/kg, using 3
CC doses at 1-3 week intervals; and for topical applicn. to prevent wound
CC infection, pref. using isotonic saline soln. of concn. 25-250 microg/mg.
CC The DNA encoding the binding protein and the hybrid protein may be
CC immobilised on a carrier and used to diagnose staphylococcal infections.
CC (Updated on 25-MAR-2003 to correct PA field.)

XX Sequence 1018 AA;

Query Match 96.3%; Score 206; DB 1; Length 1018;

Best Local Similarity 97.4%; Pred. No. 3.9e-20;

Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QNKGNSFEEDTEKDKPKYEHGNNIIDIDFDSVPHING 38

DB 784 QNKGNSFEEDTEKDKPKYEHGNNIIDIDFDSVPHING 821

AAU37245 standard; protein: 1018 AA.

AAU37245;

14-FEB-2002 (first entry)

Staphylococcus aureus cellular proliferation protein #1415.

Antisense; prokaryotic cellular proliferation protein; antibiotic;

antibacterial; drug design.

Staphylococcus aureus.

```

PN MO200170955-A2.
XX
XX 27-SEP-2001.
PD
XX
PF 21-MAR-2001; 2001WO-US009180.
XX
PR 21-MAR-2000; 2000US-0191078P.
PR 23-MAY-2000; 2000US-0206848P.
PR 26-MAY-2000; 2000US-0207727P.
PR 23-OCT-2000; 2000US-0242578P.
PR 27-NOV-2000; 2000US-0253625P.
PR 22-DEC-2000; 2000US-0257931P.
PR 16-FEB-2001; 2001US-0269308P.
XX
XX (ELIT-) ELITRA PHARM INC.
XX
XX Haselbeck R, Ohlsen KL, Zyskind JW, Wall D, Trawick JD, Carr GJ;
PI Yamamoto RT, Xu HH;
PI
XX WPI; 2001-611495/70.
DR N-PSDB; AAS55104.
XX
XX New polynucleotides for the identification and development of
PT antibiotics, comprise sequences of antisense nucleic acids.
XX
XX Example 3; SEQ ID NO 12838; 511pp; English.
XX
XX The invention relates to antisense inhibitors of genes essential to
CC prokaryotic cellular proliferation, their use in identifying the genes,
CC their use in the discovery of novel antibiotics, the essential genes
CC themselves and the encoded proteins. The prokaryotes used are Escherichia
CC coli, Staphylococcus aureus, Salmonella typhi, Klebsiella pneumoniae,
CC Pseudomonas aeruginosa and Enterococcus faecalis. The invention is also
CC useful for the identification of potential new targets for antibiotic
CC development. The antisense nucleic acids can also be used to identify
CC proteins used in proliferation, to express these proteins, and to obtain
CC antibodies capable of binding to the expressed proteins. The proteins can
CC be used to screen compounds in rational drug discovery programmes. The
CC antisense nucleic acid sequence is also useful to screen for homologous
CC nucleic acids which are required for cell proliferation in a wide variety
CC of organisms. The present sequence represents an essential prokaryotic
CC cellular proliferation protein. Note: The sequence data for this patent
CC did not form part of the printed specification, but was obtained in
CC electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 1018 AA;
SQ
Query Match 96.3%; Score 206; DB 4; Length 1018;
Best Local Similarity 97.4%; Pred. No. 3.9e-20;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 QNKGNSFPEDTEKDKPKYEHGNIIDIDFDSVPHING 38
Db 784 QNKGNSFPEDTEKDKPKYEHGNIIDIDFDSVPHING 821

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XX
XX 27-SEP-2001.
PD
XX
PF 21-MAR-2001; 2001WO-US009180.
XX
PR 21-MAR-2000; 2000US-0191078P.
PR 23-MAY-2000; 2000US-0206848P.
PR 26-MAY-2000; 2000US-0207727P.
PR 23-OCT-2000; 2000US-0242578P.
PR 27-NOV-2000; 2000US-0253625P.
PR 22-DEC-2000; 2000US-0257931P.
PR 16-FEB-2001; 2001US-0269308P.
XX
XX (ELIT-) ELITRA PHARM INC.
XX
XX Haselbeck R, Ohlsen KL, Zyskind JW, Wall D, Trawick JD, Carr GJ;
PI Yamamoto RT, Xu HH;
PI
XX WPI; 2001-611495/70.
DR N-PSDB; AAS52160.
XX
XX New polynucleotides for the identification and development of
PT antibiotics, comprise sequences of antisense nucleic acids.
XX
XX Example 3; SEQ ID NO 5797; 511pp; English.
XX
XX The invention relates to antisense inhibitors of genes essential to
CC prokaryotic cellular proliferation, their use in identifying the genes,
CC their use in the discovery of novel antibiotics, the essential genes
CC themselves and the encoded proteins. The prokaryotes used are Escherichia
CC coli, Staphylococcus aureus, Salmonella typhi, Klebsiella pneumoniae,
CC Pseudomonas aeruginosa and Enterococcus faecalis. The invention is also
CC useful for the identification of potential new targets for antibiotic
CC development. The antisense nucleic acids can also be used to identify
CC proteins used in proliferation, to express these proteins, and to obtain
CC antibodies capable of binding to the expressed proteins. The proteins can
CC be used to screen compounds in rational drug discovery programmes. The
CC antisense nucleic acid sequence is also useful to screen for homologous
CC nucleic acids which are required for cell proliferation in a wide variety
CC of organisms. The present sequence represents an essential prokaryotic
CC cellular proliferation protein. Note: The sequence data for this patent
CC did not form part of the printed specification, but was obtained in
CC electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 1018 AA;
SQ
Query Match 96.3%; Score 206; DB 4; Length 1018;
Best Local Similarity 97.4%; Pred. No. 3.9e-20;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 QNKGNSFPEDTEKDKPKYEHGNIIDIDFDSVPHING 38
Db 784 QNKGNSFPEDTEKDKPKYEHGNIIDIDFDSVPHING 821

```

```

RESULT 7
AAU34301
ID AAU34301 standard; protein; 1018 AA.
XX
XX AAU34301;
AC
XX
XX 14-FEB-2002 (first entry)
DT
XX
XX Staphylococcus aureus cellular proliferation protein #577.
DE
XX
XX Antisense; prokaryotic cellular proliferation protein; antibiotic;
KM antibacterial; drug design.
XX
XX Staphylococcus aureus.
OS
XX
XX MO200170955-A2.
PN

```

```

RESULT 8
ABJ18922
ID ABJ18922 standard; protein; 1018 AA.
XX
XX ABJ18922;
AC
XX
XX 06-MAR-2003 (first entry)
DT
XX
XX Pathogen specific antigen related staphylococcal protein SEQ ID No 68.
DE
XX
XX Antibacterial; virucide; fungicide; protozoacide; cytostatic; anti-HIV;
KM hyperimmune; serum-reactive; antigen; pathogen; tumour; allergen;
KM auto-immunity; vaccine; staphylococcal infection; antibody; cancer;
KM autoimmune disease; HIV; hepatitis.
XX
XX Staphylococcus sp.
OS
XX
XX

```

PN W0200259148-A2.
 XX
 PD 01-AUG-2002.
 XX
 XX 21-JAN-2002; 2002MO-EP000546.
 PF
 XX 26-JAN-2001; 2001AT-00000130.
 PR
 PA (CISTEM) CISTEM BIOTECHNOLOGIES GMBH.
 XX
 XX Meinke A, Nagy E, Von Ahnen U, Klade C, Henies T, Zauner M;
 PI Minh DB, Vytvytska O, Eitz H, Dryla A, Welchhart T, Hafner M;
 PI Tempelmeier B;
 XX
 DR WPI; 2003-075410/07.
 XX
 PT Identifying, isolating and producing hyperimmune serum-reactive antigens
 PT from a pathogen, for preparing vaccine or medicament for treating or
 PT preventing e.g. staphylococcal infections, comprises providing antibody
 PT preparation.
 PT
 XX Example 7; Page 157; 252pp; English.
 PS
 XX The invention relates to a novel method for identifying, isolating and
 CC producing hyperimmune serum-reactive antigens from a pathogen, tumour,
 CC allergen, a tissue or host prone to auto-immunity, where the antigens are
 CC used in a vaccine, comprises providing antibody preparation from a plasma
 CC pool of a type of animal, or individual sera with antibodies against the
 CC specific pathogen, tumour, allergen, tissue or host prone to auto-
 CC immunity. The hyperimmune serum-reactive antigens comprising any of the
 CC 62 sequences of 53-261 amino acids fully defined in the specification,
 CC or their hyperimmune fragments are useful for the manufacture of a
 CC pharmaceutical preparation, particularly a vaccine against staphylococcal
 CC infections or colonisation against *S. aureus* or *S. epidermidis*. The
 CC preparation of antibodies is useful for the manufacture of a medicament
 CC for treating or preventing staphylococcal infections or colonisation
 CC against *S. aureus* or *S. epidermidis*. The antibody preparations may also
 CC be used for diagnostic and imaging purposes. Other conditions that can be
 CC treated include cancer, autoimmune diseases or infections caused by viral
 CC (e.g. HIV, hepatitis A, B or C), fungal or protozoan pathogens. This
 CC sequence represents a staphylococcal protein relating to the method for
 CC identifying and producing pathogen specific antigens of the invention
 CC
 XX
 SQ Sequence 1018 AA;
 XX
 Query Match 96.3%; Score 206; DB 6; Length 1018;
 Best Local Similarity 97.4%; Pred. No. 3.9e-20;
 Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 QNKGNSFPEDTEKDKPKYEHGNNIIDIDPSVPHNG 38
 |||||
 DB 784 QNKGNSFEEDTEKDKPKYEHGNNIIDIDPSVPHNG 821
 |||||
 RESULT 9
 ID AAM72537 standard; protein; 1018 AA.
 XX
 AC AAM72537;
 XX
 DT 20-NOV-2003 (first entry)
 XX
 DE Staphylococcus aureus protein #1777.
 XX
 KM Antibacterial; vaccine; gene therapy; infection; sepsis; diagnosis;
 KM enzymatic assay; antibiotic target.
 XX
 OS Staphylococcus aureus.
 XX
 PN W0200294868-A2.
 XX
 PD 28-NOV-2002.
 PT

PF 27-MAR-2002; 2002MO-IB002637.
 XX
 XX 27-MAR-2001; 2001GB-00007661.
 PR
 XX (CHIR-) CHIRON SPA.
 XX
 PA Masignani V, Mora M, Scarselli M;
 PI
 PI WPI; 2003-120786/11.
 DR
 DR N-PSDB; ACF74097.
 XX
 XX New Staphylococcus aureus protein, useful as a vaccine for treating or
 PT preventing Staphylococcal infection, specifically an infection caused by
 PT *S. aureus*, e.g. sepsis.
 PT
 XX Claim 1; SEQ ID NO 3554; 49pp; English.
 PS
 XX The invention relates to novel genes and encoded proteins from
 CC Staphylococcus aureus. A composition comprising the *S. aureus* protein, a
 CC nucleic acid encoding the protein, or an antibody to the protein, is
 CC useful as a pharmaceutical, particularly as a vaccine for treating or
 CC preventing infection due to Staphylococcus bacteria, specifically an
 CC infection caused by *S. aureus*. The composition is particularly useful for
 CC treating or preventing sepsis in a patient. The composition can also be
 CC used for diagnostics. The protein is also used in an assay for enzymatic
 CC studies and as a target for antibiotics. This sequence represents one of
 CC the novel *S. aureus* proteins of the invention
 CC
 XX
 SQ Sequence 1018 AA;
 XX
 Query Match 96.3%; Score 206; DB 6; Length 1018;
 Best Local Similarity 97.4%; Pred. No. 3.9e-20;
 Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 QNKGNSFPEDTEKDKPKYEHGNNIIDIDPSVPHNG 38
 |||||
 DB 784 QNKGNSFEEDTEKDKPKYEHGNNIIDIDPSVPHNG 821
 |||||
 RESULT 10
 ID AAM89806 standard; protein; 1027 AA.
 XX
 AC AAM89806;
 XX
 DT 16-MAR-1999 (first entry)
 XX
 DE Staphylococcus aureus protein SEQ ID #5254.
 XX
 KM Computer readable medium; vaccine; *S. aureus* infection; immunodetection;
 KM cellulitis; eyelid infection; food poisoning; osteomyelitis; therapy;
 KM skin infection; surgical wound infection; scalded skin syndrome;
 KM toxic shock syndrome.
 XX
 OS Staphylococcus aureus.
 XX
 PN EP786519-A2.
 XX
 PD 30-JUL-1997.
 XX
 PF 07-JAN-1997; 97EP-00100117.
 XX
 PR 05-JAN-1996; 96US-0009861P.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 XX
 PI Kunsch CA, Choi GH, Barash SC, Dillon PJ, Fannon MR, Rosen CA;
 PI WPI; 1997-374922/35.
 XX
 DR Polynucleotide(s) and proteins derived from Staphylococcus aureus -
 PT scored on computer readable medium and used in the production of anti-
 PT *S. aureus* vaccines.
 PT

PS Claim 23; Page 3263-3267; 3271pp; English.

XX This sequence represents a *Staphylococcus aureus* protein sequence of the

CC invention. The DNA sequences encoding the *S. aureus* proteins are recorded

CC on a computer readable medium, preferably selected from a floppy or hard

CC disk, random access memory (RAM), read-only memory (ROM) or CD-ROM.

CC Homology searches using the *S. aureus* DNA sequences allows iterative

CC functions to be assigned so that protein-encoding or regulatory regions

CC of commercial, therapeutic or industrial importance can be obtained.

CC Specifically, sequences which are likely to encode antigens have been

CC identified and these polypeptides can be used in a vaccine composition

CC against *S. aureus* infection. The polypeptides can also be used in a kit

CC for the immunodetection of *S. aureus* in a sample. *S. aureus* is implicated

CC in numerous human diseases, including cellulitis, eyelid infections, food

CC poisoning, osteomyelitis, skin and surgical wound infections, scalded

CC skin syndrome, toxic shock syndrome, etc. Organisms transfected with the

CC DNA sequences can be used for recombinant production of the polypeptides.

CC The new DNA sequences (and their fragments) are useful as primers or

CC probes for isolating homologues of any of the 5191 *S. aureus* DNA sequences

CC contained on the computer readable medium

XX

XX Sequence 1027 AA:

SO

Query Match 96.3%; Score 206; DB 2; Length 102;
Best Local Similarity 97.4%; Pred. No. 3.9e-20;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0

QY 1 ONKGNQSPEDTEKDKPKYEHGNGNIIDIDFDSVPPIHG 38
|||||
Db 793 ONKGNQSPEDTEKDKPKYEHGNGNIIDIDFDSVPPIHG 830

RESULT 11
AAR88749
ID AAR88749 standard; protein; 77 AA.

XX AAR88749;
AC
XX
XX
DT 24-SEP-1996 (first entry)
XX
XX
DE
XX
S. aureus fibronectin binding protein D2D3 polypeptide.

KM Fibronectin binding protein; D2D3; prevention; adhesion; bacteria;
KM gram positive; extra-cellular matrix protein; in-dwelling device;
KM catheter; wound; D2D3; oral pathogen; oral cavity; J2385; NCIMB 40532.
XX
XX
OS
XX
Staphylococcus aureus.

PN WO9604380-A1.
XX
XX
PD 15-FEB-1996.
XX
XX
PF 28-JUL-1995; 95WO-EP003039.
XX
XX
PR 05-AUG-1994; 94GB-00015901.
XX
XX
(SMTK) SMITHKLINE BEECHAM PLC.
XX
XX
PI Critchley IA, Dodd I, Barnett P, Mossakowska DEI;
XX
XX
DR MPI; 1996-129396/13.
XX
XX
N-PsDB; AAT12582.

PT Staphylococcus aureus fibronectin binding protein D2D3 polypeptide -
PT useful for combating infection at wound sites, surgical implants, etc.
PT and as antiadherent agent in oral hygiene.
XX
XX
PS Claim 5; Page 26; 38pp; English.

CC The present sequence is the *S. aureus* fibronectin binding protein
CC polypeptide D2D3, which can be used to prevent adhesion of (e.g. gram
CC positive) bacteria, to extra-cellular matrix proteins on in-dwelling

CC	device, e.g. catheters or in wounds. D2D3 can also be used to prevent
CC	oral pathogens from binding to extra-cellular matrix proteins, in the
CC	oral cavity. D2D3 was found to be effective at inhibiting <i>S. aureus</i> 8325-
CC	4, and 120 adhesion to fibronectin coated PHEMA coverings, at a min.
CC	adhesion inhibitor concn. of 10 mcg/ml. D2D3 was derived from the D2
CC	and D3 regions of the <i>S. aureus</i> J2385 (NCIMB 40532) fibronectin binding
CC	protein
CC	Sequence 77 AA;
XX	
Qy	Query Match 93.9%; Score 201; DB 2; Length 77;
Db	Best Local Similarity 94.7%; Pred. No. 8.6e-21;
	Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0
	1 QNKGNSPEDETKDKPYEHGNIIDIDPDSVPPIHG 38
	2 QNKGDSPEDETKDKPYEHGNIIDIDPDSVPPIHG 39
RESULT 12	
ID	AAR90937 standard; peptide; 113 AA.
XX	
AC	AAR90937;
XX	
DT	23-SEP-1996 (first entry)
XX	
DE	D3D4 polypeptide #1.
XX	
KM	Fibronectin binding protein; Fbp; <i>S. aureus</i> J2385; monoclonal antibody;
KM	infection; surgical implant; antidiherent agent; hygiene; adhesion;
KM	extracellular matrix protein; oral pathogen; oral cavity.
XX	
OS	<i>Staphylococcus aureus</i> .
XX	
FH	Key Location/Qualifiers
FT	Region 1..21
FT	/note= "D1 region fragment"
FT	Region 22..59
FT	/note= "D2 region"
FT	Region 60..98
FT	/note= "D3 region"
FT	Region 99..113
FT	/note= "D4 region"
FT	Misc-difference 113
FT	/note= "P113T"
XX	
PN	WO9604381-A1.
XX	
PD	15-FEB-1996.
XX	
PF	28-JUL-1995; 95WO-EP003040.
XX	
PR	05-AUG-1994; 94GB-00015900.
XX	
PA	(SMIK) SMITHKLINE BEECHAM PLC.
XX	
PI	Critchley IA, Dodd I, Barnett P, Mcbay DL;
XX	
DR	WPI, 1996-129397/13.
XX	
PT	Polypeptide(s) derived from <i>Staphylococcus aureus</i> fibronectin binding
PT	protein - inhibit binding of bacteria to extracellular matrix proteins,
PT	for combating infection at the site of wounds and surgical implants, and
PT	in oral hygiene.
XX	
PS	Claim 6; Page 24; 35pp; English.
XX	
CC	AAR90937-R90942 represent D3D4 polypeptides. These sequences correspond
CC	to fragments of the <i>Staphylococcus aureus</i> fibronectin binding protein
CC	(Fbp). This sequence corresponds to residues 18-130 of <i>S. aureus</i> J2385
CC	Fbp, and also contains the D2 region, and a portion of the D1 region.
CC	These sequences, and monoclonal antibodies against them can be used to

CC combat infection at the site of wounds, surgical implants and other in-
 CC dwelling devices (such as catheters), and as antiadherent agents in oral
 CC hygiene. They can also be used in the manufacture of a medicament for the
 CC prevention of adhesion of bacteria to extracellular matrix proteins
 CC present on in-dwelling devices or in wounds, or of oral pathogens to
 CC similar proteins on surfaces in the oral cavity
 XX
 SQ Sequence 113 AA;

Query Match 93.9%; Score 201; DB 2; Length 113;
 Best Local Similarity 94.7%; Pred. No. 1.4e-20;
 Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 QNKGNSFPEDTEKDKPKYEHGNIIDIDFDSVPHNG 38
 |||||
 DB 23 QNKGDSFEDTEKDKPKYEHGNIIDIDFDSVPHNG 60

RESULT 13

AA858806 standard; protein; 130 AA.

AA858806;

AC 25-MAR-2003 (revised)
 DT 30-MAR-1995 (first entry)
 XX
 XX Fibronectin binding domain D1-D4 (709-838 (P838T)).

KM Fibronectin binding protein; Fbp; fibronectin binding domain;
 KM monoclonal antibody; Mab; adhesion; Gram-positive bacterium; bacteremia;
 KW Escherichia coli.

XX Staphylococcus aureus.

PN W09418327-A1.

PD 18-AUG-1994.

PF 04-FEB-1994; 94MO-GB000215.

PR 05-FEB-1993; 93GB-00002289.

PR 20-OCT-1993; 93GB-00021592.

XX (SMIK) SMITHKLINE BEECHAM PLC.

PI Burnham MKR, Chopra I, Critchley IA, Knowles DJC;

XX WPI, 1994-279748/34.

DR Fibronectin binding protein and monoclonal antibodies specific for Fbp -
 PT useful to prevent adherence of Gram-positive bacteria to indwelling
 PT devices or wounds.

PS Disclosure; Page 30; 40pp; English.

XX Polypeptides corresponding to residues G709-T886 plus PIVPPT, G709-
 CC P838(P838T) and G709-P838 (AA858805-07, respectively) of S. aureus J2385
 CC (NCIMB 40532) Fbp type A fibronectin binding domain D1-D4 region
 CC (AA858808) were expressed in E. coli B21(DE4) and used to raise MAb
 CC specific for Fbp. (Updated on 25-MAR-2003 to correct PN field.)
 XX

SQ Sequence 130 AA;

Query Match 93.9%; Score 201; DB 2; Length 130;
 Best Local Similarity 94.7%; Pred. No. 1.6e-20;
 Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 QNKGNSFPEDTEKDKPKYEHGNIIDIDFDSVPHNG 38
 |||||
 DB 40 QNKGDSFEDTEKDKPKYEHGNIIDIDFDSVPHNG 77

RESULT 14

AA858807 standard; protein; 130 AA.

AA858807;

AC 25-MAR-2003 (revised)
 DT 30-MAR-1995 (first entry)
 XX
 XX Fibronectin binding domain D1-D4 (709-838).

KM Fibronectin binding protein; Fbp; fibronectin binding domain;
 KM monoclonal antibody; Mab; adhesion; Gram-positive bacterium; bacteremia;
 KW Escherichia coli.

XX Staphylococcus aureus.

PN W09418327-A1.

PD 18-AUG-1994.

PF 04-FEB-1994; 94MO-GB000215.

PR 05-FEB-1993; 93GB-00002289.

PR 20-OCT-1993; 93GB-00021592.

XX (SMIK) SMITHKLINE BEECHAM PLC.

PI Burnham MKR, Chopra I, Critchley IA, Knowles DJC;

XX WPI, 1994-279748/34.

DR Fibronectin binding protein and monoclonal antibodies specific for Fbp -
 PT useful to prevent adherence of Gram-positive bacteria to indwelling
 PT devices or wounds.

PS Disclosure; Page 30; 40pp; English.

XX Polypeptides corresponding to residues G709-T886 plus PIVPPT, G709-
 CC P838(P838T) and G709-P838 (AA858805-07, respectively) of S. aureus J2385
 CC (NCIMB 40532) Fbp type A fibronectin binding domain D1-D4 region
 CC (AA858808) were expressed in E. coli B21(DE4) and used to raise MAb
 CC specific for Fbp. (Updated on 25-MAR-2003 to correct PN field.)
 XX

SQ Sequence 130 AA;

Query Match 93.9%; Score 201; DB 2; Length 130;
 Best Local Similarity 94.7%; Pred. No. 1.6e-20;
 Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 QNKGNSFPEDTEKDKPKYEHGNIIDIDFDSVPHNG 38
 |||||
 DB 40 QNKGDSFEDTEKDKPKYEHGNIIDIDFDSVPHNG 77

RESULT 15

AA891202 standard; peptide; 130 AA.

AA891202;

AC 13-NOV-1996 (first entry)

XX D1-D4 fibronectin binding domains.

XX Fibronectin; oral hygiene; gingivitis; gum disease; adhesion;
 KW periodontitis; oral pathogen; caries; calculus; candidiasis; oral surgery;
 KW tissue regeneration; irrigation; toothpaste; dentifrice; mouthwash;
 KW lozenge.

OS Staphylococcus aureus.

PN W09604003-A1.

```

XX
PD 15-FEB-1996.
XX
PF 18-JUL-1995; 95WO-EP002825.
XX
PR 05-AUG-1994; 94GB-00015902.
XX
PA (SMITK ) SMITHKLINE BEECHAM PLC.
XX
PI Barnett P, Critchley IA, Dodd I;
XX
DR WPI; 1996-129122/13.
XX
PT Prevention of adherence of oral pathogens in the oral cavity, partic.
PT tooth surfaces - by application of a fibronectin binding protein or
PT polypeptide or a monoclonal antibody or fragment against it.
PS
PS Claim 5; Page 32; 41pp; English.
XX
XX Adherence of oral pathogens, particularly to tooth surface, can be
CC prevented by application of a fibronectin binding protein or polypeptide.
CC The fibronectin binding protein or polypeptide is useful in the
CC manufacture of oral hygiene compositions, eg. toothpaste, liquid
CC dentifrice, mouthwash or lozenge. They are useful to prevent the plaque-
CC related development of carious lesions, gingivitis, calculus or
CC periodontal disease and to combat oral cavity infections, e.g.
CC candidiasis. They may also be useful in oral surgery e.g. in guided
CC tissue regeneration procedures to prevent subsequent bacterial infection,
CC and for irrigation of periodontal pockets. This sequence corresponds to
CC amino acids 709-838 of the D1-D4 fibronectin binding domain of
CC Staphylococcus aureus
XX
SQ Sequence 130 AA:

```

```

Query Match          93.9%; Score 201; DB 2; Length 130
Best Local Similarity 94.7%; Pred. No. 1.6e-20;
Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

```

```

QY 1 QNKGNSFPEDTEKDKPKYEHGNIITIDIDFDSVPYHIG 38
   |||:|||||
DB 40 QNKGDSFPEDTEKDKPKYEHGNIITIDIDFDSVPYHIG 77

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Search completed: October 25, 2005, 20:21:05
 Job time : 83.8825 secs

GenCore version 5.1.6
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OM protein - protein search, using SW model

Run on: October 22, 2005, 03:51:22 ; Search time 21.1723 Seconds
(without alignments)
133.980 Million cell updates/sec

Title: US-10-731-238-46

Perfect score: 214
Sequence: 1 QKGNQSPEDTEKDKPKYEHGNNIDIDFDSVPHING 38

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA: *
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2: /cgn2_6/ptodata/1/iaa/5B COMB.pep: *
3: /cgn2_6/ptodata/1/iaa/6A COMB.pep: *
4: /cgn2_6/ptodata/1/iaa/6B COMB.pep: *
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6: /cgn2_6/ptodata/1/iaa/backfile1.pep: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	214	100.0	38	4	US-09-010-317-46 Sequence 46, Appl
2	206	96.3	38	1	US-08-234-622A-3 Sequence 3, Appl
3	206	96.3	38	4	US-09-010-317-7 Sequence 7, Appl
4	206	96.3	114	1	US-08-259-000-3 Sequence 3, Appl
5	206	96.3	139	3	US-08-856-253-8 Sequence 8, Appl
6	206	96.3	1027	4	US-08-956-171E-5254 Sequence 5254, Ap
7	206	96.3	1027	4	US-08-781-986A-5254 Sequence 5254, Ap
8	201	93.9	130	2	US-08-459-135A-7 Sequence 7, Appl
9	201	93.9	130	2	US-08-459-135A-8 Sequence 8, Appl
10	201	93.9	130	3	US-08-495-559-7 Sequence 7, Appl
11	201	93.9	130	3	US-08-495-559-8 Sequence 8, Appl
12	201	93.9	174	2	US-08-459-135A-10 Sequence 10, Appl
13	201	93.9	174	3	US-08-495-559-10 Sequence 10, Appl
14	201	93.9	176	3	US-08-495-559-6 Sequence 6, Appl
15	201	93.9	178	2	US-08-459-135A-12 Sequence 12, Appl
16	201	93.9	178	3	US-08-495-559-12 Sequence 12, Appl
17	201	93.9	181	2	US-08-459-135A-6 Sequence 6, Appl
18	200	93.5	38	1	US-08-729-767-4 Sequence 4, Appl
19	200	93.5	38	4	US-09-010-317-47 Sequence 47, Appl
20	199	93.0	38	4	US-09-010-317-48 Sequence 48, Appl
21	198	92.5	38	4	US-09-010-317-8 Sequence 8, Appl
22	198	92.5	38	4	US-09-010-317-49 Sequence 49, Appl
23	196	91.6	38	4	US-09-010-317-45 Sequence 45, Appl
24	193	90.2	174	2	US-08-459-135A-13 Sequence 13, Appl
25	193	90.2	174	3	US-08-495-559-13 Sequence 13, Appl
26	193	90.2	559	4	US-08-956-171E-5251 Sequence 5251, Ap
27	193	90.2	559	4	US-08-781-986A-5251 Sequence 5251, Ap

28	192	89.7	38	4	US-09-010-317-50 Sequence 50, Appl
29	188	87.9	38	4	US-09-010-317-36 Sequence 36, Appl
30	183	85.5	36	4	US-09-010-317-58 Sequence 58, Appl
31	180	84.1	38	1	US-08-234-622A-2 Sequence 2, Appl
32	180	84.1	38	4	US-09-010-317-5 Sequence 5, Appl
33	178	83.2	38	4	US-09-010-317-41 Sequence 41, Appl
34	175	81.8	36	4	US-09-010-317-59 Sequence 59, Appl
35	174	81.3	38	1	US-08-729-767-3 Sequence 3, Appl
36	174	81.3	38	4	US-09-010-317-37 Sequence 37, Appl
37	174	81.3	38	4	US-09-010-317-39 Sequence 39, Appl
38	173	80.8	38	4	US-09-010-317-40 Sequence 40, Appl
39	173	80.8	38	4	US-09-010-317-38 Sequence 38, Appl
40	173	80.8	38	4	US-09-010-317-42 Sequence 42, Appl
41	172	80.4	38	4	US-09-010-317-6 Sequence 6, Appl
42	172	80.4	38	4	US-09-010-317-43 Sequence 43, Appl
43	170	79.4	38	4	US-09-010-317-35 Sequence 35, Appl
44	169.5	79.2	39	4	US-09-010-317-56 Sequence 56, Appl
45	166	77.6	38	4	US-09-010-317-44 Sequence 44, Appl

ALIGNMENTS

RESULT 1
US-09-010-317-46
Sequence 46, Application US/09010317
Patent No. 6685943
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
APPLICANT: Patti, Joseph M.
APPLICANT: House-Pompeo, Karen L.
APPLICANT: Speziale, Pietro
APPLICANT: Jon, Danny
APPLICANT: Mcgavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hilder, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAMK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 46:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-09-010-317-46
Query Match 100.0%; Score 214; DB 4; Length 38;
Best Local Similarity 100.0%; Pred. No. 2.5e-23;

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/259,000
FILING DATE: 13-JUN-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: SE 8702272-9
FILING DATE: 01-JUN-1987
ATTORNEY/AGENT INFORMATION:
NAME: Meuth, Donna M
REGISTRATION NUMBER: 36,607
REFERENCE/DOCKET NUMBER: 012885-062
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 114 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-259-000-3

Query Match 96.3%; Score 206; DB 1; Length 114;
Best Local Similarity 97.4%; Pred. No. 1.3e-21;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QNKGNSFPEDTEKDKPKYEHGNIIDIDPDSVPHHG 38
DB 40 QNKGNSFPEDTEKDKPKYEHGNIIDIDPDSVPHHG 77

RESULT 5
US-08-856-253-8
Sequence 8, Application US/08856253
Patent No. 6288214
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
APPLICANT: Patti, Joseph M.
APPLICANT: House-Pompeo, Karen
APPLICANT: Sthanam, Narayana
APPLICANT: Synerky, Jindrich
TITLE OF INVENTION: COLLAGEN BINDING PROTEIN COMPOSITIONS
NUMBER OF SEQUENCES: 8
TITLE OF INVENTION: AND METHODS OF USE
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: Texas
COUNTRY: U.S.
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/856,253
FILING DATE: Concurrently Herewith
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/017,678
FILING DATE: 16-MAY-1996
ATTORNEY/AGENT INFORMATION:
NAME: Kitchell, Barbara S.
REGISTRATION NUMBER: 33,928
REFERENCE/DOCKET NUMBER: TAMK.193
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 474-7577
TELEFAX: (512) 474-7577
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:

LENGTH: 139 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-08-856-253-8

Query Match 96.3%; Score 206; DB 3; Length 139;
Best Local Similarity 97.4%; Pred. No. 1.7e-21;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QNKGNSFPEDTEKDKPKYEHGNIIDIDPDSVPHHG 38
DB 54 QNKGNSFPEDTEKDKPKYEHGNIIDIDPDSVPHHG 91

RESULT 6
US-08-956-171E-5254
Sequence 5254, Application US/08956171E
Patent No. 6593114
GENERAL INFORMATION:
APPLICANT: Charles Kunsch
Gil H. Choi
Patrick S. Dillon
Craig A. Rosen
Steven C. Barash
Michael R. Fannon
TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
NUMBER OF SEQUENCES: 5256
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COUNTRY: USA
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/956,171E
FILING DATE: 20-Oct-1997
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/009,861
FILING DATE: January 5, 1996
APPLICATION NUMBER: 08/781,986
FILING DATE: January 3, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Mark J. Hyman
REGISTRATION NUMBER: 46,789
REFERENCE/DOCKET NUMBER: PB248P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (240) 314-1224
TELEFAX: (301) 309-8439
INFORMATION FOR SEQ ID NO: 5254:
SEQUENCE CHARACTERISTICS:
LENGTH: 1027 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 5254:
US-08-956-171E-5254

Query Match 96.3%; Score 206; DB 4; Length 1027;
Best Local Similarity 97.4%; Pred. No. 1.9e-20;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QNKGNSFPEDTEKDKPKYEHGNIIDIDPDSVPHHG 38
DB 793 QNKGNSFPEDTEKDKPKYEHGNIIDIDPDSVPHHG 830

RESULT 7
US-08-781-986A-5254
; Sequence 5254, Application US/08781986A
; Patent No. 6737248
; GENERAL INFORMATION:
; APPLICANT: Charles Kunesh
; TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
; NUMBER OF SEQUENCES: 5255
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4mb storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/781,986A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Benson, Bob
; REGISTRATION NUMBER: 30,446
; REFERENCE/DOCKET NUMBER: PB248PP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 5254:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1027 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-781-986A-5254

Query Match 96.3%; Score 206; DB 4; Length 1077;
Best Local Similarity 97.4%; Pred. No. 1.9e-20;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QNKGNSPEDTEKDKPKYEHGNNIIDIDPDSVPHIHG 38
DB 793 QNKGNSPEDTEKDKPKYEHGNNIIDIDPDSVPHIHG 830

RESULT 8
US-08-459-135A-7
; Sequence 7, Application US/08459135A
; Patent No. 5955078
; GENERAL INFORMATION:
; APPLICANT: BURNHAM, Martin Karl Russel
; APPLICANT: CHOPRA, Ian
; APPLICANT: CRITCHLEY, Ian Alfred
; APPLICANT: KNOWLES, David Justin Charles
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN: MONOCLONAL ANTIBODY AND THEIR US
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corporation
; STREET: 709 Swedeland Road
; CITY: King of Prussia
; STATE: PA
; COUNTRY: U.S.A.
; ZIP: 19406-0939
; COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: Fastseq, Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/459,135A
; FILING DATE: 02-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB/94/00215
; FILING DATE: 04-Feb-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Gimmil, Edward R
; REGISTRATION NUMBER: 38,891
; REFERENCE/DOCKET NUMBER: P30591C2
; TELECOMMUNICATION INFORMATION:
; TELEFAX: 610-270-5090
; TELEPHONE: 610-270-4478
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 130 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-459-135A-7

Query Match 93.9%; Score 201; DB 2; Length 130;
Best Local Similarity 94.7%; Pred. No. 7.9e-21;
Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 QNKGNSPEDTEKDKPKYEHGNNIIDIDPDSVPHIHG 38
DB 40 QNKGNSPEDTEKDKPKYEHGNNIIDIDPDSVPHIHG 77

RESULT 9
US-08-459-135A-8
; Sequence 8, Application US/08459135A
; Patent No. 5955078
; GENERAL INFORMATION:
; APPLICANT: BURNHAM, Martin Karl Russel
; APPLICANT: CHOPRA, Ian
; APPLICANT: CRITCHLEY, Ian Alfred
; APPLICANT: KNOWLES, David Justin Charles
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN: MONOCLONAL ANTIBODY AND THEIR US
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corporation
; STREET: 709 Swedeland Road
; CITY: King of Prussia
; STATE: PA
; COUNTRY: U.S.A.
; ZIP: 19406-0939
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: Fastseq, Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/459,135A
; FILING DATE: 02-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB/94/00215
; FILING DATE: 04-Feb-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Gimmil, Edward R
; REGISTRATION NUMBER: 38,891
; REFERENCE/DOCKET NUMBER: P30591C2
; TELECOMMUNICATION INFORMATION:

TELEPHONE: 610-270-4478
TELEFAX: 610-270-5090
TELEX:
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 130 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-459-135A-8

Query Match 93.9%; Score 201; DB 2; Length 130;
Best Local Similarity 94.7%; Pred. No. 7.9e-21;
Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QNKGNSFPEDTEKDKPKYEHGNNIIDIDPDSVPHHG 38
Db 40 QNKGDSFEDTEKDKPKYEHGNNIIDIDPDSVPHHG 77

RESULT 10
US-08-495-559-7
Sequence 7, Application US/08495559A
Patent No. 6054572
GENERAL INFORMATION:
APPLICANT: BURHAM, Martin Karl Russel
APPLICANT: CHOPRA, Ian
APPLICANT: CRITCHLEY, Ian Alfred
APPLICANT: KNOWLES, David Justin Charles
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN: MONOCLONAL
TITLE OF INVENTION: ANTIBODY AND THEIR USE IN PREVENTING BACTERIAL ADHESION
FILE REFERENCE: P30591
CURRENT APPLICATION NUMBER: US/08/495,559A
CURRENT FILING DATE: 1995-08-03
EARLIER APPLICATION NUMBER: GB 9302289.5
EARLIER FILING DATE: 1993-02-05
EARLIER APPLICATION NUMBER: GB 9321592.9
EARLIER FILING DATE: 1993-10-20
NUMBER OF SEQ ID NOS: 13
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 7
LENGTH: 130
TYPE: PRT
ORGANISM: Staphylococcus aureus
US-08-495-559-7

Query Match 93.9%; Score 201; DB 3; Length 130;
Best Local Similarity 94.7%; Pred. No. 7.9e-21;
Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QNKGNSFPEDTEKDKPKYEHGNNIIDIDPDSVPHHG 38
Db 40 QNKGDSFEDTEKDKPKYEHGNNIIDIDPDSVPHHG 77

RESULT 11
US-08-495-559-8
Sequence 8, Application US/08495559A
Patent No. 6054572
GENERAL INFORMATION:
APPLICANT: BURHAM, Martin Karl Russel
APPLICANT: CHOPRA, Ian
APPLICANT: CRITCHLEY, Ian Alfred
APPLICANT: KNOWLES, David Justin Charles
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN: MONOCLONAL
TITLE OF INVENTION: ANTIBODY AND THEIR USE IN PREVENTING BACTERIAL ADHESION
FILE REFERENCE: P30591
CURRENT APPLICATION NUMBER: US/08/495,559A
CURRENT FILING DATE: 1995-08-03
EARLIER APPLICATION NUMBER: GB 9302289.5
EARLIER FILING DATE: 1993-02-05
EARLIER APPLICATION NUMBER: GB 9321592.9
EARLIER FILING DATE: 1993-10-20

NUMBER OF SEQ ID NOS: 13
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 8
LENGTH: 130
TYPE: PRT
ORGANISM: Staphylococcus aureus
US-08-495-559-8

Query Match 93.9%; Score 201; DB 3; Length 130;
Best Local Similarity 94.7%; Pred. No. 7.9e-21;
Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QNKGNSFPEDTEKDKPKYEHGNNIIDIDPDSVPHHG 38
Db 40 QNKGDSFEDTEKDKPKYEHGNNIIDIDPDSVPHHG 77

RESULT 12
US-08-459-135A-10
Sequence 10, Application US/08459135A
Patent No. 595078
GENERAL INFORMATION:
APPLICANT: BURHAM, Martin Karl Russel
APPLICANT: CHOPRA, Ian
APPLICANT: CRITCHLEY, Ian Alfred
APPLICANT: KNOWLES, David Justin Charles
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN: MONOCLONAL ANTIBODY AND THEIR USE
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
STATE: PA
COUNTRY: U.S.A.
ZIP: 19406-0939
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq, Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/459,135A
FILING DATE: 02-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB/94/00215
FILING DATE: 04-Feb-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Gimmil, Edward R
REGISTRATION NUMBER: 38,891
REFERENCE/DOCKET NUMBER: P30591C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-4478
TELEFAX: 610-270-5090
TELEX:
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 174 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: Protein
US-08-459-135A-10

Query Match 93.9%; Score 201; DB 2; Length 174;
Best Local Similarity 94.7%; Pred. No. 1.1e-20;
Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QNKGNSFPEDTEKDKPKYEHGNNIIDIDPDSVPHHG 38
Db 40 QNKGDSFEDTEKDKPKYEHGNNIIDIDPDSVPHHG 77

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? Patent No. 5955078
? GENERAL INFORMATION:
? APPLICANT: BURHAM, Martin Karl Russel
? APPLICANT: CHOPRA, Ian
? APPLICANT: CRITCHLEY, Ian Alfred
? APPLICANT: KNOWLES, David Justin Charles
? TITLE OF INVENTION: FIBROBLAST BINDING PROTEIN: MONOCLONAL ANTIBODY AND THEIR USE
? NUMBER OF SEQUENCES: 15
? CORRESPONDENCE ADDRESS:
? ADDRESSEE: SmithKline Beecham Corporation
? STREET: 709 Swedeland Road
? City: King of Prussia
? STATE: PA
? COUNTRY: U.S.A.
? ZIP: 19406-0939
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Diskette
? COMPUTER: IBM Compatible
? OPERATING SYSTEM: DOS
? SOFTWARE: Fastseq, Version 2.0
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/08/459,135A
? FILING DATE: 02-JUN-1995
? CLASSIFICATION: 435
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: PCT/GB/94/00215
? FILING DATE: 04-Feb-1994
? CLASSIFICATION: 435
? ATTORNEY/AGENT INFORMATION:
? NAME: Gimmil, Edward R
? REGISTRATION NUMBER: 38,891
? REFERENCE/DOCKET NUMBER: P30591C2
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: 610-270-4478
? TELEFAX: 610-270-5090
? TELEX:
? INFORMATION FOR SEQ ID NO: 12:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 178 amino acids
? TYPE: amino acid
? STRANDEDNESS: single
? TOPOLOGY: linear
? MOLECULE TYPE: Protein
? US-08-459-135A-12

Query Match          93.9%; Score 201; DB 2; Length 178;
Best Local Similarity 94.7%; Pred. No. 1,2e-20;
Matches    36; Conservative   1; Mismatches      1; Indels     0; Gaps      0;

QY      1 QNKGNGSPPEDETKDKPKYEHEGNNIIDIDPDSVPHIG 38
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Db       40 QNKGDQSFEEDTEKDKPKYEHEGNNIIDIDPDSVPHIG 77

Search completed: October 22, 2005, 05:46:46
Job time : 21.2223 secs
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GenCore version 5.1.6
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OM protein - protein search, using SW model

Run on: October 22, 2005, 11:35:03 ; Search time 70.1256 Seconds
(without alignments)
226.232 Million cell updates/sec

Title: US-10-731-238-46

Perfect score: 214
Sequence: 1 QNKGNSFPEDETKDKPKYEHGNIIDIPDSVPHIHG 38

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1862951 seqs, 417491010 residues

Total number of hits satisfying chosen parameters: 1862951

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0 %
Maximum Match 100 %

Listing first 45 summaries

Database :

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3: /cgn2_6/prodata/2/pubppa/US06_NEW_PUB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	214	100.0	38	18	US-10-731-238-46
2	206	96.3	38	18	US-10-731-238-7
3	206	96.3	139	9	US-09-813-820-8
4	206	96.3	1018	9	US-09-815-242-5797
5	206	96.3	1018	9	US-09-815-242-12838
6	206	96.3	1018	17	US-10-470-048B-68
7	206	96.3	1027	8	US-08-781-986A-5254
8	206	96.3	1027	15	US-10-329-624-5254
9	200	93.0	38	18	US-10-731-238-47
10	199	93.0	38	18	US-10-731-238-48
11	198	92.5	38	18	US-10-731-238-8

12	198	92.5	38	18	US-10-731-238-49	Sequence 49, Appl
13	196	91.6	38	18	US-10-731-238-45	Sequence 45, Appl
14	193	90.2	388	8	US-08-901-062-1	Sequence 1, Appl
15	193	90.2	559	8	US-08-781-986A-5251	Sequence 5251, Ap
16	193	90.2	559	15	US-10-329-624-5251	Sequence 5899, Ap
17	193	90.2	767	9	US-09-815-242-5899	Sequence 13140, A
18	193	90.2	767	9	US-09-815-242-13140	Sequence 424, App
19	193	90.2	940	17	US-10-470-048B-69	Sequence 43827, A
20	193	90.2	1038	15	US-10-282-122A-43827	Sequence 50, Appl
21	193	90.2	38	18	US-10-731-238-36	Sequence 36, Appl
22	192	89.7	38	18	US-09-815-242-5456	Sequence 5456, Ap
23	188	86.4	978	9	US-09-815-242-12686	Sequence 12686, A
24	185	86.4	1001	9	US-10-731-238-58	Sequence 58, Appl
25	185	85.5	36	18	US-10-731-238-43	Sequence 43778, A
26	183	84.6	961	15	US-10-282-122A-43778	Sequence 5, Appl
27	181	84.1	38	18	US-10-731-238-5	Sequence 41, Appl
28	180	83.2	38	18	US-10-731-238-41	Sequence 37, Appl
29	178	83.2	36	18	US-10-731-238-59	Sequence 39, Appl
30	175	81.8	38	18	US-10-731-238-37	Sequence 40, Appl
31	174	81.3	38	18	US-10-731-238-39	Sequence 38, Appl
32	174	81.3	38	18	US-10-731-238-40	Sequence 42, Appl
33	174	81.3	38	18	US-10-731-238-38	Sequence 6, Appl
34	173	80.8	38	18	US-10-731-238-42	Sequence 43, Appl
35	173	80.8	38	18	US-10-731-238-46	Sequence 35, Appl
36	172	80.4	38	18	US-10-731-238-35	Sequence 56, Appl
37	172	79.4	38	18	US-10-731-238-35	Sequence 44, Appl
38	170	79.2	38	18	US-10-731-238-56	Sequence 57, Appl
39	169.5	75.5	39	18	US-10-731-238-57	Sequence 1, Appl
40	166	77.6	39	14	US-10-287-821-1	Sequence 2, Appl
41	161.5	75.5	31	14	US-10-287-821-2	Sequence 1134, Ap
42	140	65.4	31	14	US-10-731-238-103	Sequence 103, App
43	140	65.4	37	20		
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45	77	36.0				

ALIGNMENTS

RESULT 1
US-10-731-238-46
Sequence 46, Application US/10731238
Publication No. US20050123552A1
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
Patel, Joseph M.
House-Pompeo, Karen L.
Speziale, Pietro
John, Danny
McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/731,238
FILING DATE: 10-Dec-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE: 21-Jan-1998
APPLICATION NUMBER: US 60/036,139

FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAMK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 46:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 46:
US-10-731-238-46

Query Match 100.0%; Score 214; DB 18; Length 38;
Best Local Similarity 100.0%; Pred. No. 1,1e-21;
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ONKGNQSPEDTEKDKPKYEHGNGNIIDIDFDSVPHIHG 38
Db 1 ONKGNQSPEDTEKDKPKYEHGNGNIIDIDFDSVPHIHG 38

RESULT 2
US-10-731-238-7
Sequence 7, Application US/10731238
Publication No. US20050123552A1
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
Pactl, Joseph M.
House-Pompeo, Karen L.
Speziale, Pietro
Joh, Danny
McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSER: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/731,238
FILING DATE: 10-Dec-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE: 21-Jan-1998
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAMK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>

TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-10-731-238-7

Query Match 96.3%; Score 206; DB 18; Length 38;
Best Local Similarity 97.4%; Pred. No. 1,4e-20;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ONKGNQSPEDTEKDKPKYEHGNGNIIDIDFDSVPHIHG 38
Db 1 ONKGNQSPEDTEKDKPKYEHGNGNIIDIDFDSVPHIHG 38

RESULT 3
US-09-813-820-8
Sequence 8, Application US/09813820
Patent No. US20020102262A1
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
Pactl, Joseph M.
House-Pompeo, Karen
Schanam, Narayana
Symeraky, Jindrich
TITLE OF INVENTION: COLLAGEN BINDING PROTEIN COMPOSITIONS
AND METHODS OF USE
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSER: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: Texas
COUNTRY: U.S.
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/813,820
FILING DATE: 22-Mar-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/856,253
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Kitchell, Barbara S.
REGISTRATION NUMBER: 33,928
REFERENCE/DOCKET NUMBER: TAMK:193
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
TELEFAX: (512) 474-7577
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 139 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-09-813-820-8

Query Match 96.3%; Score 206; DB 9; Length 139;
Best Local Similarity 97.4%; Pred. No. 6,5e-20;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ONKGNQSPEDTEKDKPKYEHGNGNIIDIDFDSVPHIHG 38
Db 54 ONKGNQSPEDTEKDKPKYEHGNGNIIDIDFDSVPHIHG 91

RESULT 4
US-09-815-242-5797
Sequence 5797, Application US/09815242

Patent No. US20020061569A1
GENERAL INFORMATION:
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Karl L.
APPLICANT: Zysek, Judith W.
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John D.
APPLICANT: Carr, Grant J.
APPLICANT: Yamamoto, Robert T.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 5797
LENGTH: 1018
TYPE: PRT
ORGANISM: Staphylococcus aureus
US-09-815-242-5797

Query Match 96.3%; Score 206; DB 9; Length 1018;
Best Local Similarity 97.4%; Pred. No. 7,1e-19;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QNKGNSFPEDTEKDKPKYEHGNIIDIDPDSVPHNG 38
DB 784 QNKGNSFPEDTEKDKPKYEHGNIIDIDPDSVPHNG 821

RESULT 5
US-09-815-242-12838
Sequence 12838, Application US/09815242
GENERAL INFORMATION:
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Karl L.
APPLICANT: Zysek, Judith W.
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John D.
APPLICANT: Carr, Grant J.
APPLICANT: Yamamoto, Robert T.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625

PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 12838
LENGTH: 1018
TYPE: PRT
ORGANISM: Staphylococcus aureus
US-09-815-242-12838

Query Match 96.3%; Score 206; DB 9; Length 1018;
Best Local Similarity 97.4%; Pred. No. 7,1e-19;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QNKGNSFPEDTEKDKPKYEHGNIIDIDPDSVPHNG 38
DB 784 QNKGNSFPEDTEKDKPKYEHGNIIDIDPDSVPHNG 821

RESULT 6
US-10-470-048B-68
Sequence 68, Application US/10470048B
Publication No. US2005003744A1
GENERAL INFORMATION:
APPLICANT: MEINKE ET AL.
TITLE OF INVENTION: A METHOD FOR IDENTIFICATION, ISOLATION AND PRODUCTION OF
TITLE OF INVENTION: ANTIGENS TO A SPECIFIC PATHOGEN
FILE REFERENCE: SONN.035US
CURRENT APPLICATION NUMBER: US/10/470,048B
CURRENT FILING DATE: 2003-07-25
NUMBER OF SEQ ID NOS: 603
SOFTWARE: PatentIn version 3.1
SEQ ID NO 68
LENGTH: 1018
TYPE: PRT
ORGANISM: Staphylococcus aureus
US-10-470-048B-68

Query Match 96.3%; Score 206; DB 17; Length 1018;
Best Local Similarity 97.4%; Pred. No. 7,1e-19;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QNKGNSFPEDTEKDKPKYEHGNIIDIDPDSVPHNG 38
DB 784 QNKGNSFPEDTEKDKPKYEHGNIIDIDPDSVPHNG 821

RESULT 7
US-08-781-986A-5254
Sequence 5254, Application US/08781986A
Publication No. US2003005436A1
GENERAL INFORMATION:
APPLICANT: Charles Kunsch
TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
NUMBER OF SEQUENCES: 5255
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COUNTRY: USA
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/781,986A
FILING DATE:

CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Benson, Bob
REGISTRATION NUMBER: 30,446
REFERENCE/DOCKET NUMBER: PB248PP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 5254:
SEQUENCE CHARACTERISTICS:
LENGTH: 1027 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-781-986A-5254

Query Match 96.3%; Score 206; DB 8; Length 1027;
Best Local Similarity 97.4%; Pred. No. 7.2e-19;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QNKGNSFPEDTEKDKPKYEHGNIIDIDFDSVPPIHG 38
DB 793 QNKGNSFPEDTEKDKPKYEHGNIIDIDFDSVPPIHG 830

RESULT 8
US-10-329-624-5254
Sequence 5254, Application US/10329624
Publication No. US20040043037A1
GENERAL INFORMATION:
APPLICANT: Charles Kunesh
Gil H. Choi
Patrick S. Dillon
Craig A. Rosen
Steven C. Barash
Michael R. Fannon
TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
NUMBER OF SEQUENCES: 5256
CORRESPONDENCE ADDRESS:
ADDRESSER: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COUNTRY: USA
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/329,624
FILING DATE: 27-Dec-2002
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/956,171
FILING DATE: October 20, 1997
APPLICATION NUMBER: 60/009,861
FILING DATE: January 5, 1996
APPLICATION NUMBER: 08/781,986
FILING DATE: January 3, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Mark J. Hyman
REGISTRATION NUMBER: 46,789
REFERENCE/DOCKET NUMBER: PB248P1D1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (240) 314-1224
TELEFAX: (301) 309-8439
INFORMATION FOR SEQ ID NO: 5254:
SEQUENCE CHARACTERISTICS:

LENGTH: 1027 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 5254:
US-10-329-624-5254

Query Match 96.3%; Score 206; DB 15; Length 1027;
Best Local Similarity 97.4%; Pred. No. 7.2e-19;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QNKGNSFPEDTEKDKPKYEHGNIIDIDFDSVPPIHG 38
DB 793 QNKGNSFPEDTEKDKPKYEHGNIIDIDFDSVPPIHG 830

RESULT 9
US-10-731-238-47
Sequence 47, Application US/10731238
Publication No. US20050123552A1
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
Patli, Joseph M.
House-Pompeo, Karen L.
Speziale, Pietro
Joh, Danny
McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSER: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/731,238
FILING DATE: 10-Dec-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE: 21-Jan-1998
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-Jan-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAMK:169
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 47:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 47:
US-10-731-238-47

Query Match 93.5%; Score 200; DB 18; Length 38;
Best Local Similarity 94.7%; Pred. No. 8.9e-20;
Matches 36; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 QNKGNSFPEDTEKDKPKYEHGNIIDIDFDSVPPIHG 38

```
Db      1 0NKGNSFEPDTEKDKPKYEHGNNIIDIDPDSVPHIHG 38
|||||
RESULT 10
US-10-731-238-48
; Sequence 48, Application US/10731238
; Publication No. US20050123552A1
; GENERAL INFORMATION:
; APPLICANT: Hook, Magnus
;             Patti, Joseph M.
;             House-Pompeo, Karen L.
;             Speziale, Pietro
;             John, Danny
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
; AND METHODS OF USE
; NUMBER OF SEQUENCES: 105
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: TX
; COUNTRY: USA
; ZIP: 77210-4433
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/731,238
; FILING DATE: 10-Dec-2003
; CLASSIFICATION: <Unknown>
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: US/09/010,317
; FILING DATE: 21-Jan-1998
; APPLICATION NUMBER: US 60/036,139
; FILING DATE: 21-Jan-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Hibler, David W.
; REGISTRATION NUMBER: 41,071
; REFERENCE/DOCKET NUMBER: TAMK:189
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 512-418-3000
; TELEFAX: 512-474-7577
; INFORMATION FOR SEQ ID NO: 48:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 38 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 48:
US-10-731-238-48

Query Match      93.0%; Score 199; DB 18; Length 38;
Best Local Similarity 94.7%; Pred. No. 1,2e-19;
Matches 36; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Cy      1 0NKGNSFEPDTEKDKPKYEHGNNIIDIDPDSVPHIHG 38
|||||
Db      1 0NKGNSFEPDTEKDKPKYEHGNNIIDIDPDSVPHIHG 38

RESULT 11
US-10-731-238-8
; Sequence 8, Application US/10731238
; Publication No. US20050123552A1
; GENERAL INFORMATION:
; APPLICANT: Hook, Magnus
;             Patti, Joseph M.
;             House-Pompeo, Karen L.
;             Speziale, Pietro

Job, Danny
McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/731,238
FILING DATE: 10-Dec-2003
CLASSIFICATION: <Unknown>
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE: 21-Jan-1998
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-Jan-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAMK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-10-731-238-8

Query Match      92.5%; Score 198; DB 18; Length 38;
Best Local Similarity 94.7%; Pred. No. 1,7e-19;
Matches 36; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Cy      1 0NKGNSFEPDTEKDKPKYEHGNNIIDIDPDSVPHIHG 38
|||||
Db      1 0NKGNSFEPDTEKDKPKYEHGNNIIDIDPDSVPHIHG 38

RESULT 12
US-10-731-238-49
; Sequence 49, Application US/10731238
; Publication No. US20050123552A1
; GENERAL INFORMATION:
; APPLICANT: Hook, Magnus
;             Patti, Joseph M.
;             House-Pompeo, Karen L.
;             Speziale, Pietro
;             John, Danny
;             McGavin, Martin J.
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
; AND METHODS OF USE
; NUMBER OF SEQUENCES: 105
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: TX
; COUNTRY: USA
; ZIP: 77210-4433
; COMPUTER READABLE FORM:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/731,238
FILING DATE: 10-Dec-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE: 21-Jan-1998
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAMK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 49:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 49:
US-10-731-238-49

Query Match 92.5%; Score 198; DB 18; Length 38
Best Local Similarity 94.7%; Pred. No. 1.7e-19;
Matches 36; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 QNKGNSFPEDTEKDKPKYEHGNIIDIDFDSVPHIHG 38
1 QNKGNSFPEDTEKDKPKYEHGNIIDIDFDSVPHIHG 38

DB 1 QNKGNSFPEDTEKDKPKYEHGNIIDIDFDSVPHIHG 38

RESULT 13
US-10-731-238-45
Sequence 45, Application US/10731238
Publication No. US20050123552A1
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
Patel, Joseph M.
House-Pompeo, Karen L.
Speziale, Pietro
Job, Danny
McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/731,238
FILING DATE: 10-Dec-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE: 21-Jan-1998
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997

ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAMK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 45:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 45:
US-10-731-238-45

Query Match 91.6%; Score 196; DB 18; Length 38;
Best Local Similarity 94.7%; Pred. No. 3.1e-19;
Matches 36; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 QNKGNSFPEDTEKDKPKYEHGNIIDIDFDSVPHIHG 38
1 QNKGNSFPEDTEKDKPKYEHGNIIDIDFDSVPHIHG 38

DB 1 QNKGNSFPEDTEKDKPKYEHGNIIDIDFDSVPHIHG 38

RESULT 14
US-08-901-062-1
Sequence 1, Application US/08901062
Publication No. US20020025324A1
GENERAL INFORMATION:
APPLICANT: SEALS, JONATHAN R.
TITLE OF INVENTION: RECOMBINANT BIVALENT BACTERIAL VACCINE
TITLE OF INVENTION: FOR THE PREVENTION OF MASTITIS
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: HALE AND DORR LLP
STREET: 60 State Street
CITY: Boston
STATE: MA
COUNTRY: United States Of America
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/901,062
FILING DATE: 25-JUL-1997
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Baker, Hollie L.
REGISTRATION NUMBER: 31,321
REFERENCE/DOCKET NUMBER: 106941.153
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 526-6000
TELEFAX: (617) 526-5000
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 388 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-901-062-1

Query Match 90.2%; Score 193; DB 8; Length 388;
Best Local Similarity 92.1%; Pred. No. 1.3e-17;
Matches 35; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 QNKGNSFPEDTEKDKPKYEHGNIIDIDFDSVPHIHG 38

Db 303 QNNGNOSFEEDTEKDKPKYEQGNIIIDIDFDSVPHIG 340

RESULT 15
US-08-781-986A-5251

; Sequence 5251, Application US/08781986A
; Publication No. US2003005436A1
; GENERAL INFORMATION:
; APPLICANT: Charles Kunesh
; TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
; NUMBER OF SEQUENCES: 5255
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4mb storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/781.986A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Benson, Bob
; REGISTRATION NUMBER: 30,446
; REFERENCE/DOCKET NUMBER: PB248PP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 5251:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 559 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULAR TYPE: protein
; US-08-781-986A-5251

Query Match 90.2%; Score 193; DB 8; Length 559;
Best Local Similarity 92.1%; Pred. No. 2e-17;
Matches 35; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 QNNGNOSFEEDTEKDKPKYEQGNIIIDIDFDSVPHIG 38
DB 339 QNNGNOSFEEDTEKDKPKYEQGNIIIDIDFDSVPHIG 376

Search completed: October 22, 2005, 12:09:28
Job time : 70.1256 secs

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OM protein - protein search, using sw model

Run on: October 22, 2005, 04:14:19 ; Search time 13.8905 Seconds
(without alignments)
263.219 Million cell updates/sec

Title: US-10-731-238-46

Sequence: 1 ONKGNQSPEDTEKDKPKYEHGNIIDIDFDSVPHHG 38

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	206	96.3	1018	2 A32192	fibronectin-binding
2	193	90.2	940	2 S19702	fibronectin-binding
3	193	90.2	1038	2 H90053	hypothetical prote
4	181	84.6	961	2 G90053	hypothetical prote
5	60.5	28.3	214	2 A89895	hypothetical prote
6	60	28.0	442	2 H72266	actB/chur-related
7	57.5	26.9	841	2 B82755	beta-hexosaminidas
8	56.5	26.4	788	2 T30510	viral enhancing fa
9	36	26.2	591	2 C84220	propionyl-CoA carb
10	34	25.2	264	2 C87605	hypothetical prote
11	53	24.8	218	2 A95232	ribulose-phosphate
12	53	24.8	218	2 C98096	ribulose-phosphate
13	53	24.8	413	2 T31663	isooleucin-CMA 1i
14	53	24.8	658	2 R85024	probable CDP-rich
15	52	24.5	342	2 A89846	hypothetical prote
16	52	24.3	391	1 S15617	E2 protein - human
17	52	24.3	732	2 T31629	hypothetical prote
18	52	24.3	1090	2 T00533	probable DNA2-NAM7
19	51.5	24.1	132	2 B83957	flagellar basal-bo
20	51.5	24.1	154	2 AC0242	probable exported
21	51.5	24.1	223	1 KTHU43	nucleoside-triphos
22	51	23.8	183	2 DB3840	hypothetical prote
23	51	23.8	345	2 T33906	hypothetical prote
24	51	23.8	400	2 T41569	hypothetical prote
25	51	23.8	508	1 ISHUS5	protein disulfide-
26	51	23.8	752	2 G02273	liv-1 protein - hu
27	51	23.8	1091	2 S33850	fibronectin-binding
28	50.5	23.6	160	2 AD1363	single-stranded DN
29	50.5	23.6	208	2 G34238	leukotoxin A - Pas

30	50.5	23.6	317	2 T00146	hypothetical prote
31	50.5	23.6	357	2 S21758	glutamic acid-spec
32	50.5	23.6	428	2 T32952	hypothetical prote
33	50.5	23.6	582	2 T48673	matrix metalloprot
34	50.5	23.6	582	2 I38028	matrix metalloprot
35	50.5	23.6	669	2 I38029	matrix metalloprot
36	50.5	23.6	952	2 AG1209	B. subtilis yfho p
37	50.5	23.6	955	1 A35254	leukotoxin A - Pas
38	50.5	23.6	1239	2 G02750	DNA-directed DNA p
39	50.5	23.6	2946	2 T00867	hypothetical prote
40	50	23.4	211	2 G83632	conserved hypochet
41	50	23.4	284	2 S67062	hypothetical prote
42	50	23.4	330	2 D75160	n-acetyl-gamma-glu
43	49.5	23.1	194	2 B97727	prolyl endopeptida
44	49.5	23.1	371	2 A71683	hypothetical prote
45	49.5	23.1	388	2 B87600	carbamoyl-phosphat

ALIGNMENTS

RESULT 1
A32192
fibronectin-binding protein - Staphylococcus aureus
C:Species: Staphylococcus aureus
C>Date: 31-Jul-1989 #sequence_revision 31-Jul-1989 #text_change 16-Feb-1997
C:Accession: A32192
R:Signaes, C.; Raucel, G.; Joensson, K.; Lindgren, P.E.; Anantharamaiah, G.M.; Hoeoek, proc. Natl. Acad. Sci. U.S.A. 86, 699-703, 1989
A:Title: Nucleotide sequence of the gene for a fibronectin-binding protein from Staphyl
A:Reference number: A32192; MID:8908998; PMID:2521391
A:Accession: A32192
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1018 <SIG>
A:Cross-references: GB:J04151
C:Keywords: fibronectin binding

Query Match 96.3%; Score 206; DB 2; Length 1018;
Best Local Similarity 97.4%; Pred. No. 5.7e-19;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ONKGNQSPEDTEKDKPKYEHGNIIDIDFDSVPHHG 38
Db 784 ONKGNQSPEDTEKDKPKYEHGNIIDIDFDSVPHHG 821

RESULT 2

S19702
fibronectin-binding protein B - Staphylococcus aureus
C:Species: Staphylococcus aureus
C>Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
C:Accession: S19702
R:Joensson, K.; Signaes, C.; Mueller, H.P.; Lindberg, M.
Eur. J. Biochem. 202, 1041-1048, 1991
A:Title: Two different genes encode fibronectin binding proteins in Staphylococcus aure
A:Reference number: S19702; MUID:92111475; PMID:1837266
A:Accession: S19702
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-940 <JOB>
A:Cross-references: UNIPROT:Q53682; EMBL:X62992; NID:949040; PIDD:CAA44726.1; PID:95815
C:Keywords: fibronectin binding

Query Match 90.2%; Score 193; DB 2; Length 940;
Best Local Similarity 92.1%; Pred. No. 2.7e-17;
Matches 35; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 ONKGNQSPEDTEKDKPKYEHGNIIDIDFDSVPHHG 38
Db 720 ONKGNQSPEDTEKDKPKYEHGNIIDIDFDSVPHHG 757

F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A.; Rodrigues, V.; Rosa, A.J.; de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawaak, A.; Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silveira, M.; Teshako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z

A:Reference number: A59328
A:Contents: annotation
C:Genetics:
A:Gene: XF0847

Query Match 26.3%; Score 57.5; DB 2; Length 841;
Best Local Similarity 30.0%; Pred. No. 20;
Matches 12; Conservative 8; Mismatches 15; Indels 5; Gaps 1;

QY 2 NKGNSPDPTEKPKYEHGNIIDI-----DPDSVPHI 36
DB 204 NCGPTEIPVTIHDWPRFSWRGQLDVARHFDVDTVKHV 243

RESULT 8
T30510
viral enhancing factor 2 - Lymantria dispar nuclear polyhedrosis virus

C:Species: Lymantria dispar nuclear polyhedrosis virus, LdMNPV
C>Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004

C:Accession: T30510
R/Kuzio, J.; Pearson, M.N.; Harwood, S.H.; Funk, C.J.; Evans, J.T.; Slavicek, J.M.; Rohd
Virology 253, 17-34, 1999
A:Title: Sequence and analysis of the genome of a baculovirus pathogenic for Lymantria d
A:Reference number: Z20836; MUID:9124785; PMID:9887315
A:Accession: T30510
A:Status: preliminary; translated from GB/EMBL/DBD
A:Molecule type: DNA
A:Residues: 1-788 <KUZ>
A:Cross-references: UNIPROT:Q9YMG9; EMBL:AF081810; PIDN:AACT0346.1

Query Match 26.4%; Score 56.5; DB 2; Length 788;
Best Local Similarity 54.5%; Pred. No. 26;
Matches 12; Conservative 1; Mismatches 4; Indels 5; Gaps 1;

QY 17 PKYEHGNIIDI-----DSV 33
DB 114 PLYEHGNAVAPADPKSRMSRV 135

RESULT 9

C84220
propionyl-CoA carboxylase homolog [imported] - Halobacterium sp. NRC-1

C:Species: Halobacterium sp. NRC-1
C>Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004

C:Accession: C84220
R/Mg, W.V.; Kennedy, S.P.; Mahairas, G.G.; Bergquist, B.; Pan, M.; Shukla, H.D.; Lasky, S
Leithauser, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Jabc
Jung, K.H.; Alam, M.; Freitas, T.
Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000

A:Authors: Hou, S.; Daniel, C.J.; Dennis, P.P.; Omer, A.D.; Ehardt, H.; Lowe, T.M.; Li
A:Title: Genome sequence of Halobacterium species NRC-1.
A:Reference number: A84160; MUID:20504483; PMID:11016950

A:Accession: C84220
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-591 <STO>
A:Cross-references: UNIPROT:Q9HRN1; GB:AE004437; NID:G10580213; PIDN:AAG19127.1; GSPDB:C
C:Genetics:
A:Gene: yngE
C:Superfamily: propionyl-CoA carboxylase beta chain

Query Match 26.2%; Score 56; DB 2; Length 591;
Best Local Similarity 62.5%; Pred. No. 22;
Matches 10; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 7 SPEDTEKDKPKYEHG 22
DB 573 SPYEDVEKDRPSKCHG 588

RESULT 10

C87605
hypothetical protein CC2875 [imported] - Caulobacter crescentus

C:Species: Caulobacter crescentus
C>Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004

C:Accession: C87605
R/Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J
B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolo
n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A:Title: Complete Genome Sequence of Caulobacter crescentus.
A:Reference number: A87249; MUID:21173698; PMID:11259647

A:Accession: C87605
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-264 <STO>
A:Cross-references: UNIPROT:Q9A4F9; GB:AE005673; NID:G13424491; PIDN:AAK24839.1; GSPDB:C
C:Genetics:
A:Gene: CC2875

Query Match 25.2%; Score 54; DB 2; Length 264;
Best Local Similarity 33.3%; Pred. No. 16;
Matches 11; Conservative 7; Mismatches 15; Indels 0; Gaps 0;

QY 6 QSPEDTEKDKPKYEHGNIIDDPDSVPHING 38
DB 58 QOKAEVEVELPRPAHGRHVAEDRDVPAVVG 90

RESULT 11

A95232
ribulose-phosphate 3-epimerase [imported] - Streptococcus pneumoniae (strain TIGR4)

C:Species: Streptococcus pneumoniae
C>Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 09-Jul-2004

C:Accession: A95232
R/Tetteilin, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Hei
on, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapple,
nson, T.; Hickey, E.K.; Holt, I.E.
Science 293, 498-506, 2001

A:Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison
A:Title: Complete Genome Sequence of a virulent isolate of Streptococcus pneumoniae.
A:Reference number: A95000; MUID:21357209; PMID:11463916

A:Accession: A95232
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-218 <KUR>
A:Cross-references: UNIPROT:Q97NN7; GB:AE005672; PIDN:AAK76050.1; PID:G14973490; GSPDB:C
A:Experimental source: strain TIGR4
C:Genetics:
A:Gene: SPI983
C:Superfamily: yeast ribulose-5-phosphate-epimerase

Query Match 24.8%; Score 53; DB 2; Length 218;
Best Local Similarity 52.9%; Pred. No. 17;
Matches 9; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 22 GGNIIIDDPDSVPHING 38
DB 84 GADISIHVATPHING 100

RESULT 12

C98096
ribulose-phosphate 3-epimerase (EC 5.1.3.1) [imported] - Streptococcus pneumoniae (stra

C:Species: Streptococcus pneumoniae
C>Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 09-Jul-2004

C:Accession: C98096
R/Hokings, J.A.; Alborn Jr., W.; Arnold, J.; Blaszcak, L.; Burgett, S.; Dehoff, B.S.;
e, R.; Lebanc, D.J.; Lee, L.N.; Lefkowitz, E.J.; Lu, J.; Matsushima, P.; McAhren, S.;
Y, P.; Sun, P.M.; Winkler, M.E.
J. Bacteriol. 183, 5709-5717, 2001
A:Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, S.R.

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 22, 2005, 04:10:49 ; Search time 69.6361 Seconds
(without alignments)
279.439 Million cell updates/sec

Title: US-10-731-238-46

Sequence: 1 QNKGNSPPEDEKDKYEHGNNIDPDSVPHIHG 38

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_03:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	206	96.3	1018	1 FNBA_STAAU	P14738 staphylococ
2	201	93.9	943	2 Q8NUT8	Q8NUT8 staphylococ
3	201	93.9	957	2 Q6G6H4	Q6G6H4 staphylococ
4	198	92.5	152	2 Q9AEP9	Q9AEP9 staphylococ
5	193	90.2	940	2 Q53682	Q53682 staphylococ
6	193	90.2	940	2 Q99RD2	Q99RD2 staphylococ
7	193	90.2	1038	2 Q7A3J7	Q7A3J7 staphylococ
8	185	86.4	1015	2 Q8NUT7	Q8NUT7 staphylococ
9	185	86.4	1015	2 Q6G6H3	Q6G6H3 staphylococ
10	181	84.6	961	2 Q99RD3	Q99RD3 staphylococ
11	181	84.6	961	2 Q7A3J8	Q7A3J8 staphylococ
12	181	84.6	965	2 Q6G6D5	Q6G6D5 staphylococ
13	64	29.9	367	1 Q7RB60	Q7RB60 thermococ
14	64	29.9	716	2 Q7A3J7	Q7A3J7 thermococ
15	61.5	28.7	904	2 Q54324	Q54324 sulfolobus
16	60.5	28.3	214	2 Q99UP6	Q99UP6 staphylococ
17	60.5	28.3	214	2 Q7A126	Q7A126 staphylococ
18	60.5	28.3	214	2 Q7A527	Q7A527 staphylococ
19	60.5	28.3	214	2 Q6G921	Q6G921 staphylococ
20	60.5	28.3	214	2 Q6GHL3	Q6GHL3 staphylococ
21	60	28.0	442	2 Q9X147	Q9X147 thermococ
22	60	28.0	550	2 Q91LM4	Q91LM4 eucalyptus
23	60	28.0	979	2 Q7RNI1	Q7RNI1 plasmodium
24	59.5	27.8	1257	2 Q6BM72	Q6BM72 debaryomyc
25	58.5	27.3	812	2 Q87A77	Q87A77 xyloella fas
26	57.5	26.9	841	2 Q9PF31	Q9PF31 xyloella fas
27	57.5	26.9	1349	2 Q72714	Q72714 homo sapien
28	57.5	26.9	1858	2 Q8MSU5	Q8MSU5 drosophila
29	57.5	26.9	2145	2 Q9W003	Q9W003 drosophila
30	57	26.6	288	2 Q6MEU6	Q6MEU6 paracanthamyd
31	57	26.6	826	2 Q6CM29	Q6CM29 kluyveromyc

ALIGNMENTS

32	57	26.6	1246	2	Q7UKY7	Q7UKY7 rhodospirell
33	56.5	26.4	347	2	Q8CPZ8	Q8CPZ8 staphylococ
34	56.5	26.4	788	2	Q9YMG8	Q9YMG8 lymantria d
35	56.5	26.4	926	2	Q7RBX7	Q7RBX7 plasmodium
36	56	26.2	318	2	Q7Q2S6	Q7Q2S6 anopheles g
37	56	26.2	318	2	Q8GT57	Q8GT57 cucurbita m
38	56	26.2	591	2	Q9HRN1	Q9HRN1 halobacteri
39	55	25.7	426	2	Q6ZJ47	Q6ZJ47 oryza sativ
40	55	25.7	457	2	Q9GDV3	Q9GDV3 carboxotus
41	55	25.7	477	2	Q9GDNV3	Q9GDNV3 synechococ
42	55	25.7	585	2	Q6C8E1	Q6C8E1 yarrowia li
43	55	25.7	1335	2	Q7NXC8	Q7NXC8 gloebacter
44	55	25.7	1800	2	Q81E19	Q81E19 plasmodium
45	54.5	25.5	464	2	Q9XJF6	Q9XJF6 bacterioph

RESULT 1
FNBA_STAAU STANDARD; PRT; 1018 AA.
ID FNBA_STAAU
AC P14738;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Fibronectin-binding protein precursor (FNBP).
GN Name=fnba;
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1280;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NCTC 8325-4;
RX MEDLINE=8909898; PubMed=2521391;
RA Signaes C., Raucel G., Joensen K., Lindgren P.-E.,
RA Anantharamaiah G.M., Hoeck M., Lindberg M.;
RT "Nucleotide sequence of the gene for a fibronectin-binding protein
from Staphylococcus aureus: use of this peptide sequence in the
synthesis of biologically active peptides."
RL Proc. Natl. Acad. Sci. U.S.A. 86:699-703(1989).
CC -!- FUNCTION: The ability of bacteria to bind fibronectin has been
proposed as a virulence factor enabling bacteria to colonize wound
tissues and blood clots. Binding of plasma fibronectin to the
bacterial surface might block adhesion receptors on S.aureus, thus
representing an important defense mechanism against tissue
invasion.
CC -!- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
an amide bond (Potential).
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See [http://www.ebi.ac.uk/announcements/](http://www.ebi.ac.uk/announcements)
or send an email to license@ebi.ac.uk).
CC -----
CC EMBL: J04151; AAA26632.1; -;
CC InterPro: IPR004237; Fn_bind.
CC InterPro: IPR005877; Gpos_Y5IRK.
CC InterPro: IPR001899; Gram_pos_anchor.
CC Pfam: PF00746; Gram_pos_anchor; 1.
CC Pfam: PF00746; Fn_bind; 1.
CC TIGRfams: TIGR01167; LPXTG_anchor; 1.
CC TIGRfams: TIGR01168; Y5IRK_signal; 1.
CC PROSITE: PS00847; GRAM_POS_ANCHORING; 1.
CC Cell adhesion; Cell wall; Peptidoglycan-anchor; Repeat; Signal;
CC Virulence.
CC SIGNAL 1 36
CC CHAIN 37 985 Fibronectin-binding protein.
CC PROPEP 986 1018 Removed by sortase (Potential).
FT

```
FT REPEAT 545 574 B-1.
FT REPEAT 575 604 B-2.
FT DOMAIN 745 878 4 X approximate tandem repeats,
  fibronectin-binding domain.
FT REPEAT 745 782 D-1.
FT REPEAT 783 820 D-2.
FT REPEAT 821 859 D-3.
FT REPEAT 860 878 D-4 (incomplete).
FT DOMAIN 879 948 5 X tandem repeats, Pro-rich (WR).
FT REPEAT 879 892 WR 1.
FT REPEAT 893 906 WR 2.
FT REPEAT 907 920 WR 3.
FT REPEAT 921 934 WR 4.
FT REPEAT 935 948 WR 5.
FT SITE 982 986 LpXTG sorting signal (potential).
FT MOD_RES 985 985 Pentaglycyl murein peptidoglycan amidated
  threonine (Potential).
SQ SEQUENCE 1018 AA; 111780 MW; 58175E020E81F1F CRC64;

Query Match 96.3%; Score 206; DB 1; Length 1018;
Best Local Similarity 97.4%; Pred. No. 2,4e-17;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ONKGNOSPEDETEKDKPKYEHGNIIDIDPDSVPHIHG 38
Db 784 ONKGNOSPEDETEKDKPKYEHGNIIDIDPDSVPHIHG 821

RESULT 2
Q8NU8 PRELIMINARY; PRT; 943 AA.
AC Q8NU8;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE FnbA protein.
GN Name=fnbA; Ordered locus names=MM2420;
OS Staphylococcus aureus (strain MM2).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=196620;
[1]
RN SEQUENCE FROM N.A.
RC STRAIN=MM2;
RX MEDLINE=22040717; PubMed=12044378; DOI=10.1016/S0140-6736(02)08713-5;
RA Baba T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Oguchi A.,
  Nagai Y., Iwama N., Amano K., Naito T., Kuroda H., Cui L.,
  Yamamoto K., Hiramatsu K.;
RT "Genome and virulence determinants of high virulence community-
  acquired MRSA.";
RL Lancet 359:1819-1827(2002).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
  an amide bond (By similarity).
EMBL: AP004830; BAB96285.1; -.
DR HSSP: 053653; 1N67.
DR GO: GO:0009986; C:cell surface; IEA.
DR GO: GO:0005618; C:cell wall; IEA.
DR GO: GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO: GO:0016020; C:membrane; IEA.
DR GO: GO:0007155; P:cell adhesion; IEA.
DR InterPro: IPR008966; Adhes_bact.
DR InterPro: IPR004237; Fn_bind.
DR InterPro: IPR005877; Gpos_YsIRK.
DR InterPro: IPR001899; Gram_pos_anchor.
DR Pfam: PF02986; Fn_bind.1.
DR Pfam: PF00746; Gram_pos_anchor.1.
DR TIGRfam: TIGR01167; LpXTG_anchor.1.
DR TIGRfam: TIGR01168; YsIRK_signal.1.
DR PROSITE: PS50847; GRAM_POS_ANCHORING.1.
DR Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ SEQUENCE 943 AA; 104537 MW; DA8A5F31947E1B6A CRC64;

Query Match 93.9%; Score 201; DB 2; Length 943;
Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
```

```
Best Local Similarity 94.7%; Pred. No. 9.6e-17;
Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 ONKGNOSPEDETEKDKPKYEHGNIIDIDPDSVPHIHG 38
Db 727 ONKGNOSPEDETEKDKPKYEHGNIIDIDPDSVPHIHG 764

RESULT 3
Q6G6H4 PRELIMINARY; PRT; 957 AA.
AC Q6G6H4;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Fibronectin-binding protein.
GN Name=fnbB; Ordered locus names=SAS2387;
OS Staphylococcus aureus (strain MSSA476).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=282459;
[1]
RN SEQUENCE FROM N.A.
RX PubMed=15213324; DOI=10.1073/pnas.0402521101;
RA Holden M.T.G., Feil E.J., Lindsay J.A., Peacock S.U., Day N.P.J.,
  Enright M.C., Foster T.J., Moore C.E., Hurst L., Atkin R., Barron A.,
  Bason N., Bentley S.D., Chillingworth C., Chillingworth T.,
  Churcher C., Clark L., Cronin A., Doggett J., Dowd L.,
  Fellwell T., Hance Z., Harris B., Hauser H., Holtroyd S., Jagels K.,
  James K.D., Leonard N., Line A., Mayes R., Moule S., Mungall K.,
  Ormond D., Quail M.A., Rabinowitch E., Rutherford K.M., Sanders M.,
  Sharp S., Simmonds M., Stevens K., Whitehead S., Barrett B.G.,
  Spratt B.G., Parkhill J.;
RT "Complete genomes of two clinical Staphylococcus aureus strains:
  evidence for the rapid evolution of virulence and drug resistance.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:9786-9791(2004).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
  an amide bond (By similarity).
EMBL: BX571857; CAG44201.1; -.
DR GO: GO:0009986; C:cell surface; IEA.
DR GO: GO:0005618; C:cell wall; IEA.
DR GO: GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO: GO:0016020; C:membrane; IEA.
DR GO: GO:0007155; P:cell adhesion; IEA.
DR InterPro: IPR008966; Adhes_bact.
DR InterPro: IPR004237; Fn_bind.
DR InterPro: IPR005877; Gpos_YsIRK.
DR InterPro: IPR001899; Gram_pos_anchor.
DR Pfam: PF02986; Fn_bind.1.
DR Pfam: PF00746; Gram_pos_anchor.1.
DR TIGRfam: TIGR01167; LpXTG_anchor.1.
DR TIGRfam: TIGR01168; YsIRK_signal.1.
DR PROSITE: PS50847; GRAM_POS_ANCHORING.1.
DR Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ SEQUENCE 957 AA; 105980 MW; 28F8BA7FDFD3EAF CRC64;

Query Match 93.9%; Score 201; DB 2; Length 957;
Best Local Similarity 94.7%; Pred. No. 9.7e-17;
Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 ONKGNOSPEDETEKDKPKYEHGNIIDIDPDSVPHIHG 38
Db 727 ONKGNOSPEDETEKDKPKYEHGNIIDIDPDSVPHIHG 764

RESULT 4
Q9AEP9 PRELIMINARY; PRT; 152 AA.
AC Q9AEP9;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Fibronectin-binding protein (Fragment).
```

GN	Name=fnb:			
OS	Staphylococcus aureus.			
OC	Bacteria; Firmicutes; Bacillales; Staphylococcus.			
OX	NCBI_TaxID=1280;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=CMRSA-1;			
RX	MEDLINE=21246681; Pubmed=11349044;			
DOI=10.1128/IAI.69.6.3791-3799.2001;				
RA	Rice K., Huesca M., Vaz D., McGavin M.J.;			
RT	"Variance in fibrinectin binding and fmb locus polymorphisms in			
RT	Staphylococcus aureus: Identification of antigenic variation in a			
RT	fibrinectin binding protein adhesin of the epidemic CMRSA-1 strain of			
RT	methicillin-resistant S. aureus";			
RL	Infect. Immun. 69:3791-3799(2001).			
DR	EMBL: AY029184; AAK31588.1; "			
FT	NON TER	1		
FT	NON TER	152	152	
SO	SEQUENCE	152 AA;	17193 MW;	CFA3913C2B11C025 CRC64;

```

DE  Fnb protein.
GN  Name=fnd; OrderedLocuNames=SA2291;
OS  Staphylococcus aureus (strain N315).
OC  Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX  NCBI_TaxId=158879;
RN  [1]
RP  SEQUENCE FROM N.A.
RX  MEDLINE=2111952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2;
RA  Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
RA  Cui L., Oguchi A., Aoki K.-I., Nagai Y., Iian J.-Q., Ito T.,
RA  Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hoshyama A.,
RA  Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kikito C.,
RA  Sekimizu K., Hirakawa H., Oshima K., Furuya K., Yabuuchi J.,
RA  Kanetsu M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
RA  Hattori M., Ogasawara N., Hayaishi H., Hiramatsu K.,
RT  "Whole genome sequencing of methicillin-resistant Staphylococcus
RT  aureus";
RL  Lancet 357:1225-1240(2001).
CC  -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC  an amide bond (By similarity).
DR  EMBL; AP003137; BAB43594.1; -.
DR  GO; GO:0009986; C:cell surface; IEA.
DR  GO; GO:0005618; C:cell wall; IEA.
DR  GO; GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR  GO; GO:0016020; C:membrane; IEA.
DR  GO; GO:0007155; P:cell adhesion; IEA.
DR  InterPro; IPR008966; Adhes_bact.
DR  InterPro; IPR004237; Fn_bind.
DR  InterPro; IPR005877; Gpos_YsIRK.
DR  InterPro; IPR001899; Gram_pos_anchor.
DR  Pfam; PF00746; Gram_pos_anchor; 1.
DR  Pfam; PF04650; YsIRK_signal; 1.
DR  TIGRPFAM; TIGR01167; LPXTG_anchor; 1.
DR  TIGRPFAM; TIGR01168; YsIRK_signal; 1.
DR  PROSITE; PS50847; GRAM_POS_ANCHORING; 1.
KW  Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ  SEQUENCE 1038 AA; 113618 MW; 666BFBFBFBFB12 CRC64;

Query Match          90.2%; Score 193; DB 2; Length 1038;
Best Local Similarity 92.1%; Pred. No. 1,1e-15;
Matches 35; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY  1 QNKGNSFEDTEKDKPKYEHGCGNIIDIDFDSVPFHIG 38
DB  780 QNKGNSFEDTEKDKPKYEHGCGNIIDIDFDSVPFHIG 817

RESULT 8
Q8NUU7 PRELIMINARY; PRT; 1015 AA.
AC Q8NUU7;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Fnb protein.
GN Name=fnd; OrderedLocuNames=NM2421;
OS Staphylococcus aureus (strain MM2).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxId=156620;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=MM2;
RX MEDLINE=22040717; PubMed=12044378; DOI=10.1016/S0140-6736(02)08713-5;
RA Baba T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Oguchi A.,
RA Nagai Y., Iwano N., Asano K., Naimi T., Kuroda H., Cui L.,
RA Yamamoto K., Hiramatsu K.;
RT "Genome and virulence determinants of high virulence community-
RT acquired MRSA";
RL Lancet 359:1819-1827(2002).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC an amide bond (By similarity).
EMBL; AP004830; BAB96286.1; -.

```

```

DR  GO; GO:0009986; C:cell surface; IEA.
DR  GO; GO:0005618; C:cell wall; IEA.
DR  GO; GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR  GO; GO:0016020; C:membrane; IEA.
DR  GO; GO:0007155; P:cell adhesion; IEA.
DR  InterPro; IPR008966; Adhes_bact.
DR  InterPro; IPR004237; Fn_bind.
DR  InterPro; IPR005877; Gpos_YsIRK.
DR  InterPro; IPR001899; Gram_pos_anchor.
DR  Pfam; PF02986; Gram_pos_anchor; 1.
DR  Pfam; PF00746; Gram_pos_anchor; 1.
DR  Pfam; PF04650; YsIRK_signal; 1.
DR  TIGRPFAM; TIGR01167; LPXTG_anchor; 1.
DR  TIGRPFAM; TIGR01168; YsIRK_signal; 1.
DR  PROSITE; PS50847; GRAM_POS_ANCHORING; 1.
KW Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ SEQUENCE 1015 AA; 111145 MW; D0F9281BB64D44D2 CRC64;

Query Match          86.4%; Score 185; DB 2; Length 1015;
Best Local Similarity 89.5%; Pred. No. 1,1e-14;
Matches 34; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY  1 QNKGNSFEDTEKDKPKYEHGCGNIIDIDFDSVPFHIG 38
DB  785 QNKGNSFEDTEKDKPKYEHGCGNIIDIDFDSVPFHIG 822

RESULT 9
Q6G6H3 PRELIMINARY; PRT; 1015 AA.
AC Q6G6H3;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Fibronectin-binding protein.
GN OrderedLocuNames=SA82388;
OS Staphylococcus aureus (strain MSSA476).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxId=282459;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=15213324; DOI=10.1073/pnas.0402521101;
RX Holden M.T.G., Fell E.J., Lindsay J.A., Peacock S.D., Day N.P.J.,
RX Broughton M.C., Foster T.J., Moore C.E., Hurst L., Atkin R., Barron A.,
RX Bason N., Bentley S.D., Chillingworth C., Chillingworth T.,
RX Churcher C., Clark L., Corton C., Cronin A., Doggett J., Dowd L.,
RX Felwell T., Hance Z., Harris B., Haubert A., Holtroyd S., Jagels K.,
RX James K.D., Leonard N., Line A., Mayes R., Moule S., Mungall K.,
RX Ormond D., Quail M.A., Rabinowitch E., Rutherford K.M., Sanders M.,
RX Sharp S., Simmonds M., Stevens K., Whitehead S., Barrett B.G.,
RX Spratt B.G., Parkhill J.;
RT "Complete genomes of two clinical Staphylococcus aureus strains:
RT evidence for the rapid evolution of virulence and drug resistance.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:9786-9791(2004).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC an amide bond (By similarity).
EMBL; BX571857; CAG44202.1; -.
DR  GO; GO:0009986; C:cell surface; IEA.
DR  GO; GO:0005618; C:cell wall; IEA.
DR  GO; GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR  GO; GO:0016020; C:membrane; IEA.
DR  GO; GO:0007155; P:cell adhesion; IEA.
DR  InterPro; IPR008966; Adhes_bact.
DR  InterPro; IPR004237; Fn_bind.
DR  InterPro; IPR005877; Gpos_YsIRK.
DR  InterPro; IPR001899; Gram_pos_anchor.
DR  Pfam; PF02986; Fn_bind; 1.
DR  Pfam; PF00746; Gram_pos_anchor; 1.
DR  Pfam; PF04650; YsIRK_signal; 1.
DR  TIGRPFAM; TIGR01167; LPXTG_anchor; 1.
DR  TIGRPFAM; TIGR01168; YsIRK_signal; 1.
DR  PROSITE; PS50847; GRAM_POS_ANCHORING; 1.
KW Cell wall; Complete proteome; Peptidoglycan-anchor.

```

SQ SEQUENCE 1015 AA; 111145 MW; D0F9281BB64D4D2 CRC64;
 Query Match 86.4%; Score 185; DB 2; Length 1015;
 Best Local Similarity 89.5%; Pred. No. 1.1e-14;
 Matches 34; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 QNKGNSFPEDTEKDKRYEHGNIIDIDPDSVPHNG 38
 |||||
 DB 785 QNKGNSFPEDTEKDKRYEHGNIIDIDPDSVPHNG 822

RESULT 10
 ID Q99RD3 PRELIMINARY; PRT; 961 AA.
 AC Q99RD3;
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Fibronectin-binding protein homolog.
 GN Name=fndb; OrderedlocusNames=SAV2502;
 OS Staphylococcus aureus (strain Mu50 / ATCC 700699).
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 OX NCBI_TaxID=158878;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Mu50 / ATCC 700699;
 RX MEDLINE=21311952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2;
 RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
 RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Iian J.-Q., Ito T.,
 RA Kanamori M., Matsunaru H., Maruyama A., Murakami H., Hosoyama A.,
 RA Mizutani U. Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
 RA Kanehisa M., Yamauchi A., Oshima K., Furuya K., Yoshino C., Shiba T.,
 RA Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
 RT "Whole genome sequencing of methicillin-resistant Staphylococcus
 aureus."
 RL Lancet 357:1225-1240(2001).
 CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
 an amide bond (By similarity).
 DR EMBL; AP003137; BAB3593.1; -;
 DR PIR; G90053; G90053.
 DR HSSP; Q53653; 1N67.
 DR GO; GO:0009986; C:cell surface; IEA.
 DR GO; GO:0005618; C:cell wall; IEA.
 DR GO; GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0007155; P:cell adhesion; IEA.
 DR InterPro; IPR008966; Adhes_bact.
 DR InterPro; IPR005877; Gpos_YsIRK.
 DR InterPro; IPR001899; Gram_pos_anchor.
 DR Pfam; PF02986; Fn_bind.1.
 DR Pfam; PF00746; Gram_pos_anchor.1.
 DR Pfam; PF04650; YsIRK_signal.1.
 DR TIGRFAMs; TIGR01167; LPXTG_anchor.1.
 DR TIGRFAMs; TIGR01168; YsIRK_signal.1.
 DR PROSITE; PS50847; GRAM_POS_ANCHORING.1.
 KW Cell wall, Complete proteome, Peptidoglycan-anchor.
 SQ SEQUENCE 961 AA; 106010 MW; 364940F884EA4101 CRC64;

Query Match 84.6%; Score 181; DB 2; Length 961;
 Best Local Similarity 86.8%; Pred. No. 3.5e-14;
 Matches 33; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 QNKGNSFPEDTEKDKRYEHGNIIDIDPDSVPHNG 38
 |||||
 DB 731 QNKGNSFPEDTEKDKRYEHGNIIDIDPDSVPHNG 768

RESULT 11
 ID Q7A3J8 PRELIMINARY; PRT; 961 AA.
 AC Q7A3J8;

DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE fndb protein.
 GN Name=fndb; OrderedlocusNames=SA2290;
 OS Staphylococcus aureus (strain N315).
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 OX NCBI_TaxID=158879;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC MEDLINE=21311952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2;
 RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
 RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Iian J.-Q., Ito T.,
 RA Kanamori M., Matsunaru H., Maruyama A., Murakami H., Hosoyama A.,
 RA Mizutani U. Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
 RA Sekimizu K., Hiraoka H., Kihara S., Goto S., Yabuzaki J.,
 RA Kanehisa M., Yamauchi A., Oshima K., Furuya K., Yoshino C., Shiba T.,
 RA Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
 RT "Whole genome sequencing of methicillin-resistant Staphylococcus
 aureus."
 RL Lancet 357:1225-1240(2001).
 CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
 an amide bond (By similarity).
 DR EMBL; AP003137; BAB3593.1; -;
 DR PIR; G90053; G90053.
 DR GO; GO:0009986; C:cell surface; IEA.
 DR GO; GO:0005618; C:cell wall; IEA.
 DR GO; GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0007155; P:cell adhesion; IEA.
 DR InterPro; IPR008966; Adhes_bact.
 DR InterPro; IPR004237; Fn_bind.
 DR InterPro; IPR005877; Gpos_YsIRK.
 DR InterPro; IPR001899; Gram_pos_anchor.
 DR Pfam; PF02986; Fn_bind.1.
 DR Pfam; PF00746; Gram_pos_anchor.1.
 DR Pfam; PF04650; YsIRK_signal.1.
 DR TIGRFAMs; TIGR01167; LPXTG_anchor.1.
 DR TIGRFAMs; TIGR01168; YsIRK_signal.1.
 DR PROSITE; PS50847; GRAM_POS_ANCHORING.1.
 KW Cell wall, Complete proteome, Peptidoglycan-anchor.
 SQ SEQUENCE 961 AA; 106010 MW; 364940F884EA4101 CRC64;

Query Match 84.6%; Score 181; DB 2; Length 961;
 Best Local Similarity 86.8%; Pred. No. 3.5e-14;
 Matches 33; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 QNKGNSFPEDTEKDKRYEHGNIIDIDPDSVPHNG 38
 |||||
 DB 731 QNKGNSFPEDTEKDKRYEHGNIIDIDPDSVPHNG 768

RESULT 12
 ID Q6GDUS PRELIMINARY; PRT; 965 AA.
 AC Q6GDUS;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Fibronectin-binding protein.
 GN Name=fndb; OrderedlocusNames=SA2520;
 OS Staphylococcus aureus (strain MRS4252).
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 OX NCBI_TaxID=282458;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC PubMed=15213324; DOI=10.1073/pnas.0402521101;
 RA Holden M.T.G., Feil E.J., Lindsay J.A., Peacock S.J., Day N.P.J.,
 RA Enright M.C., Foster T.J., Moore C.E., Hurst L., Atkin R., Barron A.,
 RA Baeson N., Bentley S.D., Chillingworth C., Chillingworth T.,
 RA Churcher C., Clark L., Corton A., Cronin A., Doggett J., Dowd L.,
 RA Feltwell T., Hance Z., Hauser B., Hauser H., Holtroyd S., Jørgensen K.,
 RA James K.D., Lennard N., Line A., Mayes R., Moule S., Mungall K.,
 RA Ormond D., Quail M.A., Rabinowitch E., Rutherford K.M., Sanders M.,

RA Sharp S., Simmonds M., Stevens K., Whitehead S., Barrett B.3.,
 RA Spratt B.G., Parkhill J.,
 RT "Complete genomes of two clinical *Staphylococcus aureus* strains:
 RT evidence for the rapid evolution of virulence and drug resistance."
 RL Proc. Natl. Acad. Sci. U.S.A. 101:9786-9791(2004).
 CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
 CC an amide bond (By similarity).
 DR EMBL: BX571856; CAC41560.1; -.
 DR GO: GO:0009986; C:cell surface; IEA.
 DR GO: GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
 DR GO: GO:0016020; C:membrane; IEA.
 DR GO: GO:007155; P:cell adhesion; IEA.
 DR InterPro: IPR008966; Adhes_bact.
 DR InterPro: IPR004237; Fn_bind.
 DR InterPro: IPR005877; Gpos_YsIRK.
 DR InterPro: IPR001899; Gram_pos_anchor.
 DR Pfam: PF02986; Fn_bind; 1.
 DR Pfam: PF00746; Gram_pos_anchor; 1.
 DR Pfam: PF04650; YsIRK_signal; 1.
 DR TIGRfam: TIGR01167; LPXG_anchor; 1.
 DR TIGRfam: TIGR01168; YsIRK_signal; 1.
 DR PROSITE: PS00847; GRAM_POS_ANCHORING; 1.
 DR Cell wall; Complete proteome; Peptidoglycan-anchor.
 SQ SEQUENCE 965 AA; 105691 MW; 2982E132164D0551 CRC64;

Query Match 84.6%; Score 181; DB 2; Length 965.
 Best Local Similarity 86.8%; Pred. No. 3; Se-14;
 Matches 33; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 ONKNSPFEDTEKDKRYEHGNIIDIDPDSVPHIH 38
 Db 749 QNSGNSFEDTREDKRYEGSNIIDIDPDSVPHIH 786

RESULT 13
 COBD_THETN STANDARD; PRT; 367 AA.
 AC QGR5U4;
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Putative threonine-phosphate decarboxylase (EC 4.1.1.81) (L-threonine-
 DE O-3-phosphate decarboxylase).
 GN Name=cobd; OrderedLocNames=TTRE0380;
 OS Thermoanaerobacter tengcongensis.
 OC Bacteria; Firmicutes; Clostridia; Thermoanaerobacteriales;
 OC Thermoanaerobacteriaceae; Thermoanaerobacter.
 OX NCBI_TaxID=119072;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=MB4 / JCM 11007;
 RX MEDLINE=21992816; PubMed=11997336; DOI=10.1101/gr.219302;
 RA Bao Q., Tian Y., Li W., Xu Z., Xuan Z., Hu S., Dong W., Yang J.,
 RA Chen Y., Xue Y., Xu Y., Lai X., Huang L., Dong X., Ma Y., Jing L.,
 RA Tan H., Chen R., Wang J., Yu J., Yang H.;
 RT "A complete sequence of the *T. tengcongensis* genome."
 RL Genome Res. 12:689-700(2002).
 CC -1- FUNCTION: Decarboxylates L-threonine-O-3-phosphate to yield (R)-1-
 CC amino-2-propanol O-2-phosphate, the precursor for the linkage
 CC between the nucleotide loop and the cortin ring in cobalamin (By
 CC similarity).
 CC -1- CATALYTIC ACTIVITY: L-threonine O-3-phosphate = (R)-1-aminopropan-
 CC 2-yl phosphate + CO(2).
 CC -1- COFACTOR: Pyridoxal phosphate (By similarity).
 CC -1- PATHWAY: Adenosylcobalamin biosynthesis; conversion of
 CC adenosylcobyrinic acid to adenosylcobinamide.
 CC -1- SIMILARITY: Belongs to the class-II pyridoxal-phosphate-dependent
 CC aminotransferase family.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: AE013011; AM23667.1; -.
 DR HSSP: P97084; ILCS.
 DR InterPro: IPR001176; ACC synthase.
 DR InterPro: IPR004839; Aminotransferase_I/II.
 DR InterPro: IPR001917; Aminotransferase_II.
 DR InterPro: IPR005860; COBD.
 DR Pfam: PF00155; Aminotran_1_2; 1.
 DR PRINTS: PR00753; ACCSYNTHASE.
 DR TIGRfam: TIGR01140; COBD; 1.
 DR PROSITE: PS00599; AA_TRANSFER_CLASS_2; FALSE NEG.
 DR Cobalamin biosynthesis; Complete proteome; Lyase; Pyridoxal phosphate.
 FT BINDING 213 213 Pyridoxal phosphate (By similarity).
 SQ SEQUENCE 367 AA; 42396 MW; 2925127E1F8435 CRC64;

Query Match 29.9%; Score 64; DB 1; Length 367;
 Best Local Similarity 57.1%; Pred. No. 9; 9;
 Matches 16; Conservative 2; Mismatches 4; Indels 6; Gaps 2;

QY 10 EDTEDKRYEHGNIID----IDPDS 32
 Db 2 KEGERMKP-YEHGNIYDQGNLIDFSS 28

RESULT 14
 Q7RB60 PRELIMINARY; PRT; 716 AA.
 AC Q7RB60;
 DT 01-MAR-2004 (TREMBLrel. 26, Created)
 DT 01-MAR-2004 (TREMBLrel. 26, Last sequence update)
 DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
 DE Hypothetical protein.
 GN Name=PY06288;
 OS Plasmodium yoelii yoelii.
 OC Eukaryota; Alveolata; Apicomplexa; Haemosporidia; Plasmodium.
 OX NCBI_TaxID=73239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=17XNL;
 RX PubMed=12368865; DOI=10.1038/nature01099;
 RA Carlson J.M., Anguillo S.V., Suh B.B., Koil T.W., Petrea M.,
 RA Silva J.C., Ermolaeva M.D., Allen J.E., Selengut J.D., Koo H.L.,
 RA Peterson J.D., Pop M., Kosack D.S., Shumway M.F., Bidwell S.L.,
 RA Shallom S.J., van Aken S.E., Riedmuller S.B., Feldlyum T.V.,
 RA Cho J.K., Quackenbush J., Sedegah M., Shoaihi A., Cummings L.M.,
 RA Florens L., Yates F.R., III, Raine J.D., Sinden R.E., Harris M.A.,
 RA Cunningham D.A., Preiser P.R., Bergman L.W., Vaidya A.B.,
 RA van Lin L.H., Jansz C.J., Waters A.P., Smith H.O., White O.R.,
 RA Salzberg S.L., Venter J.C., Fraser C.M., Hoffman S.L., Gardner M.J.,
 RA Carnuci D.J.;
 RT "Genome sequence and comparative analysis of the model rodent malaria
 RT parasite *Plasmodium yoelii yoelii*."
 RL Nature 419:512-519(2002).
 CC -1- CAUTION: The sequence shown here is derived from an
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.
 CC CC EMBL: AABL01002106; BAA18479.1; -.
 CC DR InterPro: IPR008941; TPR-like.
 CC KW Hypothetical protein.
 SQ SEQUENCE 716 AA; 86599 MW; E11BE234A397B6F7 CRC64;

Query Match 29.9%; Score 64; DB 2; Length 716;
 Best Local Similarity 34.3%; Pred. No. 21;
 Matches 12; Conservative 7; Mismatches 16; Indels 0; Gaps 0;

QY 2 NKGNQSPFEDTEKDKRYEHGNIIDIDPDSVPHI 36
 Db 109 NNNEHTWEKKKQKSKFPNNNNIFDVSYEYVKI 143

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OM protein - protein search, using sw model

Run on: October 25, 2005, 19:38:38 ; Search time 83.8325 Seconds
(without alignments)
175.313 Million cell updates/sec

Title: US-10-731-238-47

Perfect score: 214
Sequence: 1 QNKGNSFEPDTEKDKRYEHGNIIDFDVPHIHG 38

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seque, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: Geneseq_16Dec04:*
2: geneseqp1980s:*
3: geneseqp1990s:*
4: geneseqp2000s:*
5: geneseqp2001s:*
6: geneseqp2002s:*
7: geneseqp2003as:*
8: geneseqp2003bs:*
9: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	214	100.0	38	2	AAW65703 Fibronec
2	206	96.3	38	2	AAW65663 Fibronec
3	206	96.3	134	2	AAV29087 S. aureus
4	206	96.3	139	2	AAW31556 Fibronec
5	206	96.3	1018	1	AAW82115 Staphyloc
6	206	96.3	1018	4	AAU37245 Staphyloc
7	206	96.3	1018	4	AAU34301 Staphyloc
8	206	96.3	1018	6	ABJ18922 Staphyloc
9	206	96.3	1018	6	ABW72537 Staphyloc
10	206	96.3	1027	2	AAW89806 Staphyloc
11	201	93.9	77	2	AAW88749 S. aureus
12	201	93.9	113	2	AAW90937 D3D4 poly
13	201	93.9	130	2	AAW58806 Fibronec
14	201	93.9	130	2	AAW58807 Fibronec
15	201	93.9	130	2	AAW91202 D1-D4 fib
16	201	93.9	130	2	AAW91201 D1-D4 fib
17	201	93.9	162	2	AAW90942 D3D4 poly
18	201	93.9	164	2	AAW90938 D3D4 poly
19	201	93.9	174	2	AAW58808 Fbp fibro
20	201	93.9	174	2	AAW91203 D1-D4 fib
21	201	93.9	181	2	AAW58805 Fibronec
22	201	93.9	181	2	AAW91200 D1-D4 fib
23	200	93.5	38	1	AAW80661 Protein w
24	200	93.5	38	1	AAW82117 Fibronec
25	200	93.5	38	2	AAW65702 Fibronec

26	199	93.0	38	2	AAW65704 Fibronec
27	198	92.5	38	2	AAW65664 Fibronec
28	198	92.5	38	2	AAW65705 Fibronec
29	196	91.6	38	2	AAW65701 Fibronec
30	193	90.2	134	2	AAW29088 S. aureus
31	193	90.2	559	2	AAW89803 Staphyloc
32	193	90.2	767	4	AAU34403 Staphyloc
33	193	90.2	767	4	AAU37547 Staphyloc
34	193	90.2	940	2	AAW07070 Fibronec
35	193	90.2	940	6	AAW09111 Pathogen
36	193	90.2	948	6	ADA89470 Staphyloc
37	193	90.2	948	6	ABJ18923 Pathogen
38	193	90.2	948	6	ABW72536 Staphyloc
39	193	90.2	1038	6	ABU5903 Protein e
40	192	89.7	38	2	AAW65706 Fibronec
41	188	87.9	38	2	AAW65693 Fibronec
42	185	86.4	978	4	AAU33960 Staphyloc
43	185	86.4	1001	4	AAU37093 Staphyloc
44	184	86.0	134	2	AAW29089 Cloned fi
45	183	85.5	36	2	AAW65714 Fibronec

ALIGNMENTS

RESULT 1
AAW65703 standard; peptide; 38 AA.
ID AAW65703:
AC AAW65703:
DT 16-OCT-1998 (first entry)
DE Fibronectin binding protein-derived peptide #47.
XX microbial surface components recognising adhesive matrix molecule;
XX MSCRAMM; fibronectin; fibronectin-binding protein; antibody; epitope;
KM antibiotic; bacterial infection; antibiotic-resistant strain.
KM
XX
OS Synthetic.
OS Staphylococcus aureus.
XX
XX WO9831389-A2.
XX
XX 23-JUL-1998.
XX
XX 21-JAN-1998; 98WO-US001222.
XX
XX 21-JAN-1997; 97US-0036139P.
XX
XX (TEXA) UNIV TEXAS A & M SYSTEM.
XX
XX Hooeok M, Patcl JM, House-Pompeo KL, Speziale P, Joh D;
XX Mcgavin MJ;
XX WPI; 1998-413816/35.
XX
XX Example 8; Page 102; 201p; English.
The invention relates to antibodies that bind to a fibronectin-binding domain of a fibronectin-binding protein, and inhibit binding of the protein to fibronectin. Also claimed are: (1) isolated peptides of a fibronectin-binding protein that do not bind to fibronectin; (2) fusion protein containing at least one peptide of a fibronectin-binding protein linked to a second amino acid sequence; (3) nucleic acid encoding the isolated peptide of (1). Antibodies, the isolated peptides of (1) and the nucleic acids are all useful for immunisation (active or passive) and (by inhibiting binding of bacteria to fibronectin) for preventing or treating infection in humans or other animals, particularly by staphylococci or

CC streptococci, e.g. meningitis, otitis media, pneumonia, endocarditis,
 CC mastitis in cattle, abortion in horses and many others. Since the
 CC antibodies block binding of bacteria, they should be effective against
 CC antibiotic-resistant strains, and may replace antibiotic therapy or
 CC increase its effectiveness. Sequences AAW65701-706 represent a series of
 CC synthetic peptides based on the D2 region of *S. aureus* fibronectin
 CC binding protein A. They were synthesised to contain mutations

XX Sequence 38 AA;
 SQ

Query Match 100.0%; Score 214; DB 2; Length 36;
 Best Local Similarity 100.0%; Pred. No. 8.3e-23;
 Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QNKGNSFEPDTEKDKPKYEHGNIIDIDFDSVPHIHG 38
 DB 1 QNKGNSFEPDTEKDKPKYEHGNIIDIDFDSVPHIHG 38

RESULT 2
 ID AAW65663 standard; peptide; 38 AA.
 XX AAW65663;
 AC 16-OCT-1998 (first entry)
 DT Fibronectin binding protein-derived peptide #7.
 DE
 XX microbial surface components recognising adhesive matrix molecule;
 KM MSCRAMM; fibronectin; fibronectin-binding protein; antibody; epitope;
 KM antibiotic; bacterial infection; antibiotic-resistant strain.
 XX
 OS Synthetic.
 OS Staphylococcus aureus.
 XX
 PN WO9831389-A2.
 PD 23-JUL-1998.
 PF 21-JAN-1998; 98WO-US001222.
 PR 21-JAN-1997; 97US-0036139P.
 PA (TEXA) UNIV TEXAS A & M SYSTEM.
 PI Hoeek M, Patti JW, House-Pompeo KL, Speciale P, Joh D:
 PI McGavin MJ;
 XX WPI; 1998-413816/35.
 DR WPI; 1998-413816/35.
 XX
 PT Antibody that binds to fibronectin-binding protein, preventing its
 PT binding to fibronectin - used to treat or prevent bacteria. infection,
 PT especially by Staphylococci and Streptococci.
 XX
 PS Example 2; Page 92; 201pp; English.
 XX
 CC The invention relates to antibodies that bind to a fibronectin-binding
 CC domain of a fibronectin-binding protein, and inhibit binding of the
 CC protein to fibronectin. Also claimed are: (1) isolated peptides of a
 CC fibronectin-binding protein that do not bind to fibronectin; (2) fusion
 CC protein containing at least one peptide of a fibronectin-binding protein
 CC linked to a second amino acid sequence; (3) nucleic acid encoding the
 CC isolated peptide of (1). Antibodies, the isolated peptides of (1) and the
 CC nucleic acids are all useful for immunisation (active or passive) and (by
 CC inhibiting binding of bacteria to fibronectin) for preventing or treating
 CC infection in humans or other animals, particularly by staphylococci or
 CC streptococci, e.g. meningitis, otitis media, pneumonia, endocarditis,
 CC mastitis in cattle, abortion in horses and many others. Since the
 CC antibodies block binding of bacteria, they should be effective against
 CC antibiotic-resistant strains, and may replace antibiotic therapy or
 CC increase its effectiveness. Sequences AAW65659-68 represent synthetic
 CC epitopes from the fibronectin binding domains DU and DI-D4 of the *S.*

CC aureus fnbA gene
 XX
 SQ Sequence 38 AA;
 QY Query Match 96.3%; Score 206; DB 2; Length 38;
 DB Best Local Similarity 97.4%; Pred. No. 1.1e-21;
 Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QNKGNSFEPDTEKDKPKYEHGNIIDIDFDSVPHIHG 38
 DB 1 QNKGNSFEPDTEKDKPKYEHGNIIDIDFDSVPHIHG 38

RESULT 3
 ID AAY29087 standard; protein; 134 AA.
 XX AAY29087;
 AC 28-SEP-1999 (first entry)
 DT
 DE S. aureus fibronectin binding protein A (Fnba) binding domain.
 XX
 XX Bovine herpes virus-2; BHV-2; cytokine; immune response; immunogen; IL;
 KM interleukin; colony stimulating factor; CSF; interferon; IFN; TNF;
 KM tumour necrosis factor; recombinant virus; vaccine; mucosal disease;
 KM mastitis; breast cancer; stress-induced disease; binding domain; Fnba;
 KM fibronectin binding protein.
 XX
 OS Staphylococcus aureus.
 OS
 PN WO9916892-A1.
 PD 08-APR-1999.
 PF 29-SEP-1998; 98WO-GB002927.
 PR 29-SEP-1997; 97GB-00020633.
 XX (UYBR-) UNIV BRISTOL.
 PA Bradley AJ, Duffas WP;
 PI WPI; 1999-255101/21.
 DR N-PSDB; AAX91504.
 PT New bovine herpes virus-2 vectors.
 PT
 XX Example 2; Fig 8A-B; 130pp; English.
 PS
 CC The invention provides bovine herpes virus-2 (BHV-2) based vectors that
 CC comprise at least one cytokine-encoding DNA sequence. The expression of
 CC cytokines in mammals can up-regulate immune responses to the immunogens.
 CC The cytokine is selected from interleukins (IL), colony stimulating
 CC factors (CSF), interferons (IFN) and tumour necrosis factors (TNF). The
 CC BHV-2 based vector or recombinant virus can be used as vaccines. They can
 CC be used for preventing or treating a mucosal disease in a subject, e.g.
 CC ruminants, cattle, sheep, goats, dogs, cats, horses, or man, particularly
 CC mastitis in cows or breast cancers in humans. They can also be used for
 CC preventing or treating a stress-induced disease. The present sequence
 CC represents the binding domain of a previously published *S. aureus*
 CC fibronectin binding protein A (Fnba) sequence. The Fnba binding domain
 CC gene sequence FNBB, cloned for use in this invention has 97.8 percent
 CC identity when compared to the previously published Fnba and Fnbb gene
 CC sequences

XX Sequence 134 AA;
 SQ

Query Match 96.3%; Score 206; DB 2; Length 134;
 Best Local Similarity 97.4%; Pred. No. 5.2e-21;
 Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QNKGNSFEPDTEKDKPKYEHGNIIDIDFDSVPHIHG 38

DB 40 QNKGNSFEDTEKDKPTEHGSNIIDIDPDSVPHIHG 77

RESULT 4

ID AAW31556 standard; protein; 139 AA.

AAW31556;

27-AUG-2003 (revised)

25-MAR-2003 (revised)

21-MAY-1998 (first entry)

Fibronectin-binding MSCRAMM derivative pOD.

Microbial surface component regionising adhesive matrix molecule; MSCRAMM;

adhesin; vaccine; immunisation; diagnosis; therapy; mastitis.

Staphylococcus aureus.

Key Location/Qualifiers

Peptide 1..12

/note= "vector pOE30-derived peptide"

MO9743314-A2.

20-NOV-1997.

14-MAY-1997; 97MO-US008210.

16-MAY-1996; 96US-0017678P.

(TEXA) UNIV TEXAS A & M SYSTEM.

(UABR-) UAB RES FOUND.

Hoeek M, Patti JM, House-Dompeo K, Stahanam N, Symersky J;

WPI; 1998-008801/01.

Antibody that interacts with collagen binding domain of Staphylococcal

cna gene product - useful to prevent bacterial sepsis in animal infected

with Staphylococcus aureus.

Disclosure; Page 91; 143pp; English.

This protein comprises Staphylococcus aureus fibronectin-binding

microbial surface component regionising adhesive matrix molecule (MSCRAMM)

derivative pOD, plus a vector-derived N-terminal peptide. The invention

relates to claimed nucleic acid sequences (see AAT93436-38) encoding S.

aureus collagen binding protein (CBP) epitopes M17, M31 and M55 (see

AAW31552-54) that confer protection against S. aureus infection. CBP

protein and antigenic epitopes are contemplated for use in the treatment

of pathological infections, especially to prevent bacterial adhesion to

collagen. The epitopes are also contemplated for use in the preparation

of vaccines and as carrier proteins in vaccine formulations, as well as

in the formulation of compositions for the prevention of S. aureus

infection. PCR3 and pOD (see AAW31556) were used to raise anti-MSCRAMM

polyclonal antibodies used in passive immunisation against bovine

mastitis. (Updated on 25-MAR-2003 to correct PI field.) (Updated on 27-

AUG-2003 to correct OS field.)

Sequence 139 AA;

Query Match 96.3%; Score 206; DB 2; Length 139;

Best Local Similarity 97.4%; Pred. No. 5,4e-21;

Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

1 QNKGNSFEDTEKDKPTEHGSNIIDIDPDSVPHIHG 38

54 QNKGNSFEDTEKDKPTEHGSNIIDIDPDSVPHIHG 91

RESULT 5
ID AAP82115 standard; protein; 1018 AA.

AAP82115;

25-MAR-2003 (revised)

05-JAN-1990 (first entry)

Fibronectin binding protein.

Fibronectin binding protein; S. aureus; immunisation; mastitis; ruminants;

wound infection; diagnosis.

Staphylococcus aureus.

EP294349-A.

30-MAY-1988; 88EP-00850188.

01-JUN-1987; 87SE-00002272.

(ALFA) ALFA LAVAL AGRIC INT AB.

Lindberg MK, Signas LC, Wadstrom TM, Froman G;

WPI; 1988-347978/49.

P-P-SDB; AAP82115.

Hybrid DNA encoding Staphylococcus aureus fibronectin binding protein -

useful for immunisation and topical application to prevent staphylococcal

infections.

Disclosure; Fig. 8A:1-8A:2; 23pp; English.

The S. aureus fibronectin binding protein may be included in a hybrid

protein. The protein may be used to immunise ruminants against

staphylococcal mastitis, pref. when given at 0.5-5 microg/kg, using 3

doses at 1-3 week intervals; and for topical applicn. to prevent wound

infection, pref. using isotonic saline soln. of concn. 25-250 microg/mg.

The DNA encoding the binding protein and the hybrid protein may be

immobilised on a carrier and used to diagnose staphylococcal infections.

(Updated on 25-MAR-2003 to correct PA field.)

Sequence 1018 AA;

Query Match 96.3%; Score 206; DB 1; Length 1018;

Best Local Similarity 97.4%; Pred. No. 6e-20;

Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

1 QNKGNSFEDTEKDKPTEHGSNIIDIDPDSVPHIHG 38

784 QNKGNSFEDTEKDKPTEHGSNIIDIDPDSVPHIHG 821

RESULT 6

ID AAU37245 standard; protein; 1018 AA.

AAU37245;

14-FEB-2002 (first entry)

Staphylococcus aureus cellular proliferation protein #1415.

Antisense; prokaryotic cellular proliferation protein; antibiotic;

antibacterial; drug design.

Staphylococcus aureus.

```

PN WO200170955-A2.
XX
XX PD
XX 27-SEP-2001.
PF
XX 21-MAR-2001; 2001WO-US009180.
XX
XX 21-MAR-2000; 2000US-0191078P.
PR 23-MAY-2000; 2000US-0206848P.
PR 26-MAY-2000; 2000US-0207727P.
PR 23-OCT-2000; 2000US-0242578P.
PR 27-NOV-2000; 2000US-0253625P.
PR 22-DEC-2000; 2000US-0257931P.
PR 16-FEB-2001; 2001US-0263308P.
XX
XX (ELIT-) ELITRA PHARM INC.
XX
XX Haeselbeck R, Ohlsen KU, Zyskind JW, Wall D, Trawick JD, Carr GJ;
PI Yamamoto RT, Xu HH;
XX
XX WPI; 2001-611495/70.
DR N-PDB; AAS55104.
XX
XX New polynucleotides for the identification and development of
PT antibiotics, comprise sequences of antisense nucleic acids.
XX
XX Example 3; SEQ ID NO 12838; 511pp; English.
XX
XX The invention relates to antisense inhibitors of genes essential to
CC prokaryotic cellular proliferation, their use in identifying the genes,
CC their use in the discovery of novel antibiotics, the essential genes
CC themselves and the encoded proteins. The prokaryotes used are Escherichia
CC coli, Staphylococcus aureus, Salmonella typhi, Klebsiella pneumoniae,
CC Pseudomonas aeruginosa and Enterococcus faecalis. The invention is also
CC useful for the identification of potential new targets for antibiotic
CC development. The antisense nucleic acids can also be used to identify
CC proteins used in proliferation, to express these proteins, and to obtain
CC antibodies capable of binding to the expressed proteins. The proteins can
CC be used to screen compounds in rational drug discovery programmes. The
CC antisense nucleic acid sequence is also useful to screen for homologous
CC nucleic acids which are required for cell proliferation in a wide variety
CC of organisms. The present sequence represents an essential prokaryotic
CC cellular proliferation protein. Note: The sequence data for this patent
CC did not form part of the printed specification, but was obtained in
CC electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 1018 AA;
Query Match 96.3%; Score 206; DB 4; Length 1018;
Best Local Similarity 97.4%; Pred. No. 66-20;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 ONKGNQSFEPDEKDKPKYEHGNGNIIIDDFDSVPVPHIG 38
| | | | | | | | | | | | | | | | | | | | | | | | | |
| | | | | | | | | | | | | | | | | | | | | | | | | |
Db 784 ONKGNQSFEPDEKDKPKYEHGNGNIIIDDFDSVPVPHIG 821
RESULT 7
AAU34301 ebandardj, protein; 1018 AA.
XX
XX AC AAU34301;
XX
XX 14-FEB-2002 (first entry)
XX
XX Staphylococcus aureus cellular proliferation protein #577.
XX Antisense; prokaryotic cellular proliferation protein; antibiotic;
KM antibacterial; drug design.
XX
XX Staphylococcus aureus.
XX
XX WO200170955-A2.

```

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XX 27-SEP-2001.
XD
PF 21-MAR-2001; 2001WO-US0009180.
PR 21-MAR-2000; 2000US-0191078P.
PR 23-MAR-2000; 2000US-0206848P.
PR 26-MAY-2000; 2000US-0207727P.
PR 23-OCT-2000; 2000US-0242578P.
PR 27-NOV-2000; 2000US-0253625P.
PR 22-DEC-2000; 2000US-0257931P.
PR 16-FEB-2001; 2001US-0269308P.
XX
PA (ELIT-) ELITRA PHARM INC.
XX
XX Haasebeck R, Ohlsen KL, Zyskind JW, Wall D, Trawick JD, Carr GJ;
PI Yamamoto RT, Xu HH;
XX
DR WPI: 2001-611495/70.
DR N-PSDB; AAS52160.
XX
XX New polynucleotides for the identification and development of
PT antibiotics, comprise sequences of antisense nucleic acids.
XX
XX Example 3; SEQ ID NO 5797; 511pp; English.
XX
XX The invention relates to antisense inhibitors of genes essential to
CC prokaryotic cellular proliferation, their use in identifying the genes,
CC their use in the discovery of novel antibiotics, the essential genes
CC themselves and the encoded proteins. The prokaryotes used are Escherichia
CC coli, Staphylococcus aureus, Salmonella typhi, Klebsiella pneumoniae,
CC Pseudomonas aeruginosa and Enterococcus faecalis. The invention is also
CC useful for the identification of potential new targets for antibiotic
CC development. The antisense nucleic acids can also be used to identify
CC proteins used in proliferation, to express these proteins, and to obtain
CC antibodies capable of binding to the expressed proteins. The proteins can
CC be used to screen compounds in rational drug discovery programmes. The
CC antisense nucleic acid sequence is also useful to screen for homologous
CC nucleic acids which are required for cell proliferation in a wide variety
CC of organisms. The present sequence represents an essential prokaryotic
CC cellular proliferation protein. Note: The sequence data for this patent
CC did not form part of the printed specification, but was obtained in
CC electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX
SQ Sequence 1018 AA;
XX
XX Query Match 96.3%; Score 206; DB 4; Length 1018;
XX Best Local Similarity 97.4%; Pred. No. 6e-20; 1; Indels 0; Gaps 0;
XX Matches 37; Conservative 0; Mismatches 1;
XX
XX 1 QNKGNSFEEDTKDKPYRHEHGNIIIDPDSVPHNG 38
XX |||||||
XX 784 QNKGNSFEEDTKDKPYRHEHGNIIIDPDSVPHNG 821
XX
XX RESULT 8
XX ABJ18922
XX ID ABJ18922 standard; protein; 1018 AA.
XX
XX AC ABJ18922;
XX
XX DT 06-MAR-2003 (first entry)
XX
XX Pathogen specific antigen related staphylococcal protein SEQ ID No 68.
XX
XX Antibacterial; virucide; fungicide; protozoacide; cytostatic; anti-HIV;
XX hyperimmune; serum-reactive; antigen; pathogen; tumour; allergen;
XX auto-immunity; vaccine; staphylococcal infection; antibody; cancer;
XX autoimmune disease; HIV; hepatitis.
XX
XX Staphylococcus sp.
XX

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PN MO200259148-A2.
 XX 01-AUG-2002.
 XX 21-JAN-2002; 2002MO-BP000546.
 PF 26-JAN-2001; 2001AT-00000130.
 XX
 XX (CIST-) CISTEM BIOTECHNOLOGIES GMBH.
 XX
 PI Meinke A, Nagy E, Von Ahnen U, Klade C, Henics T, Zauner W;
 PI Minh DB, Vytvytska O, Etz H, Dryla A, Weichert T, Hafner M;
 PI Tempelmeier B;
 XX
 DR WPI; 2003-075410/07.
 XX
 PT Identifying, isolating and producing hyperimmune serum-reactive antigens
 PT from a pathogen, for preparing vaccine or medicament for treating or
 PT preventing e.g. staphylococcal infections, comprises providing antibody
 PT preparation.
 PT
 PS Example 7; Page 157; 252pp; English.
 XX
 CC The invention relates to a novel method for identifying, isolating and
 CC producing hyperimmune serum-reactive antigens from a pathogen, tumour,
 CC allergen, a tissue or host prone to auto-immunity, where the antigens are
 CC used in a vaccine, comprises providing antibody preparation from a plasma
 CC pool of a type of animal, or individual sera with antibodies against the
 CC specific pathogen, tumour, allergen, tissue or host prone to auto-
 CC immunity. The hyperimmune serum-reactive antigens comprising any of the
 CC 62 sequences of 53-2261 amino acids fully defined in the specification,
 CC or their hyperimmune fragments are useful for the manufacture of a
 CC pharmaceutical preparation, particularly a vaccine against staphylococcal
 CC infections or colonisation against *S. aureus* or *S. epidermidis*. The
 CC preparation of antibodies is useful for the manufacture of a medicament
 CC for treating or preventing staphylococcal infections or colonisation
 CC against *S. aureus* or *S. epidermidis*. The antibody preparations may also
 CC be used for diagnostic and imaging purposes. Other conditions that can be
 CC treated include cancer, autoimmune diseases or infections caused by viral
 CC (e.g. HIV, hepatitis A, B or C), fungal or protozoan pathogens. This
 CC sequence represents a staphylococcal protein relating to the method for
 CC identifying and producing pathogen specific antigens of the invention
 CC
 XX
 SQ Sequence 1018 AA;
 Query Match 96.3%; Score 206; DB 6; Length 1018;
 Best Local Similarity 97.4%; Pred. No. 6e-20; Indels 0; Gaps 0;
 Matches 37; Conservative 0; Mismatches 1;
 QY 1 QNKGNSFEDPTEDKPKYEHGNIIDIDPSVPHNG 38
 DB 784 QNKGNSFEDPTEDKPKYEHGNIIDIDPSVPHNG 821
 RESULT 9
 ID ABM72537 standard; protein; 1018 AA.
 AC ABM72537;
 XX
 DT 20-NOV-2003 (first entry)
 XX
 DE Staphylococcus aureus protein #1777.
 XX
 KW Antibacterial; vaccine; gene therapy; infection; sepsis; diagnosis;
 KW enzymatic assay; antibiotic target.
 XX
 OS Staphylococcus aureus.
 XX
 PN MO200294868-A2.
 XX
 PD 28-NOV-2002.

PF 27-MAR-2002; 2002MO-IB002637.
 XX
 XX 27-MAR-2001; 2001GB-00007661.
 XX
 XX (CHIR-) CHIRON SPA.
 PA
 XX
 PI Maignani V, Mora M, Scarselli M;
 XX
 DR WPI; 2003-120786/11.
 DR N-PSDB; ACF74097.
 XX
 PT New Staphylococcus aureus protein, useful as a vaccine for treating or
 PT preventing Staphylococcus aureus infection, specifically an infection caused by
 PT *S. aureus*, e.g. sepsis.
 PT
 PS Claim 1; SEQ ID NO 3554; 49pp; English.
 XX
 CC The invention relates to novel genes and encoded proteins from
 CC Staphylococcus aureus. A composition comprising the *S. aureus* protein, a
 CC nucleic acid encoding the protein, or an antibody to the protein, is
 CC useful as a pharmaceutical, particularly as a vaccine for treating or
 CC preventing infection due to Staphylococcus bacteria, specifically an
 CC infection caused by *S. aureus*. The composition is particularly useful for
 CC treating or preventing sepsis in a patient. The composition can also be
 CC used for diagnostics. The protein is also used in an assay for enzymatic
 CC studies and as a target for antibiotics. This sequence represents one of
 CC the novel *S. aureus* proteins of the invention
 CC
 XX
 SQ Sequence 1018 AA;
 Query Match 96.3%; Score 206; DB 6; Length 1018;
 Best Local Similarity 97.4%; Pred. No. 6e-20; Indels 0; Gaps 0;
 Matches 37; Conservative 0; Mismatches 1;
 QY 1 QNKGNSFEDPTEDKPKYEHGNIIDIDPSVPHNG 38
 DB 784 QNKGNSFEDPTEDKPKYEHGNIIDIDPSVPHNG 821
 RESULT 10
 ID AAM89806 standard; protein; 1027 AA.
 AC AAM89806;
 XX
 DT 16-MAR-1999 (first entry)
 XX
 DE Staphylococcus aureus protein SEQ ID #5254.
 XX
 KW Computer readable medium; vaccine; *S. aureus* infection; immunodetection;
 KW cellulitis; eyelid infection; food poisoning; osteomyelitis; therapy;
 KW skin infection; surgical wound infection; scalded skin syndrome;
 KW toxic shock syndrome.
 XX
 OS Staphylococcus aureus.
 XX
 PN EP786519-A2.
 PN
 PD 30-JUL-1997.
 XX
 PF 07-JAN-1997; 97EP-00100117.
 XX
 PR 05-JAN-1996; 96US-0009861P.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 XX
 PI Kunsch CA, Choi GH, Barash SC, Dillon PJ, Fannon MR, Rosen CA;
 XX
 DR WPI; 1997-374922/35.
 DR
 XX Polynucleotide(s) and proteins derived from Staphylococcus aureus -
 PT stored on computer readable medium and used in the production of anti-
 PT *S. aureus* vaccines.

CC combat infection at the site of wounds, surgical implants and other in-
 CC dwelling devices (such as catheters), and as adherent agents in oral
 CC hygiene. They can also be used in the manufacture of a medicament for the
 CC prevention of adhesion of bacteria to extracellular matrix proteins
 CC present on in-dwelling devices or in wounds, or of oral pathogens to
 CC similar proteins on surfaces in the oral cavity
 XX
 SQ Sequence 113 AA;

Query Match 93.9%; Score 201; DB 2; Length 113;
 Best Local Similarity 94.7%; Pred. No. 2.2e-20;
 Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 QNKGNSFEPDTEKDKPKYEHGNIIDIDPDSVPHHG 38
 DB 23 QNKGDSFEPDTEKDKPKYEHGNIIDIDPDSVPHHG 60

RESULT 13

AAR58806 standard; protein; 130 AA.

XX AAR58806;

XX 25-MAR-2003 (revised)
 DT 30-MAR-1995 (first entry)

XX Fibronectin binding domain D1-D4 (709-838(P838T)).

XX Fibronectin binding protein; Fbp; fibronectin binding domain;
 KW monoclonal antibody; MAb; adhesion; Gram-positive bacterium; bacteremia;
 KM Escherichia coli.

XX Staphylococcus aureus.

XX W09418327-A1.

XX 18-AUG-1994.

XX 04-FEB-1994; 94MO-GB000215.

XX 05-FEB-1993; 93GB-00002289.
 PR 20-OCT-1993; 93GB-00021592.

XX (SMIK) SMITHKLINE BEECHAM PLC.

XX Burnham MKR, Chopra I, Critchley IA, Knowles DJC;

XX WPI; 1994-279748/34.

XX Fibronectin binding protein and monoclonal antibodies specific for Fbp -
 PT useful to prevent adherence of Gram-positive bacteria to indwelling
 PT devices or wounds.

XX Disclosure; Page 30; 40pp; English.

XX Polypeptides corresponding to residues G709-T886 plus PRTVPT, G709-
 CC P838(P838T) and G709-P838 (AAR58805-07, respectively) of S. aureus J2385
 CC (NCIMB 40532) Fbp type A fibronectin binding domain D1-D4 region
 CC (AAR58808) were expressed in E. coli BL21 (DE4) and used to raise MAbs
 CC specific for Fbp. (Updated on 25-MAR-2003 to correct PN field.)

XX Sequence 130 AA;

Query Match 93.9%; Score 201; DB 2; Length 130;
 Best Local Similarity 94.7%; Pred. No. 2.6e-20;
 Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 QNKGNSFEPDTEKDKPKYEHGNIIDIDPDSVPHHG 38
 DB 40 QNKGDSFEPDTEKDKPKYEHGNIIDIDPDSVPHHG 77

RESULT 14

AAR58807 standard; protein; 130 AA.

XX AAR58807;

XX 25-MAR-2003 (revised)

DT 30-MAR-1995 (first entry)

XX Fibronectin binding domain D1-D4 (709-838).

XX Fibronectin binding protein; Fbp; fibronectin binding domain;
 KW monoclonal antibody; MAb; adhesion; Gram-positive bacterium; bacteremia;
 KM Escherichia coli.

XX Staphylococcus aureus.

XX W09418327-A1.

XX 18-AUG-1994.

XX 04-FEB-1994; 94MO-GB000215.

XX 05-FEB-1993; 93GB-00002289.
 PR 20-OCT-1993; 93GB-00021592.

XX (SMIK) SMITHKLINE BEECHAM PLC.

XX Burnham MKR, Chopra I, Critchley IA, Knowles DJC;

XX WPI; 1994-279748/34.

XX Fibronectin binding protein and monoclonal antibodies specific for Fbp -
 PT useful to prevent adherence of Gram-positive bacteria to indwelling
 PT devices or wounds.

XX Disclosure; Page 30; 40pp; English.

XX Polypeptides corresponding to residues G709-T886 plus PRTVPT, G709-
 CC P838(P838T) and G709-P838 (AAR58805-07, respectively) of S. aureus J2385
 CC (NCIMB 40532) Fbp type A fibronectin binding domain D1-D4 region
 CC (AAR58808) were expressed in E. coli BL21 (DE4) and used to raise MAbs
 CC specific for Fbp. (Updated on 25-MAR-2003 to correct PN field.)

XX Sequence 130 AA;

Query Match 93.9%; Score 201; DB 2; Length 130;
 Best Local Similarity 94.7%; Pred. No. 2.6e-20;
 Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 QNKGNSFEPDTEKDKPKYEHGNIIDIDPDSVPHHG 38
 DB 40 QNKGDSFEPDTEKDKPKYEHGNIIDIDPDSVPHHG 77

RESULT 15

AAR91202 standard; peptide; 130 AA.

XX AAR91202;

DT 13-NOV-1996 (first entry)

XX D1-D4 fibronectin binding domains.

XX Fibronectin; oral hygiene; gingivitis; gum disease; adhesion;
 KW periodontitis; oral pathogen; caries; calculus; candidiasis; oral surgery;
 KW tissue regeneration; irrigation; toothpaste; dentifrice; mouthwash;
 KW lozenge.

XX Staphylococcus aureus.

XX W09604003-A1.

XX 15-FEB-1996.
 PD 18-JUL-1995; 95WO-EP002825.
 PF 05-AUG-1994; 94GB-00015902.
 PR (SMRK) SMITHKLINE BEECHAM PLC.
 XX Barnett P, Critchley IA, Dodd I;
 PI WPI; 1996-129122/13.
 DR
 XX
 PT Prevention of adherence of oral pathogens in the oral cavity, partic.
 PT tooth surfaces - by application of a fibronectin binding protein or
 PT polypeptide or a monoclonal antibody or fragment against it.
 PS Claim 5; Page 32; 41pp; English.
 XX
 CC Adherence of oral pathogens, particularly to tooth surface, can be
 CC prevented by application of a fibronectin binding protein or polypeptide.
 CC The fibronectin binding protein or polypeptide is useful in the
 CC manufacture of oral hygiene compositions, eg. toothpaste, liquid
 CC dentifrice, mouthwash or lozenge. They are useful to prevent the plaque-
 CC related development of carious lesions, gingivitis, calculus or
 CC periodontal disease and to combat oral cavity infections, eg.
 CC candidiasis. They may also be useful in oral surgery e.g. in guided
 CC tissue regeneration procedures to prevent subsequent bacterial infection,
 CC and for irrigation of periodontal pockets. This sequence corresponds to
 CC amino acids 709-838 of the D1-D4 fibronectin binding domain of
 CC Staphylococcus aureus
 XX
 SQ Sequence 130 AA;

Query Match 93.9%; Score 201; DB 2; Length 130;
 Best Local Similarity 94.7%; Pred. No. 2.6e-20;
 Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 QNKGNSFEPDTEKDKPKYEHGNIIDIDFDSVPHIHG 38
 |||:|||||
 Db 40 QNKGDSFEPDTEKDKPKYEHGNIIDIDFDSVPHIHG 77

Search completed: October 25, 2005, 20:21:05
 Job time : 83.8825 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 22, 2005, 03:51:22 ; Search time 21.1723 Seconds
(without alignments)
133.980 Million cell updates/sec

Title: US-10-731-238-47

Sequence: 1 QNKGNSFPDTEKDKPKYEHGNIIDIDFDSVPHHG 38

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:
1: /cgn2_6/ptodata/1/iaa/5A.COMB.pep.*
2: /cgn2_6/ptodata/1/iaa/5B.COMB.pep.*
3: /cgn2_6/ptodata/1/iaa/6A.COMB.pep.*
4: /cgn2_6/ptodata/1/iaa/6B.COMB.pep.*
5: /cgn2_6/ptodata/1/iaa/PTUS.COMB.pep.*
6: /cgn2_6/ptodata/1/iaa/backfile1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	214	100.0	38	4	US-09-010-317-47 Sequence 47, Appl
2	206	96.3	38	1	US-08-234-622A-3 Sequence 3, Appl
3	206	96.3	38	4	US-09-010-317-7 Sequence 7, Appl
4	206	96.3	114	1	US-08-259-000-3 Sequence 3, Appl
5	206	96.3	139	3	US-08-856-253-8 Sequence 8, Appl
6	206	96.3	1027	4	US-08-956-171E-5254 Sequence 5254, Ap
7	206	96.3	1027	4	US-08-781-986A-5254 Sequence 5254, Ap
8	201	93.9	130	2	US-08-459-135A-7 Sequence 7, Appl
9	201	93.9	130	2	US-08-459-135A-8 Sequence 8, Appl
10	201	93.9	130	3	US-08-495-559-7 Sequence 8, Appl
11	201	93.9	130	3	US-08-495-559-8 Sequence 8, Appl
12	201	93.9	174	2	US-08-459-135A-10 Sequence 10, Appl
13	201	93.9	174	3	US-08-495-559-6 Sequence 6, Appl
14	201	93.9	176	3	US-08-495-559-10 Sequence 10, Appl
15	201	93.9	178	2	US-08-459-135A-12 Sequence 12, Appl
16	201	93.9	178	2	US-08-495-559-12 Sequence 12, Appl
17	201	93.9	181	2	US-08-459-135A-6 Sequence 6, Appl
18	200	93.5	38	1	US-08-729-767-4 Sequence 4, Appl
19	200	93.5	38	4	US-09-010-317-46 Sequence 46, Appl
20	199	93.0	38	4	US-09-010-317-48 Sequence 48, Appl
21	198	92.5	38	4	US-09-010-317-8 Sequence 8, Appl
22	198	92.5	38	4	US-09-010-317-49 Sequence 49, Appl
23	196	91.6	38	4	US-09-010-317-45 Sequence 45, Appl
24	193	90.2	174	2	US-08-459-135A-13 Sequence 13, Appl
25	193	90.2	174	3	US-08-495-559-13 Sequence 13, Appl
26	193	90.2	559	4	US-08-956-171E-5251 Sequence 5251, Ap
27	193	90.2	559	4	US-08-781-986A-5251 Sequence 5251, Ap

28	192	89.7	38	4	US-09-010-317-50 Sequence 50, Appl
29	188	87.9	38	4	US-09-010-317-37 Sequence 37, Appl
30	183	85.5	36	4	US-09-010-317-58 Sequence 58, Appl
31	180	84.1	38	1	US-08-234-622A-2 Sequence 2, Appl
32	180	84.1	38	4	US-09-010-317-5 Sequence 5, Appl
33	178	83.2	38	4	US-09-010-317-41 Sequence 41, Appl
34	175	81.8	36	4	US-09-010-317-59 Sequence 59, Appl
35	174	81.3	38	1	US-08-729-767-3 Sequence 3, Appl
36	174	81.3	38	4	US-09-010-317-36 Sequence 36, Appl
37	174	81.3	38	4	US-09-010-317-39 Sequence 39, Appl
38	174	81.3	38	4	US-09-010-317-40 Sequence 40, Appl
39	173	80.8	38	4	US-09-010-317-38 Sequence 38, Appl
40	173	80.8	38	4	US-09-010-317-42 Sequence 42, Appl
41	172	80.4	38	4	US-09-010-317-6 Sequence 6, Appl
42	172	80.4	38	4	US-09-010-317-43 Sequence 43, Appl
43	170	79.4	38	4	US-09-010-317-35 Sequence 35, Appl
44	169.5	79.2	39	4	US-09-010-317-56 Sequence 56, Appl
45	166	77.6	38	4	US-09-010-317-44 Sequence 44, Appl

ALIGNMENTS

RESULT 1
US-09-010-317-47
Sequence 47, Application US/09010317
Patent No. 6685943
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
APPLICANT: Patti, Joseph M.
APPLICANT: House-Pompeo, Karen L.
APPLICANT: Spiale, Pietro
APPLICANT: Jon, Danny
APPLICANT: McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
TITLE OF INVENTION: AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAMK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-5000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 47:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-09-010-317-47
Query Match 100.0%; Score 214; DB 4; Length 38;
Best Local Similarity 100.0%; Pred. No. 3.3e-23;

Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QNKGNSFEDTEKDKPKYEHGNIIDIDPDSVPHHG 38
Db 1 QNKGNSFEDTEKDKPKYEHGNIIDIDPDSVPHHG 38

RESULT 2

US-08-234-622A-3
; Sequence 3, Application US/08234622A
; Patent No. 5440014
; GENERAL INFORMATION:
; APPLICANT: HOOK, Magnus
; APPLICANT: MCGAVIN, Martin
; APPLICANT: RAUCCI, Giuseppe
; TITLE OF INVENTION: A FIBRONECTIN BINDING PEPTIDE
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Doane, Swecker & Mathis
; STREET: P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/234,622A
; FILING DATE: 28-APR-1994
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: SE 9002617-0
; FILING DATE: 10-AUG-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: NO PCT/SE91/00534
; FILING DATE: 09-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Meuth, Donna M
; REGISTRATION NUMBER: 36,607
; REFERENCE/DOCKET NUMBER: 012885-044
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6620
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 38 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-234-622A-3

Query Match 96.3%; Score 206; DB 1; Length 38;
Best Local Similarity 97.4%; Pred. No. 4,4e-22;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QNKGNSFEDTEKDKPKYEHGNIIDIDPDSVPHHG 38
Db 1 QNKGNSFEDTEKDKPKYEHGNIIDIDPDSVPHHG 38

RESULT 3

US-09-010-317-7
; Sequence 7, Application US/09010317
; Patent No. 6685943
; GENERAL INFORMATION:
; APPLICANT: Hook, Magnus
; APPLICANT: Patli, Joseph M.
; APPLICANT: House-Pompeo, Karen L.
; APPLICANT: Speziale, Pietro

; APPLICANT: Joh, Danny
; APPLICANT: McGavin, Martin J.
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
; TITLE OF INVENTION: AND METHODS OF USE
; NUMBER OF SEQUENCES: 105
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: TX
; COUNTRY: USA
; ZIP: 77210-4433

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/010,317
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/036,139
; FILING DATE: 21-JAN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Hibler, David W.
; REGISTRATION NUMBER: 41,071
; REFERENCE/DOCKET NUMBER: TANK:189
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 512-418-3000
; TELEFAX: 512-474-7577
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 38 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
US-09-010-317-7

Query Match 96.3%; Score 206; DB 4; Length 38;
Best Local Similarity 97.4%; Pred. No. 4,4e-22;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QNKGNSFEDTEKDKPKYEHGNIIDIDPDSVPHHG 38
Db 1 QNKGNSFEDTEKDKPKYEHGNIIDIDPDSVPHHG 38

RESULT 4

US-08-259-000-3
; Sequence 3, Application US/08259000
; Patent No. 5571514
; GENERAL INFORMATION:
; APPLICANT: HOOK, Magnus
; APPLICANT: LINDBERG, Martin Kjell
; APPLICANT: SIGNAS, Lars Christer
; APPLICANT: MADSTROM, Torkel Mikael
; APPLICANT: FROMAN, Gunnar
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN AS WELL AS
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Doane, Swecker & Mathis
; STREET: P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/259,000
FILING DATE: 13-JUN-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: SE 8702272-9
FILING DATE: 01-JUN-1987
ATTORNEY/AGENT INFORMATION:
NAME: Meuth, Donna M
REGISTRATION NUMBER: 36,607
REFERENCE/DOCKET NUMBER: 012885-062
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 114 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-259-000-3

Query Match 96.3%; Score 206; DB 1; Length 114;
Best Local Similarity 97.4%; Pred. No. 1,7e-21;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QNKGNSFEDTEKDKPKYEHGNIIDIDPSVPHNG 38
Db 40 QNKGNSFEDTEKDKPKYEHGNIIDIDPSVPHNG 77

RESULT 5
US-08-556-253-8
Sequence 8, Application US/08856253
Patent No. 6288214
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
APPLICANT: Patli, Joseph M.
APPLICANT: House-Pompeo, Karen
APPLICANT: Sthanam, Narayana
APPLICANT: Symersky, Jindrich
TITLE OF INVENTION: COLLAGEN BINDING PROTEIN COMPOSITIONS
TITLE OF INVENTION: AND METHODS OF USE
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: Texas
COUNTRY: U.S.
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/856,253
FILING DATE: Concurrently Herewith
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/017,678
FILING DATE: 16-MAY-1996
ATTORNEY/AGENT INFORMATION:
NAME: Kitchell, Barbara S.
REGISTRATION NUMBER: 33,928
REFERENCE/DOCKET NUMBER: TAWK.193
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
TELEFAX: (512) 474-7577
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:

LENGTH: 139 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-08-556-253-8

Query Match 96.3%; Score 206; DB 3; Length 139;
Best Local Similarity 97.4%; Pred. No. 2.2e-21;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QNKGNSFEDTEKDKPKYEHGNIIDIDPSVPHNG 38
Db 54 QNKGNSFEDTEKDKPKYEHGNIIDIDPSVPHNG 91

RESULT 6
US-08-956-171E-5254
Sequence 5254, Application US/08956171E
Patent No. 6593114
GENERAL INFORMATION:
APPLICANT: Charles Kunsch
Gil H. Choi
Patrick S. Dillon
Craig A. Rosen
Steven C. Barash
Michael R. Fannon
TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
NUMBER OF SEQUENCES: 5256
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COUNTRY: USA
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/956,171E
FILING DATE: 20-Oct-1997
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/009,861
FILING DATE: January 5, 1996
APPLICATION NUMBER: 08/781,986
FILING DATE: January 3, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Mark J. Hyman
REGISTRATION NUMBER: 46,789
REFERENCE/DOCKET NUMBER: PB248P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (240) 314-1224
TELEFAX: (301) 309-8439
INFORMATION FOR SEQ ID NO: 5254:
SEQUENCE CHARACTERISTICS:
LENGTH: 1027 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 5254:
US-08-956-171E-5254

Query Match 96.3%; Score 206; DB 4; Length 1027;
Best Local Similarity 97.4%; Pred. No. 2.5e-20;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QNKGNSFEDTEKDKPKYEHGNIIDIDPSVPHNG 38
Db 793 QNKGNSFEDTEKDKPKYEHGNIIDIDPSVPHNG 830

RESULT 7
US-08-781-986A-5254
Sequence 5254, Application US/08781986A
Patent No. 6737248
GENERAL INFORMATION:
APPLICANT: Charles Kunesch
TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
NUMBER OF SEQUENCES: 5255
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COUNTRY: USA
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4MB storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/781,986A
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
ATTORNEY/AGENT INFORMATION:
NAME: Benson, Bob
REGISTRATION NUMBER: 30,446
REFERENCE/DOCKET NUMBER: PB248PP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 5254:
SEQUENCE CHARACTERISTICS:
LENGTH: 1027 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-781-986A-5254

Query Match 96.3%; Score 206; DB 4; Length 1027;
Best Local Similarity 97.4%; Pred. No. 2.5e-20;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QNKGNSFEPTDKPKYEHGNIIDIDFDSVPHHG 38
DB 793 QNKGNSFEPTDKPKYEHGNIIDIDFDSVPHHG 830

RESULT 8
US-08-459-135A-7
Sequence 7, Application US/08459135A
Patent No. 5955078
GENERAL INFORMATION:
APPLICANT: BURNHAM, Martin Karl Russel
APPLICANT: CHOPRA, Ian Alfred
APPLICANT: CRITCHLEY, Ian Alfred
APPLICANT: KNOWLES, David Justin Charles
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN: MONOCLONAL ANTIBODY AND THEIR US
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
STATE: PA
COUNTRY: U.S.A.
ZIP: 19406-0939
COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: Fastseq, Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/459,135A
FILING DATE: 02-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB/94/00215
FILING DATE: 04-Feb-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Gimm1, Edward R
REGISTRATION NUMBER: 38,891
REFERENCE/DOCKET NUMBER: P30591C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-4478
TELEFAX: 610-270-5090
TELEX:
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 130 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-459-135A-7

Query Match 93.9%; Score 201; DB 2; Length 130;
Best Local Similarity 94.7%; Pred. No. 1e-20;
Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 QNKGNSFEPTDKPKYEHGNIIDIDFDSVPHHG 38
DB 40 QNKGNSFEPTDKPKYEHGNIIDIDFDSVPHHG 77

RESULT 9
US-08-459-135A-8
Sequence 8, Application US/08459135A
Patent No. 5955078
GENERAL INFORMATION:
APPLICANT: BURNHAM, Martin Karl Russel
APPLICANT: CHOPRA, Ian Alfred
APPLICANT: CRITCHLEY, Ian Alfred
APPLICANT: KNOWLES, David Justin Charles
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN: MONOCLONAL ANTIBODY AND THEIR US
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
STATE: PA
COUNTRY: U.S.A.
ZIP: 19406-0939
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: Fastseq, Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/459,135A
FILING DATE: 02-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB/94/00215
FILING DATE: 04-Feb-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Gimm1, Edward R
REGISTRATION NUMBER: 38,891
REFERENCE/DOCKET NUMBER: P30591C2
TELECOMMUNICATION INFORMATION:

TELEPHONE: 610-270-4478
TELEFAX: 610-270-5090
TELEX:
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 130 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-459-135A-8

Query Match 93.9%; Score 201; DB 2; Length 130;
Best Local Similarity 94.7%; Pred. No. 1e-20;
Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 QNKGNSFEPDTEKDKPKYEHGNIIDIDFDSVPHHG 38
DB 40 QNKGDSFEDTEKDKPKYEHGNIIDIDFDSVPHHG 77

RESULT 10
US-08-495-559-7
Sequence 7, Application US/08495559A
Patent No. 6034572
GENERAL INFORMATION:
APPLICANT: BURHAM, Martin Karl Russel
APPLICANT: CHOPRA, Ian
APPLICANT: CRITCHLEY, Ian Alfred
APPLICANT: KNOWLES, David Justin Charles
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN: MONOCLONAL
TITLE OF INVENTION: ANTIBODY AND THEIR USE IN PREVENTING BACTERIAL ADHESION
FILE REFERENCE: P30591
CURRENT APPLICATION NUMBER: US/08/495,559A
CURRENT FILING DATE: 1995-08-03
EARLIER APPLICATION NUMBER: GB 9302289.5
EARLIER FILING DATE: 1993-02-05
EARLIER APPLICATION NUMBER: GB 9321592.9
EARLIER FILING DATE: 1993-10-20
NUMBER OF SEQ ID NOS: 13
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 7
LENGTH: 130
TYPE: PRT
ORGANISM: Staphylococcus aureus
US-08-495-559-7

Query Match 93.9%; Score 201; DB 3; Length 130;
Best Local Similarity 94.7%; Pred. No. 1e-20;
Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 QNKGNSFEPDTEKDKPKYEHGNIIDIDFDSVPHHG 38
DB 40 QNKGDSFEDTEKDKPKYEHGNIIDIDFDSVPHHG 77

RESULT 11
US-08-495-559-8
Sequence 8, Application US/08495559A
Patent No. 6034572
GENERAL INFORMATION:
APPLICANT: BURHAM, Martin Karl Russel
APPLICANT: CHOPRA, Ian
APPLICANT: CRITCHLEY, Ian Alfred
APPLICANT: KNOWLES, David Justin Charles
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN: MONOCLONAL
TITLE OF INVENTION: ANTIBODY AND THEIR USE IN PREVENTING BACTERIAL ADHESION
FILE REFERENCE: P30591
CURRENT APPLICATION NUMBER: US/08/495,559A
CURRENT FILING DATE: 1995-08-03
EARLIER APPLICATION NUMBER: GB 9302289.5
EARLIER FILING DATE: 1993-02-05
EARLIER APPLICATION NUMBER: GB 9321592.9
EARLIER FILING DATE: 1993-10-20

NUMBER OF SEQ ID NOS: 13
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 8
LENGTH: 130
TYPE: PRT
ORGANISM: Staphylococcus aureus
US-08-495-559-8

Query Match 93.9%; Score 201; DB 3; Length 130;
Best Local Similarity 94.7%; Pred. No. 1e-20;
Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 QNKGNSFEPDTEKDKPKYEHGNIIDIDFDSVPHHG 38
DB 40 QNKGDSFEDTEKDKPKYEHGNIIDIDFDSVPHHG 77

RESULT 12
US-08-459-135A-10
Sequence 10, Application US/08459135A
Patent No. 5955078
GENERAL INFORMATION:
APPLICANT: BURHAM, Martin Karl Russel
APPLICANT: CHOPRA, Ian
APPLICANT: CRITCHLEY, Ian Alfred
APPLICANT: KNOWLES, David Justin Charles
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN: MONOCLONAL ANTIBODY AND THEIR USE
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
STATE: PA
COUNTRY: U.S.A.
ZIP: 19406-0939
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq, Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/459,135A
FILING DATE: 02-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB/94/00215
FILING DATE: 04-Feb-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Gimmil, Edward R
REGISTRATION NUMBER: 38,891
REFERENCE/DOCKET NUMBER: P30591C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-4478
TELEFAX: 610-270-5090
TELEX:
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 174 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: Protein
US-08-459-135A-10

Query Match 93.9%; Score 201; DB 2; Length 174;
Best Local Similarity 94.7%; Pred. No. 1e-20;
Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 QNKGNSFEPDTEKDKPKYEHGNIIDIDFDSVPHHG 38
DB 40 QNKGDSFEDTEKDKPKYEHGNIIDIDFDSVPHHG 77

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RESULT 13
US-08-495-559-10
; Sequence 10, Application US/08495559A
; Patent No. 6054572
; GENERAL INFORMATION:
; APPLICANT: BURHAM, Martin Karl Russel
; APPLICANT: CHOPRA, Ian
; APPLICANT: CRITCHLEY, Ian Alfred
; APPLICANT: KNOWLES, David Justin Charles
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN: MONOCLONAL
; TITLE OF INVENTION: ANTIBODY AND THEIR USE IN PREVENTING BACTERIAL ADHESION
; FILE REFERENCE: P30591
; CURRENT APPLICATION NUMBER: US/08/495,559A
; EARLIER FILING DATE: 1995-08-03
; EARLIER APPLICATION NUMBER: GB 9302289.5
; EARLIER FILING DATE: 1993-02-05
; EARLIER APPLICATION NUMBER: GB 9321592.9
; EARLIER FILING DATE: 1993-10-20
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 10
; LENGTH: 174
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-08-495-559-10

Query Match      93.9%; Score 201; DB 3; Length 174;
Best Local Similarity 94.7%; Pred. No. 1,4e-20;
Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1 QNKGNSFEPDTEKDKPKYEHGNIIDIDPDSVPHNG 38
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Db      40 QNKGDSFEPDTEKDKPKYEHGNIIDIDPDSVPHNG 77

RESULT 14
US-08-495-559-6
; Sequence 6, Application US/08495559A
; Patent No. 6054572
; GENERAL INFORMATION:
; APPLICANT: BURHAM, Martin Karl Russel
; APPLICANT: CHOPRA, Ian
; APPLICANT: CRITCHLEY, Ian Alfred
; APPLICANT: KNOWLES, David Justin Charles
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN: MONOCLONAL
; TITLE OF INVENTION: ANTIBODY AND THEIR USE IN PREVENTING BACTERIAL ADHESION
; FILE REFERENCE: P30591
; CURRENT APPLICATION NUMBER: US/08/495,559A
; EARLIER FILING DATE: 1995-08-03
; EARLIER APPLICATION NUMBER: GB 9302289.5
; EARLIER FILING DATE: 1993-02-05
; EARLIER APPLICATION NUMBER: GB 9321592.9
; EARLIER FILING DATE: 1993-10-20
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 176
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-08-495-559-6

Query Match      93.9%; Score 201; DB 3; Length 176
Best Local Similarity 94.7%; Pred. No. 1.5e-20;
Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
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; Patent No. 5955078
; GENERAL INFORMATION:
; APPLICANT: BURHAM, Martin Karl Russel
; APPLICANT: CHOPRA, Ian
; APPLICANT: CRITCHLEY, Ian Alfred
; APPLICANT: KNOWLES, David Justin Charles
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN: MONOCLONAL ANTIBODY AND THEIR USE
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corporation
; STREET: 709 Swedeland Road
; CITY: King of Prussia
; STATE: PA
; COUNTRY: U.S.A.
; ZIP: 19406-0939
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: Fastseq, Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/459,135A
; FILING DATE: 02-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB/94/00215
; FILING DATE: 04-Feb-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Gimm1, Edward R
; REGISTRATION NUMBER: 38,891
; REFERENCE/DOCKET NUMBER: P30591C2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-270-4478
; TELEFAX: 610-270-5090
; TELEX:
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 178 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Protein
US-08-459-135A-12

Query Match      93.9%; Score 201; DB 2; Length 178;
Best Local Similarity 94.7%; Pred. No. 1.5e-20;
Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1 QNKGNSFEPDTEKDKPKYEHGNIIDIDPDSVPHNG 38
      40 QNKGDSFEPDTEKDKPKYEHGNIIDIDPDSVPHNG 77

Db      40 QNKGDSFEPDTEKDKPKYEHGNIIDIDPDSVPHNG 77
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Search completed: October 22, 2005, 05:46:46
Job time : 21.2223 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using SW model

Run on: October 22, 2005, 11:35:03 ; Search time 70.1256 Seconds
(without alignments)
226.232 Million cell updates/sec

Title: US-10-731-238-47

Perfect score: 214
Sequence: 1 QNKGNSFPEPTKDKPKYEHGNIIDFDSVPHITG 38

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1862951 seqs, 417491010 residues

Total number of hits satisfying chosen parameters: 1862951

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database:

1: Published Applications_AA:
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3: /cgn2_6/prodata/2/pubppa/PCT_NEW_PUB.pep:*
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22: /cgn2_6/prodata/2/pubppa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	206	96.3	38	18	US-10-731-238-7
3	206	96.3	139	9	US-09-813-820-8
4	206	96.3	1018	9	US-09-815-242-5797
5	206	96.3	1018	9	US-09-815-242-12838
6	206	96.3	1018	17	US-10-470-048B-68
7	206	96.3	1027	8	US-08-781-986A-5254
8	206	96.3	1027	15	US-10-339-624-5254
9	200	93.0	38	18	US-10-731-238-46
10	199	93.0	38	18	US-10-731-238-48
11	198	92.5	38	18	US-10-731-238-8

12	198	92.5	38	18	US-10-731-238-49	Sequence 49, Appl
13	196	91.6	38	18	US-10-731-238-45	Sequence 45, Appl
14	193	90.2	388	8	US-08-901-062-1	Sequence 1, Appl
15	193	90.2	559	8	US-10-329-624-5251	Sequence 5251, Ap
16	193	90.2	559	15	US-10-329-624-5251	Sequence 5899, Ap
17	193	90.2	767	9	US-09-815-242-5899	Sequence 13140, A
18	193	90.2	767	9	US-09-815-242-13140	Sequence 424, App
19	193	90.2	940	17	US-10-470-048B-424	Sequence 69, Appl
20	193	90.2	948	17	US-10-470-048B-69	Sequence 43827, A
21	193	90.2	1038	15	US-10-282-122A-43827	Sequence 50, Appl
22	192	89.7	38	18	US-10-731-238-37	Sequence 37, Appl
23	188	87.9	38	18	US-10-731-238-37	Sequence 5456, Ap
24	185	86.4	978	9	US-09-815-242-5456	Sequence 12686, A
25	185	86.4	1001	9	US-09-815-242-12686	Sequence 58, Appl
26	183	85.5	36	18	US-10-731-238-58	Sequence 43778, A
27	181	84.6	961	15	US-10-282-122A-43778	Sequence 5, Appl
28	180	84.1	38	18	US-10-731-238-5	Sequence 41, Appl
29	178	83.2	38	18	US-10-731-238-41	Sequence 59, Appl
30	175	81.8	36	18	US-10-731-238-59	Sequence 36, Appl
31	174	81.3	38	18	US-10-731-238-39	Sequence 39, Appl
32	174	81.3	38	18	US-10-731-238-39	Sequence 40, Appl
33	174	81.3	38	18	US-10-731-238-40	Sequence 38, Appl
34	173	80.8	38	18	US-10-731-238-38	Sequence 42, Appl
35	173	80.8	38	18	US-10-731-238-42	Sequence 6, Appl
36	172	80.4	38	18	US-10-731-238-6	Sequence 43, Appl
37	172	80.4	38	18	US-10-731-238-43	Sequence 35, Appl
38	170	79.4	38	18	US-10-731-238-35	Sequence 56, Appl
39	169.5	79.2	39	18	US-10-731-238-56	Sequence 44, Appl
40	166	77.6	38	18	US-10-731-238-44	Sequence 57, Appl
41	161.5	75.5	39	18	US-10-731-238-57	Sequence 1, Appl
42	140	65.4	30	14	US-10-287-821-1	Sequence 2, Appl
43	140	65.4	31	14	US-10-287-821-2	Sequence 1133, Ap
44	85.5	40.0	37	20	US-11-066-697-1134	Sequence 103, App
45	77	36.0	14	18	US-10-731-238-103	

ALIGNMENTS

RESULT 1
US-10-731-238-47
Sequence 47, Application US/1071238
Publication No. US20050123552A1
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
Patel, Joseph M.
House-Pompeo, Karen L.
Speziale, Pietro
Joh, Danny
McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/731.238
FILING DATE: 10-Dec-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/010.317
FILING DATE: 21-Jan-1998
APPLICATION NUMBER: US 60/036,139


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; FILING DATE: 21-JAN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Hibler, David W.
; REGISTRATION NUMBER: 41,071
; REFERENCE/DOCKET NUMBER: TAMK:189
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 512-418-3000
; TELEFAX: 512-474-7577
; INFORMATION FOR SEQ ID NO: 47:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 38 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 47:
US-10-731-238-47

Query Match          100.0%; Score 214; DB 18; Length 38;
Best Local Similarity 100.0%; Pred. No. 1.3e-21;
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  QNKGNSFEPDTEKDKPKYEHGNIIDIDFDSVPHIHG 38
Db      1  QNKGNSFEPDTEKDKPKYEHGNIIDIDFDSVPHIHG 38

RESULT 2
US-10-731-238-7
; Sequence 7, Application US/10731238
; Publication No. US20050123552A1
; GENERAL INFORMATION:
; APPLICANT: Hook, Magnus
;             Patti, Joseph M.
;             House-Pompeo, Karen L.
;             Speziale, Pietro
;             Jon, Danny
;             McGavin, Martin J.
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
; NUMBER OF SEQUENCES: 105
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: TX
; COUNTRY: USA
; ZIP: 77210-4433
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/731,238
; FILING DATE: 10-Dec-2003
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/010,317
; FILING DATE: 21-Jan-1998
; APPLICATION NUMBER: US 60/036,139
; FILING DATE: 21-JAN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Hibler, David W.
; REGISTRATION NUMBER: 41,071
; REFERENCE/DOCKET NUMBER: TAMK:189
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 512-418-3000
; TELEFAX: 512-474-7577
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 38 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
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; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-10-731-238-7

Query Match          96.3%; Score 206; DB 18; Length 38;
Best Local Similarity 97.4%; Pred. No. 1.5e-20;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Db      1  QNKGNSFEPDTEKDKPKYEHGNIIDIDFDSVPHIHG 38

RESULT 3
US-09-813-820-8
; Sequence 8, Application US/09813820
; Patent No. US20020102262A1
; GENERAL INFORMATION:
; APPLICANT: Hook, Magnus
;             Patti, Joseph M.
;             House-Pompeo, Karen
;             Schanam, Narayana
;             Symersky, Jindrich
; TITLE OF INVENTION: COLLAGEN BINDING PROTEIN COMPOSITIONS
; AND METHODS OF USE
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: U.S.
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/813,820
; FILING DATE: 22-Mar-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/856,253
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Kirchell, Barbara S.
; REGISTRATION NUMBER: 33,928
; REFERENCE/DOCKET NUMBER: TAMK:193
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (512) 418-3000
; TELEFAX: (512) 474-7577
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 139 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-09-813-820-8

Query Match          96.3%; Score 206; DB 9; Length 139;
Best Local Similarity 97.4%; Pred. No. 7e-20;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1  QNKGNSFEPDTEKDKPKYEHGNIIDIDFDSVPHIHG 38
Db      54 QNKGNSFEPDTEKDKPKYEHGNIIDIDFDSVPHIHG 91

RESULT 4
US-09-815-242-5797
; Sequence 5797, Application US/09815242
```

```
Patent No. US20020061569A1
GENERAL INFORMATION:
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Karl L.
APPLICANT: Zyskind, Judith W.
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John D.
APPLICANT: Carr, Grant J.
APPLICANT: Yamamoto, Robert T.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in
FILE REFERENCE: ELITRA.01A
CURRENT APPLICATION NUMBER: US/09/815,242
PRIOR FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 5797
LENGTH: 1018
TYPE: PRT
ORGANISM: Staphylococcus aureus
US-09-815-242-5797

Query Match          96.3%; Score 206; DB 9; Length 1018;
Best Local Similarity 97.4%; Pred. No. 7,2e-19;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 QNKGNSFEPDTEKDKPKYEHGNIIDIDPDSVPHING 38
DB      784 QNKGNSFEPDTEKDKPKYEHGNIIDIDPDSVPHING 821

RESULT 5
US-09-815-242-12838
Sequence 12838, Application US/09815242
Patent No. US20020061569A1
GENERAL INFORMATION:
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Karl L.
APPLICANT: Zyskind, Judith W.
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John D.
APPLICANT: Carr, Grant J.
APPLICANT: Yamamoto, Robert T.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in
FILE REFERENCE: ELITRA.01A
CURRENT APPLICATION NUMBER: US/09/815,242
PRIOR FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 5797
LENGTH: 1018
TYPE: PRT
ORGANISM: Staphylococcus aureus
US-09-815-242-5797
```

```
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 12838
LENGTH: 1018
TYPE: PRT
ORGANISM: Staphylococcus aureus
US-09-815-242-12838

Query Match          96.3%; Score 206; DB 9; Length 1018;
Best Local Similarity 97.4%; Pred. No. 7,2e-19;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 QNKGNSFEPDTEKDKPKYEHGNIIDIDPDSVPHING 38
DB      784 QNKGNSFEPDTEKDKPKYEHGNIIDIDPDSVPHING 821

RESULT 6
US-10-470-048B-68
Sequence 68, Application US/10470048B
Publication No. US2005003744A1
GENERAL INFORMATION:
APPLICANT: MEINKE ET AL.
TITLE OF INVENTION: A METHOD FOR IDENTIFICATION, ISOLATION AND PRODUCTION OF
FILE REFERENCE: SONN.035US
CURRENT APPLICATION NUMBER: US/10/470,048B
CURRENT FILING DATE: 2003-07-25
NUMBER OF SEQ ID NOS: 603
SOFTWARE: PatentIn version 3.1
SEQ ID NO 68
LENGTH: 1018
TYPE: PRT
ORGANISM: Staphylococcus aureus
US-10-470-048B-68

Query Match          96.3%; Score 206; DB 17; Length 1018;
Best Local Similarity 97.4%; Pred. No. 7,2e-19;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 QNKGNSFEPDTEKDKPKYEHGNIIDIDPDSVPHING 38
DB      784 QNKGNSFEPDTEKDKPKYEHGNIIDIDPDSVPHING 821

RESULT 7
US-08-781-986A-5254
Sequence 5254, Application US/08781986A
Publication No. US20030054436A1
GENERAL INFORMATION:
APPLICANT: Charles Kunsch
TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
NUMBER OF SEQUENCES: 5255
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COUNTRY: USA
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/781,986A
FILING DATE:
```

```
/ CLASSIFICATION: 435
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER:
/ FILING DATE:
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Benson, Bob
/ REGISTRATION NUMBER: 30,446
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (301) 309-8504
/ TELEFAX: (301) 309-8512
/ INFORMATION FOR SEQ ID NO: 5254:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 1027 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ US-08-781-986A-5254

Query Match          96.3%; Score 206; DB 8; Length 1027;
Best Local Similarity 97.4%; Pred. No. 7,3e-19;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 QNKGNSFEPDTEKDKPKYEHGNGNIIDIDPDSVPHIIG 38
DB      793 QNKGNSFEPDTEKDKPKYEHGNGNIIDIDPDSVPHIIG 830

RESULT 8
US-10-329-624-5254
/ Sequence 5254, Application US/10329624
/ Publication No. US20040043037A1
/ GENERAL INFORMATION:
/ APPLICANT: Charles Kunsch
/           Gil H. Choi
/           Patrick S. Dillon
/           Craig A. Rosen
/           Steven C. Barash
/           Michael R. Fannon
/ TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
/ NUMBER OF SEQUENCES: 5256
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Human Genome Sciences, Inc.
/ STREET: 9410 Key West Avenue
/ CITY: Rockville
/ STATE: Maryland
/ COUNTRY: USA
/ ZIP: 20850
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Diskette, 3.50 inch, 1.4mb storage
/ COMPUTER: HP Vectra 486/33
/ OPERATING SYSTEM: MSDOS version 6.2
/ SOFTWARE: ASCII Text
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/10/329,624
/ FILING DATE: 27-Dec-2002
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/956,171
/ FILING DATE: October 20, 1997
/ APPLICATION NUMBER: 60/009,861
/ FILING DATE: January 5, 1996
/ APPLICATION NUMBER: 08/781,986
/ FILING DATE: January 3, 1997
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Mark J. Hyman
/ REGISTRATION NUMBER: 46,789
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (240) 314-1224
/ TELEFAX: (301) 309-8439
/ INFORMATION FOR SEQ ID NO: 5254:
/ SEQUENCE CHARACTERISTICS:
```

```
/ LENGTH: 1027 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ SEQUENCE DESCRIPTION: SEQ ID NO: 5254:
US-10-329-624-5254

Query Match          96.3%; Score 206; DB 15; Length 1027;
Best Local Similarity 97.4%; Pred. No. 7,3e-19;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 QNKGNSFEPDTEKDKPKYEHGNGNIIDIDPDSVPHIIG 38
DB      793 QNKGNSFEPDTEKDKPKYEHGNGNIIDIDPDSVPHIIG 830

RESULT 9
US-10-731-238-46
/ Sequence 46, Application US/10731238
/ Publication No. US20050123552A1
/ GENERAL INFORMATION:
/ APPLICANT: Hook, Magnus
/           Patti, Joseph M.
/           House-Pompeo, Karen L.
/           Speziale, Pietro
/           Joh, Danny
/           McGavin, Martin J.
/ TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
/ AND METHODS OF USE
/ NUMBER OF SEQUENCES: 105
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Arnold, White & Durkee
/ STREET: P.O. Box 4433
/ CITY: Houston
/ STATE: TX
/ COUNTRY: USA
/ ZIP: 77210-4433
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/10/731,238
/ FILING DATE: 10-Dec-2003
/ CLASSIFICATION: <Unknown>
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US/09/010,317
/ FILING DATE: 21-Jan-1998
/ APPLICATION NUMBER: US 60/036,139
/ FILING DATE: 21-Jan-1997
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Hibler, David W.
/ REGISTRATION NUMBER: 41,071
/ REFERENCE/DOCKET NUMBER: TAMK:189
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 512-418-3000
/ TELEFAX: 512-474-7577
/ INFORMATION FOR SEQ ID NO: 46:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 38 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: <Unknown>
/ TOPOLOGY: linear
/ SEQUENCE DESCRIPTION: SEQ ID NO: 46:
US-10-731-238-46

Query Match          93.5%; Score 200; DB 18; Length 38;
Best Local Similarity 94.7%; Pred. No. 1e-19;
Matches 36; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 QNKGNSFEPDTEKDKPKYEHGNGNIIDIDPDSVPHIIG 38
```

Db 1 QNKGNSFEDTEKDKRYEHGNIIDIDPDSVPHNG 38

RESULT 10

US-10-731-238-48
Sequence 48, Application US/10731238
Publication No. US20050123552A1

GENERAL INFORMATION:

APPLICANT: Hook, Magnus
Patli, Joseph M.
House-Pompeo, Karen L.
Speziale, Pietro
John, Danny

TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
AND METHODS OF USE

NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS: 105

ADDRESSER: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston

STATE: TX
COUNTRY: USA
ZIP: 77210-4433

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/731.238
FILING DATE: 10-Dec-2003
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/010.317
FILING DATE: 21-Jan-1998
APPLICATION NUMBER: US 60/036.139

FILING DATE: 21-Jan-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.

REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAMK:189
TELECOMMUNICATION INFORMATION:

TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577

INFORMATION FOR SEQ ID NO: 48:

SEQUENCE CHARACTERISTICS:

LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>

TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 48:

US-10-731-238-48

Query Match 93.0%; Score 199; DB 18; Length 38;
Best Local Similarity 94.7%; Pred. No. 1,4e-19;

Matches 36; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 QNKGNSFEDTEKDKRYEHGNIIDIDPDSVPHNG 38

Db 1 QNKGNSFEDTEKDKRYEHGNIIDIDPDSVPHNG 38

RESULT 11

US-10-731-238-8
Sequence 8, Application US/10731238
Publication No. US20050123552A1

GENERAL INFORMATION:

APPLICANT: Hook, Magnus
Patli, Joseph M.
House-Pompeo, Karen L.
Speziale, Pietro

John, Danny

McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
AND METHODS OF USE

NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS: 105

ADDRESSER: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston

STATE: TX
COUNTRY: USA
ZIP: 77210-4433

COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/731.238
FILING DATE: 10-Dec-2003
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/010.317
FILING DATE: 21-Jan-1998

APPLICATION NUMBER: US 60/036.139
FILING DATE: 21-Jan-1997
ATTORNEY/AGENT INFORMATION:

NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAMK:189

TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577

INFORMATION FOR SEQ ID NO: 8:

SEQUENCE CHARACTERISTICS:

LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>

TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 8:

US-10-731-238-8

Query Match 92.5%; Score 198; DB 18; Length 38;
Best Local Similarity 94.7%; Pred. No. 1,9e-19;

Matches 36; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 QNKGNSFEDTEKDKRYEHGNIIDIDPDSVPHNG 38

Db 1 QNKGNSFEDTEKDKRYEHGNIIDIDPDSVPHNG 38

US-10-731-238-49

Sequence 49, Application US/10731238
Publication No. US20050123552A1

GENERAL INFORMATION:

APPLICANT: Hook, Magnus
Patli, Joseph M.
House-Pompeo, Karen L.

Speziale, Pietro
John, Danny

McGavin, Martin J.

TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
AND METHODS OF USE

NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS: 105

ADDRESSER: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston

STATE: TX
COUNTRY: USA
ZIP: 77210-4433

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/731,238
FILING DATE: 10-Dec-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE: 21-Jan-1998
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAMK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 49:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 49:
US-10-731-238-49
Query Match 92.5%; Score 198; DB 18; Length 38;
Best Local Similarity 94.7%; Pred. No. 1,9e-19;
Matches 36; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 QNKGNSPEPTDKPKYEHGNIIDIDFDSVPHHG 38
DB 1 QNKGNSPEPTDKPKYEHGNIIDIDFDSVPHHG 38
RESULT 13
US-10-731-238-45
Sequence 45, Application US/10731238
Publication No. US20050123552A1
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
Pacti, Joseph M.
House-Pompeo, Karen L.
Speziale, Pietro
Jon, Danny
McGavin, Martin J.
TITLE OF INVENTION: FIBROBLAST BINDING PROTEIN COMPOSITIONS
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/731,238
FILING DATE: 10-Dec-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE: 21-Jan-1998
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997

ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAMK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 45:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 45:
US-10-731-238-45
Query Match 91.6%; Score 196; DB 18; Length 38;
Best Local Similarity 94.7%; Pred. No. 3,5e-19;
Matches 36; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 QNKGNSPEPTDKPKYEHGNIIDIDFDSVPHHG 38
DB 1 QNKGNSPEPTDKPKYEHGNIIDIDFDSVPHHG 38
RESULT 14
US-08-901-062-1
Sequence 1, Application US/08901062
Publication No. US20020025324A1
GENERAL INFORMATION:
APPLICANT: SEALS, JONATHAN R.
TITLE OF INVENTION: RECOMBINANT BIVALENT BACTERIAL VACCINE
TITLE OF INVENTION: FOR THE PREVENTION OF MASTITIS
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: HALE AND DORR LLP
STREET: 60 State Street
CITY: Boston
STATE: MA
COUNTRY: United States Of America
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/901,062
FILING DATE: 25-JUL-1997
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Baker, Hollie L.
REGISTRATION NUMBER: 31,321
REFERENCE/DOCKET NUMBER: 106941.153
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 526-6000
TELEFAX: (617) 526-5000
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-901-062-1
Query Match 90.2%; Score 193; DB 8; Length 388;
Best Local Similarity 92.1%; Pred. No. 1,4e-17;
Matches 35; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 QNKGNSPEPTDKPKYEHGNIIDIDFDSVPHHG 38

DB 303 QNNGNSFEEDTEKPKYEQGNIDIDFDSVPHHG 340

RESULT 15
US-08-781-986A-5251

; Sequence 5251, Application US/08781986A
; Publication No. US2003005436A1

; GENERAL INFORMATION:

; APPLICANT: Charles Kunsch

; TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences

; NUMBER OF SEQUENCES: 5255

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Human Genome Sciences, Inc.

; STREET: 9410 Key West Avenue

; CITY: Rockville

; STATE: Maryland

; COUNTRY: USA

; ZIP: 20850

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage

; COMPUTER: HP Vectra 486/33

; OPERATING SYSTEM: MSDOS version 6.2

; SOFTWARE: ASCII Text

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/781,986A

; FILING DATE:

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER:

; FILING DATE:

; ATTORNEY/AGENT INFORMATION:

; NAME: Benson, Bob

; REGISTRATION NUMBER: 30,446

; REFERENCE/DOCKET NUMBER: PB248PP

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (301) 309-8504

; TELEFAX: (301) 309-8512

; INFORMATION FOR SEQ ID NO: 5251:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 559 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULAR TYPE: protein

; US-08-781-986A-5251

Query Match 90.2%; Score 193; DB 8; Length 559;

Best local similarity 92.1%; Pred. No. 2,1e-17;

Matches 35; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 ONKNGSFEEDTEKPKYEQGNIDIDFDSVPHHG 38

DB 339 QNNGNSFEEDTEKPKYEQGNIDIDFDSVPHHG 376

Search completed: October 22, 2005, 12:09:29
Job time : 71.1256 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 22, 2005, 04:14:19 ; Search time 13.8905 Seconds
(without alignments)
263.219 Million cell updates/sec

Title: US-10-731-238-47

Perfect score: 214
Sequence: 1 QNKGNSFEPDTEKDKRYEHGNIIDIDFDSVPHIHG 38

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	206	96.3	1018	2 A32192	fibronectin-binding
2	193	90.2	940	2 S19702	fibronectin-binding
3	193	90.2	1038	2 H80053	hypothetical prote
4	181	84.6	961	2 G90053	hypothetical prote
5	60	28.0	214	2 A89895	hypothetical prote
6	56.5	26.4	788	2 T30510	vital enhancing fa
7	54	25.2	284	2 S67062	hypothetical prote
8	54	25.2	442	2 H72266	actB/chur-related
9	54	25.2	658	2 R85024	probable CHP-rich
10	53.5	25.0	169	2 B97562	peptidyl prolyl ci
11	53.5	25.0	169	2 A12782	peptidyl prolyl ci
12	53	24.8	218	2 A95232	ribulose-phosphate
13	53	24.8	218	2 C98096	ribulose-phosphate
14	53	24.8	511	1 S31308	aldehyde dehydrog
15	52.5	24.5	160	2 A01363	single-stranded DN
16	52.5	24.5	317	2 T00146	hypothetical prote
17	52.5	24.5	1007	2 T32285	hypothetical prote
18	52.5	24.5	1952	2 T48814	hypothetical prote
19	52	24.3	113	2 S76792	hypothetical prote
20	52	24.3	333	2 G81132	NiFeR3/SMN family
21	52	24.3	333	2 H81888	hypothetical prote
22	52	24.3	790	2 T47959	hypothetical prote
23	52	24.3	2722	2 T20532	hypothetical prote
24	52	24.3	2738	2 E88320	protein F07A11.6 l
25	52	24.3	2957	2 T33152	hypothetical prote
26	51.5	24.1	328	2 S51458	hypothetical prote
27	51.5	24.1	609	2 A30311	protein kinase C (
28	51.5	24.1	1226	2 S44824	F54P2.1 protein -
29	51	23.8	183	2 D83840	hypothetical prote

30	51	23.8	388	2 S36500	E2 protein - human
31	51	23.8	391	1 S15617	E2 protein - human
32	51	23.8	545	2 G84219	hypothetical prote
33	51	23.8	591	2 C84220	proplyonyl-CoA carb
34	51	23.8	610	2 T22540	hypothetical prote
35	51	23.8	920	2 T18852	hypothetical prote
36	50.5	23.6	203	2 T36102	hypothetical prote
37	50.5	23.6	406	2 H84590	hypothetical prote
38	50.5	23.6	455	2 C95001	Mes/Ycf62 family
39	50.5	23.6	425	2 B97873	conserved hypothet
40	50.5	23.6	952	2 AG1209	B. subtilis Yfho p
41	50	23.4	161	2 T17253	hypothetical prote
42	50	23.4	385	2 S75963	hypothetical prote
43	50	23.4	413	2 T31663	leoleucine-tRNA li
44	49.5	23.1	159	2 AB1445	single-stranded DN
45	49.5	23.1	305	2 D97169	uncharacterized pr

ALIGNMENTS

RESULT 1
A32192
fibronectin-binding protein - Staphylococcus aureus
C:Species: Staphylococcus aureus
C>Date: 31-Jul-1989 #sequence_revision 31-Jul-1989 #text_change 16-Feb-1997
C:Accession: A32192
R:Signaes, C.; Raucchi, G.; Joensson, K.; Lindgren, P.E.; Anantharamaiah, G.M.; Hoeoek,
Proc. Natl. Acad. Sci. U.S.A. 86, 699-703, 1989
A:Title: Nucleotide sequence of the gene for a fibronectin-binding protein from Staphyl
A:Reference number: A32192; MUID:8908998; PMID:2521391
A:Accession: A32192
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1018 <SIG>
A:Cross-references: GB:J04151
C:Keywords: fibronectin binding

Query Match 96.3%; Score 206; DB 2; Length 1018;
Best Local Similarity 97.4%; Pred. No. 2.2e-19;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QNKGNSFEPDTEKDKRYEHGNIIDIDFDSVPHIHG 38
Db 784 QNKGNSFEPDTEKDKRYEHGNIIDIDFDSVPHIHG 821

RESULT 2

S19702
fibronectin-binding protein B - Staphylococcus aureus
C:Species: Staphylococcus aureus
C>Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
C:Accession: S19702
R:Joensson, K.; Signaes, C.; Mueller, H.P.; Lindberg, M.
Eur. J. Biochem. 202, 1041-1048, 1991
A:Title: Two different genes encode fibronectin binding proteins in Staphylococcus aure
A:Reference number: S19702; MUID:92111475; PMID:1837266
A:Accession: S19702
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-940 <JOB>
A:Cross-references: UNIPROT:Q53682; EMBL:X62992; NID:949040; PIDD:CAA44726.1; PID:95815
C:Keywords: fibronectin binding

Query Match 90.2%; Score 193; DB 2; Length 940;
Best Local Similarity 92.1%; Pred. No. 1.1e-17;
Matches 35; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 QNKGNSFEPDTEKDKRYEHGNIIDIDFDSVPHIHG 38
Db 720 QNKGNSFEPDTEKDKRYEHGNIIDIDFDSVPHIHG 757

RESULT 3

hypothetical protein fmb [imported] - Staphylococcus aureus (strain N315)
H90053
C/Species: Staphylococcus aureus
C/Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C/Accession: H90053
R/Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Ogura, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kato, C.; Sekimizu, K.; C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
A/Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.
A/Reference number: A89758; PMID:21311952; PMID:11418146
A/Accession: H90053
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-1038 <KUR>
A/Cross-references: UNIPROT:Q99RD2; GB:BA000018; PID:g13702453; PIDN:BA843594.1; GSPDB:G
A/Experimental source: strain N315
C/Genetics:
A/Gene: fmb

Query Match 90.2%; Score 193; DB 2; Length 1038;
Best Local Similarity 92.1%; Pred. No. 1.2e-17;
Matches 35; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 QNKGNSFEDTEKDKRYEHGNIIDIDPDSPVPHIHG 38
|||||

DB 780 QNKGNSFEDTEKDKRYEHGNIIDIDPDSPVPHIHG 817
|||||

RESULT 4

hypothetical protein fmb [imported] - Staphylococcus aureus (strain N315)
G90053
C/Species: Staphylococcus aureus
C/Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C/Accession: G90053
R/Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Ogura, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kato, C.; Sekimizu, K.; C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
A/Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.
A/Reference number: A89758; PMID:21311952; PMID:11418146
A/Accession: G90053
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-961 <KUR>
A/Cross-references: UNIPROT:Q99RD3; GB:BA000018; PID:g13702452; PIDN:BA843593.1; GSPDB:G
A/Experimental source: strain N315
C/Genetics:
A/Gene: fmb

Query Match 84.6%; Score 181; DB 2; Length 961;
Best Local Similarity 86.8%; Pred. No. 4.7e-16;
Matches 33; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 QNKGNSFEDTEKDKRYEHGNIIDIDPDSPVPHIHG 38
|||||

DB 731 QNKGNSFEDTEKDKRYEHGNIIDIDPDSPVPHIHG 768
|||||

RESULT 5

hypothetical protein cfxE [imported] - Staphylococcus aureus (strain N315)
A89895
C/Species: Staphylococcus aureus
C/Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C/Accession: A89895
R/Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Ogura, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kato, C.; Sekimizu, K.; C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
A/Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.
A/Reference number: A89758; PMID:21311952; PMID:11418146
A/Accession: A89895

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-214 <KUR>

A/Cross-references: UNIPROT:Q99UP6; GB:BA000018; PID:g13701022; PIDN:BA842317.1; GSPDB:G

A/Experimental source: strain N315

C/Genetics:

A/Gene: cfxE

C/Superfamily: yeast ribulose-5-phosphate-epimerase

Query Match 28.0%; Score 60; DB 2; Length 214;
Best Local Similarity 55.6%; Pred. No. 1.6;
Matches 10; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 20 EHGADMIHSTPHIH 37
|||||

DB 80 EHGADMIHSTPHIH 97
|||||

RESULT 6

vital enhancing factor 2 - Lymantria dispar nuclear polyhedrosis virus
T30510
C/Species: Lymantria dispar nuclear polyhedrosis virus, LdMNPV
C/Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
C/Accession: T30510
R/Kuzio, J.; Pearson, M.N.; Harwood, S.H.; Funk, C.J.; Evans, J.T.; Slavicek, J.M.; Rohlf, Virology 253, 17-34, 1999
A/Title: Sequence and analysis of the genome of a baculovirus pathogenic for Lymantria dispar.
A/Reference number: Z20836; PMID:99124785; PMID:9887315
A/Accession: T30510
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-788 <KUZ>
A/Cross-references: UNIPROT:Q9YMG8; EMBL:AF081810; PIDN:AC70346.1

Query Match 26.4%; Score 56.5; DB 2; Length 788;
Best Local Similarity 54.5%; Pred. No. 21;
Matches 12; Conservative 1; Mismatches 4; Indels 5; Gaps 1;

QY 17 PKYEHGNIIDIDF-----DSV 33
|||||

DB 114 PKYEHGNAVADFKRMRDSV 135
|||||

RESULT 7

hypothetical protein YOR174w - yeast (Saccharomyces cerevisiae)
S67062
N/Alternate names: hypothetical protein O3630
C/Species: Saccharomyces cerevisiae
C/Date: 12-Jul-1996 #sequence_revision 12-Jul-1996 #text_change 09-Jul-2004
C/Accession: S67062; S67066
R/Bordone, R.; Camasses, A.; Madania, A.; Martin, R.P.; Poch, O.; Tarasov, I.A.; Wine, submitted to the Protein Sequence Database, July 1996
A/Reference number: S67032
A/Accession: S67062
A/Molecule type: DNA
A/Residues: 1-284 <BOR>
A/Cross-references: UNIPROT:Q12143; EMBL:Z75082; NID:g1420422; PID:e252055; PID:g1420422
A/Experimental source: strain S288C
R/Hughes, B.; Pohl, T.M.
submitted to the Protein Sequence Database, July 1996
A/Reference number: S66685
A/Accession: S67066
A/Molecule type: DNA
A/Residues: 1-284 <HUG>
A/Cross-references: EMBL:Z75082; NID:g1420422; PID:e252055; PID:g1420423; MIPS:YOR174w
A/Experimental source: strain S288C
C/Genetics:
A/Gene: SGD:MED4
A/Cross-references: SGD:S0005700
A/Map position: 15R

Query Match 25.2%; Score 54; DB 2; Length 284;
Best Local Similarity 43.5%; Pred. No. 14;

Matches 10; Conservative 4; Mismatches 9; Indels 0; Gaps 0;
Qy 9 EPPTEKDKPKYEHGNIIDIDFDSVPHI 31
Db 255 EADNTKDKKEENNDALDLD 277

RESULT 8
H72266
asEB/chur-related protein - Thermotoga maritima (strain MSB8)

C/Species: Thermotoga maritima
C/Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004

C/Accession: H72266
R/Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.V.; Haft, D.H.; Hickey
Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.;
C.M.

Nature 399, 323-329, 1999

A/Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome seq

A/Reference number: A72200; MUID:59287316; PMID:10360571

A/Accession: H72266

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-442 <AN>

A/Cross-references: UNIPROT:Q9Y147; GB:AE001787; GB:AE000512; NID:94981882; PIDN:AD3639

A/Experimental source: strain MSB8

C/Genetics:

A/Map position: TM1324

Query Match 25.2%; Score 54; DB 2; Length 442;

Best Local Similarity 35.3%; Pred. No. 24;

Matches 12; Conservative 5; Mismatches 11; Indels 6; Gaps 1;

Qy 9 EPPTE-----KDKPKYEHGNIIDIDFDSVPHI 36

Db 44 DPDEIRPEEWLSIKKDIYGVYDDEPDEIHL 77

RESULT 9
F85024
probable CHP-rich zinc finger protein [imported] - Arabidopsis thaliana

C/Species: Arabidopsis thaliana (mouse-ear cress)

C/Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004

C/Accession: F85024

R/anonymous, The European Union Arabidopsis Genome Sequencing Consortium, The Cold Spring

Nature 402, 769-777, 1999

A/Title: Sequence and analysis of chromosome 4 of the plant Arabidopsis thaliana.

A/Reference number: A85001; MUID:20083488; PMID:10617198

A/Accession: F85024

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-658 <STO>

A/Cross-references: UNIPROT:Q9SY19; GB:NC_001268; NID:97268576; PIDN:CAB80685.1; GSPDB:C

C/Genetics:

A/Map position: 4

Query Match 25.2%; Score 54; DB 2; Length 658;

Best Local Similarity 30.8%; Pred. No. 38;

Matches 12; Conservative 9; Mismatches 16; Indels 2; Gaps 1;

Qy 1 QNKGNSFEPTEKDKPKYEHGNIIDIDFDSVPHI 37

Db 448 KDEGRCYACDRLNGFKYGNKAFVRCISISEPHI 486

RESULT 10
B97562

peptidyl prolyl cis-trans isomerase (AF203881) [imported] - Agrobacterium tumefaciens (8

C/Species: Agrobacterium tumefaciens

C/Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 09-Jul-2004

C/Accession: B97562

R/Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman,

A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.;

Science 294, 2323-2328, 2001

A/Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum

A/Reference number: A97359; MUID:21608551; PMID:11743194

A/Accession: B97562

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-169 <KUR>

A/Cross-references: UNIPROT:Q8UE86; GB:AE007869; PIDN:AAK87451.1; PID:915156769; GSPDB:C

C/Genetics:

A/Map position: circular chromosome

C/Superfamily: peptidylprolyl isomerase; cyclophilin homology

Query Match 25.0%; Score 53.5; DB 2; Length 169;

Best Local Similarity 31.0%; Pred. No. 8.9;

Matches 13; Conservative 7; Mismatches 7; Indels 15; Gaps 2;

Qy 3 KGNQSFEP-----DTEKDKPKYEHGNIIDIDFDSVPHI 38

Db 69 KGSESRFPARAGSGSEKEDLKA-----FSALPHVRG 101

RESULT 11
A12782

peptidyl prolyl cis-trans isomerase [imported] - Agrobacterium tumefaciens (strain C58,

C/Species: Agrobacterium tumefaciens

C/Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 09-Jul-2004

C/Accession: A12782

R/Wood, D.W.; Secubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, 'I

erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kutyavln, T.; Levy, R.; Li, M.; Mccliel

, Karp, P.; Romero, P.; Zhang, S.

Science 294, 2317-2323, 2001

A/Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,

ster, B.W.

A/Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.

A/Reference number: AB2577; MUID:21608550; PMID:11743193

A/Accession: A12782

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-169 <KUR>

A/Cross-references: UNIPROT:Q8UE86; GB:AE00688; PIDN:AA42679.1; PID:917740113; GSPDB:C

A/Experimental source: strain C58 (Dupont)

C/Genetics:

A/Map position: circular chromosome

C/Superfamily: peptidylprolyl isomerase; cyclophilin homology

Query Match 25.0%; Score 53.5; DB 2; Length 169;

Best Local Similarity 31.0%; Pred. No. 8.9;

Matches 13; Conservative 7; Mismatches 7; Indels 15; Gaps 2;

Qy 3 KGNQSFEP-----DTEKDKPKYEHGNIIDIDFDSVPHI 38

Db 69 KGSESRFPARAGSGSEKEDLKA-----FSALPHVRG 101

RESULT 12
A95232

ribulose-phosphate 3-epimerase [imported] - Streptococcus pneumoniae (strain TIGR4)

C/Species: Streptococcus pneumoniae

C/Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 09-Jul-2004

C/Accession: A95232

R/Rettelin, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Hei

son, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapfle,

neon, T.; Hickey, E.K.; Holt, I.E.

Science 293, 498-506, 2001

A/Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison

A/Title: Complete Genome Sequence of a virulent isolate of Streptococcus pneumoniae.

A/Reference number: A95000; MUID:21357209; PMID:11463916

A/Accession: A95232

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-218 <KUR>

A:Cross-references: UNIPROT:Q97NN7; GB:AE005672; PIDN:AAK76050.1; PID:gl4973490; GSPDB:C
 A:Experimental source: strain TIGR4
 C:Genetics:
 A:Gene: SP1983
 C:Superfamily: yeast ribulose-5-phosphate-epimerase

Query Match 24.8%; Score 53; DB 2; Length 218;
 Best Local Similarity 52.9%; Pred. No. 14;
 Matches 9; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

OY 22 GGNIIDPDSVPHHG 38
 DB 84 GADIISIHVATPHHG 100

RESULT 13

C98096
 ribulose-phosphate 3-epimerase (EC 5.1.3.1) [imported] - Streptococcus pneumoniae (strain
 C:Species: Streptococcus pneumoniae
 C:Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 09-Jul-2004
 C:Accession: C98096

R:Hosts: J.A.; Albom Jr., W.; Arnold, J.; Blaszcak, L.; Burgett, S.; Dehoff, B.S.; E
 e, R.; Leblanc, D.J.; Lee, L.N.; Lefkowitz, E.J.; Lu, J.; Matsushima, P.; McAhren, S.; M
 y, P.; Sun, P.M.; Winkler, M.E.
 J. Bacteriol. 183, 5709-5717, 2001
 A:Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baliz, R.H.; Jaekunas, S.R.;
 A:Title: Genome of the Bacterium Streptococcus pneumoniae Strain Ke.
 A:Reference number: A97872; MUID:21429245; PMID:11544234

A:Accession: C98096
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-218 <RUI>
 A:Cross-references: UNIPROT:Q8NDN5; GB:AE007317; PIDN:ALU0600.1; PID:gl5459482; GSPDB:C

C:Genetics:
 A:Gene: rpe
 C:Superfamily: yeast ribulose-5-phosphate-epimerase
 C:Keywords: isomerase

Query Match 24.8%; Score 53; DB 2; Length 218;
 Best Local Similarity 52.9%; Pred. No. 14;
 Matches 9; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

OY 22 GGNIIDPDSVPHHG 38
 DB 84 GADIISIHVATPHHG 100

RESULT 14

S31308
 aldehyde dehydrogenase (NAD) (EC 1.2.1.3) 2 precursor, mitochondrial - yeast (Saccharomy
 C:Species: Saccharomyces cerevisiae
 C:Date: 28-May-1993 #sequence_revision 31-Jan-1997 #text_change 09-Jul-2004
 C:Accession: S31308

R:Phien, J
 submitted to the EMBL Data Library, October 1992
 A:Reference number: S31308
 A:Accession: S31308
 A:Molecule type: DNA
 A:Residues: 1-511 <THI>

A:Cross-references: UNIPROT:P32872; EMBL:Z17314; NID:g3361; PID:CAA78962.1; PID:g3362
 C:Comment: This form is probably mitochondrial.
 C:Genetics:

A:Gene: ALD2
 C:Function:
 A:Description: catalyzes the oxidation of an aldehyde to an acid using NAD+ and water
 A:Note: enzymes with this activity are involved in diverse metabolic pathways in various
 C:Superfamily: NAD-dependent aldehyde dehydrogenase; aldehyde dehydrogenase homology
 C:Keywords: alcohol metabolism; mitochondrion; NAD; oxidoreductase

F:1-21/Domain: transit peptide (mitochondrion) #status predicted <TMP>
 F:22-511/Product: aldehyde dehydrogenase (NAD+) 2 #status predicted <MAT>
 F:80-351/Domain: aldehyde dehydrogenase homology <ALDD>
 F:297-331/Active site: GLU Cys #status predicted
 F:403/Binding site: NAD (Cys) #status predicted

Query Match 24.8%; Score 53; DB 1; Length 511;
 Best Local Similarity 39.4%; Pred. No. 38;
 Matches 13; Conservative 5; Mismatches 7; Indels 8; Gaps 2;

OY 4 GNSFEPTEKDKPKYHGGNIIDPDSVPHI 36
 DB 361 GN-PFESDT-----RYGPQIKIEPDSIPRL 385

RESULT 15

AD1363
 single-stranded DNA-binding protein homolog lmo2308 [imported] - Listeria monocytogenes
 C:Species: Listeria monocytogenes
 C:Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004

C:Accession: AD1363
 R:Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloeker
 .; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurgey, O.; Entian, K.D.; Fainl, H
 D.; Jones, L.M.; Karst, U.
 Science 294, 849-852, 2001

A:Authors: Kref, J.; Kuhn, M.; Kunst, F.; Kurapk, G.; Madueno, E.; Maitournam, A.; Ma
 ok, C.; Schlueter, T.; Simoes, N.; Tietze, A.; Vazquez-Boland, J.A.; Voos, H.; Wehland,
 A:Title: Comparative genomes of Listeria species.
 A:Reference number: AB1077; MUID:21537279; PMID:11679669

A:Accession: AD1363
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-160 <GLA>

A:Cross-references: UNIPROT:Q8Y4X1; GB:NC_003210; PIDN:CAD00386.1; PID:gl6411778; GSPDB
 A:Experimental source: strain EGD-e
 C:Genetics:

A:Gene: lmo2308
 C:Superfamily: single-strand binding protein; single-stranded DNA-binding protein homolo

Query Match 24.5%; Score 52.5; DB 2; Length 160;
 Best Local Similarity 31.7%; Pred. No. 11;
 Matches 13; Conservative 5; Mismatches 16; Indels 7; Gaps 1;

OY 1 QNKGK-----QSFEPTEKDKPKYHGGNIIDPDSVP 34
 DB 119 QKNKYSNNQTSYRADTSQKSDSPASGKPRIDNEDLP 159

Search completed: October 22, 2005, 06:09:54
 Job time : 14.8905 secs

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OM protein - protein search, using sw model

Run on: October 22, 2005, 04:10:49 ; Search time 69.6361 Seconds
(without alignments)
279.439 Million cell updates/sec

Title: US-10-731-238-47

Perfect score: 214
Sequence: 1 QNKGNSFEDTEKDKPKTEHGSNIIDIPDSVPHIHG 38

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_03 : *
1: uniprot_sprot : *
2: uniprot_trembl : *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	206	96.3	1018	1 FNBA_STAU	P14738 staphylococ
2	201	93.9	943	2 Q8NUT8	Q8NUT8 staphylococ
3	201	93.9	957	2 Q6G6H4	Q6G6H4 staphylococ
4	198	92.5	152	2 Q9ABP9	Q9ABP9 staphylococ
5	193	90.2	940	2 Q51682	Q51682 staphylococ
6	193	90.2	1038	2 Q99RD2	Q99RD2 staphylococ
7	193	90.2	1038	2 Q7A3J7	Q7A3J7 staphylococ
8	185	86.4	1015	2 Q8NUT7	Q8NUT7 staphylococ
9	185	86.4	1015	2 Q6G6H3	Q6G6H3 staphylococ
10	181	84.6	961	2 Q99RD3	Q99RD3 staphylococ
11	181	84.6	961	2 Q7A3J8	Q7A3J8 staphylococ
12	181	84.6	965	2 Q6GDU5	Q6GDU5 staphylococ
13	63	29.4	367	1 COBD_THETN	COBD_THETN
14	61.5	28.7	904	2 Q54324	Q54324 sulfolobus
15	60	28.0	214	2 Q99UP6	Q99UP6 staphylococ
16	60	28.0	214	2 Q7A126	Q7A126 staphylococ
17	60	28.0	214	2 Q7A527	Q7A527 staphylococ
18	60	28.0	214	2 Q6G9Z1	Q6G9Z1 staphylococ
19	60	28.0	214	2 Q6GHL3	Q6GHL3 staphylococ
20	59	27.6	716	2 Q7RB60	Q7RB60 plasmodium
21	59	27.6	979	2 Q7RNJ1	Q7RNJ1 plasmodium
22	58.5	27.3	101	2 Q68YV3	Q68YV3 vaccinium c
23	58	27.1	470	2 Q6K182	Q6K182 mycoplasma
24	57.5	26.9	626	2 Q6D823	Q6D823 erwina car
25	57.5	26.9	188	2 Q9HEC9	Q9HEC9 neurospora
26	57	26.6	188	1 SGB_ENTFA	SGB_ENTFA
27	57	26.6	644	2 Q6MEU6	Q6MEU6 enterococcu
28	57	26.6	644	2 Q41940	Q41940 murid herpe
29	57	26.6	644	2 Q83342	Q83342 murid herpe
30	57	26.6	2049	2 Q8IDA9	Q8IDA9 plasmodium d
31	56.5	26.4	788	2 Q9YWG8	Q9YWG8 lymantria d

ALIGNMENTS

RESULT 1	FNBA_STAU	STANDARD;	PRT;	1018 AA.
AC P14738;				
DT 01-APR-1990 (Rel. 14, Created)				
DT 01-APR-1990 (Rel. 14, Last sequence update)				
DT 25-OCT-2004 (Rel. 45, Last annotation update)				
DE Fibronectin-binding protein precursor (FNBP).				
GN Name=fnba;				
OS Staphylococcus aureus.				
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.				
OX NCBI_TaxID=1280;				
RN [1]				
RP SEQUENCE FROM N.A.				
RC STRAIN=NCTC 8325-4;				
RX MEDLINE=89098998; PubMed=2521391;				
RA Signaes C., Raucel G., Joensson K., Lindgren P.-E.,				
RA Anantharamiah G.M., Hoock M., Lindberg M.;				
RT "Nucleotide sequence of the gene for a fibronectin-binding protein				
RT from Staphylococcus aureus: use of this peptide sequence in the				
RT synthesis of biologically active peptides."				
RL Proc. Natl. Acad. Sci. U.S.A. 86:699-703(1989).				
CC -1- FUNCTION: The ability of bacteria to bind fibronectin has been				
CC proposed as a virulence factor enabling bacteria to colonize wound				
CC tissues and blood clots. Binding of plasma fibronectin to the				
CC bacterial surface might block adhesion receptors on S.aureus, thus				
CC representing an important defense mechanism against tissue				
CC invasion.				
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by				
CC an amide bond (Potential).				
CC -----				
CC This SWISS-PROT entry is copyright. It is produced through a collaboration				
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -				
CC the European Bioinformatics Institute. There are no restrictions on its				
CC use by non-profit institutions as long as its content is in no way				
CC modified and this statement is not removed. Usage by and for commercial				
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/				
CC or send an email to license@isb-sib.ch).				
CC -----				
CC EMBL: J04151; AAA26632.1; -;				
DR InterPro: IPR004237; Fn_bind.				
DR InterPro: IPR005877; Gpos_XSIRK.				
DR InterPro: IPR001899; Gram_pos_anchor.				
DR Pfam: PF02986; Fn_bind. 1.				
DR Pfam: PF00746; Gram_pos_anchor; 1.				
DR Pfam: PF04650; XSIRK_signal; 1.				
DR TIGRFAMs: TIGR01167; LpxNG_anchor; 1.				
DR TIGRFAMs: TIGR01166; XSIRK_signal; 1.				
DR PROSITE: PS50847; GRAM_POS_ANCHORING; 1.				
DR Cell adhesion; Cell wall; Peptidoglycan-anchor; Repeat; Signal;				
DR Virulence.				
FT SIGNAL 1 36				
FT CHAIN 37 985				
FT PROPEP 986 1018				
				Fibronectin-binding protein.
				Removed by sortase (Potential).

32	56.5	26.4	844	2	Q7SH90	Q7SH90 oryza sativ
33	56.5	26.4	1257	2	Q6BM72	Q6BM72 debaromyce
34	55.5	25.9	889	1	ZCHR_HUMAN	ZCHR_HUMAN homo sapien
35	55	25.7	288	2	Q761A0	Q761A0 chinese yam
36	55	25.7	288	2	Q761A1	Q761A1 chinese yam
37	55	25.7	288	2	Q761A2	Q761A2 chinese yam
38	55	25.7	288	2	Q761A3	Q761A3 chinese yam
39	55	25.7	288	2	Q761A4	Q761A4 chinese yam
40	55	25.7	288	2	Q761A5	Q761A5 chinese yam
41	55	25.7	288	2	Q761A6	Q761A6 chinese yam
42	55	25.7	288	2	Q761A7	Q761A7 chinese yam
43	55	25.7	288	2	Q761A8	Q761A8 chinese yam
44	55	25.7	288	2	Q761A9	Q761A9 chinese yam
45	55	25.7	288	2	Q761B0	Q761B0 chinese yam

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FT REPEAT 545 574 B-1.
FT REPEAT 575 604 B-2.
FT DOMAIN 745 878 4 X approximate tandem repeats,
FT fibronectin-binding domain.
FT REPEAT 745 782 D-1.
FT REPEAT 763 820 D-2.
FT REPEAT 821 859 D-3.
FT REPEAT 860 878 D-4 (incomplete).
FT DOMAIN 879 948 5 X tandem repeats, Pro-rich (WR).
FT REPEAT 879 892 WR 1.
FT REPEAT 893 906 WR 2.
FT REPEAT 907 920 WR 3.
FT REPEAT 921 934 WR 4.
FT REPEAT 935 948 WR 5.
FT SITE 982 986 LpXTG sorting signal (Potential).
FT MOD_RES 985 985 Pentaglycyl murein peptidoglycan amidated
FT threonine (Potential).
SQ SEQUENCE 1018 AA; 111780 MW; 58175E0020E81F1F CRC64;

Query Match 96.3%; Score 206; DB 1; Length 1013;
Best Local Similarity 97.4%; Pred. No. 3.4e-18;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QNKGNSFEPDTEKDKPKYEHGNIIDIDFDSVPHIHG 38
DB 784 QNKGNSFEPDTEKDKPKYEHGNIIDIDFDSVPHIHG 821

RESULT 2
Q8NU8 PRELIMINARY; PRT; 943 AA.
ID Q8NU8
AC Q8NU8;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE FndB protein.
GN Name=fndB; Ordered locus names=NM_420;
OS Staphylococcus aureus (strain MW2).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=196620;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NM2;
RA MEDLINE=22040717; PubMed=12044378; DOI=10.1016/S0140-6736(12)08713-5;
RA Baba T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Oguchi A.,
RA Nagai Y., Iwama N., Amano K., Naito T., Kuroda H., Cui L.,
RA Yamamoto K., Hiramoto K.;
RT "Genome and virulence determinants of high virulence community-
RT acquired MRSA."
RL Lancet 359:1819-1827(2002).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC an amide bond (By similarity).
EMBL: AF004830; BAB96285.1; -.
DR HSSP: Q53653; 1N67.
DR GO: GO:000986; C:cell surface; IEA.
DR GO: GO:0005618; C:cell wall; IEA.
DR GO: GO:0009775; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO: GO:0016020; C:membrane; IEA.
DR GO: GO:0007155; P:cell adhesion; IEA.
DR InterPro: IPR008966; Adhes_bact.
DR InterPro: IPR004237; Fn_bind.
DR InterPro: IPR005877; Gpos_YsIRK.
DR InterPro: IPR001899; Gram_pos_anchor.
DR Pfam: PF02986; Fn_bind_1.
DR Pfam: PF00746; Gram_pos_anchor; 1.
DR TIGRfam: TIGR01167; LpXTG_anchor; 1.
DR TIGRfam: TIGR01168; YsIRK_signal; 1.
DR PROSITE: PS50847; GRAM_POS_ANCHORING; 1.
KM Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ SEQUENCE 943 AA; 104537 MW; DA8A5F31947E1B6A CRC64;

Query Match 93.9%; Score 201; DB 2; Length 943.

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Best Local Similarity 94.7%; Pred. No. 1.4e-17;
Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 QNKGNSFEPDTEKDKPKYEHGNIIDIDFDSVPHIHG 38
DB 727 QNKGNSFEPDTEKDKPKYEHGNIIDIDFDSVPHIHG 764

RESULT 3
ID Q6G6H4 PRELIMINARY; PRT; 957 AA.
AC Q6G6H4;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Fibronectin-binding protein.
GN Name=fndB; Ordered locus names=SAS2387;
OS Staphylococcus aureus (strain MSSA476).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=282459;
RN [1]
RP SEQUENCE FROM N.A.
RC PubMed=15213324; DOI=10.1073/pnas.0402521101;
RX Holden M.T.G., Fell E.J., Linday J.A., Peacock S.J., Day N.P.J.,
RA Enright M.C., Foster T.J., Moore C.E., Hurst L., Atkin R., Barron A.,
RA Bason N., Bentley S.D., Chillingworth C., Chillingworth T.,
RA Churcher C., Clark L., Cotton C., Cronin A., Doggett J., Dowd L.,
RA Fellwell T., Hance Z., Harris B., Hauser H., Holroyd S., Jagels K.,
RA James K.D., Lennard N., Line A., Mayes R., Moule S., Mungall K.,
RA Ormond D., Quail M.A., Rabinowitch E., Rutherford K.M., Sanders M.,
RA Sharp S., Simmonds M., Stevens K., Whitehead S., Barrett B.G.,
RA Spratt B.G., Parkhill J.;
RT "Complete genomes of two clinical Staphylococcus aureus strains:
RT evidence for the rapid evolution of virulence and drug resistance."
RL Proc. Natl. Acad. Sci. U.S.A. 101:9786-9791(2004).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC an amide bond (By similarity).
EMBL: BX571857; CAG44201.1; -.
DR GO: GO:000986; C:cell surface; IEA.
DR GO: GO:0005618; C:cell wall; IEA.
DR GO: GO:0009775; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO: GO:0016020; C:membrane; IEA.
DR GO: GO:0007155; P:cell adhesion; IEA.
DR InterPro: IPR008966; Adhes_bact.
DR InterPro: IPR004237; Fn_bind.
DR InterPro: IPR005877; Gpos_YsIRK.
DR InterPro: IPR001899; Gram_pos_anchor.
DR Pfam: PF02986; Fn_bind_1.
DR Pfam: PF00746; Gram_pos_anchor; 1.
DR TIGRfam: TIGR01167; LpXTG_signal; 1.
DR TIGRfam: TIGR01168; YsIRK_signal; 1.
DR PROSITE: PS50847; GRAM_POS_ANCHORING; 1.
KM Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ SEQUENCE 957 AA; 105980 MW; 28F8BA7FFDFD3EAF CRC64;

Query Match 93.9%; Score 201; DB 2; Length 957;
Best Local Similarity 94.7%; Pred. No. 1.5e-17;
Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 QNKGNSFEPDTEKDKPKYEHGNIIDIDFDSVPHIHG 38
DB 727 QNKGNSFEPDTEKDKPKYEHGNIIDIDFDSVPHIHG 764

RESULT 4
ID Q9AEP9 PRELIMINARY; PRT; 152 AA.
AC Q9AEP9;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Fibronectin-binding protein (Fragment).

```

GN Name=fnd;
 OS Staphylococcus aureus.
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 OX NCBI_TaxId=1280;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CMRSA-1;
 RX MEDLINE=21246681; PubMed=11349044;
 RI DOI=10.1128/IAI.69.6.3791-3799.2001;
 RA Rice K., Huesca M., Vaz D., McGavin M.J.;
 RT "variance in fibronectin binding and fnb locus polymorphisms in
 RT Staphylococcus aureus: identification of antigenic variation in a
 RT fibronectin binding protein adhesin of the epidemic CMRSA-1 strain of
 RT methicillin-resistant S. aureus.";
 RL Infect. Immun. 69:3791-3799 (2001).
 DR EMBL: AY029184; AAK31588.1; -
 FT NON_TER 1 152
 FT SEQUENCE 152 AA; 17193 MW; CPA3913C2B11C025 CRC64;
 SQ

Query Match 92.5%; Score 198; DB 2; Length 152;
 Best Local Similarity 94.7%; Pred. No. 4.5e-18;
 Matches 36; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 ONKNGSFEPDTEKDKPKYEHGNIIDIDFDSVPHING 38
 DB 77 ONKNGSFEPDTEKDKPKYEHGNIIDIDFDSVPHING 114

RESULT 5
 ID O53682 PRELIMINARY; PRT; 940 AA.
 AC O53682;
 DT 01-NOV-1996 (TREMblrel. 01, Created)
 DT 01-NOV-1996 (TREMblrel. 01, Last sequence update)
 DT 01-MAR-2004 (TREMblrel. 26, Last annotation update)
 DE Fibronectin binding protein B.
 GN Name=fndb;
 OS Staphylococcus aureus.
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 OX NCBI_TaxId=1280;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=8325-4;
 RX MEDLINE=92111475; PubMed=1837266;
 RI Johnson K., Sigmas C., Muller H.P., Lindberg M.;
 RT "Two different genes encode fibronectin binding proteins in
 RT Staphylococcus aureus. The complete nucleotide sequence and
 RT characterization of the second gene.";
 RL Eur. J. Biochem. 202:1041-1048 (1991).
 CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
 CC an amide bond (By similarity).
 DR EMBL: X62992; CAAA4726.1; -
 DR PIR: S19702; S19702.
 DR HSP; O53653; IN67.
 DR GO: GO:0009986; C:cell surface; IEA.
 DR GO: GO:0005618; C:cell wall; IEA.
 DR GO: GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
 DR GO: GO:0016020; C:membrane; IEA.
 DR GO: GO:0007155; P:cell adhesion; IEA.
 DR InterPro: IPR008966; Adhes_bact.
 DR InterPro: IPR004237; Fn_bind.
 DR InterPro: IPR005877; Gpos_YsIRK.
 DR InterPro: IPR001899; Gram_pos_anchor.
 DR Pfam: PF02986; Fn_bind; 2.
 DR Pfam: PF00746; Gram_pos_anchor; 1.
 DR Pfam: PF04650; YsIRK_signal; 1.
 DR TIGRFAMs: TIGR01167; LPXTG_anchor; 1.
 DR TIGRFAMs: TIGR01168; YsIRK_signal; 1.
 DR PROSITE: PSS0847; GRAM_POS_ANCHORING; 1.
 KW Cell wall; Peptidoglycan-anchor.
 SQ SEQUENCE 940 AA; 10355 MW; E35FBBCA907AE345 CRC64;
 SC

Query Match 90.2%; Score 193; DB 2; Length 940;
 Best Local Similarity 92.1%; Pred. No. 1.6e-16;
 Matches 35; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 ONKNGSFEPDTEKDKPKYEHGNIIDIDFDSVPHING 38
 DB 720 ONKNGSFEPDTEKDKPKYEHGNIIDIDFDSVPHING 757

RESULT 6
 ID Q99RD2 PRELIMINARY; PRT; 1038 AA.
 AC Q99RD2;
 DT 01-JUN-2001 (TREMblrel. 17, Created)
 DT 01-JUN-2001 (TREMblrel. 17, Last sequence update)
 DT 01-MAR-2004 (TREMblrel. 26, Last annotation update)
 DE Fibronectin-binding protein homolog.
 GN Name=fnd; OrderLocName=SAV2503;
 OS Staphylococcus aureus (strain Mu50 / ATCC 700699).
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 OX NCBI_TaxId=158878;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Mu50 / ATCC 700699;
 RX MEDLINE=21311952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2;
 RI Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
 RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Iian J.-Q., Ito T.,
 RA Kanamori M., Matsumaru H., Maruyama A., Murakami H., Haseyama A.,
 RA Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
 RA Sekimizu K., Hirakawa H., Kohara S., Goto S., Yabuuchi J.,
 RA Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
 RA Hattori M., Ogasawara N., Hayaishi H., Hirakawa K.;
 RT "Whole genome sequencing of methicillin-resistant Staphylococcus
 RT aureus.";
 RL Lancet 357:1225-1240 (2001).
 CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
 CC an amide bond (By similarity).
 DR EMBL: AP003365; BAB58665.1; -
 DR PIR: H90053; H90053.
 DR GO: GO:0009986; C:cell surface; IEA.
 DR GO: GO:0005618; C:cell wall; IEA.
 DR GO: GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
 DR GO: GO:0016020; C:membrane; IEA.
 DR GO: GO:0007155; P:cell adhesion; IEA.
 DR InterPro: IPR008966; Adhes_bact.
 DR InterPro: IPR004237; Fn_bind.
 DR InterPro: IPR005877; Gpos_YsIRK.
 DR InterPro: IPR001899; Gram_pos_anchor.
 DR Pfam: PF02986; Fn_bind; 1.
 DR Pfam: PF00746; Gram_pos_anchor; 1.
 DR Pfam: PF04650; YsIRK_signal; 1.
 DR TIGRFAMs: TIGR01167; LPXTG_anchor; 1.
 DR TIGRFAMs: TIGR01168; YsIRK_signal; 1.
 DR PROSITE: PSS0847; GRAM_POS_ANCHORING; 1.
 KW Cell wall; Complete proteome; Peptidoglycan-anchor.
 SQ SEQUENCE 1038 AA; 113618 MW; 66BFBFBFBFB12 CRC64;
 SC

Query Match 90.2%; Score 193; DB 2; Length 1038;
 Best Local Similarity 92.1%; Pred. No. 1.6e-16;
 Matches 35; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 ONKNGSFEPDTEKDKPKYEHGNIIDIDFDSVPHING 38
 DB 780 ONKNGSFEPDTEKDKPKYEHGNIIDIDFDSVPHING 817

RESULT 7
 ID Q7A3J7 PRELIMINARY; PRT; 1038 AA.
 AC Q7A3J7;
 DT 05-JUL-2004 (TREMblrel. 27, Created)
 DT 05-JUL-2004 (TREMblrel. 27, Last sequence update)
 DT 05-JUL-2004 (TREMblrel. 27, Last annotation update)

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DE  Fnb protein.
GN  Name=fnd; OrderedLocusNames=SA2291;
OC  Staphylococcus aureus (strain N315).
OS  Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX  NCBI_TaxId=158879;
RN  [1]
RP  SEQUENCE FROM N.A.
RX  MEDLINE=2111952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2;
RA  Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
RA  Cui L., Oguchi A., Aoki K.-I., Nagai Y., Lian J.-Q., Ito T.,
RA  Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyma A.,
RA  Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
RA  Sekimizu K., Hirakawa H., Kohara S., Goto S., Yabuzaki J.,
RA  Kanetsu K., Yamashita A., Ohnaka K., Furuya K., Yoshino C., Shiba T.,
RA  Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.,
RT  "Whole genome sequencing of methicillin-resistant Staphylococcus
RT  aureus".
RL  Lancet 357:1225-1240(2001).
CC  -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC  an amide bond (By similarity).
DR  EMBL; AP003137; BAB43594.1; -.
DR  GO; GO:0009986; C:cell surface; IEA.
DR  GO; GO:0005618; C:cell wall; IEA.
DR  GO; GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR  GO; GO:0016020; C:membrane; IEA.
DR  GO; GO:0007155; P:cell adhesion; IEA.
DR  InterPro; IPR008966; Adhes_bact.
DR  InterPro; IPR004237; Fn_bind.
DR  InterPro; IPR001899; Gram_pos_anchor.
DR  Pfam; PR02986; Fn_bind_1.
DR  Pfam; PF04650; YSIRK_signal; 1.
DR  TIGRPFAM; TIGR01167; LPXTG_anchor; 1.
DR  TIGRPFAM; TIGR01168; YSIRK_signal; 1.
DR  PROSITE; PS50847; GRAM_POS_ANCHORING; 1.
KW  Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ  SEQUENCE 1038 AA; 113618 MW; 666BFBFBFBEB12 CRC64;

Query Match      90.2%; Score 193; DB 2; Length 1033;
Best Local Similarity 92.1%; Pred. No. 1.8e-16;
Matches 35; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY  1 QNKGNSFEDPTKDKPKYKHGNGNIIDIDFDSVPHIH 38
DB  780 QNKGNSFEDPTKDKPKYKHGNGNIIDIDFDSVPHIH 817

RESULT 8
ID  Q8NUU7          PRELIMINARY;      PRT; 1015 AA.
AC  Q8NUU7;
DT  01-OCT-2002 (TREMBLrel. 22, Created)
DT  01-OCT-2002 (TREMBLrel. 22, Last sequence update)
DT  01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE  Fnb protein.
GN  Name=fnd; OrderedLocusNames=NM2421;
OC  Staphylococcus aureus (strain MW2).
OS  Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX  NCBI_TaxId=156620;
RN  [1]
RP  SEQUENCE FROM N.A.
RX  STRAIN=MW2;
RX  MEDLINE=22040717; PubMed=12044378; DOI=10.1016/S0140-6736(02)08713-5;
RA  Baba T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Oguchi A.,
RA  Nagai Y., Iwama N., Amano K., Naimi T., Kuroda H., Cui L.,
RA  Yamamoto K., Hiramatsu K.;
RT  "Genome and virulence determinants of high virulence community-
RT  acquired MRSA".
RL  Lancet 359:1819-1827(2002).
CC  -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC  an amide bond (By similarity).
EMBL; AP004830; BAB96286.1; -.

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DR  GO; GO:0009986; C:cell surface; IEA.
DR  GO; GO:0005618; C:cell wall; IEA.
DR  GO; GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR  GO; GO:0016020; C:membrane; IEA.
DR  GO; GO:0007155; P:cell adhesion; IEA.
DR  InterPro; IPR008966; Adhes_bact.
DR  InterPro; IPR004237; Fn_bind.
DR  InterPro; IPR001899; Gram_pos_anchor.
DR  InterPro; IPR008966; Gram_pos_anchor.
DR  Pfam; PR02986; Fn_bind_1.
DR  Pfam; PF04650; YSIRK_signal; 1.
DR  TIGRPFAM; TIGR01167; LPXTG_anchor; 1.
DR  TIGRPFAM; TIGR01168; YSIRK_signal; 1.
DR  PROSITE; PS50847; GRAM_POS_ANCHORING; 1.
KW  Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ  SEQUENCE 1015 AA; 111145 MW; D0F9281B864D44D2 CRC64;

Query Match      86.4%; Score 185; DB 2; Length 1015;
Best Local Similarity 89.5%; Pred. No. 2e-15;
Matches 34; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY  1 QNKGNSFEDPTKDKPKYKHGNGNIIDIDFDSVPHIH 38
DB  785 QNKGNSFEDPTKDKPKYKHGNGNIIDIDFDSVPHIH 822

RESULT 9
ID  Q6G6H3          PRELIMINARY;      PRT; 1015 AA.
AC  Q6G6H3;
DT  05-JUL-2004 (TREMBLrel. 27, Created)
DT  05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DT  05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE  Fibronectin-binding protein.
GN  OrderedLocusNames=SA52388;
OS  Staphylococcus aureus (strain MSSA476).
OC  Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX  NCBI_TaxId=282459;
RN  [1]
RP  SEQUENCE FROM N.A.
RX  PubMed=15213324; DOI=10.1073/pnas.0402521101;
RA  Holden M.T.G., Fell E.J., Linday J.A., Peacock S.J., Day N.P.J.,
RA  Enright M.C., Foster T.J., Moore C.E., Hurst L., Atkin R., Barton A.,
RA  Bacon N., Bentley S.P., Chillingworth C., Chillingworth T.,
RA  Churcher C., Clark L., Corton C., Cronin A., Doggett J., Dowd L.,
RA  Felwell T., Hance Z., Harris B., Hauser H., Holtroyd S., Jagels K.,
RA  James K.D., Lennard N., Line A., Mayes R., Moule S., Mungall K.,
RA  Ormond D., Quail M.A., Rabinowitsch E., Rutherford K.M., Sanders M.,
RA  Sharp S., Simmonds M., Stevens K., Whitehead S., Barrett B.G.,
RA  Spratt B.G., Parkhill J.;
RT  "Complete genomes of two clinical Staphylococcus aureus strains:
RT  evidence for the rapid evolution of virulence and drug resistance.";
RL  Proc. Natl. Acad. Sci. U.S.A. 101:9786-9791(2004).
CC  -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC  an amide bond (By similarity).
DR  EMBL; BK571857; CAG44202.1; -.
DR  GO; GO:0009986; C:cell surface; IEA.
DR  GO; GO:0005618; C:cell wall; IEA.
DR  GO; GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR  GO; GO:0016020; C:membrane; IEA.
DR  GO; GO:0007155; P:cell adhesion; IEA.
DR  InterPro; IPR008966; Adhes_bact.
DR  InterPro; IPR004237; Fn_bind.
DR  InterPro; IPR005877; Gpos_YSIRK.
DR  InterPro; IPR001899; Gram_pos_anchor.
DR  Pfam; PR02986; Fn_bind_1.
DR  Pfam; PF04650; YSIRK_signal; 1.
DR  TIGRPFAM; TIGR01167; LPXTG_anchor; 1.
DR  TIGRPFAM; TIGR01168; YSIRK_signal; 1.
DR  PROSITE; PS50847; GRAM_POS_ANCHORING; 1.
KW  Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ  SEQUENCE 1015 AA; 111145 MW; D0F9281B864D44D2 CRC64;

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SQ SEQUENCE 1015 AA; 111145 MW; D0F9281BB64D4D2 CRC64;
 Query Match 86.4%; Score 185; DB 2; Length 1015;
 Best Local Similarity 89.5%; Pred. No. 2e-15;
 Matches 34; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 Oy 1 QNKGNSFEPDTEKDKRYEGHGNIIIDPDSVPHNG 38
 |||||
 DB 785 QNKGNSFEPDTEKDKRYEGHGNIIIDPDSVPHNG 822
 |||||
 RESULT 10
 Q99RD3 PRELIMINARY; PRT; 961 AA.
 AC Q99RD3;
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Fibronectin-binding protein homolog.
 GN Name=fnbB; OrderedLocNames=SAV2502;
 OS Staphylococcus aureus (strain Mu50 / ATCC 700699).
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 NC NCBI_TaxID=158878;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Mu50 / ATCC 700699;
 RA MEDLINE=21311952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2;
 RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
 RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Iian J.-O., Ito T.,
 RA Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,
 RA Mizutani U. Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
 RA Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
 RA Kanehisa M., Yamauchi A., Oshima K., Furuya K., Yoshino C., Shiba T.,
 RA Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
 RT "Whole genome sequencing of methicillin-resistant Staphylococcus
 aureus.";
 RL Lancet 357:1225-1240(2001).
 CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
 an amide bond (By similarity).
 DR EMBL: AP003365; BAB58664.1; -.
 DR PIR: G90053; G90053.
 DR HSBP; Q53653; IN67.
 DR GO: GO:0009986; C:cell surface; IEA.
 DR GO: GO:0005618; C:cell wall; IEA.
 DR GO: GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
 DR GO: GO:0016020; C:membrane; IEA.
 DR GO: GO:0007155; P:cell adhesion; IEA.
 DR InterPro: IPR008966; Adhes_bact.
 DR InterPro: IPR004237; Fn_bind.
 DR InterPro: IPR005877; Gpos_YsIRK.
 DR InterPro: IPR001899; Gram_pos_anchor.
 DR Pfam: PF02986; Fn_bind; 1.
 DR Pfam: PF00746; Gram_pos_anchor; 1.
 DR Pfam: PF04650; YsIRK_signal; 1.
 DR TIGRFAMs: TIGR01167; LpxTG_anchor; 1.
 DR TIGRFAMs: TIGR01168; YsIRK_signal; 1.
 DR PROSITE: PS50847; GRAM_POS_ANCHORING; 1.
 KW Cell wall, Complete proteome; Peptidoglycan-anchor.
 SQ SEQUENCE 961 AA; 106010 MW; 364940F884EA4101 CRC64;
 Query Match 84.6%; Score 181; DB 2; Length 961;
 Best Local Similarity 86.8%; Pred. No. 6.4e-15;
 Matches 33; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
 Oy 1 QNKGNSFEPDTEKDKRYEGHGNIIIDPDSVPHNG 38
 |||||
 DB 731 QNKGNSFEPDTEKDKRYEGHGNIIIDPDSVPHNG 768
 |||||
 RESULT 11
 Q7A3J8 PRELIMINARY; PRT; 961 AA.
 ID Q7A3J8
 AC Q7A3J8;

DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE FnbB protein.
 GN Name=fnbB; OrderedLocNames=SA2290;
 OS Staphylococcus aureus (strain N315).
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 NC NCBI_TaxID=158879;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21311952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2;
 RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
 RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Iian J.-O., Ito T.,
 RA Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,
 RA Mizutani U. Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
 RA Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
 RA Kanehisa M., Yamauchi A., Oshima K., Furuya K., Yoshino C., Shiba T.,
 RA Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
 RT "Whole genome sequencing of methicillin-resistant Staphylococcus
 aureus.";
 RL Lancet 357:1225-1240(2001).
 CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
 an amide bond (By similarity).
 DR EMBL: AP003337; BAB43593.1; -.
 DR GO: GO:0009986; C:cell surface; IEA.
 DR GO: GO:0005618; C:cell wall; IEA.
 DR GO: GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
 DR GO: GO:0016020; C:membrane; IEA.
 DR GO: GO:0007155; P:cell adhesion; IEA.
 DR InterPro: IPR008966; Adhes_bact.
 DR InterPro: IPR004237; Fn_bind.
 DR InterPro: IPR005877; Gpos_YsIRK.
 DR InterPro: IPR001899; Gram_pos_anchor.
 DR Pfam: PF02986; Fn_bind; 1.
 DR Pfam: PF00746; Gram_pos_anchor; 1.
 DR Pfam: PF04650; YsIRK_signal; 1.
 DR TIGRFAMs: TIGR01167; LpxTG_anchor; 1.
 DR TIGRFAMs: TIGR01168; YsIRK_signal; 1.
 DR PROSITE: PS50847; GRAM_POS_ANCHORING; 1.
 KW Cell wall, Complete proteome; Peptidoglycan-anchor.
 SQ SEQUENCE 961 AA; 106010 MW; 364940F884EA4101 CRC64;
 Query Match 84.6%; Score 181; DB 2; Length 961;
 Best Local Similarity 86.8%; Pred. No. 6.4e-15;
 Matches 33; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
 Oy 1 QNKGNSFEPDTEKDKRYEGHGNIIIDPDSVPHNG 38
 |||||
 DB 731 QNKGNSFEPDTEKDKRYEGHGNIIIDPDSVPHNG 768
 |||||
 RESULT 12
 Q6GDUS PRELIMINARY; PRT; 965 AA.
 ID Q6GDUS
 AC Q6GDUS;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Fibronectin-binding protein.
 GN Name=fnbA; OrderedLocNames=SA2580;
 OS Staphylococcus aureus (strain MRSA252).
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 NC NCBI_TaxID=282458;
 RN [1]
 RP SEQUENCE FROM N.A.
 RP PubMed=15213324; DOI=10.1073/pnas.0402521101;
 RA Holden M.T.G., Feil E.J., Lindsey J.A., Peacock S.J., Day N.P.J.,
 RA Enright M.C., Foster T.J., Moore C.E., Hurst L., Atkin R., Barron A.,
 RA Baeson N., Bentley S.D., Chillingworth C., Chillingworth T.,
 RA Churcher C., Clark L., Corton C., Cronin A., Doggett J., Dowd L.,
 RA Feltwell T., Hance Z., Harris B., Hauser H., Holtroyd S., Jagsels K.,
 RA James K.D., Lennard N., Line A., Mayes R., Moule S., Mungall K.,
 RA Ormond D., Quail M.A., Rabinowitsch E., Rutherford K.M., Sanders M.,


```

RA Sharp S., Simmonds M., Stevens K., Whitehead S., Barrell E.G.,
RA Spratt B.G., Parkhill J.: "Complete genomes of two clinical Staphylococcus aureus strains:
RT evidence for the rapid evolution of virulence and drug resistance.";
CC Proc. Natl. Acad. Sci. U.S.A. 101:9786-9791(2004).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC an amide bond (By similarity).
DR EMBL: BX571856; CAG41560.1; -.
DR GO: GO:0009986; Cell surface; IEA.
DR GO: GO:0009275; Cell wall (sensu Gram-positive Bacteria); IEA.
DR GO: GO:0016020; Membrane; IEA.
DR GO: GO:0007155; P-cell adhesion; IEA.
DR InterPro: IPR008966; Adhes_bact.
DR InterPro: IPR004237; Fn_bind.
DR InterPro: IPR005877; GPOB_Ysirk.
DR InterPro: IPR001899; Gram_pos_anchor.
DR Pfam: PF02986; Fn_bind; 1.
DR Pfam: PF00746; Gram_pos_anchor; 1.
DR TIGRPFAM: TIGR01167; LPXTG_anchor; 1.
DR TIGRPFAM: TIGR01168; Ysirk_signal; 1.
DR PROSITE: PS50847; GRAM_POS_ANCHORING; 1.
DR Cell wall; Complete proteome; Peptidoglycan-anchor.
DR KW
DR SEQUENCE 965 AA; 105691 MW; 2982E132164D0551 CRC64;

Query Match 84.6%; Score 181; DB 2; Length 965;
Best Local Similarity 86.8%; Pred. No. 6; Se-15;
Matches 33; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 QNKGNSFEPDTEKDKPKYEHGNIIDIDFDSVPHNG 38
DB 749 QNKGNSFEPDTEKDKPKYEGNGNIIDIDFDSVPHNG 786

RESULT 13
COBD_THETN STANDARD; PRT; 367 AA.
AC 08R5T4;
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Putative threonine-phosphate decarboxylase (EC 4.1.1.81) ("threonine-
DE O-3-phosphate decarboxylase").
GN Name-cobd; Ordered locus names=TTE0380;
OS Thermoaerobacter tengcongensis;
OC Bacteria; Firmicutes; Clostridia; Thermoaerobacteriales;
OC Thermoaerobacteriaceae; Thermoaerobacter.
OX NCBI_TaxID=119072;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MB4 / JCM 11007;
RX MEDLINE=21992816; PubMed=11997336; DOI=10.1101/gr.219302;
RA Bao Q., Tian Y., Li W., Xu Z., Xuan Z., Hu S., Dong W., Yang J.,
RA Chen Y., Xue Y., Xu Y., Lai X., Huang L., Dong X., Ma Y., Jing L.,
RA Tan H., Chen R., Wang J., Yu J., Yang H.;
RT "A complete sequence of the T. tengcongensis genome.";
RL Genome Res. 12:689-700(2002).
CC -1- FUNCTION: Decarboxylates L-threonine-O-3-phosphate to yield (R)-1-
CC amino-2-pyranol O-2-phosphate, the precursor for the linkage
CC between the nucleotide loop and the corrin ring in cobalamin (By
CC similarity).
CC -1- CATALYTIC ACTIVITY: L-threonine O-3-phosphate = (R)-1-(iminopropan-
CC 2-yl phosphate + CO(2).
CC -1- COFACTOR: Pyridoxal phosphate (By similarity).
CC -1- PATHWAY: Adenosylcobalamin biosynthesis; conversion of
CC adenosylcobyrinic acid to adenosylcobinamide.
CC -1- SIMILARITY: Belongs to the class-II pyridoxal-phosphate-dependent
CC aminotransferase family.
-----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: AE011011; AAM2667.1; -.
DR HSSP: P97084; ILCS.
DR InterPro: IPR001176; ACC synthase.
DR InterPro: IPR004839; Aminotransferase_I/II.
DR InterPro: IPR001917; Aminotransferase_II.
DR InterPro: IPR005860; COBD.
DR Pfam: PF00155; Aminotran_1_2; 1.
DR PRINTS: PR00753; ACCSYNTHASE.
DR TIGRPFAM: TIGR01140; COBD; 1.
DR PROSITE: PS00599; AA_TRANSFER_CLASS_2; FALSE_NEG.
DR Cobalamin biosynthesis; Complete proteome; Lyase; Pyridoxal phosphate.
DR FT BINDING 213 213
DR SEQUENCE 367 AA; 42396 MW; 2925127EE1F8435 CRC64;

Query Match 29.4%; Score 63; DB 1; Length 367;
Best Local Similarity 64.0%; Pred. No. 8; 4;
Matches 16; Conservative 0; Mismatches 3; Indels 6; Gaps 2;

QY 13 EKDCKPYEHGNIID----IDFDS 32
DB 5 EKDCKP-YEHGNIYDQGNLIDFSS 28

RESULT 14
QY 054324 PRELIMINARY; PRT; 904 AA.
AC 054324;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE ORF904; Method: conceptual translation supplied by author.
DE Sulfolobus islandicus.
OS Sulfolobus islandicus.
OC Archaea; Crenarchaeota; Thermoprotei; Sulfolobales; Sulfolobaceae;
OC Sulfolobus.
OX NCBI_TaxID=43080;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=REN1H1;
RX MEDLINE=96271189; PubMed=8700967; DOI=10.1006/plas.1996.0016;
RA Keeling P.J., Klenk H.P., Singh R.K., Feeley O., Schleper C.,
RA Zillig W., Doolittle W.F., Senses C.W.;
RT "Complete nucleotide sequence of the Sulfolobus islandicus multicopy
RT plasmid pRN1.";
RL Plasmid 35:141-144(1996).
DR EMBL: U36383; AAC4411.1; -.
DR PDB: 1RNI; X-ray; A=40-255.
DR PDB: 1RO0; X-ray; A=40-255.
DR PDB: 1RO2; X-ray; A=40-255.
DR InterPro: IPR004968; Pox_D5.
DR InterPro: IPR006500; Primase_C.
DR InterPro: IPR009058; Wing_hix_DNA_bnd.
DR Pfam: PF03288; Pox_D5; 1.
DR TIGRPFAM: TIGR01613; primase_Cterm; 1.
DR Plasmid.
DR KW
DR SEQUENCE 904 AA; 105816 MW; 3726CC107BC6E57F CRC64;

Query Match 28.7%; Score 61.5; DB 2; Length 904;
Best Local Similarity 38.9%; Pred. No. 37;
Matches 14; Conservative 6; Mismatches 11; Indels 5; Gaps 1;

QY 2 NKGNSFEPDTEKDKPKY-----EHGNIIDIDFDS 32
DB 29 NSGNKDFSSNFSERIRYAKWFLHGFNFIIDPDS 64

RESULT 15
QY 099UP6 PRELIMINARY; PRT; 214 AA.
ID 099UP6

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AC Q99UP6; 01-JUN-2001 (TrEMBLrel. 17, Created)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Ribulose-5-phosphate 3-epimerase homolog.
 GN Name-cfse; OrderedlocusNames=SAV1222;
 OS Staphylococcus aureus (strain Mu50 / ATCC 700699).
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 OX NCBI_TaxID=158878;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Mu50 / ATCC 700699;
 RX MEDLINE=21311952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2;
 RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kodayashi I.,
 RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Iian J.-Q., Ito T.,
 RA Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,
 RA Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
 RA Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
 RA Kanehisa M., Yamashita A., Oshida K., Furuya K., Yoshino C., Shiba T.,
 RA Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
 RT "Whole genome sequencing of methicillin-resistant Staphylococcus
 aureus.";
 RT Lancet 357:1225-1240(2001).
 CC -1- SIMILARITY: Belongs to the ribulose-phosphate 3-epimerase family.
 DR EMBL; AF003361; BAB57384.1; -.
 DR PIR; A89895; A89895.
 DR HSSP; Q43843; IRPX.
 DR GO; GO:0016853; F:isomerase activity; IEA.
 DR GO; GO:0004750; F:ribulose-phosphate 3-epimerase activity; IEA.
 DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
 DR InterPro; IPR011060; RibP_bind_barrel.
 DR Pfam; PF00834; Ribul_P_3_epim; 1.
 DR TIGRFAMs; TIGR01163; rpe; 1.
 DR PROSITE; PS01085; RIBUL_P_3_EPIMER_1; 1.
 DR PROSITE; PS01086; RIBUL_P_3_EPIMER_2; 1.
 DR Carbohydrate metabolism; Complete proteome; Isomerase.
 KW SEQUENCE 214 AA; 23572 MW; C0F62869FE242CA3 CRC64;
 SQ

Query Match 28.0%; Score 60; DB 2; Length 214;
 Best Local Similarity 55.6%; Pred. No. 11;
 Matches 10; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Qy 20 EHGNIDIDSDSVPHH 37
 |||::|||:
 Db 80 EHGDWISIHVESTPHH 97

Search completed: October 22, 2005, 06:06:09
 Job time : 70.6361 secs

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OM protein - protein search, using sw model

Run on: October 25, 2005, 19:38:38 ; Search time 83.8325 Seconds
(without alignments)
175.313 Million cell updates/sec

Title: US-10-731-238-45

Perfect score: 213

Sequence: 1 ONKGNQSPEDTEKDKPKYHGNQNIIDIDFDSVPHIHG 38

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database: A_Geneseq_16Dec04:*

1: geneseqp1808:*
2: geneseqp1908:*
3: geneseqp2008:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	213	100.0	38	2	AAW65701	AAW65701 Fibronect
2	202	94.8	38	2	AAW65663	AAW65663 Fibronect
3	202	94.8	134	2	AAV29087	AAV29087 S. aureus
4	202	94.8	139	2	AAW31556	AAW31556 Fibronect
5	202	94.8	1018	1	AAW82115	AAW82115 Fibronect
6	202	94.8	1018	4	AAU37245	AAU37245 Staphyloc
7	202	94.8	1018	4	AAU34301	AAU34301 Staphyloc
8	202	94.8	1018	6	ABW18922	ABW18922 Pathogen
9	202	94.8	1018	6	ABW72537	ABW72537 Staphyloc
10	202	94.8	1037	2	AAW69806	AAW69806 Staphyloc
11	197	92.5	77	2	AAW88749	AAW88749 S. aureus
12	197	92.5	113	2	AAW90937	AAW90937 D3D4 poly
13	197	92.5	130	2	AAW58806	AAW58806 Fibronect
14	197	92.5	130	2	AAW58807	AAW58807 Fibronect
15	197	92.5	130	2	AAW91202	AAW91202 D1-D4 fib
16	197	92.5	130	2	AAW91201	AAW91201 D1-D4 fib
17	197	92.5	162	2	AAW99942	AAW99942 D3D4 poly
18	197	92.5	164	2	AAW90938	AAW90938 D3D4 poly
19	197	92.5	174	2	AAW58808	AAW58808 Fdp fibro
20	197	92.5	174	2	AAW91203	AAW91203 D1-D4 fib
21	197	92.5	181	2	AAW58805	AAW58805 Fibronect
22	197	92.5	181	2	AAW91200	AAW91200 D1-D4 fib
23	196	92.0	38	1	AAW80661	AAW80661 Protein w
24	196	92.0	38	1	AAW82117	AAW82117 Fibronect
25	196	92.0	38	2	AAW65703	AAW65703 Fibronect

26	196	92.0	38	2	AAW65702	AAW65702 Fibronect
27	195	91.5	38	2	AAW65704	AAW65704 Fibronect
28	194	91.1	38	2	AAW65664	AAW65664 Fibronect
29	194	91.1	38	2	AAW65705	AAW65705 Fibronect
30	189	88.7	134	2	AAW29088	AAW29088 S. aureus
31	189	88.7	559	2	AAW89803	AAW89803 Staphyloc
32	189	88.7	767	4	AAU34403	AAU34403 Staphyloc
33	189	88.7	767	4	AAU37547	AAU37547 Staphyloc
34	189	88.7	940	2	AAW07070	AAW07070 Fibronect
35	189	88.7	940	6	AAW19111	AAW19111 Pathogen
36	189	88.7	948	6	ADA89470	ADA89470 Staphyloc
37	189	88.7	948	6	ABJ18923	ABJ18923 Pathogen
38	189	88.7	948	6	ABW72536	ABW72536 Staphyloc
39	189	88.7	1038	6	ABU15903	ABU15903 Protein e
40	187	87.8	38	2	AAW65691	AAW65691 Fibronect
41	181	85.0	978	4	AAU33960	AAU33960 Staphyloc
42	181	85.0	1001	4	AAU37093	AAU37093 Staphyloc
43	180	84.5	134	2	AAW29089	AAW29089 Cloned f1
44	179	84.0	36	2	AAW65714	AAW65714 Fibronect
45	177	83.1	961	6	ABU15854	ABU15854 Protein e

ALIGNMENTS

RESULT 1
AAW65701 AAW65701 standard; peptide; 38 AA.
XX
AC AAW65701;
XX
DT 16-OCT-1998 (first entry)
XX
DE Fibronectin binding protein-derived peptide #45.
XX
KW microfil surface components recognising adhesive matrix molecule;
KW MSCRAMM; fibronectin; fibronectin-binding protein; antibody; epitope;
KW antibiotic; bacterial infection; antibiotic-resistant strain.
XX
OS Synthetic.
OS Staphylococcus aureus.
XX
PN WO9813389-A2.
XX
PD 23-JUL-1998.
XX
PF 21-JAN-1998; 98WO-US001222.
XX
PR 21-JAN-1997; 97US-0036139P.
XX
PA (TEXA) UNITV TEXAS A & M SYSTEM.
XX
PI Hoecek M, Patti JM, House-Pompeo KL, Speziale P, Joh D;
PI Mcgavin MJ;
XX
DR WPI; 1998-413816/35.
XX
PT Antibody that binds to fibronectin-binding protein, preventing its
PT binding to fibronectin - used to treat or prevent bacterial infection,
PT especially by Staphylococci and Streptococci.
XX
PS Example 8; Page 102; 201pp; English.
XX
CC The invention relates to antibodies that bind to a fibronectin-binding
CC domain of a fibronectin-binding protein, and inhibit binding of the
CC protein to fibronectin. Also claimed are: (1) isolated peptides of a
CC fibronectin-binding protein that do not bind to fibronectin; (2) fusion
CC protein containing at least one peptide of a fibronectin-binding protein
CC linked to a second amino acid sequence; (3) nucleic acid encoding the
CC isolated peptide of (1). Antibodies, the isolated peptides of (1) and the
CC nucleic acids are all useful for immunisation (active or passive) and (by
CC inhibiting binding of bacteria to fibronectin) for preventing or treating
CC infection in humans or other animals, particularly by staphylococci or

CC streptococci, e.g. meningitis, otitis media, pneumonia, endocarditis,
CC mastitis in cattle, abortion in horses and many others. Since the
CC antibodies block binding of bacteria, they should be effective against
CC antibiotic-resistant strains, and may replace antibiotic therapy or
CC increase its effectiveness. Sequences AAW65701-706 represent a series of
CC synthetic peptides based on the D2 region of *S. aureus* fibronectin
CC binding protein A. They were synthesised to contain mutations
XX
SQ Sequence 38 AA;
Query Match 100.0%; Score 213; DB 2; Length 38;
Best Local Similarity 100.0%; Pred. No. 8.4e-23;
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 QNKGNSPEEDTEKDKPYEHGNIIDIDFDSVPHIG 38
DB 1 QNKGNSPEEDTEKDKPYEHGNIIDIDFDSVPHIG 38
RESULT 2
AAW65663 ID AAW65663 standard; peptide; 38 AA.
XX
AC AAW65663;
XX
DT 16-OCT-1998 (first entry)
XX
DE Fibronectin binding protein-derived peptide #7.
XX
KW microbial surface components recognising adhesive matrix molecule;
KW MSCRAMM; fibronectin-binding protein; antibody; epitope;
KW antibiotic; bacterial infection; antibiotic-resistant strain.
XX
OS Synthetic.
OS Staphylococcus aureus.
XX
PN MO9831389-A2.
XX
PD 23-JUL-1998.
XX
PF 21-JAN-1998; 98WO-US001222.
XX
PR 21-JAN-1997; 97US-0036139P.
XX
PA (TEXA) UNIV TEXAS A & M SYSTEM.
XX
XX Hosoeck M, Patci JM, House-Pompeo KL, Speciale P, Joh D;
PI McGavin MJ;
XX WPI, 1998-413816/35.
DR
XX
XX Antibody that binds to fibronectin-binding protein, preventing its
XX binding to fibronectin - used to treat or prevent bacterial infection,
XX especially by Staphylococci and Streptococci.
XX
XX Example 2; Page 92; 201pp; English.
XX
XX The invention relates to antibodies that bind to a fibronectin-binding
XX domain of a fibronectin-binding protein, and inhibit binding of the
XX protein to fibronectin. Also claimed are: (1) isolated peptides of a
XX fibronectin-binding protein that do not bind to fibronectin; (2) fusion
XX protein containing at least one peptide of a fibronectin-binding protein
XX linked to a second amino acid sequence; (3) nucleic acid encoding the
XX isolated peptide of (1). Antibodies, the isolated peptides of (1) and the
XX nucleic acids are all useful for immunisation (active or passive) and (by
XX inhibiting binding of bacteria to fibronectin) for preventing or treating
XX infection in humans or other animals, particularly by staphylococci or
XX streptococci, e.g. meningitis, otitis media, pneumonia, endocarditis,
XX mastitis in cattle, abortion in horses and many others. Since the
XX antibodies block binding of bacteria, they should be effective against
XX antibiotic-resistant strains, and may replace antibiotic therapy or
XX increase its effectiveness. Sequences AAW65659-68 represent synthetic
XX epitopes from the fibronectin binding domains DU and D1-D4 of the S.

CC aureus fnbA gene
XX
SQ Sequence 38 AA;
Query Match 94.8%; Score 202; DB 2; Length 38;
Best Local Similarity 97.4%; Pred. No. 3.1e-21;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 QNKGNSPEEDTEKDKPYEHGNIIDIDFDSVPHIG 38
DB 1 QNKGNSPEEDTEKDKPYEHGNIIDIDFDSVPHIG 38
RESULT 3
AAV29087 ID AAV29087 standard; protein; 134 AA.
XX
AC AAV29087;
XX
DT 28-SEP-1999 (first entry)
XX
DE *S. aureus* fibronectin binding protein A (FnBA) binding domain.
XX
DE Bovine herpes virus-2; BHV-2; cytokine; immune response; immunogen; IL;
XX interleukin; colony stimulating factor; CSF; interferon; IFN; TNF;
KW tumour necrosis factor; recombinant virus; vaccine; mucosal disease;
KW mastitis; breast cancer; stress-induced disease; binding domain; FnBA;
KW fibronectin binding protein.
XX
XX Staphylococcus aureus.
OS
XX
XX MO9916892-A1.
XX
XX 08-APR-1999.
XX
XX 29-SEP-1998; 98WO-GB002927.
XX
XX 29-SEP-1997; 97GB-00020633.
XX
XX (UTBR-) UNIV BRISTOL.
PA
XX
XX Bradley AJ, Duffae WPH;
PI WPI, 1999-255101/21.
XX
DR N-PSDB; AAX91504.
XX
XX New bovine herpes virus-2 vectors.
PT
XX
XX Example 2; Fig 8A-B; 130pp; English.
XX
XX The invention provides bovine herpes virus-2 (BHV-2) based vectors that
XX comprise at least one cytokine-encoding DNA sequence. The expression of
XX cytokines in mammals can up-regulate immune responses to the immunogens.
XX The cytokine is selected from interleukins (IL), colony stimulating
XX factors (CSF), interferons (IFN) and tumour necrosis factors (TNF). The
XX BHV-2 based vector or recombinant virus can be used as vaccines. They can
XX be used for preventing or treating a mucosal disease in a subject, e.g.
XX ruminants, cattle, sheep, goats, dogs, cats, horses, or man, particularly
XX mastitis in cows or breast cancers in humans. They can also be used for
XX preventing or treating a stress-induced disease. The present sequence
XX represents the binding domain of a previously published *S. aureus*
XX fibronectin binding protein A (FnBA) sequence. The FnB binding domain
XX gene sequence FnBAB, cloned for use in this invention has 97.8 percent
XX identity when compared to the previously published FnBA and FnBB gene
XX sequences
XX
SQ Sequence 134 AA;
Query Match 94.8%; Score 202; DB 2; Length 134;
Best Local Similarity 97.4%; Pred. No. 1.4e-20;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 QNKGNSPEEDTEKDKPYEHGNIIDIDFDSVPHIG 38

DB 40 QNKGNSFEEDTEKDKPKYEHGNIIDIDFDSVPHIHG 77

RESULT 4
AAW31556 standard; protein; 139 AA.

AAW31556;

27-AUG-2003 (revised)
25-MAR-2003 (revised)
21-MAY-1998 (first entry)

Fibronectin-binding MSCRAMM derivative POD.

Fibronectin; POD; collagen binding protein; sepsis; infection;
microbial surface component recognising adhesive matrix molecule; MSCRAMM;
adhesin; vaccine; immunisation; diagnosis; therapy; mastitis.

Staphylococcus aureus.

Key Location/Qualifiers

Peptide 1..12 /note="vector pQE30-derived peptide"

MO9743314-A2.

20-NOV-1997.

14-MAY-1997; 97MO-US008210.

16-MAY-1996; 96US-0017678P.

(TEXA) UNIV TEXAS A & M SYSTEM.

(UABR-) UAB RES FOUND.

Hoeck M, Patti JM, House-Pompeo K, Sthanam N, Symersky J;

WPI; 1998-008801/01.

Antibody that interacts with collagen binding domain of Staphylococcal
cna gene product - useful to prevent bacterial sepsis in animal infected
with Staphylococcus aureus.

Disclosure; Page 91; 143pp; English.

This protein comprises Staphylococcus aureus fibronectin-binding
microbial surface component recognising adhesive matrix molecule (MSCRAMM)
derivative POD, plus a vector-derived N-terminal peptide. The invention
relates to claimed nucleic acid sequences (see AAT93436-38) encoding S.
aureus collagen binding protein (CBP) epitopes M17, M31 and M55 (see
AAW31552-54) that confer protection against S. aureus infection. CBP
protein and antigenic epitopes are contemplated for use in the treatment
of pathological infections, especially to prevent bacterial adhesion to
collagen. The epitopes are also contemplated for use in the preparation
of vaccines and as carrier proteins in vaccine formulations, as well as
in the formulation of compositions for the prevention of S. aureus
infection. pCF33 and POD (see AAW31556) were used to raise anti-MSCRAMM
polyclonal antibodies used in passive immunisation against bovine
mastitis. (Updated on 25-MAR-2003 to correct PI field.) (Updated on 27-
AUG-2003 to correct OS field.)

Sequence 139 AA;

Query Match 94.8%; Score 202; DB 2; Length 139;

Best Local Similarity 97.4%; Pred. No. 1.5e-20;

Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

1 QNKGNSFEEDTEKDKPKYEHGNIIDIDFDSVPHIHG 38

54 QNKGNSFEEDTEKDKPKYEHGNIIDIDFDSVPHIHG 91

RESULT 5
AAP82115 standard; protein; 1018 AA.

AAP82115;

25-MAR-2003 (revised)
05-JAN-1990 (first entry)

Fibronectin binding protein.

Fibronectin binding protein; S. aureus; immunisation; mastitis; ruminants;
wound infection; diagnosis.

Staphylococcus aureus.

EP294349-A.

07-DEC-1988.

30-MAY-1988; 88EP-00850188.

01-JUN-1987; 87SE-00002272.

(ALFA) ALFA LAVAL AGRIC INT AB.

Lindberg MK, Signas LC, Wadstrom TM, Froman G;

WPI; 1988-347978/49.

P-PsDB; AAP82115.

Hybrid DNA encoding Staphylococcus aureus fibronectin binding protein -
useful for immunisation and topical application to prevent staphylococcal
infections.

Disclosure; Fig. 8A:1-8A:2; 23pp; English.

The S. aureus fibronectin binding protein may be included in a hybrid
protein. The protein may be used to immunise ruminants against
staphylococcal mastitis, pref. when given at 0.5-5 microg/kg, using 3
doses at 1-3 week intervals; and for topical applic. to prevent wound
infection, pref. using isotonic saline soln. of concn. 25-250 microg/mg.
The DNA encoding the binding protein and the hybrid protein may be
immobilised on a carrier and used to diagnose staphylococcal infections.
(Updated on 25-MAR-2003 to correct PA field.)

Sequence 1018 AA;

Query Match 94.8%; Score 202; DB 1; Length 1018;

Best Local Similarity 97.4%; Pred. No. 1.7e-19;

Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

1 QNKGNSFEEDTEKDKPKYEHGNIIDIDFDSVPHIHG 38

784 QNKGNSFEEDTEKDKPKYEHGNIIDIDFDSVPHIHG 821

RESULT 6

AAU37245 standard; protein; 1018 AA.

AAU37245;

14-FEB-2002 (first entry)

Staphylococcus aureus cellular proliferation protein #1415.

Antisense; prokaryotic cellular proliferation protein; antibiotic;
antibacterial; drug design.

Staphylococcus aureus.

```
PN WO200170955-A2.
XX
XX 27-SEP-2001.
PD
XX
XX 21-MAR-2001; 2001WO-US009180.
PF
XX
XX 21-MAR-2000; 2000US-0191078P.
PR 21-MAR-2000; 2000US-0191078P.
PR 23-MAY-2000; 2000US-0206848P.
PR 26-MAY-2000; 2000US-0207727P.
PR 23-OCT-2000; 2000US-0242578P.
PR 27-NOV-2000; 2000US-0253625P.
PR 22-DEC-2000; 2000US-0257931P.
PR 16-FEB-2001; 2001US-0269308P.
XX
XX (ELIT-) ELITRA PHARM INC.
PA
XX
XX Haselbeck R, Ohlsen KU, Zyskind JW, Wall D, Trawick JD, Carr GJ;
PI Yamamoto RT, Xu HH;
PI
XX WPI; 2001-611495/70.
DR N-PSDB; AAS55104.
XX
XX New polynucleotides for the identification and development of
PT antibiotics, comprise sequences of antisense nucleic acids.
PT
XX
XX Example 3; SEQ ID NO 12838; 511pp; English.
PS
XX
XX The invention relates to antisense inhibitors of genes essential to
CC prokaryotic cellular proliferation, their use in identifying the genes,
CC their use in the discovery of novel antibiotics, the essential genes
CC themselves and the encoded proteins. The prokaryotes used are Escherichia
CC coli, Staphylococcus aureus, Salmonella typhi, Klebsiella pneumoniae,
CC Pseudomonas aeruginosa and Enterococcus faecalis. The invention is also
CC useful for the identification of potential new targets for antibiotic
CC development. The antisense nucleic acids can also be used to identify
CC antibodies used in proliferation, to express these proteins, and to obtain
CC antibodies capable of binding to the expressed proteins. The proteins can
CC be used to screen compounds in rational drug discovery programmes. The
CC antisense nucleic acid sequence is also useful to screen for homologous
CC nucleic acids which are required for cell proliferation in a wide variety
CC of organisms. The present sequence represents an essential prokaryotic
CC cellular proliferation protein. Note: The sequence data for this patent
CC did not form part of the printed specification, but was obtained in
CC electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
CC
XX
XX Sequence 1018 AA:
SQ
XX
XX Query Match 94.8%; Score 202; DB 4; Length 1018;
XX Best Local Similarity 97.4%; Pred. No. 1.7e-19;
XX Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
XX
XX 27-SEP-2001.
PD
XX
XX 21-MAR-2001; 2001WO-US009180.
PF
XX
XX 21-MAR-2000; 2000US-0191078P.
PR 21-MAR-2000; 2000US-0191078P.
PR 23-MAY-2000; 2000US-0206848P.
PR 26-MAY-2000; 2000US-0207727P.
PR 23-OCT-2000; 2000US-0242578P.
PR 27-NOV-2000; 2000US-0253625P.
PR 22-DEC-2000; 2000US-0257931P.
PR 16-FEB-2001; 2001US-0269308P.
XX
XX (ELIT-) ELITRA PHARM INC.
PA
XX
XX Haselbeck R, Ohlsen KU, Zyskind JW, Wall D, Trawick JD, Carr GJ;
PI Yamamoto RT, Xu HH;
PI
XX WPI; 2001-611495/70.
DR N-PSDB; AAS52160.
XX
XX New polynucleotides for the identification and development of
PT antibiotics, comprise sequences of antisense nucleic acids.
PT
XX
XX Example 3; SEQ ID NO 5797; 511pp; English.
PS
XX
XX The invention relates to antisense inhibitors of genes essential to
CC prokaryotic cellular proliferation, their use in identifying the genes,
CC their use in the discovery of novel antibiotics, the essential genes
CC themselves and the encoded proteins. The prokaryotes used are Escherichia
CC coli, Staphylococcus aureus, Salmonella typhi, Klebsiella pneumoniae,
CC Pseudomonas aeruginosa and Enterococcus faecalis. The invention is also
CC useful for the identification of potential new targets for antibiotic
CC development. The antisense nucleic acids can also be used to identify
CC antibodies used in proliferation, to express these proteins, and to obtain
CC antibodies capable of binding to the expressed proteins. The proteins can
CC be used to screen compounds in rational drug discovery programmes. The
CC antisense nucleic acid sequence is also useful to screen for homologous
CC nucleic acids which are required for cell proliferation in a wide variety
CC of organisms. The present sequence represents an essential prokaryotic
CC cellular proliferation protein. Note: The sequence data for this patent
CC did not form part of the printed specification, but was obtained in
CC electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
CC
XX
XX Sequence 1018 AA:
SQ
XX
XX Query Match 94.8%; Score 202; DB 4; Length 1018;
XX Best Local Similarity 97.4%; Pred. No. 1.7e-19;
XX Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

FN WO200259148-A2.
 XX
 PD 01-AUG-2002.
 XX
 PF 21-JAN-2002; 2002WO-BF000546.
 XX
 PR 26-JAN-2001; 2001AT-00000130.
 XX
 PA (CIST-) CISTEM BIOTECHNOLOGIES GMBH.
 XX
 PI Meinke A, Nagy B, Von Ahnen U, Klade C, Henics T, Zauner M;
 PI Minh DB, Vytvytska O, Etz H, Dryla A, Weichhart T, Hafner M;
 PI Tempelmeier B;
 XX
 DR WPI; 2003-075410/07.
 XX
 PT Identifying, isolating and producing hyperimmune serum-reactive antigens
 PT from a pathogen, for preparing vaccine or medicament for treating or
 PT preventing e.g. staphylococcal infections, comprises providing antibody
 PT preparation.
 PT
 PS Example 7; Page 157; 252pp; English.
 XX
 CC The invention relates to a novel method for identifying, isolating and
 CC producing hyperimmune serum-reactive antigens from a pathogen, tumour,
 CC allergen, a tissue or host prone to auto-immunity, where the antigens are
 CC used in a vaccine, comprises providing antibody preparation from a plasma
 CC pool of a type of animal, or individual sera with antibodies against the
 CC specific pathogen, tumour, allergen, tissue or host prone to auto-
 CC immunity. The hyperimmune serum-reactive antigens comprising any of the
 CC 62 sequences of 53-2261 amino acids fully defined in the specification,
 CC or their hyperimmune fragments are useful for the manufacture of a
 CC pharmaceutical preparation, particularly a vaccine against staphylococcal
 CC infections or colonisation against *S. aureus* or *S. epidermidis*. The
 CC preparation of antibodies is useful for the manufacture of a medicament
 CC for treating or preventing staphylococcal infections or colonisation
 CC against *S. aureus* or *S. epidermidis*. The antibody preparations may also
 CC be used for diagnostic and imaging purposes. Other conditions that can be
 CC treated include cancer, autoimmune diseases or infections caused by viral
 CC (e.g. HIV, hepatitis A, B or C), fungal or protozoan pathogens. This
 CC sequence represents a staphylococcal protein relating to the method for
 CC identifying and producing pathogen specific antigens of the invention
 CC
 XX
 SQ Sequence 1018 AA;
 XX
 Query Match 94.8%; Score 202; DB 6; Length 1018;
 Best Local Similarity 97.4%; Pred. No. 1,7e-19;
 Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 XX
 QY 1 QNKGNSPEDTEKDKPKYEHGNIIDIDFDSVPHING 38
 Db 784 QNKGNSPEDTEKDKPKYEHGNIIDIDFDSVPHING 821
 XX
 RESULT 9
 ABM72537
 ID ABM72537 standard; protein; 1018 AA.
 XX
 AC ABM72537;
 XX
 DT 20-NOV-2003 (first entry)
 XX
 DE Staphylococcus aureus protein #1777.
 XX
 KM Antibacterial; vaccine; gene therapy; infection; sepsis; diagnosis;
 KM enzymatic assay; antibiotic target.
 XX
 OS Staphylococcus aureus.
 XX
 PN WO200294868-A2.
 XX
 PD 28-NOV-2002.
 XX

PF 27-MAR-2002; 2002WO-IB002637.
 XX
 PR 27-MAR-2001; 2001GB-00007661.
 XX
 PA (CHIR-) CHIRON SPA.
 XX
 PI Masignani V, Mora M, Scarselli M;
 PI WPI; 2003-120786/11.
 XX
 DR N-PSDB; ACF74097.
 XX
 PT New Staphylococcus aureus protein, useful as a vaccine for treating or
 PT preventing Staphylococcal infection, specifically an infection caused by
 PT *S. aureus*, e.g. sepsis.
 XX
 PS Claim 1; SEQ ID NO 3554; 49pp; English.
 XX
 CC The invention relates to novel genes and encoded proteins from
 CC Staphylococcus aureus. A composition comprising the *S. aureus* protein, a
 CC nucleic acid encoding the protein, or an antibody to the protein, is
 CC useful as a pharmaceutical, particularly as a vaccine for treating or
 CC preventing infection due to Staphylococcus bacteria, specifically an
 CC infection caused by *S. aureus*. The composition is particularly useful for
 CC treating or preventing sepsis in a patient. The composition can also be
 CC used for diagnostics. The protein is also used in an assay for enzymatic
 CC studies and as a target for antibiotics. This sequence represents one of
 CC the novel *S. aureus* proteins of the invention
 CC
 XX
 SQ Sequence 1018 AA;
 XX
 Query Match 94.8%; Score 202; DB 6; Length 1018;
 Best Local Similarity 97.4%; Pred. No. 1,7e-19;
 Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 XX
 QY 1 QNKGNSPEDTEKDKPKYEHGNIIDIDFDSVPHING 38
 Db 784 QNKGNSPEDTEKDKPKYEHGNIIDIDFDSVPHING 821
 XX
 RESULT 10
 AAW89806
 ID AAW89806 standard; protein; 1027 AA.
 XX
 AC AAW89806;
 XX
 DT 16-MAR-1999 (first entry)
 XX
 DE Staphylococcus aureus protein SEQ ID #5254.
 XX
 KM Computer readable medium; vaccine; *S. aureus* infection; immunodetection;
 KM cellulitis; eyelid infection; food poisoning; osteomyelitis; therapy;
 KM skin infection; surgical wound infection; scalded skin syndrome;
 KM toxic shock syndrome.
 XX
 OS Staphylococcus aureus.
 XX
 PN EP786519-A2.
 XX
 PD 30-JUL-1997.
 XX
 DT 07-JAN-1997; 97EP-00100117.
 XX
 PR 05-JAN-1996; 96US-0009861P.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 XX
 PI Kunsch CA, Choi GH, Barash SC, Dillon PJ, Fannon MR, Rosen CA;
 PI WPI; 1997-374922/35.
 XX
 DR Polynucleotide(s) and proteins derived from Staphylococcus aureus -
 XX PT stored on computer readable medium and used in the production of anti-
 PT *S. aureus* vaccines.
 XX


```

XX Claim 23; Page 3263-3267; 3271pp; English.
PS
XX This sequence represents a Staphylococcus aureus protein sequence of the
XX invention. The DNA sequences encoding the S.aureus proteins are recorded
XX on a computer readable medium, preferably selected from a floppy or hard
XX disk, random access memory (RAM), read-only memory (ROM) or CD-ROM.
XX Homology searches using the S.aureus DNA sequences allows putative
XX functions to be assigned so that protein-encoding or regulatory regions
XX of commercial, therapeutic or industrial importance can be contained.
XX Specifically, sequences which are likely to encode antigens have been
XX identified and these polypeptides can be used in a vaccine composition
XX against S.aureus infection. The polypeptides can also be used in a kit
XX for the immunodetection of S.aureus in a sample. S.aureus is implicated
XX in numerous human diseases, including cellulitis, eyelid infections, food
XX poisoning, osteomyelitis, skin and surgical wound infections, scaled
XX skin syndrome, toxic shock syndrome, etc. Organisms transformed with the
XX DNA sequences can be used for recombinant production of the polypeptides.
XX The new DNA sequences (and their fragments) are useful as primers or
XX probes for isolating homologues of any of the 5191 S.aureus DNA sequences
XX contained on the computer readable medium
XX
SQ Sequence 1027 AA;

Query Match          94.8%; Score 202; DB 2; Length 1027;
Best Local Similarity 97.4%; Pred. No. 1,7e-19;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 ONKGNQSPEDTEKDKPKYEHGNIIDIDPDSVPHIHG 38
Db 793 ONKGNQSPEDTEKDKPKYEHGNIIDIDPDSVPHIHG 830

RESULT 11
AAR88749
ID AAR88749 standard; protein; 77 AA.
XX
AC AAR88749;
XX
DT 24-SEP-1996 (first entry)
XX
DE S. aureus fibronectin binding protein D2D3 polypeptide.
XX
KW Fibronectin binding protein; D2D3; prevention; adhesion; bacteria;
KW gram positive; extracellular matrix protein; in-dwelling device;
KW catheter; wound; D2D3; oral pathogen; oral cavity; J2385; NCIMB 40532.
XX
OS Staphylococcus aureus.
XX
PN WO9604380-A1.
XX
PD 15-FEB-1996.
XX
PF 28-JUL-1995; 95WO-EP003039.
XX
PR 05-AUG-1994; 94GB-00015901.
XX
PA (SMIK ) SMITHKLINE BEECHAM PLC.
XX
PI Critchley IA, Dodd I, Barnett P, Mossakowska DEI;
XX
DR WPI; 1996-129396/13.
XX
DR N-FEDB; AAT12582.
XX
PT Staphylococcus aureus fibronectin binding protein D2D3 polypeptide -
PT useful for combating infection at wound sites, surgical implants, etc.
PT and as antiadherent agent in oral hygiene.
XX
PS Claim 5; Page 26; 38pp; English.
XX
XX The present sequence is the S. aureus fibronectin binding protein
XX polypeptide D2D3, which can be used to prevent adhesion of (e.g. gram
XX positive) bacteria, to extra-cellular matrix proteins on in-c-welling

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CC devices, e.g. catheters or in wounds. D2D3 can also be used to prevent
CC oral pathogens from binding to extra-cellular matrix proteins, in the
CC oral cavity. D2D3 was found to be effective at inhibiting S. aureus 8325-
CC 4, and 120 adhesion to fibronectin coated PMMA coverings, at a min.
CC addresson inhibitor concn. of 10 microg/ml. D2D3 was derived from the D2
CC and D3 regions of the S. aureus J2385 (NCIMB 40532) fibronectin binding
CC protein
XX
SQ Sequence 77 AA;

Query Match          92.5%; Score 197; DB 2; Length 77;
Best Local Similarity 94.7%; Pred. No. 3.8e-20;
Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 ONKGNQSPEDTEKDKPKYEHGNIIDIDPDSVPHIHG 38
Db 2 ONKGDQSPEDTEKDKPKYEHGNIIDIDPDSVPHIHG 39

RESULT 12
AAR90937
ID AAR90937 standard; peptide; 113 AA.
XX
AC AAR90937;
XX
DT 23-SEP-1996 (first entry)
XX
DE D3D4 polypeptide #1.
XX
KW Fibronectin binding protein; Fbp; S.aureus J2385; monoclonal antibody;
KW infection; surgical implant; antiadherent agent; hygiene; adhesion;
KW extracellular matrix protein; oral pathogen; oral cavity.
XX
OS Staphylococcus aureus.
XX
FH Key
FH Region
FH /note= "D1 region fragment"
FT 22..59
FT /note= "D2 region"
FT 60..98
FT /note= "D3 region"
FT 99..113
FT /note= "D4 region"
FT Misc-difference 113
FT /note= "P113T"
XX
PN WO9604381-A1.
XX
PD 15-FEB-1996.
XX
PF 28-JUL-1995; 95WO-EP003040.
XX
PR 05-AUG-1994; 94GB-00015900.
XX
PA (SMIK ) SMITHKLINE BEECHAM PLC.
XX
PI Critchley IA, Dodd I, Barnett P, Mcbay DL;
XX
DR WPI; 1996-129397/13.
XX
PT Polypeptide(s) derived from Staphylococcus aureus fibronectin binding
PT protein - inhibit binding of bacteria to extracellular matrix proteins,
PT for combating infection at the site of wounds and surgical implants, and
PT in oral hygiene.
XX
PS Claim 6; Page 24; 35pp; English.
XX
XX AAR90937-R90942 represent D3D4 polypeptides. These sequences correspond
XX to fragments of the Staphylococcus aureus fibronectin binding protein
XX (Fbp). This sequence corresponds to residues 18-130 of S.aureus J2385
XX Fbp, and also contains the D2 region, and a portion of the D1 region.
XX These sequences, and monoclonal antibodies against them can be used to

```

CC combat infection at the site of wounds, surgical implants and other in-
 CC dwelling devices (such as catheters), and as antiadherent agents in oral
 CC hygiene. They can also be used in the manufacture of a medicament for the
 CC prevention of adhesion of bacteria to extracellular matrix proteins
 CC present on in-dwelling devices or in wounds, or of oral pathogens to
 CC similar proteins on surfaces in the oral cavity
 CC
 SQ Sequence 113 AA;

Query Match 92.5%; Score 197; DB 2; Length 113;
 Best Local Similarity 94.7%; Pred. No. 6e-20;
 Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 QNKGNSPEEDTEKDKPKYEHGNIIDIDPSVPHIHG 38
 DB 23 QNKGDSFEDTEKDKPKYEHGNIIDIDPSVPHIHG 60

RESULT 13
 AAR58806
 ID AAR58806 standard; protein; 130 AA.

AC AAR58806;
 XX
 XX 25-MAR-2003 (revised)
 DT 30-MAR-1995 (first entry)
 DE Fibronectin binding domain D1-D4(709-838(P838T)).
 XX
 XX Fibronectin binding protein; Fbp; fibronectin binding domain;
 KW monoclinal antibody; Mab; adhesion; Gram-positive bacterium; bacteremia;
 KW Escherichia coli.
 XX
 OS Staphylococcus aureus.
 XX
 PN WO9418327-A1.
 XX
 PD 18-AUG-1994.
 XX
 PF 04-FEB-1994; 94WO-GB000215.
 XX
 PR 05-FEB-1993; 93GB-00002289.
 PR 20-OCT-1993; 93GB-00021592.
 XX
 PA (SMIK) SMITHKLINE BEECHAM PLC.
 XX
 PI Burnham MKR, Chopra I, Critchley IA, Knowles DJC;
 XX
 DR WPI; 1994-279748/34.
 XX
 PT Fibronectin binding protein and monoclonal antibodies specific for Fbp -
 PT useful to prevent adherence of Gram-positive bacteria to indwelling
 PT devices or wounds.
 XX
 PS Disclosure; Page 30; 40pp; English.
 XX
 CC Polypeptides corresponding to residues G709-T886 plus PPIVPT, G709-
 CC P838(P838T) and G709-P838 (AAR58805-07, respectively) of S. aureus J2385
 CC (NCIMB 40532) Fbp type A fibronectin binding domain D1-D4 region
 CC (AAR58808) were expressed in E. coli BL21(DE4) and used to raise MBs
 CC specific for Fbp. (Updated on 25-MAR-2003 to correct PN field.)
 CC
 XX
 SQ Sequence 130 AA;

Query Match 92.5%; Score 197; DB 2; Length 130;
 Best Local Similarity 94.7%; Pred. No. 7.2e-20;
 Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 QNKGNSPEEDTEKDKPKYEHGNIIDIDPSVPHIHG 38
 DB 40 QNKGDSFEDTEKDKPKYEHGNIIDIDPSVPHIHG 77

RESULT 14
 AAR58807
 ID AAR58807 standard; protein; 130 AA.

AC AAR58807;
 XX
 XX 25-MAR-2003 (revised)
 DT 30-MAR-1995 (first entry)
 DE Fibronectin binding domain D1-D4(709-838).
 XX
 XX Fibronectin binding protein; Fbp; fibronectin binding domain;
 KW monoclinal antibody; Mab; adhesion; Gram-positive bacterium; bacteremia;
 KW Escherichia coli.
 XX
 OS Staphylococcus aureus.
 XX
 PN WO9418327-A1.
 XX
 PD 18-AUG-1994.
 XX
 PF 04-FEB-1994; 94WO-GB000215.
 XX
 PR 05-FEB-1993; 93GB-00002289.
 PR 20-OCT-1993; 93GB-00021592.
 XX
 PA (SMIK) SMITHKLINE BEECHAM PLC.
 XX
 PI Burnham MKR, Chopra I, Critchley IA, Knowles DJC;
 XX
 DR WPI; 1994-279748/34.
 XX
 PT Fibronectin binding protein and monoclonal antibodies specific for Fbp -
 PT useful to prevent adherence of Gram-positive bacteria to indwelling
 PT devices or wounds.
 XX
 PS Disclosure; Page 30; 40pp; English.
 XX
 CC Polypeptides corresponding to residues G709-T886 plus PPIVPT, G709-
 CC P838(P838T) and G709-P838 (AAR58805-07, respectively) of S. aureus J2385
 CC (NCIMB 40532) Fbp type A fibronectin binding domain D1-D4 region
 CC (AAR58808) were expressed in E. coli BL21(DE4) and used to raise MBs
 CC specific for Fbp. (Updated on 25-MAR-2003 to correct PN field.)
 CC
 XX
 SQ Sequence 130 AA;

Query Match 92.5%; Score 197; DB 2; Length 130;
 Best Local Similarity 94.7%; Pred. No. 7.2e-20;
 Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 QNKGNSPEEDTEKDKPKYEHGNIIDIDPSVPHIHG 38
 DB 40 QNKGDSFEDTEKDKPKYEHGNIIDIDPSVPHIHG 77

RESULT 15
 AAR91202
 ID AAR91202 standard; peptide; 130 AA.

AC AAR91202;
 XX
 XX 13-NOV-1996 (first entry)
 DT
 XX
 DE D1-D4 fibronectin binding domains.
 XX
 XX Fibronectin; oral hygiene; gingivitis; gum disease; adhesion;
 KW periodontitis; oral pathogen; caries; calculus; candidiasis; oral surgery;
 KW tissue regeneration; irrigation; toothpaste; dentifrice; mouthwash;
 KW lozenge.
 XX
 OS Staphylococcus aureus.
 XX
 PN WO9604003-A1.

```

XX 15-FEB-1996.
PD
XX
XX 18-JUL-1995; 95WO-EP002825.
PF
XX
XX 05-AUG-1994; 94GB-00015902.
PR
XX
XX (SMIK ) SMITHKLINE BEECHAM PLC.
PA
XX
XX Barnett P, Critchley IA, Dodd I;
PI
XX
XX WPI; 1996-129122/13.
DR
XX
PT Prevention of adherence of oral pathogens in the oral cavity, partic.
PT tooth surfaces - by application of a fibronectin binding protein or
PT polypeptide or a monoclonal antibody or fragment against it.
XX
XX
XX Claim 5; Page 32; 41pp; English.
PS
XX
XX Adherence of oral pathogens, particularly to tooth surfaces, can be
XX prevented by application of a fibronectin binding protein or polypeptide.
XX The fibronectin binding protein or polypeptide is useful in the
XX manufacture of oral hygiene compositions, eg. toothpaste, liquid
XX dentifrice, mouthwash or lozenge. They are useful to prevent the plaque-
XX related development of carious lesions, gingivitis, calculus or
XX periodontal disease and to combat oral cavity infections, eg
XX candidiasis. They may also be useful in oral surgery e.g. in guided
XX tissue regeneration procedures to prevent subsequent bacterial infection,
XX and for irrigation of periodontal pockets. This sequence corresponds to
XX amino acids 709-838 of the D1-D4 fibronectin binding domain of
XX Staphylococcus aureus
XX
XX Sequence 130 AA:
SQ

```

```

Query Match 92.5%; Score 197; DB 2; Length 130;
Best Local Similarity 94.7%; Pred. No. 7.2e-20;
Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

```

```

QY 1 ONKGNQSPEDTEKDKPYEHGNIIDIDFDSVPHIHG 38
   |||:| | | | | | | | | | | | | | | | |
Db 40 ONKGDQSFEDTEKDKPYEHGNIIDIDFDSVPHIHG 77

```

Search completed: October 25, 2005, 20:21:05
 Job time : 84.8825 secs

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OM protein - protein search, using sw model

Run on: October 25, 2005, 19:38:38 ; Search time 83.8325 Seconds
(without alignments)
175.313 Million cell updates/sec

Title: US-10-731-238-48

Perfect score: 213
Sequence: 1 QNKGQSFEEPTKDKPKYEHGNTIDPDSVPHHG 38

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04.*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	213	100.0	38	2	AAW65704 Fibronect
2	205	96.2	38	2	AAW65663 Fibronect
3	205	96.2	134	2	AAW29087 S. aureus
4	205	96.2	139	2	AAW31556 Fibronect
5	205	96.2	1018	1	AAW82115 Fibronect
6	205	96.2	1018	4	AAU37245 Staphyloc
7	205	96.2	1018	4	AAU34301 Staphyloc
8	205	96.2	1018	6	ABJ18922 Patchogen
9	205	96.2	1018	6	ABM72537 Staphyloc
10	205	96.2	1027	2	AAW89806 Staphyloc
11	200	93.9	77	2	AAW88749 S. aureus
12	200	93.9	113	2	AAW90937 D3D4 poly
13	200	93.9	130	2	AAW58806 Fibronect
14	200	93.9	130	2	AAW58807 Fibronect
15	200	93.9	130	2	AAW91202 D1-D4 fib
16	200	93.9	130	2	AAW91201 D1-D4 fib
17	200	93.9	162	2	AAW90942 D3D4 poly
18	200	93.9	164	2	AAW90938 D3D4 poly
19	200	93.9	174	2	AAW58808 Bdp fibro
20	200	93.9	174	2	AAW91203 D1-D4 fib
21	200	93.9	181	2	AAW58805 Fibronect
22	200	93.9	181	2	AAW91200 D1-D4 fib
23	199	93.4	38	1	AAW80661 Protein w
24	199	93.4	38	1	AAW82117 Fibronect
25	199	93.4	38	2	AAW65703 Fibronect

26	199	93.4	38	2	AAW65702	AAW65702 Fibronect
27	197	92.5	38	2	AAW65664	AAW65664 Fibronect
28	197	92.5	38	2	AAW65705	AAW65705 Fibronect
29	195	91.5	38	2	AAW65701	AAW65701 Fibronect
30	192	90.1	134	2	AAW29088	AAW29088 S. aureus
31	192	90.1	559	2	AAW89803	AAW89803 Staphyloc
32	192	90.1	767	4	AAU34403	AAU34403 Staphyloc
33	192	90.1	767	4	AAU37547	AAU37547 Staphyloc
34	192	90.1	940	2	AAW07070	AAW07070 Fibronect
35	192	90.1	940	6	ABJ19111	ABJ19111 Patchogen
36	192	90.1	948	6	ADA89470	ADA89470 Staphyloc
37	192	90.1	948	6	ABJ18923	ABJ18923 Patchogen
38	192	90.1	948	6	ABM72536	ABM72536 Staphyloc
39	192	90.1	1038	6	ABU15903	ABU15903 Protein e
40	187	87.8	38	2	AAW65694	AAW65694 Fibronect
41	184	86.4	978	4	AAU33960	AAU33960 Staphyloc
42	184	86.4	1001	4	AAU37093	AAU37093 Staphyloc
43	183	85.9	134	2	AAW29089	AAW29089 Cloned f1
44	182	85.4	36	2	AAW65714	AAW65714 Fibronect
45	180	84.5	961	6	ABU15854	ABU15854 Protein e

ALIGNMENTS

RESULT 1
ID AAW65704 standard; peptide; 38 AA.
XX AC AAW65704;
XX DT 16-OCT-1998 (first entry)

XX DE Fibronectin binding protein-derived peptide #48.

XX KM microbial surface components recognising adhesive molecule;
KW MSCRAMM; fibronectin; fibronectin-binding protein; antibody; epitope;
KW antibiotic; bacterial infection; antibiotic-resistant strain.

XX OS Synthetic.
XX OS Staphylococcus aureus.

XX PN W09831389-A2.

XX PD 23-JUL-1998.

XX PF 21-JAN-1998; 98WO-US001222.

XX PR 21-JAN-1997; 97US-0036139P.

XX PA (TEXA) UNIV TEXAS A & M SYSTEM.

XX PI Hoeseok M, Patti JM, House-Pompeo KL, Speziale P, Joh D;
PI Mogavvin MJ;
DR WPI; 1998-413816/35.

XX PT Antibody that binds to fibronectin-binding protein, preventing its
XX binding to fibronectin - used to treat or prevent bacterial infection,
XX especially by Staphylococci and Streptococci.

XX Example 8; Page 102; 201pp; English.

The invention relates to antibodies that bind to a fibronectin-binding domain of a fibronectin-binding protein, and inhibit binding of the protein to fibronectin. Also claimed are: (1) isolated peptides of a fibronectin-binding protein that do not bind to fibronectin; (2) fusion protein containing at least one peptide of a fibronectin-binding protein linked to a second amino acid sequence; (3) nucleic acid encoding the isolated peptide of (1). Antibodies, the isolated peptides of (1) and the nucleic acids are all useful for immunisation (active or passive) and (by inhibiting binding of bacteria to fibronectin) for preventing or treating infection in humans or other animals, particularly by staphylococci or

CC streptococci, e.g. meningitis, otitis media, pneumonia, endocarditis,
 CC mastitis in cattle, abortion in horses and many others. Since the
 CC antibodies block binding of bacteria, they should be effective against
 CC antibiotic-resistant strains, and may replace antibiotic therapy or
 CC increase its effectiveness. Sequences AAM65701-706 represent a series of
 CC synthetic peptides based on the D2 region of *S. aureus* fibronectin
 CC binding protein A. They were synthesised to contain mutations

XX Sequence 38 AA;

SO Query Match 100.0%; Score 213; DB 2; Length 34;
 Best Local Similarity 100.0%; Pred. No. 1.8e-23;
 Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 QNKGNSFEETPEKDKPKYEHGNIIDIDFDSVPHIHG 38
 DB 1 QNKGNSFEETPEKDKPKYEHGNIIDIDFDSVPHIHG 38

RESULT 2
 ID AAM65663 standard; peptide; 38 AA.
 XX AAM65663;

AC AAM65663;
 XX 16-OCT-1998 (first entry)
 DT
 DE Fibronectin binding protein-derived peptide #7.

XX microbial surface components recognising adhesive matrix molecule;
 KM MSCRAMM; fibronectin; fibronectin-binding protein; antibody; epitope;
 XX antibiotic; bacterial infection; antibiotic-resistant strain.

OS Synthetic.
 OS *Staphylococcus aureus*.
 XX WO9831389-A2.

PN 23-JUL-1998.

PF 21-JAN-1998; 98WO-US001222.

PR 21-JAN-1997; 97US-0036139P.

PA (TEXA) UNIV TEXAS A & M SYSTEM.

PI Hoeek M, Paci JW, House-Pompeo KL, Speziale P, Joh D:

PI McGavin MJ;

DR WPI; 1998-413816/35.

XX Antibody that binds to fibronectin-binding protein, preventing its
 PT binding to fibronectin - used to treat or prevent bacteria. infection,
 PT especially by *Staphylococci* and *Streptococci*.

XX Example 2; Page 92; 201pp; English.

XX The invention relates to antibodies that bind to a fibronectin-binding
 CC domain of a fibronectin-binding protein, and inhibit binding of the
 CC protein to fibronectin. Also claimed are: (1) isolated peptides of a
 CC fibronectin-binding protein that do not bind to fibronectin; (2) fusion
 CC protein containing at least one peptide of a fibronectin-binding protein
 CC linked to a second amino acid sequence; (3) nucleic acid encoding the
 CC isolated peptide of (1). Antibodies, the isolated peptides of (1) and the
 CC nucleic acids are all useful for immunisation (active or passive) and (by
 CC inhibiting binding of bacteria to fibronectin) for preventing or treating
 CC infection in humans or other animals, particularly by *staphylococci* or
 CC *streptococci*, e.g. meningitis, otitis media, pneumonia, endocarditis,
 CC mastitis in cattle, abortion in horses and many others. Since the
 CC antibodies block binding of bacteria, they should be effective against
 CC antibiotic-resistant strains, and may replace antibiotic therapy or
 CC increase its effectiveness. Sequences AAM65659-68 represent synthetic
 CC peptides from the fibronectin binding domains DU and DI-D4 of the *S.*

CC *aureus* fnbA gene
 XX Sequence 38 AA;

SO Query Match 96.2%; Score 205; DB 2; Length 38;
 Best Local Similarity 97.4%; Pred. No. 2.7e-22;
 Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 QNKGNSFEETPEKDKPKYEHGNIIDIDFDSVPHIHG 38
 DB 1 QNKGNSFEETPEKDKPKYEHGNIIDIDFDSVPHIHG 38

RESULT 3
 ID AAY29087 standard; protein; 134 AA.
 XX AAY29087;

AC AAY29087;
 XX 28-SEP-1999 (first entry)
 DT
 DE *S. aureus* fibronectin binding protein A (FnBA) binding domain.

XX Bovine herpes virus-2; BHV-2; cytokine; immune response; immunogen; IL;
 KM interleukin; colony stimulating factor; CSF; interferon; IFN; TNF;
 KM tumour necrosis factor; recombinant virus; vaccine; mucosal disease;
 KM mastitis; breast cancer; stress-induced disease; binding domain; FnBA;
 KM fibronectin binding protein.

XX *Staphylococcus aureus*.
 OS WO9916892-A1.

PN 08-APR-1999.

PF 29-SEP-1998; 98WO-GB002927.

PR 29-SEP-1997; 97GB-00020633.

PA (UYBR-) UNIV BRISTOL.

PI Bradley AJ, Duffas WPH;

XX WPI; 1999-255101/21.

DR N-PSDB; AAX91504.

PT New bovine herpes virus-2 vectors.

XX Example 2; Fig 8A-B; 130pp; English.

XX The invention provides bovine herpes virus-2 (BHV-2) based vectors that
 CC comprise at least one cytokine-encoding DNA sequence. The expression of
 CC cytokines in mammals can up-regulate immune responses to the immunogens.
 CC The cytokine is selected from interleukins (IL), colony stimulating
 CC factors (CSF), interferons (IFN) and tumour necrosis factors (TNF). The
 CC BHV-2 based vector or recombinant virus can be used as vaccines. They can
 CC be used for preventing or treating a mucosal disease in a subject, e.g.
 CC ruminants, cattle, sheep, goats, dogs, cats, horses, or man, particularly
 CC mastitis in cows or breast cancers in humans. They can also be used for
 CC preventing or treating a stress-induced disease. The present sequence
 CC represents the binding domain of a previously published *S. aureus*
 CC fibronectin binding protein A (FnBA) sequence. The FnB binding domain
 CC gene sequence FnNB, cloned for use in this invention has 97.8 percent
 CC identity when compared to the previously published FnBA and FnBB gene
 CC sequences

XX Sequence 134 AA;

SO Query Match 96.2%; Score 205; DB 2; Length 134;
 Best Local Similarity 97.4%; Pred. No. 1.3e-21;
 Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 QNKGNSFEETPEKDKPKYEHGNIIDIDFDSVPHIHG 38

Db 40 QNKGNSFEEDTEKDKPKYEHGNIIDIDPDSVPHING 77

RESULT 4

AAW31556 standard; protein: 139 AA.

AAW31556;

27-AUG-2003 (revised)

25-MAR-2003 (revised)

21-MAY-1998 (first entry)

Fibronectin-binding MSCRAMM derivative POD.

microbial surface component region; sepsis; infection; MSCRAMM;

adhesin; vaccine; immunisation; diagnosis; therapy; mastitis.

Staphylococcus aureus.

Key Location/Qualifiers

Peptide 1..12 /note="vector POE30-derived peptide"

MO9743314-A2.

20-NOV-1997.

14-MAY-1997; 97WO-US008210.

16-MAY-1996; 96US-0017678P.

(TEXA) UNIV TEXAS A & M SYSTEM.

(UABR-) UAB RES FOUND.

Hoeek M, Fatti JM, House-Pompeo K, Sthanam N, Symersky J;

WPI; 1998-008801/01.

Antibody that interacts with collagen binding domain of Staphylococcal

PT cna gene product - useful to prevent bacterial sepsis in animal infected

with Staphylococcus aureus.

Disclousure; Page 91; 143pp; English.

This protein comprises Staphylococcus aureus fibronectin-binding

microbial surface component region; sepsis; infection; MSCRAMM)

derivative POD, plus a vector-derived N-terminal peptide. The invention

relates to claimed nucleic acid sequences (see AA93336-38) encoding S.

aureus collagen binding protein (CBP) epitopes M17, M31 and M55 (see

AAW31552-54) that confer protection against S. aureus infection. CBP

protein and antigenic epitopes are contemplated for use in the treatment

of pathological infections, especially to prevent bacterial adhesion to

collagen. The epitopes are also contemplated for use in the preparation

of vaccines and as carrier proteins in vaccine formulations, as well as

in the formulation of compositions for the prevention of S. aureus

infection. pCRf33 and pOD (see AAW31556) were used to raise anti-MSCRAMM

polyclonal antibodies used in passive immunisation against bovine

mastitis. (Updated on 25-MAR-2003 to correct PI field.) (Updated on 27-

AUG-2003 to correct OS field.)

Sequence 139 AA;

Query Match 96.2%; Score 205; DB 2; Length 139;

Best Local Similarity 97.4%; Pred. No. 1.4e-21;

Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

1 QNKGNSFEEDTEKDKPKYEHGNIIDIDPDSVPHING 38

54 QNKGNSFEEDTEKDKPKYEHGNIIDIDPDSVPHING 91

RESULT 5
AAP82115 standard; protein: 1018 AA.

AAP82115;

25-MAR-2003 (revised)

05-JUN-1990 (first entry)

Fibronectin binding protein.

Fibronectin binding protein; S. aureus; immunisation; mastitis; ruminants;

wound infection; diagnosis.

Staphylococcus aureus.

EP294349-A.

07-DEC-1988.

30-MAY-1988; 88EP-00850188.

01-JUN-1987; 87SE-00002272.

(ALFA) ALFA LAVAL AGRIC INT AB.

Lindberg MK, Signas LC, Wadstrom TM, Froman G;

WPI; 1988-347978/49.

Hybrid DNA encoding Staphylococcus aureus fibronectin binding protein -

useful for immunisation and topical application to prevent staphylococcal

infections.

Disclousure; Fig. 8A:1-8A:2; 23pp; English.

The S.aureus fibronectin binding protein may be included in a hybrid

protein. The protein may be used to immunise ruminants against

staphylococcal mastitis, pref. when given at 0.5-5 microg/kg, using 3

doses at 1-3 week intervals; and for topical applicn. to prevent wound

infection, pref. using isotonic saline soln. of concn. 25-250 microg/mg.

The DNA encoding the binding protein and the hybrid protein may be

immobilised on a carrier and used to diagnose staphylococcal infections.

(Updated on 25-MAR-2003 to correct PA field.)

Sequence 1018 AA;

Query Match 96.2%; Score 205; DB 1; Length 1018;

Best Local Similarity 97.4%; Pred. No. 1.6e-20;

Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

1 QNKGNSFEEDTEKDKPKYEHGNIIDIDPDSVPHING 38

784 QNKGNSFEEDTEKDKPKYEHGNIIDIDPDSVPHING 821

RESULT 6

AAU37245 standard; protein: 1018 AA.

AAU37245;

14-FEB-2002 (first entry)

Staphylococcus aureus cellular proliferation protein #1415.

Antisense; prokaryotic cellular proliferation protein; antibiotic;

antibacterial; drug design.

Staphylococcus aureus.

```

PN      WO200170955-A2.
XX
XX      27-SEP-2001.
PD
XX
XX      21-MAR-2001; 2001WO-US009180.
PF
XX
XX      21-MAR-2000; 2000US-0191078P.
PR      23-MAY-2000; 2000US-0206848P.
PR      26-MAY-2000; 2000US-0207277P.
PR      23-OCT-2000; 2000US-0242578P.
PR      27-NOV-2000; 2000US-0253625P.
PR      22-DEC-2000; 2000US-0257931P.
PR      16-FEB-2001; 2001US-0269308P.
XX
XX      (ELIT-) ELITRA PHARM INC.
XX
XX      Haselbeck R, Ohlsen KL, Zyskind JW, Wall D, Trawick JT, Carr GJ;
PI      Yamamoto RT, Xu HH;
PI      WPI; 2001-611495/70.
XX      N-PSDB; AAS55104.
DR
XX
XX      New polynucleotides for the identification and development of
PT      antibiotics, comprise sequences of antisense nucleic acids.
XX
XX      Example 3; SEQ ID NO 12838; 511pp; English.
XX
XX      The invention relates to antisense inhibitors of genes essential to
CC      prokaryotic cellular proliferation, their use in identifying the genes,
CC      their use in the discovery of novel antibiotics, the essential genes
CC      themselves and the encoded proteins. The prokaryotes used are Escherichia
CC      coli, Staphylococcus aureus, Salmonella typhi, Klebsiella pneumoniae,
CC      Pseudomonas aeruginosa and Enterococcus faecalis. The invention is also
CC      useful for the identification of potential new targets for antibiotic
CC      development. The antisense nucleic acids can also be used to identify
CC      proteins used in proliferation, to express these proteins, and to obtain
CC      antibodies capable of binding to the expressed proteins. The proteins can
CC      be used to screen compounds in rational drug discovery programmes. The
CC      antisense nucleic acid sequence is also useful to screen for homologous
CC      nucleic acids which are required for cell proliferation in a wide variety
CC      of organisms. The present sequence represents an essential prokaryotic
CC      cellular proliferation protein. Note: The sequence data for this patent
CC      did not form part of the printed specification, but was obtained in
CC      electronic format directly from WIPO at
CC      ftp.wipo.int/pub/published_pct_sequences
XX
XX      Sequence 1018 AA;
SQ
XX
XX      Query Match          96.2%; Score 205; DB 4; Length 1018;
XX      Best Local Similarity 97.4%; Pred. No. 1.6e-20;
XX      Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY      1 QNKGNSFEPEPTKDKPKYEHGNIIDIDFDSVPHHG 38
DB      784 QNKGNSFEPEPTKDKPKYEHGNIIDIDFDSVPHHG 821

```

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XX
XX      27-SEP-2001.
PD
XX
XX      21-MAR-2001; 2001WO-US009180.
PF
XX
XX      21-MAR-2000; 2000US-0191078P.
PR      23-MAY-2000; 2000US-0206848P.
PR      26-MAY-2000; 2000US-0207277P.
PR      23-OCT-2000; 2000US-0242578P.
PR      27-NOV-2000; 2000US-0253625P.
PR      22-DEC-2000; 2000US-0257931P.
PR      16-FEB-2001; 2001US-0269308P.
XX
XX      (ELIT-) ELITRA PHARM INC.
XX
XX      Haselbeck R, Ohlsen KL, Zyskind JW, Wall D, Trawick JD, Carr GJ;
PI      Yamamoto RT, Xu HH;
PI      WPI; 2001-611495/70.
XX      N-PSDB; AAS52160.
DR
XX
XX      New polynucleotides for the identification and development of
PT      antibiotics, comprise sequences of antisense nucleic acids.
XX
XX      Example 3; SEQ ID NO 5797; 511pp; English.
XX
XX      The invention relates to antisense inhibitors of genes essential to
CC      prokaryotic cellular proliferation, their use in identifying the genes,
CC      their use in the discovery of novel antibiotics, the essential genes
CC      themselves and the encoded proteins. The prokaryotes used are Escherichia
CC      coli, Staphylococcus aureus, Salmonella typhi, Klebsiella pneumoniae,
CC      Pseudomonas aeruginosa and Enterococcus faecalis. The invention is also
CC      useful for the identification of potential new targets for antibiotic
CC      development. The antisense nucleic acids can also be used to identify
CC      proteins used in proliferation, to express these proteins, and to obtain
CC      antibodies capable of binding to the expressed proteins. The proteins can
CC      be used to screen compounds in rational drug discovery programmes. The
CC      antisense nucleic acid sequence is also useful to screen for homologous
CC      nucleic acids which are required for cell proliferation in a wide variety
CC      of organisms. The present sequence represents an essential prokaryotic
CC      cellular proliferation protein. Note: The sequence data for this patent
CC      did not form part of the printed specification, but was obtained in
CC      electronic format directly from WIPO at
CC      ftp.wipo.int/pub/published_pct_sequences
XX
XX      Sequence 1018 AA;
SQ
XX
XX      Query Match          96.2%; Score 205; DB 4; Length 1018;
XX      Best Local Similarity 97.4%; Pred. No. 1.6e-20;
XX      Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY      1 QNKGNSFEPEPTKDKPKYEHGNIIDIDFDSVPHHG 38
DB      784 QNKGNSFEPEPTKDKPKYEHGNIIDIDFDSVPHHG 821

```

```

RESULT 7
AAU34301
ID      AAU34301 standard; protein; 1018 AA.
XX
XX      AAU34301;
AC
XX
XX      14-FEB-2002 (first entry)
DT
XX
XX      Staphylococcus aureus cellular proliferation protein #577.
DE
XX
XX      Antisense; prokaryotic cellular proliferation protein; antibiotic;
KW      antibacterial; drug design.
KW      apHy]ococcus aureus.
XX
XX      00170955-A2.

```

```

RESULT 8
ABJ18922
ID      ABJ18922 standard; protein; 1018 AA.
XX
XX      ABJ18922;
AC
XX
XX      06-MAR-2003 (first entry)
DT
XX
XX      Pathogen specific antigen related staphylococcal protein SEQ ID No 68.
DE
XX
XX      Antibacterial; virucide; fungicide; protozoacide; cytostatic; anti-HIV;
KW      hyperimmune; serum-reactive; antigen; pathogen; tumour; allergen;
KW      auto-immunity; vaccine; staphylococcal infection; antibody; cancer;
KW      autoimmune disease; HIV; hepatitis.
XX
XX      Staphylococcus sp.
XX

```

PN WO200259148-A2.
 XX
 PD 01-AUG-2002.
 XX
 PF 21-JAN-2002; 2002WO-EP000546.
 XX
 PR 26-JAN-2001; 2001AT-00000130.
 XX
 PA (CIST-) CISTEM BIOTECHNOLOGIES GMBH.
 XX
 PI Meinke A, Nagy E, Von Ahnen U, Klade C, Henics T, Zauner W;
 PI Minh DB, Vytvyrska O, Etz H, Dryla A, Weichhart T, Hafner M;
 PI Tempelmeier B;
 DR WPI; 2003-075410/07.
 XX
 PT Identifying, isolating and producing hyperimmune serum-reactive antigens
 PT from a pathogen, for preparing vaccine or medicament for treating or
 PT preventing e.g. staphylococcal infections, comprises providing antibody
 PT preparation.
 PS
 XX Example 7; Page 157; 252pp; English.
 CC The invention relates to a novel method for identifying, isolating and
 CC producing hyperimmune serum-reactive antigens from a pathogen, tumour,
 CC allergen, a tissue or host prone to auto-immunity, where the antigens are
 CC used in a vaccine, comprises providing antibody preparation from a plasma
 CC pool of a type of animal, or individual sera with antibodies against the
 CC specific pathogen, tumour, allergen, tissue or host prone to auto-
 CC immunity. The hyperimmune serum-reactive antigens comprising any of the
 CC 62 sequences of 53-2261 amino acids fully defined in the specification,
 CC or their hyperimmune fragments are useful for the manufacture of a
 CC pharmaceutical preparation, particularly a vaccine against staphylococcal
 CC infections or colonisation against *S. aureus* or *S. epidermidis*. The
 CC preparation of antibodies is useful for the manufacture of a medicament
 CC for treating or preventing staphylococcal infections or colonisation
 CC against *S. aureus* or *S. epidermidis*. The antibody preparations may also
 CC be used for diagnostic and imaging purposes. Other conditions that can be
 CC treated include cancer, autoimmune diseases or infections caused by viral
 CC (e.g. HIV, hepatitis A, B or C), fungal or protozoan pathogens. This
 CC sequence represents a staphylococcal protein relating to the method for
 CC identifying and producing pathogen specific antigens of the invention
 CC
 XX
 SQ Sequence 1018 AA;
 Query Match 96.2%; Score 205; DB 6; Length 1018;
 Best Local Similarity 97.4%; Pred. No. 1,6e-20;
 Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 QNKGNSFEEPTKDKPKYEHGNIIDIDFSVPHHG 38
 Db 784 QNKGNSFEEPTKDKPKYEHGNIIDIDFSVPHHG 821
 RESULT 9
 ABM72537
 ID ABM72537 standard; protein; 1018 AA.
 XX
 AC ABM72537;
 XX
 DT 20-NOV-2003 (first entry)
 XX
 DE Staphylococcus aureus protein #1777.
 XX
 KW Antibacterial; vaccine; gene therapy; infection; sepsis; diagnosis;
 KW enzymatic assay; antibiotic target.
 XX
 OS Staphylococcus aureus.
 XX
 PN WO200294868-A2.
 PD 28-NOV-2002.
 XX

PF 27-MAR-2002; 2002WO-IB002637.
 XX
 PR 27-MAR-2001; 2001GB-00007661.
 XX
 PA (CHIR-) CHIRON SPA.
 XX
 PI Masignani V, Mora M, Scarselli M;
 DR WPI; 2003-120786/11.
 DR N-PSDB; ACF74097.
 XX
 PT New Staphylococcus aureus protein, useful as a vaccine for treating or
 PT preventing Staphylococcal infection, specifically an infection caused by
 PT *S. aureus*, e.g. sepsis.
 PS
 XX Claim 1; SEQ ID NO 3554; 49pp; English.
 CC The invention relates to novel genes and encoded proteins from
 CC Staphylococcus aureus. A composition comprising the *S. aureus* protein, a
 CC nucleic acid encoding the protein, or an antibody to the protein, is
 CC useful as a pharmaceutical, particularly as a vaccine for treating or
 CC preventing infection due to Staphylococcus bacteria, specifically an
 CC infection caused by *S. aureus*. The composition is particularly useful for
 CC treating or preventing sepsis in a patient. The composition can also be
 CC used for diagnostics. The protein is also used in an assay for enzymatic
 CC studies and as a target for antibiotics. This sequence represents one of
 CC the novel *S. aureus* proteins of the invention
 CC
 XX
 SQ Sequence 1018 AA;
 Query Match 96.2%; Score 205; DB 6; Length 1018;
 Best Local Similarity 97.4%; Pred. No. 1,6e-20;
 Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 QNKGNSFEEPTKDKPKYEHGNIIDIDFSVPHHG 38
 Db 784 QNKGNSFEEPTKDKPKYEHGNIIDIDFSVPHHG 821
 RESULT 10
 AAM89806
 ID AAM89806 standard; protein; 1027 AA.
 XX
 AC AAM89806;
 XX
 DT 16-MAR-1999 (first entry)
 XX
 DE Staphylococcus aureus protein SEQ ID #5254.
 XX
 KW Computer readable medium; vaccine; *S. aureus* infection; immunodetection;
 KW cellulitis; eyelid infection; food poisoning; osteomyelitis; therapy;
 KW skin infection; surgical wound infection; scalded skin syndrome;
 KW toxic shock syndrome.
 XX
 OS Staphylococcus aureus.
 XX
 PN EP786519-A2.
 PD 30-JUL-1997.
 XX
 PF 07-JAN-1997; 97EP-00100117.
 XX
 PR 05-JAN-1996; 96US-0009861P.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 XX
 PI Kunesh CA, Choi GH, Barash SC, Dillon PJ, Fannon MR, Rosen CA;
 DR WPI; 1997-374922/35.
 XX
 PT Polynucleotide(s) and proteins derived from Staphylococcus aureus -
 PT stored on computer readable medium and used in the production of anti-
 PT *S. aureus* vaccines.
 XX

XX Claim 23; Page 3263-3267; 3271pp; English.
 XX This sequence represents a Staphylococcus aureus protein sequence of the
 CC invention. The DNA sequences encoding the S. aureus proteins are recorded
 CC on a computer readable medium, preferably selected from a floppy or hard
 CC disk, random access memory (RAM), read-only memory (ROM) or CD-ROM.
 CC Homology searches using the S. aureus DNA sequences allows putative
 CC functions to be assigned so that protein-encoding or regulatory regions
 CC of commercial, therapeutic or industrial importance can be obtained.
 CC Specifically, sequences which are likely to encode antigens have been
 CC identified and these polypeptides can be used in a vaccine composition
 CC against S. aureus infection. The polypeptides can also be used in a kit
 CC for the immunodetection of S. aureus in a sample. S. aureus is implicated
 CC in numerous human diseases, including cellulitis, eyelid infections, food
 CC poisoning, osteomyelitis, skin and surgical wound infections, scalded
 CC skin syndrome, toxic shock syndrome, etc. Organisms transformed with the
 CC DNA sequences can be used for recombinant production of the polypeptides.
 CC The new DNA sequences (and their fragments) are useful as primers or
 CC probes for isolating homologues of any of the 5191 S. aureus DNA sequences
 CC contained on the computer readable medium
 CC
 SQ Sequence 1027 AA;
 Query Match 96.2%; Score 205; DB 2; Length 1077;
 Best Local Similarity 97.4%; Pred. No. 1.7e-20;
 Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 QNKGNSFEPTKDKPKYEHGNIIDIDFDSVPHIHG 38
 DB 793 QNKGNSFEPTKDKPKYEHGNIIDIDFDSVPHIHG 830
 RESULT 11
 AAR8749
 ID AAR8749 standard; protein; 77 AA.
 AC AAR8749;
 DT 24-SEP-1996 (first entry)
 DE S. aureus fibronectin binding protein D2D3 polypeptide.
 DE Fibronectin binding protein; D2D3; prevention; adhesion; bacteria;
 KW gram positive; extra-cellular matrix protein; in-dwelling device;
 KW catheter; wound; D2D3; oral pathogen; oral cavity; J2385; NCIMB 40532.
 OS Staphylococcus aureus.
 PN WO9604380-A1.
 PD 15-FEB-1996.
 PF 28-JUL-1995; 95WO-EP003039.
 PR 05-AUG-1994; 94GB-00015901.
 PA (SMIK) SMITHKLINE BEECHAM PLC.
 PI Critchley IA, Dodd I, Barnett P, Mossakowska DEI;
 DR WPI; 1996-129396/13.
 DR N-PDB; AAT12582.
 XX Staphylococcus aureus fibronectin binding protein D2D3 polypeptide -
 PT useful for combating infection at wound sites, surgical implants, etc.
 PT and as antichelent agent in oral hygiene.
 PS Claim 5; Page 26; 38pp; English.
 e present sequence is the S. aureus fibronectin binding protein
 D2D3, which can be used to prevent adhesion of (e.g. gram
 active) bacteria, to extra-cellular matrix proteins on in-dwelling

CC devices, e.g. catheters or in wounds. D2D3 can also be used to prevent
 CC oral pathogens from binding to extra-cellular matrix proteins, in the
 CC oral cavity. D2D3 was found to be effective at inhibiting S. aureus 8325-
 CC 4, and 120 adhesion to fibronectin coated PMMA coverlips, at a min.
 CC adhesion inhibitor concn. of 10 microg/ml. D2D3 was derived from the D2
 CC and D3 regions of the S. aureus J2385 (NCIMB 40532) fibronectin binding
 CC protein
 CC
 SQ Sequence 77 AA;
 Query Match 93.9%; Score 200; DB 2; Length 77;
 Best Local Similarity 94.7%; Pred. No. 3.5e-21;
 Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 1 QNKGNSFEPTKDKPKYEHGNIIDIDFDSVPHIHG 38
 DB 2 QNKGNSFEPTKDKPKYEHGNIIDIDFDSVPHIHG 39
 RESULT 12
 AAR90937
 ID AAR90937 standard; peptide; 113 AA.
 AC AAR90937;
 DT 23-SEP-1996 (first entry)
 DE D3D4 polypeptide #1.
 DE Fibronectin binding protein; Fbp; S. aureus J2385; monoclonal antibody;
 KW infection; surgical implant; antichelent agent; hygiene; adhesion;
 KW extracellular matrix protein; oral pathogen; oral cavity.
 OS Staphylococcus aureus.
 PN WO9604381-A1.
 PD 15-FEB-1996.
 PF 28-JUL-1995; 95WO-EP003040.
 PR 05-AUG-1994; 94GB-00015900.
 PA (SMIK) SMITHKLINE BEECHAM PLC.
 PI Critchley IA, Dodd I, Barnett P, Mcbay DL;
 DR WPI; 1996-129397/13.
 PT Polypeptide(s) derived from Staphylococcus aureus fibronectin binding
 PT protein - inhibit binding of bacteria to extracellular matrix proteins,
 PT for combating infection at the site of wounds and surgical implants, and
 PT in oral hygiene.
 PS Claim 6; Page 24; 35pp; English.
 AAR90937-R90942 represent D3D4 polypeptides. These sequences correspond
 CC to fragments of the Staphylococcus aureus fibronectin binding protein
 CC (Fbp). This sequence corresponds to residues 18-130 of S. aureus J2385
 CC Fbp, and also contains the D2 region, and a portion of the D1 region.
 CC These sequences, and monoclonal antibodies against them can be used to

CC combat infection at the site of wounds, surgical implants and other in-
 CC dwelling devices (such as catheters), and as antiadherent agents in oral
 CC hygiene. They can also be used in the manufacture of a medicament for the
 CC prevention of adhesion of bacteria to extracellular matrix proteins
 CC present on in-dwelling devices or in wounds, or of oral pathogens to
 CC similar proteins on surfaces in the oral cavity
 XX
 SQ Sequence 113 AA;

Query Match 93.9%; Score 200; DB 2; Length 113;
 Best Local Similarity 94.7%; Pred. No. 5.6e-21;
 Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 QNKGNSFEPTKDKPKYEHGNIIDIDPSVPHNG 38
 |||||:|||||
 DB 23 QNKGDSFEPTKDKPKYEHGNIIDIDPSVPHNG 60

RESULT 13

AA58806 standard; protein; 130 AA.

AA58806;

AC AAR58806;
 XX
 DT 25-MAR-2003 (revised)
 DT 30-MAR-1995 (first entry)

DE Fibronectin binding domain D1-D4 (709-838 (P838T)).

KW Fibronectin binding protein; Fbp; fibronectin binding domain;
 KM monoclonal antibody; Mab; adhesion; Gram-positive bacterium; bacteremia;
 XX Escherichia coli.

OS Staphylococcus aureus.

PN WO9418327-A1.

PD 18-AUG-1994.

PF 04-FEB-1994; 94WO-GB000215.

PR 05-FEB-1993; 93GB-00002289.

PR 20-OCT-1993; 93GB-00021592.

PA (SMIK) SMITHKLINE BEECHAM PLC.

PI Burnham MKR, Chopra I, Critchley IA, Knowles DJC;

DR WPI; 1994-279748/34.

XX Fibronectin binding protein and monoclonal antibodies specific for Fbp -
 PT useful to prevent adherence of Gram-positive bacteria to indwelling
 PT devices or wounds.

PS Disclosure; Page 30; 40pp; English.

XX Polypeptides corresponding to residues G709-T886 plus PPIVPT, G709-
 CC P838(P838T) and G709-P838 (AAR58805-07, respectively) of S. aureus J2385
 CC (NCIMB 40532) Fbp type A fibronectin binding domain D1-D4 region
 CC (AAR58808) were expressed in E. coli BL21(DE4) and used to raise Mabs
 CC specific for Fbp. (Updated on 25-MAR-2003 to correct PN field.)
 XX

SQ Sequence 130 AA;

Query Match 93.9%; Score 200; DB 2; Length 130;
 Best Local Similarity 94.7%; Pred. No. 6.7e-21;
 Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 QNKGNSFEPTKDKPKYEHGNIIDIDPSVPHNG 38
 |||||:|||||
 DB 40 QNKGDSFEPTKDKPKYEHGNIIDIDPSVPHNG 77

RESULT 14

AA58807 standard; protein; 130 AA.

AA58807;

AC AAR58807;
 XX
 DT 25-MAR-2003 (revised)
 DT 30-MAR-1995 (first entry)

DE Fibronectin binding domain D1-D4 (709-838).

KW Fibronectin binding protein; Fbp; fibronectin binding domain;
 KM monoclonal antibody; Mab; adhesion; Gram-positive bacterium; bacteremia;
 XX Escherichia coli.

OS Staphylococcus aureus.

PN WO9418327-A1.

PD 18-AUG-1994.

PF 04-FEB-1994; 94WO-GB000215.

PR 05-FEB-1993; 93GB-00002289.

PR 20-OCT-1993; 93GB-00021592.

PA (SMIK) SMITHKLINE BEECHAM PLC.

PI Burnham MKR, Chopra I, Critchley IA, Knowles DJC;

DR WPI; 1994-279748/34.

XX Fibronectin binding protein and monoclonal antibodies specific for Fbp -
 PT useful to prevent adherence of Gram-positive bacteria to indwelling
 PT devices or wounds.

PS Disclosure; Page 30; 40pp; English.

XX Polypeptides corresponding to residues G709-T886 plus PPIVPT, G709-
 CC P838(P838T) and G709-P838 (AAR58805-07, respectively) of S. aureus J2385
 CC (NCIMB 40532) Fbp type A fibronectin binding domain D1-D4 region
 CC (AAR58808) were expressed in E. coli BL21(DE4) and used to raise Mabs
 CC specific for Fbp. (Updated on 25-MAR-2003 to correct PN field.)
 XX

SQ Sequence 130 AA;

Query Match 93.9%; Score 200; DB 2; Length 130;
 Best Local Similarity 94.7%; Pred. No. 6.7e-21;
 Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 QNKGNSFEPTKDKPKYEHGNIIDIDPSVPHNG 38
 |||||:|||||
 DB 40 QNKGDSFEPTKDKPKYEHGNIIDIDPSVPHNG 77

RESULT 15

AA91202 standard; peptide; 130 AA.

AA91202;

DT 13-NOV-1996 (first entry)

DE D1-D4 fibronectin binding domains.

XX Fibronectin; oral hygiene; gingivitis; gum disease; adhesion;
 KM periodontitis; oral pathogen; caries; calculus; candidiasis; oral surgery;
 KM tissue regeneration; irrigation; toothpaste; dentifrice; mouthwash;
 XX lozenge.

OS Staphylococcus aureus.

PN WO9604003-A1.

XX 15-FEB-1996.
 PD
 XX
 XX 18-JUL-1995; 95WO-EP02825.
 PF
 XX
 XX 05-AUG-1994; 94GB-00015902.
 PR
 XX
 XX (SMK) SMITHKLINE BEECHAM PLC.
 PA
 XX
 XX Barnett P, Critchley IA, Dodd I;
 PI
 XX
 XX WPI; 1996-129122/13.
 DR
 XX
 XX
 PT Prevention of adherence of oral pathogens in the oral cavity, partic.
 PT Tooth surfaces - by application of a fibronectin binding protein or
 PT polypeptide or a monoclonal antibody or fragment against it.
 PS
 XX Claim 5; Page 32; 41pp; English.
 XX
 CC Adherence of oral pathogens, particularly to tooth surfaces, can be
 CC prevented by application of a fibronectin binding protein or polypeptide.
 CC The fibronectin binding protein or polypeptide is useful in the
 CC manufacture of oral hygiene compositions, eg. toothpaste, liquid
 CC dentifrice, mouthwash or lozenge. They are useful to prevent the plaque-
 CC related development of carious lesions, gingivitis, calculus or
 CC periodontal disease and to combat oral cavity infections, eg.
 CC candidiasis. They may also be useful in oral surgery e.g. in guided
 CC tissue regeneration procedures to prevent subsequent bacterial infection,
 CC and for irrigation of periodontal pockets. This sequence corresponds to
 CC amino acids 709-838 of the D1-D4 fibronectin binding domain of
 CC Staphylococcus aureus
 XX
 SQ Sequence 130 AA;

Query Match 93.9%; Score 200; DB 2; Length 130;
 Best Local Similarity 94.7%; Pred. No. 6.7e-21;
 Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 QNKGNSFEETKDKPKYEHGNIIDIDFDSVPHIHG 38
 |||:|||||
 DB 40 QNKGDSFEEDTEKDKPKYEHGNIIDIDFDSVPHIHG 77

Search completed: October 25, 2005, 20:21:06
 Job time : 84.8825 secs

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OM protein - protein search, using sw model

Run on: October 25, 2005, 19:38:38 ; Search time 26.4734 Seconds
(without alignments)
175.313 Million cell updates/sec

Title: US-10-731-238-62

Perfect score: 64
Sequence: 1 SPEEDTEKDKPK 12

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:*
1: geneseq19808:*
2: geneseq19908:*
3: geneseq20008:*
4: geneseq20018:*
5: geneseq20028:*
6: geneseq20038:*
7: geneseq20038s:*
8: geneseq20048s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	64	100.0	12	2	AAW65718
2	64	100.0	30	4	AAB82164
3	64	100.0	30	7	ADC69221
4	64	100.0	31	7	ADC69222
5	64	100.0	38	1	AAPE8661
6	64	100.0	38	1	AAPE8217
7	64	100.0	38	2	AAW65664
8	64	100.0	38	2	AAW65705
9	64	100.0	38	2	AAW65663
10	64	100.0	77	2	AAW88749
11	64	100.0	113	2	AAW8937
12	64	100.0	130	2	AAW88806
13	64	100.0	130	2	AAW88807
14	64	100.0	130	2	AAW91202
15	64	100.0	130	2	AAW91201
16	64	100.0	134	2	AAW92088
17	64	100.0	134	2	AAW92087
18	64	100.0	139	2	AAW91556
19	64	100.0	162	2	AAW90942
20	64	100.0	164	2	AAW90938
21	64	100.0	174	2	AAW88808
22	64	100.0	174	2	AAW91203
23	64	100.0	181	2	AAW88805
24	64	100.0	181	2	AAW91200
25	64	100.0	559	2	AAW89803

26	64	100.0	767	4	AAU34403	AAU34403	Staphylococcus aureus
27	64	100.0	767	4	AAU37547	AAU37547	Staphylococcus aureus
28	64	100.0	940	2	AAW07070	AAW07070	Fibronectin
29	64	100.0	940	6	ABU19111	ABU19111	Staphylococcus aureus
30	64	100.0	948	6	ADA89470	ADA89470	Staphylococcus aureus
31	64	100.0	948	6	ABJ18923	ABJ18923	Staphylococcus aureus
32	64	100.0	948	6	ABW72536	ABW72536	Staphylococcus aureus
33	64	100.0	978	4	AAU33960	AAU33960	Staphylococcus aureus
34	64	100.0	1001	4	AAU37093	AAU37093	Staphylococcus aureus
35	64	100.0	1018	4	AAW82115	AAW82115	Staphylococcus aureus
36	64	100.0	1018	4	AAU37245	AAU37245	Staphylococcus aureus
37	64	100.0	1018	4	AAU34301	AAU34301	Staphylococcus aureus
38	64	100.0	1018	6	ABW18922	ABW18922	Staphylococcus aureus
39	64	100.0	1018	6	ABW72537	ABW72537	Staphylococcus aureus
40	64	100.0	1027	2	AAW89806	AAW89806	Staphylococcus aureus
41	64	100.0	1038	6	ABU15903	ABU15903	Staphylococcus aureus
42	60	93.8	14	2	AAW65761	AAW65761	Staphylococcus aureus
43	60	93.8	38	1	AAW80660	AAW80660	Staphylococcus aureus
44	60	93.8	38	1	AAW82116	AAW82116	Fibronectin
45	60	93.8	38	2	AAW65662	AAW65662	Fibronectin

ALIGNMENTS

RESULT 1
ID AAW65718 standard; peptide; 12 AA.
XX

AC AAW65718;
XX

DT 16-OCT-1998 (first entry)
XX

DE Fibronectin binding protein-derived peptide #62.
XX

XX microbial surface components recognising adhesive matrix molecule;
XX MSCRAMM; fibronectin; fibronectin-binding protein; antibody; epitope;
KW

KW antibiotic; bacterial infection; antibiotic-resistant strain.
KW

XX Synthetic.
OS

OS Staphylococcus aureus.
XX

PN W09831369-A2.
XX

PD 23-JUL-1998.
XX

PF 21-JAN-1998; 98WO-US001222.
XX

PR 21-JAN-1997; 97US-0036139P.
XX

PA (TEXA) UNIV TEXAS A & M SYSTEM.
XX

PI Hoeck M, Patti JM, House-Pompeo KL, Speziale P, Joh D;
PI McGavin MJ;
PI

DR WPI; 1998-413816/35.
XX

XX Antibody that binds to fibronectin-binding protein, preventing its
XX binding to fibronectin - used to treat or prevent bacterial infection,
XX especially by Staphylococci and Streptococci.
XX

PT

PT

PS Example 9, Page 109; 201PP; English.
XX

XX The invention relates to antibodies that bind to a fibronectin-binding
XX domain of a fibronectin-binding protein, and inhibit binding of the
XX protein to fibronectin. Also claimed are: (1) isolated peptides of a
XX fibronectin-binding protein that do not bind to fibronectin; (2) fusion
XX protein containing at least one peptide of a fibronectin-binding protein
XX linked to a second amino acid sequence; (3) nucleic acid encoding the
XX isolated peptide of (1). Antibodies, the isolated peptides of (1) and the
XX nucleic acids are all useful for immunisation (active or passive) and (by
XX inhibiting binding of bacteria to fibronectin) for preventing or treating
XX infection in humans or other animals, particularly by staphylococci or

CC streptococci, e.g. meningitis, otitis media, pneumonia, endocarditis,
 CC mastitis in cattle, abortion in horses and many others. Since the
 CC antibodies block binding of bacteria, they should be effective against
 CC antibiotic-resistant strains, and may replace antibiotic therapy or
 CC increase its effectiveness. The present sequence is shown in the
 CC specification

XX
 SQ Sequence 12 AA:

Query Match 100.0%; Score 64; DB 2; Length 12;
 Best Local Similarity 100.0%; Pred. No. 0.00048;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SPEEDTEKDKPK 12
 |||||
 DB 1 SPEEDTEKDKPK 12

RESULT 2

ID AAB82164 standard; peptide; 30 AA.

XX AAB82164;

DT 20-JUL-2001 (first entry)

XX Peptide fragment of fibronectin-binding protein, FnBP.

XX Antibacterial; antiallergic; cytostatic; TH1 immune response inducer;

KW vaccine; infectious disease; allergy; cancer;

KM fibronectin-binding protein; FnBP.

OS Staphylococcus aureus.

XX WO200126682-A2.

PD 19-APR-2001.

XX 13-OCT-2000; 2000WO-US028443.

PR 14-OCT-1999; 99GB-00024351.

PA (DOWC) DOW CHEM CO.

PI Brennan F;

DR WPI; 2001-281838/29.

PT Increasing the level of TH1-type responses to molecules, used to treat
 PT infectious diseases, allergies and cancer, comprises conjugating the
 PT molecule to a plant virus.

PS Disclosure; Page 56; 89pp; English.

CC The present invention relates to a method for increasing the level of a
 CC TH1-type immune response to a molecule. The method comprising conjugating
 CC the molecule to a heterologous peptide expressed by a plant virus, and
 CC administering the conjugate to an animal. The method is useful for
 CC treating infectious diseases, allergies and cancer, by administering
 CC appropriate antigens conjugated to a plant virus. The present sequence is
 CC a peptide fragment of the fibronectin-binding protein, FnBP, of
 CC Staphylococcus aureus. This peptide was used to generate a chimeric virus
 CC particle of coxsackie B virus (CPMV) for use in the present invention

XX
 SQ Sequence 30 AA:

Query Match 100.0%; Score 64; DB 4; Length 30;
 Best Local Similarity 100.0%; Pred. No. 0.0013;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SPEEDTEKDKPK 12
 |||||
 DB 8 SPEEDTEKDKPK 19

RESULT 3
 ID ADC69221 standard; peptide; 30 AA.

XX ADC69221;

DT 18-DEC-2003 (first entry)

XX Fibronectin binding protein B (FnBP) D2 peptide.

KW Fibronectin binding protein A; FnBP; fibronectin binding protein B;

KM FnBP; antibody; staphylococcal infection; D2 peptide; fibronectin;

OS Staphylococcus aureus.

XX US2003153022-A1.

PD 14-AUG-2003.

XX 05-NOV-2002; 2002US-00287821.

PR 05-NOV-2001; 2001US-0330964P.

PA (PART/) PARTI J M.

PA (PATE/) PATEL P.

PA (HAUL/) HALL A.

PA (DOWA/) DOMANSKI P.

PA (SYRI/) SYRIBEYS P.

PA (HUTC/) HUTCHINS J T.

PI Patel JM, Patel P, Hall A, Domanski P, Syrbey P, Hutchins JT;

DR WPI; 2003-801749/75.

PT Monoclonal antibody for treating or preventing staphylococcal infections

XX binds specified fibronectin binding protein from Staphylococcus aureus.

XX Claim 10; SEQ ID NO 1; 12pp; English.

PS The invention relates to a new monoclonal antibody that binds fibronectin

CC binding proteins from Staphylococcus aureus, including fibronectin

CC binding protein A (FnBP) and fibronectin binding protein B (FnBPB). The

CC antibody is useful in treating, preventing or diagnosing staphylococcal

CC infections in a human or animal. The antibody is capable of recognising

CC Staphylococcus aureus with high affinity. It also inhibits binding of

CC staphylococcal bacteria to fibronectin. This sequence represents an FnBPB

CC D2 peptide of the invention.

XX
 SQ Sequence 30 AA:

Query Match 100.0%; Score 64; DB 7; Length 30;
 Best Local Similarity 100.0%; Pred. No. 0.0013;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SPEEDTEKDKPK 12
 |||||
 DB 8 SPEEDTEKDKPK 19

KW Fndpb; antibody; staphylococcal infection; D2 peptide; fibronectin;
 KW antibacterial; immunostimulant.
 XX Synthetic.
 OS Staphylococcus aureus.
 PN US2003153022-A1.
 XX 14-AUG-2003.
 PD 05-NOV-2002; 2002US-00287821.
 PF 05-NOV-2001; 2001US-0330964P.
 PR 05-NOV-2001; 2001US-0330964P.
 XX (PATE/) PATTI J M.
 PA (PATE/) PATEL P.
 PA (HALL/) HALL A.
 PA (DOMA/) DOMANSKI P.
 PA (SYRI/) SYRIBEYS P.
 PA (HUTC/) HUTCHINS J T.
 PI Patel JM, Patel P, Hall A, Domanski P, Syribey P, Hutchins JT;
 DR WPI; 2003-801749/75.
 PT Monoclonal antibody for treating or preventing staphylococcal infections
 PT binds specified fibronectin binding protein from Staphylococcus aureus.
 XX Claim 10; SEQ ID NO 2; 12pp; English.
 PS The invention relates to a new monoclonal antibody that binds fibronectin
 CC binding proteins from Staphylococcus aureus, including fibronectin
 CC binding protein A (FndpA) and fibronectin binding protein B (FndpB). The
 CC antibody is useful in treating, preventing or diagnosing staphylococcal
 CC infections in a human or animal. The antibody is capable of recognising
 CC Staphylococcus aureus with high affinity. It also inhibits binding of
 CC Staphylococcal bacteria to fibronectin. This sequence represents a
 CC modified FndpB D2 peptide of the invention.
 XX Sequence 31 AA;
 SQ
 Query Match 100.0%; Score 64; DB 7; Length 31;
 Best Local Similarity 100.0%; Pred. No. 0.0013;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 SPEEDTEKDKPK 12
 DB 9 SPEEDTEKDKPK 20
 RESULT 5
 AAP80661
 ID AAP80661 standard; protein; 38 AA.
 XX AAP80661;
 AC 25-MAR-2003 (revised)
 DT 07-OCT-1990 (first entry)
 DE Protein with fibronectin binding ability.
 XX Hybrid DNA molecule; fibronectin binding; mastitis; ruminants;
 KW wound infection.
 XX Staphylococcus aureus.
 OS Staphylococcus aureus.
 PN EP294349-A.
 XX 07-DEC-1988.
 PD 30-MAY-1988; 88EP-00850188.
 PF 01-JUN-1987; 87SE-00002272.
 PR

XX (ALFA) ALFA LAVAL AGRIC INT AB.
 PA Lindberg MK, Signas LC, Wadstrom TM, Froman G;
 PI WPI; 1988-347978/49.
 DR N-PADB; AAN81098.
 XX Hybrid DNA encoding Staphylococcus aureus fibronectin binding protein -
 PT useful for immunisation and topical application to prevent staphylococcal
 PT infections.
 PS Claim 11; Page 12; 23pp; English.
 XX The peptide has fibronectin binding ability. It is useful for immunising
 CC ruminants against staphylococcal mastitis, pref. when used at 0.5-5
 CC micrograms/kg, using 3 doses given at 1-3 week intervals; for topical
 CC application to prevent wound infection, using an isotonic saline soln. of
 CC concn. 25-250 micrograms/ml; and, when immobilised on a carrier, for
 CC diagnosing staphylococcal infections. (Updated on 25-MAR-2003 to correct
 CC PF field.) (Updated on 25-MAR-2003 to correct PA field.)
 XX Sequence 38 AA;
 SQ
 Query Match 100.0%; Score 64; DB 1; Length 38;
 Best Local Similarity 100.0%; Pred. No. 0.0016;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 SPEEDTEKDKPK 12
 DB 8 SPEEDTEKDKPK 19
 RESULT 6
 AAP82117
 ID AAP82117 standard; protein; 38 AA.
 XX AAP82117;
 AC 25-MAR-2003 (revised)
 DT 05-JAN-1990 (first entry)
 DE Fibronectin binding protein.
 XX Fibronectin binding protein; S.aureus; immunisation; mastitis; ruminants;
 KW wound infection; diagnosis.
 XX Staphylococcus aureus.
 OS Staphylococcus aureus.
 PN EP294349-A.
 XX 07-DEC-1988.
 PD 30-MAY-1988; 88EP-00850188.
 PF 01-JUN-1987; 87SE-00002272.
 PR (ALFA) ALFA LAVAL AGRIC INT AB.
 XX Lindberg MK, Signas LC, Wadstrom TM, Froman G;
 PI WPI; 1988-347978/49.
 DR N-PADB; AAN82055.
 XX Hybrid DNA encoding Staphylococcus aureus fibronectin binding protein -
 PT useful for immunisation and topical application to prevent staphylococcal
 PT infections.
 PS Claim 11; Page 12; 23pp; English.
 XX The S.aureus fibronectin binding protein may be included in a hybrid
 CC protein. The protein may be used to immunise ruminants against
 CC staphylococcal mastitis, pref. when given at 0.5-5 microg/kg, using 3

CC doses at 1-3 week intervals; and for topical applicn. to prevent wound
 CC infection, pref. using isotonic saline soln. of concn. 25-250 microg/mg.
 CC The DNA encoding the binding protein and the hybrid protein may be
 CC immobilised on a carrier and used to diagnose staphylococcal infections.
 CC (updated on 25-MAR-2003 to correct PA field.)
 CC

XX Sequence 38 AA;

QY Query Match 100.0%; Score 64; DB 1; Length 38;
 Best Local Similarity 100.0%; Pred. No. 0.0016;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 SPEEDTEKDKPK 12
 8 SPEEDTEKDKPK 19

RESULT 7

AAW65664
 ID AAW65664 standard; peptide; 38 AA.

XX AAW65664;

XX 16-OCT-1998 (first entry)

XX Fibronectin binding protein-derived peptide #8.

XX microbial surface components recognising adhesive matrix molecule;
 KM MSCRAMM; fibronectin; fibronectin-binding protein; antibody; epitope;
 KM antibiotic; bacterial infection; antibiotic-resistant strain.

XX Synthetic.

OS Staphylococcus aureus.

XX WO981389-A2.

XX 23-JUL-1998.

XX 21-JAN-1998; 98WO-US001222.

XX 21-JAN-1997; 97US-0036139P.

XX (TEXA) UNIV TEXAS A & M SYSTEM.

XX Hoeoek M, Patti JM, House-Pompeo KL, Speziale P, Joh D;
 PI Mcgavin MJ;

XX WPI; 1998-413816/35.

XX Antibody that binds to fibronectin-binding protein, preventing its
 PT binding to fibronectin - used to treat or prevent bacterial infection,
 PT especially by Staphylococci and Streptococci.

XX Example 2; Page 92; 201pp; English.

XX The invention relates to antibodies that bind to a fibronectin-binding
 CC domain of a fibronectin-binding protein, and inhibit binding of the
 CC protein to fibronectin. Also claimed are: (1) isolated peptides of a
 CC fibronectin-binding protein that do not bind to fibronectin; (2) fusion
 CC protein containing at least one peptide of a fibronectin-binding protein
 CC linked to a second amino acid sequence; (3) nucleic acid encoding the
 CC isolated peptide of (1). Antibodies, the isolated peptides of (1) and the
 CC nucleic acids are all useful for immunisation (active or passive) and (by
 CC inhibiting binding of bacteria to fibronectin) for preventing or treating
 CC infection in humans or other animals, particularly by staphylococci or
 CC streptococci, e.g. meningitis, otitis media, pneumonia, endocarditis,
 CC mastitis in cattle, abortion in horses and many others. Since the
 CC antibodies block binding of bacteria, they should be effective against
 CC antibiotic-resistant strains, and may replace antibiotic therapy or
 CC increase its effectiveness. Sequences AAW65659-68 represent synthetic
 CC epitopes from the fibronectin binding domains DU and DI-D4 of the S.
 CC aureus fnbA gene
 XX

SQ Sequence 38 AA;

QY Query Match 100.0%; Score 64; DB 2; Length 38;
 Best Local Similarity 100.0%; Pred. No. 0.0016;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 SPEEDTEKDKPK 12
 7 SPEEDTEKDKPK 18

RESULT 8

AAW65705
 ID AAW65705 standard; peptide; 38 AA.

XX AAW65705;

XX 16-OCT-1998 (first entry)

XX Fibronectin binding protein-derived peptide #49.

XX microbial surface components recognising adhesive matrix molecule;
 KM MSCRAMM; fibronectin; fibronectin-binding protein; antibody; epitope;
 KM antibiotic; bacterial infection; antibiotic-resistant strain.

XX Synthetic.

OS Staphylococcus aureus.

XX WO981389-A2.

XX 23-JUL-1998.

XX 21-JAN-1998; 98WO-US001222.

XX 21-JAN-1997; 97US-0036139P.

XX (TEXA) UNIV TEXAS A & M SYSTEM.

XX Hoeoek M, Patti JM, House-Pompeo KL, Speziale P, Joh D;
 PI Mcgavin MJ;

XX WPI; 1998-413816/35.

XX Antibody that binds to fibronectin-binding protein, preventing its
 PT binding to fibronectin - used to treat or prevent bacterial infection,
 PT especially by Staphylococci and Streptococci.

XX Example 8; Page 102; 201pp; English.

XX The invention relates to antibodies that bind to a fibronectin-binding
 CC domain of a fibronectin-binding protein, and inhibit binding of the
 CC protein to fibronectin. Also claimed are: (1) isolated peptides of a
 CC fibronectin-binding protein that do not bind to fibronectin; (2) fusion
 CC protein containing at least one peptide of a fibronectin-binding protein
 CC linked to a second amino acid sequence; (3) nucleic acid encoding the
 CC isolated peptide of (1). Antibodies, the isolated peptides of (1) and the
 CC nucleic acids are all useful for immunisation (active or passive) and (by
 CC inhibiting binding of bacteria to fibronectin) for preventing or treating
 CC infection in humans or other animals, particularly by staphylococci or
 CC streptococci, e.g. meningitis, otitis media, pneumonia, endocarditis,
 CC mastitis in cattle, abortion in horses and many others. Since the
 CC antibodies block binding of bacteria, they should be effective against
 CC antibiotic-resistant strains, and may replace antibiotic therapy or
 CC increase its effectiveness. Sequences AAW65701-706 represent a series of
 CC synthetic peptides based on the D2 region of S. aureus fibronectin
 CC binding protein A. They were synthesised to contain mutations
 XX

SQ Sequence 38 AA;

QY Query Match 100.0%; Score 64; DB 2; Length 38;
 Best Local Similarity 100.0%; Pred. No. 0.0016;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SPEEDTEKDKPK 12
 DB 7 SPEEDTEKDKPK 18

RESULT 9

AAW65663
 ID AAW65663 standard; peptide; 38 AA.

AAW65663;

16-OCT-1998 (first entry)

Fibronectin binding protein-derived peptide #7.

microbial surface components recognising adhesive matrix molecule;

MSCRAMM; fibronectin; fibronectin-binding protein; antibody; epitope;

antibiotic; bacterial infection; antibiotic-resistant strain.

Synthetic.

Staphylococcus aureus.

MO981389-A2.

23-JUL-1998.

21-JAN-1998; 98MO-US001222.

21-JAN-1997; 97US-0036139P.

(TEXA) UNIV TEXAS A & M SYSTEM.

Hoeoek M, Patti JM, House-Pompeo KL, Speciale P, Joh D;

Mogavin MJ;

WPI; 1998-413816/35.

Antibody that binds to fibronectin-binding protein, preventing its

binding to fibronectin - used to treat or prevent bacterial infection,

especially by Staphylococci and Streptococci.

Example 2; Page 92; 201pp; English.

The invention relates to antibodies that bind to a fibronectin-binding

domain of a fibronectin-binding protein, and inhibit binding of the

protein to fibronectin. Also claimed are: (1) isolated peptides of a

fibronectin-binding protein that do not bind to fibronectin; (2) fusion

protein containing at least one peptide of a fibronectin-binding protein

linked to a second amino acid sequence; (3) nucleic acid encoding the

isolated peptide of (1). Antibodies, the isolated peptides of (1) and the

nucleic acids are all useful for immunisation (active or passive) and (by

inhibiting binding of bacteria to fibronectin) for preventing or treating

infection in humans or other animals, particularly by staphylococci or

streptococci, e.g. meningitis, otitis media, pneumonia, endocarditis,

CC mastitis in cattle, abortion in horses and many others. Since the

CC antibodies block binding of bacteria, they should be effective against

CC antibiotic-resistant strains, and may replace antibiotic therapy or

increase its effectiveness. Sequences AAW65659-68 represent synthetic

epitopes from the fibronectin binding domains DU and DI-D4 of the S.

aureus fmbA gene

CC aureus fmbA gene

CC Sequence 38 AA;

SO Query Match 100.0%; Score 64; DB 2; Length 38;

Best Local Similarity 100.0%; Pred. No. 0.0016;

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SPEEDTEKDKPK 12

DB 7 SPEEDTEKDKPK 18

RESULT 10

AAR88749
 ID AAR88749 standard; protein; 77 AA.

AAR88749;

24-SEP-1996 (first entry)

S. aureus fibronectin binding protein D2D3 polypeptide.

Fibronectin binding protein; D2D3; prevention; adhesion; bacteria;

gram positive; extra-cellular matrix protein; in-dwelling device;

catheter; wound; D2D3; oral pathogen; oral cavity; J2385; NCIMB 40532.

Staphylococcus aureus.

MO9604380-A1.

15-FEB-1996.

28-JUL-1995; 95MO-EP003039.

05-AUG-1994; 94GB-00015901.

(SMIK) SMITHKLINE BEECHAM PLC.

Critchley IA, Dodd I, Barnett P, Mossakowska DEI;

WPI; 1996-129396/13.

N-PSDB; AAT12582.

Staphylococcus aureus fibronectin binding protein D2D3 polypeptide -

useful for combating infection at wound sites, surgical implants, etc.

and as antiadherent agent in oral hygiene.

Claim 5; Page 26; 38pp; English.

The present sequence is the S. aureus fibronectin binding protein

polypeptide D2D3, which can be used to prevent adhesion of (e.g. gram

positive) bacteria, to extra-cellular matrix proteins on in-dwelling

devices, e.g. catheters or in wounds. D2D3 can also be used to prevent

oral pathogens from binding to extra-cellular matrix proteins, in the

oral cavity. D2D3 was found to be effective at inhibiting S. aureus 8325-

4, and 120 adhesion to fibronectin coated PMMA coverslips, at a min.

adhesion inhibitor concn. of 10 microg/ml. D2D3 was derived from the D2

and D3 regions of the S. aureus J2385 (NCIMB 40532) fibronectin binding

protein

Sequence 77 AA;

Query Match 100.0%; Score 64; DB 2; Length 77;

Best Local Similarity 100.0%; Pred. No. 0.0034;

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SPEEDTEKDKPK 12

DB 8 SPEEDTEKDKPK 19

RESULT 11

AAAR90937

ID AAR90937 standard; peptide; 113 AA.

AAAR90937;

23-SEP-1996 (first entry)

D2D4 polypeptide #1.

Fibronectin binding protein; Fbp; S.aureus J2385; monoclonal antibody;

infection; surgical implant; antiadherent agent; hygiene; adhesion;

extracellular matrix protein; oral pathogen; oral cavity.

Staphylococcus aureus.


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XX Key Location/Qualifiers
FH Region 1..21
FT Region /note= "D1 region fragment"
FT Region 22..59
FT Region /note= "D2 region"
FT Region 60..98
FT Region /note= "D3 region"
FT Region 99..113
FT Region /note= "D4 region"
FT Misc-difference 113
FT /note= "P113T"
XX
XX WO9604381-A1.
XX
XX 15-FEB-1996.
XX
XX 28-JUL-1995; 95WO-EP003040.
XX
XX 05-AUG-1994; 94GB-00015900.
XX
XX (SMIK ) SMITHKLINE BEECHAM PLC.
XX
XX Critchley IA, Dodd I, Barnett P, Mcbay DL;
XX
XX WPI; 1996-129397/13.
XX
XX Polypeptide(s) derived from Staphylococcus aureus fibronectin binding
XX protein - inhibit binding of bacteria to extracellular matrix proteins,
XX for combating infection at the site of wounds and surgical implants, and
XX in oral hygiene.
XX
XX Claim 6; Page 24; 35pp; English.
XX
XX AAR90937-R90942 represent D3D4 polypeptides. These sequences correspond
XX to fragments of the Staphylococcus aureus fibronectin binding protein
XX (Fbp). This sequence corresponds to residues 18-130 of S. aureus J2385
XX Fbp, and also contains the D2 region, and a portion of the D1 region.
XX These sequences, and monoclonal antibodies against them can be used to
XX combat infection at the site of wounds, surgical implants and other in-
XX dwelling devices (such as catheters), and as antiadherent agents in oral
XX hygiene. They can also be used in the manufacture of a medicament for the
XX prevention of adhesion of bacteria to extracellular matrix proteins
XX present on in-dwelling devices or in wounds, or of oral pathogens to
XX similar proteins on surfaces in the oral cavity
XX
XX Sequence 113 AA;
XX
XX Query Match 100.0%; Score 64; DB 2; Length 113;
XX Best Local Similarity 100.0%; Pred. No. 0.0051;
XX Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 SPEEDTEKDKPK 12
XX |||||
XX 29 SPEEDTEKDKPK 40
XX
XX
XX RESULT 12
XX AAR58806
XX ID AAR58806 standard; protein; 130 AA.
XX
XX AAR58806;
XX
XX 25-MAR-2003 (revised)
XX DT 30-MAR-1995 (first entry)
XX
XX Fibronectin binding domain D1-D4 (709-838 (P838T)).
XX
XX Fibronectin binding protein; Fbp; fibronectin binding domain;
XX monoclonal antibody; Mab; adhesion; Gram-positive bacterium; bacteremia;
XX Escherichia coli.
XX
XX Staphylococcus aureus.
XX

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XX
XX WO9418327-A1.
XX
XX 18-AUG-1994.
XX
XX 04-FEB-1994; 94WO-GB000215.
XX
XX 05-FEB-1993; 93GB-00002289.
XX PR 20-OCT-1993; 93GB-00021592.
XX
XX (SMIK ) SMITHKLINE BEECHAM PLC.
XX
XX Burnham MKR, Chopra I, Critchley IA, Knowles DJC;
XX
XX WPI; 1994-279748/34.
XX
XX Fibronectin binding protein and monoclonal antibodies specific for Fbp -
XX useful to prevent adherence of Gram-positive bacteria to indwelling
XX devices or wounds.
XX
XX Disclosure; Page 30; 40pp; English.
XX
XX Polypeptides corresponding to residues G709-T886 plus PIVPT, G709-
XX P838 (P838T) and G709-P838 (AAR58805-07, respectively) of S. aureus J2385
XX (NCIMB 40532) Fbp type A fibronectin binding domain D1-D4 region
XX (AAR58808) were expressed in E. coli BL21 (DE4) and used to raise MBs
XX specific for Fbp. (Updated on 25-MAR-2003 to correct PN field.)
XX
XX Sequence 130 AA;
XX
XX Query Match 100.0%; Score 64; DB 2; Length 130;
XX Best Local Similarity 100.0%; Pred. No. 0.0059;
XX Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 SPEEDTEKDKPK 12
XX |||||
XX 46 SPEEDTEKDKPK 57
XX
XX
XX RESULT 13
XX AAR58807
XX ID AAR58807 standard; protein; 130 AA.
XX
XX AAR58807;
XX
XX 25-MAR-2003 (revised)
XX DT 30-MAR-1995 (first entry)
XX
XX Fibronectin binding domain D1-D4 (709-838) .
XX
XX Fibronectin binding protein; Fbp; fibronectin binding domain;
XX monoclonal antibody; Mab; adhesion; Gram-positive bacterium; bacteremia;
XX Escherichia coli.
XX
XX Staphylococcus aureus.
XX
XX WO9418327-A1.
XX
XX 18-AUG-1994.
XX
XX 04-FEB-1994; 94WO-GB000215.
XX
XX 05-FEB-1993; 93GB-00002289.
XX PR 20-OCT-1993; 93GB-00021592.
XX
XX (SMIK ) SMITHKLINE BEECHAM PLC.
XX
XX Burnham MKR, Chopra I, Critchley IA, Knowles DJC;
XX
XX WPI; 1994-279748/34.
XX
XX Fibronectin binding protein and monoclonal antibodies specific for Fbp -
XX useful to prevent adherence of Gram-positive bacteria to indwelling
XX

```

PT devices or wounds.
 XX Disclosure; Page 30; 40pp; English.
 PS
 XX
 CC Polypeptides corresponding to residues G709-T886 plus PPIVPT, G709-
 CC P838(P838T) and G709-P838 (AAR58805-07, respectively) of S. aureus J385
 CC (NCIMB 40532) Fbp type A fibronectin binding domain D1-D4 region
 CC (AAR58808) were expressed in E. coli BL21(DE4) and used to raise MAbs
 CC specific for Fbp. (Updated on 25-MAR-2003 to correct PN field.)
 CC
 XX
 SQ Sequence 130 AA;
 Query Match 100.0%; Score 64; DB 2; Length 130;
 Best Local Similarity 100.0%; Pred. No. 0.0059;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 SFEEDTEKDKPK 12
 DB 46 SFEEDTEKDKPK 57
 RESULT 14
 AAR91202 standard; peptide; 130 AA.
 XX AAR91202;
 AC
 XX
 DT 13-NOV-1996 (first entry)
 XX
 DE D1-D4 fibronectin binding domains.
 XX
 XX Fibronectin; oral hygiene; gingivitis; gum disease; adhesion;
 KW periodontis; oral pathogen; caries; calculus; candidiasis; oral surgery;
 KM tissue regeneration; irrigation; toothpaste; dentifrice; mouthwash;
 KM lozenge.
 XX
 OS Staphylococcus aureus.
 XX
 PN WO9604003-A1.
 XX
 PD 15-FEB-1996.
 XX
 PF 18-JUL-1995; 95WO-EP002825.
 XX
 PR 05-AUG-1994; 94GB-00015902.
 XX
 PA (SMIK) SMITHKLINE BEECHAM PLC.
 XX
 PI Barnett P, Critchley IA, Dodd I;
 PT WPI; 1996-129122/13.
 DR
 PT Prevention of adherence of oral pathogens in the oral cavity, partic.
 PT tooth surfaces - by application of a fibronectin binding protein or
 PT polypeptide or a monoclonal antibody or fragment against it.
 XX
 PS Claim 5; Page 32; 41pp; English.
 XX
 CC Adherence of oral pathogens, particularly to tooth surfaces, can be
 CC prevented by application of a fibronectin binding protein or polypeptide.
 CC The fibronectin binding protein or polypeptide is useful in the
 CC manufacture of oral hygiene compositions, eg. toothpaste, liquid
 CC dentifrice, mouthwash or lozenge. They are useful to prevent the plaque-
 CC related development of carious lesions, gingivitis, calculus or
 CC periodontal disease and to combat oral cavity infections, e.g.
 CC candidiasis. They may also be useful in oral surgery e.g. in guided
 CC tissue regeneration procedures to prevent subsequent bacterial infection,
 CC and for irrigation of periodontal pockets. This sequence corresponds to
 CC amino acids 709-838 of the D1-D4 fibronectin binding domain of
 CC Staphylococcus aureus
 XX
 SQ Sequence 130 AA;

Query Match 100.0%; Score 64; DB 2; Length 130;
 Best Local Similarity 100.0%; Pred. No. 0.0059;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 SFEEDTEKDKPK 12
 DB 46 SFEEDTEKDKPK 57
 RESULT 15
 AAR91201 standard; peptide; 130 AA.
 XX AAR91201;
 AC
 XX
 DT 13-NOV-1996 (first entry)
 XX
 DE D1-D4 fibronectin binding domains.
 XX
 XX Fibronectin; oral hygiene; gingivitis; gum disease; adhesion;
 KW periodontis; oral pathogen; caries; calculus; candidiasis; oral surgery;
 KM tissue regeneration; irrigation; toothpaste; dentifrice; mouthwash;
 KM lozenge.
 XX
 OS Staphylococcus aureus.
 XX
 PN WO9604003-A1.
 XX
 PD 15-FEB-1996.
 XX
 PF 18-JUL-1995; 95WO-EP002825.
 XX
 PR 05-AUG-1994; 94GB-00015902.
 XX
 PA (SMIK) SMITHKLINE BEECHAM PLC.
 XX
 PI Barnett P, Critchley IA, Dodd I;
 PT WPI; 1996-129122/13.
 DR
 PT Prevention of adherence of oral pathogens in the oral cavity, partic.
 PT tooth surfaces - by application of a fibronectin binding protein or
 PT polypeptide or a monoclonal antibody or fragment against it.
 XX
 PS Claim 5; Page 31-32; 41pp; English.
 XX
 CC Adherence of oral pathogens, particularly to tooth surfaces, can be
 CC prevented by application of a fibronectin binding protein or polypeptide.
 CC The fibronectin binding protein or polypeptide is useful in the
 CC manufacture of oral hygiene compositions, eg. toothpaste, liquid
 CC dentifrice, mouthwash or lozenge. They are useful to prevent the plaque-
 CC related development of carious lesions, gingivitis, calculus or
 CC periodontal disease and to combat oral cavity infections, e.g.
 CC candidiasis. They may also be useful in oral surgery e.g. in guided
 CC tissue regeneration procedures to prevent subsequent bacterial infection,
 CC and for irrigation of periodontal pockets. This sequence corresponds to
 CC amino acids 709-838 of the D1-D4 fibronectin binding domain of
 CC Staphylococcus aureus with a P838T substitution
 XX
 SQ Sequence 130 AA;
 Query Match 100.0%; Score 64; DB 2; Length 130;
 Best Local Similarity 100.0%; Pred. No. 0.0059;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 SFEEDTEKDKPK 12
 DB 46 SFEEDTEKDKPK 57
 Search completed: October 25, 2005, 20:21:10
 Job time : 27.5234 secs

the Edge Blank (uspro)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 22, 2005, 03:51:22 ; Search time 6.68599 Seconds
(without alignments)
133.980 Million cell updates/sec

Title: US-10-731-238-62
Perfect score: 64
Sequence: 1 SFEEDTEKDKPK 12

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents_Aa:*
1: /cgn2_6/prodata/1/aa/5A-COMB.pep.*
2: /cgn2_6/prodata/1/aa/5B-COMB.pep.*
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4: /cgn2_6/prodata/1/aa/6B-COMB.pep.*
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6: /cgn2_6/prodata/1/aa/backfile1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	64	100.0	12	4	US-09-010-317-62
2	64	100.0	38	1	US-08-234-622A-3
3	64	100.0	38	1	US-08-729-767-4
4	64	100.0	38	4	US-09-010-317-7
5	64	100.0	38	4	US-09-010-317-8
6	64	100.0	38	4	US-09-010-317-9
7	64	100.0	114	1	US-08-259-000-3
8	64	100.0	130	2	US-08-459-135A-7
9	64	100.0	130	2	US-08-459-135A-8
10	64	100.0	130	3	US-08-495-559-7
11	64	100.0	130	3	US-08-495-559-8
12	64	100.0	139	3	US-08-856-253-8
13	64	100.0	174	2	US-08-459-135A-10
14	64	100.0	174	2	US-08-459-135A-13
15	64	100.0	174	3	US-08-495-559-10
16	64	100.0	174	3	US-08-495-559-13
17	64	100.0	176	3	US-08-495-559-6
18	64	100.0	178	3	US-08-459-135A-12
19	64	100.0	178	3	US-08-459-559-12
20	64	100.0	181	2	US-08-459-135A-6
21	64	100.0	559	4	US-08-956-171E-5251
22	64	100.0	559	4	US-08-781-986A-5251
23	64	100.0	1027	4	US-08-956-171E-5254
24	64	100.0	1027	4	US-08-781-986A-5254
25	60	93.8	14	4	US-09-010-317-105
26	60	93.8	38	1	US-08-234-622A-2
27	60	93.8	38	1	US-08-729-767-3

28	60	93.8	38	4	US-09-010-317-5	Sequence 5, Appl
29	60	93.8	38	4	US-09-010-317-6	Sequence 6, Appl
30	60	93.8	38	4	US-09-010-317-43	Sequence 43, Appl
31	60	93.8	39	4	US-09-010-317-56	Sequence 56, Appl
32	60	93.8	39	4	US-09-010-317-41	Sequence 57, Appl
33	58	90.6	38	4	US-09-010-317-41	Sequence 41, Appl
34	58	90.6	38	4	US-09-010-317-46	Sequence 46, Appl
35	58	90.6	38	4	US-09-010-317-47	Sequence 47, Appl
36	57	89.1	38	4	US-09-010-317-48	Sequence 48, Appl
37	54	84.4	10	4	US-09-010-317-2	Sequence 2, Appl
38	54	84.4	18	4	US-09-010-317-36	Sequence 36, Appl
39	54	84.4	38	4	US-09-010-317-37	Sequence 37, Appl
40	54	84.4	38	4	US-09-010-317-39	Sequence 39, Appl
41	54	84.4	38	4	US-09-010-317-40	Sequence 40, Appl
42	54	84.4	38	4	US-09-010-317-45	Sequence 45, Appl
43	53	82.8	38	4	US-09-010-317-38	Sequence 38, Appl
44	53	82.8	38	4	US-09-010-317-42	Sequence 42, Appl
45	52	81.2	10	4	US-09-010-317-85	Sequence 85, Appl

ALIGNMENTS

RESULT 1
US-09-010-317-62
Sequence 62, Application US/09010317
Patent No. 6685943
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
APPLICANT: Patti, Joseph M.
APPLICANT: House-Pompeo, Karen L.
APPLICANT: Speziale, Pietro
APPLICANT: Jon, Danny
APPLICANT: McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
TITLE OF INVENTION: AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hblber, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAMK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 62:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-09-010-317-62
Query Match 100.0%; Score 64; DB 4; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.00019;

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SPEEDTEKDKPK 12
| | | | | | | | | |
DB 1 SPEEDTEKDKPK 12

RESULT 2

US-08-234-622A-3
; Sequence 3, Application US/08234622A

; Patent No. 5440014

; GENERAL INFORMATION:

; APPLICANT: HOOK, Magnus

; APPLICANT: MCGAVIN, Martin

; APPLICANT: RAUCCI, Giuseppe

; TITLE OF INVENTION: A FIBRONECTIN BINDING PEPTIDE

; NUMBER OF SEQUENCES: 4

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Burns, Doane, Swecker & Mathis

; STREET: P.O. Box 1404

; CITY: Alexandria

; STATE: Virginia

; COUNTRY: United States

; ZIP: 22313-1404

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/234,622A

; FILING DATE: 28-APR-1994

; CLASSIFICATION: 530

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: SE 9002617-0

; FILING DATE: 10-AUG-1990

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: NO PCT/SE91/00534

; FILING DATE: 09-AUG-1991

; ATTORNEY/AGENT INFORMATION:

; NAME: Meuth, Donna M

; REGISTRATION NUMBER: 36,607

; REFERENCE/DOCKET NUMBER: 012885-044

; TELEPHONE: (703) 836-6620

; TELEFAX: (703) 836-2021

; INFORMATION FOR SEQ ID NO: 3:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 38 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

US-08-234-622A-3

Query Match 100.0%; Score 64; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 0.00062;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SPEEDTEKDKPK 12
| | | | | | | | | |
DB 7 SPEEDTEKDKPK 18

RESULT 3

US-08-729-767-4

; Sequence 4, Application US/08729767

; Patent No. 570702

; GENERAL INFORMATION:

; APPLICANT: HOOK, Magnus

; APPLICANT: LINDBERG, Martin Kjell

; APPLICANT: SIGNAS, Lars Christer

; APPLICANT: WADSTROM, Torkel Mikael

; APPLICANT: FROMAN, Gunnar

; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN AS WELL AS

; NUMBER OF SEQUENCES: 6

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Burns, Doane, Swecker & Mathis, L.L.P.

; STREET: P.O. Box 1404

; CITY: Alexandria

; STATE: Virginia

; COUNTRY: United States

; ZIP: 22313-1404

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/729,767

; FILING DATE: 07-OCT-1996

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/259,000

; FILING DATE: 13-JUN-1994

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/007,817

; FILING DATE: 22-JAN-1993

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/201,028

; FILING DATE: 01-JUN-1988

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: SE 8702272-9

; FILING DATE: 01-JUN-1987

; ATTORNEY/AGENT INFORMATION:

; NAME: McGowan, Malcolm K.

; REGISTRATION NUMBER: 39,300

; REFERENCE/DOCKET NUMBER: 012889-036

; TELEPHONE: (703) 836-6620

; TELEFAX: (703) 836-2021

; INFORMATION FOR SEQ ID NO: 4:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 38 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: protein

US-08-729-767-4

Query Match 100.0%; Score 64; DB 1; Length 38;
Best Local Similarity 100.0%; Pred. No. 0.00062;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SPEEDTEKDKPK 12
| | | | | | | | | |
DB 8 SPEEDTEKDKPK 19

RESULT 4

US-09-010-317-7

; Sequence 7, Application US/09010317

; Patent No. 6685943

; GENERAL INFORMATION:

; APPLICANT: Hook, Magnus

; APPLICANT: Patel, Joseph M.

; APPLICANT: House-Pompeo, Karen L.

; APPLICANT: Speciale, Pietro

; APPLICANT: Joh, Danny

; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS

; NUMBER OF SEQUENCES: 105

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Arnold, White & Durkee

STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: TX
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION/DOCKET NUMBER: TAMK:189
REFERENCE/DOCKET INFORMATION:
TELEPHONE: 512-474-7577
TELEFAX: 512-418-3000
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-09-010-317-7
Query Match 100.0%; Score 64; DB 4; Length 38;
Best Local Similarity 100.0%; Pred. No. 0.00062; Indels 0;
Matches 12; Conservative 0; Mismatches 0; Gaps 0;
OY 1 SPEEDTEKDKPK 12
DB 7 SPEEDTEKDKPK 18
RESULT 5
US-09-010-317-8
Sequence 8, Application US/09010317
GENERAL INFORMATION:
PATENT NO. 6685943
APPLICANT: Hook, Magnus
APPLICANT: Patti, Joseph M.
APPLICANT: House-Pompeo, Karen L.
APPLICANT: Speziale, Pietro
APPLICANT: John, Danny
APPLICANT: McGavin, Martin J.
TITLE OF INVENTION: FIBROBLAST BINDING PROTEIN COMPOSITIONS
TITLE OF INVENTION: AND METHODS OF USE
NUMBER OF SEQUENCES: 105
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: TX
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/036,139

FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION/DOCKET NUMBER: TAMK:189
REFERENCE/DOCKET INFORMATION:
TELEPHONE: 512-474-7577
TELEFAX: 512-418-3000
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-09-010-317-8
Query Match 100.0%; Score 64; DB 4; Length 38;
Best Local Similarity 100.0%; Pred. No. 0.00062; Indels 0;
Matches 12; Conservative 0; Mismatches 0; Gaps 0;
OY 1 SPEEDTEKDKPK 12
DB 7 SPEEDTEKDKPK 18
RESULT 6
US-09-010-317-49
Sequence 49, Application US/09010317
GENERAL INFORMATION:
PATENT NO. 6685943
APPLICANT: Hook, Magnus
APPLICANT: Patti, Joseph M.
APPLICANT: House-Pompeo, Karen L.
APPLICANT: Speziale, Pietro
APPLICANT: John, Danny
APPLICANT: McGavin, Martin J.
TITLE OF INVENTION: FIBROBLAST BINDING PROTEIN COMPOSITIONS
TITLE OF INVENTION: AND METHODS OF USE
NUMBER OF SEQUENCES: 105
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: TX
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION/DOCKET NUMBER: TAMK:189
REFERENCE/DOCKET INFORMATION:
TELEPHONE: 512-474-7577
TELEFAX: 512-418-3000
INFORMATION FOR SEQ ID NO: 49:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-09-010-317-49

Query Match 100.0%; Score 64; DB 4; Length 38;
Best Local Similarity 100.0%; Pred. No. 0.0006;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SPEEDTEKDKPK 12
DB 7 SPEEDTEKDKPK 18

RESULT 7

US-08-259-000-3
Sequence 3, Application US/08259000
Patent No. 551514
GENERAL INFORMATION:
APPLICANT: HOOK, Magnus
APPLICANT: LINDBERG, Martin Kjell
APPLICANT: SIGNAS, Lars Christer
APPLICANT: MADSTROM, Torkei Mikael
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN
NUMBER OF SEQUENCES: 4
TITLE OF INVENTION: ITS PREPARATION
CORRESPONDENCE ADDRESS:
ADDRESSEE: Burns, Doane, Swecker & Mathis
STREET: P O Box 1404
CITY: Alexandria
STATE: Virginia
COUNTRY: United States
ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/259,000
FILING DATE: 13-JUN-1994
CLASSIFICATION: 435
PRIOR APPLICATION NUMBER:
APPLICATION NUMBER: SE 8702272-9
FILING DATE: 01-JUN-1987
ATTORNEY/AGENT INFORMATION:
NAME: Meuth, Donna M
REGISTRATION NUMBER: 36,607
REFERENCE/DOCKET NUMBER: 012885-062
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 114 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-259-000-3

Query Match 100.0%; Score 64; DB 1; Length 114;
Best Local Similarity 100.0%; Pred. No. 0.0019;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SPEEDTEKDKPK 12
DB 46 SPEEDTEKDKPK 57

RESULT 8

US-08-459-135A-7
Sequence 7, Application US/08459135A
Patent No. 5955078
GENERAL INFORMATION:
APPLICANT: BURHAM, Martin Karl Russel
APPLICANT: CHOPRA, Ian

APPLICANT: CRITCHLEY, Ian Alfred
TITLE OF INVENTION: KNOWLES, David Justin Charles
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
STATE: PA
COUNTRY: U.S.A.
ZIP: 19406-0939
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
OPERATING SYSTEM: DOS
SOFTWARE: Faastseq, Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/459,135A
FILING DATE: 02-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION NUMBER:
APPLICATION NUMBER: PCT/GB/94/00215
FILING DATE: 04-Feb-1994
ATTORNEY/AGENT INFORMATION:
NAME: Gimm, Edward R
REGISTRATION NUMBER: 38,891
REFERENCE/DOCKET NUMBER: P30591C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-4478
TELEFAX: 610-270-5090
TELEX:

INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 130 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-459-135A-7

Query Match 100.0%; Score 64; DB 2; Length 130;
Best Local Similarity 100.0%; Pred. No. 0.0022;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SPEEDTEKDKPK 12
DB 46 SPEEDTEKDKPK 57

RESULT 9

US-08-459-135A-8
Sequence 8, Application US/08459135A
Patent No. 5955078
GENERAL INFORMATION:
APPLICANT: BURHAM, Martin Karl Russel
APPLICANT: CHOPRA, Ian
APPLICANT: CRITCHLEY, Ian Alfred
TITLE OF INVENTION: KNOWLES, David Justin Charles
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
STATE: PA
COUNTRY: U.S.A.
ZIP: 19406-0939
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
OPERATING SYSTEM: DOS
SOFTWARE: Faastseq, Version 2.0
CURRENT APPLICATION DATA:

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; APPLICATION NUMBER: US/08/459,135A
; FILING DATE: 02-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB/94/00215
; FILING DATE: 04-Feb-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Gimmil, Edward R
; REGISTRATION NUMBER: 38,891
; REFERENCE/DOCKET NUMBER: P30591C2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-270-4478
; TELEFAX: 610-270-5090
;
; TELEX:
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 130 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
;
US-08-459-135A-8

Query Match          100.0%; Score 64; DB 3; Length 130;
Best Local Similarity 100.0%; Pred. No. 0.0022;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 SPEEDTEKDKPK 12
Db      46 SPEEDTEKDKPK 57

RESULT 10
; Sequence 7, Application US/08495559A
; Patent No. 6054572
; GENERAL INFORMATION:
; APPLICANT: BURHAM, Martin Karl Russel
; APPLICANT: CHOPRA, Ian
; APPLICANT: CRITCHLEY, Ian Alfred
; APPLICANT: KNOWLES, David Justin Charles
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN: MONOCLONAL
; TITLE OF INVENTION: ANTIBODY AND THEIR USE IN PREVENTING BACTERIAL ADHESION
; FILE REFERENCE: P30591
; CURRENT APPLICATION NUMBER: US/08/495,559A
; CURRENT FILING DATE: 1995-08-03
; EARLIER APPLICATION NUMBER: GB 9302289.5
; EARLIER FILING DATE: 1993-02-05
; EARLIER APPLICATION NUMBER: GB 9321592.9
; EARLIER FILING DATE: 1993-10-20
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 7
; LENGTH: 130
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
;
US-08-495-559-7

Query Match          100.0%; Score 64; DB 3; Length 130;
Best Local Similarity 100.0%; Pred. No. 0.0022;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 SPEEDTEKDKPK 12
Db      46 SPEEDTEKDKPK 57

RESULT 11
US-08-495-559-8
; Sequence 8, Application US/08495559A
; Patent No. 6054572
; GENERAL INFORMATION:
; APPLICANT: BURHAM, Martin Karl Russel
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; APPLICANT: CHOPRA, Ian
; APPLICANT: CRITCHLEY, Ian Alfred
; APPLICANT: KNOWLES, David Justin Charles
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN: MONOCLONAL
; TITLE OF INVENTION: ANTIBODY AND THEIR USE IN PREVENTING BACTERIAL ADHESION
; FILE REFERENCE: P30591
; CURRENT APPLICATION NUMBER: US/08/495,559A
; CURRENT FILING DATE: 1995-08-03
; EARLIER APPLICATION NUMBER: GB 9302289.5
; EARLIER FILING DATE: 1993-02-05
; EARLIER APPLICATION NUMBER: GB 9321592.9
; EARLIER FILING DATE: 1993-10-20
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 8
; LENGTH: 130
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
;
US-08-495-559-8

Query Match          100.0%; Score 64; DB 3; Length 130;
Best Local Similarity 100.0%; Pred. No. 0.0022;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 SPEEDTEKDKPK 12
Db      46 SPEEDTEKDKPK 57

RESULT 12
US-08-856-253-8
; Sequence 8, Application US/08856253
; Patent No. 6288214
; GENERAL INFORMATION:
; APPLICANT: Hook, Magnus
; APPLICANT: Patti, Joseph M.
; APPLICANT: House-Pompeo, Karen
; APPLICANT: Stahanam, Narayana
; APPLICANT: Symersky, Jindrich
; TITLE OF INVENTION: COLLAGEN BINDING PROTEIN COMPOSITIONS
; TITLE OF INVENTION: AND METHODS OF USE
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: U.S.
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/856,253
; FILING DATE: Concurrently Herewith
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/017,678
; FILING DATE: 16-MAY-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Kitchell, Barbara S.
; REGISTRATION NUMBER: 33,928
; REFERENCE/DOCKET NUMBER: TAMK:193
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (512) 418-3000
; TELEFAX: (512) 474-7577
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 139 amino acids
; TYPE: amino acid
; STRANDEDNESS:
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TOPOLOGY: linear
US-08-856-253-8

Query Match 100.0%; Score 64; DB 3; Length 135;
Best Local Similarity 100.0%; Pred. No. 0.0023;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SPEEDTEKDKPK 12
Db 60 SPEEDTEKDKPK 71

RESULT 13

US-08-459-135A-10
Sequence 10, Application US/08459135A
Patent No. 5955078
GENERAL INFORMATION:
APPLICANT: BURNHAM, Martin Karl Russel
APPLICANT: CHOPRA, Ian
APPLICANT: CRITCHLEY, Ian Alfred
APPLICANT: KNOWLES, David Justin Charles
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN: MONOCLONAL ANTIBODY AND THEIR US
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
STATE: PA
COUNTRY: U.S.A.
ZIP: 19406-0939
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: Fastseq, Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/459,135A
FILING DATE: 02-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB/94/00215
FILING DATE: 04-Feb-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Gimm, Edward R
REGISTRATION NUMBER: 38,891
REFERENCE/DOCKET NUMBER: P30591C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-4478
TELEFAX: 610-270-5090
TELEX:
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 174 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: Protein
US-08-459-135A-10

Query Match 100.0%; Score 64; DB 2; Length 174;
Best Local Similarity 100.0%; Pred. No. 0.0023;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SPEEDTEKDKPK 12
Db 46 SPEEDTEKDKPK 57

RESULT 14
US-08-459-135A-13
Sequence 13, Application US/08459135A
Pat No. 5955078
GENERAL INFORMATION:

APPLICANT: BURNHAM, Martin Karl Russel
APPLICANT: CHOPRA, Ian
APPLICANT: CRITCHLEY, Ian Alfred
APPLICANT: KNOWLES, David Justin Charles
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN: MONOCLONAL ANTIBODY AND THEIR US
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
STATE: PA
COUNTRY: U.S.A.
ZIP: 19406-0939
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: Fastseq, Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/459,135A
FILING DATE: 02-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB/94/00215
FILING DATE: 04-Feb-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Gimm, Edward R
REGISTRATION NUMBER: 38,891
REFERENCE/DOCKET NUMBER: P30591C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-4478
TELEFAX: 610-270-5090
TELEX:
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 174 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: Protein
US-08-459-135A-13

Query Match 100.0%; Score 64; DB 2; Length 174;
Best Local Similarity 100.0%; Pred. No. 0.0023;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SPEEDTEKDKPK 12
Db 46 SPEEDTEKDKPK 57

RESULT 15
US-08-495-559-10
Sequence 10, Application US/08495559A
Patent No. 6054572
GENERAL INFORMATION:
APPLICANT: BURNHAM, Martin Karl Russel
APPLICANT: CHOPRA, Ian
APPLICANT: CRITCHLEY, Ian Alfred
APPLICANT: KNOWLES, David Justin Charles
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN: MONOCLONAL
TITLE OF INVENTION: ANTIBODY AND THEIR USE IN PREVENTING BACTERIAL ADHESION
FILE REFERENCE: P30591
CURRENT APPLICATION NUMBER: US/08/495,559A
CURRENT FILING DATE: 1995-08-03
EARLIER APPLICATION NUMBER: GB 9302289.5
EARLIER FILING DATE: 1993-02-05
EARLIER APPLICATION NUMBER: GB 9321592.9
EARLIER FILING DATE: 1993-10-20
NUMBER OF SEQ ID NOS: 13
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 10

; LENGTH: 174
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-08-495-559-10

Query Match 100.0%; Score 64; DB 3; Length 174;
Best Local Similarity 100.0%; Pred. No. 0.0029;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 46 SFEDTETKDKPK 57

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OM protein - protein search, using sw model

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Title: US-10-731-238-62

Perfect score: 64

Sequence: 1 SPEEDTEKDKPK 12

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Searched: 1862951 seqs, 417491010 residues

Total number of hits satisfying chosen parameters: 1862951

Minimum DB seq length: 0
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Maximum Match 100%
Listing first 45 summaries

Database :

Published Applications_AA:*

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- 2: /cgn2_6/prodata/2/pubppaa/PCT_NEW_PUB.pep:*
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- 11: /cgn2_6/prodata/2/pubppaa/US09C_PUBCOMB.pep:*
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- 13: /cgn2_6/prodata/2/pubppaa/US10_PUBCOMB.pep:*
- 14: /cgn2_6/prodata/2/pubppaa/US10C_PUBCOMB.pep:*
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- 19: /cgn2_6/prodata/2/pubppaa/US11_PUBCOMB.pep:*
- 20: /cgn2_6/prodata/2/pubppaa/US11_NEW_PUB.pep:*
- 21: /cgn2_6/prodata/2/pubppaa/US60_NEW_PUB.pep:*
- 22: /cgn2_6/prodata/2/pubppaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	64	100.0	12	US-10-731-238-62	Sequence 62, Appl
2	64	100.0	30	US-10-287-821-1	Sequence 1, Appl
3	64	100.0	31	US-10-287-821-2	Sequence 2, Appl
4	64	100.0	38	US-10-731-238-7	Sequence 7, Appl
5	64	100.0	38	US-10-731-238-8	Sequence 8, Appl
6	64	100.0	38	US-10-731-238-8	Sequence 8, Appl
7	64	100.0	139	US-09-813-820-8	Sequence 49, Appl
8	64	100.0	388	US-08-901-062-1	Sequence 8, Appl
9	64	100.0	559	US-08-781-986A-5251	Sequence 5251, Ap
10	64	100.0	559	US-10-329-624-5251	Sequence 5251, Ap
11	64	100.0	767	US-09-815-242-5899	Sequence 5899, Ap

12	64	100.0	767	9	US-09-815-242-13140	Sequence 13140, A
13	64	100.0	940	17	US-10-470-048B-424	Sequence 424, App
14	64	100.0	948	17	US-10-470-048B-69	Sequence 69, Appl
15	64	100.0	978	9	US-09-815-242-5456	Sequence 5456, Ap
16	64	100.0	1001	9	US-09-815-242-12886	Sequence 12886, A
17	64	100.0	1018	9	US-09-815-242-5797	Sequence 5797, Ap
18	64	100.0	1018	9	US-09-815-242-12838	Sequence 12838, A
19	64	100.0	1018	17	US-10-470-048B-68	Sequence 68, Appl
20	64	100.0	1027	8	US-08-781-986A-5254	Sequence 5254, Ap
21	64	100.0	1027	15	US-10-329-624-5254	Sequence 5254, Ap
22	64	100.0	1038	15	US-10-282-122A-43827	Sequence 43827, A
23	60	93.8	14	18	US-10-731-238-105	Sequence 105, App
24	60	93.8	38	18	US-10-731-238-5	Sequence 5, Appl
25	60	93.8	38	18	US-10-731-238-6	Sequence 6, Appl
26	60	93.8	38	18	US-10-731-238-43	Sequence 43, Appl
27	60	93.8	39	18	US-10-731-238-56	Sequence 56, Appl
28	60	93.8	39	18	US-10-731-238-57	Sequence 57, Appl
29	60	93.8	39	18	US-10-731-238-46	Sequence 46, Appl
30	58	90.6	38	18	US-10-731-238-41	Sequence 41, Appl
31	58	90.6	38	18	US-10-731-238-46	Sequence 46, Appl
32	58	90.6	38	18	US-10-731-238-47	Sequence 47, Appl
33	57	89.1	38	18	US-10-731-238-48	Sequence 48, Appl
34	54	84.4	10	18	US-10-731-238-2	Sequence 2, Appl
35	54	84.4	38	18	US-10-731-238-36	Sequence 36, Appl
36	54	84.4	38	18	US-10-731-238-37	Sequence 37, Appl
37	54	84.4	38	18	US-10-731-238-39	Sequence 39, Appl
38	54	84.4	38	18	US-10-731-238-40	Sequence 40, Appl
39	54	84.4	38	18	US-10-731-238-45	Sequence 45, Appl
40	53	82.8	38	18	US-10-731-238-38	Sequence 38, Appl
41	53	82.8	38	18	US-10-731-238-42	Sequence 42, Appl
42	52	81.2	10	18	US-10-731-238-85	Sequence 85, Appl
43	52	81.2	36	18	US-10-731-238-58	Sequence 58, Appl
44	52	81.2	36	18	US-10-731-238-59	Sequence 59, Appl
45	52	81.2	38	18	US-10-731-238-50	Sequence 50, Appl

ALIGNMENTS

RESULT 1
US-10-731-238-62
Sequence 62, Application US/10731238
Publication No. US20050123552A1
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
Patel, Joseph M.
House-Pompeo, Karen L.
Speziale, Pietro
Joh, Danny
McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSER: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/731.238
FILING DATE: 10-Dec-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/010.317
FILING DATE: 21-Jan-1998
APPLICATION NUMBER: US 60/036.139

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; FILING DATE: 21-JAN-1997
; ATTORNEY/AGENT INFORMATION:
;   NAME: Hibler, David W.
;   REGISTRATION NUMBER: 41,071
;   REFERENCE/DOCKET NUMBER: TAMK:189
; TELECOMMUNICATION INFORMATION:
;   TELEPHONE: 512-418-3000
;   TELEFAX: 512-474-7577
; INFORMATION FOR SEQ ID NO: 62:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH: 12 amino acids
;     TYPE: amino acid
;     STRANDEDNESS: <Unknown>
;     TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 62:
US-10-731-238-62

Query Match      100.0%; Score 64; DB 18; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.0016;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 SPEEDTEKDKPK 12
DB      1 SPEEDTEKDKPK 12

RESULT 2
US-10-287-821-1
; Sequence 1, Application US/10287821
; Publication No. US20030153022A1
; GENERAL INFORMATION:
;   APPLICANT: PATTI, Joseph M.
;   TITLE OF INVENTION: MONOCLONAL ANTIBODIES TO THE FIBRONECTIN BINDING PROTEIN. . .
;   FILE REFERENCE: P07427US01/BAS
;   CURRENT APPLICATION NUMBER: US/10/287,821
;   CURRENT FILING DATE: 2002-11-05
;   PRIOR APPLICATION NUMBER: 60/330,964
;   PRIOR FILING DATE: 2001-11-05
;   NUMBER OF SEQ ID NOS: 2
;   SOFTWARE: PatentIn version 3.1
;   SEQ ID NO 1
;   LENGTH: 30
;   TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-10-287-821-1

Query Match      100.0%; Score 64; DB 14; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.0041;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 SPEEDTEKDKPK 12
DB      8 SPEEDTEKDKPK 19

RESULT 3
US-10-287-821-2
; Sequence 2, Application US/10287821
; Publication No. US20030153022A1
; GENERAL INFORMATION:
;   APPLICANT: PATTI, Joseph M.
;   TITLE OF INVENTION: MONOCLONAL ANTIBODIES TO THE FIBRONECTIN BINDING PROTEIN. . .
;   FILE REFERENCE: P07427US01/BAS
;   CURRENT APPLICATION NUMBER: US/10/287,821
;   CURRENT FILING DATE: 2002-11-05
;   PRIOR APPLICATION NUMBER: 60/330,964
;   PRIOR FILING DATE: 2001-11-05
;   NUMBER OF SEQ ID NOS: 2
;   SOFTWARE: PatentIn version 3.1
;   SEQ ID NO 2
;   LENGTH: 31
;   TYPE: PRT
; ORGANISM: Staphylococcus aureus
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US-10-287-821-2

Query Match      100.0%; Score 64; DB 14; Length 31;
Best Local Similarity 100.0%; Pred. No. 0.0043;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 SPEEDTEKDKPK 12
DB      9 SPEEDTEKDKPK 20

RESULT 4
US-10-731-238-7
; Sequence 7, Application US/10731238
; Publication No. US20050123552A1
; GENERAL INFORMATION:
;   APPLICANT: Hook, Magnus
;   PATTI, Joseph M.
;   House-Pompeo, Karen L.
;   Speziale, Pietro
;   Job, Danny
;   McGavin, Martin J.
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
;   AND METHODS OF USE
;   NUMBER OF SEQUENCES: 105
;   CORRESPONDENCE ADDRESS:
;   ADDRESSER: Arnold, White & Durkee
;   STREET: P.O. Box 4433
;   CITY: Houston
;   STATE: TX
;   COUNTRY: USA
;   ZIP: 77210-4433
; COMPUTER READABLE FORM:
;   MEDIUM TYPE: floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: PatentIn Release #1.0, Version #1.30
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/10/731,238
;   FILING DATE: 10-Dec-2003
;   CLASSIFICATION: <Unknown>
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US/09/010,317
;   FILING DATE: 21-Jan-1998
;   APPLICATION NUMBER: US 60/036,139
;   FILING DATE: 21-JAN-1997
; ATTORNEY/AGENT INFORMATION:
;   NAME: Hibler, David W.
;   REGISTRATION NUMBER: 41,071
;   REFERENCE/DOCKET NUMBER: TAMK:189
; TELECOMMUNICATION INFORMATION:
;   TELEPHONE: 512-418-3000
;   TELEFAX: 512-474-7577
; INFORMATION FOR SEQ ID NO: 7:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH: 38 amino acids
;     TYPE: amino acid
;     STRANDEDNESS: <Unknown>
;     TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-10-731-238-7

Query Match      100.0%; Score 64; DB 18; Length 38;
Best Local Similarity 100.0%; Pred. No. 0.0053;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 SPEEDTEKDKPK 12
DB      7 SPEEDTEKDKPK 18

RESULT 5
US-10-731-238-8
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Sequence 8, Application US/10731238
Publication No. US20050123552A1
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
Pattl, Joseph M.
House-Pompeo, Karen L.
Speziale, Pietro
Joh, Danny
McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/731,238
FILING DATE: 10-Dec-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE: 21-Jan-1998
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TWMK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-10-731-238-8
Query Match 100.0%; Score 64; DB 18; Length 38;
Best Local Similarity 100.0%; Pred. No. 0.0053;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 SPEEDTEKDKPK 12
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Db 7 SPEEDTEKDKPK 18
RESULT 6
US-10-731-238-49
Sequence 49, Application US/10731238
Publication No. US20050123552A1
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
Pattl, Joseph M.
House-Pompeo, Karen L.
Speziale, Pietro
Joh, Danny
McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:

ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/731,238
FILING DATE: 10-Dec-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE: 21-Jan-1998
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TWMK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 49:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 49:
US-10-731-238-49
Query Match 100.0%; Score 64; DB 18; Length 38;
Best Local Similarity 100.0%; Pred. No. 0.0053;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 SPEEDTEKDKPK 12
|||
Db 7 SPEEDTEKDKPK 18
RESULT 7
US-09-813-820-8
Sequence 8, Application US/09813820
Patent No. US20020102262A1
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
Pattl, Joseph M.
House-Pompeo, Karen
Sthanam, Narayana
Symerky, Jindrich
TITLE OF INVENTION: COLLAGEN BINDING PROTEIN COMPOSITIONS
AND METHODS OF USE
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: Texas
COUNTRY: U.S.
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/813,820
FILING DATE: 22-Mar-2001

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; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/856,253
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Kitchell, Barbara S.
; REGISTRATION NUMBER: 33,928
; REFERENCE/DOCKET NUMBER: TAMK.193
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (512) 418-3000
; TELEFAX: (512) 474-7577
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 139 amino acids
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-09-813-820-8

Query Match      100.0%; Score 64; DB 9; Length 139;
Best Local Similarity 100.0%; Pred. No. 0.02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 SPEEDTEKDKPK 12
DB      60 SPEEDTEKDKPK 71

RESULT 8
US-08-901-062-1
; Sequence 1, Application US/08901062
; Publication No. US20020025324A1
; GENERAL INFORMATION:
; APPLICANT: SEALS, JONATHAN R.
; TITLE OF INVENTION: RECOMBINANT BIVALENT BACTERIAL VACCIN;
; TITLE OF INVENTION: FOR THE PREVENTION OF MASTITIS
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HALB AND DORR LLP
; STREET: 60 State Street
; CITY: Boston
; STATE: MA
; COUNTRY: United States Of America
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/901,062
; FILING DATE: 25-JUL-1997
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Baker, Hollie L.
; REGISTRATION NUMBER: 31,321
; REFERENCE/DOCKET NUMBER: 106941.153
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 526-6000
; TELEFAX: (617) 526-5000
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 388 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
US-08-901-062-1

Query Match      100.0%; Score 64; DB 8; Length 388;
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; Best Local Similarity 100.0%; Pred. No. 0.06;
; Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 SPEEDTEKDKPK 12
DB      309 SPEEDTEKDKPK 320

RESULT 9
US-08-781-986A-5251
; Sequence 5251, Application US/08781986A
; Publication No. US20030054436A1
; GENERAL INFORMATION:
; APPLICANT: Charles Kunesh
; TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
; NUMBER OF SEQUENCES: 5253
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4mb storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/781,986A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Benson, Bob
; REGISTRATION NUMBER: 30,446
; REFERENCE/DOCKET NUMBER: PB248PP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 5251:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 559 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-781-986A-5251

Query Match      100.0%; Score 64; DB 8; Length 559;
Best Local Similarity 100.0%; Pred. No. 0.088;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 SPEEDTEKDKPK 12
DB      345 SPEEDTEKDKPK 356

RESULT 10
US-10-329-624-5251
; Sequence 5251, Application US/10329624
; Publication No. US20040043037A1
; GENERAL INFORMATION:
; APPLICANT: Charles Kunesh
; Gail H. Choi
; Patrick S. Dillon
; Craig A. Rosen
; Steven C. Barash
; Michael R. Fannon
; TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
; NUMBER OF SEQUENCES: 5256
```

CORRESPONDENCE ADDRESS:
ADDRESSER: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COUNTRY: USA
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/329,624
FILING DATE: 27-Dec-2002
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 08/956,171
FILING DATE: October 20, 1997
APPLICATION NUMBER: 60/009,861
FILING DATE: January 5, 1996
APPLICATION NUMBER: 08/781,986
FILING DATE: January 3, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Mark J. Hyman
REGISTRATION NUMBER: 46,789
REFERENCE/DOCKET NUMBER: PB248P1D1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (240) 314-1224
TELEFAX: (301) 309-8439
INFORMATION FOR SEQ ID NO: 5251:
SEQUENCE CHARACTERISTICS:
LENGTH: 559 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 5251:
US-10-329-624-5251
Query Match 100.0%; Score 64; DB 15; Length 559;
Best Local Similarity 100.0%; Pred. No. 0.088;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 SPEEDTEKDKPK 12
Db 345 SPEEDTEKDKPK 356
RESULT 11
US-09-815-242-5899
Sequence 5899, Application US/09815242
Patent No. US20020061569A1
GENERAL INFORMATION:
APPLICANT: Haeselbeck, Robert
APPLICANT: Ohlsen, Karl L.
APPLICANT: Zyskind, Judith W.
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John D.
APPLICANT: Carr, Grant J.
APPLICANT: Yamamoto, Robert T.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in
FILE REFERENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: US/09/815,242
PRIORITY APPLICATION NUMBER: 60/191,078
PRIORITY FILING DATE: 2000-03-21
PRIORITY FILING DATE: 2000-03-21
PRIORITY APPLICATION NUMBER: 60/206,848
PRIORITY FILING DATE: 2000-05-23
PRIORITY APPLICATION NUMBER: 60/207,727
PRIORITY FILING DATE: 2000-05-26
PRIORITY APPLICATION NUMBER: 60/242,578

PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 5899
LENGTH: 767
TYPE: PRT
ORGANISM: Staphylococcus aureus
US-09-815-242-5899
Query Match 100.0%; Score 64; DB 9; Length 767;
Best Local Similarity 100.0%; Pred. No. 0.12;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 SPEEDTEKDKPK 12
Db 726 SPEEDTEKDKPK 737
RESULT 12
US-09-815-242-13140
Sequence 13140, Application US/09815242
Patent No. US20020061569A1
GENERAL INFORMATION:
APPLICANT: Haeselbeck, Robert
APPLICANT: Ohlsen, Karl L.
APPLICANT: Zyskind, Judith W.
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John D.
APPLICANT: Carr, Grant J.
APPLICANT: Yamamoto, Robert T.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in
FILE REFERENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: US/09/815,242
PRIORITY APPLICATION NUMBER: 60/191,078
PRIORITY FILING DATE: 2000-03-21
PRIORITY FILING DATE: 2000-05-23
PRIORITY APPLICATION NUMBER: 60/206,848
PRIORITY FILING DATE: 2000-05-26
PRIORITY APPLICATION NUMBER: 60/207,727
PRIORITY FILING DATE: 2000-10-23
PRIORITY APPLICATION NUMBER: 60/253,625
PRIORITY FILING DATE: 2000-11-27
PRIORITY APPLICATION NUMBER: 60/257,931
PRIORITY FILING DATE: 2000-12-22
PRIORITY APPLICATION NUMBER: 60/269,308
PRIORITY FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 13140
LENGTH: 767
TYPE: PRT
ORGANISM: Staphylococcus aureus
US-09-815-242-13140
Query Match 100.0%; Score 64; DB 9; Length 767;
Best Local Similarity 100.0%; Pred. No. 0.12;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 SPEEDTEKDKPK 12
Db 726 SPEEDTEKDKPK 737


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RESULT 13
US-10-470-048B-424
; Sequence 424, Application US/10470048B
; Publication No. US20050037444A1
; GENERAL INFORMATION:
; APPLICANT: MEINKE ET AL.
; TITLE OF INVENTION: A METHOD FOR IDENTIFICATION, ISOLATION AND PRODUCTION OF
; FILE REFERENCE: SONN.035US
; CURRENT APPLICATION NUMBER: US/10/470,048B
; FILING DATE: 2003-07-25
; NUMBER OF SEQ ID NOS: 603
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 424
; LENGTH: 940
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-10-470-048B-424

Query Match      100.0%; Score 64; DB 17; Length 940;
Best Local Similarity 100.0%; Pred. No. 0.15;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 SPEEDTEKDKPK 12
      |||||
Db      726 SPEEDTEKDKPK 737

RESULT 14
US-10-470-048B-69
; Sequence 69, Application US/10470048B
; Publication No. US20050037444A1
; GENERAL INFORMATION:
; APPLICANT: MEINKE ET AL.
; TITLE OF INVENTION: A METHOD FOR IDENTIFICATION, ISOLATION AND PRODUCTION OF
; FILE REFERENCE: SONN.035US
; CURRENT APPLICATION NUMBER: US/10/470,048B
; FILING DATE: 2003-07-25
; NUMBER OF SEQ ID NOS: 603
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 69
; LENGTH: 948
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-10-470-048B-69

Query Match      100.0%; Score 64; DB 17; Length 948;
Best Local Similarity 100.0%; Pred. No. 0.15;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 SPEEDTEKDKPK 12
      |||||
Db      734 SPEEDTEKDKPK 745

RESULT 15
US-09-815-242-5456
; Sequence 5456, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haseldeck, Robert
; APPLICANT: Ohlsen, Karl L.
; APPLICANT: Zyckind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; FILE REFERENCE: ELITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815,242

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; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5456
; LENGTH: 978
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-09-815-242-5456

Query Match      100.0%; Score 64; DB 9; Length 978;
Best Local Similarity 100.0%; Pred. No. 0.16;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 SPEEDTEKDKPK 12
      |||||
Db      768 SPEEDTEKDKPK 779

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Search completed: October 22, 2005, 12:09:33
 Job time : 22.1449 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using SW model

Run on: October 22, 2005, 04:14:19 ; Search time 4.38647 Seconds
(without alignments)
263.219 Million cell updates/sec

Title: US-10-731-238-62

Sequence: 1 SFEEDTEKDKPK 12

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	64	100.0	940	2 S19702	fibronectin-binding
2	64	100.0	1018	2 A32192	fibronectin-binding
3	64	100.0	1038	2 H90053	hypothetical prote
4	60	93.8	961	2 G90053	hypothetical prote
5	44	68.8	591	2 C84220	proplyl-CoA card
6	43	67.2	467	2 AG0771	probable two-compo
7	43	67.2	1074	2 T01906	hypothetical prote
8	41	64.1	193	2 H6938	conserved hypochet
9	41	64.1	250	2 C85040	hypothetical prote
10	41	64.1	4869	2 S66572	tyandine receptor
11	40	62.5	236	2 T20726	hypothetical prote
12	40	62.5	325	2 T18283	hypothetical prote
13	40	62.5	467	2 F90989	sensor protein for
14	40	62.5	467	2 A85835	sensor protein (fo
15	40	62.5	467	2 E64974	sensor kinase Bae
16	40	62.5	817	2 F83073	probable ATP-depen
17	40	62.5	821	2 T16412	hypothetical prote
18	39	60.9	238	1 Q0B74	US4 protein - huma
19	39	60.9	502	2 T14286	embryogenic callus
20	39	60.9	665	2 T51780	hypothetical prote
21	39	60.9	1129	2 T25635	hypothetical prote
22	39	60.9	1175	2 T25634	hypothetical prote
23	38	59.4	56	2 S74259	tropoin T 3, fast
24	38	59.4	67	2 S48660	tropoin T 1, fast
25	38	59.4	184	1 TPRB1W	tropoin I, slow s
26	38	59.4	187	1 TPRB1W	tropoin I, slow s
27	38	59.4	187	1 B44786	tropoin I, slow s
28	38	59.4	258	2 I53021	tropoin T - human
29	38	59.4	269	1 WZVZ13	I3 protein - vacci

30	38	59.4	269	2 T37340	30K DNA binding ph
31	38	59.4	269	2 G72157	L3L protein - vari
32	38	59.4	269	2 A36843	K3L protein - vari
33	38	59.4	269	2 T28495	hypothetical prote
34	38	59.4	430	2 T04678	hypothetical prote
35	38	59.4	517	1 A39038	1-caldesmon, nonmu
36	38	59.4	539	2 T16400	hypothetical prote
37	38	59.4	602	2 T42401	ubiquitin cholest
38	38	59.4	689	4 S30392	hypothetical RTVL-
39	38	59.4	734	2 B42680	nucleolus-cytoplas
40	38	59.4	771	1 A33430	h-caldesmon - chic
41	38	59.4	845	2 A45669	neurofilament trip
42	38	59.4	849	2 S00030	neurofilament trip
43	38	59.4	1259	2 T32901	hypothetical prote
44	37	57.8	51	2 I66796	fetal tropoin T 3
45	37	57.8	56	2 I53073	fetal tropoin T 2

ALIGNMENTS

RESULT 1

S19702
Fibronectin-binding protein B - Staphylococcus aureus
C:Species: Staphylococcus aureus
C>Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
C/Accession: S19702
R:Joensson, K.; Signaes, C.; Mueller, H.P.; Lindberg, M.
Eur. J. Biochem. 202, 1041-1048, 1991
A:Title: Two different genes encode fibronectin binding proteins in Staphylococcus aure
A:Reference number: S19702; PMID:92111475; PMID:1837266
A/Accession: S19702
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-940 <JOB>
A/Cross-references: UNIPROT:Q53682; EMBL:X62992; NID:949040; PIDN:CAA44726.1; PID:95815
C/Keywords: fibronectin binding

Query Match

Best Local Similarity 100.0%; Score 64; DB 2; Length 940;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SFEEDTEKDKPK 12
DB 726 SFEEDTEKDKPK 737

RESULT 2

A32192
Fibronectin-binding protein - Staphylococcus aureus
C:Species: Staphylococcus aureus
C>Date: 31-Jul-1989 #sequence_revision 31-Jul-1989 #text_change 16-Feb-1997
C/Accession: A32192
R:Signaes, C.; Rancu, G.; Joensson, K.; Lindgren, P.E.; Anantharamiah, G.M.; Hoeoek,
Proc. Natl. Acad. Sci. U.S.A. 86, 699-703, 1989
A:Title: Nucleotide sequence of the gene for a fibronectin-binding protein from Staphyl
A:Reference number: A32192; PMID:8908998; PMID:2521391
A/Accession: A32192
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-1018 <SIG>
A/Cross-references: GB:U04151
C/Keywords: fibronectin binding

Query Match

Best Local Similarity 100.0%; Score 64; DB 2; Length 1018;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SFEEDTEKDKPK 12
DB 790 SFEEDTEKDKPK 801

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RESULT 3
H90053
Hypothetical protein fnb [imported] - Staphylococcus aureus (strain N315)
C:Species: Staphylococcus aureus
C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C:Accession: H90053
R:Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguc
ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.;
C.; Shiba, T.; Hatori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
A:Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.
A:Reference number: A89758; PMID:21311952; PMID:11418146
A:Accession: H90053
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1038 <KUR>
A:Cross-references: UNIPROT:Q99RD2; GB:BA000018; PID:g13702453; PIDN:BA843594.1; GSPDB:G
A:Experimental source: strain N315
C:Genetics:
A:Gene: fnb

Query Match          100.0%; Score 64; DB 2; Length 1038;
Best Local Similarity 100.0%; Pred. No. 0.0087;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SPEEDTEKDKPK 12
    |||||
Db 786 SFEEDTEKDKPK 797

RESULT 4
G90053
Hypothetical protein fnb [imported] - Staphylococcus aureus (strain N315)
C:Species: Staphylococcus aureus
C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C:Accession: G90053
R:Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguc
ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.;
C.; Shiba, T.; Hatori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
A:Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.
A:Reference number: A89758; PMID:21311952; PMID:11418146
A:Accession: G90053
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-961 <KUR>
A:Cross-references: UNIPROT:Q99RD3; GB:BA000018; PID:g13702452; PIDN:BA843593.1; GSPDB:G
A:Experimental source: strain N315
C:Genetics:
A:Gene: fnb

Query Match          93.8%; Score 60; DB 2; Length 961;
Best Local Similarity 91.7%; Pred. No. 0.038;
Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SFEEDTEKDKPK 12
    |||||
Db 699 SFEEDTEKDKPK 710

RESULT 5
C84220
Propionyl-CoA carboxylase homolog [imported] - Halobacterium sp. NRC-1
C:Species: Halobacterium sp. NRC-1
C:Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
C:Accession: C84220
R:Ng, W.V.; Kennedy, S.P.; Mahaires, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Laaky, S
; Leitbauer, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Jabc
Jung, K.H.; Alam, M.; Freilae, T.
Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000
A:Authors: Hou, S.; Daniele, C.J.; Dennis, P.P.; Omer, A.D.; Ehardt, H.; Lowe, T.M.; Li
A:Title: Genome sequence of Halobacterium species NRC-1.
A:Reference number: A84160; PMID:20504483; PMID:11016950
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A:Accession: C84220
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-591 <STO>
A:Cross-references: UNIPROT:Q9HRN1; GB:AE004437; NID:g10580213; PIDN:AA619127.1; GSPDB:G
A:Gene: yngE
C:Superfamily: propionyl-CoA carboxylase beta chain

Query Match          68.8%; Score 44; DB 2; Length 591;
Best Local Similarity 72.7%; Pred. No. 12;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 SFEEDTEKDKPK 11
    |||||
Db 573 SFEEDTEKDKPK 583

RESULT 6
AG0771
Probable two-component system sensor kinase (EC 2.7.3.-) [imported] - Salmonella enterica
C:Species: Salmonella enterica subsp. enterica serovar Typh
A:Note: this species has also been called Salmonella typhi
C:Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
C:Accession: AG0771
R:Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher,
th, T.; Conerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar,
, S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A:Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.
A:Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov
A:Reference number: AB0502; PMID:21534947; PMID:11677608
A:Accession: AG0771
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-467 <PAR>
A:Cross-references: GB:AL53382; PIDN:CM02493.1; PID:g16503357; GSPDB:GN00176
C:Genetics:
A:Gene: STY2343
C:Keywords: phosphotransferase

Query Match          67.2%; Score 43; DB 2; Length 467;
Best Local Similarity 63.6%; Pred. No. 14;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 SFEEDTEKDKPK 11
    |||||
Db 84 SFEHDNRDKPK 94

RESULT 7
T01906
Hypothetical protein T12H20.3 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 26-Feb-1999 #sequence_revision 26-Feb-1999 #text_change 09-Jul-2004
C:Accession: T01906
R:Cotton, M.; Graves, T.; Suterer, C.; Modde, T.
submitted to the EMBL Data Library, July 1998
A:Description: The sequence of A. thaliana T12H20.
A:Reference number: Z14453
A:Accession: T01906
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-1074 <COT>
A:Cross-references: UNIPROT:O82491; EMBL:AF080119; NID:g3600029; PID:g3600033
A:Experimental source: cultivar Columbia
C:Genetics:
A:Map position: 4
A:Note: T12H20.3

Query Match          67.2%; Score 43; DB 2; Length 1074;
Best Local Similarity 58.3%; Pred. No. 33;
Matches 7; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
```

OY 1 SFEDETKDKPK 12
 ||:|||||:
 Db 459 SFEDEDEBKPR 470

RESULT 8

conserved hypothetical protein ypmQ - Bacillus subtilis

C:Species: Bacillus subtilis

C>Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004

C:Accession: H69938

R:Kumai, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azavedo, V.; Beret, C.; Bron, S.; Brouillet, S.; Bruchli, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Chik, A.; Ehrlich, S.D.; Emerson, P.T.; Entian, K.D.; Eyring, J.; Fabbri, C.; Ferrara, E.

Nature 390, 249-256, 1997

A:Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Gallizzi, A.; Gallier, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.

Koeber, P.; Konings, G.; Krogan, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois, A.; Lauter, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maue, Y. M.; Ogawa, K.; Ogihara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portet, Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadate, Y.; Sato, T.; Scanlon, A.; Schmitt, M.; Schmitt, S.; Schreier, R.; Scofield, P.; Tognoni, A.; Tosato, V.; Uchiyama, T.; Walters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K.

A:Authors: Yoshikawa, H.F.; Zumbstein, E.; Yoshikawa, H.; Danchin, A.

A>Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.

A:Reference number: A63580; PMID:98044033; PMID:9384377

A:Accession: H69938

A:Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-193 <KUN>

A:Cross-references: UNIPROT:P54178; GB:Z99115; GB:AL009126; NID:G2634478; PIDN:CAB14093.

A:Experimental source: strain 168

A:Gene: ypmQ

C:Superfamily: immunodominant protein

Query Match 64.1%; Score 41; DB 2; Length 193;
 Best Local Similarity 66.7%; Pred. No. 12;
 Matches 8; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 1 SFEDETKDKPK 12
 ||:|||||:
 Db 93 SFEVDENDKPK 104

RESULT 9

hypothetical protein AT4903170 [imported] - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)

C>Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004

C:Accession: C85040

R:Anonymous, The European Union Arabidopsis Genome Sequencing Consortium, The Cold Spring Nature 402, 769-777, 1999

A>Title: Sequence and analysis of chromosome 4 of the plant Arabidopsis thaliana.

A:Reference number: A85001; PMID:20083488; PMID:10617198

A:Accession: C85040

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-250 <STO>

A:Cross-references: UNIPROT:Q9ZRI4; GB:NC_001268; NID:G7270187; PIDN:CAB77802.1; GSPDB:C

C:Gene: AT4903170

A:Map position: 4

Query Match 64.1%; Score 41; DB 2; Length 250;
 Best Local Similarity 70.0%; Pred. No. 15;
 Matches 7; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

OY 3 EEDTEKDKPK 12
 ||:|||||:
 Db 77 EEDTEKDKPK 86

RESULT 10

ryanodine receptor type 3 - chicken

C:Species: Gallus gallus (chicken)

C>Date: 14-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004

C:Accession: S66572

R:Ohtani, L.; Marziani, G.; Conti, A.; Chaleworth, A.; Sorrentino, V.

Biochem. J. 315, 207-216, 1996

A>Title: Alpha and beta isoforms of ryanodine receptor from chicken skeletal muscle are

A:Reference number: S66572; PMID:96207583; PMID:8670108

A:Accession: S66572

A:Status: preliminary; nucleic acid sequence not shown

A:Molecule type: mRNA

A:Residues: 1-4809 <OTT>

A:Cross-references: UNIPROT:Q90985; EMBL:X95267; NID:G1212911; PIDN:CAA64563.1; PID:G12

C:Superfamily: ryanodine receptor; transcription initiation factor sigma region 1 homol

Query Match 64.1%; Score 41; DB 2; Length 4869;
 Best Local Similarity 77.8%; Pred. No. 3,6e+02;
 Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 3 EEDTEKDKPK 11
 ||:|||||:
 Db 3546 EEDTEKDKPK 3554

RESULT 11

hypothetical protein F10G8.7 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004

C:Accession: T20726

R:Basham, V.

submitted to the EMBL Data Library, September 1996

A:Reference number: Z19315

A:Accession: T20726

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-296 <WLL>

A:Cross-references: UNIPROT:Q93456; EMBL:Z80216; PIDN:CAB02283.1; GSPDB:GN00019; CESP:F

A:Experimental source: clone F10G8

C:Gene: CESP:F10G8.7

A:Map position: 1

A:Insertions: 53/1; 129/3; 153/3; 187/3; 209/2; 249/2

Query Match 62.5%; Score 40; DB 2; Length 296;
 Best Local Similarity 72.7%; Pred. No. 27;
 Matches 8; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 2 EEDTEKDKPK 12
 ||:|||||:
 Db 52 EEDTEKDKPK 62

RESULT 12

hypothetical protein G5 - slime mold (Dictyostelium discoideum)

C:Species: Dictyostelium discoideum

C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004

C:Accession: T18283

R:Riebel, J.; Gonzalez, C.M.; Gonzalez, S.T.; Pilkington, K.J.; Kiyosawa, H.; Hugl

Genetics 148, 1117-1125, 1998

A>Title: Dictyostelium discoideum nuclear plasmid Ddp5 is a chimera related to the Ddp1

A:Reference number: Z14684; PMID:98198836; PMID:9539429

A:Accession: T18283

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-325 <RIE>

A:Cross-references: UNIPROT:O44016; EMBL:U00796; NID:G2702254; PID:G2702258; PIDN:AC18

C:Gene: G5

A:introns: 85/1

Query Match 62.5%; Score 40; DB 2; Length 325;
Best Local Similarity 80.0%; Pred. No. 30;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 SEDTEKDKKP 12
DB 227 EEDKEKDKKP 236

RESULT 13

P90989
Sensor protein for Baer [imported] - Escherichia coli (strain O157:H7, substrain RMD 05
C:Species: Escherichia coli
C:Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 09-Jul-2004
C:Accession: P90989
R:Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.
gawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001
A:Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and gene
A:Reference number: A99629; MUID:21156231; PMID:11258796
A:Accession: P90989
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-467 <NAV>
A:Cross-references: UNIPROT:Q8X712; GB:BA000007; PIDN:BA836309.1; PID:G13362355; GSPDB:C
A:Experimental source: strain O157:H7, substrain RMD 0509952
C:Genetics:
A:Gene: ECE2886

Query Match 62.5%; Score 40; DB 2; Length 467;
Best Local Similarity 63.6%; Pred. No. 44;
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 SPEEDTEKDKP 11
DB 84 SPEHDNSEDKP 94

RESULT 14

A85835
Sensor protein (for Baer) [imported] - Escherichia coli (strain O157:H7, substrain EDL93
C:Species: Escherichia coli
C:Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
C:Accession: A85835
R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew
Miller, L.; Grothbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca,
Nature 409, 529-533, 2001
A:Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A:Reference number: A85480; MUID:21074935; PMID:11206551
A:Accession: A85835
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-467 <STO>
A:Cross-references: UNIPROT:Q8X712; GB:AE005174; NID:G12516284; PIDN:AA657141.1; GSPDB:C
A:Experimental source: strain O157:H7, substrain EDL933
C:Genetics:
A:Gene: baes

Query Match 62.5%; Score 40; DB 2; Length 467;
Best Local Similarity 63.6%; Pred. No. 44;
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 SPEEDTEKDKP 11
DB 84 SPEHDNSEDKP 94

RESULT 15

E64974
sensory kinase Baes (EC 2.7.3.-) - Escherichia coli (strain K-12)
N:Alternate names: signal transduction protein

C:Species: Escherichia coli

C:Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 09-Jul-2004

C:Accession: E64974; JX0282

R:Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Co

A.; Rose, D.J.; Mau, B.; Shao, Y.

Science 277, 1453-1462, 1997

A:Title: The complete genome sequence of Escherichia coli K-12.

A:Reference number: A64720; MUID:97426617; PMID:9278503

A:Accession: E64974

A:Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-467 <BLAT>

A:Cross-references: UNIPROT:P30847; GB:AE000297; GB:U00096; NID:G1788382; PIDN:AACT5139.

A:Experimental source: strain K-12, substrain MG1655

R:Nagasawa, S.; Ishige, K.; Mizuno, T.

J. Biochem. 114, 350-357, 1993

A:Title: Novel members of the two-component signal transduction genes in Escherichia coli

A:Reference number: JX0282; MUID:94110256; PMID:8282725

A:Accession: JX0282

A:Molecule type: DNA

A:Residues: 1-413, 'VPA', 'VPA', '422-467 <NAG>

A:Cross-references: GB:D14054; NID:9216530; PIDN:BA003140.1; PID:G1003646; PID:G216532

C:Genetics:

A:Gene: baes

C:Keywords: autophosphorylation; phosphohistidine; phosphoprotein; phosphotransferase; s

F:12-32/Domain: transmembrane #status predicted <TM1>

F:168-186/Domain: transmembrane #status predicted <TM2>

F:219-458/Domain: sensor histidine kinase homology <SHK>

F:250/Binding site: phosphate (His) (covalent) (by autophosphorylation) #status predicted

Query Match 62.5%; Score 40; DB 2; Length 467;
Best Local Similarity 63.6%; Pred. No. 44;
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 SPEEDTEKDKP 11
DB 84 SPEHDNSEDKP 94

Search completed: October 22, 2005, 06:10:00
Job time: 5.38647 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model.

Run on: October 22, 2005, 04:10:49 ; Search time 21.9903 Seconds
(without alignments)
279.439 Million cell updates/sec

Title: US-10-731-238-62
Perfect score: 64
Sequence: 1 SFEDTREDKDKPK 12

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: UniProt_03.*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted to have a
score greater than or equal to the score of the result being printed.
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	64	100.0	152	Q9AEP9	Q9AEP9 staphylococ
2	64	100.0	940	Q53682	Q53682 staphylococ
3	64	100.0	943	Q8NUU8	Q8NUU8 staphylococ
4	64	100.0	957	Q6G6H4	Q6G6H4 staphylococ
5	64	100.0	1015	Q8NUU7	Q8NUU7 staphylococ
6	64	100.0	1015	Q6G6H3	Q6G6H3 staphylococ
7	64	100.0	1018	FNBA_STANU	FNBA_STANU
8	64	100.0	1038	Q9ARD2	Q9ARD2 staphylococ
9	64	100.0	1038	Q9ARD3	Q9ARD3 staphylococ
10	60	93.8	961	Q7A3J7	Q7A3J7 staphylococ
11	60	93.8	961	Q7A3J8	Q7A3J8 staphylococ
12	60	93.8	965	Q6GDU5	Q6GDU5 staphylococ
13	44	68.8	574	Q7YZ15	Q7YZ15 nematostell
14	44	68.8	591	Q9HRN1	Q9HRN1 halobacteri
15	43	67.2	467	Q8ZSF4	Q8ZSF4 salmonella
16	43	67.2	467	Q8ZNP9	Q8ZNP9 salmonella
17	43	67.2	1074	Q8Z491	Q8Z491 arabidopsis
18	43	65.6	359	Q6VM19	Q6VM19 medicago tr
19	42	65.6	622	Q8J1G1	Q8J1G1 brachydanio
20	42	65.6	815	Q6BYE9	Q6BYE9 debaryomyce
21	42	65.6	829	Q72CT7	Q72CT7 desulfovibr
22	41	64.1	118	Q6K3O5	Q6K3O5 oryza sativ
23	41	64.1	193	YPMO_BACSU	YPMO_BACSU bacillus su
24	41	64.1	250	Q9ZRI4	Q9ZRI4 arabidopsis
25	41	64.1	359	Q64T22	Q64T22 bacteroides
26	41	64.1	416	NAP5_HUMAN	NAP5_homo sapien
27	41	64.1	472	Q7RME2	Q7RME2 plasmodium
28	41	64.1	569	Q8SR48	Q8SR48 encephalitio
29	41	64.1	793	Q7TJL3	Q7TJL3 brachydanio
30	41	64.1	820	STL_CHLCV	STL_CHLCV chlamydomo
31	41	64.1	1213	Q6C8W7	Q6C8W7 yarrowia li

ALIGNMENTS

32	41	64.1	4007	2	Q7SH24	Q7sh24 neurospora
33	41	64.1	4869	2	Q90985	Q90985 gallus gall
34	40	62.5	154	2	Q7RR09	Q7rr09 plasmodium
35	40	62.5	197	2	Q23872	Q23872 dictyostel
36	40	62.5	278	2	Q8KFP8	Q8kfp8 chlorobium
37	40	62.5	278	2	Q7ZW15	Q7zw15 brachydanio
38	40	62.5	325	2	Q44016	Q44016 dictyostel
39	40	62.5	338	2	Q9N1T8	Q9n1t8 canis fami
40	40	62.5	465	2	Q95KN1	Q95kn1 canis fami
41	40	62.5	467	1	BAES_ECOLI	BAES_ecoli escherichia
42	40	62.5	467	1	Q8H8X6	Q8h8x6 oryza sativ
43	40	62.5	467	2	Q8X712	Q8x712 escherichia
44	40	62.5	467	2	Q83ML1	Q83ml1 shigella fl
45	40	62.5	552	2	Q9P5P6	Q9p5p6 neurospora

RESULT 1

Q9AEP9	PRELIMINARY;	PRT;	152 AA.
ID Q9AEP9;			
DT 01-JUN-2001 (TrEMBLrel. 17, Created)			
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)			
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)			
DE Fibronectin-binding protein (Fragment).			
GN Name=fnb;			
OS Staphylococcus aureus.			
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.			
OX NCBI_TaxID=1280;			
RN [1]			
RP SEQUENCE FROM N.A.			
RC STRAIN=CMRSA-1;			
RX MEDLINE=2124681; PubMed=11349044;			
RY DOI=10.1128/IAI.69.6.3791-3799.2001;			
RA Rice K., Huebner M., Vaz D., McGavin M.J.;			
RT "Variance in fibronectin binding and fnb locus polymorphisms in a			
RT Staphylococcus aureus: identification of antigenic variation in a			
RT fibronectin binding protein adhesin of the epidemic CMRSA-1 strain of			
RT methicillin-resistant S. aureus.";			
RL Infect. Immun. 69:3791-3799(2001).			
DR EMBL; AY029184; AKK31588.1; --.			
FT NON_TER			
FT NON_TER			
SQ SEQUENCE 152 AA; 17193 MW; CFA3913C2B11C025 CRC64;			
Query Match 100.0%; Score 64; DB 2; Length 152;			
Best Local Similarity 100.0%; Pred. No. 0.023;			
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
QY 1 SFEDTREDKDKPK 12			
DB 45 SFEDTREDKDKPK 56			
RESULT 2			
ID Q53682	PRELIMINARY;	PRT;	940 AA.
AC Q53682;			
DT 01-NOV-1996 (TrEMBLrel. 01, Created)			
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)			
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)			
DE Fibronectin binding protein B.			
GN Name=fnbB;			
OS Staphylococcus aureus.			
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.			
OX NCBI_TaxID=1280;			
RN [1]			
RP SEQUENCE FROM N.A.			
RC STRAIN=8325-4;			
RX MEDLINE=92111475; PubMed=1837266;			
RA Jonsson K., Sigmas C., Muller H.P., Lindberg M.;			

```
RT "Two different genes encode fibronectin binding proteins in
RT Staphylococcus aureus. The complete nucleotide sequence and
RT characterization of the second gene."
RT Eur. J. Biochem. 202;1041-1048(1991).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC an amide bond (By similarity).
DR EMBL: X62997; CAA44726.1; -.
DR FIR: S19702; S19702.
DR HSSP: Q53653; IN67.
DR GO: GO:0009986; C:cell surface; IEA.
DR GO: GO:0005618; C:cell wall; IEA.
DR GO: GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO: GO:0016020; C:membrane; IEA.
DR GO: GO:0007155; P:cell adhesion; IEA.
DR InterPro: IPR008966; Adhes_bact.
DR InterPro: IPR004237; Fn_bind.
DR InterPro: IPR005877; Gpos_Ysirk.
DR Pfam: PF02986; Fn_bind_2; -.
DR Pfam: PF00746; Gram_pos_anchor; 1.
DR Pfam: PF04650; Ysirk_signal; 1.
DR TIGRfams: TIGR01167; Lpxtg_anchor; 1.
DR TIGRfams: TIGR01168; Ysirk_signal; 1.
DR PROSITE: PS50847; GRAM_POS_ANCHORING; 1.
KW Cell wall; Peptidoglycan-anchor.
SQ SEQUENCE 940 AA; 103555 MW; E35FBBCA907AE345 CRC64;

Query Match 100.0%; Score 64; DB 2; Length 943;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SFEEDTEKDKPK 12
DB 726 SFEEDTEKDKPK 737

RESULT 3
ID Q8NU08 PRELIMINARY; PRT; 943 AA.
AC Q8NU08;
DT 01-OCT-2002 (TREMBlrel. 22, Created)
DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE FnBb protein.
GN Name=fnBb; OrderedLocustNames=MM2420;
OS Staphylococcus aureus (strain MM2).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=196620;
RA Nagai Y., Iwama N., Asano K., Naimi T., Kuroda H., Cui L.,
RA Yamamoto K., Hiramatsu K.;
RT "Genome and virulence determinants of high virulence community-
RT acquired MRSA."
RL Lancet 359:1819-1827(2002).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC an amide bond (By similarity).
DR EMBL: AP004830; BAB96285.1; -.
DR HSSP: Q53653; IN67.
DR GO: GO:0009986; C:cell surface; IEA.
DR GO: GO:0005618; C:cell wall; IEA.
DR GO: GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO: GO:0016020; C:membrane; IEA.
DR GO: GO:0007155; P:cell adhesion; IEA.
DR InterPro: IPR008966; Adhes_bact.
DR InterPro: IPR004237; Fn_bind.
DR InterPro: IPR005877; Gpos_Ysirk.
DR Pfam: PF02986; Fn_bind; 1.
DR Pfam: PF00746; Gram_pos_anchor; 1.
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```
DR Pfam: PF04650; Ysirk_signal; 1.
DR TIGRfams: TIGR01167; Lpxtg_anchor; 1.
DR TIGRfams: TIGR01168; Ysirk_signal; 1.
DR PROSITE: PS50847; GRAM_POS_ANCHORING; 1.
KW Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ SEQUENCE 943 AA; 104537 MW; DA8A5F31947E1B6A CRC64;

Query Match 100.0%; Score 64; DB 2; Length 943;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SFEEDTEKDKPK 12
DB 733 SFEEDTEKDKPK 744

RESULT 4
ID Q6G6H4 PRELIMINARY; PRT; 957 AA.
AC Q6G6H4;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE Fibronectin-binding protein.
GN Name=fnBb; OrderedLocustNames=SAS2387;
OS Staphylococcus aureus (strain MSSA476).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=282459;
RA Bason N., Bentley S.D., Chillingworth C., Chillingworth T.,
RA Churcher C., Clark L., Cotton C., Cronin A., Doggett J., Dowd L.,
RA Feltham D., Hance Z., Harris B., Hauser H., Holtroyd S., Jagels K.,
RA James K.D., Lennard N., Line A., Mayes R., Mouton R., Mungall K.,
RA Ormond S., Quail M.A., Rabinowitch B., Rutherford K.M., Sanders M.,
RA Sharp S., Simmonds M., Stevens K., Whitehead S., Barrett B.G.,
RA Spratt B.G., Parkhill J.;
RT "Complete genomes of two clinical Staphylococcus aureus strains:
RT evidence for the rapid evolution of virulence and drug resistance."
RL Proc. Natl. Acad. Sci. U.S.A. 101:9786-9791(2004).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC an amide bond (By similarity).
DR EMBL: BX571857; CAG44201.1; -.
DR GO: GO:0009986; C:cell surface; IEA.
DR GO: GO:0005618; C:cell wall; IEA.
DR GO: GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO: GO:0016020; C:membrane; IEA.
DR GO: GO:0007155; P:cell adhesion; IEA.
DR InterPro: IPR008966; Adhes_bact.
DR InterPro: IPR004237; Fn_bind.
DR InterPro: IPR005877; Gpos_Ysirk.
DR InterPro: IPR001899; Gram_pos_anchor.
DR Pfam: PF02986; Fn_bind; 1.
DR Pfam: PF00746; Gram_pos_anchor; 1.
DR Pfam: PF04650; Ysirk_signal; 1.
DR TIGRfams: TIGR01167; Lpxtg_anchor; 1.
DR TIGRfams: TIGR01168; Ysirk_signal; 1.
DR PROSITE: PS50847; GRAM_POS_ANCHORING; 1.
KW Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ SEQUENCE 957 AA; 105980 MW; 28F8BA7FFPFDSEAF CRC64;

Query Match 100.0%; Score 64; DB 2; Length 957;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SFEEDTEKDKPK 12
DB 733 SFEEDTEKDKPK 744
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RESULT 5
Q8NU07 ID Q8NU07 PRELIMINARY; PRT; 1015 AA.
AC Q8NU07;
DT 01-OCT-2002 (TREMBlrel. 22, Created)
DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Fnd protein.
GN Name=fnd; OrderedLocuNames=NM2421;
OS Staphylococcus aureus (strain MM2).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=196620;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MM2;
RX MEDLINE=22040717; PubMed=12044378; DOI=10.1016/S0140-6736(02)08713-5;
RA Baba T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Oguchi A.,
RA Nagai Y., Iwama N., Asano K., Naimi T., Kuroda H., Cui L.,
RA Yamamoto K., Hiratsugu K.,
RT "Genome and virulence determinants of high virulence community-
RT acquired MRSA."
RL Lancet 359:1819-1827(2002).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC an amide bond (By similarity).
DR EMBL: AP004830; BAB96286.1; -
DR GO: GO:0009986; C:cell surface; IEA.
DR GO: GO:0005618; C:cell wall; IEA.
DR GO: GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO: GO:0016020; C:membrane; IEA.
DR GO: GO:0007155; P:cell adhesion; IEA.
DR InterPro: IPR008966; Adhes_bact.
DR InterPro: IPR004237; Fn_bind.
DR InterPro: IPR005877; Gpos_YsIRK.
DR InterPro: IPR01899; Gram_pos_anchor.
DR Pfam: PF02986; Fn_bind. 1.
DR Pfam: PF00746; Gram_pos_anchor; 1.
DR TIGRFAMs: TIGR01167; LpxTG_anchor; 1.
DR TIGRFAMs: TIGR01168; YsIRK_signal; 1.
DR PROSITE: PS50847; GRAM_POS_ANCHORING; 1.
KW Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ SEQUENCE 1015 AA; 111145 MW; D0F9281BB64D4D2 CRC64;

Query Match 100.0%; Score 64; DB 2; Length 1015;
Best Local Similarity 100.0%; Pred. No. 0.15;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SPEEDTEKDKPK 12
DB 791 SPEEDTEKDKPK 802

RESULT 6
Q6G6H3 ID Q6G6H3 PRELIMINARY; PRT; 1015 AA.
AC Q6G6H3;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE Fibronectin-binding protein.
GN OrderedLocuNames=5AS238;
OS Staphylococcus aureus (strain MSSA476).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=282459;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=15213324; DOI=10.1073/pnas.0402521101;
RA Holden M.T.G., Fell E.J., Lindsay J.A., Peacock S.J., Day N.P.J.,
RA Enright M.C., Foster T.J., Moore C.E., Hurst L., Atkin R., Barron A.,
RA Baon N., Bentley S.D., Chillingworth C., Chillingworth T.,
RA Churcher C., Clark L., Cotton C., Cronin A., Doggett J., Dowd L.,
RA Felwell T., Hance Z., Harris B., Hauser H., Holroyd S., Jagsels K.,
RA James K.D., Lennard N., Line A., Mayes R., Moutle S., Mungall K.,

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RA Ormond D., Quail M.A., Rabinowitz E., Rutherford K.M., Sanders M.,
RA Sharp S., Simmonds M., Stevens K., Whitehead S., Barrell B.G.,
RA Spratt B.G., Parkhill J.,
RT "Complete genomes of two clinical Staphylococcus aureus strains:
RT evidence for the rapid evolution of virulence and drug resistance."
RL Proc. Natl. Acad. Sci. U.S.A. 101:9786-9791(2004).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC an amide bond (By similarity).
DR EMBL: BX571857; CAG44202.1; -
DR GO: GO:0009986; C:cell surface; IEA.
DR GO: GO:0005618; C:cell wall; IEA.
DR GO: GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO: GO:0016020; C:membrane; IEA.
DR GO: GO:0007155; P:cell adhesion; IEA.
DR InterPro: IPR008966; Adhes_bact.
DR InterPro: IPR004237; Fn_bind.
DR InterPro: IPR005877; Gpos_YsIRK.
DR InterPro: IPR01899; Gram_pos_anchor.
DR Pfam: PF02986; Fn_bind. 1.
DR Pfam: PF00746; Gram_pos_anchor; 1.
DR TIGRFAMs: TIGR01167; LpxTG_anchor; 1.
DR TIGRFAMs: TIGR01168; YsIRK_signal; 1.
DR PROSITE: PS50847; GRAM_POS_ANCHORING; 1.
KW Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ SEQUENCE 1015 AA; 111145 MW; D0F9281BB64D4D2 CRC64;

Query Match 100.0%; Score 64; DB 2; Length 1015;
Best Local Similarity 100.0%; Pred. No. 0.15;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SPEEDTEKDKPK 12
DB 791 SPEEDTEKDKPK 802

RESULT 7
FNBA_STRAU ID FNBA_STRAU STANDARD; PRT; 1018 AA.
AC P14738;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Fibronectin-binding protein precursor (FNBP).
GN Name=fndb;
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1280;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=NCTC 8325-4; PubMed=2521391;
RA Signaers C., Raucel G., Joensson K., Lindgren P.-E.,
RA Anantharamaiah G.M., Hoeck M., Lindberg M.,
RT "Nucleotide sequence of the gene for a fibronectin-binding protein
RT from Staphylococcus aureus: use of this peptide sequence in the
RT synthesis of biologically active peptides."
RL Proc. Natl. Acad. Sci. U.S.A. 86:769-703(1989).
CC -1- FUNCTION: The ability of bacteria to bind fibronectin has been
CC proposed as a virulence factor enabling bacteria to colonize wound
CC tissues and blood clots. Binding of plasma fibronectin to the
CC bacterial surface might block adhesion receptors on S.aureus, thus
CC representing an important defense mechanism against tissue
CC invasion.
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC an amide bond (Potential).
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.ebi.ac.uk/announcements/)

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CC or send an email to license@sb-std.ch).
CC -----
DR EMBL: J04151; AAA2632.1; -.
DR InterPro: IPR004237; Fn_bind.
DR InterPro: IPR005877; Gpos_YsIRK.
DR InterPro: IPR001899; Gram_pos_anchor.
DR Pfam: PF02986; Fn_bind; 1.
DR Pfam: PF00746; Gram_pos_anchor; 1.
DR Pfam: PF04650; YsIRK_signal; 1.
DR TIGRPFAM: TIGR01167; LPXTG_anchor; 1.
DR TIGRPFAM: TIGR01168; YsIRK_signal; 1.
DR PROSITE: PSS0847; GRAM_POS_ANCHORING; 1.
DR Cell adhesion, Cell wall, Peptidoglycan-anchor; Repeat; Signal;
KM Virulence.
KW
FT CHAIN 1 36
FT SIGNAL 37 985
FT PROPEP 986 1018
FT REPEAT 545 574
FT REPEAT 575 604
FT DOMAIN 745 878
FT REPEAT 745 782
FT REPEAT 783 820
FT REPEAT 821 859
FT REPEAT 860 878
FT DOMAIN 879 948
FT REPEAT 879 892
FT REPEAT 893 906
FT REPEAT 907 920
FT REPEAT 921 934
FT REPEAT 935 948
FT SITE 982 985
FT MOD_RES 985 985
SQ SEQUENCE 1018 AA; 111780 MW; 58175B020E81F1F CRC64;

Query Match 100.0%; Score 64; DB 1; Length 101;
Best Local Similarity 100.0%; Pred. No. 0.15;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SPEEDTEKDKPK 12
DB 790 SPEEDTEKDKPK 801

RESULT 8
O99RD2 PRELIMINARY; PRT; 1038 AA.
AC O99RD2;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Fibronectin-binding protein homolog.
GN Name=fnb; OrderedlocusNames=SAV2503.
OS Staphylococcus aureus (strain Mu50 / ATCC 700699).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=158878;
RX MEDLINE=21311952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2;
RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Iian J.-Q., Ito T.,
RA Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,
RA Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
RA Sekimizu K., Hirakawa H., Kohara S., Goto S., Yabuzaki J.,
RA Kanehisa M., Yamaehita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
RA Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
RT aureus."
RL Lancet 357:1225-1240(2001).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
an amide bond (By similarity).
```

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DR EMBL: AP003365; BAB58665.1; -.
DR PIR: H90053; H90053.
DR GO: GO:0009986; C:cell surface; IEA.
DR GO: GO:0005618; C:cell wall; IEA.
DR GO: GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO: GO:0016020; C:membrane; IEA.
DR GO: GO:0007155; P:cell adhesion; IEA.
DR InterPro: IPR008966; Adhes_bact.
DR InterPro: IPR004237; Fn_bind.
DR InterPro: IPR005877; Gpos_YsIRK.
DR InterPro: IPR001899; Gram_pos_anchor.
DR Pfam: PF02986; Fn_bind; 1.
DR Pfam: PF00746; Gram_pos_anchor; 1.
DR Pfam: PF04650; YsIRK_signal; 1.
DR TIGRPFAM: TIGR01167; LPXTG_anchor; 1.
DR TIGRPFAM: TIGR01168; YsIRK_signal; 1.
DR PROSITE: PSS0847; GRAM_POS_ANCHORING; 1.
DR Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ SEQUENCE 1038 AA; 113618 MW; 666BF6BF2BFEB12 CRC64;

Query Match 100.0%; Score 64; DB 2; Length 1038;
Best Local Similarity 100.0%; Pred. No. 0.16;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SPEEDTEKDKPK 12
DB 786 SPEEDTEKDKPK 797

RESULT 9
O7A3J7 PRELIMINARY; PRT; 1038 AA.
AC O7A3J7;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Fnb protein.
GN Name=fnb; OrderedlocusNames=SA2291.
OS Staphylococcus aureus (strain N315).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=158879;
RX MEDLINE=21311952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2;
RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Iian J.-Q., Ito T.,
RA Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,
RA Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
RA Sekimizu K., Hirakawa H., Kohara S., Goto S., Yabuzaki J.,
RA Kanehisa M., Yamaehita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
RA Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
RT aureus."
RL Lancet 357:1225-1240(2001).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
an amide bond (By similarity).
EMBL: AP003337; BAB43594.1; -.
DR GO: GO:0009986; C:cell surface; IEA.
DR GO: GO:0005618; C:cell wall; IEA.
DR GO: GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO: GO:0016020; C:membrane; IEA.
DR GO: GO:0007155; P:cell adhesion; IEA.
DR InterPro: IPR008966; Adhes_bact.
DR InterPro: IPR004237; Fn_bind.
DR InterPro: IPR005877; Gpos_YsIRK.
DR InterPro: IPR001899; Gram_pos_anchor.
DR Pfam: PF02986; Fn_bind; 1.
DR Pfam: PF00746; Gram_pos_anchor; 1.
DR Pfam: PF04650; YsIRK_signal; 1.
DR TIGRPFAM: TIGR01167; LPXTG_anchor; 1.
DR TIGRPFAM: TIGR01168; YsIRK_signal; 1.
DR PROSITE: PSS0847; GRAM_POS_ANCHORING; 1.
DR Cell wall; Complete proteome; Peptidoglycan-anchor.
```

SQ SEQUENCE 1038 AA; 113618 MW; 666BF6BF2BF6B12 CRC64;
 Query Match 100.0%; Score 64; DB 2; Length 1038;
 Best Local Similarity 100.0%; Pred. No. 0.16;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SPEEDTEKDKPK 12
 |||||
 DB 786 SPEEDTEKDKPK 797

RESULT 10
 Q99RD3 PRELIMINARY; PRT; 961 AA.
 AC Q99RD3; 01-JUN-2001 (TrEMBLrel. 17, Created)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Fibronectin-binding protein homolog.
 GN Name=fnb8; OrderedLocustNames=SAV2502;
 OS Staphylococcus aureus (strain M50 / ATCC 700699).
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 NCBI_TaxID=158878;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=M50 / ATCC 700699;
 RX MEDLINE=21311952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2;
 RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
 RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Lian J.-Q., Ito T.,
 RA Kanamori M., Matsunaru H., Maruyama A., Murakami H., Hosoyama A.,
 RA Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
 RA Sekimizu K., Hirakawa H., Kunara S., Goto S., Yabuzaki J.,
 RA Kanehisa M., Yamaashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
 RA Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
 RT "Whole genome sequencing of methicillin-resistant Staphylococcus
 aureus."
 RL Lancet 357:1225-1240(2001).
 CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
 an amide bond (By similarity).
 DR EMBL: AP003365; BAB58664.1; -;
 DR PIR: G90053; G90053.
 DR HSP; Q53653; I167.
 DR GO: GO:0009986; C:cell surface; IEA.
 DR GO: GO:0005618; C:cell wall; IEA.
 DR GO: GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
 DR GO: GO:0016020; C:membrane; IEA.
 DR GO: GO:0007155; P:cell adhesion; IEA.
 DR InterPro: IPR008966; Adhes_bact.
 DR InterPro: IPR004237; Fn_bind.
 DR InterPro: IPR001899; Gram_pos_anchor.
 DR Pfam: PF02986; Fn_bind; 1.
 DR Pfam: PF00746; Gram_pos_anchor; 1.
 DR Pfam: PF04650; YSIRK_signal; 1.
 DR TIGRFAMs: TIGR01167; LPXTG_anchor; 1.
 DR TIGRFAMs: TIGR01168; YSIRK_signal; 1.
 DR PROSITE: PS50847; GRAM_POS_ANCHORING; 1.
 KW Cell wall; Complete proteome; Peptidoglycan-anchor.
 SQ SEQUENCE 961 AA; 106010 MW; 364940F884EA4101 CRC64;

Query Match 93.8%; Score 60; DB 2; Length 961;
 Best Local Similarity 91.7%; Pred. No. 0.62;
 Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SPEEDTEKDKPK 12
 |||||
 DB 699 SPEEDTEKDKPK 710

RESULT 11
 Q7A3J8 PRELIMINARY; PRT; 961 AA.
 AC Q7A3J8;

DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DE FnbB protein.
 GN Name=fnb8; OrderedLocustNames=SA2290;
 OS Staphylococcus aureus (strain N315).
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 NCBI_TaxID=158879;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21311952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2;
 RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
 RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Lian J.-Q., Ito T.,
 RA Kanamori M., Matsunaru H., Maruyama A., Murakami H., Hosoyama A.,
 RA Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
 RA Sekimizu K., Hirakawa H., Kunara S., Goto S., Yabuzaki J.,
 RA Kanehisa M., Yamaashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
 RA Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
 RT "Whole genome sequencing of methicillin-resistant Staphylococcus
 aureus."
 RL Lancet 357:1225-1240(2001).
 CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
 an amide bond (By similarity).
 DR EMBL: AP003337; BAB43593.1; -;
 DR GO: GO:0009986; C:cell surface; IEA.
 DR GO: GO:0005618; C:cell wall; IEA.
 DR GO: GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
 DR GO: GO:0016020; C:membrane; IEA.
 DR GO: GO:0007155; P:cell adhesion; IEA.
 DR InterPro: IPR008966; Adhes_bact.
 DR InterPro: IPR004237; Fn_bind.
 DR InterPro: IPR005877; Gpos_YSIRK.
 DR InterPro: IPR001899; Gram_pos_anchor.
 DR Pfam: PF02986; Fn_bind; 1.
 DR Pfam: PF00746; Gram_pos_anchor; 1.
 DR Pfam: PF04650; YSIRK_signal; 1.
 DR TIGRFAMs: TIGR01167; LPXTG_anchor; 1.
 DR TIGRFAMs: TIGR01168; YSIRK_signal; 1.
 DR PROSITE: PS50847; GRAM_POS_ANCHORING; 1.
 KW Cell wall; Complete proteome; Peptidoglycan-anchor.
 SQ SEQUENCE 961 AA; 106010 MW; 364940F884EA4101 CRC64;

Query Match 93.8%; Score 60; DB 2; Length 961;
 Best Local Similarity 91.7%; Pred. No. 0.62;
 Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SPEEDTEKDKPK 12
 |||||
 DB 699 SPEEDTEKDKPK 710

RESULT 12
 Q6GDUS PRELIMINARY; PRT; 965 AA.
 AC Q6GDUS;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Fibronectin-binding protein.
 GN Name=fnbA; OrderedLocustNames=SA2580;
 OS Staphylococcus aureus (strain MRSA252).
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 NCBI_TaxID=282458;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX PubMed=15213324; DOI=10.1073/pnas.0402521101;
 RA Holden M.T.G., Feil E.J., Lindsay J.A., Peacock S.J., Day N.P.J.,
 RA Enright M.C., Foster T.J., Moore C.E., Hurst L., Atkin R., Barron A.,
 RA Baeson N., Bentley S.D., Chillingworth C., Chillingworth T.,
 RA Churcher C., Clark L., Corton C., Cronin A., Doggett J., Dowd L.,
 RA Feltwell T., Hance Z., Hauser H., Holtroyd S., Jørgensen K.,
 RA James K.D., Lennard N., Line A., Mayes R., Moule S., Mungall K.,
 RA Ormond D., Quail M.A., Rabinowitsch E., Rutherford K.M., Sanders M.,

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RA Sharp S., Simmonds M., Stevens K., Whitehead S., Barrell B.G.,
RA Spratt B.G., Parkhill J.,
RT "Complete genomes of two clinical Staphylococcus aureus strains:
RT Evidence for the rapid evolution of virulence and drug resistance.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:9786-9791(2004).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC an amide bond (By similarity).
DR EMBL: BX571856; CAG41560.1; -.
DR GO: GO:0009986; C:cell surface; IEA.
DR GO: GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO: GO:0016020; C:membrane; IEA.
DR GO: GO:0007155; P:cell adhesion; IEA.
DR InterPro: IPR008966; Adhes_bact.
DR InterPro: IPR004237; Fn_bind.
DR InterPro: IPR005877; Gpos_YsIRK.
DR InterPro: IPR001899; Gram_pos_anchor.
DR Pfam: PF02986; Fn_bind_1.
DR Pfam: PF00746; Gram_pos_anchor; 1.
DR Pfam: PF04650; YsIRK_signal; 1.
DR TIGRfams: TIGR01167; LPXTG_anchor; 1.
DR TIGRfams: TIGR01168; YsIRK_signal; 1.
DR PROSITE: PS50847; GRAM_POS_ANCHORING; 1.
KW Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ SEQUENCE 965 AA; 105691 MW; 2982E132164D0551 CRC64;

Query Match 93.8%; Score 60; DB 2; Length 965;
Best Local Similarity 91.7%; Pred. No. 0.63;
Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SPEEDTEKDKPK 12
DB 755 SPEEDTEEDKPK 766

RESULT 13
QY215 PRELIMINARY; PRT; 574 AA.
AC QY215;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE 90-kDa heat-shock protein (Fragment).
GN Name=hsp90;
OS Nematostella vectensis.
OC Eukaryota; Metazoa; Chordata; Anthozoa; Zoantharia; Actinopteria;
OC Edwardsiidae; Nematostellidae.
OC NCBI_TaxID=45351;
OX NCBI_TaxID=45351;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22707964; PubMed=12823451;
RA Rokas A., King N., Finmerly J., Carroll S.B.;
RT "Conflicting phylogenetic signals at the base of the metazoa tree.";
RL Evol. Dev. 5:346-359(2003).
DR EMBL: AY226090; AAP51222.1; -.
DR HSSP: P07900; IBYO.
DR GO: GO:0005524; F:ATP binding; IEA.
DR GO: GO:0051082; F:unfolding protein binding; IEA.
DR GO: GO:0006457; P:protein folding; IEA.
DR InterPro: IPR009079; 4_helix_cytokine.
DR InterPro: IPR003594; ATPbind_ATPase.
DR InterPro: IPR001404; Hsp90.
DR Pfam: PF02518; HATPase_C; 1.
DR Pfam: PF00183; HSP90; 1.
DR SMART: SM00387; HATPase_C; 1.
DR PROSITE: PS00298; HSP90_1.
FT NON_TER 1
FT NON_TER 574
SQ SEQUENCE 574 AA; 66236 MW; FB9BD1FE5284C10 CRC64;

Query Match 68.8%; Score 44; DB 2; Length 574;
Best Local Similarity 80.0%; Pred. No. 1.3e+02;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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QY 3 EEDTEKDKPK 12
DB 223 EEDGDKDKPK 232

RESULT 14
QYHNT1 PRELIMINARY; PRT; 591 AA.
AC QYHNT1;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Propionyl-CoA carboxylase homolog.
GN Name=yngE; Ordered locus names=VNG0623G;
OS Halobacterium sp. (strain NRC-1 / ATCC 700922 / JCM 11081).
OC Archaea; Euryarchaeota; Halobacteria; Halobacteriales;
OC Halobacteriaceae; Halobacterium.
OC NCBI_TaxID=64091;
OX NCBI_TaxID=64091;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20504483; PubMed=11016950; DOI=10.1073/pnas.190337797;
RA Ng W.V., Kennedy S.P., Mahatras G.G., Bergquist B., Pan M.,
RA Shukla H.D., Laasy S.R., Baliga N.S., Thorsson V., Strogna J.,
RA Swartzell S., Welt D., Hall J., Dahl T.A., Welt R., Goo Y.A.,
RA Leitbauer B., Keller K., Cruz R., Danson M.J., Hough D.W.,
RA Maddocks D.G., Jablonksi P.E., Krebs M.P., Angewine C.M., Dale H.,
RA Isewarger T.A., Peck R.F., Pohlstroder M., Spudich J.L., Jung K.-H.,
RA Alam M., Freitas T., Hou S., Daniels C.J., Dennis P.P., Omer A.D.,
RA Ebhardt H., Lowe T.M., Liang P., Riley M., Hood L., DasSarma S.;
RT "Genome sequence of Halobacterium species NRC-1.";
RL Proc. Natl. Acad. Sci. U.S.A. 97:12176-12181(2000).
DR EMBL: AF005010; AAG19127.1; -.
DR FTR: C84220; C84220.
DR HSSP: Q8GBW6; 1ON3.
DR GO: GO:0009343; C:biotin carboxylase complex; IEA.
DR GO: GO:0004075; F:biotin carboxylase activity; IEA.
DR InterPro: IPR000022; Carboxyl_trans.
DR Pfam: PF01039; Carboxyl_trans; 1.
KW Complete proteome.
SQ SEQUENCE 591 AA; 64547 MW; 0EC5ACF9008A225C CRC64;

Query Match 68.8%; Score 44; DB 2; Length 591;
Best Local Similarity 72.7%; Pred. No. 1.3e+02;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 SPEEDTEKDKPK 11
DB 573 SPEEDTEKDKPK 583

RESULT 15
Q825F4 PRELIMINARY; PRT; 467 AA.
AC Q825F4;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Putative two-component system sensor kinase (EC 2.7.3.-).
GN Name=baeS; Ordered locus names=STY2343, l0742;
OS Salmonella typhi.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Salmonella.
OC NCBI_TaxID=601;
OX NCBI_TaxID=601;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=CT18;
RX MEDLINE=21534947; PubMed=11677608; DOI=10.1038/35101607;
RA Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain J.,
RA Churcher C.M., Mungall K.L., Bentley S.D., Holden M.T.G., Sebatina M.,
RA Baker S., Basham D., Brooks K., Chillingworth T., Connerton P.,
RA Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J.,
RA Felwell T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jagsels K.,
RA Krogh A., Larsen T.S., Leather S., Moule S., O'Garra P., Parry C.,

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RA Quail M.A., Rutherford K.M., Simmonds M., Skelton J., Stevens K.,
 RA Whitehead S., Barrell B.G.;
 RT "Complete genome sequence of a multiple drug resistant *Salmonella*
 RT enterica serovar Typhi CT18.";
 RL Nature 413:848-852(2001).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Ty2 / ATCC 700931;
 RX MEDLINE=22531367; PubMed=12644504;
 RX DOI=10.1128/JB.185.7.2330-2337.2003;
 RA Deng W., Liou S.-R., Plunkett G. III, Mayhew G.F., Rose D.J.,
 RA Burland V., Kodyanski V., Schwartz D.C., Blattner F.R.;
 RT "Comparative genomics of *Salmonella enterica* serovar Typhi strains Ty2
 RT and CT18.";
 RL J. Bacteriol. 185:2330-2337(2003).
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
 CC -1- SIMILARITY: Contains 1 histidine kinase domain.
 DR EMBL; AL627273; CAD02493.1; -.
 DR EMBL; AE016836; AAC068435.1; -.
 DR GO; GO:0016021; C:Integral to membrane; IEA.
 DR GO; GO:0005524; F:ATP binding; IEA.
 DR GO; GO:0016301; F:Kinase activity; IEA.
 DR GO; GO:0016740; F:transferase activity; IEA.
 DR GO; GO:0000155; F:two-component sensor molecule activity; IEA.
 DR GO; GO:0007600; P:sensory perception; IEA.
 DR GO; GO:0000160; P:two-component signal transduction system (p. . .); IEA.
 DR Pfam; PF00672; HAMP; 1.
 DR Pfam; PF02518; HATPase_C; 1.
 DR Pfam; PF00512; HsKA; 1.
 DR PRINTS; PR00344; BCTRSENSOR.
 DR PRINTS; PR01780; LANTIREGPROT.
 DR SMART; SM00304; HAMP; 1.
 DR SMART; SM00387; HATPase_C; 1.
 DR SMART; SM00388; HsKA; 1.
 DR PROSITE; PSS0865; HAMP; 1.
 DR PROSITE; PSS0109; HIS_KIN; 1.
 KM Complete proteome; Kinase; Phosphorylation; Sensory transduction;
 KM Transferase; Transmembrane.
 SQ SEQUENCE 467 AA; 52132 MW; FACG945D10B16D CRC64;

Query March 67.2%; Score 43; DB 2; Length 467;
 Best Local Similarity 63.6%; Pred. NO. 1.5e+02;
 Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 SPEEDTEKDP 11
 ||| | :|||
 Db 84 SFHHNDRDKP 94

Search completed: October 22, 2005, 06:06:22
 Job time : 23.9903 secs

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OM protein - protein search, using SW model

Run on: October 25, 2005, 19:38:38 ; Search time 22.0612 Seconds
(without alignments)
175.313 Million cell updates/sec

Title: US-10-731-238-63

Perfect score: 52

Sequence: 1 QNSGNQSFEE 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

A_Geneseq_16Dec04: *
1: geneseqp19808: *
2: geneseqp19908: *
3: geneseqp20008: *
4: geneseqp20018: *
5: geneseqp20028: *
6: geneseqp20038: *
7: geneseqp20048: *
8: geneseqp20058: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	52	100.0	10	2 AAW65719	AAW65719 Fibrinect
2	52	100.0	38	1 AAP80660	AAP80660 Protein w
3	52	100.0	38	1 AAP82116	AAP82116 Fibrinect
4	52	100.0	38	1 AAW65695	AAW65695 Fibrinect
5	52	100.0	38	2 AAW65662	AAW65662 Fibrinect
6	52	100.0	38	2 AAW65696	AAW65696 Fibrinect
7	52	100.0	38	2 AAW65697	AAW65697 Fibrinect
8	52	100.0	38	2 AAW65694	AAW65694 Fibrinect
9	52	100.0	38	2 AAW65699	AAW65699 Fibrinect
10	52	100.0	38	2 AAW65661	AAW65661 Fibrinect
11	52	100.0	38	2 AAW65698	AAW65698 Fibrinect
12	52	100.0	39	2 AAW65712	AAW65712 Fibrinect
13	52	100.0	39	2 AAW65713	AAW65713 Fibrinect
14	52	100.0	130	2 AAR58806	AAR58806 Fibrinect
15	52	100.0	130	2 AAR58807	AAR58807 Fibrinect
16	52	100.0	130	2 AAR51202	AAR51202 D1-D4 fib
17	52	100.0	130	2 AAR91201	AAR91201 D1-D4 fib
18	52	100.0	134	2 AAY28089	AAY28089 Cloned fi
19	52	100.0	134	2 AAY28088	AAY28088 S. aureus
20	52	100.0	134	2 AAY29087	AAY29087 S. aureus
21	52	100.0	139	2 AAW31556	AAW31556 Fibrinect
22	52	100.0	174	2 AAR58808	AAR58808 Fbp fibro
23	52	100.0	174	2 AAR91203	AAR91203 D1-D4 fib
24	52	100.0	181	2 AAR58805	AAR58805 Fibrinect
25	52	100.0	181	2 AAR91200	AAR91200 D1-D4 fib

ALIGNMENTS

RESULT 1
AAW65719 standard; peptide; 10 AA.
XX
AC AAW65719;
XX
DT 16-OCT-1998 (first entry)
XX
DE Fibrinectin binding protein-derived peptide #63.
XX
XX microbial surface components recognising adhesive matrix molecule;
KW MSCRAMM; fibrinectin; fibrinectin-binding protein; antibody; epitope;
KW antibiotic; bacterial infection; antibiotic-resistant strain.
XX
OS Synthetic.
OS Staphylococcus aureus.
XX
PN W09831389-A2.
XX
XX 23-JUL-1998.
XX
PF 21-JAN-1998; 98WO-US001222.
XX
PR 21-JAN-1997; 97US-0036139P.
XX
XX (TEXA) UNIV TEXAS A & M SYSTEM.
XX
XX Hoeoek M, Patil JM, House-Pompeo KL, Speziale P, Joh D;
PI McGavin MJ;
XX WPI; 1998-413816/35.
XX
XX
XX The invention relates to antibodies that bind to a fibrinectin-binding
XX domain of a fibrinectin-binding protein, and inhibit binding of the
XX protein to fibrinectin. Also claimed are: (1) isolated peptides of a
XX fibrinectin-binding protein that do not bind to fibrinectin; (2) fusion
XX protein containing at least one peptide of a fibrinectin-binding protein
XX linked to a second amino acid sequence; (3) nucleic acid encoding the
XX isolated peptide of (1). Antibodies, the isolated peptides of (1) and the
XX nucleic acids are all useful for immunisation (active or passive) and (by
XX inhibiting binding of bacteria to fibrinectin) for preventing or treating
XX infection in humans or other animals, particularly by staphylococci or

CC streptococci, e.g. meningitis, otitis media, pneumonia, endocarditis,
 CC mastitis in cattle, abortion in horses and many others. Since the
 CC antibodies block binding of bacteria, they should be effective against
 CC antibiotic-resistant strains, and may replace antibiotic therapy or
 CC increase its effectiveness. Sequences AAW65719-41 and AAW65658 represent
 CC peptides which were synthesised to span the D1 motif and the N-terminal
 CC 18 amino acids of D2, with each peptide overlapping by eight amino acids
 CC with the previous sequence
 XX
 SQ Sequence 10 AA;

Query Match 100.0%; Score 52; DB 2; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.0037;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QNSGNOSFEE 10
 |||||
 1 QNSGNOSFEE 10

RESULT 2
 ID AAW60660 standard; protein; 38 AA.

XX AAW60660;
 XX
 AC 25-MAR-2003 (revised)
 DT 07-OCT-1990 (first entry)
 XX
 DE Protein with fibronectin binding ability.
 XX
 XX Hybrid DNA molecule; fibronectin binding; mastitis; ruminants;
 KM wound infection.
 XX

XX Staphylococcus aureus.

XX EP294349-A.

XX 07-DEC-1988.

XX 30-MAY-1988; 88BP-00850188.

XX 01-JUN-1987; 87SE-00002272.

XX (ALFA) ALFA LAVAL AGRIC INT AB.

XX Lindberg MK, Signas LC, Wadstrom TM, Froman G;

XX WPI; 1988-347978/49.

XX N-PSDB; AAN81097.

PT Hybrid DNA encoding Staphylococcus aureus fibronectin binding protein -
 PT useful for immunisation and topical application to prevent staphylococcal
 PT infections.

PS Claim 11; Page 12; 23pp; English.

CC The peptide has fibronectin binding ability. It is useful for immunising
 CC ruminants against staphylococcal mastitis, pref. when used at 0.5-5
 CC micrograms/kg, using 3 doses given at 1-3 week intervals; for topical
 CC application to prevent wound infection, using an isotonic saline soln. of
 CC concn. 25-250 micrograms/ml; and, when immobilised on a carrier, for
 CC diagnosing staphylococcal infections. (Updated on 25-MAR-2003 to correct
 CC PF field.) (Updated on 25-MAR-2003 to correct PA field.)

XX Sequence 38 AA;

Query Match 100.0%; Score 52; DB 1; Length 38;
 Best Local Similarity 100.0%; Pred. No. 0.016;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QNSGNOSFEE 10
 |||||

DB 2 QNSGNOSFEE 11

RESULT 3
 ID AAW82116 standard; protein; 38 AA.

XX AAW82116;

XX 25-MAR-2003 (revised)

DT 05-JAN-1990 (first entry)

XX Fibronectin binding protein.

XX Fibronectin binding protein; S.aureus; immunisation; mastitis; ruminants;

XX wound infection; diagnosis.

XX Staphylococcus aureus.

XX EP294349-A.

XX 07-DEC-1988.

XX 30-MAY-1988; 88BP-00850188.

XX 01-JUN-1987; 87SE-00002272.

XX (ALFA) ALFA LAVAL AGRIC INT AB.

XX Lindberg MK, Signas LC, Wadstrom TM, Froman G;

XX WPI; 1988-347978/49.

XX N-PSDB; AAN82054.

PT Hybrid DNA encoding Staphylococcus aureus fibronectin binding protein -
 PT useful for immunisation and topical application to prevent staphylococcal
 PT infections.
 PS Claim 11; Page 12; 23pp; English.

CC The S.aureus fibronectin binding protein may be included in a hybrid
 CC protein. The protein may be used to immunise ruminants against
 CC staphylococcal mastitis, pref. when given at 0.5-5 microg/kg, using 3
 CC doses at 1-3 week intervals; and for topical applicn. to prevent wound
 CC infection, pref. using isotonic saline soln. of concn. 25-250 microg/mg.
 CC The DNA encoding the binding protein and the hybrid protein may be
 CC immobilised on a carrier and used to diagnose staphylococcal infections.
 CC (Updated on 25-MAR-2003 to correct PA field.)

XX Sequence 38 AA;

Query Match 100.0%; Score 52; DB 1; Length 38;
 Best Local Similarity 100.0%; Pred. No. 0.016;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QNSGNOSFEE 10
 |||||
 2 QNSGNOSFEE 11

RESULT 4
 ID AAW65695 standard; peptide; 38 AA.

XX AAW65695;

XX 16-OCT-1998 (first entry)

XX Fibronectin binding protein-derived peptide #39.

XX microbial surface components recognising adhesive matrix molecule;
 KM MSCRAMM; fibronectin; fibronectin-binding protein; antibody; epitope;
 KM antibiotic; bacterial infection; antibiotic-resistant strain.

```

XX OS Synthetic.
XX OS Staphylococcus aureus.
XX PN MO9831389-A2.
XX PD 23-JUL-1998.
XX PF 21-JAN-1998; 98WO-US001222.
XX PR 21-JAN-1997; 97US-0036139P.
XX PA (TEXA ) UNIV TEXAS A & M SYSTEM.
XX PI Hoeoek M, Patti JM, House-Pompeo KL, Speziale P, Joh D;
XX PI Mcgavln MJ;
XX DR WPI, 1998-413816/35.
XX PS
XX PT Antibody that binds to fibronectin-binding protein, preventing its
XX PT binding to fibronectin - used to treat or prevent bacterial infection,
XX PT especially by Staphylococci and Streptococci.
XX PS Example 8, Page 102; 201pp; English.
XX CC
XX CC The invention relates to antibodies that bind to a fibronectin-binding
XX CC domain of a fibronectin-binding protein, and inhibit binding of the
XX CC protein to fibronectin. Also claimed are: (1) isolated peptides of a
XX CC fibronectin-binding protein that do not bind to fibronectin; (2) fusion
XX CC protein containing at least one peptide of a fibronectin-binding protein
XX CC linked to a second amino acid sequence; (3) nucleic acid encoding the
XX CC isolated peptide of (1). Antibodies, the isolated peptides of (1) and the
XX CC isolated acids are all useful for immunisation (active or passive) and (by
XX CC inhibiting binding of bacteria to fibronectin) for preventing or treating
XX CC infection in humans or other animals, particularly by staphylococci or
XX CC streptococci, e.g. meningitis, otitis media, pneumonia, endocarditis,
XX CC mastitis in cattle, abortion in horses and many others. Since the
XX CC antibodies block binding of bacteria, they should be effective against
XX CC antibiotic-resistant strains, and may replace antibiotic therapy or
XX CC increase its effectiveness. Sequences AAM65691-700 represent a series of
XX CC synthetic peptides based on the D1 region of S. aureus fibronectin
XX CC binding protein A. They were synthesised to contain mutations
XX CC
XX SQ
XX Query Match 100.0%; Score 52; DB 2; Length 38;
XX Best Local Similarity 100.0%; Pred. No. 0.016;
XX Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 QNSGNQSFEE 10
Db 1 QNSGNQSFEE 10
XX
XX RESULT 5
XX ID AAM65662 standard; peptide; 38 AA.
XX AC AAM65662;
XX DT 16-OCT-1998 (first entry)
XX DE Fibronectin binding protein-derived peptide #6.
XX KM microbial surface components recognising adhesive matrix molecule;
XX KM MSCRAM; fibronectin; fibronectin-binding protein; antibody; epitope;
XX KM antibiotic; bacterial infection; antibiotic-resistant strain.
XX OS Synthetic.
XX OS Staphylococcus aureus.
XX PN MO9831389-A2.
XX

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PD 23-JUL-1998.
XX PF 21-JAN-1998; 98WO-US001222.
XX PR 21-JAN-1997; 97US-0036139P.
XX PA (TEXA ) UNIV TEXAS A & M SYSTEM.
XX PI Hoeoek M, Patti JM, House-Pompeo KL, Speziale P, Joh D;
XX PI Mcgavln MJ;
XX DR WPI, 1998-413816/35.
XX PS
XX PT Antibody that binds to fibronectin-binding protein, preventing its
XX PT binding to fibronectin - used to treat or prevent bacterial infection,
XX PT especially by Staphylococci and Streptococci.
XX PS Example 2; Page 92; 201pp; English.
XX CC
XX CC The invention relates to antibodies that bind to a fibronectin-binding
XX CC domain of a fibronectin-binding protein, and inhibit binding of the
XX CC protein to fibronectin. Also claimed are: (1) isolated peptides of a
XX CC fibronectin-binding protein that do not bind to fibronectin; (2) fusion
XX CC protein containing at least one peptide of a fibronectin-binding protein
XX CC linked to a second amino acid sequence; (3) nucleic acid encoding the
XX CC isolated peptide of (1). Antibodies, the isolated peptides of (1) and the
XX CC isolated acids are all useful for immunisation (active or passive) and (by
XX CC inhibiting binding of bacteria to fibronectin) for preventing or treating
XX CC infection in humans or other animals, particularly by staphylococci or
XX CC streptococci, e.g. meningitis, otitis media, pneumonia, endocarditis,
XX CC mastitis in cattle, abortion in horses and many others. Since the
XX CC antibodies block binding of bacteria, they should be effective against
XX CC antibiotic-resistant strains, and may replace antibiotic therapy or
XX CC increase its effectiveness. Sequences AAM65659-68 represent synthetic
XX CC epitopes from the fibronectin binding domains DU and D1-D4 of the S.
XX CC aureus fnba gene
XX CC
XX SQ
XX Query Match 100.0%; Score 52; DB 2; Length 38;
XX Best Local Similarity 100.0%; Pred. No. 0.016;
XX Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 QNSGNQSFEE 10
Db 1 QNSGNQSFEE 10
XX
XX RESULT 6
XX ID AAM65696 standard; peptide; 38 AA.
XX AC AAM65696;
XX DT 16-OCT-1998 (first entry)
XX DE Fibronectin binding protein-derived peptide #40.
XX KM microbial surface components recognising adhesive matrix molecule;
XX KM MSCRAM; fibronectin; fibronectin-binding protein; antibody; epitope;
XX KM antibiotic; bacterial infection; antibiotic-resistant strain.
XX OS Synthetic.
XX OS Staphylococcus aureus.
XX PN MO9831389-A2.
XX PD 23-JUL-1998.
XX PF 21-JAN-1998; 98WO-US001222.
XX PR 21-JAN-1997; 97US-0036139P.
XX

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PA (TEXA) UNIV TEXAS A & M SYSTEM.
 XX Hoeoek M, Patti JM, House-Pompeo KL, Speziale P, Joh D;
 PI Mcgavayn MJ;
 XX WPI; 1998-413816/35.
 DR
 XX Antibody that binds to fibronectin-binding protein, preventing its
 PT binding to fibronectin - used to treat or prevent bacterial infection,
 PT especially by Staphylococci and Streptococci.
 PS Example 8; Page 102; 201pp; English.
 XX
 CC The invention relates to antibodies that bind to a fibronectin-binding
 CC domain of a fibronectin-binding protein, and inhibit binding of the
 CC protein to fibronectin. Also claimed are: (1) isolated peptides of a
 CC fibronectin-binding protein that do not bind to fibronectin; (2) fusion
 CC protein containing at least one peptide of a fibronectin-binding protein
 CC linked to a second amino acid sequence; (3) nucleic acid encoding the
 CC isolated peptide of (1). Antibodies, the isolated peptides of (1) and the
 CC nucleic acids are all useful for immunisation (active or passive) and (by
 CC inhibiting binding of bacteria to fibronectin) for preventing or treating
 CC infection in humans or other animals, particularly by staphylococci or
 CC streptococci, e.g. meningitis, otitis media, pneumonia, endocarditis,
 CC mastitis in cattle, abortion in horses and many others. Since the
 CC antibodies block binding of bacteria, they should be effective against
 CC antibiotic-resistant strains, and may replace antibiotic therapy or
 CC increase its effectiveness. Sequences AAW65691-700 represent a series of
 CC synthetic peptides based on the D1 region of S. aureus fibronectin
 CC binding protein A. They were synthesised to contain mutations
 XX
 SQ Sequence 38 AA;
 QY
 Query Match 100.0%; Score 52; DB 2; Length 38;
 Best Local Similarity 100.0%; Pred. No. 0.016;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 DB 1 QNSGNSFEE 10
 1 QNSGNSFEE 10
 RESULT 7
 ID AAW65697 standard; peptide; 38 AA.
 XX
 AC AAW65697;
 XX
 DT 16-OCT-1998 (first entry)
 XX
 DE Fibronectin binding protein-derived peptide #41.
 XX
 KM microbial surface components recognising adhesive matrix molecule;
 KM MSCRAMM; fibronectin; fibronectin-binding protein; antibody; epitope;
 KM antibiotic; bacterial infection; antibiotic-resistant strain.
 OS Synthetic.
 OS Staphylococcus aureus.
 XX
 PN WO9831389-A2.
 XX
 PD 23-JUL-1998.
 XX
 PF 21-JAN-1998; 98WO-US001222.
 XX
 PR 21-JAN-1997; 97US-0036139P.
 XX
 PA (TEXA) UNIV TEXAS A & M SYSTEM.
 XX
 PI Hoeoek M, Patti JM, House-Pompeo KL, Speziale P, Joh D;
 PI Mcgavayn MJ;
 XX WPI; 1998-413816/35.

XX
 XX Antibody that binds to fibronectin-binding protein, preventing its
 PT binding to fibronectin - used to treat or prevent bacterial infection,
 PT especially by Staphylococci and Streptococci.
 PS Example 8; Page 102; 201pp; English.
 XX
 CC The invention relates to antibodies that bind to a fibronectin-binding
 CC domain of a fibronectin-binding protein, and inhibit binding of the
 CC protein to fibronectin. Also claimed are: (1) isolated peptides of a
 CC fibronectin-binding protein that do not bind to fibronectin; (2) fusion
 CC protein containing at least one peptide of a fibronectin-binding protein
 CC linked to a second amino acid sequence; (3) nucleic acid encoding the
 CC isolated peptide of (1). Antibodies, the isolated peptides of (1) and the
 CC nucleic acids are all useful for immunisation (active or passive) and (by
 CC inhibiting binding of bacteria to fibronectin) for preventing or treating
 CC infection in humans or other animals, particularly by staphylococci or
 CC streptococci, e.g. meningitis, otitis media, pneumonia, endocarditis,
 CC mastitis in cattle, abortion in horses and many others. Since the
 CC antibodies block binding of bacteria, they should be effective against
 CC antibiotic-resistant strains, and may replace antibiotic therapy or
 CC increase its effectiveness. Sequences AAW65691-700 represent a series of
 CC synthetic peptides based on the D1 region of S. aureus fibronectin
 CC binding protein A. They were synthesised to contain mutations
 XX
 SQ Sequence 38 AA;
 QY
 Query Match 100.0%; Score 52; DB 2; Length 38;
 Best Local Similarity 100.0%; Pred. No. 0.016;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 DB 1 QNSGNSFEE 10
 1 QNSGNSFEE 10
 RESULT 8
 ID AAW65694 standard; peptide; 38 AA.
 XX
 AC AAW65694;
 XX
 DT 16-OCT-1998 (first entry)
 XX
 DE Fibronectin binding protein-derived peptide #38.
 XX
 KM microbial surface components recognising adhesive matrix molecule;
 KM MSCRAMM; fibronectin; fibronectin-binding protein; antibody; epitope;
 KM antibiotic; bacterial infection; antibiotic-resistant strain.
 OS Synthetic.
 OS Staphylococcus aureus.
 XX
 PN WO9831389-A2.
 XX
 PD 23-JUL-1998.
 XX
 PF 21-JAN-1998; 98WO-US001222.
 XX
 PR 21-JAN-1997; 97US-0036139P.
 XX
 PA (TEXA) UNIV TEXAS A & M SYSTEM.
 XX
 PI Hoeoek M, Patti JM, House-Pompeo KL, Speziale P, Joh D;
 PI Mcgavayn MJ;
 XX WPI; 1998-413816/35.
 XX
 PT Antibody that binds to fibronectin-binding protein, preventing its
 PT binding to fibronectin - used to treat or prevent bacterial infection,
 PT especially by Staphylococci and Streptococci.
 PS Example 8; Page 102; 201pp; English.

XX The invention relates to antibodies that bind to a fibronectin-binding
 CC domain of a fibronectin-binding protein, and inhibit binding of the
 CC protein to fibronectin. Also claimed are: (1) isolated peptides of a
 CC fibronectin-binding protein that do not bind to fibronectin; (2) fusion
 CC protein containing at least one peptide of a fibronectin-binding protein
 CC linked to a second amino acid sequence; (3) nucleic acid encoding the
 CC isolated peptide of (1). Antibodies, the isolated peptides of (1) and the
 CC nucleic acids are all useful for immunisation (active or passive) and (by
 CC inhibiting binding of bacteria to fibronectin) for preventing or treating
 CC infection in humans or other animals, particularly by staphylococci or
 CC streptococci, e.g. meningitis, otitis media, pneumonia, endocarditis,
 CC mastitis in cattle, abortion in horses and many others. Since the
 CC antibodies block binding of bacteria, they should be effective against
 CC antibiotic-resistant strains, and may replace antibiotic therapy or
 CC increase its effectiveness. Sequences AAW65691-700 represent a series of
 CC synthetic peptides based on the D1 region of *S. aureus* fibronectin
 CC binding protein A. They were synthesised to contain mutations

XX Sequence 38 AA;

Query Match 100.0%; Score 52; DB 2; Length 38;

Best Local Similarity 100.0%; Pred. No. 0.016;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QNSGNSFEE 10
 |||||
 Db 1 QNSGNSFEE 10

RESULT 9
 AAW65699
 ID AAW65699 standard; peptide; 38 AA.

XX AAW65699;

DT 16-OCT-1998 (first entry)

XX Fibronectin binding protein-derived peptide #43.

XX microbial surface components recognising adhesive matrix molecule;
 KM MSCRAMM; fibronectin; fibronectin-binding protein; antibody; epitope;
 KM antibiotic; bacterial infection; antibiotic-resistant strain.

XX Synthetic.
 OS Staphylococcus aureus.

XX W09831389-A2.

XX 23-JUL-1998.

XX 21-JAN-1998; 98WO-US001222.

XX 21-JAN-1997; 97US-0036139P.

XX (TEXA) UNIV TEXAS A & M SYSTEM.

XX Hosoe M, Patti JM, House-Pompeo KL, Speziale P, Joh D;
 PI Mcgavin MJ;

XX WPI; 1998-413816/35.

XX Antibody that binds to fibronectin-binding protein, preventing its
 PT binding to fibronectin - used to treat or prevent bacterial infection,
 PT especially by Staphylococci and Streptococci.

XX Example 8; Page 102; 201pp; English.

XX The invention relates to antibodies that bind to a fibronectin-binding
 CC domain of a fibronectin-binding protein, and inhibit binding of the
 CC protein to fibronectin. Also claimed are: (1) isolated peptides of a
 CC fibronectin-binding protein that do not bind to fibronectin; (2) fusion
 CC protein containing at least one peptide of a fibronectin-binding protein

CC linked to a second amino acid sequence; (3) nucleic acid encoding the
 CC isolated peptide of (1). Antibodies, the isolated peptides of (1) and the
 CC nucleic acids are all useful for immunisation (active or passive) and (by
 CC inhibiting binding of bacteria to fibronectin) for preventing or treating
 CC infection in humans or other animals, particularly by staphylococci or
 CC streptococci, e.g. meningitis, otitis media, pneumonia, endocarditis,
 CC mastitis in cattle, abortion in horses and many others. Since the
 CC antibodies block binding of bacteria, they should be effective against
 CC antibiotic-resistant strains, and may replace antibiotic therapy or
 CC increase its effectiveness. Sequences AAW65691-700 represent a series of
 CC synthetic peptides based on the D1 region of *S. aureus* fibronectin
 CC binding protein A. They were synthesised to contain mutations

XX Sequence 38 AA;

Query Match 100.0%; Score 52; DB 2; Length 38;

Best Local Similarity 100.0%; Pred. No. 0.016;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QNSGNSFEE 10
 |||||
 Db 1 QNSGNSFEE 10

RESULT 10
 AAW65661
 ID AAW65661 standard; peptide; 38 AA.

XX AAW65661;

DT 16-OCT-1998 (first entry)

XX Fibronectin binding protein-derived peptide #5.

XX microbial surface components recognising adhesive matrix molecule;
 KM MSCRAMM; fibronectin; fibronectin-binding protein; antibody; epitope;
 KM antibiotic; bacterial infection; antibiotic-resistant strain.

XX Synthetic.
 OS Staphylococcus aureus.

XX W09831389-A2.

XX 23-JUL-1998.

XX 21-JAN-1998; 98WO-US001222.

XX 21-JAN-1997; 97US-0036139P.

XX (TEXA) UNIV TEXAS A & M SYSTEM.

XX Hosoe M, Patti JM, House-Pompeo KL, Speziale P, Joh D;
 PI Mcgavin MJ;

XX WPI; 1998-413816/35.

XX Antibody that binds to fibronectin-binding protein, preventing its
 PT binding to fibronectin - used to treat or prevent bacterial infection,
 PT especially by Staphylococci and Streptococci.

XX Example 2; Page 92; 201pp; English.

XX The invention relates to antibodies that bind to a fibronectin-binding
 CC domain of a fibronectin-binding protein, and inhibit binding of the
 CC protein to fibronectin. Also claimed are: (1) isolated peptides of a
 CC fibronectin-binding protein that do not bind to fibronectin; (2) fusion
 CC protein containing at least one peptide of a fibronectin-binding protein
 CC linked to a second amino acid sequence; (3) nucleic acid encoding the
 CC isolated peptide of (1). Antibodies, the isolated peptides of (1) and the
 CC nucleic acids are all useful for immunisation (active or passive) and (by
 CC inhibiting binding of bacteria to fibronectin) for preventing or treating
 CC infection in humans or other animals, particularly by staphylococci or
 CC streptococci, e.g. meningitis, otitis media, pneumonia, endocarditis,

CC mastitis in cattle, abortion in horses and many others. Since the
 CC antibodies block binding of bacteria, they should be effective against
 CC antibiotic-resistant strains, and may replace antibiotic therapy or
 CC increase its effectiveness. Sequences AAW65659-68 represent synthetic
 CC epitopes from the fibronectin binding domains D1 and D1-D4 of the S.
 CC aureus fnbA gene
 XX
 SQ Sequence 38 AA;
 QY 1 QNSGNOSFEE 10
 DB 1 QNSGNOSFEE 10
 Query Match 100.0%; Score 52; DB 2; Length 38;
 Best Local Similarity 100.0%; Pred. No. 0.016;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 RESULT 11
 AAW65698 standard; peptide; 38 AA.
 AC AAW65698;
 DT 16-OCT-1998 (first entry)
 DE Fibronectin binding protein-derived peptide #42.
 OS Microbial surface components recognising adhesive matrix molecule;
 KM MSCRAM; fibronectin; fibronectin-binding protein; antibody; epitope;
 KM antibiotic; bacterial infection; antibiotic-resistant strain.
 OS Synthetic.
 OS Staphylococcus aureus.
 PN WO9831389-A2.
 PD 23-JUL-1998.
 PF 21-JAN-1998; 98WO-US001222.
 PR 21-JAN-1997; 97US-0036139P.
 PA (TEXA) UNIV TEXAS A & M SYSTEM.
 PI Hoeoek M, Patti JM, House-Pompeo KL, Speziale P, Joh D,
 PI McGavin MJ;
 DR WPI; 1998-413816/35.
 XX Antibody that binds to fibronectin-binding protein, preventing its
 PT binding to fibronectin - used to treat or prevent bacterial infection,
 PT especially by Staphylococci and Streptococci.
 XX
 PS Example 8; Page 102; 201pp; English.
 CC The invention relates to antibodies that bind to a fibronectin-binding
 CC domain of a fibronectin-binding protein, and inhibit binding of the
 CC protein to fibronectin. Also claimed are: (1) isolated peptides of a
 CC fibronectin-binding protein that do not bind to fibronectin; (2) fusion
 CC protein containing at least one peptide of a fibronectin-binding protein
 CC linked to a second amino acid sequence; (3) nucleic acid encoding the
 CC isolated peptide of (1). Antibodies, the isolated peptides of (1) and the
 CC nucleic acids are all useful for immunisation (active or passive) and (by
 CC inhibiting binding of bacteria to fibronectin) for preventing or treating
 CC infection in humans or other animals, particularly by staphylococci or
 CC streptococci, e.g. meningitis, otitis media, pneumonia, endocarditis,
 CC mastitis in cattle, abortion in horses and many others. Since the
 CC antibodies block binding of bacteria, they should be effective against
 CC antibiotic-resistant strains, and may replace antibiotic therapy or
 CC increase its effectiveness. Sequences AAW65691-700 represent a series of
 CC synthetic peptides based on the D1 region of S. aureus fibronectin
 CC binding protein A. They were synthesised to contain mutations

XX
 SQ Sequence 38 AA;
 QY 1 QNSGNOSFEE 10
 DB 1 QNSGNOSFEE 10
 Query Match 100.0%; Score 52; DB 2; Length 38;
 Best Local Similarity 100.0%; Pred. No. 0.016;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 RESULT 12
 AAW65712 standard; peptide; 39 AA.
 AC AAW65712;
 DT 16-OCT-1998 (first entry)
 DE Fibronectin binding protein-derived peptide #56.
 OS Microbial surface components recognising adhesive matrix molecule;
 KM MSCRAM; fibronectin; fibronectin-binding protein; antibody; epitope;
 KM antibiotic; bacterial infection; antibiotic-resistant strain.
 OS Synthetic.
 OS Staphylococcus aureus.
 PN WO9831389-A2.
 PD 23-JUL-1998.
 PF 21-JAN-1998; 98WO-US001222.
 PR 21-JAN-1997; 97US-0036139P.
 PA (TEXA) UNIV TEXAS A & M SYSTEM.
 PI Hoeoek M, Patti JM, House-Pompeo KL, Speziale P, Joh D,
 PI McGavin MJ;
 DR WPI; 1998-413816/35.
 XX Antibody that binds to fibronectin-binding protein, preventing its
 PT binding to fibronectin - used to treat or prevent bacterial infection,
 PT especially by Staphylococci and Streptococci.
 XX
 PS Example 8; Page 104; 201pp; English.
 CC The invention relates to antibodies that bind to a fibronectin-binding
 CC domain of a fibronectin-binding protein, and inhibit binding of the
 CC protein to fibronectin. Also claimed are: (1) isolated peptides of a
 CC fibronectin-binding protein that do not bind to fibronectin; (2) fusion
 CC protein containing at least one peptide of a fibronectin-binding protein
 CC linked to a second amino acid sequence; (3) nucleic acid encoding the
 CC isolated peptide of (1). Antibodies, the isolated peptides of (1) and the
 CC nucleic acids are all useful for immunisation (active or passive) and (by
 CC inhibiting binding of bacteria to fibronectin) for preventing or treating
 CC infection in humans or other animals, particularly by staphylococci or
 CC streptococci, e.g. meningitis, otitis media, pneumonia, endocarditis,
 CC mastitis in cattle, abortion in horses and many others. Since the
 CC antibodies block binding of bacteria, they should be effective against
 CC antibiotic-resistant strains, and may replace antibiotic therapy or
 CC increase its effectiveness. The present sequence is shown in the
 CC specification
 XX
 SQ Sequence 39 AA;
 QY 1 QNSGNOSFEE 10
 DB 1 QNSGNOSFEE 10
 Query Match 100.0%; Score 52; DB 2; Length 39;
 Best Local Similarity 100.0%; Pred. No. 0.016;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 QNSGNOSFEE 10
 |||||
 DB 1 QNSGNOSFEE 10

RESULT 13

AAW65713
 ID AAW65713 standard; peptide; 39 AA.

XX AC AAW65713;

XX DT 16-OCT-1998 (first entry)

XX DE Fibronectin binding protein-derived peptide #57.

XX KM microbial surface components recognising adhesive matrix molecule;

XX KM MRCRAMM; fibronectin; fibronectin-binding protein; antibody; epitope;

XX KM antibiotic; bacterial infection; antibiotic-resistant strain.

XX OS Synthetic.

XX OS Staphylococcus aureus.

XX PN WO9831389-A2.

XX PD 23-JUL-1998.

XX PF 21-JAN-1998; 98WO-US001222.

XX PR 21-JAN-1997; 97US-0036139P.

XX PA (TEXA) UNIV TEXAS A & M SYSTEM.

XX PI Hoeoek M, Patti JM, House-Pompeo KL, Speciale P, Joh D;

XX PI McGavin MJ;

XX DR WPI; 1998-413816/35.

XX PT Antibody that binds to fibronectin-binding protein, preventing its

XX PT binding to fibronectin - used to treat or prevent bacterial infection,

XX PT especially by Staphylococci and Streptococci.

XX PS Example 8; Page 104; 201pp; English.

XX CC The invention relates to antibodies that bind to a fibronectin-binding

XX CC domain of a fibronectin-binding protein, and inhibit binding of the

XX CC protein to fibronectin. Also claimed are: (1) isolated peptides of a

XX CC fibronectin-binding protein that do not bind to fibronectin; (2) fusion

XX CC protein containing at least one peptide of a fibronectin-binding protein

XX CC linked to a second amino acid sequence; (3) nucleic acid encoding the

XX CC isolated peptide of (1). Antibodies, the isolated peptides of (1) and the

XX CC nucleic acids are all useful for immunisation (active or passive) and (by

XX CC inhibiting binding of bacteria to fibronectin) for preventing or treating

XX CC infection in humans or other animals, particularly by staphylococci or

XX CC streptococci, e.g. meningitis, otitis media, pneumonia, endocarditis,

XX CC mastitis in cattle, abortion in horses and many others. Since the

XX CC antibodies block binding of bacteria, they should be effective against

XX CC antibiotic-resistant strains, and may replace antibiotic therapy or

XX CC increase its effectiveness. The present sequence is shown in the

XX CC specification

XX CC Sequence 39 AA;

XX CC Query Match

XX CC Best Local Similarity 100.0%; Score 52; DB 2; Length 39;

XX CC Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 QNSGNOSFEE 10
 |||||
 DB 1 QNSGNOSFEE 10

RESULT 14

AAAS8806

ID AAR58806 standard; protein; 130 AA.
 XX AC AAR58806;

XX DT 25-MAR-2003 (revised)

XX DT 30-MAR-1995 (first entry)

XX DE Fibronectin binding domain D1-D4 (709-838 (P838T)).

XX KM Fibronectin binding protein; Fbp; fibronectin binding domain;

XX KM monoclonal antibody; Mab; adhesion; Gram-positive bacterium; bacteremia;

XX KM Escherichia coli.

XX OS Staphylococcus aureus.

XX PN WO9418327-A1.

XX PD 18-AUG-1994.

XX PF 04-FEB-1994; 94WO-GB000215.

XX PR 05-FEB-1993; 93GB-00002289.

XX PR 20-OCT-1993; 93GB-00021592.

XX PA (SMIX) SMITHKLINE BEECHAM PLC.

XX PI Burnham MKR, Chopra I, Critchley IA, Knowles DJC;

XX PI WPI; 1994-279748/34.

XX DR WPI; 1994-279748/34.

XX XX Fibronectin binding protein and monoclonal antibodies specific for Fbp -

XX PT useful to prevent adherence of Gram-positive bacteria to indwelling

XX PT devices or wounds.

XX PS Disclosure; Page 30; 40pp; English.

XX CC Polypeptides corresponding to residues G709-T886 plus PRIVPT, G709-

XX CC P838(P838T) and G709-P838 (AAR58805-07, respectively) of S. aureus 72385

XX CC (NCIMB 40532) Fbp type A fibronectin binding domain D1-D4 region

XX CC (AAR58808) were expressed in E. coli BL21(DE4) and used to raise MAb

XX CC specific for Fbp. (Updated on 25-MAR-2003 to correct PN field.)

XX CC Sequence 130 AA;

XX CC Query Match

XX CC Best Local Similarity 100.0%; Score 52; DB 2; Length 130;

XX CC Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 QNSGNOSFEE 10
 |||||
 DB 2 QNSGNOSFEE 11

RESULT 15

AAAS8807

ID AAR58807 standard; protein; 130 AA.

XX AC AAR58807;

XX DT 25-MAR-2003 (revised)

XX DT 30-MAR-1995 (first entry)

XX DE Fibronectin binding domain D1-D4 (709-838).

XX KM Fibronectin binding protein; Fbp; fibronectin binding domain;

XX KM monoclonal antibody; Mab; adhesion; Gram-positive bacterium; bacteremia;

XX KM Escherichia coli.

XX OS Staphylococcus aureus.

XX PN WO9418327-A1.

XX PD 18-AUG-1994.

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XX 04-FEB-1994; 94WO-GB000215.
PF
XX
XX 05-FEB-1993; 93GB-0002289.
PR
XX 20-OCT-1993; 93GB-00021592.
PR
XX
XX (SMIK ) SMITHKLINE BEECHAM PLC.
XX
XX Burnham MKR, Chopra I, Critchley IA, Knowles DJC;
PI
XX
XX WPI; 1994-279748/34.
DR
XX
XX Fibronectin binding protein and monoclonal antibodies specific for Fbp -
PT useful to prevent adherence of Gram-positive bacteria to indwelling
PT devices or wounds.
XX
XX
XX Disclosure; Page 30; 40pp; English.
PS
XX
XX Polypeptides corresponding to residues G709-T886 plus PPIVPT, G709-
CC P838(P838T) and G709-P838 (AAR58805-07, respectively) of S. aureus J2385
CC (NCIMB 40532) Fbp type A fibronectin binding domain D1-D4 region
CC (AAR58808) were expressed in E. coli BL21(DE4) and used to raise MAbs
CC specific for Fbp. (Updated on 25-MAR-2003 to correct PN field.)
XX
XX
XX Sequence 130 AA;
SQ

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Query Match 100.0%; Score 52; DB 2; Length 130;
Best Local Similarity 100.0%; Pred. No. 0.06;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 QNSGNQSFEF 10
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Db 2 QNSGNQSFEF 11

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Search completed: October 25, 2005, 20:21:10
 Job time : 22.112 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 22, 2005, 03:51:22 ; Search time 5.57166 Seconds
(without alignments)
133.980 Million cell updates/sec

Title: US-10-731-238-63

Perfect score: 52

Sequence: 1 QNSGNSFREE 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA: *
1: /cgn2_6/ptodata/1/1aa/5A.COMB.pep: *
2: /cgn2_6/ptodata/1/1aa/5B.COMB.pep: *
3: /cgn2_6/ptodata/1/1aa/6A.COMB.pep: *
4: /cgn2_6/ptodata/1/1aa/6B.COMB.pep: *
5: /cgn2_6/ptodata/1/1aa/PCUS.COMB.pep: *
6: /cgn2_6/ptodata/1/1aa/backfile1.pep: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	52	100.0	10	4	US-09-010-317-63
2	52	100.0	38	1	US-08-234-622A-2
3	52	100.0	38	1	US-08-729-767-3
4	52	100.0	38	4	US-09-010-317-5
5	52	100.0	38	4	US-09-010-317-6
6	52	100.0	38	4	US-09-010-317-38
7	52	100.0	38	4	US-09-010-317-39
8	52	100.0	38	4	US-09-010-317-40
9	52	100.0	38	4	US-09-010-317-41
10	52	100.0	38	4	US-09-010-317-42
11	52	100.0	38	4	US-09-010-317-43
12	52	100.0	39	4	US-09-010-317-56
13	52	100.0	39	4	US-09-010-317-57
14	52	100.0	114	4	US-08-259-000-3
15	52	100.0	130	2	US-08-459-135A-7
16	52	100.0	130	2	US-08-459-135A-8
17	52	100.0	130	3	US-08-495-559-7
18	52	100.0	130	3	US-08-495-559-8
19	52	100.0	139	3	US-08-856-253-8
20	52	100.0	174	2	US-08-459-135A-10
21	52	100.0	174	2	US-08-459-135A-13
22	52	100.0	174	3	US-08-495-559-10
23	52	100.0	174	3	US-08-495-559-13
24	52	100.0	176	3	US-08-495-559-6
25	52	100.0	178	2	US-08-459-135A-12
26	52	100.0	178	2	US-08-495-559-12
27	52	100.0	181	2	US-08-459-135A-6

28	52	100.0	559	4	US-08-956-171E-5251	Sequence 5251, Ap
29	52	100.0	559	4	US-08-781-986A-5251	Sequence 5251, Ap
30	52	100.0	1027	4	US-08-956-171E-5254	Sequence 5254, Ap
31	52	100.0	1027	4	US-08-781-986A-5254	Sequence 5254, Ap
32	48	92.3	10	4	US-09-010-317-82	Sequence 82, Appl
33	48	92.3	36	4	US-09-010-317-58	Sequence 58, Appl
34	48	92.3	36	4	US-09-010-317-59	Sequence 59, Appl
35	48	92.3	38	1	US-08-234-622A-3	Sequence 3, Appl
36	48	92.3	38	1	US-08-729-767-4	Sequence 4, Appl
37	48	92.3	38	4	US-09-010-317-7	Sequence 8, Appl
38	48	92.3	38	4	US-09-010-317-8	Sequence 49, Appl
39	48	92.3	38	4	US-09-010-317-48	Sequence 48, Appl
40	48	92.3	38	4	US-09-010-317-49	Sequence 37, Appl
41	47	90.4	38	4	US-09-010-317-37	Sequence 36, Appl
42	46	88.5	38	4	US-09-010-317-36	Sequence 8, Appl
43	46	88.5	686	4	US-09-653-839-8	Sequence 8, Appl
44	46	88.5	686	4	US-10-202-619-8	Sequence 6, Appl
45	46	88.5	702	4	US-09-653-839-6	Sequence 6, Appl

ALIGNMENTS

RESULT 1
US-09-010-317-63
Sequence 63, Application US/09010317
Patent No. 6685943
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
APPLICANT: Patti, Joseph M.
APPLICANT: House-Pompeo, Karen L.
APPLICANT: Speziale, Pietro
APPLICANT: Jon, Danny
APPLICANT: Mcgavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAMK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 63:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-09-010-317-63
Query Match 100.0%; Score 52; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0018;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QNSGNSFEE 10
| | | | | | | | | |
Db 1 QNSGNSFEE 10

RESULT 2
US-08-234-622A-2
; Sequence 2, Application US/08234622A
; Patent No. 5440014
; GENERAL INFORMATION:
; APPLICANT: HOOK, Magnus
; APPLICANT: MCGAVIN, Martin
; APPLICANT: RAUCCI, Giuseppe
; TITLE OF INVENTION: A FIBRONECTIN BINDING PEPTIDE
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Doane, Swecker & Mathis
; STREET: P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/234,622A
; FILING DATE: 28-APR-1994
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: SE 9002617-0
; FILING DATE: 10-AUG-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/SE91/00534
; FILING DATE: 09-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Meuth, Donna M
; REGISTRATION NUMBER: 36,607
; REFERENCE/DOCKET NUMBER: 012885-044
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 38 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-234-622A-2

Query Match 100.0%; Score 52; DB 1; Length 38;
Best Local Similarity 100.0%; Pred. No. 0.0076;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QNSGNSFEE 10
| | | | | | | | | |
Db 1 QNSGNSFEE 10

RESULT 3
US-08-729-767-3
; Sequence 3, Application US/08729767
; Patent No. 5770702
; GENERAL INFORMATION:
; APPLICANT: HOOK, Magnus
; APPLICANT: LINDBERG, Martin Kjell
; APPLICANT: SIGNS, Lars Christer
; APPLICANT: WADSTROM, Torkel Mikael

; APPLICANT: FROMAN, Gunnar
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN AS WELL AS
; ITS PREPARATION
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Doane, Swecker & Mathis, L.L.P.
; STREET: P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/729,767
; FILING DATE: 07-OCT-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/259,000
; FILING DATE: 13-JUN-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/007,817
; FILING DATE: 22-JAN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/201,028
; FILING DATE: 01-JUN-1988
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: SE 8702272-9
; FILING DATE: 01-JUN-1987
; ATTORNEY/AGENT INFORMATION:
; NAME: McGowan, Malcolm K.
; REGISTRATION NUMBER: 39,300
; REFERENCE/DOCKET NUMBER: 012889-036
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 38 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-729-767-3

Query Match 100.0%; Score 52; DB 1; Length 38;
Best Local Similarity 100.0%; Pred. No. 0.0076;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QNSGNSFEE 10
| | | | | | | | | |
Db 2 QNSGNSFEE 11

RESULT 4
US-09-010-317-5
; Sequence 5, Application US/09010317
; Patent No. 6685943
; GENERAL INFORMATION:
; APPLICANT: Hook, Magnus
; APPLICANT: Patti, Joseph M.
; APPLICANT: House-Pompeo, Karen L.
; APPLICANT: Speziale, Pietro
; APPLICANT: Jon, Danny
; APPLICANT: McGavin, Martin J.
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
; NUMBER OF SEQUENCES: 105
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee

STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TANK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-09-010-317-5

Query Match 100.0%; Score 52; DB 4; Length 38;
Best Local Similarity 100.0%; Pred. No. 0.0076;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QNSGNQSFEE 10
Db 1 QNSGNQSFEE 10

RESULT 5
US-09-010-317-6
Sequence 6, Application US/09010317
Patent No. 6685943
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
APPLICANT: Patti, Joseph M.
APPLICANT: House-Pompeo, Karen L.
APPLICANT: Speziale, Pietro
APPLICANT: Joh, Danny
APPLICANT: McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
NUMBER OF SEQUENCES: 105
TITLE OF INVENTION: AND METHODS OF USE
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/036,139

FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TANK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-09-010-317-6

Query Match 100.0%; Score 52; DB 4; Length 38;
Best Local Similarity 100.0%; Pred. No. 0.0076;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QNSGNQSFEE 10
Db 1 QNSGNQSFEE 10

RESULT 6
US-09-010-317-38
Sequence 38, Application US/09010317
Patent No. 6685943
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
APPLICANT: Patti, Joseph M.
APPLICANT: House-Pompeo, Karen L.
APPLICANT: Speziale, Pietro
APPLICANT: Joh, Danny
APPLICANT: McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
NUMBER OF SEQUENCES: 105
TITLE OF INVENTION: AND METHODS OF USE
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TANK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 38:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-09-010-317-38

Query Match 100.0%; Score 52; DB 4; Length 38
Best Local Similarity 100.0%; Pred. No. 0.0076;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QNSGNSFEE 10
Db 1 QNSGNSFEE 10

RESULT 7

US-09-010-317-39
Sequence 39, Application US/09010317
Patent No. 6685943
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
APPLICANT: Patti, Joseph M.
APPLICANT: House-Pompeo, Karen L.
APPLICANT: Speziale, Pietro
APPLICANT: John, Danny
APPLICANT: McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
TITLE OF INVENTION: AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/010.317
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAMK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 39:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-09-010-317-39

Query Match

100.0%; Score 52; DB 4; Length 38;
Best Local Similarity 100.0%; Pred. No. 0.0076;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QNSGNSFEE 10
Db 1 QNSGNSFEE 10

RESULT 8

US-09-010-317-40
Sequence 40, Application US/09010317
Patent No. 6685943
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
APPLICANT: Patti, Joseph M.

APPLICANT: House-Pompeo, Karen L.
APPLICANT: Speziale, Pietro
APPLICANT: John, Danny
APPLICANT: McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
TITLE OF INVENTION: AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/010.317
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAMK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 40:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-09-010-317-40

Query Match

100.0%; Score 52; DB 4; Length 38;
Best Local Similarity 100.0%; Pred. No. 0.0076;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QNSGNSFEE 10
Db 1 QNSGNSFEE 10

RESULT 9

US-09-010-317-41
Sequence 41, Application US/09010317
Patent No. 6685943
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
APPLICANT: Patti, Joseph M.
APPLICANT: House-Pompeo, Karen L.
APPLICANT: Speziale, Pietro
APPLICANT: John, Danny
APPLICANT: McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
TITLE OF INVENTION: AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Releasee #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAMK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 41:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-09-010-317-41

Query Match 100.0%; Score 52; DB 4; Length 38;
Best Local Similarity 100.0%; Pred. No. 0.0076;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QNSGNSFEE 10
| | | | | | | | | |
Db 1 QNSGNSFEE 10

RESULT 10
US-09-010-317-42
Sequence 42, Application US/09010317
Patent No. 6685943
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
APPLICANT: Patti, Joseph M.
APPLICANT: House-Pompeo, Karen L.
APPLICANT: Speziale, Pietro
APPLICANT: John, Danny
APPLICANT: McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
NUMBER OF SEQUENCES: 105
TITLE OF INVENTION: AND METHODS OF USE
CLASSIFICATION:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Releasee #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAMK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 41:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-09-010-317-43

TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 42:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-09-010-317-42

Query Match 100.0%; Score 52; DB 4; Length 38;
Best Local Similarity 100.0%; Pred. No. 0.0076;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QNSGNSFEE 10
| | | | | | | | | |
Db 1 QNSGNSFEE 10

RESULT 11
US-09-010-317-43
Sequence 43, Application US/09010317
Patent No. 6685943
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
APPLICANT: Patti, Joseph M.
APPLICANT: House-Pompeo, Karen L.
APPLICANT: Speziale, Pietro
APPLICANT: John, Danny
APPLICANT: McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
NUMBER OF SEQUENCES: 105
TITLE OF INVENTION: AND METHODS OF USE
CLASSIFICATION:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Releasee #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAMK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 43:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-09-010-317-43

Query Match 100.0%; Score 52; DB 4; Length 38;
Best Local Similarity 100.0%; Pred. No. 0.0076;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QNSGNSFEE 10
| | | | | | | | | |
Db 1 QNSGNSFEE 10

RESULT 12
US-09-010-317-56
; Sequence 56, Application US/09010317
; Patent No. 6685943
; GENERAL INFORMATION:
; APPLICANT: Hook, Magnus
; APPLICANT: Patti, Joseph M.
; APPLICANT: House-Pompeo, Karen L.
; APPLICANT: Speziale, Pietro
; APPLICANT: Job, Danny
; APPLICANT: Mcgavin, Martin J.
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
; TITLE OF INVENTION: AND METHODS OF USE
; NUMBER OF SEQUENCES: 105
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: TX
; COUNTRY: USA
; ZIP: 77210-4433
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/010,317
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/036,139
; FILING DATE: 21-JAN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Hibler, David W.
; REGISTRATION NUMBER: 41,071
; REFERENCE/DOCKET NUMBER: TANK:189
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 512-418-3000
; TELEFAX: 512-474-7577
; INFORMATION FOR SEQ ID NO: 56:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 39 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; US-09-010-317-56
Query Match 100.0%; Score 52; DB 4; Length 39;
Best Local Similarity 100.0%; Pred. No. 0.0078;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 QNSGNSFEE 10
Db 1 QNSGNSFEE 10
RESULT 13
US-09-010-317-57
; Sequence 57, Application US/09010317
; Patent No. 6685943
; GENERAL INFORMATION:
; APPLICANT: Hook, Magnus
; APPLICANT: Patti, Joseph M.
; APPLICANT: House-Pompeo, Karen L.
; APPLICANT: Speziale, Pietro
; APPLICANT: Job, Danny
; APPLICANT: Mcgavin, Martin J.
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
; TITLE OF INVENTION: AND METHODS OF USE
; NUMBER OF SEQUENCES: 105

; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: TX
; COUNTRY: USA
; ZIP: 77210-4433
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/010,317
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/036,139
; FILING DATE: 21-JAN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Hibler, David W.
; REGISTRATION NUMBER: 41,071
; REFERENCE/DOCKET NUMBER: TANK:189
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 512-418-3000
; TELEFAX: 512-474-7577
; INFORMATION FOR SEQ ID NO: 57:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 39 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; US-09-010-317-57
Query Match 100.0%; Score 52; DB 4; Length 39;
Best Local Similarity 100.0%; Pred. No. 0.0078;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 QNSGNSFEE 10
Db 1 QNSGNSFEE 10
RESULT 14
US-08-259-000-3
; Sequence 3, Application US/08259000
; Patent No. 5571514
; GENERAL INFORMATION:
; APPLICANT: HOOK, Magnus
; APPLICANT: LINDBERG, Martin Kjell
; APPLICANT: SIGNAS, Lars Christer
; APPLICANT: MADSTROM, Torkel Mikael
; APPLICANT: FROMAN, Gunnar
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN AS WELL AS
; TITLE OF INVENTION: ITS PREPARATION
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Doane, Swecker & Mathis
; STREET: P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/259,000
; FILING DATE: 13-JUN-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:

APPLICATION NUMBER: SE 8702272-9
FILING DATE: 01-JUN-1987
ATTORNEY/AGENT INFORMATION:
NAME: Meuth, Donna M
REGISTRATION NUMBER: 36,607
REFERENCE/DOCKET NUMBER: 012885-062
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 114 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-259-000-3

Query Match 100.0%; Score 52; DB 1; Length 114;
Best Local Similarity 100.0%; Pred. No. 0.025;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ONSGNSFEE 10
DB 2 ONSGNSFEE 11

RESULT 15

US-08-459-135A-7
Sequence 7, Application US/08459135A
Patent No. 5955078
GENERAL INFORMATION:
APPLICANT: BURHAM, Martin Karl Russel
APPLICANT: CHOPRA, Ian
APPLICANT: CRITCHLEY, Ian Alfred
APPLICANT: KNOWLES, David Justin Charles
TITLE OF INVENTION: FIBROBLAST BINDING PROTEIN: MONOCLONAL ANTIBODY AND THEIR US
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
STATE: PA
COUNTRY: U.S.A.
ZIP: 19406-0939
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: Fastseq, Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/459,135A
FILING DATE: 02-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB/94/00215
FILING DATE: 04-Feb-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Glimm, Edward R
REGISTRATION NUMBER: 38,891
REFERENCE/DOCKET NUMBER: P30591C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-4478
TELEFAX: 610-270-5090
TELEX:
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 130 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-459-135A-7

Query Match 100.0%; Score 52; DB 2; Length 130;
Best Local Similarity 100.0%; Pred. No. 0.025;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ONSGNSFEE 10
DB 2 ONSGNSFEE 11

Search completed: October 22, 2005, 05:46:51
Job time : 6.62166 secs

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OM protein - protein search, using sw model

Run on: October 22, 2005, 11:35:03 ; Search time 18.4541 Seconds
(without alignments)
226.232 Million cell updates/sec

Title: US-10-731-238-63

Perfect score: 52

Sequence: 1 QNSGNSFEE 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1862951 seqs, 417491010 residues

Total number of hits satisfying chosen parameters: 1862951

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA:*

1: /cgn2_6/ptodata/2/pubppa/US07_PUBCOMB.pep:*

2: /cgn2_6/ptodata/2/pubppa/PCT_NEW_PUB.pep:*

3: /cgn2_6/ptodata/2/pubppa/US06_NEW_PUB.pep:*

4: /cgn2_6/ptodata/2/pubppa/US06_PUBCOMB.pep:*

5: /cgn2_6/ptodata/2/pubppa/US07_NEW_PUB.pep:*

6: /cgn2_6/ptodata/2/pubppa/PCTUS_PUBCOMB.pep:*

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8: /cgn2_6/ptodata/2/pubppa/US08_PUBCOMB.pep:*

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11: /cgn2_6/ptodata/2/pubppa/US09C_PUBCOMB.pep:*

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18: /cgn2_6/ptodata/2/pubppa/US10_NEW_PUB.pep:*

19: /cgn2_6/ptodata/2/pubppa/US11A_PUBCOMB.pep:*

20: /cgn2_6/ptodata/2/pubppa/US11_NEW_PUB.pep:*

21: /cgn2_6/ptodata/2/pubppa/US60_NEW_PUB.pep:*

22: /cgn2_6/ptodata/2/pubppa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	52	100.0	10	US-10-731-238-63	Sequence 63, Appl
2	52	100.0	38	US-10-731-238-5	Sequence 5, Appl
3	52	100.0	38	US-10-731-238-6	Sequence 6, Appl
4	52	100.0	38	US-10-731-238-38	Sequence 38, Appl
5	52	100.0	38	US-10-731-238-39	Sequence 39, Appl
6	52	100.0	38	US-10-731-238-40	Sequence 40, Appl
7	52	100.0	38	US-10-731-238-41	Sequence 41, Appl
8	52	100.0	38	US-10-731-238-42	Sequence 42, Appl
9	52	100.0	38	US-10-731-238-43	Sequence 43, Appl
10	52	100.0	39	US-10-731-238-56	Sequence 56, Appl
11	52	100.0	39	US-10-731-238-57	Sequence 57, Appl

12	52	100.0	139	9	US-09-813-820-8	Sequence 8, Appl
13	52	100.0	388	8	US-08-901-062-1	Sequence 1, Appl
14	52	100.0	559	8	US-08-781-986A-5251	Sequence 5251, Ap
15	52	100.0	559	15	US-10-329-624-5251	Sequence 5251, Ap
16	52	100.0	767	9	US-09-815-242-5899	Sequence 5899, Ap
17	52	100.0	767	9	US-09-815-242-13140	Sequence 13140, A
18	52	100.0	940	17	US-10-470-046B-424	Sequence 424, Ap
19	52	100.0	948	17	US-10-470-046B-69	Sequence 69, Appl
20	52	100.0	961	15	US-10-282-122A-43778	Sequence 43778, A
21	52	100.0	978	9	US-09-815-242-5456	Sequence 5456, Ap
22	52	100.0	1001	9	US-09-815-242-12686	Sequence 12686, A
23	52	100.0	1018	9	US-09-815-242-5797	Sequence 5797, Ap
24	52	100.0	1018	9	US-09-815-242-12838	Sequence 12838, A
25	52	100.0	1018	17	US-10-470-046B-68	Sequence 68, Appl
26	52	100.0	1027	8	US-08-781-986A-5254	Sequence 5254, Ap
27	52	100.0	1027	15	US-10-329-624-5254	Sequence 5254, Ap
28	52	100.0	1038	15	US-10-282-122A-43827	Sequence 43827, A
29	49	94.2	30	14	US-10-287-821-1	Sequence 1, Appl
30	49	94.2	31	14	US-10-287-821-2	Sequence 2, Appl
31	48	92.3	10	18	US-10-731-238-82	Sequence 82, Appl
32	48	92.3	36	18	US-10-731-238-58	Sequence 58, Appl
33	48	92.3	36	18	US-10-731-238-59	Sequence 59, Appl
34	48	92.3	38	18	US-10-731-238-7	Sequence 7, Appl
35	48	92.3	38	18	US-10-731-238-8	Sequence 8, Appl
36	48	92.3	38	18	US-10-731-238-48	Sequence 48, Appl
37	48	92.3	38	18	US-10-731-238-37	Sequence 37, Appl
38	47	90.4	38	18	US-10-731-238-37	Sequence 37, Appl
39	46	88.5	38	18	US-10-731-238-36	Sequence 36, Appl
40	46	88.5	686	16	US-10-760-709-8	Sequence 8, Appl
41	46	88.5	702	14	US-10-116-519-11	Sequence 11, Appl
42	46	88.5	702	15	US-10-390-585-9	Sequence 9, Appl
43	46	88.5	702	15	US-10-055-569A-39	Sequence 39, Appl
44	46	88.5	702	15	US-10-275-107-47	Sequence 47, Appl
45	46	88.5	702	16	US-10-760-709-6	Sequence 6, Appl

ALIGNMENTS

RESULT 1
US-10-731-238-63
Sequence 63, Application US/10711238
Publication No. US20050123552A1
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
Patli, Joseph M.
House-Pompeo, Karen L.
Speziale, Pietro
Joh, Danny
McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/731.238
FILING DATE: 10-Dec-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/010.317
FILING DATE: 21-Jan-1998
APPLICATION NUMBER: US 60/036.139

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;
; FILING DATE: 21-JAN-1997
; ATTORNEY/AGENT INFORMATION:
;   NAME: Hibler, David W.
;   REGISTRATION NUMBER: 41,071
;   REFERENCE/DOCKET NUMBER: TAMK:189
; TELECOMMUNICATION INFORMATION:
;   TELEPHONE: 512-418-3000
;   TELEFAX: 512-474-7577
; INFORMATION FOR SEQ ID NO: 63:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH: 10 amino acids
;     TYPE: amino acid
;     STRANDEDNESS: <Unknown>
;     TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 63:
US-10-731-238-63

Query Match      100.0%; Score 52; DB 18; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.0057;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 10NSGNOSFEE 10
Db      1 10NSGNOSFEE 10

RESULT 2
US-10-731-238-5
; Sequence 5, Application US/10731238
; Publication No. US20050123552A1
; GENERAL INFORMATION:
;   APPLICANT: Hook, Magnus
;             Partl, Joseph M.
;             House-Pompeo, Karen L.
;             Speziale, Pietro
;             John, Danny
;             McGavin, Martin J.
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
; AND METHODS OF USE
; NUMBER OF SEQUENCES: 105
; CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Arnold, White & Durkee
;   STREET: P.O. Box 4433
;   CITY: Houston
;   STATE: TX
;   COUNTRY: USA
;   ZIP: 77210-4433
; COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/10/731,238
;   FILING DATE: 10-Dec-2003
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US/09/010,317
;   FILING DATE: 21-Jan-1998
;   APPLICATION NUMBER: US 60/036,139
;   FILING DATE: 21-JAN-1997
; ATTORNEY/AGENT INFORMATION:
;   NAME: Hibler, David W.
;   REGISTRATION NUMBER: 41,071
;   REFERENCE/DOCKET NUMBER: TAMK:189
; TELECOMMUNICATION INFORMATION:
;   TELEPHONE: 512-418-3000
;   TELEFAX: 512-474-7577
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 38 amino acids
;   TYPE: amino acid
;   STRANDEDNESS: <Unknown>
;   TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-10-731-238-5

Query Match      100.0%; Score 52; DB 18; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.0057;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 10NSGNOSFEE 10
Db      1 10NSGNOSFEE 10
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;
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-10-731-238-5

Query Match      100.0%; Score 52; DB 18; Length 38;
Best Local Similarity 100.0%; Pred. No. 0.024;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 10NSGNOSFEE 10
Db      1 10NSGNOSFEE 10

RESULT 3
US-10-731-238-6
; Sequence 6, Application US/10731238
; Publication No. US20050123552A1
; GENERAL INFORMATION:
;   APPLICANT: Hook, Magnus
;             Partl, Joseph M.
;             House-Pompeo, Karen L.
;             Speziale, Pietro
;             John, Danny
;             McGavin, Martin J.
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
; AND METHODS OF USE
; NUMBER OF SEQUENCES: 105
; CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Arnold, White & Durkee
;   STREET: P.O. Box 4433
;   CITY: Houston
;   STATE: TX
;   COUNTRY: USA
;   ZIP: 77210-4433
; COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/10/731,238
;   FILING DATE: 10-Dec-2003
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US/09/010,317
;   FILING DATE: 21-Jan-1998
;   APPLICATION NUMBER: US 60/036,139
;   FILING DATE: 21-JAN-1997
; ATTORNEY/AGENT INFORMATION:
;   NAME: Hibler, David W.
;   REGISTRATION NUMBER: 41,071
;   REFERENCE/DOCKET NUMBER: TAMK:189
; TELECOMMUNICATION INFORMATION:
;   TELEPHONE: 512-418-3000
;   TELEFAX: 512-474-7577
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 38 amino acids
;   TYPE: amino acid
;   STRANDEDNESS: <Unknown>
;   TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-10-731-238-6

Query Match      100.0%; Score 52; DB 18; Length 38;
Best Local Similarity 100.0%; Pred. No. 0.024;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 10NSGNOSFEE 10
Db      1 10NSGNOSFEE 10
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RESULT 4
US-10-731-238-38
; Sequence 38, Application US/10731238
; Publication No. US20050123552A1
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
             Patti, Joseph M.
             House-Pompeo, Karen L.
             Speziale, Pietro
             Joh, Danny
             McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSER: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/731,238
FILING DATE: 10-Dec-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE: 21-Jan-1998
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-Jan-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAMK.189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 38:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 38:
US-10-731-238-38

Query Match      100.0%; Score 52; DB 18; Length 38;
Best Local Similarity 100.0%; Pred. No. 0.024;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  QNSGNSFEE 10
        |||||||
Db      1  QNSGNSFEE 10

RESULT 5
US-10-731-238-39
; Sequence 39, Application US/10731238
; Publication No. US20050123552A1
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
             Patti, Joseph M.
             House-Pompeo, Karen L.
             Speziale, Pietro
             Joh, Danny
             McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
AND METHODS OF USE

```

```

NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSER: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/731,238
FILING DATE: 10-Dec-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE: 21-Jan-1998
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-Jan-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAMK.189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 39:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 39:
US-10-731-238-39

Query Match      100.0%; Score 52; DB 18; Length 38;
Best Local Similarity 100.0%; Pred. No. 0.024;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  QNSGNSFEE 10
        |||||||
Db      1  QNSGNSFEE 10

RESULT 6
US-10-731-238-40
; Sequence 40, Application US/10731238
; Publication No. US20050123552A1
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
             Patti, Joseph M.
             House-Pompeo, Karen L.
             Speziale, Pietro
             Joh, Danny
             McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSER: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30

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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/731,238
FILING DATE: 10-Dec-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE: 21-Jan-1998
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-Jan-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAMK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 40:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 40:
US-10-731-238-40

Query Match 100.0%; Score 52; DB 18; Length 38;
Best Local Similarity 100.0%; Pred. No. 0.024;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QNSGNOSFEE 10
Db 1 QNSGNOSFEE 10

RESULT 7
US-10-731-238-41
Sequence 41, Application US/10731238
Publication No. US20050123552A1
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
Patti, Joseph M.
House-Pompeo, Karen L.
Speziale, Pietro
John, Danny
McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/731,238
FILING DATE: 10-Dec-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE: 21-Jan-1998
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-Jan-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAMK:189

TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 41:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 41:
US-10-731-238-41

Query Match 100.0%; Score 52; DB 18; Length 38;
Best Local Similarity 100.0%; Pred. No. 0.024;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QNSGNOSFEE 10
Db 1 QNSGNOSFEE 10

RESULT 8
US-10-731-238-42
Sequence 42, Application US/10731238
Publication No. US20050123552A1
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
Patti, Joseph M.
House-Pompeo, Karen L.
Speziale, Pietro
John, Danny
McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/731,238
FILING DATE: 10-Dec-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE: 21-Jan-1998
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-Jan-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAMK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 42:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 42:
US-10-731-238-42

Query Match 100.0%; Score 52; DB 18; Length 38;

Best Local Similarity 100.0%; Pred. No. 0.024;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QNSGNSFEE 10
|||||
Db 1 QNSGNSFEE 10

RESULT 9

US-10-731-238-43
; Sequence 43, Application US/10731238
; Publication No. US20050123552A1

GENERAL INFORMATION:

APPLICANT: Hook, Magnus
Patli, Joseph M.
House-Pompeo, Karen L.
Speziale, Pietro
Joh, Danny

TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
AND METHODS OF USE

NUMBER OF SEQUENCES: 105

CORRESPONDENCE ADDRESS:

ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433

CITY: Houston

STATE: TX

COUNTRY: USA

ZIP: 77210-4433

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/731,238

FILING DATE: 10-Dec-2003

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/010,317

FILING DATE: 21-Jan-1998

APPLICATION NUMBER: US 60/036,139

FILING DATE: 21-JAN-1997

ATTORNEY/AGENT INFORMATION:

NAME: Hibler, David W.

REGISTRATION NUMBER: 41,071

REFERENCE/DOCKET NUMBER: TAMK.189

TELECOMMUNICATION INFORMATION:

TELEPHONE: 512-418-3000

TELEFAX: 512-474-7577

INFORMATION FOR SEQ ID NO: 43:

SEQUENCE CHARACTERISTICS:

LENGTH: 38 amino acids

TYPE: amino acid

STRANDEDNESS: <Unknown>

TOPOLOGY: linear

SEQUENCE DESCRIPTION: SEQ ID NO: 43:

Query Match 100.0%; Score 52; DB 18; Length 38;
Best Local Similarity 100.0%; Pred. No. 0.024;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QNSGNSFEE 10
|||||
Db 1 QNSGNSFEE 10

RESULT 10

US-10-731-238-56
; Sequence 56, Application US/10731238
; Publication No. US20050123552A1
; GENERAL INFORMATION:

APPLICANT: Hook, Magnus
Patli, Joseph M.
House-Pompeo, Karen L.
Speziale, Pietro
Joh, Danny

TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
AND METHODS OF USE

NUMBER OF SEQUENCES: 105

CORRESPONDENCE ADDRESS:

ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433

CITY: Houston

STATE: TX

COUNTRY: USA

ZIP: 77210-4433

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/731,238

FILING DATE: 10-Dec-2003

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/010,317

FILING DATE: 21-Jan-1998

APPLICATION NUMBER: US 60/036,139

FILING DATE: 21-JAN-1997

ATTORNEY/AGENT INFORMATION:

NAME: Hibler, David W.

REGISTRATION NUMBER: 41,071

REFERENCE/DOCKET NUMBER: TAMK.189

TELECOMMUNICATION INFORMATION:

TELEPHONE: 512-418-3000

TELEFAX: 512-474-7577

INFORMATION FOR SEQ ID NO: 56:

SEQUENCE CHARACTERISTICS:

LENGTH: 39 amino acids

TYPE: amino acid

STRANDEDNESS: <Unknown>

TOPOLOGY: linear

SEQUENCE DESCRIPTION: SEQ ID NO: 56:

Query Match 100.0%; Score 52; DB 18; Length 39;
Best Local Similarity 100.0%; Pred. No. 0.024;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QNSGNSFEE 10
|||||
Db 1 QNSGNSFEE 10

RESULT 11

US-10-731-238-57
; Sequence 57, Application US/10731238
; Publication No. US20050123552A1

GENERAL INFORMATION:

APPLICANT: Hook, Magnus
Patli, Joseph M.
House-Pompeo, Karen L.
Speziale, Pietro
Joh, Danny

TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
AND METHODS OF USE

NUMBER OF SEQUENCES: 105

CORRESPONDENCE ADDRESS:

ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433

CITY: Houston

STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/731,238
FILING DATE: 10-Dec-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE: 21-Jan-1998
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAMK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 57:
SEQUENCE CHARACTERISTICS:
LENGTH: 39 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 57:
US-10-731-238-57

Query Match 100.0%; Score 52; DB 18; Length 39;
Best Local Similarity 100.0%; Pred. No. 0.024;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QNSGNOSFEE 10
DB 1 QNSGNOSFEE 10

RESULT 12
US-09-813-820-8
Sequence 8, Application US/09813820
Patent No. US20020102262A1
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
Patti, Joseph M.
House-Pompeo, Karen
Sthanam, Narayana
Symerky, Jindrich
TITLE OF INVENTION: COLLAGEN BINDING PROTEIN COMPOSITIONS
AND METHODS OF USE
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: Texas
COUNTRY: U.S.
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/813,820
FILING DATE: 22-Mar-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/856,253

FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Kitchell, Barbara S.
REGISTRATION NUMBER: 33,928
REFERENCE/DOCKET NUMBER: TAMK:193
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
TELEFAX: (512) 474-7577
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 139 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-09-813-820-8

Query Match 100.0%; Score 52; DB 9; Length 139;
Best Local Similarity 100.0%; Pred. No. 0.094;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QNSGNOSFEE 10
DB 16 QNSGNOSFEE 25

RESULT 13
US-08-901-062-1
Sequence 1, Application US/08901062
Publication No. US20020025324A1
GENERAL INFORMATION:
APPLICANT: SEALS, JONATHAN R.
TITLE OF INVENTION: RECOMBINANT BIVALENT BACTERIAL VACCINE
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: HALE AND DORR LLP
STREET: 60 State Street
CITY: Boston
STATE: MA
COUNTRY: United States Of America
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/901,062
FILING DATE: 25-JUL-1997
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Baker, Hollie L.
REGISTRATION NUMBER: 31,321
REFERENCE/DOCKET NUMBER: 106941.153
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 526-6000
TELEFAX: (617) 526-5000
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 388 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-901-062-1

Query Match 100.0%; Score 52; DB 8; Length 388;
Best Local Similarity 100.0%; Pred. No. 0.28;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QNSGNOSFEE 10
| | | | |
Db 265 QNSGNOSFEE 274

RESULT 14

US-08-781-986A-5251
; Sequence 5251, Application US/08781986A
; Publication No. US20030054436A1
; GENERAL INFORMATION:
; APPLICANT: Charles Kunsch
; TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
; NUMBER OF SEQUENCES: 5255
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4mb storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/781,986A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Benson, Bob
; REGISTRATION NUMBER: 30,446
; REFERENCE/DOCKET NUMBER: PB248PP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 5251:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 559 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-781-986A-5251

Query Match 100.0%; Score 52; DB 8; Length 559;

Best Local Similarity 100.0%; Pred. No. 0.41;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QNSGNOSFEE 10
| | | | |
Db 301 QNSGNOSFEE 310

RESULT 15

US-10-329-624-5251
; Sequence 5251, Application US/10329624
; Publication No. US20040043037A1
; GENERAL INFORMATION:
; APPLICANT: Charles Kunsch
; Gil H. Choi
; Patrick S. Dillon
; Craig A. Rosen
; Steven C. Barash
; Michael R. Pannon
; TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
; NUMBER OF SEQUENCES: 5256
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue

CITY: Rockville
STATE: Maryland
COUNTRY: USA
ZIP: 20850

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.50 inch, 1.4mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/329,624

FILING DATE: 27-Dec-2002

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/956,171

FILING DATE: October 20, 1997

APPLICATION NUMBER: 60/009,861

FILING DATE: January 5, 1996

APPLICATION NUMBER: 08/781,986

FILING DATE: January 3, 1997

ATTORNEY/AGENT INFORMATION:

NAME: Mark J. Hyman

REGISTRATION NUMBER: 46,789

REFERENCE/DOCKET NUMBER: PB248P1D1

TELECOMMUNICATION INFORMATION:

TELEPHONE: (240) 314-1224

TELEFAX: (301) 309-8439

INFORMATION FOR SEQ ID NO: 5251:

SEQUENCE CHARACTERISTICS:

LENGTH: 559 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 5251:

US-10-329-624-5251

Query Match 100.0%; Score 52; DB 15; Length 559;

Best Local Similarity 100.0%; Pred. No. 0.41;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QNSGNOSFEE 10
| | | | |
Db 301 QNSGNOSFEE 310

Search completed: October 22, 2005, 12:09:34
Job time : 19.4541 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 22, 2005, 04:14:19 ; Search time 3.65539 Seconds
(without alignments)
263.219 Million cell updates/sec

Title: US-10-731-238-63

Perfect score: 52
Sequence: 1 ONSGNOSFEE 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	52	100.0	940	2 S19702	fibronectin-binding
2	52	100.0	961	2 G90053	hypothetical prote
3	52	100.0	1018	2 A32192	fibronectin-binding
4	52	100.0	1038	2 H90053	hypothetical prote
5	38	73.1	918	2 A55277	hexokinase (EC 2.7
6	37	71.2	333	2 C84792	hypothetical prote
7	37	71.2	358	2 S45911	hypothetical prote
8	36	69.2	310	2 J10091	beta-lactamase (EC
9	36	69.2	478	2 T16170	hypothetical prote
10	36	69.2	642	2 T39376	hypothetical DAG-b
11	35	67.3	1184	2 T41515	coiled coil protei
12	35	67.3	1962	2 A32634	lactocarpin (EC 3.4
13	34	65.4	155	1 RMBYR6	DNA-directed RNA p
14	34	65.4	160	2 G95213	hypothetical prote
15	34	65.4	164	2 H98077	hypothetical prote
16	34	65.4	461	2 S33420	probable subtilisi
17	34	65.4	551	2 S51941	pinunin I precursor
18	34	65.4	1113	2 S73327	MG140 homolog - My
19	34	65.4	2366	2 S10317	toxin B - Clostrid
20	33	63.5	267	2 H86548	polymorphic outer
21	33	63.5	282	2 S31258	probable membrane
22	33	63.5	296	2 B40257	RNA15 protein - ye
23	33	63.5	376	1 QGBEW2	U53 protein - hum
24	33	63.5	548	2 T28910	hypothetical prote
25	33	63.5	566	2 S52676	probable membrane
26	33	63.5	767	2 T41344	probable zinc-fing
27	33	63.5	835	2 S63463	hypothetical prote
28	33	63.5	1747	2 A54121	collagen alpha-4 c
29	32	61.5	149	2 T41481	very hypothetical

30	32	61.5	170	2 S77460	hypothetical prote
31	32	61.5	182	2 J31245	20K protein - Bac1
32	32	61.5	182	2 B32255	hypothetical 20K p
33	32	61.5	203	2 H83802	holliday junction
34	32	61.5	213	2 S26055	2-dehydro-3-deoxy-
35	32	61.5	269	2 T16702	hypothetical prote
36	32	61.5	271	2 T47978	splicing factor RS
37	32	61.5	276	2 H96816	hypothetical prote
38	32	61.5	301	2 T01193	reverse transcript
39	32	61.5	344	2 T40908	hypothetical prote
40	32	61.5	362	1 A28517	severin - slime mo
41	32	61.5	382	2 S75823	threonine synthase
42	32	61.5	429	2 AH3294	cell cycle protein
43	32	61.5	479	2 G71957	probable outer mem
44	32	61.5	509	2 D95053	transcription regu
45	32	61.5	584	2 B84668	ethylene-insensiti

ALIGNMENTS

RESULT 1

S19702
fibronectin-binding protein B - Staphylococcus aureus
C:Species: Staphylococcus aureus
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
C:Accession: S19702
R:Joensuu, K.; Signaes, C.; Mueller, H.P.; Lindberg, M.
Eur. J. Biochem. 202, 1041-1048, 1991
A:Title: Two different genes encode fibronectin binding proteins in Staphylococcus aureus
A:Reference number: S19702; PMID:92111475; PMID:1837266
A:Accession: S19702
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-940 <JOE>
A:Cross-references: UNIPROT:O53682; EMBL:X62992; NID:949040; PIDN:CAA44726.1; PID:958155
C:Keywords: fibronectin binding

Query Match 100.0%; Score 52; DB 2; Length 940;
Best Local Similarity 100.0%; Pred. No. 0.062;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ONSGNOSFEE 10
Db 682 ONSGNOSFEE 691

RESULT 2

G90053
hypothetical protein fnbB [imported] - Staphylococcus aureus (strain N315)
C:Species: Staphylococcus aureus
C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C:Accession: G90053
R:Kuroda, M.; Ohba, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Ogu
ma, A.; Mitutani, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.;
C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
A:Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.
A:Reference number: A89758; PMID:21311952; PMID:11418146
A:Accession: G90053
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-961 <KUR>
A:Cross-references: UNIPROT:Q99RD3; GB:BA000018; PID:g13702452; PIDN:BA843593.1; GSPDB:
A:Experimental source: strain N315
C:Genetics:
A:Gene: fnbB

Query Match 100.0%; Score 52; DB 2; Length 961;
Best Local Similarity 100.0%; Pred. No. 0.064;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 ONSGNOSFEE 10

DB 693 QNSGNOSFEE 702

RESULT 3

A:192 fibronectin-binding protein - Staphylococcus aureus

C:Species: Staphylococcus aureus

C>Date: 31-Jul-1989 #sequence_revision 31-Jul-1989 #text_change 16-Feb-1997

C:Accession: A32192

R:Signaet, C.; Raucel, G.; Joansson, K.; Lindgren, P.E.; Anantaramaiah, G.M.; Hoeck, M.

Proc. Natl. Acad. Sci. U.S.A. 86, 699-703, 1989

A:Title: Nucleotide sequence of the gene for a fibronectin-binding protein from Staphylococcus aureus

A:Reference number: A32192; PMID:8908998; PMID:2521391

A:Accession: A32192

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-1018 <SIG>

A:Cross-references: GB:J04151

C:Keywords: fibronectin binding

Query Match 100.0%; Score 52; DB 2; Length 10:8;
Best Local Similarity 100.0%; Pred. No. 0.068;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QNSGNOSFEE 10
DB 746 QNSGNOSFEE 755

RESULT 4

A:192 fibronectin-binding protein fmb [imported] - Staphylococcus aureus (strain N315)

C:Species: Staphylococcus aureus

C>Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004

C:Accession: H90053

R:Kuroda, M.; Ohno, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Ogura, A.; Mizutani-Uji, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Gato, C.; Sekimizu, K.; C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hirama, S.; K.

Lancet 357, 1225-1240, 2001

A:Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.

A:Reference number: A89758; PMID:21311952; PMID:11418146

A:Accession: H90053

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-1038 <KUR>

A:Cross-references: UNIPROT:Q99RD2; GB:BA000018; PID:G13702453; PIDN:BABA3594.1; GSPDB:G

A:Experimental source: strain N315

C:Genetics:

A:Gene: fmb

Query Match 100.0%; Score 52; DB 2; Length 1038;
Best Local Similarity 100.0%; Pred. No. 0.069;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QNSGNOSFEE 10
DB 742 QNSGNOSFEE 751

RESULT 5

A:5277 hexokinase (EC 2.7.1.1) 1 - bovine

C:Species: Bos primigenius taurus (cattle)

C>Date: 10-Feb-1995 #sequence_revision 10-Feb-1995 #text_change 07-Mar-1999

C:Accession: A55277; A43643

R:Griffin, L.D.; Gelb, B.D.; Wheeler, D.A.; Davison, D.; Adams, V.; McCabe, E.R.

Genomics 11, 1014-1024, 1991

A:Title: Mammalian hexokinase 1: evolutionary conservation and structure to function

A:Reference number: A55277; PMID:92147096; PMID:1783373

A:Accession: A55277

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-918 <GR1>

A:Experimental source: brain

A>Note: sequence modified after extraction from NCBI backbone

A>Note: sequence extracted from NCBI backbone (NCBI:80765; NCBI:80767)

R:Griffin, L.D.; Macgregor, G.R.; Wuzny, D.M.; Harter, J.; Cook, R.G.; McCabe, E.R.B.

Biochem. Med. Metab. Biol. 41, 125-131, 1989

A:Title: Synthesis and characterization of a bovine hexokinase 1 cDNA probe by mixed oli

A:Reference number: A43643; PMID:89247146; PMID:2719857

A:Accession: A43643

A:Status: preliminary

A:Molecule type: protein

A:Residues: 11-51 <GR2>

C:Superfamily: human hexokinase I; hexokinase homology

C:Keywords: ATP; duplication; glycolysis; phosphotransferase

F:31459/Domain: hexokinase homology <HXK1>

F:479-907/Domain: hexokinase homology <HXK2>

Query Match 73.1%; Score 38; DB 2; Length 918;
Best Local Similarity 77.8%; Pred. No. 32;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 NSGNOSFEE 10
DB 735 NSGNOSFEE 743

RESULT 6

A:4792 hypothetical protein At2g37400 [imported] - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)

C>Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004

C:Accession: C84792

R:Lin, X.; Keul, S.; Rounleay, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanKen, S.E.; Umeyam, L.; Tallon, L.

euus, D.; Nieman, W.C.; White, O.; Eisen, J.A.; Salberg, S.L.; Frazer, C.M.; Venter, J.

Nature 402, 761-768, 1999

A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.

A:Reference number: A84420; PMID:20083487; PMID:10617197

A:Accession: C84792

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-333 <STO>

A:Cross-references: UNIPROT:Q9ZU86; GB:AE002093; NID:G4056493; PIDN:AA098059.1; GSPDB:G

C:Genetics:

A:Gene: At2g37400

A:Map position: 2

Query Match 71.2%; Score 37; DB 2; Length 333;
Best Local Similarity 70.0%; Pred. No. 17;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 QNSGNOSFEE 10
DB 105 QNSGNOSFEE 114

RESULT 7

A:5911 hypothetical protein YBR053c - yeast (Saccharomyces cerevisiae)

N:Alternate names: hypothetical protein YBR0506

C:Species: Saccharomyces cerevisiae

A:Variety: strain S288C

C>Date: 26-Aug-1994 #sequence_revision 09-Sep-1994 #text_change 09-Jul-2004

C:Accession: S45911; S49508; S55852

R:Aljinovic, G.; Pohl, F.M.; Pohl, T.M.

submitted to the Protein Sequence Database, August 1994

A:Reference number: S45906

A:Accession: S45911

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-358 <ALJ>

A:Cross-references: UNIPROT:P38235; EMBL:Z35922; NID:G536286; PIDN:CAA84996.1; PID:G5362

R:Aljinovic, G.

submitted to the EMBL Data Library, October 1994

A;Description: Sequence and analysis of 24 kb on chromosome II of *Saccharomyces cerevisiae*
 A;Reference number: S49503
 A;Accession: S49508
 A;Molecule type: DNA
 A;Residues: 1-358 <RL2>
 A;Cross-references: EMBL:Z46260; NID:G5559942; PIDN:CAA6396.1; PID:G5559949
 R;Aljinovic, G.; Pohl, T.M.
 Yeast 11, 475-479, 1995
 A;Title: Sequence and analysis of 24 kb on chromosome II of *Saccharomyces cerevisiae*.
 A;Reference number: S55846; MUID:95321020; PMID:7597852
 A;Accession: S55852
 A;Status: nucleic acid sequence not shown; translation not shown
 A;Molecule type: DNA
 A;Residues: 1-358 <ALM>
 A;Cross-references: EMBL:Z46260; NID:G5559942; PIDN:CAA6396.1; PID:G5559949
 A;Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1994
 C;Genetics:
 A;Cross-references: SGD:S0000257
 A;Map position: 2R

Query Match 71.2%; Score 37; DB 2; Length 358;
 Best Local Similarity 77.8%; Pred. No. 18;
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 QNSGNOSFE 9
 Db 240 KNSNOSFE 248

RESULT 8
 JL0091
 beta-lactamase (EC 3.5.2.6) precursor - *Bacillus* sp. (strain 170)
 N;Alternate names: lipo-penicillinase
 C;Species: *Bacillus* sp.
 C;Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 20-Jun-2000
 C;Accession: JL0091
 R;Kato, C.; Nakano, Y.; Horikoshi, K.
 Arch. Microbiol. 151, 91-94, 1989
 A;Title: The nucleotide sequence of the lipo-penicillinase gene of alkalophilic *Bacillus*
 A;Reference number: JL0091; MUID:89245965; PMID:2655551
 A;Accession: JL0091
 A;Molecule type: mRNA
 A;Residues: 1-310 <KAT>
 A;Cross-references: GB:D10848; NID:G216225; PIDN:BA01621.1; PID:G216226
 C;Superfamily: beta-lactamase I
 C;Keywords: hydrolase; lipoprotein
 F;1-29/Domain: signal sequence #status predicted <SIG>
 F;30-310/Product: beta-lactamase #status predicted <MAT>
 F;89/Active site: Ser #status predicted

Query Match 69.2%; Score 36; DB 2; Length 310;
 Best Local Similarity 75.0%; Pred. No. 24;
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 QNSGNOSF 8
 Db 46 ENTGNOSF 53

RESULT 9
 T16170
 hypothetical protein F26F4.4 - *Caenorhabditis elegans*
 C;Species: *Caenorhabditis elegans*
 C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
 C;Accession: T16170
 R;Fulton, L.
 submitted to the EMBL Data Library, March 1996
 A;Description: The sequence of *C. elegans* cosmid F26F4.
 A;Reference number: Z18471
 A;Accession: T16170
 A;Status: preliminary; translated from GB/EMBL/DBJ
 A;Molecule type: DNA
 A;Residues: 1-478 <FUL>

A;Cross-references: UNIPROT:Q19819; EMBL:U12964; NID:G1213452; PID:G529202; PIDN:AAA912
 A;Experimental source: strain Bristol N2
 C;Genetics:
 A;Gene: CSP:F26F4.4
 A;Introns: 47/2; 81/2; 125/3; 171/3; 214/1; 236/2; 343/3; 444/1

Query Match 69.2%; Score 36; DB 2; Length 478;
 Best Local Similarity 100.0%; Pred. No. 38;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QNSGNOS 7
 Db 246 QNSGNOS 252

RESULT 10
 T39376
 hypothetical DAG-binding domain protein SPBC12C2.05C - fission yeast (*Schizosaccharomyces pombe*)
 C;Species: *Schizosaccharomyces pombe*
 C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
 C;Accession: T39376
 R;Devlin, K.; Churcher, C.M.; Barrett, B.G.; Rajandream, M.A.; Walsh, S.V.
 submitted to the EMBL Data Library, September 1995
 A;Reference number: Z21849
 A;Accession: T39376
 A;Status: preliminary; translated from GB/EMBL/DBJ
 A;Molecule type: DNA
 A;Residues: 1-642 <DEV>
 A;Cross-references: UNIPROT:Q09746; EMBL:Z54140; PIDN:CAA90818.1; GSPDB:GN00066; SPDB: S:
 A;Experimental source: strain 972h-; cosmid c12C2
 C;Genetics:
 A;Gene: SPDB:SPBC12C2.05C
 A;Map position: 1
 A;Intons: 13/3; 22/3; 44/1; 84/2; 430/1; 549/1; 637/2
 F;398-447/Domain: protein kinase C zinc-binding repeat homology <KZN>

Query Match 69.2%; Score 36; DB 2; Length 642;
 Best Local Similarity 87.5%; Pred. No. 53;
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 NSGNOSFE 9
 Db 348 NSGNOSFE 355

RESULT 11
 T41515
 coiled coil protein - fission yeast (*Schizosaccharomyces pombe*)
 C;Species: *Schizosaccharomyces pombe*
 C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
 C;Accession: T41515
 R;Murphy, L.; Harris, D.; Wood, V.; Rajandream, M.A.; Barrett, B.G.
 submitted to the EMBL Data Library, March 1999
 A;Reference number: Z21999
 A;Accession: T41515
 A;Status: preliminary; translated from GB/EMBL/DBJ
 A;Molecule type: DNA
 A;Residues: 1-1184 <MUR>
 A;Cross-references: UNIPROT:Q9Y7U0; EMBL:AL049522; PIDN:CAB40018.1; GSPDB:GN00068; SP
 A;Experimental source: strain 972h-; cosmid c63
 C;Genetics:
 A;Gene: SPDB:SPCC63.14
 A;Map position: 3

Query Match 67.3%; Score 35; DB 2; Length 1184;
 Best Local Similarity 60.0%; Pred. No. 1,6e+02;
 Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 QNSGNOSFE 10
 Db 812 ESSGNNEFE 821


```
RESULT 12
A2634
Lactococpin (EC 3.4.21.96) precursor [similarity] - lactococcus lactis subsp. cremoris (E
N:Alternate names: cell envelope-associated serine protease prtp
C:Species: Lactococcus lactis subsp. cremoris
C>Date: 21-May-1990 #sequence_revision 21-May-1990 #ext_change 21-Jul-2000
C:Accession: A32634
R:Voe, P.; Simons, G.; Slezew, R.J.; de Voe, W.M.
J. Biol. Chem. 264, 13579-13585, 1989
A:Title: Primary structure and organization of the gene for a procaryotic, cell envelope
A:Reference number: A32634; MUID:89340435; PMID:2760036
A:Accession: A32634
A:Molecule type: DNA
A:Residues: 1-1962 <VOS>
A:Cross-references: GB:U09662; GB:M26310; NID:g149476; PIDN:AAA03533.1; PID:g149478
A:Note: the authors translated the codon GGT for residue 1103 as Tyr
A:Note: part of this sequence, including the amino end of the mature protein, were deter
C:Genetics:
A:Genome: plasmid
C:Superfamily: lactococpin; subtilisin homology
C:Keywords: hydrolase; serine proteinase; transmembrane protein
F:1-33/Domain: signal sequence #status predicted <Sig>
F:34-187/Domain: propeptide #status predicted <PRO>
F:188-1962/Product: serine proteinase, cell-envelope-associated #status predicted <MAT>
F:208-634/Domain: subtilisin homology #status atypical <SBT>
F:1938-1955/Domain: transmembrane #status predicted <TMM>

Query Match
Best Local Similarity 67.3%; Score 35; DB 2; Length 1962;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 NSGNQSFEE 10
DB 353 NSGNQTFED 361

RESULT 13
RNBRY6
DNA-directed RNA polymerase (EC 2.7.7.6) chain RPO26 - yeast (Saccharomyces cerevisiae)
N:Alternate names: DNA-directed RNA polymerase 23k chain; LNA-directed RNA polymerase II
C:Species: Saccharomyces cerevisiae
C>Date: 30-Sep-1992 #sequence_revision 30-Sep-1992 #ext_change 09-Jul-2004
C:Accession: S13307; A36352; B34588; A38846; S58817
R:Archambault, J.; Schappert, K.T.; Friesen, J.D.
Mol. Cell. Biol. 10, 6123-6131, 1990
A:Title: A suppressor of an RNA polymerase II mutation of Sa:charomyces cerevisiae encod
A:Reference number: A36352; MUID:91061718; PMID:2247052
A:Accession: S13307
A:Molecule type: DNA
A:Residues: 1-155 <ARCI>
A:Cross-references: UNIPROT:P20435; EMBL:M33924; NID:g172452; PIDN:AAA34989.1; PID:g1724
A:Accession: A36352
A:Molecule type: mRNA
A:Residues: 1-155 <MOY2>
A:Cross-references: GB:M33924; NID:g172452; PIDN:AAA34989.1; PID:g172453
R:Moylechik, N.A.; Liao, S.M.; Kolodziej, P.A.; Young, R.A.
Genes. Dev. 4, 313-323, 1990
A:Title: Subunits shared by eukaryotic nuclear RNA polymerases.
A:Reference number: A34588; MUID:90249736; PMID:2186966
A:Accession: B34588
A:Status: not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 1-155 <MOY1>
A:Cross-references: GB:X53288; NID:g287823; PIDN:CAA37382.1; PIT:g287824
A:Accession: A38846
A:Molecule type: protein
A:Residues: 48-60;99-115 <MOY2>
R:Miller, N.
Submitted to the EMBL Data Library, April 1995
A:Subcloning: The sequence of S. cerevisiae cosmid 9677.
A:Reference number: S58816
A:Accession: S58817
A:Molecule type: DNA
```

```
A:Residues: 1-155 <ML>
A:Cross-references: EMBL:U25841; NID:g786295; PIDN:AB64616.1; PID:g786304; GSPDB:GND
C:Comment: This protein is a subunit of DNA-directed RNA polymerases I, II, and III.
C:Genetics:
A:Gene: SGD:RPO26; RPB6; MIPS:YPR187W
A:Cross-references: SGD:50006391; MIPS:YPR187W
A:Map position: 16R
A:Introns: 7/2
C:Superfamily: DNA-directed RNA polymerase chain RPO26
C:Keywords: nucleotidyltransferase
F:3-42/Region: acidic
F:65-97/Region: basic

Query Match
Best Local Similarity 65.4%; Score 34; DB 1; Length 155;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 2 NSGNQSFEE 10
DB 9 NDGNENFED 17

RESULT 14
G95213
Hypothetical protein SPI831 [imported] - Streptococcus pneumoniae (strain TIGR4)
C:Species: Streptococcus pneumoniae
C>Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #ext_change 09-Jul-2004
C:Accession: G95213
R:Teitelin, H.; Nelson, K.E.; Paulsen, I.T.; Bisen, J.A.; Read, T.D.; Peterson, S.; Head
on, J.D.; Unayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtapple,
neon, T.; Hickey, B.K.; Holt, I.E.
Science 293, 498-506, 2001
A:Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison,
A:Title: Complete genome sequence of a virulent isolate of Streptococcus pneumoniae.
A:Reference number: A95000; MUID:21357209; PMID:11463916
A:Accession: G95213
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-160 <KUP>
A:Cross-references: UNIPROT:Q97P13; GB:AE005672; PIDN:AAK75904.1; PID:g14973332; GSPDB G
A:Experimental source: strain TIGR4
C:Genetics:
A:Gene: SPI831

Query Match
Best Local Similarity 65.4%; Score 34; DB 2; Length 160;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 QNSGNQSFEE 10
DB 123 QNNQNTKTFEE 132

RESULT 15
H98077
Hypothetical protein spr1650 [imported] - Streptococcus pneumoniae (strain R6)
C:Species: Streptococcus pneumoniae
C>Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #ext_change 09-Jul-2004
C:Accession: H98077
R:Hoskins, J.A.; Albom Jr., W.; Arnold, J.; Blaszcak, L.; Burgett, S.; DeHoff, B.S.;
e, R.; LeBlanc, D.J.; Lee, L.N.; Lefkowitz, E.J.; Lu, J.; Matsushima, P.; McAhren, S.;
Y, P.; Sun, P.M.; Winkler, M.E.
J. Bacteriol. 183, 5709-5717, 2001
A:Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaekunas, S.R.;
A:Title: Genome of the Bacterium Streptococcus pneumoniae Strain R6.
A:Reference number: A97872; MUID:21429245; PMID:11544234
A:Accession: H98077
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-164 <KUR>
A:Cross-references: UNIPROT:Q8CYD1; GB:AE007317; PIDN:AAU0453.1; PID:g15459321; GSPDB
C:Genetics:
A:Gene: spr1650
```

Query Match 65.4%; Score 34; DB 2; Length 164;
Best Local Similarity 60.0%; Pred. No. 30;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 QNSGNOSFEE 10
||:|::|||
Db 127 QNNQNKTFEE 136

Search completed: October 22, 2005, 06:10:01
Job time : 4.65539 secs

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GenCore version 5.1.6
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OM protein - protein search, using SW model

Run on: October 22, 2005, 04:10:49 ; Search time 18.3253 Seconds
(without alignments)
279,439 Million cell updates/sec

Title: US-10-731-238-63

Sequence: 1 QNSGNQSFEE 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1613378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database: UniProt_03:*

1: uniprot_sprot:*

2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	52	100.0	940	2 Q53682	Q53682 staphylococ
2	52	100.0	943	2 Q8NU08	Q8NU08 staphylococ
3	52	100.0	957	2 Q6G6H4	Q6G6H4 staphylococ
4	52	100.0	961	2 Q99RD3	Q99RD3 staphylococ
5	52	100.0	961	2 Q7A3J8	Q7A3J8 staphylococ
6	52	100.0	965	2 Q6GDU5	Q6GDU5 staphylococ
7	52	100.0	1015	2 Q8NU07	Q8NU07 staphylococ
8	52	100.0	1015	2 Q6G6H3	Q6G6H3 staphylococ
9	52	100.0	1018	1 FMBA_STAAU	P14738 staphylococ
10	52	100.0	1038	2 Q99RD2	Q99RD2 staphylococ
11	52	100.0	1038	2 Q7A3J7	Q7A3J7 staphylococ
12	49	94.2	152	2 Q9AEP9	Q9AEP9 staphylococ
13	46	88.5	702	1 CANB_HUMAN	Q9UMGQ homo sapien
14	38	73.1	538	1 Q64V15	Q64V15 bacteroides
15	38	73.1	1576	2 Q6IRN6	Q6IRN6 xenopus lae
16	37	71.2	257	2 Q8EGW3	Q8EGW3 shewanella
17	37	71.2	333	2 Q8L9J2	Q8L9J2 arabidopsis
18	37	71.2	333	2 Q8ZUS6	Q8ZUS6 arabidopsis
19	37	71.2	358	1 YBQ3_YEAST	P38235 saccharomyc
20	37	71.2	358	2 Q6O5F3	Q6O5F3 saccharomyc
21	37	71.2	918	1 HXK1_BOVIN	P27595 bos taurus
22	36	69.2	245	2 Q7MF77	Q7MF77 vibrio vuln
23	36	69.2	310	2 Q45414	Q45414 bacillus sp
24	36	69.2	447	2 Q19819	Q19819 cenorhabdi
25	36	69.2	508	2 Q6FQ62	Q6FQ62 candida gla
26	36	69.2	642	1 YB65_SCHPO	Q09746 schizosacch
27	36	69.2	698	2 Q72E00	Q72E00 desulfovibr
28	36	69.2	799	2 Q6KHP9	Q6KHP9 mycoplasma
29	36	69.2	1291	2 Q6CAW1	Q6CAW1 yarrowia li
30	36	69.2	2149	2 Q8IFK7	Q8IFK7 plasmodium
31	35	67.3	103	2 Q8PTY3	Q8PTY3 methanosarc

32	35	67.3	150	2 Q64B80	Q64B80 uncultured
33	35	67.3	275	2 Q6C8T6	Q6C8T6 yarrowia li
34	35	67.3	375	2 Q76B90	Q76B90 prunus aviu
35	35	67.3	433	2 Q94478	Q94478 dictyostell
36	35	67.3	975	2 Q68CQ8	Q68CQ8 homo sapien
37	35	67.3	1184	2 Q9Y7U0	Q9Y7U0 schizosacch
38	35	67.3	1902	1 P3P_LACLC	P15292 lactococcu
39	35	67.3	2104	2 Q8IKF9	Q8IKF9 plasmodium
40	34	65.4	137	2 Q8R7G8	Q8R7G8 thermosae
41	34	65.4	155	1 RP86_YEAST	P20435 saccharomyc
42	34	65.4	160	2 Q97P13	Q97P13 streptococc
43	34	65.4	164	2 Q8CYD1	Q8CYD1 streptococc
44	34	65.4	165	2 Q6V8M0	Q6V8M0 rhodothermu
45	34	65.4	229	2 Q8RLG0	Q8RLG0 bradyrhizob

ALIGNMENTS

RESULT 1	Q53682	PRELIMINARY;	PRT;	940 AA.
AC	Q53682;			
DT	01-NOV-1996 (TREMBlrel. 01, Created)			
DT	01-NOV-1996 (TREMBlrel. 01, Last sequence update)			
DT	01-MAR-2004 (TREMBlrel. 26, Last annotation update)			
DE	Fibronectin binding protein B.			
GN	Name=fnbB;			
OS	Staphylococcus aureus.			
OC	Bacteria; Firmicutes; Bacillales; Staphylococcus.			
OX	NCBI_TaxID=1280;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=8325-4;			
RX	MEDLINE=9211475; PubMed=1837266;			
RA	Johnson K., Sigmas C., Muller H.P., Lindberg M.;			
RT	"Two different genes encode fibronectin binding proteins in			
RT	Staphylococcus aureus. The complete nucleotide sequence and			
RT	characterization of the second gene."			
RL	Bur. J. Biochem. 202:1041-1048 (1991).			
CC	-1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by			
CC	an amide bond (By similarity).			
DR	EMBL: X62992; CAA44726.1; -.			
DR	PIR: S19702; S19702.			
DR	HSP; Q53653; IN67.			
DR	GO: GO:0009986; C:cell surface; IEA.			
DR	GO: GO:0005618; C:cell wall; IEA.			
DR	GO: GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.			
DR	GO: GO:0016020; C:membrane; IEA.			
DR	GO: GO:007155; P:cell adhesion; IEA.			
DR	InterPro: IPR008966; Adhes_bact.			
DR	InterPro: IPR004237; Fn_bind.			
DR	InterPro: IPR005877; Gpos_YsIRK.			
DR	InterPro: IPR001899; Gram_pos_anchor.			
DR	Pfam: PF02986; Fn_bind_2			
DR	Pfam: PF00746; Gram_pos_anchor; 1.			
DR	Pfam: PF04650; YsIRK_signal; 1.			
DR	TIGRFAMs: TIGR01167; LPTXG_anchor; 1.			
DR	TIGRFAMs: TIGR01168; YsIRK_signal; 1.			
DR	PROSITE: PS50847; GRAM_POS_ANCHORING; 1.			
DR	Cell wall; peptidoglycan-anchor.			
DR	SEQUENCE 940 AA; 103555 MW; B35FBBCA907AE345 CRC64;			
QY	Query Match	100.0%;	Score 52;	DB 2; Length 940;
Db	Best Local Similarity	100.0%;	Pred. No. 0.34;	
	Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
	1 QNSGNQSFEE 10			
	682 QNSGNQSFEE 691			

RESULT 2

```
Q8NU8      PRELIMINARY;      PRT;      943 AA.
ID Q8NU8;
AC Q8NU8;
DT 01-OCT-2002 (TREMBLrel. 22, Created)
DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE FndB protein.
GN Name=fndB; OrderedLocusNames=MM2420;
OS Staphylococcus aureus (strain MM2).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=196620;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MM2;
RX MEDLINE=2040717; PubMed=12044378; DOI=10.1016/S0140-6736(02)08713-5;
RA Baba T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Oguchi A.,
RA Nagai Y., Iwano N., Asano K., Naimi T., Kuroda H., Cui L.,
RA Yamamoto K., Hiramatsu K.;
RT "Genome and virulence determinants of high virulence community-
RT acquired MRSA.";
RL Lancet 359:1819-1827(2002).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC an amide bond (By similarity).
DR EMBL: AP004830; BAB96285.1; -.
DR HSSP: OS3653; 1N67.
DR GO: GO:0009986; C:cell surface; IEA.
DR GO: GO:0005618; C:cell wall; IEA.
DR GO: GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO: GO:0016020; C:membrane; IEA.
DR GO: GO:0007155; P:cell adhesion; IEA.
DR InterPro: IPR008966; Adhes_bact.
DR InterPro: IPR004237; Fn_bind.
DR InterPro: IPR005877; Gpos_YSTRK.
DR InterPro: IPR001899; Gram_pos_anchor.
DR Pfam: PF02986; Fn_bind; 1.
DR Pfam: PF00746; Gram_pos_anchor; 1.
DR TIGRfams: TIGR01167; LPTXG_anchor; 1.
DR TIGRfams: TIGR01168; YSTRK_signal; 1.
DR PROSITE: PS50847; GRAM_POS_ANCHORING; 1.
DR Cell wall; Complete proteome; Peptidoglycan-anchor.
KW SEQUENCE 943 AA; 104537 MW; DABA5F31947E1B6A CRC64;
SQ
Query Match 100.0%; Score 52; DB 2; Length 943;
Best Local Similarity 100.0%; Pred. No. 0.34;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ONSGNOSFEE 10
DB 689 QNSGNOSFEE 698
RESULT 3
Q6G6H4 PRELIMINARY; PRT; 957 AA.
ID Q6G6H4;
AC Q6G6H4;
DT 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE Fibronectin-binding protein.
GN Name=fnbB; OrderedLocusNames=SA52387;
OS Staphylococcus aureus (strain MSSA476).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=282459;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=15213324; DOI=10.1073/pnas.0402521101;
RA Holden M.T.G., Fell E.J., Lindsay J.A., Peacock S.J., Day N.P.J.,
RA Enright M.C., Foster T.J., Moore C.E., Hurst V., Atkin R., Iatton A.,
RA Bason N., Bentley S.D., Chillingworth C., Chillingworth T.,
RA Churcher C., Clark L., Cotton C., Cronin A., Doggett J., Dowd L.,
RA Feltwell T., Hance Z., Harris B., Hauser H., Holtroyd S., Jaseels K.,
RA James K.D., Lennard N., Line A., Mayes R., Moule S., Mungall K.,
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RA Ormond D., Quail M.A., Rabinowitch E., Rutherford K.M., Sanders M.,
RA Sharp S., Simmonds M., Stevens K., Whitehead S., Barrell B.G.,
RA Spratt B.G., Parkhill J.;
RT "Complete genomes of two clinical Staphylococcus aureus strains:
RT evidence for the rapid evolution of virulence and drug resistance.";
RT Proc. Natl. Acad. Sci. U.S.A. 101:9786-9791(2004).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC an amide bond (By similarity).
DR EMBL: BX571857; CAG44201.1; -.
DR GO: GO:0009986; C:cell surface; IEA.
DR GO: GO:0005618; C:cell wall; IEA.
DR GO: GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO: GO:0016020; C:membrane; IEA.
DR GO: GO:0007155; P:cell adhesion; IEA.
DR InterPro: IPR008966; Adhes_bact.
DR InterPro: IPR004237; Fn_bind.
DR InterPro: IPR005877; Gpos_YSTRK.
DR InterPro: IPR001899; Gram_pos_anchor.
DR Pfam: PF02986; Fn_bind; 1.
DR Pfam: PF00746; Gram_pos_anchor; 1.
DR TIGRfams: TIGR01167; LPTXG_anchor; 1.
DR TIGRfams: TIGR01168; YSTRK_signal; 1.
DR PROSITE: PS50847; GRAM_POS_ANCHORING; 1.
DR Cell wall; Complete proteome; Peptidoglycan-anchor.
KW SEQUENCE 957 AA; 105980 MW; 28F8BA7FFDFD3EAF CRC64;
SQ
Query Match 100.0%; Score 52; DB 2; Length 957;
Best Local Similarity 100.0%; Pred. No. 0.35;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ONSGNOSFEE 10
DB 689 QNSGNOSFEE 698
RESULT 4
Q99RD3 PRELIMINARY; PRT; 961 AA.
ID Q99RD3;
AC Q99RD3;
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE Fibronectin-binding protein homolog.
GN Name=fnbB; OrderedLocusNames=SAV2502;
OS Staphylococcus aureus (strain Mu50 / ATCC 700699).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=158878;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=Mu50 / ATCC 700699;
RX MEDLINE=21311952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2;
RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Iian J.-Q., Ito T.,
RA Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosooya A.,
RA Mizutani-Ul Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
RA Sekimizu K., Hirakawa H., Kohara S., Goto S., Yabuzaki J.,
RA Kaneshita M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
RA Hattori M., Ogasawara N., Hayaishi H., Hiramatsu K.;
RT "Whole genome sequencing of methicillin-resistant Staphylococcus
RT aureus.";
RL Lancet 357:1225-1240(2001).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC an amide bond (By similarity).
DR EMBL: AP003365; BAB58664.1; -.
DR PIR: G90053; G90053.
DR HSSP: OS3653; 1N67.
DR GO: GO:0009986; C:cell surface; IEA.
DR GO: GO:0005618; C:cell wall; IEA.
DR GO: GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO: GO:0016020; C:membrane; IEA.
DR GO: GO:0007155; P:cell adhesion; IEA.
DR InterPro: IPR008966; Adhes_bact.
```

DR InterPro; IPR004237; Fn_bind.
 DR InterPro; IPR005877; Gpos_YsIRK.
 DR InterPro; IPR001899; Gram_pos_anchor.
 DR Pfam; PF02986; Fn_bind; 1.
 DR Pfam; PF00746; Gram_pos_anchor; 1.
 DR Pfam; PF04650; YsIRK_signal; 1.
 DR TIGRPFAM; TIGR01167; LPTXG_anchor; 1.
 DR TIGRPFAM; TIGR01168; YsIRK_signal; 1.
 DR PROSITE; PS50847; GRAM_POS_ANCHORING; 1.
 KW Cell wall; Complete proteome; Peptidoglycan-anchor.
 SO SEQUENCE 961 AA; 106010 MW; 364940F884EA4101 CRC64;

Query Match 100.0%; Score 52; DB 2; Length 961;
 Best Local Similarity 100.0%; Pred. No. 0.35;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QNSGNOSFEE 10
 DB 693 QNSGNOSFEE 702

RESULT 5
 ID 07A3J8 PRELIMINARY; PRT; 961 AA.
 AC 07A3J8;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE FndB protein.
 GN Name=fndB; Ordered locus names=SA2290;
 OS Staphylococcus aureus (strain N315).
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 NCBI_Taxid=158879;
 RX MEDLINE=21311952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2;
 RP SEQUENCE FROM N.A.
 RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
 RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Iian J.-O., Ito T.,
 RA Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyma A.,
 RA Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Katto C.,
 RA Sekimizu K., Hirakawa H., Kohara S., Goto S., Yabuuchi J.,
 RA Kaneshita M., Yamashita A., Ohnaka K., Furuya K., Yoshino C., Shiba T.,
 RA Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.,
 RT "Whole genome sequencing of methicillin-resistant Staphylococcus
 aureus";
 RL Lancet 357:1225-1240(2001).
 CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
 an amide bond (By similarity).
 CC EMBL; AP003137; BAB43593.1; -;
 DR GO; GO:0009986; C:cell surface; IEA.
 DR GO; GO:0005618; C:cell wall (sensu Gram-positive Bacteria); IEA.
 DR GO; GO:000975; C:cell wall (sensu Gram-positive Bacteria); IEA.
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0007155; P:cell adhesion; IEA.
 DR InterPro; IPR008966; Adhes_Bact.
 DR InterPro; IPR004237; Fn_bind.
 DR InterPro; IPR005877; Gpos_YsIRK.
 DR InterPro; IPR001899; Gram_pos_anchor.
 DR Pfam; PF02986; Fn_bind; 1.
 DR Pfam; PF00746; Gram_pos_anchor; 1.
 DR Pfam; PF04650; YsIRK_signal; 1.
 DR TIGRPFAM; TIGR01167; LPTXG_anchor; 1.
 DR TIGRPFAM; TIGR01168; YsIRK_signal; 1.
 DR PROSITE; PS50847; GRAM_POS_ANCHORING; 1.
 KW Cell wall; Complete proteome; Peptidoglycan-anchor.
 SO SEQUENCE 961 AA; 106010 MW; 364940F884EA4101 CRC64;

Query Match 100.0%; Score 52; DB 2; Length 961;
 Best Local Similarity 100.0%; Pred. No. 0.35;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 QNSGNOSFEE 10
 DB 693 QNSGNOSFEE 702

DB 693 QNSGNOSFEE 702

RESULT 6
 ID 06GDU5 PRELIMINARY; PRT; 965 AA.
 AC 06GDU5;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Fibronectin-binding protein.
 GN Name=fndB; Ordered locus names=SA2580;
 OS Staphylococcus aureus (strain MRSA252).
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 NCBI_Taxid=282458;
 RX PubMed=15213324; DOI=10.1073/pnas.0402521101;
 RA Holden M.T.G., Fell E.J., Lindsay J.A., Peacock S.J., Day N.P.J.,
 RA Enright N.C., Foster T.J., Moore C.E., Hurst L., Atkin R., Barton A.,
 RA Bason N., Bentley S.D., Chillingworth C., Chillingworth T.,
 RA Churcher C., Clark L., Corton C., Cronin A., Doggett J., Dowd L.,
 RA Felwell T., Hance Z., Harris B., Hauser A., Holtroyd S., Jagels K.,
 RA James K.D., Lennard N., Line A., Mayes R., Moulé S., Mungall K.,
 RA Ormrod D., Quail M.A., Rabinowitch E., Rutherford K.M., Sanders M.,
 RA Sharp S., Simmonds M., Stevens K., Whitehead S., Barrett B.G.,
 RA Spratt B.G., Parkhill J.;
 RT "Complete genomes of two clinical Staphylococcus aureus strains:
 evidence for the rapid evolution of virulence and drug resistance.";
 RL Proc. Natl. Acad. Sci. U.S.A. 101:9786-9791(2004).
 CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
 an amide bond (By similarity).
 CC EMBL; BX571856; CAG41560.1; -;
 DR GO; GO:0009986; C:cell surface; IEA.
 DR GO; GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0007155; P:cell adhesion; IEA.
 DR InterPro; IPR008966; Adhes_Bact.
 DR InterPro; IPR004237; Fn_bind.
 DR InterPro; IPR005877; Gpos_YsIRK.
 DR InterPro; IPR001899; Gram_pos_anchor.
 DR Pfam; PF02986; Fn_bind; 1.
 DR Pfam; PF00746; Gram_pos_anchor; 1.
 DR Pfam; PF04650; YsIRK_signal; 1.
 DR TIGRPFAM; TIGR01167; LPTXG_anchor; 1.
 DR TIGRPFAM; TIGR01168; YsIRK_signal; 1.
 DR PROSITE; PS50847; GRAM_POS_ANCHORING; 1.
 KW Cell wall; Complete proteome; Peptidoglycan-anchor.
 SO SEQUENCE 965 AA; 105691 MW; 2982E132164D0551 CRC64;

Query Match 100.0%; Score 52; DB 2; Length 965;
 Best Local Similarity 100.0%; Pred. No. 0.35;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QNSGNOSFEE 10
 DB 749 QNSGNOSFEE 758

RESULT 7
 ID 08NUU7 PRELIMINARY; PRT; 1015 AA.
 AC 08NUU7;
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE FndB protein.
 GN Name=fndB; Ordered locus names=MW2421;
 OS Staphylococcus aureus (strain MW2).
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 NCBI_Taxid=196620;
 RP SEQUENCE FROM N.A.

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RC STRAIN=NM2;
RX MEDLINE=22040717; PubMed=12044378; DOI=10.1016/S0140-6736(02)08713-5;
RA Baba T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Oguchi A.,
RA Nagai Y., Iwama N., Asano K., Naito T., Kuroda H., Cui L.,
RA Yamamoto K., Hiramatsu K.;
RT "Genome and virulence determinants of high virulence community-
RT acquired MRSA.";
RL Lancet 359:1819-1827(2002).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC an amide bond (By similarity).
CC EMBL, AP004830; BAB96286.1; -.
DR GO: GO:0009986; C:cell surface; IEA.
DR GO: GO:0005618; C:cell wall; IEA.
DR GO: GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO: GO:0016020; C:membrane; IEA.
DR GO: GO:0007155; P:cell adhesion; IEA.
DR InterPro: IPR008966; Adhes_bact.
DR InterPro: IPR004237; Fn_bind.
DR InterPro: IPR001899; Gram_pos_anchor.
DR Pfam: PF02986; Fn_bind; 1.
DR Pfam: PF00746; Gram_pos_anchor; 1.
DR Pfam: PF04650; YSIRK_signal; 1.
DR TIGRFAMs: TIGR01167; LpxTG_anchor; 1.
DR TIGRFAMs: TIGR01168; YSIRK_signal; 1.
DR PROSITE: PS50847; GRAM_POS_ANCHORING; 1.
DR Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ SEQUENCE 1015 AA; 111145 MW; D0F9281BB64D4D2 CRC64;

Query Match 100.0%; Score 52; DB 2; Length 1015;
Best Local Similarity 100.0%; Pred. No. 0.37;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QNSGNQSFEE 10
DB 747 QNSGNQSFEE 756

RESULT 8
O6G6H3 PRELIMINARY; PRT; 1015 AA.
ID O6G6H3;
AC O6G6H3;
DT 05-JUL-2004 (TREMblrel. 27, Created)
DT 05-JUL-2004 (TREMblrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMblrel. 27, Last annotation update)
DE Fibronectin-binding protein.
GN OrderedLocustNames=SA62388;
OS Staphylococcus aureus (strain MSSA476).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
CX NCBI_TaxId=282459;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=15213324; DOI=10.1073/pnas.0402521101;
RA Holden M.T.G., Fell B.J., Lindsay J.A., Peacock S.U., Day N.P.J.,
RA Enright M.C., Foster T.J., Moore C.E., Hurst L., Actin R., Barron A.,
RA Baason N., Bentley S.D., Chillingworth C., Chillingworth T.,
RA Churcher C., Clark L., Cotton C., Cronin A., Doggett J., Dowd L.,
RA Felwell T., Hance Z., Harris B., Hauser H., Holroyd S., Jagels K.,
RA James K.D., Leonard N., Line A., Mayes R., Moule S., Mungall K.,
RA Ormond D., Quail M.A., Rabinowitch E., Rutherford K.M., Sanders M.,
RA Sharp S., Simmonds M., Stevens K., Whitehead S., Barrett B.G.,
RA Spratt B.G., Parkhill J.;
RT "Complete genomes of two clinical Staphylococcus aureus strains:
RT evidence for the rapid evolution of virulence and drug resistance.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:9786-9791(2004).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC an amide bond (By similarity).
CC EMBL, BS571857; CAG44202.1; -.
DR GO: GO:0009986; C:cell surface; IEA.
DR GO: GO:0005618; C:cell wall; IEA.
DR GO: GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO: GO:0016020; C:membrane; IEA.
DR GO: GO:0007155; P:cell adhesion; IEA.

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DR InterPro: IPR008966; Adhes_bact.
DR InterPro: IPR004237; Fn_bind.
DR InterPro: IPR005877; Gpos_YSIRK.
DR InterPro: IPR001899; Gram_pos_anchor.
DR Pfam: PF02986; Fn_bind; 1.
DR Pfam: PF00746; Gram_pos_anchor; 1.
DR Pfam: PF04650; YSIRK_signal; 1.
DR TIGRFAMs: TIGR01167; LpxTG_anchor; 1.
DR TIGRFAMs: TIGR01168; YSIRK_signal; 1.
DR PROSITE: PS50847; GRAM_POS_ANCHORING; 1.
DR Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ SEQUENCE 1015 AA; 111145 MW; D0F9281BB64D4D2 CRC64;

Query Match 100.0%; Score 52; DB 2; Length 1015;
Best Local Similarity 100.0%; Pred. No. 0.37;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QNSGNQSFEE 10
DB 747 QNSGNQSFEE 756

RESULT 9
FNBA_STAAU STANDARD; PRT; 1018 AA.
ID FNBA_STAAU
AC P14738;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Fibronectin-binding protein precursor (FNBP).
GN Name=fnba;
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
CX NCBI_TaxId=1280;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=NTC 8325-4;
RX MEDLINE=89098998; PubMed=2521391;
RA Signaes C., Raucet G., Joensson K., Lindgren P.-E.,
RA Anantharamaiah G.M., Hoeoek M., Lindberg M.;
RT "Nucleotide sequence of the gene for a fibronectin-binding protein
RT from Staphylococcus aureus: use of this peptide sequence in the
RT synthesis of biologically active peptides.";
RL Proc. Natl. Acad. Sci. U.S.A. 86:699-703(1989).
CC -1- FUNCTION: The ability of bacteria to bind fibronectin has been
CC proposed as a virulence factor enabling bacteria to colonize wound
CC tissues and blood clots. Binding of plasma fibronectin to the
CC bacterial surface might block adhesion receptors on S.aureus, thus
CC representing an important defense mechanism against tissue
CC invasion.
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC an amide bond (Potential).
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@sib-sib.ch).
CC EMBL, J04151; AAA26632.1; -.
DR InterPro: IPR004237; Fn_bind.
DR InterPro: IPR005877; Gpos_YSIRK.
DR InterPro: IPR001899; Gram_pos_anchor.
DR Pfam: PF02986; Fn_bind; 1.
DR Pfam: PF00746; Gram_pos_anchor; 1.
DR Pfam: PF04650; YSIRK_signal; 1.
DR TIGRFAMs: TIGR01167; LpxTG_anchor; 1.
DR TIGRFAMs: TIGR01168; YSIRK_signal; 1.
DR PROSITE: PS50847; GRAM_POS_ANCHORING; 1.
DR Cell adhesion; Cell wall; Peptidoglycan-anchor; Repeat; Signal;
DR Cell adhesion; Cell wall; Peptidoglycan-anchor; Repeat; Signal;
KM Virulence.

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FT SIGNAL 1 36
FT CHAIN 37 985 Fibronectin-binding protein.
FT PROPEP 986 1018 Removed by sortase (Potential).
FT REPEAT 545 574 B-1.
FT REPEAT 575 604 B-2.
FT DOMAIN 745 878 4 X approximate tandem repeats,
  fibronectin-binding domain.
FT REPEAT 745 782 D-1.
FT REPEAT 783 820 D-2.
FT REPEAT 821 859 D-3.
FT REPEAT 860 878 D-4 (incomplete).
FT DOMAIN 879 948 5 X tandem repeats, Pro-rich (WR).
FT REPEAT 879 892 WR 1.
FT REPEAT 893 906 WR 2.
FT REPEAT 907 920 WR 3.
FT REPEAT 921 934 WR 4.
FT REPEAT 935 948 WR 5.
FT SITE 982 986 LPTXG sorting signal (potential).
FT MOD_RES 985 985 Pentaglycyl murein peptidoglycan amidated
  chreonine (potential).
SQ SEQUENCE 1018 AA; 111780 MW; 58175E0020E81F1F CRC64;

Query Match 100.0%; Score 52; DB 1; Length 1018;
Best Local Similarity 100.0%; Pred. No. 0.37;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QNSGNSFEE 10
Db 746 QNSGNSFEE 755

RESULT 10
Q99RD2 PRELIMINARY; PRT; 1038 AA.
ID Q99RD2
AC Q99RD2
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Fibronectin-binding protein homolog.
GN Name=fnb; OrderedLocustNames=SAV2503;
OS Staphylococcus aureus (strain Mu50 / ATCC 706069).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
NCBI_TaxID=158878;
OX
RN
RP SEQUENCE FROM N.A.
RC STRAIN=Mu50 / ATCC 706069;
RX MEDLINE=21311952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2;
RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
  Cui L., Oguchi A., Aoki K.-I., Nagai Y., Lian J.-Q., Ito T.,
  Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hoshoyama A.,
  Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
  Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
  Kanehisa M., Yamashita A., Oshima K., Saito K., Yoshino C., Shiba T.,
  Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
  "Whole genome sequencing of methicillin-resistant Staphylococcus
  aureus."
RT Lancer 357:1225-1240 (2001).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
  an amide bond (By similarity).
EMBL, AP003365; BAB5865.1; -.
DR GO: GO:0009986; C:cell surface; IEA.
DR GO: GO:0005618; C:cell wall; IEA.
DR GO: GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO: GO:0016020; C:membrane; IEA.
DR GO: GO:007155; P:cell adhesion; IEA.
DR InterPro: IPR004237; Fp_bind.
DR InterPro: IPR008966; Adhes_bact.
DR InterPro: IPR005877; Gpos_YsIRK.
DR InterPro: IPR001899; Gram_pos_anchor.
DR Pfam: PF02986; Fp_bind. 1.
DR Pfam: PF04650; YsIRK_signal. 1.
DR TIGRFAMs: TIGR01167; LPTXG_anchor. 1.
DR TIGRFAMs: TIGR01168; YsIRK_signal. 1.
DR PROSITE: PS50847; GRAM_POS_ANCHORING. 1.
KW Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ SEQUENCE 1038 AA; 113618 MW; 666BF6BF2BFBB12 CRC64;

Query Match 100.0%; Score 52; DB 2; Length 1038;
Best Local Similarity 100.0%; Pred. No. 0.38;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QNSGNSFEE 10
Db 742 QNSGNSFEE 751

RESULT 11
Q7A3J7 PRELIMINARY; PRT; 1038 AA.
ID Q7A3J7
AC Q7A3J7
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Fnb protein.
GN Name=fnb; OrderedLocustNames=SA2291;
OS Staphylococcus aureus (strain N315).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
NCBI_TaxID=158879;
OX
RN
RP SEQUENCE FROM N.A.
RC MEDLINE=21311952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2;
RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
  Cui L., Oguchi A., Aoki K.-I., Nagai Y., Lian J.-Q., Ito T.,
  Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hoshoyama A.,
  Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
  Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
  Kanehisa M., Yamashita A., Oshima K., Saito K., Yoshino C., Shiba T.,
  Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
  "Whole genome sequencing of methicillin-resistant Staphylococcus
  aureus."
RT Lancer 357:1225-1240 (2001).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
  an amide bond (By similarity).
EMBL, AP003337; BAB3594.1; -.
DR GO: GO:0009986; C:cell surface; IEA.
DR GO: GO:0005618; C:cell wall; IEA.
DR GO: GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO: GO:0016020; C:membrane; IEA.
DR GO: GO:0007155; P:cell adhesion; IEA.
DR InterPro: IPR008966; Adhes_bact.
DR InterPro: IPR004237; Fp_bind.
DR InterPro: IPR005877; Gpos_YsIRK.
DR InterPro: IPR001899; Gram_pos_anchor.
DR Pfam: PF02986; Fp_bind. 1.
DR Pfam: PF00746; Gram_pos_anchor. 1.
DR Pfam: PF04650; YsIRK_signal. 1.
DR TIGRFAMs: TIGR01167; LPTXG_anchor. 1.
DR TIGRFAMs: TIGR01168; YsIRK_signal. 1.
DR PROSITE: PS50847; GRAM_POS_ANCHORING. 1.
KW Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ SEQUENCE 1038 AA; 113618 MW; 666BF6BF2BFBB12 CRC64;

Query Match 100.0%; Score 52; DB 2; Length 1038;
Best Local Similarity 100.0%; Pred. No. 0.38;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QNSGNSFEE 10
Db 742 QNSGNSFEE 751

RESULT 12
Q9AEP9 PRELIMINARY; PRT; 152 AA.
ID Q9AEP9

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DR TIGRFAMs: TIGR01167; LPTXG_anchor. 1.
DR TIGRFAMs: TIGR01168; YsIRK_signal. 1.
DR PROSITE: PS50847; GRAM_POS_ANCHORING. 1.
DR Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ SEQUENCE 1038 AA; 113618 MW; 666BF6BF2BFBB12 CRC64;

Query Match 100.0%; Score 52; DB 2; Length 1038;
Best Local Similarity 100.0%; Pred. No. 0.38;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QNSGNSFEE 10
Db 742 QNSGNSFEE 751

RESULT 11
Q7A3J7 PRELIMINARY; PRT; 1038 AA.
ID Q7A3J7
AC Q7A3J7
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Fnb protein.
GN Name=fnb; OrderedLocustNames=SA2291;
OS Staphylococcus aureus (strain N315).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
NCBI_TaxID=158879;
OX
RN
RP SEQUENCE FROM N.A.
RC MEDLINE=21311952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2;
RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
  Cui L., Oguchi A., Aoki K.-I., Nagai Y., Lian J.-Q., Ito T.,
  Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hoshoyama A.,
  Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
  Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
  Kanehisa M., Yamashita A., Oshima K., Saito K., Yoshino C., Shiba T.,
  Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
  "Whole genome sequencing of methicillin-resistant Staphylococcus
  aureus."
RT Lancer 357:1225-1240 (2001).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
  an amide bond (By similarity).
EMBL, AP003337; BAB3594.1; -.
DR GO: GO:0009986; C:cell surface; IEA.
DR GO: GO:0005618; C:cell wall; IEA.
DR GO: GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO: GO:0016020; C:membrane; IEA.
DR GO: GO:0007155; P:cell adhesion; IEA.
DR InterPro: IPR008966; Adhes_bact.
DR InterPro: IPR004237; Fp_bind.
DR InterPro: IPR005877; Gpos_YsIRK.
DR InterPro: IPR001899; Gram_pos_anchor.
DR Pfam: PF02986; Fp_bind. 1.
DR Pfam: PF00746; Gram_pos_anchor. 1.
DR Pfam: PF04650; YsIRK_signal. 1.
DR TIGRFAMs: TIGR01167; LPTXG_anchor. 1.
DR TIGRFAMs: TIGR01168; YsIRK_signal. 1.
DR PROSITE: PS50847; GRAM_POS_ANCHORING. 1.
KW Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ SEQUENCE 1038 AA; 113618 MW; 666BF6BF2BFBB12 CRC64;

Query Match 100.0%; Score 52; DB 2; Length 1038;
Best Local Similarity 100.0%; Pred. No. 0.38;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QNSGNSFEE 10
Db 742 QNSGNSFEE 751

RESULT 12
Q9AEP9 PRELIMINARY; PRT; 152 AA.
ID Q9AEP9

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AC 09AP9;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Fibronectin-binding protein (Fragment).
GN Name=fnb;
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxId=1280;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=CMRSA-1;
RX DOI=10.1128/IAI.69.6.3791-3799.2001;
RA Rice K., Huesca M., Vaz D., McGavin M.J.;
RT "Variance in fibronectin binding and fnb locus polymorphisms in
RT Staphylococcus aureus: identification of antigenic variation in a
RT fibronectin binding protein adhesin of the epidemic CMRSA-1 strain of
RT methicillin-resistant S. aureus.";
RL Infect. Immun. 69:3791-3799(2001).
DR EMBL; AY029184; AAK31588.1; -.
FT NON TER 1
FT NON TER 152
SQ SEQUENCE 152 AA; 17193 MW; CFA3913C2B11C025 CRC64;

Query Match 94.2%; Score 49; DB 2; Length 152;
Best Local Similarity 90.0%; Pred. No. 0.17;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ONSGNSFEE 10
DB 1 ONSGNSFEE 10

RESULT 13
CANB_HUMAN STANDARD; PRT; 702 AA.
AC 09JUN06; 08MAR05;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Calpain 11 (EC 3.4.22.-) (Calcium-activated neutral proteinase 11)
DE (CAMP 11).
GN Name=CAPN11;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxId=9606;
RN (1)
RP SEQUENCE FROM N.A.
RX MEDLINE=9335989; PubMed=10409436; DOI=10.1006/geno.1999.5659;
RA Dear T.N., Moller A., Boehm T.;
RT "CAPN11: a calpain with high mRNA levels in testis and located on
RT chromosome 6.";
RL Genomics 59:243-247(1999).
RN (2)
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan K., Moore T., Max S.I., Wang J., Heien F.,
RA Datchenko L., Marusik K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M.J., Udell T.B., Toshiyuki S., Carninci P., Prange C.,
RA Brownstein M.J., Soares M.B., Bonaldi M.F., Casavant T.L., Schetz T.E.,
RA Raha S.S., Loggellano N.A., Peters G.J., Abramson R.D., Muljy S.J.,
RA Bosak S.A., McKernan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.V., Hilyk R.A.,
RA Villalón D.K., Muzny K.C., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,

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RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield V.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -1- FUNCTION: Calcium-regulated non-lysosomal thiol-protease which
CC catalyze limited proteolysis of substrates involved in
CC cytoskeletal remodeling and signal transduction.
CC -1- CATALYTIC ACTIVITY: Broad endopeptidase specificity.
CC -1- SUBUNIT: Heterodimer of a large (catalytic) and a small
CC (regulatory) subunit.
CC -1- TISSUE SPECIFICITY: Highest expression in testis.
CC -1- SIMILARITY: Belongs to the peptidase C2 family.
CC -1- SIMILARITY: Contains 1 calpain catalytic domain.
CC -1- SIMILARITY: Contains 2 EF-hand calcium-binding domains.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AJ242832; CAB52137.1; -.
DR EMBL; BC033733; AAK3733.1; -.
DR HSSP; Q07009; IMDW.
DR MEROPS; C02.013; -.
DR Genew; HGNC:1478; CAPN11.
DR MIM; 604822; -.
DR GO; GO:0004198; F:calpain activity; TAS.
DR GO; GO:0008233; F:peptidase activity; TAS.
DR InterPro; IPR002048; EF-hand.
DR InterPro; IPR001983; EF-hand-like.
DR InterPro; IPR000169; Pept_cys_acsite.
DR InterPro; IPR001300; Peptidase_C2.
DR Pfam; PR01067; Calpain_III; 1.
DR Pfam; PR00036; ehand_2; 1.
DR Pfam; PR00648; Peptidase_C2; 1.
DR PRINTS; PR00704; CALPAIN.
DR SMART; SM00720; calpain_III; 1.
DR SMART; SM00230; CysPC; 1.
DR SMART; SM00054; EPH; 2.
DR PROSITE; PSS0203; CALPAIN_CAT; 1.
DR PROSITE; PSS0018; EF_HAND; 2.
DR PROSITE; PSS00640; THIOL_PROTEASE_ASN; FALSE_NEG.
DR PROSITE; PSS00139; THIOL_PROTEASE_CYS; 1.
DR PROSITE; PSS00639; THIOL_PROTEASE_HIS; FALSE_NEG.
KW Calcium-binding; Hydrolase; Multigene family; Thiol protease.
FT DOMAIN 42 341
FT DOMAIN 342 514
FT DOMAIN 515 530
FT DOMAIN 531 701
FT CA_BIND 586 597
FT CA_BIND 616 627
FT DOMAIN 651 662
FT DOMAIN 681 692
FT ACT_SITE 102 102
FT ACT_SITE 259 259
FT ACT_SITE 283 283
FT CONFLICT 404 404
SQ SEQUENCE 702 AA; 80582 MW; 3A618682B9674FAE CRC64;

Query Match 88.5%; Score 46; DB 1; Length 702;
Best Local Similarity 90.0%; Pred. No. 3.6;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ONSGNSFEE 10
DB 22 ONSGNSFEE 31

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RESULT 14
Q64VL5 PRELIMINARY; PRT; 538 AA.
ID 064VL5;
AC 064VL5;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DE Putative outer membrane protein probably involved in nutrient
DE binding.
GN ORFNames=BP1714;
OS Bacteroides fragilis.
OC Bacteria; Bacteroidetes; Bacteroides (class); Bacteroidales;
OC Bacteroidaceae; Bacteroides.
OX NCBI_TaxID=817;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=YCH46;
RA Kuwahara T., Yamashita A., Hirakawa H., Nakayama H., Toh H., Okada N.,
RA Kuwata S., Hattori M., Hayashi T., Ohnishi Y.
RT "Genomic analysis of Bacteroides fragilis reveals extensive DNA
RT inversions regulating cell surface adaptation."
RL Proc. Natl. Acad. Sci. U.S.A. 0:0-0(2004).
DR EMBL: AP06841; BAD48461.1; -.
SQ SEQUENCE 538 AA; 60657 MW; A64A5059C6446D7D CRC64;

Query Match 73.1%; Score 38; DB 2; Length 538;
Best Local Similarity 66.7%; Pred. NO. 98;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 QNSGNSQSF 9
Db 334 QNTGNQTYE 342

RESULT 15
Q6IRN6 PRELIMINARY; PRT; 1576 AA.
ID 06IRN6;
AC 06IRN6;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE MGC83683 protein.
GN Name=MGC83683;
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Oocytes;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshitoki S., Carrinci P., Prange C.,
RA Rana S.S., Loquellano N.A., Peters G.J., Adamson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulik S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahay J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalske U., Smallus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Maira M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]

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RP SEQUENCE FROM N.A.
RC TISSUE=Oocytes;
RX MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA Richardson P.;
RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus
RT initiative."
RL Dev. Dyn. 225:384-391(2002).
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Oocytes;
RA Klein S., Strausberg R.;
RL Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL: BC070721; AAH70721.1; -.
DR InterPro: IPR001715; Calponin-like.
DR Pfam: PF00307; CH; 1.
SQ SEQUENCE 1576 AA; 175933 MW; 6C22D339E783603E CRC64;

Query Match 73.1%; Score 38; DB 2; Length 1576;
Best Local Similarity 87.5%; Pred. NO. 3,3e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QNSGNSQSF 8
Db 619 QNEGNSQSF 626

Search completed: October 22, 2005, 06:06:24
Job time : 20.3253 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 25, 2005, 19:38:38 ; Search time 22.0612 Seconds
(without alignments)
175.313 Million cell updates/sec

Title: US-10-731-238-64

Perfect score: 52

Sequence: 1 SCNQSFEDDT 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

A_Geneseq_16Dec04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003s:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	52	100.0	10	2	AAW65720 Fibronec
2	52	100.0	38	1	AAW65720 Fibronec
3	52	100.0	38	1	AAW65720 Fibronec
4	52	100.0	38	1	AAW65720 Fibronec
5	52	100.0	38	2	AAW65662 Fibronec
6	52	100.0	38	2	AAW65662 Fibronec
7	52	100.0	38	2	AAW65697 Fibronec
8	52	100.0	38	2	AAW65697 Fibronec
9	52	100.0	38	2	AAW65697 Fibronec
10	52	100.0	38	2	AAW65697 Fibronec
11	52	100.0	38	2	AAW65697 Fibronec
12	52	100.0	38	2	AAW65697 Fibronec
13	52	100.0	38	2	AAW65697 Fibronec
14	52	100.0	38	2	AAW65697 Fibronec
15	52	100.0	38	2	AAW65697 Fibronec
16	52	100.0	38	2	AAW65697 Fibronec
17	52	100.0	38	2	AAW65697 Fibronec
18	52	100.0	38	2	AAW65697 Fibronec
19	52	100.0	38	2	AAW65697 Fibronec
20	52	100.0	38	2	AAW65697 Fibronec
21	52	100.0	38	2	AAW65697 Fibronec
22	52	100.0	38	2	AAW65697 Fibronec
23	52	100.0	38	2	AAW65697 Fibronec
24	52	100.0	38	2	AAW65697 Fibronec
25	52	100.0	38	2	AAW65697 Fibronec

26	52	100.0	767	4	AAU37547
27	52	100.0	940	6	AAW65720
28	52	100.0	940	6	AAW65720
29	52	100.0	948	6	AAW65720
30	52	100.0	948	6	AAW65720
31	52	100.0	948	6	AAW65720
32	52	100.0	948	6	AAW65720
33	52	100.0	948	6	AAW65720
34	52	100.0	948	6	AAW65720
35	52	100.0	948	6	AAW65720
36	52	100.0	948	6	AAW65720
37	52	100.0	948	6	AAW65720
38	52	100.0	948	6	AAW65720
39	52	100.0	948	6	AAW65720
40	52	100.0	948	6	AAW65720
41	52	100.0	948	6	AAW65720
42	52	100.0	948	6	AAW65720
43	52	100.0	948	6	AAW65720
44	52	100.0	948	6	AAW65720
45	52	100.0	948	6	AAW65720

ALIGNMENTS

RESULT 1
AAW65720 standard; peptide, 10 AA.
AAW65720:
16-OCT-1998 (first entry)
Fibronec binding protein-derived peptide #64.
microbial surface components recognising adhesive matrix molecule;
MSCRAMM; fibronec; fibronec-binding protein; antibody; epitope;
antibiotic; bacterial infection; antibiotic-resistant strain.
Synthetic.
Staphylococcus aureus.
W09831389-A2.
23-JUL-1998.
21-JAN-1998; 98WO-US001222.
21-JAN-1997; 97US-0036139P.
(TEXA) UNIV TEXAS A & M SYSTEM.
Hoeok M, Patti JM, House-Pompeo KL, Speziale P, Joh D;
Megavir M;
WPI; 1998-413816/35.
Antibody that binds to fibronec-binding protein, preventing its
binding to fibronec - used to treat or prevent bacterial infection,
especially by Staphylococci and Streptococci.
Example 9; Page 109; 201PP; English.
The invention relates to antibodies that bind to a fibronec-binding
domain of a fibronec-binding protein, and inhibit peptides of the
protein to fibronec. Also claimed are: (1) isolated peptides of a
fibronec-binding protein that do not bind to fibronec; (2) fusion
protein containing at least one peptide of a fibronec-binding protein
linked to a second amino acid sequence; (3) nucleic acid encoding the
isolated peptide of (1). Antibodies, the isolated peptides of (1) and the
nucleic acids are all useful for immunisation (active or passive) and (by
inhibiting binding of bacteria to fibronec) for preventing or treating
infection in humans or other animals, particularly by staphylococci or

CC streptococci, e.g. meningitis, otitis media, pneumonia, endocarditis,
 CC mastitis in cattle, abortion in horses and many others. Since the
 CC antibodies block binding of bacteria, they should be effective against
 CC antibiotic-resistant strains, and may replace antibiotic therapy or
 CC increase its effectiveness. Sequences AAW65719-41 and AAW35658 represent
 CC peptides which were synthesised to span the D1 motif and the N-terminal
 CC 18 amino acids of D2, with each peptide overlapping by eight amino acids
 CC with the previous sequence
 XX
 SQ Sequence 10 AA;

Query Match 100.0%; Score 52; DB 1; Length 38.
 Best Local Similarity 100.0%; Pred. No. 0.0018;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGNQSFEDT 10
 Db 1 SGNQSFEDT 10

RESULT 2
 AAP80660
 ID AAP80660 standard; protein; 38 AA.
 XX
 AC AAP80660;

XX 25-MAR-2003 (revised)
 DT 07-OCT-1990 (first entry)
 XX
 XX Protein with fibronectin binding ability.

XX Hybrid DNA molecule; fibronectin binding; mastitis; ruminants;
 KM wound infection.

XX Staphylococcus aureus.

XX EP294349-A.

XX 07-DEC-1988.

XX 30-MAY-1988; 88EP-00850188.

XX 01-JUN-1987; 87SE-00002272.

XX (ALFA) ALFA LAVAL AGRIC INT AB.

XX Lindberg MK, Signas LC, Wadstrom TM, Froman G;

XX WPI; 1988-347978/49.

DR N-PSDB; AAN81097.

XX Hybrid DNA encoding Staphylococcus aureus fibronectin binding protein -
 PT useful for immunisation and topical application to prevent staphylococcal
 PT infections.
 XX

PS Claim 11; Page 12; 23pp; English.

XX The peptide has fibronectin binding ability. It is useful for immunising
 CC ruminants against staphylococcal mastitis, pref. when used at 0.5-5
 CC micrograms/kg, using 3 doses given at 1-3 week intervals; for topical
 CC application to prevent wound infection, using an isotonic saline soln. of
 CC concn. 25-250 micrograms/ml; and, when immobilised on a carrier, for
 CC diagnosing staphylococcal infections. (Updated on 25-MAR-2003 to correct
 CC PF field.) (Updated on 25-MAR-2003 to correct PA field.)
 XX

SQ Sequence 38 AA;

Query Match 100.0%; Score 52; DB 1; Length 38;
 Best Local Similarity 100.0%; Pred. No. 0.0085;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 SGNQSFEDT 10
 Db 1 SGNQSFEDT 10

Db 4 SGNQSFEDT 13

RESULT 3
 AAP82116
 ID AAP82116 standard; protein; 38 AA.

XX AAP82116;

XX 25-MAR-2003 (revised)

DT 05-JUN-1990 (first entry)

XX Fibronectin binding protein.

XX Fibronectin binding protein; S.aureus; immunisation; mastitis; ruminants;
 KM wound infection; diagnosis.

XX Staphylococcus aureus.

XX EP294349-A.

XX 07-DEC-1988.

XX 30-MAY-1988; 88EP-00850188.

XX 01-JUN-1987; 87SE-00002272.

XX (ALFA) ALFA LAVAL AGRIC INT AB.

XX Lindberg MK, Signas LC, Wadstrom TM, Froman G;

XX WPI; 1988-347978/49.

DR N-PSDB; AAN82054.

XX Hybrid DNA encoding Staphylococcus aureus fibronectin binding protein -
 PT useful for immunisation and topical application to prevent staphylococcal
 PT infections.
 XX

PS Claim 11; Page 12; 23pp; English.

XX The S.aureus fibronectin binding protein may be included in a hybrid
 CC protein. The protein may be used to immunise ruminants against
 CC staphylococcal mastitis, pref. when given at 0.5-5 microg/kg, using 3
 CC doses at 1-3 week intervals; and for topical applicn. to prevent wound
 CC infection, pref. using isotonic saline soln. of concn. 25-250 microg/mg.
 CC The DNA encoding the binding protein and the hybrid protein may be
 CC immobilised on a carrier and used to diagnose staphylococcal infections.
 CC (Updated on 25-MAR-2003 to correct PA field.)
 XX

SQ Sequence 38 AA;

Query Match 100.0%; Score 52; DB 1; Length 38;
 Best Local Similarity 100.0%; Pred. No. 0.0085;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGNQSFEDT 10
 Db 4 SGNQSFEDT 13

RESULT 4
 AAW65662
 ID AAW65662 standard; peptide; 38 AA.

XX AAW65662;

XX 16-OCT-1998 (first entry)

XX Fibronectin binding protein-derived peptide #6.

XX microbial surface components recognising adhesive matrix molecule;
 KM MSCRAMM; fibronectin; fibronectin-binding protein; antibody; epitope;
 KM antibiotic; bacterial infection; antibiotic-resistant strain.

```

XX OS Synthetic.
XX OS Staphylococcus aureus.
XX PN W09831389-A2.
XX PD 23-JUL-1998.
XX PF 21-JAN-1998; 98WO-US001222.
XX PR 21-JAN-1997; 97US-0036139P.
XX (TEXA ) UNIV TEXAS A & M SYSTEM.
XX PA Hoeoek M, Patti JM, House-Pompeo KL, Speziale P, Joh D;
XX PI Mcgavin MJ;
XX DR WPI; 1998-413816/35.
XX
XX PT Antibody that binds to fibronectin-binding protein, preventing its
XX binding to fibronectin - used to treat or prevent bacterial infection,
XX especially by Staphylococci and Streptococci.
XX
XX PS Example 2; Page 92; 201pp; English.
XX
XX CC The invention relates to antibodies that bind to a fibronectin-binding
XX domain of a fibronectin-binding protein, and inhibit binding of the
XX protein to fibronectin. Also claimed are: (1) isolated peptides of a
XX fibronectin-binding protein that do not bind to fibronectin; (2) fusion
XX protein containing at least one peptide of a fibronectin-binding protein
XX linked to a second amino acid sequence; (3) nucleic acid encoding the
XX isolated peptide of (1). Antibodies, the isolated peptides of (1) and the
XX nucleic acids are all useful for immunisation (active or passive) and (by
XX inhibiting binding of bacteria to fibronectin) for preventing or treating
XX infection in humans or other animals, particularly by staphylococci or
XX streptococci, e.g. meningitis, otitis media, pneumonia, endocarditis,
XX mastitis in cattle, abortion in horses and many others. Since the
XX antibodies block binding of bacteria, they should be effective against
XX antibiotic-resistant strains, and may replace antibiotic therapy or
XX increase its effectiveness. Sequences AAW65659-68 represent synthetic
XX epitopes from the fibronectin binding domains DU and DI-D4 of the S.
XX aureus fnBA gene
XX
XX SQ Sequence 38 AA:
XX
XX Query Match 100.0%; Score 52; DB 2; Length 38;
XX Best Local Similarity 100.0%; Pred. No. 0.0085;
XX Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 SGNQSFEDT 10
XX |||||
XX 3 SGNQSFEDT 12
XX
XX Db
XX
XX RESULT 5
XX ID AAW65696 standard; peptide; 38 AA.
XX
XX AC AAW65696;
XX
XX DT 16-OCT-1998 (first entry)
XX
XX DE Fibronectin binding protein-derived peptide #40.
XX
XX KW microbial surface components recognising adhesive matrix molecule;
XX MSCRAMM; fibronectin; fibronectin-binding protein; antibody; epitope;
XX antibiotic; bacterial infection; antibiotic-resistant strain.
XX
XX OS Synthetic.
XX OS Staphylococcus aureus.
XX
XX PN W09831389-A2.
XX
XX

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PD PD 23-JUL-1998.
XX XX 21-JAN-1998; 98WO-US001222.
XX PF 21-JAN-1997; 97US-0036139P.
XX PR 21-JAN-1997; 97US-0036139P.
XX (TEXA ) UNIV TEXAS A & M SYSTEM.
XX PA Hoeoek M, Patti JM, House-Pompeo KL, Speziale P, Joh D;
XX PI Mcgavin MJ;
XX DR WPI; 1998-413816/35.
XX
XX PT Antibody that binds to fibronectin-binding protein, preventing its
XX binding to fibronectin - used to treat or prevent bacterial infection,
XX especially by Staphylococci and Streptococci.
XX
XX PS Example 8; Page 102; 201pp; English.
XX
XX CC The invention relates to antibodies that bind to a fibronectin-binding
XX domain of a fibronectin-binding protein, and inhibit binding of the
XX protein to fibronectin. Also claimed are: (1) isolated peptides of a
XX fibronectin-binding protein that do not bind to fibronectin; (2) fusion
XX protein containing at least one peptide of a fibronectin-binding protein
XX linked to a second amino acid sequence; (3) nucleic acid encoding the
XX isolated peptide of (1). Antibodies, the isolated peptides of (1) and the
XX nucleic acids are all useful for immunisation (active or passive) and (by
XX inhibiting binding of bacteria to fibronectin) for preventing or treating
XX infection in humans or other animals, particularly by staphylococci or
XX streptococci, e.g. meningitis, otitis media, pneumonia, endocarditis,
XX mastitis in cattle, abortion in horses and many others. Since the
XX antibodies block binding of bacteria, they should be effective against
XX antibiotic-resistant strains, and may replace antibiotic therapy or
XX increase its effectiveness. Sequences AAW65691-700 represent a series of
XX synthetic peptides based on the DI region of S. aureus fibronectin
XX binding protein A. They were synthesised to contain mutations
XX
XX SQ Sequence 38 AA:
XX
XX Query Match 100.0%; Score 52; DB 2; Length 38;
XX Best Local Similarity 100.0%; Pred. No. 0.0085;
XX Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 SGNQSFEDT 10
XX |||||
XX 3 SGNQSFEDT 12
XX
XX Db
XX
XX RESULT 6
XX ID AAW65697 standard; peptide; 38 AA.
XX
XX AC AAW65697;
XX
XX DT 16-OCT-1998 (first entry)
XX
XX DE Fibronectin binding protein-derived peptide #41.
XX
XX KW microbial surface components recognising adhesive matrix molecule;
XX MSCRAMM; fibronectin; fibronectin-binding protein; antibody; epitope;
XX antibiotic; bacterial infection; antibiotic-resistant strain.
XX
XX OS Synthetic.
XX OS Staphylococcus aureus.
XX
XX PN W09831389-A2.
XX
XX PD 23-JUL-1998.
XX PF 21-JAN-1998; 98WO-US001222.
XX PR 21-JAN-1997; 97US-0036139P.
XX
XX

```

2A	(TEXA) UNIV TEXAS A & M SYSTEM.
XX	
XX	Hoeoek M, Patti JM, House-Pompeo KL, Speciale P, Joh I;
P1	McGavin MO;
P1	
XX	
DR	WPI, 1998-413816/35.
XX	
PT	Antibody that binds to fibronectin-binding protein, preventing its
PT	binding to fibronectin - used to treat or prevent bacterial infection,
PT	especially by Staphylococci and Streptococci.
XX	
PS	Example 8; Page 102; 201p; English.
XX	
CC	The invention relates to antibodies that bind to a fibronectin-binding
CC	domain of a fibronectin-binding protein, and inhibit binding of the
CC	protein to fibronectin. Also claimed are: (1) isolated peptides of a
CC	fibronectin-binding protein that do not bind to fibronectin; (2) fusion
CC	protein containing at least one peptide of a fibronectin-binding protein
CC	linked to a second amino acid sequence; (3) nucleic acid encoding the
CC	isolated peptide of (1). Antibodies, the isolated peptides of (1) and the
CC	nucleic acids are all useful for immunisation (active or passive) and (by
CC	inhibiting binding of bacteria to fibronectin) for preventing or treating
CC	infection in humans or other animals, particularly by staphylococci or
CC	streptococci, e.g. meningitis, otitis media, pneumonia, endocarditis,
CC	mastitis in cattle, abortion in horses and many others. Since the
CC	antibodies block binding of bacteria, they should be effective against
CC	antibiotic-resistant strains, and may replace antibiotic therapy or
CC	enhance its effectiveness. Sequences AAM65691-700 represent a series of
CC	synthetic peptides based on the D1 region of S. aureus fibronectin
CC	binding protein A. They were synthesised to contain mutations
XX	
SQ	Sequence 38 AA;
XX	
Query_Match	100.0%; Score 52; DB 2; Length 38;
Best Local Similarity	100.0%; Pred. NO. 0.0085;
Matches 10; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
OY	1 SGNOSFEEDT 10
Db	3 SGNOSFEEDT 12
XX	
RESULT 7	
AAM65699	
ID	AAM65699 standard; peptide; 38 AA.
AC	
XX	AAM65699;
XX	
XX	16-OCT-1998 (first entry)
XX	
DE	Fibronectin binding protein-derived peptide #43.
XX	
KW	microbial surface components recognising adhesive matrix molecule;
KW	MSCRAMM; fibronectin; fibronectin-binding protein; antibody; epitope;
KW	antibiotic; bacterial infection; antibiotic-resistant strain.
XX	
XX	Synthetic.
OS	Staphylococcus aureus.
XX	
PN	WO9831389-A2.
XX	
PD	23-JUL-1998.
XX	
PF	21-JAN-1998; 98WO-US001222.
XX	
PR	21-JAN-1997; 97US-0036139P.
XX	
PA	(TEXA) UNIV TEXAS A & M SYSTEM.
XX	
P1	Hoeoek M, Patti JM, House-Pompeo KL, Speciale P, Joh D;
P1	McGavin MO;
XX	
DR	WPI, 1998-413816/35.

```

PT Antibody that binds to fibronectin-binding protein, preventing its
PT binding to fibronectin - used to treat or prevent bacterial infection,
PT especially by Staphylococci and Streptococci.
PS Example 8; Page 102; 201pp; English.
XX
CC The invention relates to antibodies that bind to a fibronectin-binding
CC domain of a fibronectin-binding protein, and inhibit binding of the
CC protein to fibronectin. Also claimed are: (1) isolated peptides of a
CC protein containing at least one peptide of a fibronectin-binding protein
CC linked to a second amino acid sequence; (3) nucleic acid encoding the
CC isolated peptide of (1). Antibodies, the isolated peptides of (1) and the
CC nucleic acids are all useful for immunisation (active or passive) and (by
CC inhibiting binding of bacteria to fibronectin) for preventing or treating
CC infection in humans or other animals, particularly by staphylococci or
CC streptococci, e.g. meningitis, otitis media, pneumonia, endocarditis,
CC mastitis in cattle, abortion in horses and many others. Since the
CC antibodies block binding of bacteria, they should be effective against
CC antibiotic-resistant strains, and may replace antibiotic therapy or
CC increase its effectiveness. Sequences AAM65691-700 represent a series of
CC synthetic peptides based on the D1 region of S. aureus fibronectin
CC binding protein A. They were synthesised to contain mutations
SQ Sequence 38 AA;
Query Match 100.0%; Score 52; DB 2; Length 38;
Best Local Similarity 100.0%; Pred. No. 0.0085;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0.
QY 1 SGNO$FDEDT 10
DB |||||
3 SGNO$FDEDT 12
RESULT 8
AAM65661
ID ID AAM65661 standard; peptide; 38 AA.
AC AAM65661;
XX
XX 16-OCT-1998 (first entry)
DT
DE Fibronectin binding protein-derived peptide #5.
XX
XX microbial surface components recognising adhesive matrix molecule;
KW MSRAWM; fibronectin; fibronectin-binding protein; antibody; epitope;
XX antibiotic; bacterial infection; antibiotic-resistant strain.
XX
XX Synthetic.
OS Staphylococcus aureus.
OS
PN WO9831389-A2.
PD
PD 23-JUL-1998.
PF 21-JAN-1998; 98WO-US001222.
PR 21-JAN-1997; 97US-0036139P.
XX
PA (TEKA ) UNIV TEXAS A & M SYSTEM.
XX
PI Hoeoek M, Palti JM, House-Pompeo KL, Speciale P, Joh D;
PI McGavin MJ;
DR WPI, 1998-413816/35.
XX
PT Antibody that binds to fibronectin-binding protein, preventing its
PT binding to fibronectin - used to treat or prevent bacterial infection,
PT especially by Staphylococci and Streptococci.
PS Example 2; Page 92; 201pp; English.

```

XX The invention relates to antibodies that bind to a fibronectin-binding
 CC domain of a fibronectin-binding protein, and inhibit binding of the
 CC protein to fibronectin. Also claimed are: (1) isolated peptides of a
 CC fibronectin-binding protein that do not bind to fibronectin; (2) fusion
 CC protein containing at least one peptide of a fibronectin-binding protein
 CC linked to a second amino acid sequence; (3) nucleic acid encoding the
 CC isolated peptide of (1). Antibodies, the isolated peptides of (1) and the
 CC nucleic acids are all useful for immunisation (active or passive) and (by
 CC inhibiting binding of bacteria to fibronectin) for preventing or treating
 CC infection in humans or other animals, particularly by staphylococci or
 CC streptococci, e.g. meningitis, otitis media, pneumonia, endocarditis,
 CC mastitis in cattle, abortion in horses and many others. Since the
 CC antibodies block binding of bacteria, they should be effective against
 CC antibiotic-resistant strains, and may replace antibiotic therapy or
 CC increase its effectiveness. Sequences AAW6569-68 represent synthetic
 CC epitopes from the fibronectin binding domains DU and DI-D4 of the S.
 CC aureus fnda gene

XX
 SQ Sequence 38 AA;

Query Match 100.0%; Score 52; DB 2; Length 38;
 Best Local Similarity 100.0%; Pred. No. 0.0085;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGNQSFEDT 10
 |||||
 DB 3 SGNQSFEDT 12

RESULT 9
 AAW65698
 ID AAW65698 standard; peptide; 38 AA.

XX AAW65698;

XX 16-OCT-1998 (first entry)

XX Fibronectin binding protein-derived peptide #42.

KM microbial surface components recognising adhesive matrix molecule;
 KM MSCRAMM; fibronectin; fibronectin-binding protein; antibody; epitope;
 KM antibiotic; bacterial infection; antibiotic-resistant strain.

OS Synthetic.
 OS Staphylococcus aureus.

XX WO9831389-A2.

XX 23-JUL-1998.

XX 21-JAN-1998; 98WO-US001222.

XX 21-JAN-1997; 97US-0036139P.

XX (TEXA) UNIV TEXAS A & M SYSTEM.

PI Hoeoek M, Patti JM, House-Pompeo KL, Speziale P, Joh D;
 PI McGavin MJ;

XX WPI; 1998-413816/35.

PT Antibody that binds to fibronectin-binding protein, preventing its
 binding to fibronectin - used to treat or prevent bacterial infection,
 PT especially by Staphylococci and Streptococci.

XX Example 8; Page 102; 201pp; English.

CC The invention relates to antibodies that bind to a fibronectin-binding
 CC domain of a fibronectin-binding protein, and inhibit binding of the
 CC protein to fibronectin. Also claimed are: (1) isolated peptides of a
 CC fibronectin-binding protein that do not bind to fibronectin; (2) fusion
 CC protein containing at least one peptide of a fibronectin-binding protein
 CC linked to a second amino acid sequence; (3) nucleic acid encoding the
 CC isolated peptide of (1). Antibodies, the isolated peptides of (1) and the
 CC nucleic acids are all useful for immunisation (active or passive) and (by
 CC inhibiting binding of bacteria to fibronectin) for preventing or treating
 CC infection in humans or other animals, particularly by staphylococci or
 CC streptococci, e.g. meningitis, otitis media, pneumonia, endocarditis,

CC linked to a second amino acid sequence; (3) nucleic acid encoding the
 CC isolated peptide of (1). Antibodies, the isolated peptides of (1) and the
 CC nucleic acids are all useful for immunisation (active or passive) and (by
 CC inhibiting binding of bacteria to fibronectin) for preventing or treating
 CC infection in humans or other animals, particularly by staphylococci or
 CC streptococci, e.g. meningitis, otitis media, pneumonia, endocarditis,
 CC mastitis in cattle, abortion in horses and many others. Since the
 CC antibodies block binding of bacteria, they should be effective against
 CC antibiotic-resistant strains, and may replace antibiotic therapy or
 CC increase its effectiveness. Sequences AAW65691-700 represent a series of
 CC synthetic peptides based on the DI region of S. aureus fibronectin
 CC binding protein A. They were synthesised to contain mutations

XX
 SQ Sequence 38 AA;

Query Match 100.0%; Score 52; DB 2; Length 38;
 Best Local Similarity 100.0%; Pred. No. 0.0085;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGNQSFEDT 10
 |||||
 DB 3 SGNQSFEDT 12

RESULT 10
 AAW65712
 ID AAW65712 standard; peptide; 39 AA.

XX AAW65712;

XX 16-OCT-1998 (first entry)

XX Fibronectin binding protein-derived peptide #56.

KM microbial surface components recognising adhesive matrix molecule;
 KM MSCRAMM; fibronectin; fibronectin-binding protein; antibody; epitope;
 KM antibiotic; bacterial infection; antibiotic-resistant strain.

OS Synthetic.
 OS Staphylococcus aureus.

XX WO9831389-A2.

XX 23-JUL-1998.

XX 21-JAN-1998; 98WO-US001222.

XX 21-JAN-1997; 97US-0036139P.

XX (TEXA) UNIV TEXAS A & M SYSTEM.

PI Hoeoek M, Patti JM, House-Pompeo KL, Speziale P, Joh D;
 PI McGavin MJ;

XX WPI; 1998-413816/35.

PT Antibody that binds to fibronectin-binding protein, preventing its
 binding to fibronectin - used to treat or prevent bacterial infection,
 PT especially by Staphylococci and Streptococci.

XX Example 8; Page 104; 201pp; English.

CC The invention relates to antibodies that bind to a fibronectin-binding
 CC domain of a fibronectin-binding protein, and inhibit binding of the
 CC protein to fibronectin. Also claimed are: (1) isolated peptides of a
 CC fibronectin-binding protein that do not bind to fibronectin; (2) fusion
 CC protein containing at least one peptide of a fibronectin-binding protein
 CC linked to a second amino acid sequence; (3) nucleic acid encoding the
 CC isolated peptide of (1). Antibodies, the isolated peptides of (1) and the
 CC nucleic acids are all useful for immunisation (active or passive) and (by
 CC inhibiting binding of bacteria to fibronectin) for preventing or treating
 CC infection in humans or other animals, particularly by staphylococci or
 CC streptococci, e.g. meningitis, otitis media, pneumonia, endocarditis,

CC mastitis in cattle, abortion in horses and many others. Since the
 CC antibodies block binding of bacteria, they should be effective against
 CC antibiotic-resistant strains, and may replace antibiotic therapy or
 CC increase its effectiveness. The present sequence is shown in the
 CC specification
 CC
 XX

SQ Sequence 39 AA;

Query Match 100.0%; Score 52; DB 2; Length 39;

Best Local Similarity 100.0%; Pred. No. 0.0088; Indels 0; Gaps 0;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SGNQSFEDT 10
 |||||
 Db 3 SGNQSFEDT 12

RESULT 11

ID AAW65713 standard; peptide; 39 AA.

XX AAW65713;

XX 16-OCT-1998 (first entry)

XX Fibronectin binding protein-derived peptide #57.

XX microbial surface components recognising adhesive matrix molecule;

XX MSCRAMM; fibronectin; fibronectin-binding protein; antibody; epitope;

XX antibiotic; bacterial infection; antibiotic-resistant strain.

XX Synthetic.

XX Staphylococcus aureus.

XX WO9831389-A2.

XX 23-JUL-1998.

XX 21-JAN-1998; 98WO-US001222.

XX 21-JAN-1997; 97US-0036139P.

XX (TEXA) UNIV TEXAS A & M SYSTEM.

XX Hoeck M, Patti JM, House-Pompeo KL, Speziale P, Joh D;

XX Mcgavin MJ;

XX WPI; 1998-413816/35.

XX Antibody that binds to fibronectin-binding protein, preventing its

XX binding to fibronectin - used to treat or prevent bacterial infection,

XX especially by Staphylococci and Streptococci.

XX Example 8; Page 104; 201pp; English.

XX The invention relates to antibodies that bind to a fibronectin-binding

XX domain of a fibronectin-binding protein, and inhibit binding of the

XX protein to fibronectin. Also claimed are: (1) isolated peptides of a

XX fibronectin-binding protein that do not bind to fibronectin (2) fusion

XX protein containing at least one peptide of a fibronectin-binding protein

XX linked to a second amino acid sequence; (3) nucleic acid encoding the

XX isolated peptide of (1). Antibodies, the isolated peptides of (1) and the

XX nucleic acids are all useful for immunisation (active or passive) and (by

XX inhibiting binding of bacteria to fibronectin) for preventing or treating

XX infection in humans or other animals, particularly by staphylococci or

XX streptococci, e.g. meningitis, otitis media, pneumonia, endocarditis,

XX mastitis in cattle, abortion in horses and many others. Since the

XX antibodies block binding of bacteria, they should be effective against

XX antibiotic-resistant strains, and may replace antibiotic therapy or

XX increase its effectiveness. The present sequence is shown in the

XX specification
 XX
 XX Sequence 39 AA;

Query Match 100.0%; Score 52; DB 2; Length 39;
 Best Local Similarity 100.0%; Pred. No. 0.0088;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SGNQSFEDT 10
 |||||
 Db 3 SGNQSFEDT 12

RESULT 12

ID AAR58806 standard; protein; 130 AA.

XX AAR58806;

XX 25-MAR-2003 (revised)

XX 30-MAR-1995 (first entry)

XX Fibronectin binding domain D1-D4 (709-838 (P838T)).

XX Fibronectin binding protein; Fbp; fibronectin binding domain;

XX monoclonal antibody; Mab; adhesion; Gram-positive bacterium; bacteremia;

XX Escherichia coli.

XX Staphylococcus aureus.

XX WO9418327-A1.

XX 18-AUG-1994.

XX 04-FEB-1994; 94WO-GB000215.

XX 05-FEB-1993; 93GB-00002289.

XX 20-OCT-1993; 93GB-00021592.

XX (SMK) SMITHKLINE BEECHAM PLC.

XX Burnham MKR, Chopra I, Critchley IA, Knowles DJ;

XX WPI; 1994-279748/34.

XX Fibronectin binding protein and monoclonal antibodies specific for Fbp -

XX devices or wounds.

XX Disclosure; Page 30; 40pp; English.

XX Polypeptides corresponding to residues G709-T886 plus PPIVPT, G709-

XX P838 (P838T) and G709-P838 (AAR58805-07, respectively) of S. aureus J2385

XX (NCIMB 40532) Fbp type A fibronectin binding domain D1-D4 region

XX (AAR58808) were expressed in E. coli BL21 (DE4) and used to raise Mab

XX specific for Fbp. (Updated on 25-MAR-2003 to correct PN field.)

XX Sequence 130 AA;

Qy 1 SGNQSFEDT 10
 |||||
 Db 4 SGNQSFEDT 13

RESULT 13

ID AAR58807 standard; protein; 130 AA.

XX AAR58807;

XX 25-MAR-2003 (revised)

XX 30-MAR-1995 (first entry)

XX Fibronectin binding domain D1-D4 (709-838).
 DE Fibronectin binding protein; Fbp; fibronectin binding domain;
 XX monoclinal antibody; Mab; adhesion; Gram-positive bacterium; bacteremia;
 KW Escherichia coli.
 XX Staphylococcus aureus.
 OS
 XX WO9418327-A1.
 PN
 XX 18-AUG-1994.
 PD
 XX 04-FEB-1994; 94WO-GB000215.
 PF
 XX 05-FEB-1993; 93GB-0002289.
 PR 20-OCT-1993; 93GB-00021592.
 XX
 XX (SMIK) SMITHKLINE BEECHAM PLC.
 PA
 XX Burnham MKR, Chopra I, Critchley IA, Knowles DJC;
 PI WPI; 1994-279748/34.
 DR
 XX Fibronectin binding protein and monoclonal antibodies specific for Fbp -
 PT useful to prevent adherence of Gram-positive bacteria to indwelling
 PT devices or wounds.
 PT
 XX
 PS Disclosure; Page 30; 40pp; English.
 XX
 XX Polypeptides corresponding to residues G709-T886 plus PPIVPT, G709-
 CC P838(P838T) and G709-P838 (AAR58805-07, respectively) of S. aureus J5385
 CC (NCIMB 40532) Fbp type A fibronectin binding domain D1-D4 region
 CC (AAR58808) were expressed in E. coli BL21(DE4) and used to raise MAb
 CC specific for Fbp. (Updated on 25-MAR-2003 to correct PN field.)
 CC
 XX Sequence 130 AA;
 SQ
 Query Match 100.0%; Score 52; DB 2; Length 130;
 Best Local Similarity 100.0%; Pred. No. 0.036;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 SGNQSFEDT 10
 DB 4 SGNQSFEDT 13
 XX
 XX RESULT 14
 ID AAR91202 standard; peptide; 130 AA.
 XX AAR91202;
 AC AAR91202;
 XX
 XX 13-NOV-1996 (first entry)
 DT
 XX
 XX D1-D4 fibronectin binding domains.
 DE
 XX Fibronectin; oral hygiene; gingivitis; gum disease; adhesion;
 KW periodontitis; oral pathogens; caries; calculus; candidiasis; oral surgery;
 KW tissue regeneration; irrigation; toothpaste; dentifrice; mouthwash;
 KW lozenge.
 XX
 XX Staphylococcus aureus.
 OS
 XX WO9604003-A1.
 PN
 XX 15-FEB-1996.
 PD
 XX 18-JUL-1995; 95WO-EP002825.
 PF
 XX 05-AUG-1994; 94GB-00015902.
 PR
 XX (SMIK) SMITHKLINE BEECHAM PLC.
 PA

XX Barnett P, Critchley IA, Dodd I;
 PI WPI; 1996-129122/13.
 DR
 XX Prevention of adherence of oral pathogens in the oral cavity, partic.
 PT tooth surfaces - by application of a fibronectin binding protein or
 PT polypeptide or a monoclonal antibody or fragment against it.
 PT
 XX
 XX Claim 5; Page 32; 41pp; English.
 PS
 XX Adherence of oral pathogens, particularly to tooth surfaces, can be
 CC prevented by application of a fibronectin binding protein or polypeptide.
 CC The fibronectin binding protein or polypeptide is useful in the
 CC manufacture of oral hygiene compositions, eg. toothpaste, liquid
 CC dentifrice, mouthwash or lozenge. They are useful to prevent the plaque-
 CC related development of carious lesions, gingivitis, calculus or
 CC periodontal disease and to combat oral cavity infections, e.g.
 CC candidiasis. They may also be useful in oral surgery e.g. in guided
 CC tissue regeneration procedures to prevent subsequent bacterial infection,
 CC and for irrigation of periodontal pockets. This sequence corresponds to
 CC amino acids 709-838 of the D1-D4 fibronectin binding domain of
 CC Staphylococcus aureus
 CC
 XX Sequence 130 AA;
 SQ
 Query Match 100.0%; Score 52; DB 2; Length 130;
 Best Local Similarity 100.0%; Pred. No. 0.036;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 SGNQSFEDT 10
 DB 4 SGNQSFEDT 13
 XX
 XX RESULT 15
 ID AAR91201 standard; peptide; 130 AA.
 XX AAR91201;
 AC AAR91201;
 XX
 XX 13-NOV-1996 (first entry)
 DT
 XX
 XX D1-D4 fibronectin binding domains.
 DE
 XX Fibronectin; oral hygiene; gingivitis; gum disease; adhesion;
 KW periodontitis; oral pathogens; caries; calculus; candidiasis; oral surgery;
 KW tissue regeneration; irrigation; toothpaste; dentifrice; mouthwash;
 KW lozenge.
 XX
 XX Staphylococcus aureus.
 OS
 XX WO9604003-A1.
 PN
 XX 15-FEB-1996.
 PD
 XX 18-JUL-1995; 95WO-EP002825.
 PF
 XX 05-AUG-1994; 94GB-00015902.
 PR
 XX (SMIK) SMITHKLINE BEECHAM PLC.
 PA
 XX Barnett P, Critchley IA, Dodd I;
 PI WPI; 1996-129122/13.
 DR
 XX Prevention of adherence of oral pathogens in the oral cavity, partic.
 PT tooth surfaces - by application of a fibronectin binding protein or
 PT polypeptide or a monoclonal antibody or fragment against it.
 PT
 XX
 XX Claim 5; Page 31-32; 41pp; English.
 PS
 XX Adherence of oral pathogens, particularly to tooth surfaces, can be

CC prevented by application of a fibronectin binding protein or polypeptide.
CC The fibronectin binding protein or polypeptide is useful in the
CC manufacture of oral hygiene compositions, eg. toothpaste, liquid
CC dentifrice, mouthwash or lozenge. They are useful to prevent the plaque-
CC related development of carious lesions, gingivitis, calculus or
CC periodontal disease and to combat oral cavity infections, e.g.
CC candidiasis. They may also be useful in oral surgery e.g. in guided
CC tissue regeneration procedures to prevent subsequent bacterial infection,
CC and for irrigation of periodontal pockets. This sequence corresponds to
CC amino acids 709-838 of the D1-D4 fibronectin binding domain of
CC Staphylococcus aureus with a P838T substitution
XX

Sequence 130 AA:

Query Match 100.0%; Score 52; DB 2; Length 130;
Best Local Similarity 100.0%; Pred. No. 0.036;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGNQSFEDT 10
| | | | | | | | | |
Db 4 SGNQSFEDT 13

Search completed: October 25, 2005, 20:21:10
Job time : 22.112 secs

(bidsn) MJD 06/10/11

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OM protein - protein search, using SW model

Run on: October 22, 2005, 03:51:22 ; Search time 5.57166 Seconds
(without alignments)
133.980 Million cell updates/sec

Title: US-10-731-238-64

Perfect score: 52

Sequence: 1 SGNQSFEDPT 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

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Issued Patents AA: *
1: /cgn2_6/ptodata/1/1aa/5A COMB.pep: *
2: /cgn2_6/ptodata/1/1aa/5B COMB.pep: *
3: /cgn2_6/ptodata/1/1aa/6A COMB.pep: *
4: /cgn2_6/ptodata/1/1aa/6B COMB.pep: *
5: /cgn2_6/ptodata/1/1aa/PCUS COMB.pep: *
6: /cgn2_6/ptodata/1/1aa/backfile1.pep: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	52	100.0	10	4	US-09-010-317-64
2	52	100.0	38	1	US-08-234-622A-2
3	52	100.0	38	1	US-08-729-767-3
4	52	100.0	38	4	US-09-010-317-5
5	52	100.0	38	4	US-09-010-317-6
6	52	100.0	38	4	US-09-010-317-40
7	52	100.0	38	4	US-09-010-317-41
8	52	100.0	38	4	US-09-010-317-42
9	52	100.0	38	4	US-09-010-317-43
10	52	100.0	39	4	US-09-010-317-56
11	52	100.0	39	4	US-09-010-317-57
12	52	100.0	114	1	US-08-259-000-3
13	52	100.0	130	2	US-08-459-135A-7
14	52	100.0	130	2	US-08-459-135A-8
15	52	100.0	130	3	US-08-495-559-7
16	52	100.0	130	3	US-08-495-559-8
17	52	100.0	139	3	US-08-856-253-8
18	52	100.0	174	2	US-08-459-135A-10
19	52	100.0	174	2	US-08-459-135A-13
20	52	100.0	174	2	US-08-495-559-10
21	52	100.0	174	3	US-08-495-559-13
22	52	100.0	176	3	US-08-495-559-6
23	52	100.0	178	2	US-08-459-135A-12
24	52	100.0	178	3	US-08-495-559-12
25	52	100.0	181	2	US-08-459-135A-6
26	52	100.0	559	4	US-08-956-171E-5251
27	52	100.0	559	4	US-08-781-986A-5251

28	52	100.0	1027	4	US-08-956-171E-5254	Sequence 5254, Ap
29	52	100.0	1027	4	US-08-781-986A-5254	Sequence 5254, Ap
30	48	92.3	10	4	US-09-010-317-83	Sequence 83, Ap
31	48	92.3	36	4	US-09-010-317-58	Sequence 58, Ap
32	48	92.3	36	4	US-09-010-317-59	Sequence 59, Ap
33	48	92.3	38	1	US-08-234-622A-3	Sequence 3, Ap
34	48	92.3	38	1	US-08-729-767-4	Sequence 4, Ap
35	48	92.3	38	4	US-09-010-317-7	Sequence 7, Ap
36	48	92.3	38	4	US-09-010-317-8	Sequence 8, Ap
37	48	92.3	38	4	US-09-010-317-49	Sequence 49, Ap
38	47	90.4	38	4	US-09-010-317-39	Sequence 39, Ap
39	46	88.5	38	4	US-09-010-317-36	Sequence 36, Ap
40	46	88.5	38	4	US-09-010-317-37	Sequence 37, Ap
41	45	86.5	38	4	US-09-010-317-38	Sequence 38, Ap
42	42	80.8	10	4	US-09-010-317-65	Sequence 65, Ap
43	42	80.8	10	4	US-09-010-317-84	Sequence 84, Ap
44	42	80.8	38	4	US-09-010-317-35	Sequence 35, Ap
45	42	80.8	38	4	US-09-010-317-46	Sequence 46, Ap

ALIGNMENTS

RESULT 1
US-09-010-317-64
Sequence 64, Application US/09010317
Patent No. 6685943
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
APPLICANT: Patti, Joseph M.
APPLICANT: House-Pompeo, Karen L.
APPLICANT: Speziale, Pietro
APPLICANT: Jon, Danny
APPLICANT: McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAMK.189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 64:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-09-010-317-64
Query Match 100.0%; Score 52; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.00057;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SGNOSFEEDT 10
|||||
Db 1 SGNOSFEEDT 10

RESULT 2

US-08-234-622A-2
; Sequence 2, Application US/08234622A
; Patent No. 5440014
; GENERAL INFORMATION:
; APPLICANT: HOOK, Magnus
; APPLICANT: MCGAVIN, Martin
; APPLICANT: RAUCCI, Giuseppe
; TITLE OF INVENTION: A FIBRONECTIN BINDING PEPTIDE
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Doane, Swecker & Mathis
; STREET: P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22131-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/234,622A
; FILING DATE: 28-APR-1994
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: SE 9002617-0
; FILING DATE: 10-AUG-1990
; PRIOR APPLICATION DATA: WO PCT/SE91/00534
; APPLICATION NUMBER: NO PCT/SE91/00534
; FILING DATE: 09-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Meuth, Donna M
; REGISTRATION NUMBER: 36,607
; REFERENCE/DOCKET NUMBER: 012885-044
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 38 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-234-622A-2

Query Match 100.0%; Score 52; DB 1; Length 38;
Best Local Similarity 100.0%; Pred. No. 0.0027;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SGNOSFEEDT 10
|||||
Db 3 SGNOSFEEDT 12

RESULT 3

US-08-729-767-3
; Sequence 3, Application US/08729767
; Patent No. 5770702
; GENERAL INFORMATION:
; APPLICANT: HOOK, Magnus
; APPLICANT: LINDBERG, Martin Kjell
; APPLICANT: SIGNAS, Lars Christer
; APPLICANT: MADSTROM, Torkel Mikael

APPLICANT: FROMAN, Gunnar
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN AS WELL AS
; TITLE OF INVENTION: ITS PREPARATION
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Doane, Swecker & Mathis, L.L.P.
; STREET: P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22131-1404

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/729,767
; FILING DATE: 07-OCT-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/259,000
; FILING DATE: 13-JUN-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/007,817
; FILING DATE: 22-JAN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/201,028
; FILING DATE: 01-JUN-1988
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: SE 8702272-9
; FILING DATE: 01-JUN-1987
; ATTORNEY/AGENT INFORMATION:
; NAME: McGowan, Malcolm K.
; REGISTRATION NUMBER: 39,300
; REFERENCE/DOCKET NUMBER: 012889-036
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 38 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-729-767-3

Query Match 100.0%; Score 52; DB 1; Length 38;
Best Local Similarity 100.0%; Pred. No. 0.0027;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SGNOSFEEDT 10
|||||
Db 4 SGNOSFEEDT 13

RESULT 4

US-09-010-317-5
; Sequence 5, Application US/09010317
; Patent No. 6685943
; GENERAL INFORMATION:
; APPLICANT: HOOK, Magnus
; APPLICANT: Patti, Joseph M.
; APPLICANT: House-Pompeo, Karen L.
; APPLICANT: Speciale, Pietro
; APPLICANT: Joh, Danny
; APPLICANT: McGavin, Martin J.
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
; TITLE OF INVENTION: AND METHODS OF USE
; NUMBER OF SEQUENCES: 105
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee

STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/036,139
ATTORNEY/AGENT INFORMATION:
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAMK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-09-010-317-5
Query Match 100.0%; Score 52; DB 4; Length 38;
Best Local Similarity 100.0%; Pred. No. 0.0027;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 SGNOSFEEDT 10
Db 3 SGNOSFEEDT 12
RESULT 5
US-09-010-317-6
Sequence 6, Application US/09010317
Patent No. 6685943
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
APPLICANT: Patti, Joseph M.
APPLICANT: House-Pompeo, Karen L.
APPLICANT: Speziale, Pietro
APPLICANT: Joh, Danny
APPLICANT: McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
TITLE OF INVENTION: AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/036,139

FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAMK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-09-010-317-6
Query Match 100.0%; Score 52; DB 4; Length 38;
Best Local Similarity 100.0%; Pred. No. 0.0027;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 SGNOSFEEDT 10
Db 3 SGNOSFEEDT 12
RESULT 6
US-09-010-317-40
Sequence 40, Application US/09010317
Patent No. 6685943
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
APPLICANT: Patti, Joseph M.
APPLICANT: House-Pompeo, Karen L.
APPLICANT: Speziale, Pietro
APPLICANT: Joh, Danny
APPLICANT: McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
TITLE OF INVENTION: AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAMK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 40:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-09-010-317-40

Query Match 100.0%; Score 52; DB 4; Length 38;
Best Local Similarity 100.0%; Pred. No. 0.0027;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGNOSFEEDT 10
| | | | | | | | | |
DB 3 SGNOSFEEDT 12

RESULT 7
US-09-010-317-41

; Sequence 41, Application US/09010317
; Patent No. 6685943
; GENERAL INFORMATION:
; APPLICANT: Hook, Magnus
; APPLICANT: Patti, Joseph M.
; APPLICANT: House-Pompeo, Karen L.
; APPLICANT: Speziale, Pietro
; APPLICANT: Joh, Danny
; APPLICANT: McGavin, Martin J.
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
; TITLE OF INVENTION: AND METHODS OF USE
; NUMBER OF SEQUENCES: 105
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: TX
; COUNTRY: USA
; ZIP: 77210-4433
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/010,317
; FILING DATE:
; STRANDEDNESS:
; TOPOLOGY: linear
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/036,139
; FILING DATE: 21-JAN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Hibler, David W.
; REGISTRATION NUMBER: 41,071
; REFERENCE/DOCKET NUMBER: TANK:189
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 512-418-3000
; TELEFAX: 512-474-7577
; INFORMATION FOR SEQ. ID NO: 41:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 38 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; US-09-010-317-41

Query Match 100.0%; Score 52; DB 4; Length 38;
Best Local Similarity 100.0%; Pred. No. 0.0027;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGNOSFEEDT 10
| | | | | | | | | |
DB 3 SGNOSFEEDT 12

RESULT 8
US-09-010-317-42

; Sequence 42, Application US/09010317
; Patent No. 6685943
; GENERAL INFORMATION:
; APPLICANT: Hook, Magnus
; APPLICANT: Patti, Joseph M.

; APPLICANT: House-Pompeo, Karen L.
; APPLICANT: Speziale, Pietro
; APPLICANT: Joh, Danny
; APPLICANT: McGavin, Martin J.
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
; TITLE OF INVENTION: AND METHODS OF USE
; NUMBER OF SEQUENCES: 105
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: TX
; COUNTRY: USA
; ZIP: 77210-4433
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/010,317
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/036,139
; FILING DATE: 21-JAN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Hibler, David W.
; REGISTRATION NUMBER: 41,071
; REFERENCE/DOCKET NUMBER: TANK:189
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 512-418-3000
; TELEFAX: 512-474-7577
; INFORMATION FOR SEQ. ID NO: 42:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 38 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; US-09-010-317-42

Query Match 100.0%; Score 52; DB 4; Length 38;
Best Local Similarity 100.0%; Pred. No. 0.0027;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGNOSFEEDT 10
| | | | | | | | | |
DB 3 SGNOSFEEDT 12

RESULT 9
US-09-010-317-43

; Sequence 43, Application US/09010317
; Patent No. 6685943
; GENERAL INFORMATION:
; APPLICANT: Hook, Magnus
; APPLICANT: Patti, Joseph M.
; APPLICANT: House-Pompeo, Karen L.
; APPLICANT: Speziale, Pietro
; APPLICANT: Joh, Danny
; APPLICANT: McGavin, Martin J.
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
; TITLE OF INVENTION: AND METHODS OF USE
; NUMBER OF SEQUENCES: 105
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: TX
; COUNTRY: USA
; ZIP: 77210-4433
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAMK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 43:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-09-010-317-43

Query Match 100.0%; Score 52; DB 4; Length 38;
Best Local Similarity 100.0%; Pred. No. 0.0027;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGNOSFEEDT 10
|||||

Db 3 SGNOSFEEDT 12

RESULT 10
US-09-010-317-56
Sequence 56, Application US/09010317
Patent No. 6685943
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
APPLICANT: Patti, Joseph M.
APPLICANT: House-Pompeo, Karen L.
APPLICANT: Speziale, Pietro
APPLICANT: John, Danny
APPLICANT: McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
TITLE OF INVENTION: AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAMK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 57:
SEQUENCE CHARACTERISTICS:
LENGTH: 39 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-09-010-317-57

Query Match 100.0%; Score 52; DB 4; Length 39;
Best Local Similarity 100.0%; Pred. No. 0.0027;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGNOSFEEDT 10
|||||

Db 3 SGNOSFEEDT 12

TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 56:
SEQUENCE CHARACTERISTICS:
LENGTH: 39 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-09-010-317-56

Query Match 100.0%; Score 52; DB 4; Length 39;
Best Local Similarity 100.0%; Pred. No. 0.0027;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGNOSFEEDT 10
|||||

Db 3 SGNOSFEEDT 12

RESULT 11
US-09-010-317-57
Sequence 57, Application US/09010317
Patent No. 6685943
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
APPLICANT: Patti, Joseph M.
APPLICANT: House-Pompeo, Karen L.
APPLICANT: Speziale, Pietro
APPLICANT: John, Danny
APPLICANT: McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
TITLE OF INVENTION: AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAMK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 57:
SEQUENCE CHARACTERISTICS:
LENGTH: 39 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-09-010-317-57

Query Match 100.0%; Score 52; DB 4; Length 39;
Best Local Similarity 100.0%; Pred. No. 0.0027;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGNOSFEEDT 10
|||||

Db 3 SGNOSFEEDT 12

RESULT 12
US-08-259-000-3
Sequence 3, Application US/08259000
Patent No. 5571514
GENERAL INFORMATION:
APPLICANT: HOOK, Magnus
APPLICANT: LINDERBERG, Martin Kjell
APPLICANT: SIGNAS, Lars Christer
APPLICANT: MADSTROM, Torkel Mikael
APPLICANT: FROMAN, Gunnar
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN AS WELL AS
TITLE OF INVENTION: ITS PREPARATION
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Burns, Doane, Swecker & Mathis
STREET: P.O. Box 1404
CITY: Alexandria
STATE: Virginia
COUNTRY: United States
ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Releasee #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/259,000
FILING DATE: 13-JUN-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: SE 8702272-9
FILING DATE: 01-JUN-1987
ATTORNEY/AGENT INFORMATION:
NAME: Meuth, Donna M
REGISTRATION NUMBER: 36,607
REFERENCE/DOCKET NUMBER: 012885-062
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 114 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-259-000-3

Query Match 100.0%; Score 52; DB 1; Length 114;
Best Local Similarity 100.0%; Pred. No. 0.0094;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGNOSFEEDT 10
DB 4 SGNOSFEEDT 13

RESULT 13
US-08-459-135A-7
Sequence 7, Application US/08459135A
Patent No. 5955078
GENERAL INFORMATION:
APPLICANT: BURNHAM, Martin Karl Russel
APPLICANT: CHOPRA, Ian
APPLICANT: CRITCHLEY, Ian Alfred
APPLICANT: KNOWLES, David Justin Charles
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN: MONOCLONAL ANTIBODY AND THEIR US
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road

CITY: King of Prussia
STATE: PA
COUNTRY: U.S.A.
ZIP: 19406-0939
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: Fastseq, Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/459,135A
FILING DATE: 02-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB/94/00215
FILING DATE: 04-Feb-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Gimm, Edward R
REGISTRATION NUMBER: 38,891
REFERENCE/DOCKET NUMBER: P30591C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-4478
TELEFAX: 610-270-5090
TELEX:
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 130 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-459-135A-7

Query Match 100.0%; Score 52; DB 2; Length 130;
Best Local Similarity 100.0%; Pred. No. 0.011;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGNOSFEEDT 10
DB 4 SGNOSFEEDT 13

RESULT 14
US-08-459-135A-8
Sequence 8, Application US/08459135A
Patent No. 5955078
GENERAL INFORMATION:
APPLICANT: BURNHAM, Martin Karl Russel
APPLICANT: CHOPRA, Ian
APPLICANT: CRITCHLEY, Ian Alfred
APPLICANT: KNOWLES, David Justin Charles
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN: MONOCLONAL ANTIBODY AND THEIR US
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
STATE: PA
COUNTRY: U.S.A.
ZIP: 19406-0939
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: Fastseq, Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/459,135A
FILING DATE: 02-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB/94/00215
FILING DATE: 04-Feb-1994
CLASSIFICATION: 435

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; ATTORNEY/AGENT INFORMATION:
;   NAME: Gimmil, Edward R
;   REGISTRATION NUMBER: 38,891
;   REFERENCE/DOCKET NUMBER: P30591C2
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: 610-270-4478
;   TELEFAX: 610-270-5090
;   TELETYPE:
;   INFORMATION FOR SEQ ID NO: 8:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH: 130 amino acids
;     TYPE: amino acid
;     TOPOLOGY: linear
;   MOLECULE TYPE: protein
;
US-08-459-135A-8

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Query Match      100.0%; Score 52; DB 2; Length 130;
Best Local Similarity 100.0%; Pred. No. 0.011;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      1 SGNQSFEDT 10
      |||||
Db      4 SGNQSFEDT 13

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RESULT 15
US-08-495-559-7
; Sequence 7, Application US/08495559A
; Patent No. 6054572
; GENERAL INFORMATION:
;   APPLICANT: BURMAN, Martin Karl Russel
;   APPLICANT: CHOPRA, Ian
;   APPLICANT: CRITCHLEY, Ian Alfred
;   APPLICANT: KNOWLES, David Justin Charles
;   TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN: MONOCLONAL
;   TITLE OF INVENTION: ANTIBODY AND THEIR USE IN PREVENTING BACTERIAL ADHESION
;   FILE REFERENCE: P30591
;   CURRENT APPLICATION NUMBER: US/08/495,559A
;   CURRENT FILING DATE: 1995-08-03
;   EARLIER APPLICATION NUMBER: GB 9302289.5
;   EARLIER FILING DATE: 1993-02-05
;   EARLIER APPLICATION NUMBER: GB 9321592.9
;   EARLIER FILING DATE: 1993-10-20
;   NUMBER OF SEQ ID NOS: 13
;   SOFTWARE: FastSeq for Windows Version 3.0
;   SEQ ID NO 7
;   LENGTH: 130
;   TYPE: PRT
;   ORGANISM: Staphylococcus aureus
US-08-495-559-7

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Query Match      100.0%; Score 52; DB 3; Length 130;
Best Local Similarity 100.0%; Pred. No. 0.011;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      1 SGNQSFEDT 10
      |||||
Db      4 SGNQSFEDT 13

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Job time : 5.62166 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 22, 2005, 11:35:03 ; Search time 18.4541 Seconds
(without alignments)
226.232 Million cell updates/sec

Title: US-10-731-238-64

Perfect score: 52

Sequence: 1 SGNQSFEDT 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1862951 seqs, 417491010 residues

Total number of hits satisfying chosen parameters: 1862951

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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2: /cgn2_6/prodata/2/pubpaa/PCT_NEW_PUB.pep:*
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11: /cgn2_6/prodata/2/pubpaa/US09C_PUBCOMB.pep:*
12: /cgn2_6/prodata/2/pubpaa/US09_NEW_PUB.pep:*
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22: /cgn2_6/prodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	52	100.0	10	US-10-731-238-64	Sequence 64, Appl
2	52	100.0	38	US-10-731-238-5	Sequence 5, Appl
3	52	100.0	38	US-10-731-238-6	Sequence 6, Appl
4	52	100.0	38	US-10-731-238-40	Sequence 40, Appl
5	52	100.0	38	US-10-731-238-41	Sequence 41, Appl
6	52	100.0	38	US-10-731-238-42	Sequence 42, Appl
7	52	100.0	38	US-10-731-238-43	Sequence 43, Appl
8	52	100.0	39	US-10-731-238-56	Sequence 56, Appl
9	52	100.0	39	US-10-731-238-57	Sequence 57, Appl
10	52	100.0	139	US-09-813-820-8	Sequence 8, Appl
11	52	100.0	388	US-08-901-062-1	Sequence 1, Appl

12	52	100.0	559	US-08-781-986A-5251	Sequence 5251, Ap
13	52	100.0	559	US-10-329-624-5251	Sequence 5251, Ap
14	52	100.0	767	US-09-815-242-5899	Sequence 5899, Ap
15	52	100.0	767	US-09-815-242-13140	Sequence 13140, A
16	52	100.0	940	US-10-470-048B-424	Sequence 424, App
17	52	100.0	948	US-10-470-048B-69	Sequence 69, Appl
18	52	100.0	961	US-10-283-122A-43778	Sequence 43778, A
19	52	100.0	978	US-09-815-242-54567	Sequence 5456, Ap
20	52	100.0	1001	US-09-815-242-12686	Sequence 12686, A
21	52	100.0	1018	US-09-815-242-57977	Sequence 5797, Ap
22	52	100.0	1018	US-09-815-242-12838	Sequence 12838, A
23	52	100.0	1018	US-10-470-048B-68	Sequence 68, Appl
24	52	100.0	1027	US-08-781-986A-5254	Sequence 5254, Ap
25	52	100.0	1027	US-10-329-624-5254	Sequence 5254, Ap
26	52	100.0	1038	US-10-283-122A-43827	Sequence 43827, A
27	49	94.2	30	US-10-287-821-1	Sequence 1, Appl
28	49	94.2	31	US-10-287-821-2	Sequence 2, Appl
29	48	92.3	10	US-10-731-238-83	Sequence 83, Appl
30	48	92.3	36	US-10-731-238-58	Sequence 58, Appl
31	48	92.3	36	US-10-731-238-59	Sequence 59, Appl
32	48	92.3	38	US-10-731-238-7	Sequence 7, Appl
33	48	92.3	38	US-10-731-238-8	Sequence 8, Appl
34	48	92.3	38	US-10-731-238-49	Sequence 49, Appl
35	47	90.4	38	US-10-731-238-39	Sequence 39, Appl
36	46	88.5	38	US-10-731-238-36	Sequence 36, Appl
37	46	88.5	38	US-10-731-238-37	Sequence 37, Appl
38	45	86.5	38	US-10-731-238-38	Sequence 38, Appl
39	42	80.8	10	US-10-731-238-65	Sequence 65, Appl
40	42	80.8	10	US-10-731-238-84	Sequence 84, Appl
41	42	80.8	38	US-10-731-238-35	Sequence 35, Appl
42	42	80.8	38	US-10-731-238-46	Sequence 46, Appl
43	42	80.8	38	US-10-731-238-47	Sequence 47, Appl
44	41	78.8	10	US-10-731-238-63	Sequence 63, Appl
45	41	78.8	18	US-10-731-238-48	Sequence 48, Appl

ALIGNMENTS

RESULT 1
US-10-731-238-64
Sequence 64, Application US/10731238
Publication No US20050123552A1
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
Patli, Joseph M.
House-Pompeo, Karen L.
Speziale, Pietro
Joh, Danny
McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/731.238
FILING DATE: 10-Dec-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/010.317
FILING DATE: 21-Jan-1998
APPLICATION NUMBER: US 60/036,139

FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAMK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 64:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 64:
US-10-731-238-64

Query Match 100.0%; Score 52; DB 18; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.0037;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGNOSFEEDT 10
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Db 1 SGNOSFEEDT 10

RESULT 2
US-10-731-238-5
Sequence 5, Application US/10731238
Publication No. US20050123552A1
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
Patti, Joseph M.
House-Pompeo, Karen L.
Speziale, Pietro
Jon, Danny
McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/731,238
FILING DATE: 10-Dec-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE: 21-Jan-1998
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAMK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>

TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-10-731-238-5

Query Match 100.0%; Score 52; DB 18; Length 38;
Best Local Similarity 100.0%; Pred. No. 0.016;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGNOSFEEDT 10
|||||
Db 3 SGNOSFEEDT 12

RESULT 3
US-10-731-238-6
Sequence 6, Application US/10731238
Publication No. US20050123552A1
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
Patti, Joseph M.
House-Pompeo, Karen L.
Speziale, Pietro
Jon, Danny
McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/731,238
FILING DATE: 10-Dec-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE: 21-Jan-1998
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAMK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-10-731-238-6

Query Match 100.0%; Score 52; DB 18; Length 38;
Best Local Similarity 100.0%; Pred. No. 0.016;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGNOSFEEDT 10
|||||
Db 3 SGNOSFEEDT 12


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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/731,238
FILING DATE: 10-Dec-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE: 21-Jan-1998
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-Jan-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAMK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 42:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 42:
US-10-731-238-42

Query Match      100.0%; Score 52; DB 18; Length 38;
Best Local Similarity 100.0%; Pred. No. 0.016;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 SGNOSFEEDT 10
Db      3 SGNOSFEEDT 12

RESULT 7
US-10-731-238-43
Sequence 43, Application US/10731238
Publication No. US20050123552A1
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
Patel, Joseph M.
House-Pompeo, Karen L.
Speziale, Pietro
Joh, Danny
McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/731,238
FILING DATE: 10-Dec-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE: 21-Jan-1998
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-Jan-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAMK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 42:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 42:
US-10-731-238-42

Query Match      100.0%; Score 52; DB 18; Length 38;
Best Local Similarity 100.0%; Pred. No. 0.016;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 SGNOSFEEDT 10
Db      3 SGNOSFEEDT 12
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 43:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 43:
US-10-731-238-43

Query Match      100.0%; Score 52; DB 18; Length 38;
Best Local Similarity 100.0%; Pred. No. 0.016;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 SGNOSFEEDT 10
Db      3 SGNOSFEEDT 12

RESULT 8
US-10-731-238-56
Sequence 56, Application US/10731238
Publication No. US20050123552A1
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
Patel, Joseph M.
House-Pompeo, Karen L.
Speziale, Pietro
Joh, Danny
McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/731,238
FILING DATE: 10-Dec-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE: 21-Jan-1998
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-Jan-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAMK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 56:
SEQUENCE CHARACTERISTICS:
LENGTH: 39 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 56:
US-10-731-238-56

Query Match      100.0%; Score 52; DB 18; Length 39;
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Best Local Similarity 100.0%; Pred. No. 0.017;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGNOSFEEDT 10
|||||
Db 3 SGNOSFEEDT 12

RESULT 9

US-10-731-238-57
Sequence 57, Application US/10731238
Publication No. US20050123552A1
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
Patti, Joseph M.
House-Pompeo, Karen L.
Speziale, Pietro
John, Danny
McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/731,238
FILING DATE: 10-Dec-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE: 21-Jan-1998
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAMK.189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 57:
SEQUENCE CHARACTERISTICS:
LENGTH: 39 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 57:
US-10-731-238-57
Query Match 100.0%; Score 52; DB 18; Length 39;
Best Local Similarity 100.0%; Pred. No. 0.017;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGNOSFEEDT 10
|||||
Db 3 SGNOSFEEDT 12

RESULT 10
US-09-813-820-8
Sequence 8, Application US/09813820
Patent No. US20020102262A1
GENERAL INFORMATION:

APPLICANT: Hook, Magnus
Patti, Joseph M.
House-Pompeo, Karen
Stinam, Narayana
Symersky, Jindrich
TITLE OF INVENTION: COLLAGEN BINDING PROTEIN COMPOSITIONS
AND METHODS OF USE
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: Texas
COUNTRY: U.S.
ZIP: 77210

COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/813,820
FILING DATE: 22-Mar-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/856,253
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Kitchell, Barbara S.
REGISTRATION NUMBER: 33,928
REFERENCE/DOCKET NUMBER: TAMK.193
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
TELEFAX: (512) 474-7577
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 139 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-09-813-820-8
Query Match 100.0%; Score 52; DB 9; Length 139;
Best Local Similarity 100.0%; Pred. No. 0.068;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGNOSFEEDT 10
|||||
Db 18 SGNOSFEEDT 27

RESULT 11
US-08-901-062-1
Sequence 1, Application US/08901062
Publication No. US20020025324A1
GENERAL INFORMATION:
APPLICANT: SEALS, JONATHAN R.
TITLE OF INVENTION: RECOMBINANT BIVALENT BACTERIAL VACCINE
AND METHODS OF USE
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: HALE AND DORR LLP
STREET: 60 State Street
CITY: Boston
STATE: MA
COUNTRY: United States Of America
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/901,062
FILING DATE: 25-JUL-1997
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Baker, Hollie L.
REGISTRATION NUMBER: 31,321
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 526-6000
TELEFAX: (617) 526-5000
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 388 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHEICAL: NO
ANTI-SENSE: NO
US-08-901-062-1

Query Match 100.0%; Score 52; DB 8; Length 388;
Best Local Similarity 100.0%; Pred. No. 0.21;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SGNOSFEEDT 10
Db 267 SGNOSFEEDT 276

RESULT 12
US-08-781-986A-5251
Sequence 5251, Application US/08781986A
Publication No. US2003005436A1
GENERAL INFORMATION:
APPLICANT: Charles Kunsch
TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
NUMBER OF SEQUENCES: 5255
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COUNTRY: USA
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4MB storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/781,986A
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Benson, Bob
REGISTRATION NUMBER: 30,446
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 5251:
SEQUENCE CHARACTERISTICS:
LENGTH: 559 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-781-986A-5251

Query Match 100.0%; Score 52; DB 8; Length 559;
Best Local Similarity 100.0%; Pred. No. 0.31;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SGNOSFEEDT 10
Db 303 SGNOSFEEDT 312

RESULT 13
US-10-329-624-5251
Sequence 5251, Application US/10329624
Publication No. US20040043037A1
GENERAL INFORMATION:
APPLICANT: Charles Kunsch
GIL H. Choi
Patrick S. Dillon
Craig A. Rosen
Steven C. Barash
Michael R. Fannon
TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
NUMBER OF SEQUENCES: 5256
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COUNTRY: USA
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4MB storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/329,624
FILING DATE: 27-Dec-2002
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/956,171
FILING DATE: October 20, 1997
APPLICATION NUMBER: 60/009,861
FILING DATE: January 5, 1996
APPLICATION NUMBER: 08/781,986
FILING DATE: January 3, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Mark J. Hyman
REGISTRATION NUMBER: 46,789
REFERENCE/DOCKET NUMBER: PB248P1D1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (240) 314-1224
TELEFAX: (301) 309-8439
INFORMATION FOR SEQ ID NO: 5251:
SEQUENCE CHARACTERISTICS:
LENGTH: 559 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 5251:
US-10-329-624-5251

Query Match 100.0%; Score 52; DB 15; Length 559;
Best Local Similarity 100.0%; Pred. No. 0.31;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SGNOSFEEDT 10
Db 303 SGNOSFEEDT 312

RESULT 14
US-09-815-242-5899

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Sequence 5899, Application US/09815242
Patent No. US20020061569A1
GENERAL INFORMATION:
APPLICANT: Haeselbeck, Robert
APPLICANT: Ohlsen, Karl L.
APPLICANT: Zykkind, Judith W.
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John D.
APPLICANT: Carr, Grant J.
APPLICANT: Yamamoto, Robert T.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 5899
LENGTH: 767
TYPE: prt
ORGANISM: Staphylococcus aureus
US-09-815-242-5899

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Query March Similarity      100.0%; Score 52; DB 9; Length 767;
Best Local Similarity      100.0%; Pred. No. 0.44;
Matches    10; Conservative    0; Mismatches    0; Indels    0; Gaps    0;

QY          1 SGNOSFEEDT 10
            |||||
Db           684 SGNOSFEEDT 693

RESULT 15
/ Sequence 13140, Application US/09815242
/ Patent No. US2002061569A1
/ GENERAL INFORMATION:
/ APPLICANT: Haselbeck, Robert
/ APPLICANT: Ohlsen, Karl L.
/ APPLICANT: Zyekind, Judith W.
/ APPLICANT: Wall, Daniel
/ APPLICANT: Trawick, John D.
/ APPLICANT: Carr, Grant J.
/ APPLICANT: Yamamoto, Robert T.
/ APPLICANT: Xu, H. Howard
/ TITLE OF INVENTION: Identification of Essential Genes in
/ TITLE OF INVENTION: Prokaryotes
/ FILE REFERENCE: ELITRA.011A
/ CURRENT APPLICATION NUMBER: US/09/815,242
/ CURRENT FILING DATE: 2001-03-21
/ PRIOR APPLICATION NUMBER: 60/191,078
/ PRIOR FILING DATE: 2000-03-21
/ PRIOR APPLICATION NUMBER: 60/206,848
/ PRIOR FILING DATE: 2000-05-23
/ PRIOR APPLICATION NUMBER: 60/207,727
/ PRIOR FILING DATE: 2000-05-26
/ PRIOR APPLICATION NUMBER: 60/242,578
/ PRIOR FILING DATE: 2000-10-23

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PRIORITY APPLICATION NUMBER: 60/253, 625
PRIORITY FILING DATE: 2000-11-27
PRIORITY APPLICATION NUMBER: 60/257, 931
PRIORITY FILING DATE: 2000-12-22
PRIORITY APPLICATION NUMBER: 60/269, 308
PRIORITY FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 13140
LENGTH: 767
TYPE: PRT
ORGANISM: Staphylococcus aureus
US-09-815-242-13140

Query Match          100.0%;   Score 52;   DB 9;   Length 767;
Best Local Similarity 100.0%;   Pred. No. 0.44;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0.

      1  GGNOSFEEDT 10
      |||||||
      684  GGNOSFEEDT 693

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Search completed: October 22, 2005, 12:09:34
Job time : 18.4541 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 22, 2005, 04:14:19 ; Search time 3.65539 Seconds
(without alignments)
263.219 Million cell updates/sec

Title: US-10-731-238-64

Perfect score: 52
Sequence: 1 SGNQSFEDPT 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : PIR 79:*

1: p1r1:*

2: p1r2:*

3: p1r3:*

4: p1r4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	52	100.0	940	2	S19702 fibronectin-binding
2	52	100.0	961	2	G90053 fibronectin prote
3	52	100.0	1018	2	A32192 fibronectin-binding
4	52	100.0	1038	2	H90053 fibronectin prote
5	40	76.9	461	2	S23420 probable subtilisin
6	37	71.2	429	2	G64649 fibronectin prote
7	36	69.2	323	2	D86847 biotin-labeled CoA
8	35	67.3	72	2	C86714 fibronectin prote
9	35	67.3	167	2	S37843 glutathione peroxi
10	35	67.3	209	2	S61906 protein YNR023w ho
11	35	67.3	234	2	S14469 asparagine-rich pr
12	35	67.3	480	2	T50511 serine-type carbox
13	35	67.3	848	2	T28055 fibronectin prote
14	35	67.3	1351	2	S44665 ZK370.4 protein -
15	35	67.3	2529	2	B64635 toxin-like outer m
16	35	67.3	416	2	S39684 yMDN protein - Bac
17	34	65.4	429	2	G71937 fibronectin prote
18	34	65.4	499	2	A30151 dihydroilpoamide d
19	34	65.4	509	2	D95053 transcription regu
20	34	65.4	526	2	C84993 peptide chain rele
21	34	65.4	526	2	D96977 peptide chain rele
22	34	65.4	531	2	H81928 translation releas
23	34	65.4	531	2	F81176 translation releas
24	34	65.4	538	2	D75381 translation releas
25	34	65.4	540	2	AC2353 peptide-chain rele
26	34	65.4	547	2	S77410 translation releas
27	33	63.5	112	2	G86756 prophage p12 prote
28	33	63.5	170	2	bcl-x short - mous
29	33	63.5	176	2	gene bcl-xshort pr

30	33	63.5	297	1	NBRT apolipoprotein H p
31	33	63.5	333	2	C84792 hypothetical prote
32	33	63.5	457	2	T26642 hypothetical prote
33	33	63.5	533	2	B96777 hypothetical prote
34	33	63.5	539	2	T02508 hypothetical prote
35	33	63.5	705	2	S54521 probable membrane
36	33	63.5	835	2	S63463 hypothetical prote
37	33	63.5	944	2	G86720 translation initia
38	33	63.5	1092	2	S42798 fibronectin-binding
39	33	63.5	1114	2	S51470 fibronectin-binding
40	33	63.5	1117	2	S33851 fibronectin-binding
41	33	63.5	1747	2	A54121 collagen alpha-4 c
42	32	61.5	109	2	S24331 hypothetical prote
43	32	61.5	189	2	C82483 hypothetical prote
44	32	61.5	191	2	AE0412 probable 2'-5' RNA
45	32	61.5	330	2	S46819 hypothetical prote

ALIGNMENTS

RESULT 1
S19702
fibronectin-binding protein B - Staphylococcus aureus
C/Species: Staphylococcus aureus
C/Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
C/Accession: S19702
R./Joensson, K.; Signaef, C.; Mueller, H.P.; Lindberg, M.
Eur. J. Biochem. 202, 1041-1048, 1991
A./Title: Two different genes encode fibronectin binding proteins in Staphylococcus aure
A./Reference number: S19702; PMID:92111475; PMID:1837266
A./Accession: S19702
A./Status: preliminary
A./Molecule type: DNA
A./Residues: 1-940 <JOB>
C./Cross-references: UNIPROT:O53682; EMBL:X62992; NID:949040; PIDN:CAA44726.1; PID:95815
C./Keywords: fibronectin binding

Query Match 100.0%; Score 52; DB 2; Length 940;
Best Local Similarity 100.0%; Pred. No. 0.056;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGNQSFEDPT 10
DB 684 SGNQSFEDPT 693

RESULT 2

G90053
hypothetical protein fmb (imported) - Staphylococcus aureus (strain N315)
C/Species: Staphylococcus aureus
C/Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C/Accession: G90053
R./Kuroda, M.; Ohba, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Ogu

ma, A.; Mizutani, U.; Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kato, C.; Sekimizu, K.;
C./Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
A./Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.

A./Reference number: A89758; PMID:21311952; PMID:11418146
A./Accession: G90053

A./Status: preliminary

A./Molecule type: DNA

A./Residues: 1-961 <KUR>

A./Cross-references: UNIPROT:Q99RD3; GB:BA000018; PID:913702452; PIDN:BA043593.1; GSPDB:

A./Experimental source: strain N315

C./Genetics: fmb

QY 1 SGNQSFEDPT 10

Query Match 100.0%; Score 52; DB 2; Length 961;
Best Local Similarity 100.0%; Pred. No. 0.058;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 695 SGNOSFEEDT 704

RESULT 3

A32192

Fibronectin-binding protein - Staphylococcus aureus

C/Species: Staphylococcus aureus

C/Date: 31-Jul-1989 #sequence_revision 31-Jul-1989 #text_change 16-Feb-1997

C/Accession: A32192

R/Signatures: C.; Raucchi, G.; Jonsson, K.; Lindgren, P.E.; Anantaramaiah, G.M.; Hoeck, M.

Proc. Natl. Acad. Sci. U.S.A. 86, 699-703, 1989

A/Title: Nucleotide sequence of the gene for a fibronectin-binding protein from Staphylococcus aureus

A/Reference number: A32192; PMID:8908998; PMID:2521391

A/Accession: A32192

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-1018 <SIG>

A/Cross-references: GB:J04151

C/Keywords: fibronectin binding

Query Match 100.0%; Score 52; DB 2; Length 1018;
Best Local Similarity 100.0%; Pred. No. 0.062;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 SGNOSFEEDT 10
|||||
748 SGNOSFEEDT 757

RESULT 4

H90053

Hypothetical protein fnb [imported] - Staphylococcus aureus (strain N315)

C/Species: Staphylococcus aureus

C/Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004

C/Accession: H90053

R/Signatures: M.; Ohba, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Ogura, A.; Mizutani-Uji, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Iatco, C.; Sekimizu, K.;

C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.

Lancet 357, 1225-1240, 2001

A/Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.

A/Reference number: A89758; PMID:21311952; PMID:11418146

A/Accession: H90053

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-1038 <KUR>

A/Cross-references: UNIPROT:Q99RD2; GB:BA000018; PID:G13702453; PIDN:BA843594.1; GSPDB:C

A/Experimental source: strain N315

C/Genetics:

A/Gene: fnb

Query Match 100.0%; Score 52; DB 2; Length 1038;
Best Local Similarity 100.0%; Pred. No. 0.063;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 SGNOSFEEDT 10
|||||
744 SGNOSFEEDT 753

RESULT 5

S23420

Probable subtilisin-like proteinase (EC 3.4.21.-) epip - Staphylococcus epidermidis

N/Alternate names: Iantibiotic epidermin biosynthesis protein epip

C/Species: Staphylococcus epidermidis

C/Date: 22-Nov-1993 #sequence_revision 01-Dec-1995 #text_change (9-Jul-2004

C/Accession: S23420

R/Schnell, N.; Engelke, G.; Augustin, J.; Rosenstein, R.; Ungermann, V.; Goetz, F.; Entl

Eur. J. Biochem. 204, 57-68, 1992

A/Title: Analysis of genes involved in the biosynthesis of Iantibiotic epidermin.

A/Reference number: S23413; PMID:92155237; PMID:11740156

A/Accession: S23420

A/Status: preliminary

A/Molecule type: DNA
A/Residues: 1-461 <SCH>
A/Cross-references: UNIPROT:P30199; EMBL:X62386; NID:G46964; PIDN:CAA44257.1; PID:G46971
C/Keywords: hydrolase; serine proteinase

Query Match 76.9%; Score 40; DB 2; Length 461;
Best Local Similarity 77.8%; Pred. No. 5.9;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

1 SGNOSFEED 9
|||||
182 SGNOSFEED 190

RESULT 6

G64649

Hypothetical protein HP1039 - Helicobacter pylori (strain 26695)

C/Species: Helicobacter pylori

C/Date: 09-Aug-1997 #sequence_revision 09-Aug-1997 #text_change 09-Jul-2004

C/Accession: G64649

R/Tomb, J.F.; White, O.; Kervajave, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.D.

Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khalak, H.G.; Glodek, A.; McKen

son, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Wathey, L.

Nature 388, 539-547, 1997

A/Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser, C.

A/Title: The complete genome sequence of the gastric pathogen Helicobacter pylori.

A/Reference number: A64520; PMID:97394467; PMID:9252185

A/Accession: G64649

A/Status: preliminary; nucleic acid sequence not shown; translation not shown

A/Molecule type: DNA

A/Residues: 1-429 <TOM>

A/Cross-references: UNIPROT:Q25682; GB:AE00611; GB:AE00511; NID:G2314173; PIDN:AAD0808

C/Genetics:

A/Start codon: GTG

Query Match 71.2%; Score 37; DB 2; Length 429;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

3 NOSFEED 9
|||||
270 NOSFEED 276

RESULT 7

D86847

biotin-[acetyl-CoA-carboxylase] ligase (EC 6.3.4.15) [imported] - Lactococcus lactis sub

N/Alternate names: bifunctional protein BifA

C/Species: Lactococcus lactis subsp. lactis

C/Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 09-Jul-2004

C/Accession: D86847

R/Bolotin, A.; Wincker, P.; Mueger, S.; Jallion, O.; Malarme, K.; Weissenbach, J.; Ehrli

Genome Res. 11, 731-753, 2001

A/Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis

A/Reference number: A86625; PMID:21235186; PMID:11337471

A/Accession: D86847

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-323 <STO>

A/Cross-references: UNIPROT:Q9CE06; GB:AE005176; PID:G12724804; PIDN:AAK05878.1; GSPDB:C

A/Experimental source: strain IL1403

C/Genetics:

A/Gene: bifA1

C/Keywords: ligase

Query Match 69.2%; Score 36; DB 2; Length 323;
Best Local Similarity 66.7%; Pred. No. 24;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

2 SGNOSFEEDT 10
|||||
62 SGNOSFEEDT 70

RESULT 8
C86714
hypothetical protein yhcC [imported] - Lactococcus lactis subsp. lactis (strain IL1403)
C/Species: Lactococcus lactis subsp. lactis
C/Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 09-Jul-2004
C/Accession: C86714
R/Bolotin, A.; Wincker, P.; Manger, S.; Jallion, O.; Malarme, K.; Weissenbach, J.; Ehrlich
Genome Res. 11, 731-753, 2001
A/Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis s8
A/Reference number: A86625; MUID:21235166; PMID:11337471
A/Accession: C86714
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-72 <STO>
A/Cross-references: UNIPROT:Q9C4L4; GB:AE005176; PID:g12723627; PIDN:AAK04813.1; GSPDB:C
A/Experimental source: strain IL1403
C/Genetics:
A/Gene: yhcC

Query Match 67.3%; Score 35; DB 2; Length 72;
Best Local Similarity 75.0%; Pred. No. 7.4;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 2 GNSQFEED 9
DB 14 GNNFED 21

RESULT 9
S37843
glutathione peroxidase homolog YKL026c - Yeast (Saccharomyces cerevisiae)
C/Species: Saccharomyces cerevisiae
C/Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 09-Jul-2004
C/Accession: S37843
R/Rieger, M.
submitted to the Protein Sequence Database, March 1994
A/Reference number: S37832
A/Accession: S37843
A/Molecule type: DNA
A/Residues: 1-167 <RIE>
A/Cross-references: UNIPROT:P36014; EMBL:Z28026; NID:g486022; PIDN:CAA01861.1; PID:g4860
A/Experimental source: strain S288C
C/Genetics:
A/Gene: SGP:GPX1; MIPS:YKL026c
A/Cross-references: SGD:S0001509
A/Map position: 11L
C/Superfamily: glutathione peroxidase

Query Match 67.3%; Score 35; DB 2; Length 167;
Best Local Similarity 75.0%; Pred. No. 19;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 2 GNSQFEED 9
DB 68 GNSQFEED 75

RESULT 10
S61906
protein YNR023w homolog - Ashbya gossypii (fragment)
C/Species: Ashbya gossypii
C/Date: 19-Mar-1997 #sequence_revision 29-Aug-1997 #text_change 09-Jul-2004
C/Accession: S61906
R/Altman-John, R.; Philippe, P.
Mol. Gen. Genet. 250, 69-80, 1996
A/Title: AGTHR4, a new selection marker for transformation of the filamentous fungus Ash
A/Reference number: S61905; MUID:96158846; PMID:8569689
A/Accession: S61906
A/Status: translation not shown
A/Molecule type: DNA
A/Residues: 1-209 <ALT>
A/Cross-references: UNIPROT:O00064; EMBL:X91046; NID:g975641; PIDN:CAA62507.1; PID:g9756

Query Match 67.3%; Score 35; DB 2; Length 209;
Best Local Similarity 60.0%; Pred. No. 24;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 1 GNSQFEED 10
DB 173 SGDDGFEDT 182

RESULT 11
S14469
asparagine-rich protein (clone 17C1) - Plasmodium falciparum (fragment)
C/Species: Plasmodium falciparum
C/Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 09-Jul-2004
C/Accession: S14469
R/Schreiber, L.; Deutsche, U.; Storch, T.; Mueller-Hill, D.
submitted to the EMBL Data Library, December 1989
A/Reference number: S14469
A/Accession: S14469
A/Molecule type: mRNA
A/Residues: 1-234 <SCH>
A/Cross-references: UNIPROT:Q25769; EMBL:X17484; NID:g9844; PID:g1335714

Query Match 67.3%; Score 35; DB 2; Length 234;
Best Local Similarity 70.0%; Pred. No. 27;
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 GNSQFEED 10
DB 29 SGNSFEHGT 38

RESULT 12
T50511
serine-type carboxypeptidase II-like protein - Arabidopsis thaliana
N/Alternate names: protein T22D6.200
C/Species: Arabidopsis thaliana (mouse-ear cress)
C/Date: 21-Jul-2000 #sequence_revision 21-Jul-2000 #text_change 09-Jul-2004
C/Accession: T50511
R/Bevan, M.; Terry, N.; Ardiles, W.; Buysaert, C.; Dasseville, R.; De Clerck, R.; De
ewes, H.W.; Rudd, S.; Lemcke, K.; Mayer, K.F.X.
submitted to the Protein Sequence Database, May 2000
A/Reference number: Z25101
A/Accession: T50511
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-480 <BEV>
A/Cross-references: UNIPROT:Q9LEV1; EMBL:AL357612
A/Experimental source: cultivar Columbia; BAC clone T22D6
C/Genetics:
A/Map position: 5
A/Introns: 92/1; 128/1; 191/1; 220/3; 318/3; 364/2; 395/2
A/Note: T22D6.200
C/Superfamily: serine carboxypeptidase

Query Match 67.3%; Score 35; DB 2; Length 480;
Best Local Similarity 77.8%; Pred. No. 59;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 2 GNSQFEED 10
DB 255 GSCSFEEDT 263

RESULT 13
T28055
hypothetical protein ZK858.1 - Caenorhabditis elegans
C/Species: Caenorhabditis elegans
C/Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C/Accession: T28055
R/White, S.
submitted to the EMBL Data Library, September 1996

A:Reference number: Z20462

A:Accession: T28055

A:Status: preliminary; translated from GB/EMBL/DBD

A:Molecule type: DNA

A:Residues: 1-848 <MIL>

A:Cross-references: UNIPROT:Q94419; EMBL:Z79759; PIDN:CAB02138.1; GSPDB:GN00019; CESP:ZK

A:Experimental source: clone ZK858

C:Genetics:

A:Gene: CESP:ZK858.1

A:Map position: 1

A:introns: 26/3; 82/3; 130/3; 195/3; 241/3; 613/1; 762/1

Query Match

Best Local Similarity 67.3%; Score 35; DB 2; Length 848;

Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GNGSFEED 9

Db 550 GNGSFEED 557

RESULT 14

S44665

ZK370.4 protein - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C>Date: 20-Feb-1995 #sequence_rev: 20-Feb-1995 #text_change (19-Sep-1997

C:Accession: S44665

R:Wilson, R.

submitted to the EMBL Data Library, August 1992

A:Description: Sequence of the C. elegans cosmid ZK370.

A:Reference number: S44662

A:Accession: S44665

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-1351 <MIL>

A:Cross-references: EMBL:M98552; NID:G156500; PID:G156504

C:Genetics:

A:introns: 21/3; 160/3; 211/2; 264/2; 313/3; 412/3; 437/1; 468/3; 502/3; 560/2; 678/3; 7

Query Match

Best Local Similarity 67.3%; Score 35; DB 2; Length 1351;

Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 GNGSFEED 9

Db 1312 GNGSFEED 1320

RESULT 15

B64635

toxin-like outer membrane protein HP0922 - Helicobacter pylori (strain 26695)

C:Species: Helicobacter pylori

C>Date: 09-Aug-1997 #sequence_rev: 09-Aug-1997 #text_change (9-Jul-2004

C:Accession: B64635

R:Tomb, J.F.; White, O.; Kierulff, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.D.;

Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khalak, H.G.; Glodek, A.; McKen-

non, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Watthey, L.

Nature 388, 539-547, 1997

A:Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karp, P.D.; Smith, H.O.; Fraser, C.

A:Title: The complete genome sequence of the gastric pathogen Helicobacter pylori.

A:Reference number: A64520; PMID:97394467; PMID:9252185

A:Accession: B64635

A:Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-2529 <TOM>

A:Cross-references: UNIPROT:Q25579; GB:AE000602; GB:AE000511; NII:G2314060; PIDN:AAD0796

Query Match

Best Local Similarity 67.3%; Score 35; DB 2; Length 2529;

Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Db 309 GNGSFEED 318

Search completed: October 22, 2005, 06:10:02
Job time : 4.65539 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using SW model

Run on: October 22, 2005, 04:10:49 ; Search time 18.3253 Seconds
(without alignments)
279.439 Million cell updates/sec

Title: US-10-731-238-64
Perfect score: 52
Sequence: 1 SGNQSFEDT 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues
Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 200000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: UniProt_03.*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	52	100.0	940	2 Q53682	Q53682 staphylococ
2	52	100.0	943	2 Q8NUH8	Q8NUH8 staphylococ
3	52	100.0	957	2 Q6G6H4	Q6G6H4 staphylococ
4	52	100.0	961	2 Q99RD3	Q99RD3 staphylococ
5	52	100.0	961	2 Q7A3J8	Q7A3J8 staphylococ
6	52	100.0	965	2 Q6GDU5	Q6GDU5 staphylococ
7	52	100.0	1015	2 Q8NUV7	Q8NUV7 staphylococ
8	52	100.0	1015	2 Q6G6H3	Q6G6H3 staphylococ
9	52	100.0	1018	1 FMBA STAU	P14738 staphylococ
10	52	100.0	1038	2 Q99RD2	Q99RD2 staphylococ
11	52	100.0	1038	2 Q7A3J7	Q7A3J7 staphylococ
12	49	94.2	152	2 Q8AEP9	Q8AEP9 staphylococ
13	49	94.2	347	2 Q8MEY6	Q8MEY6 dictyosteli
14	40	76.9	461	1 EBP1 STAP	P30199 staphylococ
15	39	75.0	654	2 Q7S2I8	Q7S2I8 neurospora
16	37	71.2	125	1 LMIP MOUSE	Q88994 rattus norv
17	37	71.2	338	2 Q88954	Q88954 rattus norv
18	37	71.2	338	2 Q922Q1	Q922Q1 mus musculu
19	37	71.2	429	2 Q9X5H1	Q9X5H1 helicobacte
20	37	71.2	429	2 Q25682	Q25682 helicobacte
21	37	71.2	789	2 CANB HUMAN	Q9UMG6 homo sapien
22	37	71.2	789	1 Q6SR79	Q6SR79 manheimia
23	36	69.2	125	1 LMIP HUMAN	Q9Y2G5 homo sapien
24	36	69.2	323	2 Q9CEQ6	Q9CEQ6 lactococcus
25	36	69.2	754	2 Q6PMP9	Q6PMP9 candida gla
26	36	69.2	775	2 Q7SAZ0	Q7SAZ0 neurospora
27	36	69.2	946	2 Q8BUH5	Q8BUH5 mus musculu
28	35	67.3	72	2 Q9CHL4	Q9CHL4 lactococcus
29	35	67.3	99	2 Q917U3	Q917U3 tt virus. o
30	35	67.3	99	2 Q917U4	Q917U4 tt virus. o
31	35	67.3	150	2 Q64B80	Q64B80 uncultured

32	35	67.3	167	1 GPX1 YEAST	P36014 saccharomyc
33	35	67.3	192	2 Q9J7M1	Q9J7M1 tt virus. o
34	35	67.3	209	2 Q00064	Q00064 ashbya goss
35	35	67.3	234	2 Q25769	Q25769 plasmodium
36	35	67.3	456	2 Q75EL9	Q75EL9 ashbya goss
37	35	67.3	480	2 Q9LEY1	Q9LEY1 arabidopsis
38	35	67.3	489	2 Q6AZI2	Q6AZI2 xenopus lae
39	35	67.3	506	2 Q7OCY8	Q7OCY8 anopheles g
40	35	67.3	507	2 Q8TKK6	Q8TKK6 anopheles g
41	35	67.3	604	2 Q9VE87	Q9VE87 drosophila
42	35	67.3	617	1 Z221 HUMAN	Q9UK13 homo sapien
43	35	67.3	679	1 FTSH BACPF	P94304 bacillus ps
44	35	67.3	697	2 Q8IQO9	Q8IQO9 drosophila
45	35	67.3	746	2 Q9WAX2	Q9WAX2 tt virus. 1

ALIGNMENTS

RESULT 1					
Q53682	ID	Q53682	PRELIMINARY;	PRT;	940 AA.
AC	Q53682;				
DT	01-NOV-1996 (TREMBLrel. 01, Created)				
DT	01-NOV-1996 (TREMBLrel. 01, Last sequence update)				
DT	01-MAR-2004 (TREMBLrel. 26, Last annotation update)				
DE	Fibronectin binding protein B.				
GN	Name=fnbB;				
OS	Staphylococcus aureus.				
OC	Bacteria; Firmicutes; Bacillales; Staphylococcus.				
OX	NCBI_TaxID=1280;				
RN	(1)				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=8325-4;				
RX	MEDLINE=9211475; Pubmed=1837266;				
RA	Johnson K., Sigman C., Muller H.P., Lindberg M.;				
RT	"Two different genes encode fibronectin binding proteins in				
RT	Staphylococcus aureus. The complete nucleotide sequence and				
RT	characterization of the second gene."				
RL	Eur. J. Biochem. 202:1041-1048 (1991).				
CC	-1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by				
CC	an amide bond (BY similarity).				
DR	EMBL; X62992; CAA44726.1; -.				
DR	PIR; S19702; S19702.				
DR	HSP; Q53653; IN67.				
DR	GO; GO:0009986; C:cell surface; IEA.				
DR	GO; GO:0005618; C:cell wall; IEA.				
DR	GO; GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.				
DR	GO; GO:0016020; C:membrane; IEA.				
DR	GO; GO:007155; P:cell adhesion; IEA.				
DR	InterPro; IPR008966; Adhes_Bact.				
DR	InterPro; IPR004237; Fn_bind.				
DR	InterPro; IPR005877; Gpos_Ysirk.				
DR	InterPro; IPR001899; Gram_pos_anchor.				
DR	Pfam; PF02986; Fn_bind_2.				
DR	Pfam; PF00746; Gram_pos_anchor; 1.				
DR	Pfam; PF04650; Ysirk_signal; 1.				
DR	TIGRFAMs; TIGR01167; LPXTG_anchor; 1.				
DR	TIGRFAMs; TIGR01168; Ysirk_signal; 1.				
DR	PROSITE; PS50847; GRAM_POS_ANCHORING; 1.				
DR	Cell wall; Peptidoglycan-anchor.				
DR	Cell wall; Peptidoglycan-anchor.				
DR	SEQUENCE 940 AA; 10355 MW; E35FBBCA907AE345 CRC64;				
DR	Query Match	100.0%;	Score 52;	DB 2;	Length 940;
DR	Best Local Similarity	100.0%;	Pred. No. 0.28;		
DR	Matches 10;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
DR	Q5	1 SGNQSFEDT 10			
DR	Db	684 SGNQSFEDT 693			
DR	RESULT 2				


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Q8NU8      PRELIMINARY;      PRT;      943 AA.
ID Q8NU8;
AC Q8NU8;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE FnbB protein.
GN Name=fnbB; OrderedLocNames=MM2420;
OS Staphylococcus aureus (strain MM2).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=196620;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MM2;
RX MEDLINE=22040717; PubMed=12044378; DOI=10.1016/S0140-7361(02)08713-5;
RA Baba T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Oguchi A.,
RA Nagai Y., Iwama N., Asano K., Naimi T., Kuroda H., Cui L.,
RA Yamamoto K., Hiramatsu K.;
RT "Genome and virulence determinants of high virulence community-
RT acquired MRSA."
RL Lancet 359:1819-1827(2002).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC an amide bond (By similarity).
DR EMBL; AP004830; BAB96285.1; -.
DR HSSP; O53653; 1N67.
DR GO; GO:0009986; C:cell surface; IEA.
DR GO; GO:0005618; C:cell wall; IEA.
DR GO; GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0007155; P:cell adhesion; IEA.
DR InterPro; IPR008966; Adhes_bact.
DR InterPro; IPR004237; Fn_bind.
DR InterPro; IPR005877; Gpos_YsIRK.
DR InterPro; IPR001899; Gram_pos_anchor.
DR Pfam; PF02986; Fn_bind.1.
DR Pfam; PF00746; Gram_pos_anchor.1.
DR Pfam; PF04650; YsIRK_signal.1.
DR TIGRfams; TIGR01167; LPXTG_anchor.1.
DR TIGRfams; TIGR01168; YsIRK_signal.1.
DR PROSITE; PS50847; GRAM_POS_ANCHORING.1.
DR Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ SEQUENCE 943 AA; 104537 MW; DABA5F31947E1B6A CRC64;

Query Match      100.0%; Score 52; DB 2; Length 943;
Best Local Similarity 100.0%; Pred. No. 0.28;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGNOSFEEDT 10
DB 691 SGNOSFEEDT 700

RESULT 3
Q6G6H4      PRELIMINARY;      PRT;      957 AA.
ID Q6G6H4;
AC Q6G6H4;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Fibronectin-binding protein.
GN Name=fnbB; OrderedLocNames=SA52387;
OS Staphylococcus aureus (strain MSSA476).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=282459;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=15213324; DOI=10.1073/pnas.0402521101;
RA Holden M.T.G., Fell E.J., Lindsay J.A., Peacock S.J., Day N.P.J.,
RA Enright M.C., Foster T.J., Moore C.E., Hurst L., Atkin R., Farron A.,
RA Bason N., Bentley S.D., Chillingworth C., Chillingworth T.,
RA Churcher C., Clark L., Cotton C., Cronin A., Doggett J., Dowd L.,
RA Felwell T., Hance Z., Harris B., Hauser H., Holtroyd S., Jagsis K.,
RA James K.D., Lennard N., Line A., Mayes R., Moule S., Mungall K.,

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RA Ormond D., Quail M.A., Rabinowitch E., Rutherford K.M., Sanders M.,
RA Sharp S., Simmonds M., Stevens K., Whitehead S., Barrell B.G.,
RA Spratt B.G., Parkhill J.;
RT "Complete genomes of two clinical Staphylococcus aureus strains:
RT evidence for the rapid evolution of virulence and drug resistance."
RT Proc. Natl. Acad. Sci. U.S.A. 101:9786-9791(2004).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC an amide bond (By similarity).
DR EMBL; BX571857; CAG44201.1; -.
DR GO; GO:0009986; C:cell surface; IEA.
DR GO; GO:0005618; C:cell wall; IEA.
DR GO; GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0007155; P:cell adhesion; IEA.
DR InterPro; IPR008966; Adhes_bact.
DR InterPro; IPR004237; Fn_bind.
DR InterPro; IPR005877; Gpos_YsIRK.
DR InterPro; IPR001899; Gram_pos_anchor.
DR Pfam; PF02986; Fn_bind.1.
DR Pfam; PF00746; Gram_pos_anchor.1.
DR Pfam; PF04650; YsIRK_signal.1.
DR TIGRfams; TIGR01167; LPXTG_anchor.1.
DR TIGRfams; TIGR01168; YsIRK_signal.1.
DR PROSITE; PS50847; GRAM_POS_ANCHORING.1.
DR Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ SEQUENCE 957 AA; 105980 MW; 28F8BA7FDFD3EAF CRC64;

Query Match      100.0%; Score 52; DB 2; Length 957;
Best Local Similarity 100.0%; Pred. No. 0.28;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGNOSFEEDT 10
DB 691 SGNOSFEEDT 700

RESULT 4
Q99RD3      PRELIMINARY;      PRT;      961 AA.
ID Q99RD3;
AC Q99RD3;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Fibronectin-binding protein homolog.
GN Name=fnbB; OrderedLocNames=SAV2502;
OS Staphylococcus aureus (strain Mu50 / ATCC 700699).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=158878;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Mu50 / ATCC 700699;
RX MEDLINE=21311952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2;
RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Lian J.-Q., Ito T.,
RA Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hoshoyama A.,
RA Mizutani-Uji Y., Takahashi N.K., Sawano T., Inoue R.-I., Katto C.,
RA Sekimizu K., Hiramatsu K., Kohara S., Goto S., Yabuuchi J.,
RA Kanihisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
RA Hattori M., Ogasawara N., Hayaishi H., Hiramatsu K.;
RT "Whole genome sequencing of methicillin-resistant Staphylococcus
RT aureus."
RL Lancet 357:1225-1240(2001).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC an amide bond (By similarity).
DR EMBL; AP003365; BAB58664.1; -.
DR PIR; G90053; G90053.
DR HSSP; O53653; 1N67.
DR GO; GO:0009986; C:cell surface; IEA.
DR GO; GO:0005618; C:cell wall; IEA.
DR GO; GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0007155; P:cell adhesion; IEA.
DR InterPro; IPR008966; Adhes_bact.

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DR InterPro; IPR004237; Fn_bind.
 DR InterPro; IPR005877; Gpos_YsIRK.
 DR InterPro; IPR001899; Gram_pos_anchor.
 DR Pfam; PF02986; Fn_bind; 1.
 DR Pfam; PF00746; Gram_pos_anchor; 1.
 DR Pfam; PF04650; YsIRK_signal; 1.
 DR TIGRFAMs; TIGR01167; LPXTG_anchor; 1.
 DR TIGRFAMs; TIGR01168; YsIRK_signal; 1.
 DR PROSITE; PS50847; GRAM_POS_ANCHORING; 1.
 KW Cell wall; Complete proteome; Peptidoglycan-anchor.
 SQ SEQUENCE 961 AA; 106010 MW; 364940f884EA4101 CRC64;

Query Match 100.0%; Score 52; DB 2; Length 961;
 Best Local Similarity 100.0%; Pred. No. 0.28;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGNOSFEEDT 10
 DB 695 SGNOSFEEDT 704

RESULT 5
 ID Q7A3J8 PRELIMINARY; PRT; 961 AA.
 AC Q7A3J8;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Fnb protein.
 GN Name=fnb; Ordered locus names=SA2290;
 OS Staphylococcus aureus (strain N315).
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 OX NCBI_TaxID=158879;
 RN [1]

RP SEQUENCE FROM N.A.
 RX MEDLINE=21311952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2;
 RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
 RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Iian J.-O., Ito T.,
 RA Kanamori M., Matsunaru H., Maruyama A., Murakami H., Hosoyama A.,
 RA Mizunuma-Uji Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
 RA Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuuchi J.,
 RA Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
 RA Hattori M., Ogasawara N., Hayashi H., Hiramoto K.;
 RT "Whole genome sequencing of methicillin-resistant Staphylococcus
 aureus."
 RL Lancet 357:1225-1240(2001).
 CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
 an amide bond (By similarity).
 CC EMBL; AP003137; BAB43593.1; -;
 DR GO; GO:0009986; C:cell surface; IEA.
 DR GO; GO:0005618; C:cell wall; IEA.
 DR GO; GO:0009375; C:cell wall (sensu Gram-positive Bacteria); IEA.
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0007155; P:cell adhesion; IEA.
 DR InterPro; IPR008966; Adhes_bact.
 DR InterPro; IPR004237; Fn_bind.
 DR InterPro; IPR005877; Gpos_YsIRK.
 DR InterPro; IPR001899; Gram_pos_anchor.
 DR Pfam; PF02986; Fn_bind; 1.
 DR Pfam; PF00746; Gram_pos_anchor; 1.
 DR Pfam; PF04650; YsIRK_signal; 1.
 DR TIGRFAMs; TIGR01167; LPXTG_anchor; 1.
 DR TIGRFAMs; TIGR01168; YsIRK_signal; 1.
 DR PROSITE; PS50847; GRAM_POS_ANCHORING; 1.
 KW Cell wall; Complete proteome; Peptidoglycan-anchor.
 SQ SEQUENCE 961 AA; 106010 MW; 364940f884EA4101 CRC64;

Query Match 100.0%; Score 52; DB 2; Length 961;
 Best Local Similarity 100.0%; Pred. No. 0.28;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 SGNOSFEEDT 10
 DB 695 SGNOSFEEDT 704

DB 695 SGNOSFEEDT 704

RESULT 6
 ID Q6GDU5 PRELIMINARY; PRT; 965 AA.
 AC Q6GDU5;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Fibronectin-binding protein.
 GN Name=fnbA; Ordered locus names=SA2580;
 OS Staphylococcus aureus (strain MRSA252).
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 OX NCBI_TaxID=282458;
 RN [1]

RP SEQUENCE FROM N.A.
 RX PubMed=15213324; DOI=10.1073/pnas.0402521101;
 RA Holden M.T.G., Fell E.J., Lindsay J.A., Peacock S.J., Day N.P.J.,
 RA Enright M.C., Foster T.J., Moore C.E., Hurst L., Ackin R., Barron A.,
 RA Bason N., Bentley S.D., Chillingworth C., Chillingworth T.,
 RA Churcher C., Clark L., Cotton C., Cronin A., Doggett J., Dowd L.,
 RA Feltham T., Hance Z., Harris B., Hauber H., Holtroyd S., Jagsels K.,
 RA James K.D., Leonard N., Line A., Mayes R., Moule S., Mungall K.,
 RA Ormond D., Quail M.A., Rabinovitch E., Rutherford K.M., Sanders M.,
 RA Sharp S., Simmonds M., Stevens K., Whitehead S., Barrett B.G.,
 RA Spratt B.G., Parkhill J.;
 RT "Complete genomes of two clinical Staphylococcus aureus strains:
 evidence for the rapid evolution of virulence and drug resistance.";
 RL Proc. Natl. Acad. Sci. U.S.A. 101:9786-9791(2004).
 CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
 an amide bond (By similarity).
 CC EMBL; BX571856; CAG41560.1; -;
 DR GO; GO:0009986; C:cell surface; IEA.
 DR GO; GO:0009375; C:cell wall (sensu Gram-positive Bacteria); IEA.
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0007155; P:cell adhesion; IEA.
 DR InterPro; IPR008966; Adhes_bact.
 DR InterPro; IPR004237; Fn_bind.
 DR InterPro; IPR005877; Gpos_YsIRK.
 DR InterPro; IPR001899; Gram_pos_anchor.
 DR Pfam; PF02986; Fn_bind; 1.
 DR Pfam; PF00746; Gram_pos_anchor; 1.
 DR Pfam; PF04650; YsIRK_signal; 1.
 DR TIGRFAMs; TIGR01167; LPXTG_anchor; 1.
 DR TIGRFAMs; TIGR01168; YsIRK_signal; 1.
 DR PROSITE; PS50847; GRAM_POS_ANCHORING; 1.
 KW Cell wall; Complete proteome; Peptidoglycan-anchor.
 SQ SEQUENCE 965 AA; 105691 MW; 2982E132164D0551 CRC64;

Query Match 100.0%; Score 52; DB 2; Length 965;
 Best Local Similarity 100.0%; Pred. No. 0.29;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGNOSFEEDT 10
 DB 751 SGNOSFEEDT 760

RESULT 7
 ID Q8NUU7 PRELIMINARY; PRT; 1015 AA.
 AC Q8NUU7;
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Fnb protein.
 GN Name=fnb; Ordered locus names=MW2421;
 OS Staphylococcus aureus (strain MW2).
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 OX NCBI_TaxID=196620;
 RN [1]
 RP SEQUENCE FROM N.A.

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RC STRAIN=WM2;
RX MEDLINE=22040717; PubMed=12044378; DOI=10.1016/S0140-6736(02)08713-5;
RA Baba T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Ojuchi A.,
RA Nagai Y., Iwama N., Asano K., Naimi T., Kuroda H., Cui L.,
RA Yamamoto K., Hiramatsu K.;
RT Genome and virulence determinants of high virulence community-
acquired MRSA";
RT Lancet 359:1819-1827(2002).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
an amide bond (By similarity).
CC EMBL, AP004830; BAB96286.1; -.
DR GO; GO:0009986; C:cell surface; IEA.
DR GO; GO:0005618; C:cell wall; IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO; GO:0007155; P:cell adhesion; IEA.
DR InterPro; IPR008966; Adhes_Bact.
DR InterPro; IPR004237; Fn_bind.
DR InterPro; IPR001899; Gram_pos_anchor.
DR Pfam; PF02986; Fn_bind; 1.
DR Pfam; PF00746; Gram_pos_anchor; 1.
DR TIGRPFAM; TIGR01167; LPXTG_anchor; 1.
DR TIGRPFAM; TIGR01167; LPXTG_anchor; 1.
DR PROSITE; PS50847; GRAM_POS_ANCHORING; 1.
KW Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ SEQUENCE 1015 AA; 11145 MW; D0F9281BB64D44D2 CRC64;

Query Match 100.0%; Score 52; DB 2; Length 1015;
Best Local Similarity 100.0%; Pred. No. 0.3;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGNQSFEDT 10
DB 749 SGNQSFEDT 758

RESULT 8
Q6G6H3 PRELIMINARY; PRT; 1015 AA.
AC Q6G6H3;
ID 06G6H3 (T-EMBLrel. 27, Created)
DT 05-JUL-2004 (T-EMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (T-EMBLrel. 27, Last sequence update)
DE Fibronectin-binding protein.
GN OrderedLocustNames=SA52338;
OS Staphylococcus aureus (strain MSSA476).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=282459;
RN [1]
RN SEQUENCE FROM N.A.
RX PubMed=15213324; DOI=10.1073/pnas.0402521101;
RA Holden M.T.G., Fell E.J., Lindsay J.A., Peacock S.J., Day N.P.J.,
RA Enright M.C., Foster T.J., Moore C.E., Hurst L., Atkin R., Barron A.,
RA Bason N., Bentley S.D., Chillingworth C., Chillingworth T.,
RA Churcher C., Clark L., Cotton C., Cronin A., Doggett J., Dowd L.,
RA Felwell T., Hance Z., Harris B., Hauser H., Holtroyd S., Jajels K.,
RA James K.D., Lennard N., Line A., Mayes R., Moule S., Mungai K.,
RA Ormond D., Quail M.A., Rabinowitsch E., Rutherford K.M., Sanders M.,
RA Sharp S., Simmonds M., Stevens K., Whitehead S., Barrett B.G.,
RA Spratt B.G., Parkhill J.;
RT "Complete genomes of two clinical Staphylococcus aureus strains:
RT evidence for the rapid evolution of virulence and drug resistance.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:9786-9791(2004).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
an amide bond (By similarity).
CC EMBL, X5571857; CAG44202.1; -.
DR GO; GO:0009986; C:cell surface; IEA.
DR GO; GO:0005618; C:cell wall; IEA.
DR GO; GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0007155; P:cell adhesion; IEA.

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DR InterPro; IPR008966; Adhes_Bact.
DR InterPro; IPR004237; Fn_bind.
DR InterPro; IPR005877; Gpos_YsIRK.
DR InterPro; IPR001899; Gram_pos_anchor.
DR Pfam; PF02986; Fn_bind; 1.
DR Pfam; PF00746; Gram_pos_anchor; 1.
DR Pfam; PF04650; YsIRK_signal; 1.
DR TIGRPFAM; TIGR01167; LPXTG_anchor; 1.
DR TIGRPFAM; TIGR01167; LPXTG_anchor; 1.
DR PROSITE; PS50847; GRAM_POS_ANCHORING; 1.
KW Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ SEQUENCE 1015 AA; 11145 MW; D0F9281BB64D44D2 CRC64;

Query Match 100.0%; Score 52; DB 2; Length 1015;
Best Local Similarity 100.0%; Pred. No. 0.3;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGNQSFEDT 10
DB 749 SGNQSFEDT 758

RESULT 9
FNBA STRAU STANDARD; PRT; 1018 AA.
ID FNBA STRAU
AC P14738;
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Fibronectin-binding protein precursor (FNBP).
GN Name=fnba;
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1280;
RN [1]
RN SEQUENCE FROM N.A.
RX STRAIN=NCTC 8325-4;
RX MEDLINE=89098998; PubMed=2521391;
RA Signaes C., Raucel G., Joensson K., Lindgren P.-E.,
RA Anantharamiah G.M., Hoesek M., Lindberg M.;
RT "Nucleotide sequence of the gene for a fibronectin-binding protein
RT from Staphylococcus aureus: use of this peptide sequence in the
RT synthesis of biologically active peptides.";
RL Proc. Natl. Acad. Sci. U.S.A. 86:699-703(1989).
CC -1- FUNCTION: The ability of bacteria to bind fibronectin has been
CC proposed as a virulence factor enabling bacteria to colonize wound
CC tissues and blood clots. Binding of plasma fibronectin to the
CC bacterial surface might block adhesion receptors on S.aureus, thus
CC representing an important defense mechanism against tissue
CC invasion.
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC an amide bond (Potential).
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.1sb-sib.ch/announce/
CC or send an email to license@1sb-sib.ch).
CC -----
DR EMBL, J04151; AAA26632.1; -.
DR InterPro; IPR004237; Fn_bind.
DR InterPro; IPR005877; Gpos_YsIRK.
DR InterPro; IPR001899; Gram_pos_anchor.
DR Pfam; PF02986; Fn_bind; 1.
DR Pfam; PF00746; Gram_pos_anchor; 1.
DR Pfam; PF04650; YsIRK_signal; 1.
DR TIGRPFAM; TIGR01167; LPXTG_anchor; 1.
DR TIGRPFAM; TIGR01167; LPXTG_anchor; 1.
DR PROSITE; PS50847; GRAM_POS_ANCHORING; 1.
KW Cell adhesion; Cell wall; Peptidoglycan-anchor; Repeat; Signal;
Virulence.

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FT SIGNAL 1 36
FT CHAIN 37 985 Fibronectin-binding protein.
FT PROPP 986 1018 Removed by sortase (Potential).
FT REPEAT 545 574 B-1.
FT REPEAT 575 604 B-2.
FT DOMAIN 745 878 4 X approximate tandem repeats,
  Fibronectin-binding domain.
FT REPEAT 745 782 D-1.
FT REPEAT 783 820 D-2.
FT REPEAT 821 859 D-3.
FT REPEAT 860 878 D-4 (incomplete).
FT DOMAIN 879 948 5 X tandem repeats, Pro-rich (WR).
FT REPEAT 879 892 WR 1.
FT REPEAT 893 906 WR 2.
FT REPEAT 907 920 WR 3.
FT REPEAT 921 934 WR 4.
FT REPEAT 935 948 WR 5.
FT SITE 982 986 LpxTG sorting signal (potential).
FT MOD_RES 985 985 Pentaglycyl murein peptidoglycan amidated
  chreonine (potential).
SQ SEQUENCE 1018 AA; 11780 MW; 581758020E81F1F CRC64;

Query Match 100.0%; Score 52; DB 1; Length 1018;
Best Local Similarity 100.0%; Pred. No. 0.3;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SGNOSFEEDT 10
Db 748 SGNOSFEEDT 757

RESULT 10
Q99RD2 PRELIMINARY; PRT; 1038 AA.
ID 099RD2;
AC Q99RD2;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Fibronectin-binding protein homolog.
GN Name=fnb; OrderedLocustNames=SAV2503;
OS Staphylococcus aureus (strain Mu50 / ATCC 700699).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=158878;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Mu50 / ATCC 700699;
RX MEDLINE=21311952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2;
RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
  Cui L., Oguchi A., Aoki K.-I., Nagai Y., Iian J.-Q., Ito T.,
  Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,
  Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
  Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
  Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
  Hattori M., Ogasawara N., Hayashi H., Hiramoto K.;
RA "Whole genome sequencing of methicillin-resistant Staphylococcus
RT aureus.";
RT Lancer 357:1225-1240(2001).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
  an amide bond (by similarity).
CC EMBL; AP003365; BAB58665.1; -.
DR PIR; H90053; H90053.
DR GO; GO:0009986; C:cell surface; IEA.
DR GO; GO:0005618; C:cell wall; IEA.
DR GO; GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:007155; P:cell adhesion; IEA.
DR InterPro; IPR008966; Adhes_bact.
DR InterPro; IPR004237; Fn_bind.
DR InterPro; IPR005877; Gpos_YsIRK.
DR InterPro; IPR001899; Gram_pos_anchor.
DR Pfam; PF02986; Fn_bind; 1.
DR Pfam; PF04650; YsIRK_signal; 1.
DR TIGRfams; TIGR01167; LpxTG_anchor; 1.
DR TIGRfams; TIGR01168; YsIRK_signal; 1.
DR PROSITE; PS50847; GRAM_POS_ANCHORING; 1.
KW Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ SEQUENCE 1038 AA; 113618 MW; 666BF6BF2BFEB12 CRC64;

Query Match 100.0%; Score 52; DB 2; Length 1038;
Best Local Similarity 100.0%; Pred. No. 0.31;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SGNOSFEEDT 10
Db 744 SGNOSFEEDT 753

RESULT 11
Q7A3J7 PRELIMINARY; PRT; 1038 AA.
ID 07A3J7;
AC Q7A3J7;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Fnb protein.
GN Name=fnb; OrderedLocustNames=SA2291;
OS Staphylococcus aureus (strain N315).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=158879;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21311952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2;
RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
  Cui L., Oguchi A., Aoki K.-I., Nagai Y., Iian J.-Q., Ito T.,
  Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,
  Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
  Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
  Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
  Hattori M., Ogasawara N., Hayashi H., Hiramoto K.;
RA "Whole genome sequencing of methicillin-resistant Staphylococcus
RT aureus.";
RT Lancer 357:1225-1240(2001).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
  an amide bond (by similarity).
CC EMBL; AP003377; BAB43594.1; -.
DR GO; GO:0009986; C:cell surface; IEA.
DR GO; GO:0005618; C:cell wall; IEA.
DR GO; GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0007155; P:cell adhesion; IEA.
DR InterPro; IPR008966; Adhes_bact.
DR InterPro; IPR004237; Fn_bind.
DR InterPro; IPR005877; Gpos_YsIRK.
DR InterPro; IPR001899; Gram_pos_anchor.
DR Pfam; PF02986; Fn_bind; 1.
DR Pfam; PF04650; YsIRK_signal; 1.
DR TIGRfams; TIGR01167; LpxTG_anchor; 1.
DR TIGRfams; TIGR01168; YsIRK_signal; 1.
DR PROSITE; PS50847; GRAM_POS_ANCHORING; 1.
KW Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ SEQUENCE 1038 AA; 113618 MW; 666BF6BF2BFEB12 CRC64;

Query Match 100.0%; Score 52; DB 2; Length 1038;
Best Local Similarity 100.0%; Pred. No. 0.31;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SGNOSFEEDT 10
Db 744 SGNOSFEEDT 753

RESULT 12
Q9AEP9 PRELIMINARY; PRT; 152 AA.
ID 09AEP9

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DR TIGRfams; TIGR01167; LpxTG_anchor; 1.
DR TIGRfams; TIGR01168; YsIRK_signal; 1.
DR PROSITE; PS50847; GRAM_POS_ANCHORING; 1.
KW Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ SEQUENCE 1038 AA; 113618 MW; 666BF6BF2BFEB12 CRC64;

Query Match 100.0%; Score 52; DB 2; Length 1038;
Best Local Similarity 100.0%; Pred. No. 0.31;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SGNOSFEEDT 10
Db 744 SGNOSFEEDT 753

RESULT 11
Q7A3J7 PRELIMINARY; PRT; 1038 AA.
ID 07A3J7;
AC Q7A3J7;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Fnb protein.
GN Name=fnb; OrderedLocustNames=SA2291;
OS Staphylococcus aureus (strain N315).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=158879;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21311952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2;
RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
  Cui L., Oguchi A., Aoki K.-I., Nagai Y., Iian J.-Q., Ito T.,
  Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,
  Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
  Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
  Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
  Hattori M., Ogasawara N., Hayashi H., Hiramoto K.;
RA "Whole genome sequencing of methicillin-resistant Staphylococcus
RT aureus.";
RT Lancer 357:1225-1240(2001).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
  an amide bond (by similarity).
CC EMBL; AP003377; BAB43594.1; -.
DR GO; GO:0009986; C:cell surface; IEA.
DR GO; GO:0005618; C:cell wall; IEA.
DR GO; GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0007155; P:cell adhesion; IEA.
DR InterPro; IPR008966; Adhes_bact.
DR InterPro; IPR004237; Fn_bind.
DR InterPro; IPR005877; Gpos_YsIRK.
DR InterPro; IPR001899; Gram_pos_anchor.
DR Pfam; PF02986; Fn_bind; 1.
DR Pfam; PF04650; YsIRK_signal; 1.
DR TIGRfams; TIGR01167; LpxTG_anchor; 1.
DR TIGRfams; TIGR01168; YsIRK_signal; 1.
DR PROSITE; PS50847; GRAM_POS_ANCHORING; 1.
KW Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ SEQUENCE 1038 AA; 113618 MW; 666BF6BF2BFEB12 CRC64;

Query Match 100.0%; Score 52; DB 2; Length 1038;
Best Local Similarity 100.0%; Pred. No. 0.31;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SGNOSFEEDT 10
Db 744 SGNOSFEEDT 753

RESULT 12
Q9AEP9 PRELIMINARY; PRT; 152 AA.
ID 09AEP9

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AC 09AEP9;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Fibronectin-binding protein (Fragment).
OS Name=fnb;
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1280;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=CMRSA-1;
RX MEDLINE=21246681; PubMed=11349044;
DOI=10.1126/IAI.69.6.3791-3799.2001;
RA Rice K., Huesca M., Vaz D., McGavin M.J.;
RT "Variation in fibronectin binding and fnb locus polymorphism in
RT Staphylococcus aureus: identification of antigenic variation in a
RT fibronectin binding protein adhesin of the epidemic CMRSA-1 strain of
RT methicillin-resistant S. aureus.";
RT Infect. Immun. 69:3791-3799(2001).
DR EMBL; AY029184; AKJ1588.1; -.
FT NON_TER 1
FT NON_TER 152
SQ SEQUENCE 152 AA; 17193 MW; CFA3913C2B11C025 CRC64;

Query Match 94.2%; Score 49; DB 2; Length 152;
Best Local Similarity 90.0%; Pred. No. 0.14;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGNQSFEEPT 10
Db 3 TGNQSFEEPT 12

RESULT 13
Q8MYE6 PRELIMINARY; PRT; 347 AA.
ID 08MYE6
AC 08MYE6;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein.
OC Dictyostelium discoideum (Slime mold).
OC Eukaryota; Mycetozoa; Dictyostelida; Dictyostelium.
OX NCBI_TaxID=44689;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=AX4;
RX MEDLINE=22092622; PubMed=12097910; DOI=10.1038/nature00847;
RA Gloeckner G., Eichinger L., Szatranski K., Pachepat J., Dear P.,
RA Lehmann R., Baumgart C., Parra G., April J.F., Gigo R., Kumpf K.,
RA Tunggal B., Cox E., Quail M.A., Platzer M., Rosenthal A., Kegel A.A.;
RT "Sequence and analysis of chromosome 2 of Dictyostelium discoideum.";
RT Nature 418:79-85(2002).
RN (2)
RP SEQUENCE FROM N.A.
RC STRAIN=AX4;
RA Baumgart C.;
RA Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC117082; AA034342.2; -.
DR InterPro; IPR005302; MOSC.
DR InterPro; IPR005303; MOSC_N.
DR Pfam; PF03473; MOSC; 1.
DR Pfam; PF03476; MOSC_N; 1.
KW Hypothetical protein.
SQ SEQUENCE 347 AA; 39327 MW; 00DF9F37AC556D89 CRC64;

Query Match 76.9%; Score 40; DB 2; Length 347;
Best Local Similarity 70.0%; Pred. No. 22;
Matches 7; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGNQSFEEPT 10
Db 1 SGNQSFEEPT 10

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Db 253 AGDKSFEEPT 262

RESULT 14
EPIP STAEP STANDARD; PRT; 461 AA.
ID EPIP STAEP
AC P30199;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Epidermin leader peptide processing serine protease epip precursor
DE (EC 3.4.21.-).
GN Name=epip;
OS Staphylococcus epidermidis.
OG Plasmid pTu 32.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1282;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=ru 3298 / DSM 3095;
RX MEDLINE=92155237; PubMed=1740156;
RA Schnell N., Engelke G., Augustin J., Rosenstein R.; Ungermann V.,
RA Goetz F., Entian K.-D.;
RT "Analysis of genes involved in the biosynthesis of lantibiotic
RT epidermin.";
RT Eur. J. Biochem. 204:57-68(1992).
RL -1- FUNCTION: Protease which cleaves the matured lantibiotic from the
modified prepeptide (Probable).
CC -1- PATHWAY: Epidermin biosynthesis; last step.
CC -1- SIMILARITY: Belongs to the peptidase S8 family.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; X62386; CAA44257.1; -.
DR PIR; S23420; S23420.
DR HSSP; P00782; 2SRT.
DR MEROPS; S08.060; -.
DR InterPro; IPR008357; Peptidase_S8_1p.
DR InterPro; IPR000209; Pept_S8_S53.
DR Pfam; PF00082; Peptidase_S8_1.
DR PRINTS; PR01779; LANTIPROCESS.
DR PRINTS; PR00723; SUBTILISIN.
DR PROSITE; PS00136; SUBTILASIN_ASP; 1.
DR PROSITE; PS00137; SUBTILASIN_HIS; 1.
DR PROSITE; PS00138; SUBTILASIN_SER; 1.
KW Hydrolase; Plasmid; Serine protease; Signal; Zymogen.
FT SIGNAL 1
FT PROPEP 24
FT CHAIN ? 461
FT ACT_SITE 149 149
FT ACT_SITE 194 194
FT ACT_SITE 402 402
SQ SEQUENCE 461 AA; 51814 MW; F2770F4F8436D906 CRC64;

Query Match 76.9%; Score 40; DB 1; Length 461;
Best Local Similarity 77.8%; Pred. No. 30;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGNQSFEEPT 9
Db 182 SGNQSFEEPT 190

RESULT 15
Q7S2L8 PRELIMINARY; PRT; 654 AA.
ID Q7S2L8

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AC 07S2L8;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein.
GN Name=NCU09130.1;
OS Neurospora crassa.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.
OX NCBI_TaxId=5141;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=OR74A;
RA Galagan J.E., Calvo S.E., Borkovich K.A., Selker E.U., Read N.D.,
RA Jaffe D., Fitzhugh W., Ma L.-J., Smirnov S., Purcell S., Rehman B.,
RA Elkins T., Engels R., Wang S., Nielsen C.B., Butler J., Endrizzi M.,
RA Qui D., Ianakiev P., Pedersen D., Nelson M., Washburne M.,
RA Selitrenikoff C.P., Kinsey J.A., Braun E.L., Zelter A., Schulte U.,
RA Kothe G.O., Jedd G., Mewes W., Staben C., Marcotte E., Greenberg D.,
RA Roy A., Foley K., Naylor J., Thomann N., Barrett R., Gnerre S.,
RA Kamal M., Kamvysselis M., Mauceli E., Bielke C., Rudd S., Fishman D.,
RA Kryzofowa S., Rasmussen C., Metzzenberg R.L., Perkins D.D., Kroken S.,
RA Cogoni C., Macino G., Catchside D., Li W., Pratt R.J., Osmani S.A.,
RA Desouza C.C., Glass L., Orbach M.J., Berglund J., Voelker R.,
RA Yarden O., Plamann M., Siller S., Dunlap J., Radford A., Aramayo R.,
RA Natvig D.O., Alex L.A., Manhaupt G., Ebbole D.J., Freitag M.,
RA Paulsen I., Sachs M.S., Lander E.S., Nisbaum C., Birren B.;
RA "The Genome Sequence of the Filamentous Fungus Neurospora crassa.";
RL Nature 0:0-0(2003).
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL: AABX01000421; EAA29666.1; -
KW Hypothetical protein.
SQ SEQUENCE 654 AA; 72779 MW; 215DF37D72DD0DC7 CRC64;

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Query Match          75.0%; Score 39; DB 2; Length 654;
Best Local Similarity 88.9%; Pred. No. 71;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 1 SGNOSFEED 9
   |||||
Db 264 SGNOSAEED 272

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Search completed: October 22, 2005, 06:06:26
 Job time : 20.3253 secs

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CC streptococci, e.g. meningitis, otitis media, pneumonia, endocarditis,
 CC mastitis in cattle; abortion in horses and many others. Since the
 CC antibodies block binding of bacteria, they should be effective against
 CC antibiotic-resistant strains, and may replace antibiotic therapy or
 CC increase its effectiveness. Sequences AAW65719-41 and AAW65658 represent
 CC peptides which were synthesised to span the D1 motif and the N-terminal
 CC 18 amino acids of D2, with each peptide overlapping by e.ght amino acids
 CC with the previous sequence
 XX
 SQ Sequence 10 AA;

Query Match 100.0%; Score 52; DB 2; Length 16;
 Best Local Similarity 100.0%; Pred. No. 0.012;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NOSFEEDTEE 10
 |||||
 DB 1 NOSFEEDTEE 10

RESULT 2
 AAP80660
 ID AAP80660 standard; protein; 38 AA.

XX AAP80660;
 AC
 XX 25-MAR-2003 (revised)
 DT 07-OCT-1990 (first entry)
 DE Protein with fibronectin binding ability.
 XX
 XX Hybrid DNA molecule; fibronectin binding; mastitis; ruminants;
 KM wound infection.
 XX

OS Staphylococcus aureus.
 PN EP294349-A.
 PD 07-DEC-1988.

XX 30-MAY-1988; 88EP-00850188.
 PF
 XX 01-JUN-1987; 87SE-00002272.
 PR
 XX (ALFA) ALFA LAVAL AGRIC INT AB.
 PA
 PI Lindberg MK, Signas LC, Wadstrom TM, Froman G;
 XX
 DR WPI; 1988-347978/49.
 DR N-PSDB; AAN61097.

XX
 PT Hybrid DNA encoding Staphylococcus aureus fibronectin binding protein -
 PT useful for immunisation and topical application to prevent staphylococcal
 PT infections.

XX
 PS Claim 11; Page 12; 23pp; English.

XX The peptide has fibronectin binding ability. It is useful for immunising
 CC ruminants against staphylococcal mastitis, pref. when used at 0.5-5
 CC micrograms/kg, using 3 doses given at 1-3 week intervals; for topical
 CC application to prevent wound infection, using an isotonic saline soln. of
 CC concn. 25-250 micrograms/ml; and, when immobilised on a carrier, for
 CC diagnosing staphylococcal infections. (Updated on 25-MAR-2003 to correct
 CC PF field.) (Updated on 25-MAR-2003 to correct PA field.)
 CC
 XX

SQ Sequence 38 AA;

Query Match 100.0%; Score 52; DB 1; Length 38;
 Best Local Similarity 100.0%; Pred. No. 0.054;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NOSFEEDTEE 10
 |||||

DB 6 NOSFEEDTEE 15

RESULT 3
 AAP82116
 ID AAP82116 standard; protein; 38 AA.

XX AAP82116;
 AC
 XX 25-MAR-2003 (revised)
 DT 05-JAN-1990 (first entry)
 DE Fibronectin binding protein.
 XX
 XX Fibronectin binding protein, S.aureus; immunisation; mastitis; ruminants;
 KM wound infection; diagnosis.
 XX

XX Staphylococcus aureus.

XX EP294349-A.
 PN 07-DEC-1988.

XX 30-MAY-1988; 88EP-00850188.
 PF
 XX 01-JUN-1987; 87SE-00002272.
 PR

XX (ALFA) ALFA LAVAL AGRIC INT AB.
 PA
 PI Lindberg MK, Signas LC, Wadstrom TM, Froman G;
 XX
 DR WPI; 1988-347978/49.
 DR N-PSDB; AAN62054.

XX Hybrid DNA encoding Staphylococcus aureus fibronectin binding protein -
 PT useful for immunisation and topical application to prevent staphylococcal
 PT infections.

XX
 PS Claim 11; Page 12; 23pp; English.

XX The S.aureus fibronectin binding protein may be included in a hybrid
 CC protein. The protein may be used to immunise ruminants against
 CC staphylococcal mastitis, pref. when given at 0.5-5 microg/kg, using 3
 CC doses at 1-3 week intervals; and for topical applicn. to prevent wound
 CC infection, pref. using isotonic saline soln. of concn. 25-250 microg/mg.
 CC The DNA encoding the binding protein and the hybrid protein may be
 CC immobilised on a carrier and used to diagnose staphylococcal infections.
 CC (Updated on 25-MAR-2003 to correct PA field.)
 CC
 XX

SQ Sequence 38 AA;

Query Match 100.0%; Score 52; DB 1; Length 38;
 Best Local Similarity 100.0%; Pred. No. 0.054;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NOSFEEDTEE 10
 |||||
 DB 6 NOSFEEDTEE 15

RESULT 4
 AAW65662
 ID AAW65662 standard; peptide; 38 AA.

XX AAW65662;
 AC
 XX 16-OCT-1998 (first entry)
 DT
 XX Fibronectin binding protein-derived peptide #6.
 DE

XX microbial surface components recognising adhesive matrix molecule;
 KM MSCRAMM; fibronectin; fibronectin-binding protein; antibody; epitope;
 KW antibiotic; bacterial infection; antibiotic-resistant strain.

```

XX OS Synthetic.
XX OS Staphylococcus aureus.
XX PN MO9831389-A2.
XX PD 23-JUL-1998.
XX PF 21-JAN-1998; 98WO-US001222.
XX PR 21-JAN-1997; 97US-0036139P.
XX PA (TEXA ) UNIV TEXAS A & M SYSTEM.
XX PI Hoeoek M, Patti JM, House-Pompeo KL, Speziale P, Joh D;
XX PI McGavin MJ;
XX DR WPI, 1998-413816/35.
XX PT Antibody that binds to fibronectin-binding protein, preventing its
XX PT binding to fibronectin - used to treat or prevent bacterial infection,
XX PT especially by Staphylococci and Streptococci.
XX PS Example 2; Page 92; 201pp; English.
XX CC The invention relates to antibodies that bind to a fibronectin-binding
XX CC domain of a fibronectin-binding protein, and inhibit binding of the
XX CC protein to fibronectin. Also claimed are: (1) isolated peptides of a
XX CC fibronectin-binding protein that do not bind to fibronectin; (2) fusion
XX CC protein containing at least one peptide of a fibronectin-binding protein
XX CC linked to a second amino acid sequence; (3) nucleic acid encoding the
XX CC isolated peptide of (1). Antibodies, the isolated peptides of (1) and the
XX CC nucleic acids are all useful for immunisation (active or passive) and (by
XX CC inhibiting binding of bacteria to fibronectin) for preventing or treating
XX CC infection in humans or other animals, particularly by staphylococci or
XX CC streptococci, e.g. meningitis, otitis media, pneumonia, endocarditis,
XX CC mastitis in cattle, abortion in horses and many others. Since the
XX CC antibodies block binding of bacteria, they should be effective against
XX CC antibiotic-resistant strains, and may replace antibiotic therapy or
XX CC increase its effectiveness. Sequences AAM6569-68 represent synthetic
XX CC epitopes from the fibronectin binding domains DU and DI-D4 of the S.
XX CC aureus fnda gene
XX CC
SQ Sequence 38 AA;
Query Match 100.0%; Score 52; DB 2; Length 38;
Best Local Similarity 100.0%; Pred. No. 0.054;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 NOSFEEDTEE 10
   |||||
   5 NOSFEEDTEE 14
Db
RESULT 5
ID AAM65699 standard; peptide; 38 AA.
XX AAM65699;
XX AC
XX DT 16-OCT-1998 (first entry)
XX DE Fibronectin binding protein-derived peptide #43.
XX KM microbial surface components recognising adhesive matrix molecule;
XX KM MSCRAMM; fibronectin; fibronectin-binding protein; antibody; epitope;
XX KM antibiotic; bacterial infection; antibiotic-resistant strain.
XX OS Synthetic.
XX OS Staphylococcus aureus.
XX PN MO9831389-A2.

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PD 23-JUL-1998.
XX PF 21-JAN-1998; 98WO-US001222.
XX PR 21-JAN-1997; 97US-0036139P.
XX PA (TEXA ) UNIV TEXAS A & M SYSTEM.
XX PI Hoeoek M, Patti JM, House-Pompeo KL, Speziale P, Joh D;
XX PI McGavin MJ;
XX DR WPI, 1998-413816/35.
XX PT Antibody that binds to fibronectin-binding protein, preventing its
XX PT binding to fibronectin - used to treat or prevent bacterial infection,
XX PT especially by Staphylococci and Streptococci.
XX PS Example 8; Page 102; 201pp; English.
XX CC The invention relates to antibodies that bind to a fibronectin-binding
XX CC domain of a fibronectin-binding protein, and inhibit binding of the
XX CC protein to fibronectin. Also claimed are: (1) isolated peptides of a
XX CC fibronectin-binding protein that do not bind to fibronectin; (2) fusion
XX CC protein containing at least one peptide of a fibronectin-binding protein
XX CC linked to a second amino acid sequence; (3) nucleic acid encoding the
XX CC isolated peptide of (1). Antibodies, the isolated peptides of (1) and the
XX CC nucleic acids are all useful for immunisation (active or passive) and (by
XX CC inhibiting binding of bacteria to fibronectin) for preventing or treating
XX CC infection in humans or other animals, particularly by staphylococci or
XX CC streptococci, e.g. meningitis, otitis media, pneumonia, endocarditis,
XX CC mastitis in cattle, abortion in horses and many others. Since the
XX CC antibodies block binding of bacteria, they should be effective against
XX CC antibiotic-resistant strains, and may replace antibiotic therapy or
XX CC increase its effectiveness. Sequences AAM6561-700 represent a series of
XX CC synthetic peptides based on the DI region of S. aureus fibronectin
XX CC binding protein A. They were synthesised to contain mutations
XX CC
SQ Sequence 38 AA;
Query Match 100.0%; Score 52; DB 2; Length 38;
Best Local Similarity 100.0%; Pred. No. 0.054;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 NOSFEEDTEE 10
   |||||
   5 NOSFEEDTEE 14
Db
RESULT 6
ID AAM65661 standard; peptide; 38 AA.
XX AAM65661;
XX AC
XX DT 16-OCT-1998 (first entry)
XX DE Fibronectin binding protein-derived peptide #5.
XX KM microbial surface components recognising adhesive matrix molecule;
XX KM MSCRAMM; fibronectin; fibronectin-binding protein; antibody; epitope;
XX KM antibiotic; bacterial infection; antibiotic-resistant strain.
XX OS Synthetic.
XX OS Staphylococcus aureus.
XX PN MO9831389-A2.
XX PD 23-JUL-1998.
XX PF 21-JAN-1998; 98WO-US001222.
XX PR 21-JAN-1997; 97US-0036139P.
XX

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PA (TEXA) UNIV TEXAS A & M SYSTEM.
 XX Hoeoek M, Patri JM, House-Pompeo KL, Speziale P, Joh H;
 PI Mcgavin MJ;
 XX WPI; 1998-413816/35.
 DR
 XX
 PT Antibody that binds to fibronectin-binding protein, preventing its
 PT binding to fibronectin - used to treat or prevent bacterial infection,
 PT especially by Staphylococci and Streptococci.
 XX
 PS Example 2; Page 92; 201pp; English.
 XX
 CC The invention relates to antibodies that bind to a fibronectin-binding
 CC domain of a fibronectin-binding protein, and inhibit binding of the
 CC protein to fibronectin. Also claimed are: (1) isolated peptides of a
 CC fibronectin-binding protein that do not bind to fibronectin; (2) fusion
 CC protein containing at least one peptide of a fibronectin-binding protein
 CC linked to a second amino acid sequence; (3) nucleic acid encoding the
 CC isolated peptide of (1). Antibodies, the isolated peptides of (1) and the
 CC nucleic acids are all useful for immunisation (active or passive) and (b)
 CC inhibiting binding of bacteria to fibronectin) for preventing or treating
 CC infection in humans or other animals, particularly by staphylococci or
 CC streptococci, e.g. meningitis, otitis media, pneumonia, endocarditis,
 CC mastitis in cattle, abortion in horses and many others. Since the
 CC antibodies block binding of bacteria, they should be effective against
 CC antibiotic-resistant strains, and may replace antibiotic therapy or
 CC increase its effectiveness. Sequences AAW65659-68 represent: synthetic
 CC epitopes from the fibronectin binding domains D1 and D1-D4 of the S.
 CC aureus fnbA gene
 CC
 SQ Sequence 38 AA;
 SQ
 Query Match 100.0%; Score 52; DB 2; Length 38;
 Best Local Similarity 100.0%; Pred. No. 0.054;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 NOSFEDTTE 10
 Db 5 NOSFEDTTE 14
 DB
 RESULT 7
 ID AAW65698 standard; peptide; 38 AA.
 XX
 AC AAW65698;
 XX
 DT 16-OCT-1998 (first entry)
 XX
 DE Fibronectin binding protein-derived peptide #42.
 XX
 KM microbial surface components recognising adhesive matrix molecule;
 KM MSCRAMM; fibronectin; fibronectin-binding protein; antibody; epitope;
 KM antibiotic; bacterial infection; antibiotic-resistant str.1.
 XX
 OS Synthetic.
 OS Staphylococcus aureus.
 OS
 PN WO9831389-A2.
 XX
 PD 23-JUL-1998.
 XX
 PF 21-JAN-1998; 98WO-US001222.
 XX
 PR 21-JAN-1997; 97US-0036139P.
 XX
 PA (TEXA) UNIV TEXAS A & M SYSTEM.
 XX
 PI Hoeoek M, Patri JM, House-Pompeo KL, Speziale P, Joh D;
 PI Mcgavin MJ;
 XX
 DR WPI; 1998-413816/35.

XX
 PT Antibody that binds to fibronectin-binding protein, preventing its
 PT binding to fibronectin - used to treat or prevent bacterial infection,
 PT especially by Staphylococci and Streptococci.
 XX
 PS Example 8; Page 102; 201pp; English.
 XX
 CC The invention relates to antibodies that bind to a fibronectin-binding
 CC domain of a fibronectin-binding protein, and inhibit binding of the
 CC protein to fibronectin. Also claimed are: (1) isolated peptides of a
 CC fibronectin-binding protein that do not bind to fibronectin; (2) fusion
 CC protein containing at least one peptide of a fibronectin-binding protein
 CC linked to a second amino acid sequence; (3) nucleic acid encoding the
 CC isolated peptide of (1). Antibodies, the isolated peptides of (1) and the
 CC nucleic acids are all useful for immunisation (active or passive) and (b)
 CC inhibiting binding of bacteria to fibronectin) for preventing or treating
 CC infection in humans or other animals, particularly by staphylococci or
 CC streptococci, e.g. meningitis, otitis media, pneumonia, endocarditis,
 CC mastitis in cattle, abortion in horses and many others. Since the
 CC antibodies block binding of bacteria, they should be effective against
 CC antibiotic-resistant strains, and may replace antibiotic therapy or
 CC increase its effectiveness. Sequences AAW65691-700 represent a series of
 CC synthetic peptides based on the D1 region of S. aureus fibronectin
 CC binding protein A. They were synthesised to contain mutations
 CC
 SQ Sequence 38 AA;
 SQ
 Query Match 100.0%; Score 52; DB 2; Length 38;
 Best Local Similarity 100.0%; Pred. No. 0.054;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 NOSFEDTTE 10
 Db 5 NOSFEDTTE 14
 DB
 RESULT 8
 ID AAW65712 standard; peptide; 39 AA.
 XX
 AC AAW65712;
 XX
 DT 16-OCT-1998 (first entry)
 XX
 DE Fibronectin binding protein-derived peptide #56.
 XX
 KM microbial surface components recognising adhesive matrix molecule;
 KM MSCRAMM; fibronectin; fibronectin-binding protein; antibody; epitope;
 KM antibiotic; bacterial infection; antibiotic-resistant strain.
 XX
 OS Synthetic.
 OS Staphylococcus aureus.
 OS
 PN WO9831389-A2.
 XX
 PD 23-JUL-1998.
 XX
 PF 21-JAN-1998; 98WO-US001222.
 XX
 PR 21-JAN-1997; 97US-0036139P.
 XX
 PA (TEXA) UNIV TEXAS A & M SYSTEM.
 XX
 PI Hoeoek M, Patri JM, House-Pompeo KL, Speziale P, Joh D;
 PI Mcgavin MJ;
 XX
 DR WPI; 1998-413816/35.
 XX
 PT Antibody that binds to fibronectin-binding protein, preventing its
 PT binding to fibronectin - used to treat or prevent bacterial infection,
 PT especially by Staphylococci and Streptococci.
 XX
 PS Example 8; Page 104; 201pp; English.

XX The invention relates to antibodies that bind to a fibronectin-binding
 CC domain of a fibronectin-binding protein, and inhibit binding of the
 CC protein to a fibronectin. Also claimed are: (1) isolated peptides of a
 CC fibronectin-binding protein that do not bind to fibronectin; (2) fusion
 CC protein containing at least one peptide of a fibronectin-binding protein
 CC linked to a second amino acid sequence; (3) nucleic acid encoding the
 CC isolated peptide of (1). Antibodies, the isolated peptides of (1) and the
 CC nucleic acids are all useful for immunisation (active or passive) and (by
 CC inhibiting binding of bacteria to fibronectin) for preventing or treating
 CC infection in humans or other animals, particularly by staphylococci or
 CC streptococci, e.g. meningitis, otitis media, pneumonia, endocarditis,
 CC mastitis in cattle, abortion in horses and many others. Since the
 CC antibodies block binding of bacteria, they should be effective against
 CC antibiotic-resistant strains, and may replace antibiotic therapy or
 CC increase its effectiveness. The present sequence is shown in the
 CC specification

XX Sequence 39 AA;

Query Match 100.0%; Score 52; DB 2; Length 39;

Best Local Similarity 100.0%; Pred. No. 0.055;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NOSFEDTEE 10

DB 5 NOSFEDTEE 14

RESULT 9
 AAM65713
 ID AAM65713 standard; peptide; 39 AA.

AC AAM65713;

DT 16-OCT-1998 (first entry)

DE Fibronectin binding protein-derived peptide #57.

XX microbial surface components recognising adhesive matrix molecule;

KW MSCRAMM; fibronectin; fibronectin-binding protein; antibody; epitope;

KM antibiotic; bacterial infection; antibiotic-resistant strain.

XX Synthetic.

OS Staphylococcus aureus.

PN MO9831389-A2.

PD 23-JUL-1998.

PF 21-JAN-1998; 98WO-US001222.

PR 21-JAN-1997; 97US-0036139P.

XX (TEXA) UNITV TEXAS A & M SYSTEM.

PA Hosook M, Pati JM, House-Pompeo KL, Speciale P, Joh D;

XX Mcgavin MJ;

PI WPI; 1998-413816/35.

DR WPI; 1998-413816/35.

XX Antibody that binds to fibronectin-binding protein, preventing its

PT binding to fibronectin - used to treat or prevent bacterial infection,

PT especially by staphylococci and streptococci.

XX Example 8; Page 104; 201pp; English.

XX The invention relates to antibodies that bind to a fibronectin-binding

CC domain of a fibronectin-binding protein, and inhibit binding of the

CC protein to fibronectin. Also claimed are: (1) isolated peptides of a

CC fibronectin-binding protein that do not bind to fibronectin; (2) fusion

CC protein containing at least one peptide of a fibronectin-binding protein

CC linked to a second amino acid sequence; (3) nucleic acid encoding the

CC isolated peptide of (1). Antibodies, the isolated peptides of (1) and the
 CC nucleic acids are all useful for immunisation (active or passive) and (by
 CC inhibiting binding of bacteria to fibronectin) for preventing or treating
 CC infection in humans or other animals, particularly by staphylococci or
 CC streptococci, e.g. meningitis, otitis media, pneumonia, endocarditis,
 CC mastitis in cattle, abortion in horses and many others. Since the
 CC antibodies block binding of bacteria, they should be effective against
 CC antibiotic-resistant strains, and may replace antibiotic therapy or
 CC increase its effectiveness. The present sequence is shown in the
 CC specification

XX Sequence 39 AA;

Query Match 100.0%; Score 52; DB 2; Length 39;

Best Local Similarity 100.0%; Pred. No. 0.055;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NOSFEDTEE 10

DB 5 NOSFEDTEE 14

RESULT 10
 AAR58806
 ID AAR58806 standard; protein; 130 AA.

AC AAR58806;

DT 25-MAR-2003 (revised)

DT 30-MAR-1995 (first entry)

DE Fibronectin binding domain D1-D4(709-838(P838T)).

XX Fibronectin binding protein; Fbp; fibronectin binding domain;

KW monoclonal antibody; MAb; adhesion; Gram-positive bacterium; bacteremia;

KM *Escherichia coli*.

XX Staphylococcus aureus.

PN WO9418327-A1.

PD 18-AUG-1994.

PF 04-FEB-1994; 94WO-GB000215.

PR 05-FEB-1993; 93GB-00002289.

PR 20-OCT-1993; 93GB-00021592.

PA (SMIK) SMITHKLINE BEECHAM PLC.

XX Burnham MKR, Chopra I, Critchley IA, Knowles DJC;

PI WPI; 1994-279748/34.

DR WPI; 1994-279748/34.

XX Fibronectin binding protein and monoclonal antibodies specific for Fbp -

PT useful to prevent adherence of Gram-positive bacteria to indwelling

PT devices or wounds.

XX Disclosure; Page 30; 40pp; English.

XX Polypeptides corresponding to residues 709-786 plus PPIVPT. 6709-

CC P838(P838T) and 6709-786 (AAR58805-07, respectively) of *S. aureus* 4385

CC (NCIMB 40532) Fbp type A fibronectin binding domain D1-D4 region MAb

CC (AAR58808) were expressed in *E. coli* BL21(DE4) and used to raise MAb

CC specific for Fbp. (Updated on 25-MAR-2003 to correct PN field.)

QY 1 NOSFEDTEE 10

DB 5 NOSFEDTEE 14

Query Match 100.0%; Score 52; DB 2; Length 130;

Best Local Similarity 100.0%; Pred. No. 0.21;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 6 NOSFEEDTEE 15

RESULT 11

ID AAR58807 standard; protein; 130 AA.

AC AAR58807;

DT 25-MAR-2003 (revised)

DT 30-MAR-1995 (first entry)

DE Fibronectin binding domain D1-D4(709-838).

KW Fibronectin binding protein; Fbp; fibronectin binding domain;
KW monoclonal antibody; Mab; adhesion; Gram-positive bacterium; bacteraemia;
KW Escherichia coli.

OS Staphylococcus aureus.

PN WO9418327-A1.

PD 18-AUG-1994.

PF 04-FEB-1994; 94WO-GB000215.

PR 05-FEB-1993; 93GB-00002289.

PR 20-OCT-1993; 93GB-00021592.

PA (SMIK) SMITHKLINE BEECHAM PLC.

PI Burnham MKR, Chopra I, Critchley IA, Knowles DUC;

PI WPI; 1994-279748/34.

PT Fibronectin binding protein and monoclonal antibodies specific for Fbp -
PT useful to prevent adherence of Gram-positive bacteria to intwelling
PT devices or wounds.

PS Disclosure; Page 30; 40pp; English.

CC POLYPEPTIDES corresponding to residues G709-T886 plus PPIVPYT, G709-
CC P838(P838T) and G709-P838(AAR58805-07, respectively) of S. aureus J2385
CC (NCIMB 40532) Fbp type A fibronectin binding domain D1-D4 region
CC (AAR58808) were expressed in E. coli BL21(DE3) and used to raise Mabs
CC specific for Fbp. (Updated on 25-MAR-2003 to correct PN file d.)

SQ Sequence 130 AA;

Query Match 100.0%; Score 52; DB 2; Length 130;
Best Local Similarity 100.0%; Pred. No. 0.21;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NOSFEEDTEE 10
DB 6 NOSFEEDTEE 15

RESULT 12

ID AAR91202 standard; peptide; 130 AA.

AC AAR91202;

DT 13-NOV-1996 (first entry)

DE D1-D4 fibronectin binding domains.

KW Fibronectin; oral hygiene; gingivitis; gum disease; adhesion;
KW periodontitis; oral pathogen; caries; calculus; candidiasis; oral surgery;
KW tissue regeneration; irrigation; toothpaste; dentifrice; mouthwash;
KW Lozenge.

OS Staphylococcus aureus.

PN WO9604003-A1.

PD 15-FEB-1996.

PF 18-JUL-1995; 95WO-EP002825.

PR 05-AUG-1994; 94GB-00015902.

PA (SMIK) SMITHKLINE BEECHAM PLC.

PI Barnett P, Critchley IA, Dodd I;

PI WPI; 1996-129122/13.

PT Prevention of adherence of oral pathogens in the oral cavity, partic.
PT tooth surfaces - by application of a fibronectin binding protein or
PT polypeptide or a monoclonal antibody or fragment against it.

PS Claim 5; Page 32; 41pp; English.

CC Adherence of oral pathogens, particularly to tooth surfaces, can be
CC prevented by application of a fibronectin binding protein or polypeptide.
CC The fibronectin binding protein or polypeptide is useful in the
CC manufacture of oral hygiene compositions, eg. toothpaste, liquid
CC dentifrice, mouthwash or lozenge. They are useful to prevent the plaque-
CC related development of carious lesions, gingivitis, calculus or
CC periodontal disease and to combat oral cavity infections, e.g.
CC candidiasis. They may also be useful in oral surgery e.g. in guided
CC tissue regeneration procedures to prevent subsequent bacterial infection,
CC and for irrigation of periodontal pockets. This sequence corresponds to
CC amino acids 709-838 of the D1-D4 fibronectin binding domain of
CC Staphylococcus aureus

SQ Sequence 130 AA;

Query Match 100.0%; Score 52; DB 2; Length 130;
Best Local Similarity 100.0%; Pred. No. 0.21;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NOSFEEDTEE 10
DB 6 NOSFEEDTEE 15

RESULT 13

ID AAR91201 standard; peptide; 130 AA.

AC AAR91201;

DT 13-NOV-1996 (first entry)

DE D1-D4 fibronectin binding domains.

KW Fibronectin; oral hygiene; gingivitis; gum disease; adhesion;
KW periodontitis; oral pathogen; caries; calculus; candidiasis; oral surgery;
KW tissue regeneration; irrigation; toothpaste; dentifrice; mouthwash;
KW Lozenge.

OS Staphylococcus aureus.

PN WO9604003-A1.

PD 15-FEB-1996.

PF 18-JUL-1995; 95WO-EP002825.

PR 05-AUG-1994; 94GB-00015902.

PA (SMIK) SMITHKLINE BEECHAM PLC.

XX Barnett P, Critchley IA, Dodd I;
 XX WPI, 1996-129122/13.
 XX
 XX Prevention of adherence of oral pathogens in the oral cavity, partic.
 XX tooth surfaces - by application of a fibronectin binding protein or
 XX polypeptide or a monoclonal antibody or fragment against it.
 XX
 XX Claim 5; Page 31-32; 41pp; English.
 XX
 XX Adherence of oral pathogens, particularly to tooth surfaces, can be
 XX prevented by application of a fibronectin binding protein or polypeptide.
 XX The fibronectin binding protein or polypeptide is useful in the
 XX manufacture of oral hygiene compositions, eg. toothpaste, liquid
 XX dentifrice, mouthwash or lozenge. They are useful to prevent the plaque-
 XX related development of carious lesions, gingivitis, calculus or
 XX periodontal disease and to combat oral cavity infections, e.g.
 XX candidiasis. They may also be useful in oral surgery e.g. in guided
 XX tissue regeneration procedures to prevent subsequent bacterial infection,
 XX and for irrigation of periodontal pockets. This sequence corresponds to
 XX amino acids 709-838 of the D1-D4 fibronectin binding domain of
 XX Staphylococcus aureus with a P838T substitution
 XX
 XX Sequence 130 AA;
 XX
 XX Query Match 100.0%; Score 52; DB 2; Length 130;
 XX Best Local Similarity 100.0%; Pred. No. 0.21;
 XX Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX
 XX 1 NOSFEEDTEE 10
 XX |||||
 XX 6 NOSFEEDTEE 15
 XX
 XX RESULT 14
 XX AAY29089
 XX ID AAY29089 standard; protein; 134 AA.
 XX
 XX AAY29089;
 XX
 XX 28-SEP-1999 (first entry)
 XX
 XX Cloned fibronectin binding protein binding domain (FnBAB) sequence.
 XX
 XX Bovine herpes virus-2; BHV-2; cytokine; immune response; immunogen; IL;
 XX interleukin; colony stimulating factor; CSF; interferon; IFN; TNF;
 XX tumour necrosis factor; recombinant virus; vaccine; mucosal disease;
 XX mastitis; breast cancer; stress-induced disease; binding domain; FnBAB;
 XX fibronectin binding protein.
 XX
 XX Staphylococcus aureus.
 XX
 XX WO916892-A1.
 XX
 XX 08-APR-1999.
 XX
 XX 29-SEP-1998; 98WO-GB002927.
 XX
 XX 29-SEP-1997; 97GB-00020633.
 XX
 XX (UYBR-) UNIV BRISTOL.
 XX
 XX Bradley AJ, Duffas WP;
 XX WPI, 1999-255101/21.
 XX DR N-PSDB; AAX91506.
 XX
 XX New bovine herpes virus-2 vectors.
 XX
 XX Example 2; Fig 8A-B; 130pp; English.
 XX
 XX The invention provides bovine herpes virus-2 (BHV-2) based vectors that

CC comprise at least one cytokine-encoding DNA sequence. The expression of
 CC cytokines in mammals can up-regulate immune responses to the immunogens.
 CC The cytokine is selected from interleukins (IL), colony stimulating
 CC factors (CSF), interferons (IFN) and tumour necrosis factors (TNF). The
 CC BHV-2 based vector or recombinant virus can be used as vaccines. They can
 CC be used for preventing or treating a mucosal disease in a subject, e.g.
 CC ruminants, cattle, sheep, goats, dogs, cats, horses, or man, particularly
 CC mastitis in cows or breast cancers in humans. They can also be used for
 CC preventing or treating a stress-induced disease. The present sequence
 CC represents a S. aureus fibronectin binding protein binding domain
 CC sequence FnBAB, the gene cloned for use in this invention. The gene has
 CC 97.8 percent identity when compared to the previously published sequences
 CC FnBA and FnBB
 XX
 XX Sequence 134 AA;
 XX
 XX Query Match 100.0%; Score 52; DB 2; Length 134;
 XX Best Local Similarity 100.0%; Pred. No. 0.22;
 XX Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX
 XX 1 NOSFEEDTEE 10
 XX |||||
 XX 6 NOSFEEDTEE 15
 XX
 XX RESULT 15
 XX AAY29088
 XX ID AAY29088 standard; protein; 134 AA.
 XX
 XX AAY29088;
 XX
 XX 28-SEP-1999 (first entry)
 XX
 XX S. aureus fibronectin binding protein B (FnBB) binding domain.
 XX
 XX Bovine herpes virus-2; BHV-2; cytokine; immune response; immunogen; IL;
 XX interleukin; colony stimulating factor; CSF; interferon; IFN; TNF;
 XX tumour necrosis factor; recombinant virus; vaccine; mucosal disease;
 XX mastitis; breast cancer; stress-induced disease; binding domain; FnBB;
 XX fibronectin binding protein.
 XX
 XX Staphylococcus aureus.
 XX
 XX WO916892-A1.
 XX
 XX 08-APR-1999.
 XX
 XX 29-SEP-1998; 98WO-GB002927.
 XX
 XX 29-SEP-1997; 97GB-00020633.
 XX
 XX (UYBR-) UNIV BRISTOL.
 XX
 XX Bradley AJ, Duffas WP;
 XX WPI, 1999-255101/21.
 XX DR N-PSDB; AAX91505.
 XX
 XX New bovine herpes virus-2 vectors.
 XX
 XX Example 2; Fig 8A-B; 130pp; English.
 XX
 XX The invention provides bovine herpes virus-2 (BHV-2) based vectors that
 CC comprise at least one cytokine-encoding DNA sequence. The expression of
 CC cytokines in mammals can up-regulate immune responses to the immunogens.
 CC The cytokine is selected from interleukins (IL), colony stimulating
 CC factors (CSF), interferons (IFN) and tumour necrosis factors (TNF). The
 CC BHV-2 based vector or recombinant virus can be used as vaccines. They can
 CC be used for preventing or treating a mucosal disease in a subject, e.g.
 CC ruminants, cattle, sheep, goats, dogs, cats, horses, or man, particularly
 CC mastitis in cows or breast cancers in humans. They can also be used for
 CC preventing or treating a stress-induced disease. The present sequence
 CC represents the binding domain of a previously published S. aureus

CC fibronectin binding protein B (FnBB) sequence. The FnB binding domain
 CC gene sequence FNBB, cloned for use in this invention has 97.8 percent
 CC identity when compared to the previously published FnBB and FnBB gene
 CC sequences

XX
 SQ Sequence 134 AA;

Query Match 100.0%; Score 52; DB 2; Length 134;
 Best Local Similarity 100.0%; Pred. No. 0.22;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NOSFEEDTEE 10
 |||||
 Db 6 NOSFEEDTEE 15

Search completed: October 25, 2005, 20:58:41
 Job time : 64.2 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 22, 2005, 05:46:56 ; Search time 17.3 Seconds
(without alignments)
43.150 Million cell updates/sec

Title: US-10-731-238-65

Perfect score: 52

Sequence: 1 NQSPFEDTDE 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA: *
1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep.*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep.*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep.*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep.*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep.*
6: /cgn2_6/ptodata/1/iaa/backfile1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	52	100.0	10	4	US-09-010-317-65 Sequence 65, Appl
2	52	100.0	38	1	US-08-234-622A-2 Sequence 2, Appl
3	52	100.0	38	1	US-08-729-767-3 Sequence 3, Appl
4	52	100.0	38	4	US-09-010-317-5 Sequence 5, Appl
5	52	100.0	38	4	US-09-010-317-6 Sequence 6, Appl
6	52	100.0	38	4	US-09-010-317-42 Sequence 42, Appl
7	52	100.0	38	4	US-09-010-317-43 Sequence 43, Appl
8	52	100.0	39	4	US-09-010-317-56 Sequence 56, Appl
9	52	100.0	39	4	US-09-010-317-57 Sequence 57, Appl
10	52	100.0	114	1	US-08-259-000-3 Sequence 3, Appl
11	52	100.0	130	2	US-08-459-135A-7 Sequence 7, Appl
12	52	100.0	130	2	US-08-459-135A-8 Sequence 8, Appl
13	52	100.0	130	3	US-08-495-559-7 Sequence 7, Appl
14	52	100.0	130	3	US-08-495-559-8 Sequence 8, Appl
15	52	100.0	139	3	US-08-856-253-8 Sequence 8, Appl
16	52	100.0	174	2	US-08-459-135A-10 Sequence 10, Appl
17	52	100.0	174	2	US-08-459-135A-13 Sequence 13, Appl
18	52	100.0	174	3	US-08-495-559-10 Sequence 10, Appl
19	52	100.0	174	3	US-08-495-559-13 Sequence 13, Appl
20	52	100.0	176	3	US-08-495-559-6 Sequence 6, Appl
21	52	100.0	178	3	US-08-459-135A-12 Sequence 12, Appl
22	52	100.0	178	3	US-08-495-559-12 Sequence 12, Appl
23	52	100.0	181	2	US-08-459-135A-6 Sequence 6, Appl
24	52	100.0	559	4	US-08-956-171E-5251 Sequence 5251, Ap
25	52	100.0	559	4	US-08-781-986A-5251 Sequence 5251, Ap
26	52	100.0	1027	4	US-08-956-171E-5254 Sequence 5254, Ap
27	52	100.0	1027	4	US-08-781-986A-5254 Sequence 5254, Ap

28	48	92.3	10	4	US-09-010-317-84 Sequence 84, Appl
29	48	92.3	36	4	US-09-010-317-58 Sequence 58, Appl
30	48	92.3	36	4	US-09-010-317-59 Sequence 59, Appl
31	48	92.3	38	1	US-08-234-622A-3 Sequence 3, Appl
32	48	92.3	38	1	US-08-729-767-4 Sequence 4, Appl
33	48	92.3	38	1	US-09-010-317-7 Sequence 7, Appl
34	48	92.3	38	4	US-09-010-317-8 Sequence 8, Appl
35	48	92.3	38	4	US-09-010-317-49 Sequence 49, Appl
36	47	90.4	38	4	US-09-010-317-41 Sequence 41, Appl
37	46	88.5	38	4	US-09-010-317-36 Sequence 36, Appl
38	46	88.5	38	4	US-09-010-317-37 Sequence 37, Appl
39	46	88.5	38	4	US-09-010-317-39 Sequence 39, Appl
40	46	88.5	38	4	US-09-010-317-40 Sequence 40, Appl
41	45	86.5	38	4	US-09-010-317-38 Sequence 38, Appl
42	42	80.8	10	4	US-09-010-317-64 Sequence 64, Appl
43	42	80.8	10	4	US-09-010-317-83 Sequence 83, Appl
44	42	80.8	38	4	US-09-010-317-35 Sequence 35, Appl
45	42	80.8	38	4	US-09-010-317-46 Sequence 46, Appl

ALIGNMENTS

RESULT 1
US-09-010-317-65
Sequence 65, Application US/09010317
Patent No. 6685943
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
APPLICANT: Patti, Joseph M.
APPLICANT: House-Pompeo, Karen L.
APPLICANT: Speziale, Pietro
APPLICANT: John, Danny
APPLICANT: McQuinn, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
TITLE OF INVENTION: AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAMK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 65:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-09-010-317-65
Query Match 100.0%; Score 52; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0034;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NOSFEDTEE 10
|||||
Db 1 NOSFEDTEE 10

RESULT 2

US-08-234-622A-2

; Sequence 2, Application US/08234622A

; Patent No. 544014

; GENERAL INFORMATION:

; APPLICANT: HOOK, Magnus

; APPLICANT: MCGAVIN, Martin

; APPLICANT: RAUCCI, Giuseppe

; TITLE OF INVENTION: A FIBRONECTIN BINDING PEPTIDE

; NUMBER OF SEQUENCES: 4

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Burns, Doane, Swecker & Mathis

; STREET: P.O. Box 1404

; CITY: Alexandria

; STATE: Virginia

; COUNTRY: United States

; ZIP: 22313-1404

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/234,622A

; FILING DATE: 28-APR-1994

; CLASSIFICATION: 530

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: SE 9002617-0

; FILING DATE: 10-AUG-1990

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: NO PCT/SE91/00534

; FILING DATE: 09-AUG-1991

; ATTORNEY/AGENT INFORMATION:

; NAME: Meuth, Donna M

; REGISTRATION NUMBER: 36,607

; REFERENCE/DOCKET NUMBER: 012885-044

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (703) 836-6620

; TELEFAX: (703) 836-2021

; INFORMATION FOR SEQ ID NO: 2:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 38 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

; US-08-234-622A-2

Query Match

Best Local Similarity 100.0%; Score 52; DB 1; Length 38;

Best Local Similarity 100.0%; Pred. No. 0.014;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NOSFEDTEE 10
|||||
Db 5 NOSFEDTEE 14

RESULT 3

US-08-729-767-3

; Sequence 3, Application US/08729767

; Patent No. 5770702

; GENERAL INFORMATION:

; APPLICANT: HOOK, Magnus

; APPLICANT: LINDERBERG, Martin Kjell

; APPLICANT: SIGNAS, Lars Christer

; APPLICANT: MADSTROM, Torkel Mikael

APPLICANT: FROMAN, Gunnar
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN AS WELL AS
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:

ADDRESSEE: Burns, Doane, Swecker & Mathis, L.L.P.

STREET: P.O. Box 1404

CITY: Alexandria

STATE: Virginia

COUNTRY: United States

ZIP: 22313-1404

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/729,767

FILING DATE: 07-OCT-1996

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/259,000

FILING DATE: 13-JUN-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/007,817

FILING DATE: 22-JAN-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/201,028

FILING DATE: 01-JUN-1988

PRIOR APPLICATION DATA:

APPLICATION NUMBER: SE 8702272-9

FILING DATE: 01-JUN-1987

ATTORNEY/AGENT INFORMATION:

NAME: McGowan, Malcolm K.

REGISTRATION NUMBER: 39,300

REFERENCE/DOCKET NUMBER: 012889-036

TELECOMMUNICATION INFORMATION:

TELEPHONE: (703) 836-6620

TELEFAX: (703) 836-2021

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 38 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-729-767-3

Query Match

Best Local Similarity 100.0%; Score 52; DB 1; Length 38;

Best Local Similarity 100.0%; Pred. No. 0.014;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NOSFEDTEE 10
|||||
Db 6 NOSFEDTEE 15

RESULT 4

US-09-010-317-5

; Sequence 5, Application US/09010317

; Patent No. 6685943

; GENERAL INFORMATION:

; APPLICANT: Hook, Magnus

; APPLICANT: Patti, Joseph M.

; APPLICANT: House-Pompeo, Karen L.

; APPLICANT: Speciale, Pietro

; APPLICANT: Job, Danny

; APPLICANT: McGavin, Martin J.

; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS

; NUMBER OF SEQUENCES: 105

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Arnold, White & Durkee

STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAMK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-09-010-317-5

Query Match 100.0%; Score 52; DB 4; Length 38;
Best local Similarity 100.0%; Pred. No. 0.014;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NOSFEEDTEE 10
|||||
DB 5 NOSFEEDTEE 14

RESULT 5
US-09-010-317-6
Sequence 6, Application US/09010317
Patent No. 6685943
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
APPLICANT: Patti, Joseph M.
APPLICANT: House-Pompeo, Karen L.
APPLICANT: Speziale, Pietro
APPLICANT: Joh, Danny
APPLICANT: McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
TITLE OF INVENTION: AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/036,139

FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAMK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-09-010-317-6

Query Match 100.0%; Score 52; DB 4; Length 38;
Best local Similarity 100.0%; Pred. No. 0.014;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NOSFEEDTEE 10
|||||
DB 5 NOSFEEDTEE 14

RESULT 6
US-09-010-317-42
Sequence 42, Application US/09010317
Patent No. 6685943
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
APPLICANT: Patti, Joseph M.
APPLICANT: House-Pompeo, Karen L.
APPLICANT: Speziale, Pietro
APPLICANT: Joh, Danny
APPLICANT: McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
TITLE OF INVENTION: AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAMK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 42:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-09-010-317-42

Query Match 100.0%; Score 52; DB 4; Length 38;
Best Local Similarity 100.0%; Pred. No. 0.014;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NOSFEEDTEE 10
| | | | | | | | | |
DB 5 NOSFEEDTEE 14

RESULT 7

US-09-010-317-43
; Sequence 43, Application US/09010317
; Patent No. 6685943
; GENERAL INFORMATION:
; APPLICANT: Hook, Magnus
; APPLICANT: Patti, Joseph M.
; APPLICANT: House-Pompeo, Karen L.
; APPLICANT: Speziale, Pietro
; APPLICANT: Joh, Danny
; APPLICANT: McGavin, Martin J.
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
; TITLE OF INVENTION: AND METHODS OF USE
; NUMBER OF SEQUENCES: 105
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: TX
; COUNTRY: USA
; ZIP: 77210-4433
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 512-418-3000
; TELEFAX: 512-474-7577
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/010,317
; FILING DATE:
; CLASSIFICATION:
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: US 60/036,139
; FILING DATE: 21-JAN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Hibler, David W.
; REGISTRATION NUMBER: 41,071
; REFERENCE/DOCKET NUMBER: TANK:189
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 512-418-3000
; TELEFAX: 512-474-7577
; INFORMATION FOR SEQ. ID NO: 43:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 38 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; US-09-010-317-43

Query Match 100.0%; Score 52; DB 4; Length 38;
Best Local Similarity 100.0%; Pred. No. 0.014;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NOSFEEDTEE 10
| | | | | | | | | |
DB 5 NOSFEEDTEE 14

RESULT 8

US-09-010-317-56
; Sequence 56, Application US/09010317
; Patent No. 6685943
; GENERAL INFORMATION:
; APPLICANT: Hook, Magnus
; APPLICANT: Patti, Joseph M.

; APPLICANT: House-Pompeo, Karen L.
; APPLICANT: Speziale, Pietro
; APPLICANT: Joh, Danny
; APPLICANT: McGavin, Martin J.
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
; TITLE OF INVENTION: AND METHODS OF USE
; NUMBER OF SEQUENCES: 105
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: TX
; COUNTRY: USA
; ZIP: 77210-4433
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/010,317
; FILING DATE:
; CLASSIFICATION:
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: US 60/036,139
; FILING DATE: 21-JAN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Hibler, David W.
; REGISTRATION NUMBER: 41,071
; REFERENCE/DOCKET NUMBER: TANK:189
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 512-418-3000
; TELEFAX: 512-474-7577
; INFORMATION FOR SEQ. ID NO: 56:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 39 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; US-09-010-317-56

Query Match 100.0%; Score 52; DB 4; Length 39;
Best Local Similarity 100.0%; Pred. No. 0.015;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NOSFEEDTEE 10
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DB 5 NOSFEEDTEE 14

RESULT 9

US-09-010-317-57
; Sequence 57, Application US/09010317
; Patent No. 6685943
; GENERAL INFORMATION:
; APPLICANT: Hook, Magnus
; APPLICANT: Patti, Joseph M.
; APPLICANT: House-Pompeo, Karen L.
; APPLICANT: Speziale, Pietro
; APPLICANT: Joh, Danny
; APPLICANT: McGavin, Martin J.
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
; TITLE OF INVENTION: AND METHODS OF USE
; NUMBER OF SEQUENCES: 105
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: TX
; COUNTRY: USA
; ZIP: 77210-4433
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAMK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ. ID NO: 57:
SEQUENCE CHARACTERISTICS:
LENGTH: 39 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-09-010-317-57

Query Match 100.0%; Score 52; DB 4; Length 39;
Best Local Similarity 100.0%; Pred. No. 0.015;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NOSPEEDTEE 10
DB 5 NOSPEEDTEE 14

RESULT 10
US-08-259-000-3
Sequence 3, Application US/08259000
Patent No. 5571514
GENERAL INFORMATION:
APPLICANT: HOOK, Magnus
APPLICANT: LINDERBERG, Martin Kjell
APPLICANT: SIGNAS, Lars Christer
APPLICANT: WADSTROM, Torkei Mikael
APPLICANT: FROMAN, Gunnar
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN AS WELL AS
TITLE OF INVENTION: ITS PREPARATION
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Burns, Doane, Swecker & Mathis
STREET: P.O. Box 1404
CITY: Alexandria
STATE: Virginia
COUNTRY: United States
ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/259,000
FILING DATE: 13-JUN-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: SE 8702272-9
FILING DATE: 01-JUN-1987
ATTORNEY/AGENT INFORMATION:
NAME: Meuth, Donna M.
REGISTRATION NUMBER: 36,607
REFERENCE/DOCKET NUMBER: 012885-062
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021

INFORMATION FOR SEQ. ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 114 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-259-000-3

Query Match 100.0%; Score 52; DB 1; Length 114;
Best Local Similarity 100.0%; Pred. No. 0.046;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NOSPEEDTEE 10
DB 6 NOSPEEDTEE 15

RESULT 11
US-08-459-135A-7
Sequence 7, Application US/08459135A
Patent No. 5955078
GENERAL INFORMATION:
APPLICANT: BURHAM, Martin Karl Russel
APPLICANT: CHOPRA, Ian
APPLICANT: CRITCHLEY, Ian Alfred
APPLICANT: KNOWLES, David Justin Charles
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN: MONOCLONAL ANTIBODY AND THEIR US
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Smithkline Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
STATE: PA
COUNTRY: U.S.A.
ZIP: 19406-0939
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM compatible
OPERATING SYSTEM: DOS
SOFTWARE: Fastseq, Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/459,135A
FILING DATE: 02-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB/94/00215
FILING DATE: 04-Feb-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Gimmil, Edward R.
REGISTRATION NUMBER: 38,891
REFERENCE/DOCKET NUMBER: P30591C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-4478
TELEFAX: 610-270-5090
TELEX:
INFORMATION FOR SEQ. ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 130 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-459-135A-7

Query Match 100.0%; Score 52; DB 2; Length 130;
Best Local Similarity 100.0%; Pred. No. 0.053;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NOSPEEDTEE 10
DB 6 NOSPEEDTEE 15

RESULT 12
US-08-459-135A-8
; Sequence 8, Application US/08459135A
; Patent No. 5955078
; GENERAL INFORMATION:
; APPLICANT: BURHAM, Martin Karl Russel
; APPLICANT: CHOPRA, Ian
; APPLICANT: CRITCHLEY, Ian Alfred
; APPLICANT: KNOWLES, David Justin Charles
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN: MONOCLONAL ANTIBODY AND THEIR US
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Smithkline Beecham Corporation
; STREET: 709 Swedeland Road
; CITY: King of Prussia
; STATE: PA
; COUNTRY: U.S.A.
; ZIP: 19406-0939
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: Fastseq, Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/459,135A
; FILING DATE: 02-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB/94/00215
; FILING DATE: 04-Feb-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Gimmil, Edward R.
; REGISTRATION NUMBER: 38,891
; REFERENCE/DOCKET NUMBER: P30591C2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-270-4478
; TELEFAX: 610-270-5090
; TELEX:
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 130 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-459-135A-8

Query Match 100.0%; Score 52; DB 2; Length 130;
Best Local Similarity 100.0%; Pred. No. 0.053;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NOSFEEDTEE 10
| | | | | | | | | |
DB 6 NOSFEEDTEE 15

RESULT 13
US-08-495-559-7
; Sequence 7, Application US/08495559A
; Patent No. 6054572
; GENERAL INFORMATION:
; APPLICANT: BURHAM, Martin Karl Russel
; APPLICANT: CHOPRA, Ian
; APPLICANT: CRITCHLEY, Ian Alfred
; APPLICANT: KNOWLES, David Justin Charles
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN: MONOCLONAL
; TITLE OF INVENTION: ANTIBODY AND THEIR USE IN PREVENTING BACTERIAL ADHESION
; FILE REFERENCE: P30591
; CURRENT APPLICATION NUMBER: US/08/495,559A
; CURRENT FILING DATE: 1995-08-03
; EARLIER APPLICATION NUMBER: GB 9302289.5
; EARLIER FILING DATE: 1993-02-05

; EARLIER APPLICATION NUMBER: GB 9321592.9
; EARLIER FILING DATE: 1993-10-20
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 7
; LENGTH: 130
; TYPE: PRP
; ORGANISM: Staphylococcus aureus
US-08-495-559-7

Query Match 100.0%; Score 52; DB 3; Length 130;
Best Local Similarity 100.0%; Pred. No. 0.053;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NOSFEEDTEE 10
| | | | | | | | | |
DB 6 NOSFEEDTEE 15

RESULT 14
US-08-495-559-8
; Sequence 8, Application US/08495559A
; Patent No. 6054572
; GENERAL INFORMATION:
; APPLICANT: BURHAM, Martin Karl Russel
; APPLICANT: CHOPRA, Ian
; APPLICANT: CRITCHLEY, Ian Alfred
; APPLICANT: KNOWLES, David Justin Charles
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN: MONOCLONAL
; TITLE OF INVENTION: ANTIBODY AND THEIR USE IN PREVENTING BACTERIAL ADHESION
; FILE REFERENCE: P30591
; CURRENT APPLICATION NUMBER: US/08/495,559A
; CURRENT FILING DATE: 1995-08-03
; EARLIER APPLICATION NUMBER: GB 9302289.5
; EARLIER FILING DATE: 1993-02-05
; EARLIER APPLICATION NUMBER: GB 9321592.9
; EARLIER FILING DATE: 1993-10-20
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 8
; LENGTH: 130
; TYPE: PRP
; ORGANISM: Staphylococcus aureus
US-08-495-559-8

Query Match 100.0%; Score 52; DB 3; Length 130;
Best Local Similarity 100.0%; Pred. No. 0.053;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NOSFEEDTEE 10
| | | | | | | | | |
DB 6 NOSFEEDTEE 15

RESULT 15
US-08-856-253-8
; Sequence 8, Application US/08856253
; Patent No. 6288214
; GENERAL INFORMATION:
; APPLICANT: Hook, Magnus
; APPLICANT: Patell, Joseph M.
; APPLICANT: House-Pompeo, Karen
; APPLICANT: Schanam, Narayana
; APPLICANT: Symersky, Jindrich
; TITLE OF INVENTION: COLLAGEN BINDING PROTEIN COMPOSITIONS
; TITLE OF INVENTION: AND METHODS OF USE
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: U.S.

ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/856,253
FILING DATE: Concurrently Herewith
CLASSIFICATION: 514
Prior APPLICATION DATA:
APPLICATION NUMBER: US 60/017,678
FILING DATE: 16-MAY-1996
ATTORNEY/AGENT INFORMATION:
NAME: Kitchell, Barbara S.
REGISTRATION NUMBER: 33,928
REFERENCE/DOCKET NUMBER: TAMK:193
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
TELEFAX: (512) 474-7577
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 139 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-08-856-253-8

Query Match 100.0%; Score 52; DB 3; Length 139;
Best Local Similarity 100.0%; Pred. No. 0.057; 0;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 NOSFEEDTEE 10
DB 20 NOSFEEDTEE 29

Search completed: October 22, 2005, 07:41:39
Job time : 17.35 secs

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OM protein - protein search, using sw model

Run on: October 22, 2005, 12:09:40 ; Search time 57.25 Seconds
(without alignments)
72.924 Million cell updates/sec

Title: US-10-731-238-65

Perfect score: 52

Sequence: 1 NOSFEEDTKE 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1862951 seqs, 417491010 residues

Total number of hits satisfying chosen parameters: 1862951

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-Processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA.*

1: /cgn2_6/prodata/2/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/prodata/2/pubpaa/PCT_NEW_PUB.pep.*
3: /cgn2_6/prodata/2/pubpaa/US06_NEW_PUB.pep.*
4: /cgn2_6/prodata/2/pubpaa/US06_PUBCOMB.pep.*
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6: /cgn2_6/prodata/2/pubpaa/PCTUS_PUBCOMB.pep.*
7: /cgn2_6/prodata/2/pubpaa/US08_NEW_PUB.pep.*
8: /cgn2_6/prodata/2/pubpaa/US08_PUBCOMB.pep.*
9: /cgn2_6/prodata/2/pubpaa/US09_PUBCOMB.pep.*
10: /cgn2_6/prodata/2/pubpaa/US09C_PUBCOMB.pep.*
11: /cgn2_6/prodata/2/pubpaa/US09C_NEW_PUB.pep.*
12: /cgn2_6/prodata/2/pubpaa/US10_PUBCOMB.pep.*
13: /cgn2_6/prodata/2/pubpaa/US10C_PUBCOMB.pep.*
14: /cgn2_6/prodata/2/pubpaa/US10C_PUBCOMB.pep.*
15: /cgn2_6/prodata/2/pubpaa/US10C_PUBCOMB.pep.*
16: /cgn2_6/prodata/2/pubpaa/US10_PUBCOMB.pep.*
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19: /cgn2_6/prodata/2/pubpaa/US11_PUBCOMB.pep.*
20: /cgn2_6/prodata/2/pubpaa/US11_NEW_PUB.pep.*
21: /cgn2_6/prodata/2/pubpaa/US60_NEW_PUB.pep.*
22: /cgn2_6/prodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	52	100.0	10	US-10-731-238-65	Sequence 65, Appl
2	52	100.0	38	US-10-731-238-5	Sequence 5, Appl
3	52	100.0	38	US-10-731-238-6	Sequence 6, Appl
4	52	100.0	38	US-10-731-238-42	Sequence 42, Appl
5	52	100.0	38	US-10-731-238-43	Sequence 43, Appl
6	52	100.0	39	US-10-731-238-56	Sequence 56, Appl
7	52	100.0	39	US-10-731-238-57	Sequence 57, Appl
8	52	100.0	139	US-09-813-820-8	Sequence 8, Appl
9	52	100.0	388	US-08-901-062-1	Sequence 1, Appl
10	52	100.0	559	US-08-781-986A-5251	Sequence 5251, Ap
11	52	100.0	559	US-10-329-624-5251	Sequence 5251, Ap

12	52	100.0	767	US-09-815-242-5899	Sequence 5899, Ap
13	52	100.0	767	US-09-815-242-13140	Sequence 13140, A
14	52	100.0	940	US-10-470-048B-424	Sequence 424, App
15	52	100.0	948	US-10-470-048B-69	Sequence 69, Appl
16	52	100.0	948	US-10-282-122A-43778	Sequence 43778, A
17	52	100.0	961	US-09-815-242-5456	Sequence 5456, Ap
18	52	100.0	978	US-09-815-242-12686	Sequence 12686, A
19	52	100.0	1001	US-09-815-242-5797	Sequence 5797, Ap
20	52	100.0	1018	US-09-815-242-12838	Sequence 12838, A
21	52	100.0	1018	US-10-470-048B-68	Sequence 68, Appl
22	52	100.0	1018	US-08-781-986A-5254	Sequence 5254, Ap
23	52	100.0	1027	US-10-329-624-5254	Sequence 5254, A
24	52	100.0	1038	US-10-282-122A-43827	Sequence 43827, Ap
25	48	92.3	10	US-10-287-821-1	Sequence 1, Appl
26	48	92.3	30	US-10-287-821-2	Sequence 2, Appl
27	48	92.3	31	US-10-287-821-2	Sequence 58, Appl
28	48	92.3	36	US-10-731-238-58	Sequence 59, Appl
29	48	92.3	36	US-10-731-238-59	Sequence 7, Appl
30	48	92.3	38	US-10-731-238-7	Sequence 8, Appl
31	48	92.3	38	US-10-731-238-8	Sequence 41, Appl
32	48	92.3	38	US-10-731-238-49	Sequence 49, Appl
33	47	90.4	38	US-10-731-238-41	Sequence 36, Appl
34	46	88.5	38	US-10-731-238-36	Sequence 37, Appl
35	46	88.5	38	US-10-731-238-37	Sequence 39, Appl
36	46	88.5	38	US-10-731-238-39	Sequence 40, Appl
37	46	88.5	38	US-10-731-238-40	Sequence 38, Appl
38	45	86.5	38	US-10-731-238-38	Sequence 64, Appl
39	42	80.8	10	US-10-731-238-64	Sequence 83, Appl
40	42	80.8	10	US-10-731-238-83	Sequence 35, Appl
41	42	80.8	38	US-10-731-238-35	Sequence 46, Appl
42	42	80.8	38	US-10-731-238-46	Sequence 47, Appl
43	42	80.8	38	US-10-731-238-47	Sequence 66, Appl
44	41	78.8	10	US-10-731-238-66	Sequence 105, App
45	41	78.8	14	US-10-731-238-105	

ALIGNMENTS

RESULT 1
US-10-731-238-65
; Sequence 65, Application US/10731238
; Publication No. US20050123552A1
; GENERAL INFORMATION:
APPLICANT: Hook, Magnus
Patel, Joseph M.
House-Pompeo, Karen L.
Speziale, Pietro
John, Danny
McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10-731-238
FILING DATE: 10-Dec-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE: 21-Jan-1998
APPLICATION NUMBER: US 60/036,139

FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAMK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 65:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 65:
US-10-731-238-65

Query Match 100.0%; Score 52; DB 18; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.027;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NOSFEEDTEE 10
|||||
DB 1 NOSFEEDTEE 10

RESULT 2
US-10-731-238-5
Sequence 5, Application US/10731238
Publication No. US20050123552A1
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
Patti, Joseph M.
House-Pompeo, Karen L.
Speziale, Pietro
Joh, Danny
McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/731,238
FILING DATE: 10-Dec-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE: 21-Jan-1998
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAMK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>

TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-10-731-238-5

Query Match 100.0%; Score 52; DB 18; Length 38;
Best Local Similarity 100.0%; Pred. No. 0.11;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NOSFEEDTEE 10
|||||
DB 5 NOSFEEDTEE 14

RESULT 3
US-10-731-238-6
Sequence 6, Application US/10731238
Publication No. US20050123552A1
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
Patti, Joseph M.
House-Pompeo, Karen L.
Speziale, Pietro
Joh, Danny
McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/731,238
FILING DATE: 10-Dec-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE: 21-Jan-1998
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAMK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-10-731-238-6

Query Match 100.0%; Score 52; DB 18; Length 38;
Best Local Similarity 100.0%; Pred. No. 0.11;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NOSFEEDTEE 10
|||||
DB 5 NOSFEEDTEE 14

RESULT 4
US-10-731-238-42
; Sequence 42, Application US/10731238
; Publication No. US20050123552A1
; GENERAL INFORMATION:
; APPLICANT: Hook, Magnus
; Patti, Joseph M.
; House-Pompeo, Karen L.
; Speciale, Pietro
; John, Danny
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
; AND METHODS OF USE
; NUMBER OF SEQUENCES: 105
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: TX
; COUNTRY: USA
; ZIP: 77210-4433
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/731,238
; FILING DATE: 10-Dec-2003
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/010,317
; FILING DATE: 21-Jan-1998
; APPLICATION NUMBER: US 60/036,139
; FILING DATE: 21-JAN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Hibler, David W.
; REGISTRATION NUMBER: 41,071
; REFERENCE/DOCKET NUMBER: TAMK:189
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 512-418-3000
; TELEFAX: 512-474-7577
; INFORMATION FOR SEQ ID NO: 42:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 38 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 42:
US-10-731-238-42
Query Match 100.0%; Score 52; DB 18; Length 38;
Best Local Similarity 100.0%; Pred. No. 0.11; 0; Indels 0; Gaps 0;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 NOSFEEDTEE 10
Db 5 NOSFEEDTEE 14
RESULT 5
US-10-731-238-43
; Sequence 43, Application US/10731238
; Publication No. US20050123552A1
; GENERAL INFORMATION:
; APPLICANT: Hook, Magnus
; Patti, Joseph M.
; House-Pompeo, Karen L.
; Speciale, Pietro
; John, Danny
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
; AND METHODS OF USE

NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/731,238
FILING DATE: 10-Dec-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE: 21-Jan-1998
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAMK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 43:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 43:
US-10-731-238-43
Query Match 100.0%; Score 52; DB 18; Length 38;
Best Local Similarity 100.0%; Pred. No. 0.11; 0; Indels 0; Gaps 0;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 NOSFEEDTEE 10
Db 5 NOSFEEDTEE 14
RESULT 6
US-10-731-238-56
; Sequence 56, Application US/10731238
; Publication No. US20050123552A1
; GENERAL INFORMATION:
; APPLICANT: Hook, Magnus
; Patti, Joseph M.
; House-Pompeo, Karen L.
; Speciale, Pietro
; John, Danny
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
; AND METHODS OF USE
; NUMBER OF SEQUENCES: 105
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: TX
; COUNTRY: USA
; ZIP: 77210-4433
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/731,238
FILING DATE: 10-Dec-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE: 21-Jan-1998
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAMK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 56:
SEQUENCE CHARACTERISTICS:
LENGTH: 39 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 56:
US-10-731-238-56

Query Match 100.0%; Score 52; DB 18; Length 39;
Best Local Similarity 100.0%; Pred. No. 0.11;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NOSFEEDTEE 10
DB 5 NOSFEEDTEE 14

RESULT 7
US-10-731-238-57
Sequence 57, Application US/10731238
Publication No. US20050123552A1
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
Patel, Joseph M.
House-Pompeo, Karen L.
Speziale, Pietro
John, Danny
McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: US
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/731,238
FILING DATE: 10-Dec-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE: 21-Jan-1998
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAMK:189

TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 57:
SEQUENCE CHARACTERISTICS:
LENGTH: 39 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 57:
US-10-731-238-57

Query Match 100.0%; Score 52; DB 18; Length 39;
Best Local Similarity 100.0%; Pred. No. 0.11;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NOSFEEDTEE 10
DB 5 NOSFEEDTEE 14

RESULT 8
US-09-813-820-8
Sequence 8, Application US/09813820
Patent No. US20020102262A1
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
Patel, Joseph M.
House-Pompeo, Karen
Sthanam, Narayana
Symeraky, Jindrich
TITLE OF INVENTION: COLLAGEN BINDING PROTEIN COMPOSITIONS
AND METHODS OF USE
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: Texas
COUNTRY: U.S.
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/813,820
FILING DATE: 22-Mar-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/856,253
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Kitchell, Barbara S.
REGISTRATION NUMBER: 33,928
REFERENCE/DOCKET NUMBER: TAMK:193
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
TELEFAX: (512) 474-7577
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 139 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-09-813-820-8

Query Match 100.0%; Score 52; DB 9; Length 139;
Best Local Similarity 100.0%; Pred. No. 0.44;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NOSFEEDTEE 10
DB 20 NOSFEEDTEE 29

RESULT 9

US-08-901-062-1
Sequence 1, Application US/08901062
Publication No. US2002025324A1
GENERAL INFORMATION:
APPLICANT: SEALS, JONATHAN R.
TITLE OF INVENTION: RECOMBINANT BIVALENT BACTERIAL VACCINE
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: HALE AND DORR LLP
STREET: 60 State Street
CITY: Boston
STATE: MA
COUNTRY: United States Of America
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/901,062
FILING DATE: 25-JUL-1997
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Baker, Hollie L.
REGISTRATION NUMBER: 31,321
REFERENCE/DOCKET NUMBER: 106941.153
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 526-6000
TELEFAX: (617) 526-5000
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 388 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO

US-08-901-062-1

Query Match 100.0%; Score 52; DB 8; Length 388;
Best Local Similarity 100.0%; Pred. No. 1.3;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NOSFEEDTEE 10
DB 269 NOSFEEDTEE 278

RESULT 10

US-08-781-986A-5251
Sequence 5251, Application US/08781986A
Publication No. US20030054436A1
GENERAL INFORMATION:
APPLICANT: Charles Kunsch
TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
NUMBER OF SEQUENCES: 5255
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COUNTRY: USA
ZIP: 20850
COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/781,986A
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Benson, Bob
REGISTRATION NUMBER: 30,446
REFERENCE/DOCKET NUMBER: PB248PP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 5251:
SEQUENCE CHARACTERISTICS:
LENGTH: 559 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein

US-08-781-986A-5251

Query Match 100.0%; Score 52; DB 8; Length 559;
Best Local Similarity 100.0%; Pred. No. 1.9;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NOSFEEDTEE 10
DB 305 NOSFEEDTEE 314

RESULT 11

US-10-329-624-5251
Sequence 5251, Application US/10329624
Publication No. US20040043037A1
GENERAL INFORMATION:
APPLICANT: Charles Kunsch
Gil H. Choi
Patrick S. Dillon
Craig A. Rosen
Steven C. Barash
Michael R. Fannon
TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
NUMBER OF SEQUENCES: 5256
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COUNTRY: USA
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/329,624
FILING DATE: 27-Dec-2002
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/956,171
FILING DATE: October 20, 1997
APPLICATION NUMBER: 60/009,861
FILING DATE: January 5, 1996
APPLICATION NUMBER: 08/781,986
FILING DATE: January 3, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Mark J. Hyman

REGISTRATION NUMBER: 46,789
REFERENCE/DOCKET NUMBER: PB248P1D1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (240) 314-1224
TELEFAX: (301) 309-8439
INFORMATION FOR SEQ ID NO: 5251:
SEQUENCE CHARACTERISTICS:
LENGTH: 559 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 5251:
US-10-329-624-5251

Query Match 100.0%; Score 52; DB 15; Length 559;
Best Local Similarity 100.0%; Pred. No. 1.9;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NOSFEEDTEE 10
DB 305 NOSFEEDTEE 314

RESULT 12
US-09-815-242-5899
Sequence 5899, Application US/09815242
Patent No. US20020061569A1
GENERAL INFORMATION:
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Karl L.
APPLICANT: Zyskind, Judith W.
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John D.
APPLICANT: Carr, Grant J.
APPLICANT: Yamamoto, Robert T.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in
FILE REFERENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 5899
LENGTH: 767
TYPE: PRT
ORGANISM: Staphylococcus aureus
US-09-815-242-5899

Query Match 100.0%; Score 52; DB 9; Length 767;
Best Local Similarity 100.0%; Pred. No. 2.7;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NOSFEEDTEE 10
DB 686 NOSFEEDTEE 695

RESULT 13
US-09-815-242-13140
Sequence 13140, Application US/09815242
Patent No. US20020061569A1
GENERAL INFORMATION:
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Karl L.
APPLICANT: Zyskind, Judith W.
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John D.
APPLICANT: Carr, Grant J.
APPLICANT: Yamamoto, Robert T.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in
FILE REFERENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 13140
LENGTH: 767
TYPE: PRT
ORGANISM: Staphylococcus aureus
US-09-815-242-13140

Query Match 100.0%; Score 52; DB 9; Length 767;
Best Local Similarity 100.0%; Pred. No. 2.7;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NOSFEEDTEE 10
DB 686 NOSFEEDTEE 695

RESULT 14
US-10-470-048B-424
Sequence 424, Application US/10470048B
Publication No. US20050037444A1
GENERAL INFORMATION:
APPLICANT: MEINKE ET AL.
TITLE OF INVENTION: A METHOD FOR IDENTIFICATION, ISOLATION AND PRODUCTION OF
FILE REFERENCE: SONN:035US
CURRENT APPLICATION NUMBER: US/10/470,048B
CURRENT FILING DATE: 2003-07-25
NUMBER OF SEQ ID NOS: 603
SOFTWARE: PatentIn version 3.1
SEQ ID NO 424
LENGTH: 940
TYPE: PRT
ORGANISM: Staphylococcus aureus
US-10-470-048B-424

Query Match 100.0%; Score 52; DB 17; Length 940;
Best Local Similarity 100.0%; Pred. No. 3.3;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NOSFEEDTEE 10

Db 686 NOSFEEDTEE 695

RESULT 15
US-10-470-048B-69
; Sequence 69, Application US/10470048B
; Publication No. US2005037444A1
; GENERAL INFORMATION:
; APPLICANT: MEINKE ET AL.
; TITLE OF INVENTION: A METHOD FOR IDENTIFICATION, ISOLATION AND PRODUCTION OF
; TITLE OF INVENTION: ANTIGENS TO A SPECIFIC PATHOGEN
; FILE REFERENCE: SONN:035US
; CURRENT APPLICATION NUMBER: US/10/470,048B
; CURRENT FILING DATE: 2003-07-25
; NUMBER OF SEQ ID NOS: 603
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 69
; LENGTH: 948
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-10-470-048B-69

Query Match 100.0%; Score 52; DB 17; Length 948;
Best Local Similarity 100.0%; Pred. No. 3.3;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NOSFEEDTEE 10
Db 694 NOSFEEDTEE 703

Search completed: October 22, 2005, 12:39:42
Job time : 58.25 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 22, 2005, 06:10:10 ; Search time 11.45 Seconds
(without alignments)
84.032 Million cell updates/sec

Title: US-10-731-238-65

Perfect score: 52
Sequence: 1 NOSFEEDTEE 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_79:.*
1: pir1:.*
2: pir2:.*
3: pir3:.*
4: pir4:.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	52	100.0	940	2	S19702 fibronectin-binding
2	52	100.0	961	2	G90053 hypohetical prote
3	52	100.0	1018	2	A32192 fibronectin-binding
4	52	100.0	1038	2	H90053 hypohetical prote
5	42	80.8	457	2	T26642 hypohetical prote
6	37	71.2	429	2	G64649 hypohetical prote
7	37	71.2	705	2	S54521 probable membrane
8	37	71.2	1879	2	T19481 hypohetical prote
9	36	69.2	199	2	A32183 tropomyosin TPM1 -
10	35	67.3	195	2	B97345 GTP cyclohydrolase
11	35	67.3	242	2	T24034 hypohetical prote
12	35	67.3	374	2	A59273 proteinase inhibit
13	35	67.3	648	2	T20358 hypohetical prote
14	35	67.3	670	2	T06742 hypohetical prote
15	35	67.3	944	2	G86720 translation initia
16	34	65.4	186	2	F81689 conserved hypohet
17	34	65.4	429	2	G71937 hypohetical prote
18	34	65.4	530	1	T44892 probable dihydrol
19	34	65.4	553	1	H70786 steroid hormone re
20	34	65.4	560	2	S27874 hypohetical prote
21	34	65.4	888	2	T25713 hypohetical prote
22	34	65.4	1066	2	S72479 Nbc-2 protein - Ne
23	34	65.4	1337	2	T13948 atypical protein K
24	33	63.5	144	1	JQ0088 phosphotransferase
25	33	63.5	167	2	S37843 glutathione peroxi
26	33	63.5	170	2	I49055 bcl-x short - mous
27	33	63.5	176	2	I67435 gene bcl-xshort pr
28	33	63.5	227	2	G71726 cell division proc
29	33	63.5	314	2	G86835 hypohetical prote

30	33	63.5	395	2	T52423
31	33	63.5	397	2	AC3110
32	33	63.5	521	2	B69222
33	33	63.5	539	2	T02508
34	33	63.5	544	2	C42653
35	33	63.5	599	2	T00948
36	33	63.5	665	2	AG1117
37	33	63.5	665	2	A11477
38	33	63.5	752	2	S64750
39	33	63.5	812	2	S43604
40	33	63.5	905	2	S29329
41	33	63.5	1388	2	T38720
42	33	63.5	1421	2	T49500
43	33	63.5	1649	2	T19938
44	33	63.5	1980	2	S54307
45	33	63.5	5255	2	T31677

ALIGNMENTS

RESULT 1

S19702

fibronectin-binding protein B - Staphylococcus aureus
C:Species: Staphylococcus aureus

C>Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #ext_change 09-Jul-2004

C:Accession: S19702
R:Joensson, K.; Signaes, C.; Mueller, H.P.; Lindberg, M.

Eur. J. Biochem. 202, 1041-1048, 1991

A>Title: Two different genes encode fibronectin binding proteins in Staphylococcus aure
A:Reference number: S19702, PMID:92111475, PMID:1837266

A:Accession: S19702

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-940 <JOE>

A:Cross-references: UNIPROT:Q53682; EMBL:X62992; NID:G49040; PIDN:CAA44726.1; PID:G5815
C:Keywords: fibronectin binding

Query Match

Best Local Similarity 100.0%; Score 52; DB 2; Length 940;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NOSFEEDTEE 10

DB 686 NOSFEEDTEE 695

RESULT 2

G90053 hypohetical protein fmb [imported] - Staphylococcus aureus (strain N315)

C:Species: Staphylococcus aureus
C>Date: 10-May-2001 #sequence_revision 10-May-2001 #ext_change 09-Jul-2004

C:Accession: G90053
R:Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Ogu

ma, A.; Mizutani, U.; Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kato, C.; Sekimizu, K.

C.; Shib, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.

Lancet 357, 1225-1240, 2001

A>Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.

A:Reference number: AB9758, PMID:21311952, PMID:11418146

A:Accession: G90053
A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-961 <KUR>
A:Cross-references: UNIPROT:Q99RD3; GB:BA000018; PID:G13702452; PIDN:BA843593.1; GSPDB:

A:Experimental source: strain N315

C:Genetic:

A:Gene: fmbB
Query Match 100.0%; Score 52; DB 2; Length 961;
Best Local Similarity 100.0%; Pred. No. 0.27;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NOSFEEDTEE 10

Db 697 NOSFEEDTEE 706

RESULT 3

A32192
fibronectin-binding protein - Staphylococcus aureus
C:Species: Staphylococcus aureus
C:Date: 31-Jul-1989 #sequence_revision 31-Jul-1989 #text_change 16-Feb-1997
C:Accession: A32192
R:Signaee, C.; Raucet, G.; Jonsson, K.; Lindgren, P.E.; Anantharamaiah, G.M.; Hoeck, M.
Proc. Natl. Acad. Sci. U.S.A. 86, 659-703, 1989
A:Title: Nucleotide sequence of the gene for a fibronectin-binding protein from Staphylococcus aureus
A:Reference number: A32192; MUID:89038998; PMID:2521391
A:Accession: A32192
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1018 <SIG>
A:Cross-references: GB:J04151
C:Keywords: fibronectin binding

Query Match 100.0%; Score 52; DB 2; Length 1018;
Best Local Similarity 100.0%; Pred. No. 0.28;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NOSFEEDTEE 10
Db 750 NOSFEEDTEE 759

RESULT 4

H90053
hypothetical protein fnb [imported] - Staphylococcus aureus (strain N315)
C:Species: Staphylococcus aureus
C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C:Accession: H90053
R:Kurda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Gai, L.; Ogura, A.; Mizutani-Uji, Y.; Kobayashi, N.; Savano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.; C.; Shiba, T.; Hatori, M.; Ogasawara, N.; Hayashi, H.; Hiramoto, K.
Lancet 357, 1225-1240, 2001
A:Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.
A:Reference number: A89758; MUID:21311952; PMID:11418146
A:Accession: H90053
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1038 <KUR>
A:Cross-references: UNIPROT:Q99RD2; GB:BA000018; PID:G13702453; PIDN:BA843594.1; GSPDB:Q
A:Experimental source: strain N315
C:Genetics:
A:Gene: fnb

Query Match 100.0%; Score 52; DB 2; Length 1031;
Best Local Similarity 100.0%; Pred. No. 0.29;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NOSFEEDTEE 10
Db 746 NOSFEEDTEE 755

RESULT 5

T26642
hypothetical protein Y37DBA.22 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 19-Jul-2004
C:Accession: T26642
R:Barlow, K.
submitted to the EMBL Data Library, October 1998
A:Reference number: Z20247
A:Accession: T26642
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-457 <WIL>

A:Cross-references: UNIPROT:Q9XWU8; EMBL:AL032626; PIDN:CAA21543.1; CESP:Y37DBA.22
A:Experimental source: clone Y37DBA
C:Genetics:
A:Gene: CESP:Y37DBA.22
A:introns: 59/3; 220/2; 363/3; 385/3; 418/3

Query Match 80.8%; Score 42; DB 2; Length 457;
Best Local Similarity 80.0%; Pred. No. 7.2;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 NOSFEEDTEE 10
Db 425 NOSFEEDTEE 434

RESULT 6

G64649
hypothetical protein HP1039 - Helicobacter pylori (strain 26955)
C:Species: Helicobacter pylori
C:Date: 09-Aug-1997 #sequence_revision 09-Aug-1997 #text_change 09-Jul-2004
C:Accession: G64649
R:Tom, J.F.; White, O.; Keriavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.D.; Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khaliq, H.G.; Glodek, A.; McKenna, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Wathey, L.
Nature 388, 539-547, 1997
A:Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpe, P.D.; Smith, H.O.; Fraser, C.
A:Title: The complete genome sequence of the gastric pathogen Helicobacter pylori.
A:Reference number: A64520; MUID:97394467; PMID:9252185
A:Accession: G64649
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-429 <TOM>
A:Cross-references: UNIPROT:Q25682; GB:AE000611; GB:AE000511; NID:G2314173; PIDN:AA00808
C:Genetics:
A:Start codon: GTG

Query Match 71.2%; Score 37; DB 2; Length 429;
Best Local Similarity 100.0%; Pred. No. 52;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NOSFEED 7
Db 270 NOSFEED 276

RESULT 7

S54521
probable membrane protein YMR163c - Yeast (Saccharomyces cerevisiae)
N:Alternate names: hypothetical protein YMR520.13c
C:Species: Saccharomyces cerevisiae
C:Date: 08-Jul-1995 #sequence_revision 01-Sep-1995 #text_change 09-Jul-2004
C:Accession: S54521; S54608
R:Hunt, S.; Bowman, S.
submitted to the EMBL Data Library, May 1995
A:Reference number: S54510
A:Accession: S54521
A:Molecule type: DNA
A:Residues: 1-705 <HUN>
A:Cross-references: UNIPROT:Q03824; GB:Z49705; EMBL:Z49700; NID:9825556; PID:9825568; EM
A:Experimental source: strain AB972
C:Genetics:
A:Gene: MIPs:YMR163c
A:Cross-references: SGD:S0004773
A:Map position: 13R
C:Superfamily: Saccharomyces cerevisiae probable membrane protein YMR163c
C:Keywords: transmembrane protein
F:215-231/Domain: transmembrane #status predicted <TW1>
F:415-431/Domain: transmembrane #status predicted <TW2>

Query Match 71.2%; Score 37; DB 2; Length 705;
Best Local Similarity 77.8%; Pred. No. 89;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 NOSFEEDTE 9
DB 569 NDSFEEDTE 577

RESULT 8
T19481
hypothetical protein C26C6.1 - *Caenorhabditis elegans*
C:Species: *Caenorhabditis elegans*
C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T19481, T25434
R:McMurray, A.
submitted to the EMBL Data Library, May 1996
A:Reference number: Z19128
A:Accession: T19481
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-1879 <W11>
A:Cross-references: UNIPROT:Q18210; EMBL:Z72503; PIDN:CAA96600.1; GSPDB:GN00019; CESP:CA
A:Experimental source: clone C26C6
R:McMurray, A.
submitted to the EMBL Data Library, May 1996
A:Reference number: Z20033
A:Accession: T25434
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-1879 <W12>
A:Cross-references: EMBL:Z72517; PIDN:CAA96697.1; GSPDB:GN00019; CESP:C26C6.1
A:Experimental source: clone T28F4
A:Gene: CESP:C26C6.1
A:Genetics:
A:Map position: 1
A:Insertions: 42/3; 295/2; 489/3; 665/2; 980/3; 1233/2; 1292/1; 1325/3; 1349/3; 1486
F:368-422/Domain: bromodomain homology <BRO3>
F:560-615/Domain: bromodomain homology <BRO2>
F:737-792/Domain: bromodomain homology <BRO3>

Query Match 71.2%; Score 37; DB 2; Length 1879;
Best Local Similarity 60.0%; Pred. No. 2.6e+02;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 NOSFEEDTE 10
DB 324 NENFEEDSEE 333

RESULT 9
A32183
tropomyosin TPM1 - yeast (*Saccharomyces cerevisiae*)
N:Alternate names: protein N2332; protein YNL079C
C:Species: *Saccharomyces cerevisiae*
C>Date: 08-Sep-1989 #sequence_revision 08-Sep-1989 #text_change 09-Jul-2004
C:Accession: A32183; S53899; S63011; S63018; S63928
R:Li, H.; Bretscher, A.
Cell 57, 233-242, 1989
A:Title: Disruption of the single tropomyosin gene in yeast results in the disappearance
A:Reference number: A32183; MUID:89195234; PMID:2649250
A:Accession: A32183
A:Molecule type: DNA
A:Residues: 1-199 <LIU>
A:Cross-references: UNIPROT:P17536; EMBL:M25501; NID:g173037; PIDN:AAA5174.1; PID:g1730
R:Poehlmann, R.; Philippesen, P.
submitted to the EMBL Data Library, April 1995
A:Reference number: S53896
A:Accession: S53899
A:Molecule type: DNA
A:Residues: 1-199 <POE>
A:Cross-references: EMBL:X86470; NID:g791101; PIDN:CAA60179.1; PID:g791105
R:Poehlmann, R.; Philippesen, P.
submitted to the Protein Sequence Database, April 1996
A:Reference number: S62997
A:Accession: S63011
A:Molecule type: DNA

A:Residues: 1-199 <POW>
A:Cross-references: EMBL:Z71355; NID:g1301970; PIDN:CAA95953.1; PID:g1301971; MIPS:YNL0
A:Experimental source: strain S288C
R:Solier-Mira, A.; Saiz, J.E.; Ballesta, J.P.G.; Remacha, M.
submitted to the Protein Sequence Database, April 1996
A:Reference number: S63018
A:Accession: S63018
A:Molecule type: DNA
A:Residues: 1-199 <SOL>
A:Cross-references: EMBL:Z71355; NID:g1301970; PIDN:CAA95953.1; PID:g1301971; MIPS:YNL0
A:Experimental source: strain S288C
R:Poehlmann, R.; Philippesen, P.
Yeast 12, 391-402, 1996
A:Title: Sequencing a cosmid clone of *Saccharomyces cerevisiae* chromosome XIV reveals 1
A:Reference number: S63925; MUID:96267764; PMID:8701611
A:Accession: S63928
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-199 <POF>
A:Cross-references: EMBL:X86470; NID:g791101; PIDN:CAA60179.1; PID:g791105
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, April 1995
A:Genetics:
A:Gene: SGD:TPM1
A:Cross-references: SGD:S0005023; MIPS:YNL079C
A:Map position: 14L
C:Superfamily: tropomyosin TPM1
C:Keywords: coiled coil; cytoskeleton

Query Match 69.2%; Score 36; DB 2; Length 199;
Best Local Similarity 70.0%; Pred. No. 35;
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 NOSFEEDTE 10
DB 126 NQLEEDLEE 135

RESULT 10
B97345
GTP cyclohydrolase I [imported] - *Clostridium acetobutylicum*
C:Species: *Clostridium acetobutylicum*
C>Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 09-Jul-2004
C:Accession: B97345
R:Noiing, U.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee
J.; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.
J. Bacteriol. 183, 4823-4838, 2001
A:Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Cl
A:Reference number: A96900; MUID:21359325; PMID:21359325
A:Accession: B97345
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-195 <KUR>
A:Cross-references: UNIPROT:Q97D54; GB:AE01437; PIDN:AAK81549.1; PID:g15026726; GSPDB:
A:Experimental source: *Clostridium acetobutylicum* ATCC824
C:Genetics:
A:Gene: CAC3626
C:Superfamily: GTP cyclohydrolase I

Query Match 67.3%; Score 35; DB 2; Length 195;
Best Local Similarity 60.0%; Pred. No. 51;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 NOSFEEDTE 10
DB 58 NKTFEEDLKE 67

RESULT 11
T24034
hypothetical protein R07E3.2 - *Caenorhabditis elegans*
C:Species: *Caenorhabditis elegans*
C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T24034

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R: Cottage, A. submitted to the EMBL Data Library, May 1995
A: Reference number: Z19832
A: Accession: T24034
A: Status: preliminary; translated from GB/EMBL/DBJ
A: Molecule type: DNA
A: Residues: 1-242 <MIL>
A: Cross-references: UNIPROT:Q21814; EMBL:Z49207; PDB:CAA69074.1; GSPDB:GN00028; CESP:R07E3
C: Genetics:
A: Gene: CESP:R07E3.2
A: Map position: X
A: Introns: 67/2; 93/3; 138/3

Query Match      67.3%  Score 35;  DB 2;  Length 242:
Best Local Similarity 66.7%  Pred. No. 64;
Matches 6;  Conservative 3;  Mismatches 0;  Indels 0;  Gaps 0;

QY      2  QSFEEDTEE 10
      :::|||||
Db      132 ETWEEDTEE 140

RESULT 12
A59273
proteinase inhibitor 8 - human
N: Alternate names: cytoplasmic antiproteinase 2 (CAP-2)
C: Species: Homo sapiens (man)
C: Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 09-Jul-2004
C: Accession: A59273
R: Sprecher, C.A.; Morgenstern, K.A.; Mathews, S.; Dahlen, J.R.; Schrader, S.K.; Foster, J. Biol. Chem. 270, 29854-29861, 1995
A: Title: Molecular cloning, expression, and partial characterization of two novel members
A: Reference number: A59273; MUID:96102039; PMID:8530382
A: Accession: A59273
A: Status: preliminary; not compared with conceptual translation
A: Molecule type: mRNA
A: Residues: 1-374 <SPR>
A: Cross-references: UNIPROT:P50452; GB:L40377; NID:g1160926; PDB:AA041939.1; PID:g1160908
A: Experimental source: tissue type placenta; note (vector lambda gtl1); gene CAP2
C: Genetics:
A: Gene: GDB:PI8; CAP2
A: Cross-references: GDB:599392; OMIM:601697
A: Map position: 18q21.3-18q21.3
C: Superfamily: Serpin
C: Keywords: proteinase inhibitor
F:333/Inhibitory site: Arg (unidentified proteinase) #status predicted

Query Match      67.3%  Score 35;  DB 2;  Length 374;
Best Local Similarity 87.5%  Pred. No. 1e+02;
Matches 7;  Conservative 0;  Mismatches 1;  Indels 0;  Gaps 0;

QY      3  SPEEDTEE 10
      |||||||
Db      120 SFAEDTEE 127

RESULT 13
T20358
hypothetical protein D2030.8 - Caenorhabditis elegans
C: Species: Caenorhabditis elegans
C: Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C: Accession: T20358
R: Wilkinson, J.
submitted to the EMBL Data Library, June 1996
A: Reference number: Z19261
A: Accession: T20358
A: Status: preliminary; translated from GB/EMBL/DBJ
A: Molecule type: DNA
A: Residues: 1-648 <MIL>
A: Cross-references: UNIPROT:P90793; EMBL:Z73906; PDB:CAA98120.1; GSPDB:GN00019; CESP:R07E3
A: Experimental source: clone D2030
C: Genetics:

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A:Gene: CESP:ID2030.8
A:Map position: 1
A:Introns: 52/3; 141/2; 177/1; 213/3; 326/3; 394/2; 438/2; 464/3; 543/3; 573/2
C:Superfamily: Caenorhabditis elegans hypothetical protein D2030.8

Query Match
Best Local Similarity 67.3%; Score 35; DB 2; Length 648;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 NOSFEEDTE 9
DB 36 SQNFEEDEE 44

RESULT 14
T06742
Hypothetical protein F15B8.30 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004
C:Accession: T06742
R:Queller, F.; Bense, V.; Rechmann, S.; Borkova, D.; Ansoorge, W.; Salanoubat, M.; Mewes,
submitted to the Protein Sequence Database, April 1999
A:Reference number: 215794
A:Accession: T06742
A:Molecule type: DNA
A:Residues: 1-670 <QUS-
A:Cross-References: UNIPROT:Q9SVZ2; EMBL:AL049660; GSPDB:GN00061; ATSP:F15B8.30
A:Experimental source: cultivar Columbia; BAC clone F15B8
C:Genetics:
A:Gene: ATSP:F15B8.30
A:Map position: 3
A:Introns: 253/2; 347/3; 410/3; 468/3; 525/3; 563/3
C:Superfamily: Arabidopsis thaliana hypothetical protein F15B8.30

Query Match
Best Local Similarity 66.7%; Score 35; DB 2; Length 670;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 NOSFEEDTE 9
DB 154 NENFEDEE 162

RESULT 15
G86720
translational initiation factor IF-2 [imported] - Lactococcus lactis subsp. lactis (strain
C:Species: Lactococcus lactis subsp. lactis
C:Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 09-Jul-2004
C:Accession: G86720
R:Boletín, A.; Winkler, P.; Mauger, S.; Jallón, O.; Malarme, K.; Weissenbach, J.; Ehrlich
Genome Res. 11, 731-753, 2001
A:Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis s8
A:Reference number: A86625; WUID:21235186; PMID:11337471
A:Accession: G86720
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-944 <STO>
A:Cross-References: UNIPROT:P58002; GB:AB005176; PID:G12723685; PIDN:AAK04865.1; GSPDB:G
A:Experimental source: strain IL1403
C:Genetics:
A:Gene: INF8
C:Superfamily: translational initiation factor IF-2; translation elongation factor Tu homo

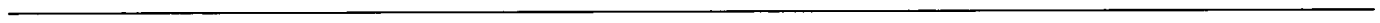
Query Match
Best Local Similarity 70.0%; Score 35; DB 2; Length 944;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 NOSFEEDTE 10
DB 396 NOSLDEDTIE 405

Search completed: October 22, 2005, 08:04:19

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Job time : 13.45 secs



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OM protein - protein search, using sw model

Run on: October 22, 2005, 06:06:36 ; Search time 55.85 Seconds
(without alignments)

91.688 Million cell updates/sec

Title: US-10-731-238-65

Perfect score: 52
Sequence: 1 NOSFEEDTEE 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database : UniProt_03 : *
1: uniprot_sprot : *
2: uniprot_trembl : *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	52	100.0	152	2	Q9AEP9
2	52	100.0	940	2	Q53682
3	52	100.0	943	2	Q8NUT8
4	52	100.0	957	2	Q6G6H4
5	52	100.0	961	2	Q99RD3
6	52	100.0	961	2	Q7A3J8
7	52	100.0	965	2	Q6GDU5
8	52	100.0	1015	2	Q8NUT7
9	52	100.0	1015	2	Q6G6H3
10	52	100.0	1018	1	FNBA_STAUA
11	52	100.0	1038	2	Q99RD2
12	52	100.0	1038	2	Q7A3J7
13	42	80.8	458	2	Q9XWU8
14	41	78.8	502	2	Q8NFC6
15	40	76.9	123	2	Q6DKA6
16	40	76.9	975	2	Q68C08
17	39	75.0	714	2	Q93ZT8
18	39	75.0	714	2	Q9LUN2
19	39	75.0	885	2	Q9GNC0
20	39	75.0	885	2	Q9VNX1
21	39	75.0	1638	2	Q869R3
22	38	73.1	169	2	Q8E534
23	37	71.2	429	2	Q9X5H1
24	37	71.2	429	2	Q25682
25	37	71.2	705	1	YK37_YEAST
26	37	71.2	1136	2	Q6FX70
27	37	71.2	1329	2	Q75JPO
28	37	71.2	1832	2	Q72700
29	37	71.2	1883	2	Q18210
30	36	69.2	199	1	TPM1_YEAST
31	36	69.2	208	2	Q72RT6

32	36	69.2	208	2	Q8F3W5	Q8F3W5 leptospira
33	36	69.2	346	2	Q8LCU2	Q8LCU2 arabidopsis
34	36	69.2	398	2	Q93VT6	Q93VT6 arabidopsis
35	36	69.2	398	2	Q7YZS1	Q7YZS1 depressaria
36	36	69.2	471	2	Q9FNN4	Q9FNN4 arabidopsis
37	36	69.2	485	2	Q9V9N1	Q9V9N1 drosophila
38	36	69.2	679	1	FTSH_BACPF	P94304 bacillus ps
39	36	69.2	841	2	Q9SHQ3	Q9SHQ3 arabidopsis
40	36	69.2	882	2	Q9VZQ9	Q9VZQ9 drosophila
41	36	69.2	946	2	Q8B0H5	Q8B0H5 mus musculus
42	35	67.3	119	2	Q7T0H6	Q7T0H6 prochloroco
43	35	67.3	136	2	Q8MQ89	Q8MQ89 caenorhabdi
44	35	67.3	195	1	GCH1_CLOAB	Q97D54 clostridium
45	35	67.3	219	2	Q6LFJ7	Q6LFJ7 plasmodium

ALIGNMENTS

RESULT 1

Q9AEP9	PRELIMINARY;	PRT;	152 AA.
AC Q9AEP9;			
DT 01-JUN-2001 (TREMBlrel. 17, Created)			
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)			
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)			
DE Fibronectin-binding protein (Fragment).			
GN Name=fnb;			
OS Staphylococcus aureus.			
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.			
OX NCBI_TaxID=1280;			
RN [1]			
RP SEQUENCE FROM N.A.			
RC STRAIN=CMRSA-1;			
RX MEDLINE=21246681; PubMed=11349044;			
RX DOI=10.1128/IAI.69.6.3791-3799.2001;			
RA Rice K., Huesca M., Vaz D., McGavin M.J.;			
"variance in fibronectin binding and fnb locus polymorphisms in			
RT Staphylococcus aureus: identification of antigenic variation in a			
RT fibronectin binding protein adhesin of the epidemic CMRSA-1 strain of			
RT methicillin-resistant S. aureus.";			
RL Infect. Immun. 69:3791-3799(2001).			
DR EMBL; AY029184; AAK31588.1; -.			
FT NON_TER			
FT NON_TER			
FT NON_TER			
SO SEQUENCE	152 AA;	17193 MW;	CFA3913C2B11C025 CRC64;

Query Match 100.0%; Score 52; DB 2; Length 152;
Best Local Similarity 100.0%; Pred. No. 0.19; Mismatches 0; Gaps 0;
Matches 10; Conservative 0; Indels 0;

QY 1 NOSFEEDTEE 10
Db 5 NOSFEEDTEE 14

RESULT 2

Q53682	PRELIMINARY;	PRT;	940 AA.
ID Q53682			
AC Q53682;			
DT 01-NOV-1996 (TREMBlrel. 01, Created)			
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)			
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)			
DE Fibronectin binding protein B.			
GN Name=fnbB;			
OS Staphylococcus aureus.			
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.			
OX NCBI_TaxID=1280;			
RN [1]			
RP SEQUENCE FROM N.A.			
RC STRAIN=8325-4;			
RX MEDLINE=92111475; PubMed=1837266;			
RA Jonsson K., Sigmas C., Muller H.P., Lindberg M.;			

RT "Two different genes encode fibronectin binding proteins :n
 RT Staphylococcus aureus. The complete nucleotide sequence and
 RT characterization of the second gene." ;
 RL Eur. J. Biochem. 202:1041-1048 (1991).
 CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
 CC an amide bond (By similarity).
 DR EMBL: X62992; CAA44726.1; -.
 DR PIR: S19702; S19702.
 DR HSSP: Q53653; 1N67.
 DR GO: GO:0009986; C:cell surface; IEA.
 DR GO: GO:0005618; C:cell wall; IEA.
 DR GO: GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
 DR GO: GO:0016020; C:membrane; IEA.
 DR GO: GO:0007155; P:cell adhesion; IEA.
 DR InterPro: IPR008966; Adhes_bact.
 DR InterPro: IPR004237; Fn_bind.
 DR InterPro: IPR005877; Gpos_YsIRK.
 DR InterPro: IPR001899; Gram_pos_anchor.
 DR Pfam: PF02986; Fn_bind; 2.
 DR Pfam: PF00746; Gram_pos_anchor; 1.
 DR Pfam: PF04650; YsIRK_signal; 1.
 DR TIGRfam: TIGR0167; LpxTG_anchor; 1.
 DR TIGRfam: TIGR0168; YsIRK_signal; 1.
 DR PROSITE: PS50847; GRAM_POS_ANCHORING; 1.
 DR Cell wall; Peptidoglycan-anchor.
 KW SEQUENCE 940 AA; 103555 MW; E35FBCA907A5345 CRC64;

Query Match 100.0%; Score 52; DB 2; Length 940
 Best Local Similarity 100.0%; Pred. No. 1.4;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NOSPEEDTEE 10
 Db 686 NOSPEEDTEE 695

RESULT 3
 Q8NU8 PRELIMINARY; PRT; 943 AA.
 ID Q8NU8;
 AC Q8NU8;
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE FnBb protein.
 GN Name=fnBb; OrderedLocustNames=MM3420;
 OS Staphylococcus aureus (strain MM2).
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 OX NCBI_TaxID=196620;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=MM2;
 RX MEDLINE=22040717; PubMed=12044378; DOI=10.1016/S0140-6736(00)08713-5;
 RA Baba T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Oguchi A.,
 RA Nagai Y., Iwama N., Asano K., Naimi T., Kuroda H., Cui L.,
 RA Yamamoto K., Hiramatsu K.;
 RA "Genome and virulence determinants of high virulence commu-ty-
 RT acquired MRSA";
 RL Lancet 359:1819-1827(2002).
 CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
 CC an amide bond (By similarity).
 DR EMBL: AP004830; BAB96285.1; -.
 DR HSSP: Q53653; 1N67.
 DR GO: GO:0009986; C:cell surface; IEA.
 DR GO: GO:0005618; C:cell wall; IEA.
 DR GO: GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
 DR GO: GO:0016020; C:membrane; IEA.
 DR GO: GO:0007155; P:cell adhesion; IEA.
 DR InterPro: IPR008966; Adhes_bact.
 DR InterPro: IPR004237; Fn_bind.
 DR InterPro: IPR005877; Gpos_YsIRK.
 DR InterPro: IPR001899; Gram_pos_anchor.
 DR Pfam: PF02986; Fn_bind; 1.
 DR Pfam: PF00746; Gram_pos_anchor; 1.

DR Pfam: PF04650; YsIRK_signal; 1.
 DR TIGRfam: TIGR0167; LpxTG_anchor; 1.
 DR TIGRfam: TIGR0168; YsIRK_signal; 1.
 DR PROSITE: PS50847; GRAM_POS_ANCHORING; 1.
 DR Cell wall; Complete proteome; Peptidoglycan-anchor.
 KW SEQUENCE 943 AA; 104537 MW; DA8A5F3194781B6A CRC64;

Query Match 100.0%; Score 52; DB 2; Length 943;
 Best Local Similarity 100.0%; Pred. No. 1.5;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NOSPEEDTEE 10
 Db 693 NOSPEEDTEE 702

RESULT 4
 Q6G6H4 PRELIMINARY; PRT; 957 AA.
 ID Q6G6H4;
 AC Q6G6H4;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Fibronectin-binding protein.
 GN Name=fnBb; OrderedLocustNames=SAS2387;
 OS Staphylococcus aureus (strain MSSA476).
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 OX NCBI_TaxID=282459;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX PubMed=15213324; DOI=10.1073/pnas.0402521101;
 RA Holden M.T.G., Fell E.J., Lindsey J.A., Peacock S.J., Day N.P.J.,
 RA Knight M.C., Foster T.J., Moore C.E., Hurst L., Ackin R., Barron A.,
 RA Baeson N., Bentley S.D., Chillingworth C., Chillingworth T.,
 RA Churcher C., Clark L., Corron C., Cronin A., Doggett J., Dowd L.,
 RA Felwell T., Hance Z., Harris B., Hauser H., Holroyd S., Jagsis K.,
 RA James K.D., Lennard N., Line A., Mayes R., Moule S., Mungall K.,
 RA Ormond D., Quail M.A., Rabinowitch E., Rutherford K.M., Sanders M.,
 RA Sharp S., Simmonds M., Stevens K., Whitehead S., Barrett B.G.,
 RA Spratt B.G., Parkhill J.;
 RA "Complete genomes of two clinical Staphylococcus aureus strains:
 RT evidence for the rapid evolution of virulence and drug resistance";
 RL Proc. Natl. Acad. Sci. U.S.A. 101:9786-9791(2004).
 CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
 CC an amide bond (By similarity).
 DR EMBL: BX571857; CAG44201.1; -.
 DR GO: GO:0009986; C:cell surface; IEA.
 DR GO: GO:0005618; C:cell wall; IEA.
 DR GO: GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
 DR GO: GO:0016020; C:membrane; IEA.
 DR GO: GO:0007155; P:cell adhesion; IEA.
 DR InterPro: IPR008966; Adhes_bact.
 DR InterPro: IPR004237; Fn_bind.
 DR InterPro: IPR005877; Gpos_YsIRK.
 DR InterPro: IPR001899; Gram_pos_anchor.
 DR Pfam: PF02986; Fn_bind; 1.
 DR Pfam: PF00746; Gram_pos_anchor; 1.
 DR Pfam: PF04650; YsIRK_signal; 1.
 DR TIGRfam: TIGR0167; LpxTG_anchor; 1.
 DR TIGRfam: TIGR0168; YsIRK_signal; 1.
 DR PROSITE: PS50847; GRAM_POS_ANCHORING; 1.
 DR Cell wall; Complete proteome; Peptidoglycan-anchor.
 KW SEQUENCE 957 AA; 105980 MW; 28F8BA7FFD0F3EAF CRC64;

Query Match 100.0%; Score 52; DB 2; Length 957;
 Best Local Similarity 100.0%; Pred. No. 1.5;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NOSPEEDTEE 10
 Db 693 NOSPEEDTEE 702

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RESULT 5
O99RD3 PRELIMINARY; PRT; 961 AA.
AC O99RD3;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE Name=fndB; OrderedLocuNames=SAV2502;
GN Name=fndB; OrderedLocuNames=SAV2502;
OS Staphylococcus aureus (strain Mu50 / ATCC 700699).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxId=158878;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=MU50 / ATCC 700699;
RC MEDLINE=21311952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2;
RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Iino J.-Q., Ito T.,
RA Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,
RA Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
RA Sekitizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
RA Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
RA Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
RT "Whole genome sequencing of methicillin-resistant Staphylococcus
RT aureus."
RL Lancet 357:1225-1240(2001).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC an amide bond (By similarity).
EMBL: AP003365; BAB58664.1; -.
DR HSP; G90053; G90053.
DR HSP; G90053; G90053.
DR GO; GO:0009986; C:cell surface; IEA.
DR GO; GO:0005618; C:cell wall; IEA.
DR GO; GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0007155; P:cell adhesion; IEA.
DR InterPro; IPR004237; Fn_bind.
DR InterPro; IPR005877; Gpos_YsIRK.
DR InterPro; IPR001899; Gram_pos_anchor.
DR Pfam; PF02986; Fn_bind.1.
DR Pfam; PF00746; Gram_pos_anchor.1.
DR Pfam; PF04650; YsIRK_signal.1.
DR TIGRFAMs; TIGR01167; LPXTG_anchor.1.
DR TIGRFAMs; TIGR01168; YsIRK_signal.1.
DR PROSITE; PSS0847; GRAM_POS_ANCHORING.1.
KW Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ SEQUENCE 961 AA; 106010 MW; 364940F884EA4101 CRC64;

Query Match 100.0%; Score 52; DB 2; Length 961;
Best Local Similarity 100.0%; Pred. No. 1.5;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NOSFEEDTEE 10
DB 697 NOSFEEDTEE 706

RESULT 6
O7A3J8 PRELIMINARY; PRT; 961 AA.
AC O7A3J8;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE FndB protein.
GN Name=fndB; OrderedLocuNames=SA2290;
OS Staphylococcus aureus (strain N315).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxId=158879;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21311952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2;
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RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
RA Chi L., Oguchi A., Aoki K.-I., Nagai Y., Iino J.-Q., Ito T.,
RA Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,
RA Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
RA Sekitizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
RA Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
RA Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
RT "Whole genome sequencing of methicillin-resistant Staphylococcus
RT aureus."
RL Lancet 357:1225-1240(2001).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC an amide bond (By similarity).
EMBL: AP003337; BAB43593.1; -.
DR GO; GO:0009986; C:cell surface; IEA.
DR GO; GO:0005618; C:cell wall; IEA.
DR GO; GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0007155; P:cell adhesion; IEA.
DR InterPro; IPR004237; Fn_bind.
DR InterPro; IPR005877; Gpos_YsIRK.
DR InterPro; IPR001899; Gram_pos_anchor.
DR Pfam; PF02986; Fn_bind.1.
DR Pfam; PF00746; Gram_pos_anchor.1.
DR Pfam; PF04650; YsIRK_signal.1.
DR TIGRFAMs; TIGR01167; LPXTG_anchor.1.
DR TIGRFAMs; TIGR01168; YsIRK_signal.1.
DR PROSITE; PSS0847; GRAM_POS_ANCHORING.1.
KW Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ SEQUENCE 961 AA; 106010 MW; 364940F884EA4101 CRC64;

Query Match 100.0%; Score 52; DB 2; Length 961;
Best Local Similarity 100.0%; Pred. No. 1.5;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NOSFEEDTEE 10
DB 697 NOSFEEDTEE 706

RESULT 7
O6GDUS PRELIMINARY; PRT; 965 AA.
AC O6GDUS;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE Fibronectin-binding protein.
GN Name=fndB; OrderedLocuNames=SA2580;
OS Staphylococcus aureus (strain MRS252).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxId=282458;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=15213324; DOI=10.1073/pnas.0402521101;
RA Holden M.T.G., Fell E.J., Lindsey J.A., Peacock S.J., Day N.P.J.,
RA Enright M.C., Foster T.J., Moore C.B., Hurst L., Atkin R., Barron A.,
RA Baeson N., Bentley S.D., Chillingworth C., Chillingworth T.,
RA Churcher C., Clark L., Cotton C., Cronin A., Doggett J., Dowd L.,
RA Felwell T., Hance Z., Harris B., Hauser H., Holtroyd S., Jagsle K.,
RA James K.D., Lennard N., Line A., Mayes R., Moule S., Mungall K.,
RA Omond D., Quail M.A., Rabinowitsch E., Rutherford K.M., Sanders M.,
RA Sharp S., Simmons M., Stevens K., Whitehead S., Barrett B.G.,
RA Spratt B.G., Parkhill J.;
RT "Complete genomes of two clinical Staphylococcus aureus strains:
RT evidence for the rapid evolution of virulence and drug resistance";
RL Proc. Natl. Acad. Sci. U.S.A. 101:9786-9791(2004).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC an amide bond (By similarity).
EMBL: BX571856; CA641560.1; -.
DR GO; GO:0009986; C:cell surface; IEA.
DR GO; GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO; GO:0016020; C:membrane; IEA.
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DR GO:0007155; P:cell adhesion; IEA.
 DR InterPro; IPR008956; Adhes_bact.
 DR InterPro; IPR004237; Fn_bind.
 DR InterPro; IPR005877; Gpos_YsIRK.
 DR InterPro; IPR001899; Gram_pos_anchor.
 DR Pfam; PF02986; Fn_bind; 1.
 DR Pfam; PF00746; Gram_pos_anchor; 1.
 DR Pfam; PF04650; YsIRK_signal; 1.
 DR TIGRfams; TIGR01167; LpxTG_anchor; 1.
 DR TIGRfams; TIGR01168; YsIRK_signal; 1.
 DR PROSITE; PS50847; GRAM_POS_ANCHORING; 1.
 DR Cell wall; Complete proteome; Peptidoglycan-anchor.
 SQ SEQUENCE 965 AA; 105691 MW; 29828132164D0551 CRC64;

Query Match 100.0%; Score 52; DB 2; Length 965;
 Best Local Similarity 100.0%; Pred. No. 1.5;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NOSFEEDTEE 10
 DB 751 NOSFEEDTEE 762

RESULT 8
 Q8NUU7 PRELIMINARY; PRT; 1015 AA.
 AC Q8NUU7; 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Fnb protein.
 GN Name=fnb; OrderedlocusNames=MW2421;
 OS Staphylococcus aureus (strain MW2).
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 OX NCBI_TaxId=196620;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=MW2;
 RX MEDLINE=2040717; PubMed=12044378; DOI=10.1016/S0140-6736(00)08713-5;
 RA Baba T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Oguchi A.,
 RA Nagai Y., Iwama N., Asano K., Naito T., Kuroda H., Cui L.,
 RA Yamamoto K., Hiramatsu K.;
 RT "Genome and virulence determinants of high virulence commu-ty-
 acquired MRSA.";
 RL Lancet 359:1819-1827(2002).
 CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
 an amide bond (By similarity).
 DR EMBL; AP004830; BAB96286.1; -;
 DR GO; GO:0009986; C:cell surface; IEA.
 DR GO; GO:0005618; C:cell wall; IEA.
 DR GO; GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0007155; P:cell adhesion; IEA.
 DR InterPro; IPR008966; Adhes_bact.
 DR InterPro; IPR004237; Fn_bind.
 DR InterPro; IPR005877; Gpos_YsIRK.
 DR InterPro; IPR001899; Gram_pos_anchor.
 DR Pfam; PF02986; Fn_bind; 1.
 DR Pfam; PF00746; Gram_pos_anchor; 1.
 DR Pfam; PF04650; YsIRK_signal; 1.
 DR TIGRfams; TIGR01167; LpxTG_anchor; 1.
 DR TIGRfams; TIGR01168; YsIRK_signal; 1.
 DR PROSITE; PS50847; GRAM_POS_ANCHORING; 1.
 DR Cell wall; Complete proteome; Peptidoglycan-anchor.
 SQ SEQUENCE 1015 AA; 111145 MW; D0F9281BB64D4D2 CRC64;

Query Match 100.0%; Score 52; DB 2; Length 1015;
 Best Local Similarity 100.0%; Pred. No. 1.6;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 NOSFEEDTEE 10
 DB 751 NOSFEEDTEE 760

RESULT 9
 Q6G6H3 PRELIMINARY; PRT; 1015 AA.
 AC Q6G6H3;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Fibronectin-binding protein.
 GN OrderedlocusNames=SA52388;
 OS Staphylococcus aureus (strain MSSA476).
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 OX NCBI_TaxId=282459;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX PubMed=15213124; DOI=10.1073/pnas.0402521101;
 RA Holden M.T.G., Fell E.J., Lindsey J.A., Peacock S.J., Day N.P.J.,
 RA Enright M.C., Foster T.J., Moore C.E., Hurst L., Atkin R., Barron A.,
 RA Bason N., Bentley S.D., Chillingworth C., Chillingworth T.,
 RA Churcher C., Clark L., Corson C., Cronin A., Doggett J., Dowd L.,
 RA Felwell T., Hance Z., Harris B., Harris A., Hayes R., Mungall K.,
 RA James K.D., Leonard N., Line A., Mayes R., Moutie S., Mungall K.,
 RA Ormond D., Quail M.A., Rabinowitch E., Rutherford K.M., Sanders M.,
 RA Sharp S., Simmonds M., Stevens K., Whitehead S., Barrett B.G.,
 RA Spratt B.G., Parkhill J.;
 RT "Complete genomes of two clinical Staphylococcus aureus strains:
 evidence for the rapid evolution of virulence and drug resistance.";
 RL Proc. Natl. Acad. Sci. U.S.A. 101:9786-9791(2004).
 CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
 an amide bond (By similarity).
 DR EMBL; BX571857; CAG44202.1; -;
 DR GO; GO:0009986; C:cell surface; IEA.
 DR GO; GO:0005618; C:cell wall; IEA.
 DR GO; GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0007155; P:cell adhesion; IEA.
 DR InterPro; IPR008966; Adhes_bact.
 DR InterPro; IPR004237; Fn_bind.
 DR InterPro; IPR005877; Gpos_YsIRK.
 DR InterPro; IPR001899; Gram_pos_anchor.
 DR Pfam; PF02986; Fn_bind; 1.
 DR Pfam; PF00746; Gram_pos_anchor; 1.
 DR Pfam; PF04650; YsIRK_signal; 1.
 DR TIGRfams; TIGR01167; LpxTG_anchor; 1.
 DR TIGRfams; TIGR01168; YsIRK_signal; 1.
 DR PROSITE; PS50847; GRAM_POS_ANCHORING; 1.
 DR Cell wall; Complete proteome; Peptidoglycan-anchor.
 SQ SEQUENCE 1015 AA; 111145 MW; D0F9281BB64D4D2 CRC64;

Query Match 100.0%; Score 52; DB 2; Length 1015;
 Best Local Similarity 100.0%; Pred. No. 1.6;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NOSFEEDTEE 10
 DB 751 NOSFEEDTEE 760

RESULT 10
 FNBA_STAUV STANDARD; PRT; 1018 AA.
 ID FNBA_STAUV
 AC P14738;
 DT 01-APR-1990 (rel. 14, Created)
 DT 01-APR-1990 (rel. 14, Last sequence update)
 DT 25-OCT-2004 (rel. 45, Last annotation update)
 DE Fibronectin-binding protein precursor (FNBP).
 GN Name=fnbpA;
 OS Staphylococcus aureus.
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 OX NCBI_TaxId=1280;
 RN [1]
 RP SEQUENCE FROM N.A.

RC STRAIN=NCTC 8325-4;
 RX MEDLINE=89089898; PubMed=2521391;
 RA Signaes C., Raucet G., Joensson K., Lindgren P.-E.,
 RA Anantharamiah G.M., Hoeck M., Lindberg M.;
 RT "Nucleotide sequence of the gene for a fibronectin-binding protein
 from *Staphylococcus aureus*: use of this peptide sequence in the
 RT synthesis of biologically active peptides.";
 RL Proc. Natl. Acad. Sci. U.S.A. 86:699-703(1989).
 CC -1- FUNCTION: The ability of bacteria to bind fibronectin has been
 CC proposed as a virulence factor enabling bacteria to colonize wound
 CC tissues and blood clots. Binding of plasma fibronectin to the
 CC bacterial surface might block adhesion receptors on *S. aureus*, thus
 CC representing an important defense mechanism against tissue
 CC invasion.
 CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
 CC an amide bond (Potential).
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL: J04151; AAA26632.1; -;
 CC InterPro: IPR004237; Fp_bind.
 CC InterPro: IPR005877; Gpos_YsIRK.
 CC InterPro: IPR001899; Gram_pos_anchor.
 CC Pfam: PF02986; Fp_bind; 1.
 CC Pfam: PF00746; Gram_pos_anchor; 1.
 CC Pfam: PF04650; YsIRK_signal; 1.
 CC TIGRPFAMs: TIGR01167; LPXTG_anchor; 1.
 CC TIGRPFAMs: TIGR01168; YsIRK_signal; 1.
 CC PROSITE: PSS0847; GRAM_POS_ANCHORING; 1.
 CC Cell adhesion; Cell wall; Peptidoglycan-anchor; Repeat; Signal;
 KW virulence.
 KM VIRULENCE.
 FT CHAIN 1 36
 FT PROPEP 37 985
 FT REPEAT 545 1018
 FT REPEAT 575 574
 FT REPEAT 575 604
 FT DOMAIN 745 878
 FT REPEAT 745 782
 FT REPEAT 783 820
 FT REPEAT 821 859
 FT REPEAT 860 878
 FT DOMAIN 879 948
 FT REPEAT 879 892
 FT REPEAT 893 906
 FT REPEAT 907 920
 FT REPEAT 921 934
 FT REPEAT 935 948
 FT SITE 982 986
 FT MOD_RES 985 985
 SQ SEQUENCE 1018 AA; 111780 MW; 58175E0020E81F1F CRC64;
 Query Match 100.0%; Score 52; DB 1; Length 1018;
 Best Local Similarity 100.0%; Pred. No. 1.6;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 NOSFEEDTEE 10
 DB 750 NOSFEEDTEE 759
 RESULT 11
 ID Q09RD2 PRELIMINARY; PRT; 1038 AA.
 AC Q09RD2;
 DT 01-JUN-2001 (TREMBlrel. 17, Created)

DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
 DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
 DE Fibronectin-binding protein homolog.
 GN Name=fib; OrderedLocuNames=SAV2503;
 OS *Staphylococcus aureus* (strain Mu50 / ATCC 700699).
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 OX NCBI_TaxId=158878;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=MU50 / ATCC 700699;
 RX MEDLINE=2111952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2;
 RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
 RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Iian J.-Q., Ito T.,
 RA Kanamori M., Matsunari H., Maruyama A., Murakami H., Hosoyama A.,
 RA Mizutani-Ui Y., Takahashi N.K., Kohara S., Goto S., Yabuzaki J.,
 RA Sekimizu K., Hiraoka H., Yamashita A., Oshima K., Furuya K., Yoshino C., Shida T.,
 RA Hattori M., Ogasawara N., Hayaishi H., Hiramatsu K.;
 RT "Whole genome sequencing of methicillin-resistant *Staphylococcus*
 RT aureus.";
 RL Lancet 357:1225-1240(2001).
 CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
 CC an amide bond (By similarity).
 CC EMBL: AF003365; BAB58665.1; -;
 CC PIR: H90053; H90053.
 CC GO: GO:000986; C:cell surface; IEA.
 CC GO: GO:0005618; C:cell wall; IEA.
 CC GO: GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
 CC GO: GO:0016020; C:membrane; IEA.
 CC GO: GO:0007155; P:cell adhesion; IEA.
 CC InterPro: IPR008966; Adhes_bact.
 CC InterPro: IPR004237; Fp_bind.
 CC InterPro: IPR005877; Gpos_YsIRK.
 CC InterPro: IPR001899; Gram_pos_anchor.
 CC Pfam: PF02986; Fp_bind; 1.
 CC Pfam: PF00746; Gram_pos_anchor; 1.
 CC Pfam: PF04650; YsIRK_signal; 1.
 CC TIGRPFAMs: TIGR01167; LPXTG_anchor; 1.
 CC TIGRPFAMs: TIGR01168; YsIRK_signal; 1.
 CC PROSITE: PSS0847; GRAM_POS_ANCHORING; 1.
 CC Cell wall; Complete proteome; Peptidoglycan-anchor.
 SQ SEQUENCE 1038 AA; 113618 MW; 666BF6BF2BFEB2 CRC64;
 Query Match 100.0%; Score 52; DB 2; Length 1038;
 Best Local Similarity 100.0%; Pred. No. 1.6;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 NOSFEEDTEE 10
 DB 746 NOSFEEDTEE 755
 RESULT 12
 ID Q7A3J7 PRELIMINARY; PRT; 1038 AA.
 AC Q7A3J7;
 DT 05-JUL-2004 (TREMBlrel. 27, Created)
 DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
 DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
 DE Fnb protein.
 GN Name=fnb; OrderedLocuNames=SA2291;
 OS *Staphylococcus aureus* (strain N315).
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 OX NCBI_TaxId=158879;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC MEDLINE=21311952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2;
 RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
 RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Iian J.-Q., Ito T.,
 RA Kanamori M., Matsunari H., Maruyama A., Murakami H., Hosoyama A.,
 RA Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
 RA Sekimizu K., Hiraoka H., Kuhara S., Goto S., Yabuzaki J.,
 RA Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,

RA Hattori M., Ogasawara N., Hayaishi H., Hiramatsu K.;
RT "Whole genome sequencing of methicillin-resistant *Staphylococcus*
RL aureus.";
CC Lancet 357:1225-1240(2001).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
an amide bond (By similarity).
DR EMBL: AP003137; BAB43594.1; -.
DR GO: GO:0009986; C:cell surface; IEA.
DR GO: GO:0005618; C:cell wall; IEA.
DR GO: GO:0003275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO: GO:0016020; C:membrane; IEA.
DR GO: GO:0007155; P:cell adhesion; IEA.
DR InterPro: IPR008966; Adhes_bact.
DR InterPro: IPR004237; Fn_bind.
DR InterPro: IPR005877; Gpos_YsIRK.
DR InterPro: IPR001899; Gram_pos_anchor.
DR Pfam: PF02986; Fn_bind; 1.
DR Pfam: PF00746; Gram_pos_anchor; 1.
DR TIGRPFAM: TIGR01167; LpxK_anchor; 1.
DR TIGRPFAM: TIGR01168; YsIRK_signal; 1.
DR PROSITE: PS00847; GRAM_POS_ANCHORING; 1.
KW Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ SEQUENCE 1038 AA; 113618 MW; 666BF6BF2BFEB12 CRC64;

Query Match 100.0%; Score 52; DB 2; Length 1038;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NOSFEEDTEE 10
|||||||
Db 746 NOSFEEDTEE 755

RESULT 13
Q9XWU8 PRELIMINARY; PRT; 458 AA.
ID Q9XWU8;
AC Q9XWU8;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein Y37D8A.22.
GN ORFNames=Y37D8A.22;
OS *Caenorhabditis elegans*.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditioidea;
OC Rhabditidae; Pelodertinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=Brieol N2;
RX MEDLINE=99069613; PubMed=9851916;
RA none;
RT "Genome sequence of the nematode *C. elegans*: A platform for
RT investigating biology.";
RL Science 282:2012-2018(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Brieol N2;
RA Barlow K.;
RL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL: AL032626; CAA21543.2; -.
DR PIR: T26642; T26642.
DR Wormbase: WBGene00012559; Y37D8A.22.
DR Wormpep: Y37D8A.22; CE31831.
KW Hypothetical protein.
SQ SEQUENCE 458 AA; 51868 MW; 1F1EF7D9DEEC069 CRC64;

Query Match 80.8%; Score 42; DB 2; Length 458;
Best Local Similarity 80.0%; Pred. No. 41;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 NOSFEEDTEE 10
|||||||
RN

Db 426 NOSFEEDTEE 435

RESULT 14
Q8NFC6 PRELIMINARY; PRT; 502 AA.
ID Q8NFC6;
AC Q8NFC6;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Ovary;
RA Guo J.H., Yu L.;
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF528529; AAM94279.1; -.
KW Hypothetical protein.
SQ SEQUENCE 502 AA; 55115 MW; C77D17CCA120FA04 CRC64;

Query Match 78.8%; Score 41; DB 2; Length 502;
Best Local Similarity 100.0%; Pred. No. 68;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SPEEDTEE 10
|||||||
Db 418 SPEEDTEE 425

RESULT 15
Q6DKA6 PRELIMINARY; PRT; 123 AA.
ID Q6DKA6;
AC Q6DKA6;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE LOC43712 protein (Fragment).
GN Name=LOC43712;
OS *Xenopus laevis* (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN (1)
RP SEQUENCE FROM N.A.
RC TISSUE=Eye;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner J., Shenmen C.M., Schuler G.D.,
RA Altshul S.F., Zeeberg B., Buetow K.H., Scheele C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Schetz T.E.,
RA Brownstein M.T., Udén T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mulhaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.U., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Huiyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriques S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shcherchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Gittwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smalls D.E., Scherch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.

```

RC TISSUE=Eye;
RX MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA Richardson P.;
RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus
RT initiative";
RL Dev. Dyn. 225:384-391(2002).
RN (3)
RP SEQUENCE FROM N.A.
RC TISSUE=Eye;
RA Klein S., Gerhard D.S.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC074456; AAH74456.1;
DR GO; GO:0005667; C:transcription factor complex; IEA.
DR GO; GO:0003702; F:RNA polymerase II transcription factor acti. . .; IEA.
DR GO; GO:0006352; P:transcription initiation; IEA.
DR InterPro; IPR009072; Histone-fold.
DR Pfam; PF02269; TFIID-18kDa; I.
FT NON_TER 1
SQ SEQUENCE 123 AA; 14188 MW; 8C3A76F7C9AB38C CRC64;

Query Match 76.9%; Score 40; DB 2; Length 123;
Best Local Similarity 70.0%; Pred. NO. 22;
Matches 7; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 NGSFEEDTER 10
DB 6 DQTFEETER 15

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Search completed: October 22, 2005, 08:00:24
 Job time : 58.85 secs

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CC	streptococci, e.g. meningitis, otitis media, pneumonia, endocarditis,
CC	mastitis in cattle, abortion in horses and many others. Since the
CC	antibodies block binding of bacteria, they should be effective against
CC	antibiotic-resistant strains, and may replace antibiotic therapy or
CC	increase its effectiveness. Sequences AAM65719-41 and AAM75658 represent
CC	peptides which were synthesised to span the D1 motif and the N-terminal
CC	18 amino acids of D2, with each peptide overlapping by eight amino acids
CC	with the previous sequence
XX	
SQ	Sequence 10 AA;
	Query Match 100.0%; Score 52; DB 2; Length 10
	Best Local Similarity 100.0%; Pred. No. 0.029;
	Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0
OY	1 SPEEDTEBDK 10
DB	1 SPEEDTEBDK 10
RESULT 2	
AAM65761	ID AAM65761 standard; peptide; 14 AA.
XX	AAM65761;
AC	
XX	16-OCT-1998 (first entry)
DT	
XX	Peptide #105.
DE	
XX	microbial surface components recognising adhesive matrix molecule;
KW	MSCRAMM; fibronectin; fibronectin-binding protein; antibody; epitope;
RW	antibiotic; bacterial infection; antibiotic-resistant strain.
KV	
XX	
OS	Synthetic.
CS	Staphylococcus aureus.
XX	
PN	WO9831389-A2.
PD	23-JUL-1998.
XX	
PJ	21-JAN-1998; 98MO-US001222.
PF	
PR	21-JAN-1997; 97US-0036133P.
XX	
PA	(TEXA) UNIV TEXAS A & M SYSTEM.
XX	
P1	Hoecek M, Patti JM, House-Pompeo KL, Speziale P, Joh D;
PI	McGavin MJ;
DR	WPI, 1998-413816/35.
PS	
XX	Disclosure, Page 173; 201pp; English.
CC	The invention relates to antibodies that bind to a fibronectin-binding
CC	domain of a fibronectin-binding protein, and inhibit binding of the
CC	protein to fibronectin. Also claimed are: (1) isolated peptides of a
CC	fibronectin-binding protein that do not bind to fibronectin; (2) fusion
CC	protein containing at least one peptide of a fibronectin-binding protein
CC	linked to a second amino acid sequence; (3) nucleic acid encoding the
CC	isolated peptide of (1). Antibodies, the isolated peptides cf (1) and the
CC	nucleic acids are all useful for immunisation (active or passive) and (by
CC	inhibiting binding of bacteria to fibronectin) for preventing or treating
CC	infection in humans or other animals, particularly by staphylococci or
CC	streptococci, e.g. meningitis, otitis media, pneumonia, endocarditis,
CC	mastitis in cattle, abortion in horses and many others. Since the
CC	antibodies block binding of bacteria, they should be effective against
CC	antibiotic-resistant strains, and may replace antibiotic therapy or
CC	increase its effectiveness. The present sequence is shown in the

```
CC specification
XX
SQ Sequence 14 AA;

Query Match      100.0%; Score 52; DB 2; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.042;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0

QY          1 SPEEDTEEDK 10
              |||||
Db           1 SFEEDTEEDK 10

RESULT 3
AAP80660
ID AAP80660 standard; protein; 38 AA.
XX
AC AAP80660;
XX
DT 25-MAR-2003 (revised)
DT 07-OCT-1990 (first entry)
XX
DE Protein with fibronectin binding ability.
KW Hybrid DNA molecule; fibronectin binding; mastitis; ruminants; wound infection.
XX
OS Staphylococcus aureus.
PN EP294349-A.
PD 07-DEC-1988.
XX
PF 30-MAY-1988; 88EP-00850188.
XX
PR 01-JUN-1987; 87SE-00002272.
PA (ALFA ) ALFA LAVAL AGRIC INT AB.
Lindberg MK, Signae LC, Wadstrom TM, Froman G;
PI MPI: 1988-347978/49.
DR N-PADB; AAN81097.
XX
PT Hybrid DNA encoding Staphylococcus aureus fibronectin binding protein - useful for immunisation and topical application to prevent staphylococcal infections.
XX
PS Claim 11; Page 12; 23pp; English.
XX
PS The peptide has fibronectin binding ability. It is useful for immunising ruminants against staphylococcal mastitis, pref. when used at 0.5-5 micrograms/kg, using 3 doses given at 1-3 week intervals; for topical application to prevent wound infection, using an isotonic saline soln. of concn. 25-250 microgram/ml; and, when immobilised on a carrier, for diagnosing staphylococcal infections. (Updated on 25-MAR-2003 to correct PF field.) (Updated on 25-MAR-2003 to correct PA field.)
CC
XX
SQ Sequence 38 AA;

Query Match      100.0%; Score 52; DB 1; Length 38;
Best Local Similarity 100.0%; Pred. No. 0.12;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0

QY          1 SPEEDTEEDK 10
              |||||
Db           8 SFEEDTEEDK 17

RESULT 4
AAP82116
ID AAP82116 standard; protein; 38 AA.
XX
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AC AAB2116;
 XX
 XX 25-MAR-2003 (revised)
 DT 05-JAN-1990 (first entry)
 XX
 XX Fibronection binding protein.
 DE
 XX Fibronection binding protein; S. aureus; immunisation; mastitis; ruminants;
 KW wound infection; diagnosis.
 XX
 XX Staphylococcus aureus.
 OS
 XX EP294349-A.
 PN
 XX 07-DEC-1988.
 PD
 XX 30-MAY-1988; 88EP-00850188.
 PF
 XX 01-JUN-1987; 87SE-00002272.
 PR
 XX (ALFA) ALFA LAVAL AGRIC INT AB.
 PA
 XX Lindberg MK, Signas LC, Wadstrom TM, Froman G;
 PI WPI; 1988-347978/49.
 XX N-PSDB; AAN82054.
 DR
 XX Hybrid DNA encoding Staphylococcus aureus fibronection binding protein -
 PT useful for immunisation and topical application to prevent staphylococcal
 PT infections.
 PT
 XX Claim 11; Page 12; 23pp; English.
 PS
 XX The S. aureus fibronection binding protein may be included in a hybrid
 CC protein. The protein may be used to immunise ruminants against
 CC staphylococcal mastitis, pref. when given at 0.5-5 microg/kg, using 3
 CC doses at 1-3 week intervals; and for topical applicn. to prevent wound
 CC infection, pref. using isotonic saline soln. of concn. 25-250 microg/mg.
 CC The DNA encoding the binding protein and the hybrid protein may be
 CC immobilised on a carrier and used to diagnose staphylococcal infections.
 CC (Updated on 25-MAR-2003 to correct PA field.)
 CC
 SQ Sequence 38 AA;
 XX
 XX Query Match 100.0%; Score 52; DB 1; Length 38;
 XX Best Local Similarity 100.0%; Pred. No. 0.12;
 XX Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 SPEEDTEBDK 10
 DB 8 SFEDTEBDK 17
 XX
 XX RESULT 5
 XX AAW65662
 ID AAW65662 standard; peptide; 38 AA.
 AC
 XX AAW65662;
 AC
 DT 16-OCT-1998 (first entry)
 DT
 XX Fibronection binding protein-derived peptide #6.
 XX
 DE microbial surface components recognising adhesive matrix molecule;
 KW MSCRAMM; fibronection; fibronection-binding protein; antibody; epitope;
 KW antibiotic; bacterial infection; antibiotic-resistant strain.
 XX
 XX Synthetic.
 OS Staphylococcus aureus.
 OS
 XX WO9831389-A2.
 PN
 XX 23-JUL-1998.
 PD

XX
 XX 21-JAN-1998; 98WO-US001222.
 PF
 XX 21-JAN-1997; 97US-0036139P.
 PR
 XX (TEXA) UNIV TEXAS A & M SYSTEM.
 PA
 XX Hoeck M, Patti JM, House-Pompeo KL, Speciale P, Joh D;
 PI McGavin MJ;
 PI WPI; 1998-413816/35.
 DR
 XX Antibody that binds to fibronection-binding protein, preventing its
 PT binding to fibronection - used to treat or prevent bacterial infection,
 PT especially by Staphylococci and Streptococci.
 PT
 XX Example 2; Page 92; 201pp; English.
 PS
 XX The invention relates to antibodies that bind to a fibronection-binding
 CC domain of a fibronection-binding protein, and inhibit binding of the
 CC protein to fibronection. Also claimed are: (1) isolated peptides of a
 CC fibronection-binding protein that do not bind to fibronection; (2) fusion
 CC protein containing at least one peptide of a fibronection-binding protein
 CC linked to a second amino acid sequence; (3) nucleic acid encoding the
 CC isolated peptide of (1). Antibodies, the isolated peptides of (1) and the
 CC nucleic acids are all useful for immunisation (active or passive) and (by
 CC inhibiting binding of bacteria to fibronection) for preventing or treating
 CC infection in humans or other animals, particularly by staphylococci or
 CC streptococci, e.g. meningitis, otitis media, pneumonia, endocarditis,
 CC mastitis in cattle, abortion in horses and many others. Since the
 CC antibodies block binding of bacteria, they should be effective against
 CC antibiotic-resistant strains, and may replace antibiotic therapy or
 CC increase its effectiveness. Sequences AAW65659-68 represent synthetic
 CC epitopes from the fibronection binding domains DU and DI-D4 of the S.
 CC aureus fnbA gene
 CC
 SQ Sequence 38 AA;
 XX
 XX Query Match 100.0%; Score 52; DB 2; Length 38;
 XX Best Local Similarity 100.0%; Pred. No. 0.12;
 XX Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 SPEEDTEBDK 10
 DB 7 SFEDTEBDK 16
 XX
 XX RESULT 6
 XX AAW65699
 ID AAW65699 standard; peptide; 38 AA.
 AC
 XX AAW65699;
 AC
 DT 16-OCT-1998 (first entry)
 DT
 XX Fibronection binding protein-derived peptide #43.
 XX
 DE microbial surface components recognising adhesive matrix molecule;
 KW MSCRAMM; fibronection; fibronection-binding protein; antibody; epitope;
 KW antibiotic; bacterial infection; antibiotic-resistant strain.
 XX
 XX Synthetic.
 OS Staphylococcus aureus.
 OS
 XX WO9831389-A2.
 PN
 XX 23-JUL-1998.
 PD
 XX 21-JAN-1998; 98WO-US001222.
 PF
 XX 21-JAN-1997; 97US-0036139P.
 PR
 XX (TEXA) UNIV TEXAS A & M SYSTEM.
 PA


```

XX Hoecek M, Patti JM, House-Pompeo KL, Speziale P, Joh D;
PI Mcgavin MJ;
XX WPI; 1998-413816/35.
XX
XX Antibody that binds to fibronectin-binding protein, preventing its
PT binding to fibronectin - used to treat or prevent bacterial infection,
PT especially by Staphylococci and Streptococci.
XX
XX Example 8; Page 102; 201pp; English.
XX
XX The invention relates to antibodies that bind to a fibronectin-binding
CC domain of a fibronectin-binding protein, and inhibit binding of the
CC protein to fibronectin. Also claimed are: (1) isolated peptides of a
CC fibronectin-binding protein that do not bind to fibronectin; (2) fusion
CC protein containing at least one peptide of a fibronectin-binding protein
CC linked to a second amino acid sequence; (3) nucleic acid encoding the
CC isolated peptide of (1). Antibodies, the isolated peptides of (1) and the
CC nucleic acids are all useful for immunisation (active or passive) and (by
CC inhibiting binding of bacteria to fibronectin) for preventing or treating
CC infection in humans or other animals, particularly by staphylococci or
CC streptococci, e.g. meningitis, otitis media, pneumonia, endocarditis,
CC mastitis in cattle, abortion in horses and many others. Since the
CC antibodies block binding of bacteria, they should be effective against
CC antibiotic-resistant strains, and may replace antibiotic therapy or
CC increase its effectiveness. Sequences AAW65691-700 represent a series of
CC synthetic peptides based on the D1 region of S. aureus fibronectin
CC binding protein A. They were synthesised to contain mutations
XX
XX
SQ Sequence 38 AA;
XX
XX Query Match 100.0%; Score 52; DB 2; Length 38;
XX Best Local Similarity 100.0%; Pred. No. 0.12;
XX Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 SPEEDTEBDK 10
XX |||||||||
XX 7 SPEEDTEBDK 16
XX
XX
XX RESULT 7
XX AAW65661
XX ID AAW65661 standard; peptide; 38 AA.
XX
XX AAW65661;
XX
XX 16-OCT-1998 (first entry)
XX
XX Fibronectin binding protein-derived peptide #5.
XX
XX microbial surface components recognising adhesive matrix molecule;
KW MSCRAMM; fibronectin; fibronectin-binding protein; antibody; epitope;
KW antibiotic; bacterial infection; antibiotic-resistant strain.
XX
XX Synthetic.
OS Staphylococcus aureus.
XX
XX WO9831389-A2.
XX
XX 23-JUL-1998.
XX
XX 21-JAN-1998; 98WO-US001222.
XX
XX 21-JAN-1997; 97US-0036139P.
XX
XX (TEXA ) UNIV TEXAS A & M SYSTEM.
XX
XX Hoecek M, Patti JM, House-Pompeo KL, Speziale P, Joh D;
PI Mcgavin MJ;
XX WPI; 1998-413816/35.
XX

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PT Antibody that binds to fibronectin-binding protein, preventing its
PT binding to fibronectin - used to treat or prevent bacterial infection,
PT especially by Staphylococci and Streptococci.
XX
XX Example 2; Page 92; 201pp; English.
XX
XX The invention relates to antibodies that bind to a fibronectin-binding
CC domain of a fibronectin-binding protein, and inhibit binding of the
CC protein to fibronectin. Also claimed are: (1) isolated peptides of a
CC fibronectin-binding protein that do not bind to fibronectin; (2) fusion
CC protein containing at least one peptide of a fibronectin-binding protein
CC linked to a second amino acid sequence; (3) nucleic acid encoding the
CC isolated peptide of (1). Antibodies, the isolated peptides of (1) and the
CC nucleic acids are all useful for immunisation (active or passive) and (by
CC inhibiting binding of bacteria to fibronectin) for preventing or treating
CC infection in humans or other animals, particularly by staphylococci or
CC streptococci, e.g. meningitis, otitis media, pneumonia, endocarditis,
CC mastitis in cattle, abortion in horses and many others. Since the
CC antibodies block binding of bacteria, they should be effective against
CC antibiotic-resistant strains, and may replace antibiotic therapy or
CC increase its effectiveness. Sequences AAW6559-68 represent synthetic
CC epitopes from the fibronectin binding domains D1 and D1-D4 of the S.
CC aureus fnbA gene
XX
XX
SQ Sequence 38 AA;
XX
XX Query Match 100.0%; Score 52; DB 2; Length 38;
XX Best Local Similarity 100.0%; Pred. No. 0.12;
XX Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 SPEEDTEBDK 10
XX |||||||||
XX 7 SPEEDTEBDK 16
XX
XX
XX RESULT 8
XX AAW65712
XX ID AAW65712 standard; peptide; 39 AA.
XX
XX AAW65712;
XX
XX 16-OCT-1998 (first entry)
XX
XX Fibronectin binding protein-derived peptide #56.
XX
XX microbial surface components recognising adhesive matrix molecule;
KW MSCRAMM; fibronectin; fibronectin-binding protein; antibody; epitope;
KW antibiotic; bacterial infection; antibiotic-resistant strain.
XX
XX Synthetic.
OS Staphylococcus aureus.
XX
XX WO9831389-A2.
XX
XX 23-JUL-1998.
XX
XX 21-JAN-1998; 98WO-US001222.
XX
XX 21-JAN-1997; 97US-0036139P.
XX
XX (TEXA ) UNIV TEXAS A & M SYSTEM.
XX
XX Hoecek M, Patti JM, House-Pompeo KL, Speziale P, Joh D;
PI Mcgavin MJ;
XX WPI; 1998-413816/35.
XX
XX Antibody that binds to fibronectin-binding protein, preventing its
PT binding to fibronectin - used to treat or prevent bacterial infection,
PT especially by Staphylococci and Streptococci.
XX
XX Example 8; Page 104; 201pp; English.
XX

```

CC The invention relates to antibodies that bind to a fibronectin-binding
 CC domain of a fibronectin-binding protein, and inhibit binding of the
 CC protein to fibronectin. Also claimed are: (1) isolated peptides of a
 CC fibronectin-binding protein that do not bind to fibronectin; (2) fusion
 CC protein containing at least one peptide of a fibronectin-binding protein
 CC linked to a second amino acid sequence; (3) nucleic acid encoding the
 CC isolated peptide of (1). Antibodies, the isolated peptides of (1) and the
 CC nucleic acids are all useful for immunisation (active or passive) and (by
 CC inhibiting binding of bacteria to fibronectin) for preventing or treating
 CC infection in humans or other animals, particularly by staphylococci or
 CC streptococci, e.g. meningitis, otitis media, pneumonia, endocarditis,
 CC mastitis in cattle, abortion in horses and many others. Since the
 CC antibodies block binding of bacteria, they should be effective against
 CC antibiotic-resistant strains, and may replace antibiotic therapy or
 CC increase its effectiveness. The present sequence is shown in the
 CC specification.

SQ Sequence 39 AA;

Query Match 100.0%; Score 52; DB 2; Length 39;
 Best Local Similarity 100.0%; Pred. No. 0.13;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SFEEDTEEDK 10
 |||||
 DB 7 SFEEDTEEDK 16

RESULT 9
 AAW65713 standard; peptide; 39 AA.

XX AAW65713;
 XX 16-OCT-1998 (first entry)
 DT
 DE Fibronectin binding protein-derived peptide #57.
 XX
 XX microbial surface components recognising adhesive matrix molecule;
 KM MSCRAMM; fibronectin; fibronectin-binding protein; antibody; epitope;
 KM antibiotic; bacterial infection; antibiotic-resistant strain.
 XX
 XX Synthetic.
 OS Staphylococcus aureus.
 XX
 XX WO9831369-A2.
 PN 23-JUL-1998.
 PD
 XX 21-JAN-1998; 98WO-US001222.
 PF
 XX 21-JAN-1997; 97US-0036139P.
 PR
 XX (TEXA) UNIV TEXAS A & M SYSTEM.
 PA Hoeoek M; Patil JM, House-Pompeo KL, Speciale P, Joh D;
 PI Megavain MJ;
 XX WPI; 1998-413816/35.
 DR
 XX The invention relates to antibodies that bind to a fibronectin-binding
 CC domain of a fibronectin-binding protein, and inhibit binding of the
 CC protein to fibronectin. Also claimed are: (1) isolated peptides of a
 CC fibronectin-binding protein that do not bind to fibronectin; (2) fusion
 CC protein containing at least one peptide of a fibronectin-binding protein
 CC linked to a second amino acid sequence; (3) nucleic acid encoding the
 CC isolated peptide of (1). Antibodies, the isolated peptides of (1) and the

CC nucleic acids are all useful for immunisation (active or passive) and (by
 CC inhibiting binding of bacteria to fibronectin) for preventing or treating
 CC infection in humans or other animals, particularly by staphylococci or
 CC streptococci, e.g. meningitis, otitis media, pneumonia, endocarditis,
 CC mastitis in cattle, abortion in horses and many others. Since the
 CC antibodies block binding of bacteria, they should be effective against
 CC antibiotic-resistant strains, and may replace antibiotic therapy or
 CC increase its effectiveness. The present sequence is shown in the
 CC specification.

SQ Sequence 39 AA;

Query Match 100.0%; Score 52; DB 2; Length 39;
 Best Local Similarity 100.0%; Pred. No. 0.13;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SFEEDTEEDK 10
 |||||
 DB 7 SFEEDTEEDK 16

RESULT 10
 AAR58806 standard; protein; 130 AA.

XX AAR58806;
 XX 25-MAR-2003 (revised)
 DT 30-MAR-1995 (first entry)
 DT
 DE Fibronectin binding domain D1-D4 (709-838(P838T)).
 XX
 XX Fibronectin binding protein; Fbp; fibronectin binding domain;
 KM monoclonal antibody; Mab; adhesion; Gram-positive bacterium; bacteraemia;
 KM Escherichia coli.
 XX
 XX Staphylococcus aureus.
 OS
 XX WO9418327-A1.
 PN 18-AUG-1994.
 PD
 PF 04-FEB-1994; 94WO-GB000215.
 XX
 XX 05-FEB-1993; 93GB-00002289.
 PR 20-OCT-1993; 93GB-00021592.
 XX
 XX (SMIK) SMITHKLINE BEECHAM PLC.
 PA Burnham MKR, Chopra I, Critchley IA, Knowles DJC;
 PI WPI; 1994-279748/34.
 DR
 XX Fibronectin binding protein and monoclonal antibodies specific for Fbp -
 PT useful to prevent adherence of Gram-positive bacteria to indwelling
 PT devices or wounds.
 PT
 XX Disclosure; Page 30; 40pp; English.
 PS
 XX Polypeptide corresponding to residues 709-786 plus PIVPPT, 6709-
 CC P838(P838T) and 6709-7838 (AAR58805-07, respectively) of S. aureus J2385
 CC (NCIMB 40532) Fbp type A fibronectin binding domain D1-D4 region Mab
 CC (AAR58808) were expressed in E. coli Buz1(DE4) and used to raise MAb
 CC specific for Fbp. (Updated on 25-MAR-2003 to correct PN field.)
 XX
 XX Sequence 130 AA;

Query Match 100.0%; Score 52; DB 2; Length 130;
 Best Local Similarity 100.0%; Pred. No. 0.46;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SFEEDTEEDK 10
 |||||

```

Db      8 SPEEDTEEDK 17

RESULT 11
AAR58807
ID      AAR58807 standard; protein; 130 AA.
XX
XX
AC      AAR58807;
XX
XX      25-MAR-2003 (revised)
DT      30-MAR-1995 (first entry)
XX
XX      Fibronectin binding domain D1-D4 (709-838) .
DE
XX
XX      Fibronectin binding protein; Fbp; fibronectin binding domain;
KW      monoclonal antibody; Mab; adhesion; Gram-positive bacterium; bacteraemia;
KW      Escherichia coli.
XX
XX      Staphylococcus aureus.
OS
XX      WO9418327-A1.
PN
XX      18-AUG-1994.
PD
XX      04-FEB-1994; 94WO-GB000215.
PF
XX      05-FEB-1993; 93GB-00002289.
PR      20-OCT-1993; 93GB-00021592.
XX
XX      (SMIK ) SMITHKLINE BEECHAM PLC.
PA
XX      Burnham MKR, Chopra I, Critchley IA, Knowles DJC;
PI      WPI; 1994-279748/34.
XX
XX      Fibronectin binding protein and monoclonal antibodies specific for Fbp -
PT      useful to prevent adherence of Gram-positive bacteria to indwelling
XX      devices or wounds.
XX
XX      Disclosure; Page 30; 40pp; English.
PS
XX
XX      Polypeptides corresponding to residues G709-T886 plus PRTVPT, G709-
CC      P838(P838T) and G709-P838 (AAR58805-07, respectively) of S. aureus J2385
CC      (NCIMB 40532) Fbp type A fibronectin binding domain D1-D4 region
CC      (AAR58808) were expressed in E. coli BL21(DE4) and used to raise MAbs
CC      specific for Fbp. (Updated on 25-MAR-2003 to correct PN field.)
XX
XX      SQ Sequence 130 AA;

Query Match      100.0%; Score 52; DB 2; Length 130;
Best Local Similarity 100.0%; Pred. No. 0.46;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 SPEEDTEEDK 10
      |||||
      8 SPEEDTEEDK 17

Db

RESULT 12
AAR91202
ID      AAR91202 standard; peptide; 130 AA.
XX
XX      AAR91202;
XX
XX      13-NOV-1996 (first entry)
DT
XX
XX      D1-D4 fibronectin binding domains.
DE
XX
XX      Fibronectin; oral hygiene; gingivitis; gum disease; adhesior;
KW      periodontitis; oral pathogen; caries; calculus; candidiasis; oral surgery;
KW      tissue regeneration; irrigation; toothpaste; dentifrice; mouthwash;
KW      lozenge.
XX
XX

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OS      Staphylococcus aureus.
XX
XX      WO9604003-A1.
PN
XX      15-FEB-1996.
PD
XX      18-JUL-1995; 95WO-EP002825.
PF
XX      05-AUG-1994; 94GB-00015902.
PR
XX      (SMIK ) SMITHKLINE BEECHAM PLC.
PA
XX      Barnett P, Critchley IA, Dodd I;
PI      WPI; 1996-129122/13.
XX
XX      Prevention of adherence of oral pathogens in the oral cavity, partic.
PT      tooth surfaces - by application of a fibronectin binding protein or
XX      polypeptide or a monoclonal antibody or fragment against it.
XX
XX      Claim 5; Page 32; 41pp; English.
PS
XX
XX      Adherence of oral pathogens, particularly to tooth surfaces, can be
CC      prevented by application of a fibronectin binding protein or polypeptide.
CC      The fibronectin binding protein or polypeptide is useful in the
CC      manufacture of oral hygiene compositions, eg. toothpaste, liquid
CC      dentifrice, mouthwash or lozenge. They are useful to prevent the plaque-
CC      related development of carious lesions, gingivitis, calculus or
CC      periodontal disease and to combat oral cavity infections, e.g.
CC      candidiasis. They may also be useful in oral surgery e.g. in guided
CC      tissue regeneration procedures to prevent subsequent bacterial infection,
CC      and for irrigation of periodontal pockets. This sequence corresponds to
CC      amino acids 709-838 of the D1-D4 fibronectin binding domain of
XX      Staphylococcus aureus
XX
XX      SQ Sequence 130 AA;

Query Match      100.0%; Score 52; DB 2; Length 130;
Best Local Similarity 100.0%; Pred. No. 0.46;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 SPEEDTEEDK 10
      |||||
      8 SPEEDTEEDK 17

Db

RESULT 13
AAR91201
ID      AAR91201 standard; peptide; 130 AA.
XX
XX      AAR91201;
XX
XX      13-NOV-1996 (first entry)
DT
XX
XX      D1-D4 fibronectin binding domains.
DE
XX
XX      Fibronectin; oral hygiene; gingivitis; gum disease; adhesion;
KW      periodontitis; oral pathogen; caries; calculus; candidiasis; oral surgery;
KW      tissue regeneration; irrigation; toothpaste; dentifrice; mouthwash;
KW      lozenge.
XX
XX      Staphylococcus aureus.
OS
XX      WO9604003-A1.
PN
XX      15-FEB-1996.
PD
XX      18-JUL-1995; 95WO-EP002825.
PF
XX      05-AUG-1994; 94GB-00015902.
PR
XX      (SMIK ) SMITHKLINE BEECHAM PLC.
PA
XX

```

PI Barnett P, Critchley IA, Dodd I;
 XX WPI; 1996-129122/13.
 DR
 XX
 PT Prevention of adherence of oral pathogens in the oral cavity, partic.
 PT tooth surfaces - by application of a fibronectin binding protein or
 PT polypeptide or a monoclonal antibody or fragment against it.
 XX
 PS Claim 5; Page 31-32; 41pp; English.
 CC Adherence of oral pathogens, particularly to tooth surfaces, can be
 CC prevented by application of a fibronectin binding protein or polypeptide.
 CC The fibronectin binding protein or polypeptide is useful in the
 CC manufacture of oral hygiene compositions, eg. toothpaste, liquid
 CC dentifrice, mouthwash or lozenge. They are useful to prevent the plaque-
 CC related development of carious lesions, gingivitis, calculus or
 CC periodontal disease and to combat oral cavity infections, e.g.
 CC candidiasis. They may also be useful in oral surgery e.g. in guided
 CC tissue regeneration procedures to prevent subsequent bacterial infection,
 CC and for irrigation of periodontal pockets. This sequence corresponds to
 CC amino acids 709-838 of the D1-D4 fibronectin binding domain of
 CC *Staphylococcus aureus* with a P838T substitution
 XX
 SQ Sequence 130 AA;
 Query Match 100.0%; Score 52; DB 2; Length 130;
 Best Local Similarity 100.0%; Pred. No. 0.46;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 SFEEDTEEDK 10
 |||||
 DB 8 SFEEDTEEDK 17
 RESULT 14
 AAY29089
 ID AAY29089 standard; protein; 134 AA.
 XX
 AC AAY29089;
 XX
 DT 28-SEP-1999 (first entry)
 XX
 DE Cloned fibronectin binding protein binding domain (FnBAB) sequence.
 XX
 KW Bovine herpes virus-2; BHV-2; cytokine; immune response; immunogen; IL;
 KW interleukin; colony stimulating factor; CSF; interferon; IFN; TNF;
 KW tumour necrosis factor; recombinant virus; vaccine; mucosal disease;
 KW mastitis; breast cancer; stress-induced disease; binding domain; FnBAB;
 KW fibronectin binding protein.
 XX
 OS *Staphylococcus aureus*.
 XX
 PN WO9916892-A1.
 XX
 PD 08-APR-1999.
 XX
 PF 29-SEP-1998; 98WO-GB002927.
 XX
 PR 29-SEP-1997; 97GB-00020633.
 XX
 PA (UYBR-) UNIV BRISTOL.
 XX
 PI Bradley AJ, Duffas WP;
 XX WPI; 1999-255101/21.
 DR N-PSDB; AAX91506.
 XX
 PT New bovine herpes virus-2 vectors.
 XX
 PS Example 2; Fig 8A-B; 130pp; English.
 CC The invention provides bovine herpes virus-2 (BHV-2) based vectors that
 CC comprise at least one cytokine-encoding DNA sequence. The expression of

CC cytokines in mammals can up-regulate immune responses to the immunogens.
 CC The cytokine is selected from interleukins (IL), colony stimulating
 CC factors (CSF), interferons (IFN) and tumour necrosis factors (TNF). The
 CC BHV-2 based vector or recombinant virus can be used as vaccines. They can
 CC be used for preventing or treating a mucosal disease in a subject, e.g.
 CC ruminants, cattle, sheep, goats, dogs, cats, horses, or man, particularly
 CC mastitis in cows or breast cancers in humans. They can also be used for
 CC preventing or treating a stress-induced disease. The present sequence
 CC represents a S. aureus fibronectin binding protein binding domain
 CC sequence FnBAB, the gene cloned for use in this invention. The gene has
 CC 97.8 percent identity when compared to the previously published sequences
 CC FnBA and FnBB
 XX
 SQ Sequence 134 AA;
 Query Match 100.0%; Score 52; DB 2; Length 134;
 Best Local Similarity 100.0%; Pred. No. 0.47;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 SFEEDTEEDK 10
 |||||
 DB 8 SFEEDTEEDK 17
 RESULT 15
 AAY29088
 ID AAY29088 standard; protein; 134 AA.
 XX
 AC AAY29088;
 XX
 DT 28-SEP-1999 (first entry)
 XX
 DE S. aureus fibronectin binding protein B (FnBB) binding domain.
 XX
 KW Bovine herpes virus-2; BHV-2; cytokine; immune response; immunogen; IL;
 KW interleukin; colony stimulating factor; CSF; interferon; IFN; TNF;
 KW tumour necrosis factor; recombinant virus; vaccine; mucosal disease;
 KW mastitis; breast cancer; stress-induced disease; binding domain; FnBB;
 KW fibronectin binding protein.
 XX
 OS *Staphylococcus aureus*.
 XX
 PN WO9916892-A1.
 XX
 PD 08-APR-1999.
 XX
 PF 29-SEP-1998; 98WO-GB002927.
 XX
 PR 29-SEP-1997; 97GB-00020633.
 XX
 PA (UYBR-) UNIV BRISTOL.
 XX
 PI Bradley AJ, Duffas WP;
 XX WPI; 1999-255101/21.
 DR N-PSDB; AAX91505.
 XX
 PT New bovine herpes virus-2 vectors.
 XX
 PS Example 2; Fig 8A-B; 130pp; English.
 CC The invention provides bovine herpes virus-2 (BHV-2) based vectors that
 CC comprise at least one cytokine-encoding DNA sequence. The expression of
 CC cytokines in mammals can up-regulate immune responses to the immunogens.
 CC The cytokine is selected from interleukins (IL), colony stimulating
 CC factors (CSF), interferons (IFN) and tumour necrosis factors (TNF). The
 CC BHV-2 based vector or recombinant virus can be used as vaccines. They can
 CC be used for preventing or treating a mucosal disease in a subject, e.g.
 CC ruminants, cattle, sheep, goats, dogs, cats, horses, or man, particularly
 CC mastitis in cows or breast cancers in humans. They can also be used for
 CC preventing or treating a stress-induced disease. The present sequence
 CC represents the binding domain of a previously published S. aureus
 CC fibronectin binding protein B (FnBB) sequence. The FnB binding domain

CC gene sequence FNAB, cloned for use in this invention has 9'.8 percent
CC identity when compared to the previously published FNBA and FNBB gene
CC sequences
XX

SQ Sequence 134 AA;

Query Match 100.0%; Score 52; DB 2; Length 134;
Best Local Similarity 100.0%; Pred. No. 0.47;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SPEEDTEEDK 10

Db 8 SPEEDTEEDK 17

Search completed: October 25, 2005, 20:58:41
Job time : 63.2 secs

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OW protein - protein search, using SW model

Run on: October 22, 2005, 05:46:56 ; Search time 17.3 Seconds
(without alignments)
43.150 Million cell updates/sec

Title: US-10-731-238-66

Perfect score: 52

Sequence: 1 SFEEDTEEDK 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

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3: /cgn2_6/ptodata/1/1aa/6A-COMB.pep.*
4: /cgn2_6/ptodata/1/1aa/6B-COMB.pep.*
5: /cgn2_6/ptodata/1/1aa/PCITUS-COMB.pep.*
6: /cgn2_6/ptodata/1/1aa/backfile1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	52	100.0	10	4	US-09-010-317-66
2	52	100.0	14	4	US-09-010-317-105
3	52	100.0	38	1	US-08-234-622A-2
4	52	100.0	38	1	US-08-729-767-3
5	52	100.0	38	4	US-09-010-317-5
6	52	100.0	38	4	US-09-010-317-6
7	52	100.0	38	4	US-09-010-317-43
8	52	100.0	39	4	US-09-010-317-56
9	52	100.0	39	4	US-09-010-317-57
10	52	100.0	114	1	US-08-259-000-3
11	52	100.0	130	2	US-08-459-135A-7
12	52	100.0	130	2	US-08-459-135A-8
13	52	100.0	130	3	US-08-495-559-7
14	52	100.0	130	3	US-08-495-559-8
15	52	100.0	139	3	US-08-856-253-8
16	52	100.0	174	2	US-08-459-135A-10
17	52	100.0	174	2	US-08-459-135A-13
18	52	100.0	174	2	US-08-495-559-10
19	52	100.0	174	3	US-08-495-559-13
20	52	100.0	176	3	US-08-495-559-6
21	52	100.0	178	2	US-08-459-135A-12
22	52	100.0	178	2	US-08-495-559-12
23	52	100.0	181	2	US-08-459-135A-6
24	52	100.0	559	4	US-08-956-171E-5251
25	52	100.0	559	4	US-08-781-986A-5251
26	52	100.0	1027	4	US-08-956-171E-5254
27	52	100.0	1027	4	US-08-781-986A-5254

28	48	92.3	10	4	US-09-010-317-85	Sequence 85, Appl
29	48	92.3	12	4	US-09-010-317-62	Sequence 62, Appl
30	48	92.3	36	4	US-09-010-317-58	Sequence 58, Appl
31	48	92.3	36	4	US-09-010-317-59	Sequence 59, Appl
32	48	92.3	38	1	US-08-234-622A-3	Sequence 3, Appl1
33	48	92.3	38	1	US-08-729-767-4	Sequence 4, Appl1
34	48	92.3	38	4	US-09-010-317-7	Sequence 7, Appl1
35	48	92.3	38	4	US-09-010-317-8	Sequence 8, Appl1
36	48	92.3	38	4	US-09-010-317-49	Sequence 49, Appl
37	46	88.5	38	4	US-09-010-317-36	Sequence 36, Appl
38	46	88.5	38	4	US-09-010-317-37	Sequence 37, Appl
39	46	88.5	38	4	US-09-010-317-39	Sequence 39, Appl
40	46	88.5	38	4	US-09-010-317-40	Sequence 40, Appl
41	46	88.5	38	4	US-09-010-317-41	Sequence 41, Appl
42	45	86.5	38	4	US-09-010-317-38	Sequence 38, Appl
43	45	86.5	38	4	US-09-010-317-42	Sequence 42, Appl
44	42	80.8	10	4	US-09-010-317-67	Sequence 67, Appl
45	42	80.8	38	4	US-09-010-317-35	Sequence 35, Appl

ALIGNMENTS

RESULT 1
US-09-010-317-66
Sequence 66, Application US/09010317
Patent No. 6685943
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
APPLICANT: Patti, Joseph M.
APPLICANT: House-Pompeo, Karen L.
APPLICANT: Spziale, Pietro
APPLICANT: John, Danny
APPLICANT: McAvain, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
TITLE OF INVENTION: AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAMK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 66:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-09-010-317-66
Query Match 100.0%; Score 52; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.007;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SPEEDTEBDK 10
|||||

Db 1 SPEEDTEBDK 10

RESULT 2

US-09-010-317-105

; Sequence 105, Application US/09010317
; Patent No. 6685943

; GENERAL INFORMATION:

; APPLICANT: Hook, Magnus

; APPLICANT: Patti, Joseph M.

; APPLICANT: House-Pompeo, Karen L.

; APPLICANT: Speziale, Pietro

; APPLICANT: McGavin, Martin J.

; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS

; TITLE OF INVENTION: AND METHODS OF USE

; NUMBER OF SEQUENCES: 105

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Arnold, White & Durkee

; STREET: P.O. Box 4433

; CITY: Houston

; STATE: TX

; COUNTRY: USA

; ZIP: 77210-4433

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Releasee #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/010,317

; FILING DATE:

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 60/036,139

; FILING DATE: 21-JAN-1997

; ATTORNEY/AGENT INFORMATION:

; NAME: Hibler, David W.

; REGISTRATION NUMBER: 41,071

; REFERENCE/DOCKET NUMBER: TAMK:169

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 512-418-3000

; TELEFAX: 512-474-7577

; INFORMATION FOR SEQ ID NO: 105:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 14 amino acids

; TYPE: amino acid

; STRANDEDNESS:

; TOPOLOGY: linear

US-09-010-317-105

Query Match 100.0%; Score 52; DB 4; Length 14;

Best Local Similarity 100.0%; Pred. No. 0.01; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SPEEDTEBDK 10
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Db 1 SPEEDTEBDK 10

RESULT 3

US-08-234-622A-2

; Sequence 2, Application US/08234622A

; Patent No. 5440014

; GENERAL INFORMATION:

; APPLICANT: Hook, Magnus

; APPLICANT: MCGAVIN, Martin

; APPLICANT: RAUCCI, Giuseppe

; TITLE OF INVENTION: A FIBRONECTIN BINDING PEPTIDE

; NUMBER OF SEQUENCES: 4

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Burns, Doane, Swecker & Mathis

; STREET: P.O. Box 1404

; CITY: Alexandria

; STATE: Virginia

; COUNTRY: United States

; ZIP: 22113-1404

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Releasee #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/234,622A

; FILING DATE: 28-APR-1994

; CLASSIFICATION: 530

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: SE 9002617-0

; FILING DATE: 10-AUG-1990

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: WO PCT/SE91/00534

; FILING DATE: 09-AUG-1991

; ATTORNEY/AGENT INFORMATION:

; NAME: Neuth, Donna M

; REGISTRATION NUMBER: 36,607

; REFERENCE/DOCKET NUMBER: 012885-044

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (703) 836-6620

; TELEFAX: (703) 836-2021

; INFORMATION FOR SEQ ID NO: 2:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 38 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

US-08-234-622A-2

Query Match 100.0%; Score 52; DB 1; Length 38;

Best Local Similarity 100.0%; Pred. No. 0.029; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SPEEDTEBDK 10
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Db 7 SPEEDTEBDK 16

RESULT 4

US-08-729-767-3

; Sequence 3, Application US/08729767

; Patent No. 5770702

; GENERAL INFORMATION:

; APPLICANT: Hook, Magnus

; APPLICANT: LINDBERG, Martin Kjell

; APPLICANT: SIGNAS, Lars Christer

; APPLICANT: MADSTROM, Torkel Mikael

; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN AS WELL AS

; TITLE OF INVENTION: ITS PREPARATION

; NUMBER OF SEQUENCES: 6

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Burns, Doane, Swecker & Mathis, L.L.P.

; STREET: P.O. Box 1404

; CITY: Alexandria

; STATE: Virginia

; COUNTRY: United States

; ZIP: 22113-1404

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Releasee #1.0, Version #1.30

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1      RESULT 5
2      US-09-010-317-5
3      : Sequence 5, Application US/09010317
4      : Patent No. 6685943
5      :
6      : GENERAL INFORMATION:
7      :
8      : APPLICANT: HOOK, Magnus
9      : APPLICANT: Patti, Joseph M.
10     : APPLICANT: House-Pompeo, Karen L.
11     : APPLICANT: Speziale, Pietro
12     : APPLICANT: Job, Danny
13     : APPLICANT: McGavin, Martin J.
14     : TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
15     : TITLE OF INVENTION: AND METHODS OF USE
16     : NUMBER OF SEQUENCES: 105
17     :
18     : CORRESPONDENCE ADDRESS:
19     : ADDRESSEE: Arnold, White & Durkee
20     : STREET: P.O. Box 4433
21     : CITY: Houston
22     : STATE: TX
23     : COUNTRY: USA
24     : ZIP: 77210-4433
25     :
26     : COMPUTER READABLE FORM:
27     : MEDIUM TYPE: Floppy disk
28     : COMPUTER: IBM PC compatible
29     : OPERATING SYSTEM: PC-DOS/MS-DOS
30     : SOFTWARE: PatentIn Release #1.0, Version #1.30
31     : CURRENT APPLICATION DATA:
32     : APPLICATION NUMBER: US/09/010,317
33     : FILING DATE:
34     : CLASSIFICATION:
35     : PRIORITY APPLICATION DATA:
36     : APPLICATION NUMBER: US 60/036,139
37     :

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1      RESULT 6
2      US-09-010-317-6
3      Sequence 6, Application US/09010317
4      Patent No. 6685943
5      GENERAL INFORMATION:
6      APPLICANT: Hook, Magnus
7      APPLICANT: Patil, Joseph M.
8      APPLICANT: House-Pompeo, Karen L.
9      APPLICANT: Speciale, Pietro
10     APPLICANT: Job, Danny
11     APPLICANT: McGeary, Martin J.
12     TITLE OF INVENTION: FIBROBLAST BINDING PROTEIN COMPOSITIONS
13     TITLE OF INVENTION: AND METHODS OF USE
14     NUMBER OF SEQUENCES: 105
15     CORRESPONDENCE ADDRESS:
16     ADDRESSEE: Arnold, White & Durkee
17     STREET: P.O. Box 4433
18     CITY: Houston
19     STATE: TX
20     COUNTRY: USA
21     ZIP: 77210-4433
22     COMPUTER READABLE FORM:
23     MEDIUM TYPE: Floppy disk
24     COMPUTER: IBM PC compatible
25     OPERATING SYSTEM: PC-DOS/MS-DOS
26     SOFTWARE: PatentIn Release #1.0, Version #1.30
27     CURRENT APPLICATION DATA:
28     APPLICATION NUMBER: US/09/010,317
29     FILING DATE:
30     CLASSIFICATION:
31     PRIOR APPLICATION DATA:
32     APPLICATION NUMBER: US 60/036,139
33     FILING DATE: 21-JAN-1997
34     ATTORNEY/AGENT INFORMATION:
35     NAME: Hibley, David W.
36     REGISTRATION NUMBER: 41,071
37     REFERENCE/DOCKET NUMBER: TAMK:169
38     TELECOMMUNICATION INFORMATION:
39     TELEPHONE: 512-418-3000
40     TELEFAX: 512-474-7577
41     INFORMATION FOR SEQ ID NO: 6:
42     SEQUENCE CHARACTERISTICS:
43     LENGTH: 38 amino acids
44     TYPE: amino acid
45     STRANDEDNESS:
46     TOPOLOGY: linear
47     US-09-010-317-6

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Query Match 100.0%; Score 52; DB 4; Length 38;
Best Local Similarity 100.0%; Pred. No. 0.029;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SPEEDTEEDK 10
| | | | | | | | | |
DB 7 SPEEDTEEDK 16

RESULT 7
US-09-010-317-43

; Sequence 43, Application US/09010317
; Patent No. 6685943
; GENERAL INFORMATION:
; APPLICANT: Hook, Magnus
; APPLICANT: Patti, Joseph M.
; APPLICANT: House-Pompeo, Karen L.
; APPLICANT: Speziale, Pietro
; APPLICANT: Joh, Danny
; APPLICANT: McGavin, Martin J.
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
; TITLE OF INVENTION: AND METHODS OF USE
; NUMBER OF SEQUENCES: 105
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: TX
; COUNTRY: USA
; ZIP: 77210-4433
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/010,317
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/036,139
; FILING DATE: 21-JAN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Hibler, David W.
; REGISTRATION NUMBER: 41,071
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 512-418-3000
; TELEFAX: 512-474-7577
; INFORMATION FOR SEQ ID NO: 43:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 38 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
US-09-010-317-43

Query Match 100.0%; Score 52; DB 4; Length 38;
Best Local Similarity 100.0%; Pred. No. 0.029;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SPEEDTEEDK 10
| | | | | | | | | |
DB 7 SPEEDTEEDK 16

RESULT 8
US-09-010-317-56

; Sequence 56, Application US/09010317
; Patent No. 6685943
; GENERAL INFORMATION:
; APPLICANT: Hook, Magnus
; APPLICANT: Patti, Joseph M.

; APPLICANT: House-Pompeo, Karen L.
; APPLICANT: Speziale, Pietro
; APPLICANT: Joh, Danny
; APPLICANT: McGavin, Martin J.
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
; TITLE OF INVENTION: AND METHODS OF USE
; NUMBER OF SEQUENCES: 105
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: TX
; COUNTRY: USA
; ZIP: 77210-4433
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/010,317
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/036,139
; FILING DATE: 21-JAN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Hibler, David W.
; REGISTRATION NUMBER: 41,071
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 512-418-3000
; TELEFAX: 512-474-7577
; INFORMATION FOR SEQ ID NO: 56:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 39 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
US-09-010-317-56

Query Match 100.0%; Score 52; DB 4; Length 39;
Best Local Similarity 100.0%; Pred. No. 0.03;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SPEEDTEEDK 10
| | | | | | | | | |
DB 7 SPEEDTEEDK 16

RESULT 9
US-09-010-317-57

; Sequence 57, Application US/09010317
; Patent No. 6685943
; GENERAL INFORMATION:
; APPLICANT: Hook, Magnus
; APPLICANT: Patti, Joseph M.
; APPLICANT: House-Pompeo, Karen L.
; APPLICANT: Speziale, Pietro
; APPLICANT: Joh, Danny
; APPLICANT: McGavin, Martin J.
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
; TITLE OF INVENTION: AND METHODS OF USE
; NUMBER OF SEQUENCES: 105
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: TX
; COUNTRY: USA
; ZIP: 77210-4433
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAMK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 57:
SEQUENCE CHARACTERISTICS:
LENGTH: 39 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-09-010-317-57

Query Match 100.0%; Score 52; DB 4; Length 39;
Best Local Similarity 100.0%; Pred. No. 0.03;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SPEEDTEBDK 10
DB 7 SPEEDTEBDK 16

RESULT 10
US-08-259-000-3
Sequence 3, Application US/08259000
Patent No. 5571514
GENERAL INFORMATION:
APPLICANT: HOOK, Magnus
APPLICANT: LINDBERG, Martin Kjell
APPLICANT: SIGNAS, Lars Christer
APPLICANT: MADSTROM, Torrel Mikael
APPLICANT: FROMAN, Gunnar
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN AS WELL AS
TITLE OF INVENTION: ITS PREPARATION
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Burns, Doane, Swecker & Mathis
STREET: P.O. Box 1404
CITY: Alexandria
STATE: Virginia
COUNTRY: United States
ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/259,000
FILING DATE: 13-JUN-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: SE 8702272-9
FILING DATE: 01-JUN-1987
ATTORNEY/AGENT INFORMATION:
NAME: Meuth, Donna M
REGISTRATION NUMBER: 36,607
REFERENCE/DOCKET NUMBER: 012885-062
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021

INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 114 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-259-000-3

Query Match 100.0%; Score 52; DB 1; Length 114;
Best Local Similarity 100.0%; Pred. No. 0.093;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SPEEDTEBDK 10
DB 8 SPEEDTEBDK 17

RESULT 11
US-08-459-135A-7
Sequence 7, Application US/08459135A
Patent No. 595078
GENERAL INFORMATION:
APPLICANT: BURNHAM, Martin Karl Russel
APPLICANT: CHOPRA, Ian
APPLICANT: CRITCHLEY, Ian Alfred
APPLICANT: KNOWLES, David Justin Charles
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN: MONOCLONAL ANTIBODY AND THEIR US
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
STATE: PA
COUNTRY: U.S.A.
ZIP: 19406-0939
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: Fastseq, Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/459,135A
FILING DATE: 02-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB/94/00215
FILING DATE: 04-Feb-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Gimmil, Edward R
REGISTRATION NUMBER: 38,891
REFERENCE/DOCKET NUMBER: P30591C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-4478
TELEFAX: 610-270-5090
TELEX:
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 130 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-459-135A-7

Query Match 100.0%; Score 52; DB 2; Length 130;
Best Local Similarity 100.0%; Pred. No. 0.11; Indels 0; Gaps 0;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SPEEDTEBDK 10
DB 8 SPEEDTEBDK 17

RESULT 12
US-08-459-135A-8
; Sequence 8, Application US/08459135A
; Patent No. 5955078
; GENERAL INFORMATION:
; APPLICANT: BURHAM, Martin Karl Russel
; APPLICANT: CHOPRA, Ian
; APPLICANT: CRITCHLEY, Ian Alfred
; APPLICANT: KNOWLES, David Justin Charles
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN: MONOCLONAL ANTIBODY AND THEIR US
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corporation
; STREET: 709 Swedeland Road
; CITY: King of Prussia
; STATE: PA
; COUNTRY: U.S.A.
; ZIP: 19406-0939
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: Fastseq, Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/459,135A
; FILING DATE: 02-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB/94/00215
; FILING DATE: 04-Feb-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Gimm1, Edward R
; REGISTRATION NUMBER: 38,891
; REFERENCE/DOCKET NUMBER: P30591C2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-270-4478
; TELEFAX: 610-270-5090
; TELEX:
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 130 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: Protein
US-08-459-135A-8
Query Match 100.0%; Score 52; DB 2; Length 130;
Best Local Similarity 100.0%; Pred. No. 0.11;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 SPEEDTEEDK 10
| | | | | | | | | |
Db 8 SFEEDTEEDK 17
RESULT 13
US-08-495-559-7
; Sequence 7, Application US/08495559A
; Patent No. 6054572
; GENERAL INFORMATION:
; APPLICANT: BURHAM, Martin Karl Russel
; APPLICANT: CHOPRA, Ian
; APPLICANT: CRITCHLEY, Ian Alfred
; APPLICANT: KNOWLES, David Justin Charles
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN: MONOCLONAL
; TITLE OF INVENTION: ANTIBODY AND THEIR USE IN PREVENTING BACTERIAL ADHESION
; FILE REFERENCE: P30591
; CURRENT APPLICATION NUMBER: US/08/495,559A
; FILING DATE: 1995-08-03
; EARLIER APPLICATION NUMBER: GB 9302289.5
; EARLIER FILING DATE: 1993-02-05

; EARLIER APPLICATION NUMBER: GB 9321592.9
; EARLIER FILING DATE: 1993-10-20
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 7
; LENGTH: 130
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-08-495-559-7
Query Match 100.0%; Score 52; DB 3; Length 130;
Best Local Similarity 100.0%; Pred. No. 0.11;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 SPEEDTEEDK 10
| | | | | | | | | |
Db 8 SFEEDTEEDK 17
RESULT 14
US-08-495-559-8
; Sequence 8, Application US/08495559A
; Patent No. 6054572
; GENERAL INFORMATION:
; APPLICANT: BURHAM, Martin Karl Russel
; APPLICANT: CHOPRA, Ian
; APPLICANT: CRITCHLEY, Ian Alfred
; APPLICANT: KNOWLES, David Justin Charles
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN: MONOCLONAL
; TITLE OF INVENTION: ANTIBODY AND THEIR USE IN PREVENTING BACTERIAL ADHESION
; FILE REFERENCE: P30591
; CURRENT APPLICATION NUMBER: US/08/495,559A
; FILING DATE: 1995-08-03
; EARLIER APPLICATION NUMBER: GB 9302289.5
; EARLIER FILING DATE: 1993-02-05
; EARLIER APPLICATION NUMBER: GB 9321592.9
; EARLIER FILING DATE: 1993-10-20
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 8
; LENGTH: 130
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-08-495-559-8
Query Match 100.0%; Score 52; DB 3; Length 130;
Best Local Similarity 100.0%; Pred. No. 0.11;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 SPEEDTEEDK 10
| | | | | | | | | |
Db 8 SFEEDTEEDK 17
RESULT 15
US-08-856-253-8
; Sequence 8, Application US/08856253
; Patent No. 6288214
; GENERAL INFORMATION:
; APPLICANT: Hook, Magnus
; APPLICANT: Patil, Joseph M.
; APPLICANT: House-Pompeo, Karen
; APPLICANT: Schanam, Narayana
; APPLICANT: Symersky, Jindrich
; TITLE OF INVENTION: COLLAGEN BINDING PROTEIN COMPOSITIONS
; TITLE OF INVENTION: AND METHODS OF USE
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: U.S.

21P: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/856,253
FILING DATE: Concurrently Herewith
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/017,678
FILING DATE: 16-MAY-1996
ATTORNEY/AGENT INFORMATION:
NAME: Kitchell, Barbara S.
REGISTRATION NUMBER: 33,928
REFERENCE/DOCKET NUMBER: TAPK:193
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
TELEFAX: (512) 474-7577
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 139 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-08-856-253-8

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 22, 2005, 12:09:40 ; Search time 57.25 Seconds
(without alignments)
72.924 Million cell updates/sec

Title: US-10-731-238-66

Perfect score: 52

Sequence: 1 SFEEDTEEDK 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1862951 seqs, 417491010 residues

Total number of hits satisfying chosen parameters: 1862951

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications_AA:*

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2: /cgn2_6/prodata/2/pubpaa/PCT_NEW_PUB.pep:*

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22: /cgn2_6/prodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	52	100.0	10	US-10-731-238-66	Sequence 66, Appl
2	52	100.0	14	US-10-731-238-105	Sequence 105, Appl
3	52	100.0	38	US-10-731-238-6	Sequence 5, Appl
4	52	100.0	38	US-10-731-238-6	Sequence 6, Appl
5	52	100.0	38	US-10-731-238-43	Sequence 43, Appl
6	52	100.0	39	US-10-731-238-56	Sequence 56, Appl
7	52	100.0	39	US-10-731-238-57	Sequence 57, Appl
8	52	100.0	139	US-09-813-820-8	Sequence 8, Appl
9	52	100.0	388	US-08-901-062-1	Sequence 1, Appl
10	52	100.0	559	US-08-781-986A-5251	Sequence 5251, Ap
11	52	100.0	559	US-10-329-624-5251	Sequence 5251, Ap

12	52	100.0	767	9	US-09-815-242-5899	Sequence 5899, Ap
13	52	100.0	767	9	US-09-815-242-13140	Sequence 13140, A
14	52	100.0	940	17	US-10-470-048B-424	Sequence 424, Appl
15	52	100.0	948	17	US-10-470-048B-69	Sequence 69, Appl
16	52	100.0	961	15	US-10-282-122A-43778	Sequence 43778, A
17	52	100.0	978	15	US-09-815-242-5456	Sequence 5456, Ap
18	52	100.0	1001	9	US-09-815-242-12686	Sequence 12686, A
19	52	100.0	1018	9	US-09-815-242-5797	Sequence 5797, Ap
20	52	100.0	1018	9	US-09-815-243-12838	Sequence 12838, A
21	52	100.0	1018	17	US-10-470-048B-68	Sequence 68, Appl
22	52	100.0	1027	8	US-08-781-986A-5254	Sequence 5254, Ap
23	52	100.0	1027	15	US-10-329-624-5254	Sequence 5254, A
24	52	100.0	1038	15	US-10-282-122A-43827	Sequence 43827, A
25	48	92.3	10	18	US-10-731-238-62	Sequence 62, Appl
26	48	92.3	12	18	US-10-287-821-1	Sequence 1, Appl
27	48	92.3	30	14	US-10-287-821-2	Sequence 2, Appl
28	48	92.3	31	14	US-10-287-821-2	Sequence 58, Appl
29	48	92.3	36	18	US-10-731-238-58	Sequence 59, Appl
30	48	92.3	36	18	US-10-731-238-59	Sequence 7, Appl
31	48	92.3	38	18	US-10-731-238-7	Sequence 8, Appl
32	48	92.3	38	18	US-10-731-238-8	Sequence 49, Appl
33	48	92.3	38	18	US-10-731-238-49	Sequence 36, Appl
34	46	88.5	38	18	US-10-731-238-36	Sequence 37, Appl
35	46	88.5	38	18	US-10-731-238-37	Sequence 39, Appl
36	46	88.5	38	18	US-10-731-238-39	Sequence 40, Appl
37	46	88.5	38	18	US-10-731-238-40	Sequence 41, Appl
38	46	88.5	38	18	US-10-731-238-41	Sequence 38, Appl
39	45	86.5	38	18	US-10-731-238-38	Sequence 42, Appl
40	45	86.5	38	18	US-10-731-238-42	Sequence 62, Appl
41	43	82.7	3051	15	US-10-144-194A-62	Sequence 67, Appl
42	43	82.7	3051	16	US-10-491-566-62	Sequence 35, Appl
43	42	80.8	10	18	US-10-731-238-67	Sequence 46, Appl
44	42	80.8	38	18	US-10-731-238-35	
45	42	80.8	38	18	US-10-731-238-46	

ALIGNMENTS

RESULT 1

US-10-731-238-66

Sequence 66, Application US/10731238

Publication No. US20050123552A1

GENERAL INFORMATION:

APPLICANT: Hook, Magnus

Patli, Joseph M.

House-Pompeo, Karen L.

Speziale, Pietro

Joh, Danny

McGavin, Martin J.

TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS

AND METHODS OF USE

NUMBER OF SEQUENCES: 105

CORRESPONDENCE ADDRESS:

ADDRESS: Arnold, White & Durkee

STREET: P.O. Box 4433

CITY: Houston

STATE: TX

COUNTRY: USA

ZIP: 77210-4433

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC Compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/731.238

FILING DATE: 10-Dec-2003

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/010.317

FILING DATE: 21-Jan-1998

APPLICATION NUMBER: US 60/036.139

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;
; FILING DATE: 21-JAN-1997
; ATTORNEY/AGENT INFORMATION:
;   NAME: Hibler, David W.
;   REGISTRATION NUMBER: 41,071
;   REFERENCE/DOCKET NUMBER: TAMK:189
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE: 512-418-3000
;     TELEFAX: 512-474-7577
; INFORMATION FOR SEQ ID NO: 66:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH: 10 amino acids
;     TYPE: amino acid
;     STRANDEDNESS: <Unknown>
;     TOPOLOGY: linear
;   SEQUENCE DESCRIPTION: SEQ ID NO: 66:
US-10-731-238-66

Query Match      100.0%; Score 52; DB 18; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.09;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SPEEDTEEDK 10
Db 1 SPEEDTEEDK 10

RESULT 2
US-10-731-238-105
; Sequence 105, Application US/10731238
; Publication No. US20050123552A1
; GENERAL INFORMATION:
;   APPLICANT: Hook, Magnus
;     Patcli, Joseph M.
;     House-Pompeo, Karen L.
;     Speziale, Pietro
;     John, Danny
;     McGavin, Martin J.
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
; NUMBER OF SEQUENCES: 105
; CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Arnold, White & Durkee
;   STREET: P.O. Box 4433
;   CITY: Houston
;   STATE: TX
;   COUNTRY: USA
;   ZIP: 77210-4433
; COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/10/731,238
;   FILING DATE: 10-Dec-2003
;   CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US/09/010,317
;   FILING DATE: 21-Jan-1998
;   APPLICATION NUMBER: US 60/036,139
;   FILING DATE: 21-JAN-1997
; ATTORNEY/AGENT INFORMATION:
;   NAME: Hibler, David W.
;   REGISTRATION NUMBER: 41,071
;   REFERENCE/DOCKET NUMBER: TAMK:189
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE: 512-418-3000
;     TELEFAX: 512-474-7577
; INFORMATION FOR SEQ ID NO: 105:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH: 14 amino acids
;     TYPE: amino acid
;     STRANDEDNESS: <Unknown>
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; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 105:
US-10-731-238-105

Query Match      100.0%; Score 52; DB 18; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SPEEDTEEDK 10
Db 1 SPEEDTEEDK 10

RESULT 3
US-10-731-238-5
; Sequence 5, Application US/10731238
; Publication No. US20050123552A1
; GENERAL INFORMATION:
;   APPLICANT: Hook, Magnus
;     Patcli, Joseph M.
;     House-Pompeo, Karen L.
;     Speziale, Pietro
;     John, Danny
;     McGavin, Martin J.
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
; AND METHODS OF USE
; NUMBER OF SEQUENCES: 105
; CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Arnold, White & Durkee
;   STREET: P.O. Box 4433
;   CITY: Houston
;   STATE: TX
;   COUNTRY: USA
;   ZIP: 77210-4433
; COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/10/731,238
;   FILING DATE: 10-Dec-2003
;   CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US/09/010,317
;   FILING DATE: 21-Jan-1998
;   APPLICATION NUMBER: US 60/036,139
;   FILING DATE: 21-JAN-1997
; ATTORNEY/AGENT INFORMATION:
;   NAME: Hibler, David W.
;   REGISTRATION NUMBER: 41,071
;   REFERENCE/DOCKET NUMBER: TAMK:189
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE: 512-418-3000
;     TELEFAX: 512-474-7577
; INFORMATION FOR SEQ ID NO: 5:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH: 38 amino acids
;     TYPE: amino acid
;     STRANDEDNESS: <Unknown>
;     TOPOLOGY: linear
;   SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-10-731-238-5

Query Match      100.0%; Score 52; DB 18; Length 38;
Best Local Similarity 100.0%; Pred. No. 0.36;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SPEEDTEEDK 10
Db 7 SPEEDTEEDK 16

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RESULT 4
US-10-731-238-6
; Sequence 6, Application US/10731238
; Publication No. US20050123552A1
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
; Patti, Joseph M.
; House-Pompeo, Karen L.
; Speziale, Pietro
; John, Danny
; McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/731,238
FILING DATE: 10-Dec-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE: 21-Jan-1998
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAMK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-418-7577
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-10-731-238-6
Query Match 100.0%; Score 52; DB 18; Length 38;
Best Local Similarity 100.0%; Pred. No. 0.36;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 SPEEDTEEDK 10
Db 7 SPEEDTEEDK 16
RESULT 5
US-10-731-238-43
; Sequence 43, Application US/10731238
; Publication No. US20050123552A1
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
; Patti, Joseph M.
; House-Pompeo, Karen L.
; Speziale, Pietro
; John, Danny
; McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
AND METHODS OF USE
```

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NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/731,238
FILING DATE: 10-Dec-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE: 21-Jan-1998
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAMK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 43:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 43:
US-10-731-238-43
Query Match 100.0%; Score 52; DB 18; Length 38;
Best Local Similarity 100.0%; Pred. No. 0.36;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 SPEEDTEEDK 10
Db 7 SPEEDTEEDK 16
RESULT 6
US-10-731-238-56
; Sequence 56, Application US/10731238
; Publication No. US20050123552A1
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
; Patti, Joseph M.
; House-Pompeo, Karen L.
; Speziale, Pietro
; John, Danny
; McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/731,238
FILING DATE: 10-Dec-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE: 21-Jan-1998
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-Jan-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAMK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 56:
SEQUENCE CHARACTERISTICS:
LENGTH: 39 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 56:
US-10-731-238-56

Query Match 100.0%; Score 52; DB 18; Length 39;
Best Local Similarity 100.0%; Pred. No. 0.37;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SPEEDTEEDK 10
DB 7 SPEEDTEEDK 16

RESULT 7
US-10-731-238-57
Sequence 57, Application US/10731238
Publication No. US20050123552A1
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
Patel, Joseph M.
House-Pompeo, Karen L.
Speziale, Pietro
John, Danny
McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/731,238
FILING DATE: 10-Dec-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE: 21-Jan-1998
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-Jan-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAMK:189

TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 57:
SEQUENCE CHARACTERISTICS:
LENGTH: 39 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 57:
US-10-731-238-57

Query Match 100.0%; Score 52; DB 18; Length 39;
Best Local Similarity 100.0%; Pred. No. 0.37;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SPEEDTEEDK 10
DB 7 SPEEDTEEDK 16

RESULT 8
US-09-813-820-8
Sequence 8, Application US/09813820
Patent No. US20020102262A1
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
Patel, Joseph M.
House-Pompeo, Karen
Shanam, Narayana
Symerky, Jindrich
TITLE OF INVENTION: COLLAGEN BINDING PROTEIN COMPOSITIONS
AND METHODS OF USE
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: Texas
COUNTRY: U.S.
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/813,820
FILING DATE: 22-Mar-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/856,253
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Kitchell, Barbara S.
REGISTRATION NUMBER: 33,928
REFERENCE/DOCKET NUMBER: TAMK:193
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
TELEFAX: (512) 474-7577
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 139 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-09-813-820-8

Query Match 100.0%; Score 52; DB 9; Length 139;
Best Local Similarity 100.0%; Pred. No. 1.4;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SPEEDTEEDK 10
DB 22 SPEEDTEEDK 31

RESULT 9
US-08-901-062-1

Sequence 1, Application US/08901062
Publication No. US20020025324A1
GENERAL INFORMATION:
APPLICANT: SEALS, JONATHAN R.
TITLE OF INVENTION: RECOMBINANT BIVALENT BACTERIAL VACCINE
TITLE OF INVENTION: FOR THE PREVENTION OF MASTITIS
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: HALE AND DORR LLP
STREET: 60 State Street
CITY: Boston
STATE: MA
COUNTRY: United States Of America
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/901,062
FILING DATE: 25-JUL-1997
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Baker, Hollie L.
REGISTRATION NUMBER: 31,321
REFERENCE/DOCKET NUMBER: 106941.153
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 526-6000
TELEFAX: (617) 526-5000
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 388 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-901-062-1

Query Match 100.0%; Score 52; DB 8; Length 388;
Best Local Similarity 100.0%; Pred. No. 4.1;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SPEEDTEEDK 10
DB 271 SPEEDTEEDK 280

RESULT 10
US-08-781-986A-5251
Sequence 5251, Application US/08781986A
Publication No. US20030054436A1
GENERAL INFORMATION:
APPLICANT: Charles Kunsch
TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
NUMBER OF SEQUENCES: 5255
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COUNTRY: USA
ZIP: 20850
COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/781,986A
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Benson, Bob
REGISTRATION NUMBER: 30,446
REFERENCE/DOCKET NUMBER: PB248PP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 5251:
SEQUENCE CHARACTERISTICS:
LENGTH: 559 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-781-986A-5251

Query Match 100.0%; Score 52; DB 8; Length 559;
Best Local Similarity 100.0%; Pred. No. 6;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SPEEDTEEDK 10
DB 307 SPEEDTEEDK 316

RESULT 11
US-10-329-624-5251

Sequence 5251, Application US/10329624
Publication No. US20040043037A1
GENERAL INFORMATION:
APPLICANT: Charles Kunsch
Gil H. Choi
Patrick S. Dillon
Craig A. Rosen
Steven C. Barash
Michael R. Fannon
TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
NUMBER OF SEQUENCES: 5256
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COUNTRY: USA
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/329,624
FILING DATE: 27-Dec-2002
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/956,171
FILING DATE: October 20, 1997
APPLICATION NUMBER: 60/009,861
FILING DATE: January 5, 1996
APPLICATION NUMBER: 08/781,986
FILING DATE: January 3, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Mark J. Hyman

REGISTRATION NUMBER: 46,789
REFERENCE/DOCKET NUMBER: PB248P1D1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (240) 314-1224
TELEFAX: (301) 309-8439
INFORMATION FOR SEQ ID NO: 5251:
SEQUENCE CHARACTERISTICS:
LENGTH: 559 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 5251:
US-10-329-624-5251

Query Match 100.0%; Score 52; DB 15; Length 559;
Best Local Similarity 100.0%; Pred. No. 6;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SPEEDTEEDK 10
Db 307 SPEEDTEEDK 316

RESULT 12
US-09-815-242-5899
Sequence 5899, Application US/09815242
Patent No. US20020061569A1
GENERAL INFORMATION:
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Karl L.
APPLICANT: Zykkind, Judith W.
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John D.
APPLICANT: Carr, Grant J.
APPLICANT: Yamamoto, Robert T.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in
FILE REFERENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 5899
LENGTH: 767
TYPE: PRT
ORGANISM: Staphylococcus aureus
US-09-815-242-5899

Query Match 100.0%; Score 52; DB 9; Length 767;
Best Local Similarity 100.0%; Pred. No. 8.3;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SPEEDTEEDK 10
Db 688 SPEEDTEEDK 697

RESULT 13
US-09-815-242-13140
Sequence 13140, Application US/09815242
Patent No. US20020061569A1
GENERAL INFORMATION:
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Karl L.
APPLICANT: Zykkind, Judith W.
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John D.
APPLICANT: Carr, Grant J.
APPLICANT: Yamamoto, Robert T.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in
FILE REFERENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 13140
LENGTH: 767
TYPE: PRT
ORGANISM: Staphylococcus aureus
US-09-815-242-13140

Query Match 100.0%; Score 52; DB 9; Length 767;
Best Local Similarity 100.0%; Pred. No. 8.3;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SPEEDTEEDK 10
Db 688 SPEEDTEEDK 697

RESULT 14
US-10-470-048B-424
Sequence 424, Application US/10470048B
Publication No. US2005003744A1
GENERAL INFORMATION:
APPLICANT: MEINKEN ET AL.
TITLE OF INVENTION: A METHOD FOR IDENTIFICATION, ISOLATION AND PRODUCTION OF
FILE REFERENCE: SONN:035US
CURRENT APPLICATION NUMBER: US/10/470,048B
CURRENT FILING DATE: 2003-07-25
NUMBER OF SEQ ID NOS: 603
SOFTWARE: PatentIn version 3.1
SEQ ID NO 424
LENGTH: 940
TYPE: PRT
ORGANISM: Staphylococcus aureus
US-10-470-048B-424

Query Match 100.0%; Score 52; DB 17; Length 940;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SPEEDTEEDK 10

Db 688 SPEEDTEEDK 697

RESULT 15
US-10-470-048B-69
; Sequence 69; Application US/10470048B
; Publication No. US2005037444A1
; GENERAL INFORMATION:
; APPLICANT: MEINKE ET AL.
; TITLE OF INVENTION: A METHOD FOR IDENTIFICATION, ISOLATION AND PRODUCTION OF
; TITLE OF INVENTION: ANTIGENS TO A SPECIFIC PATHOGEN
; FILE REFERENCE: SONN:035US
; CURRENT APPLICATION NUMBER: US/10/470,048B
; CURRENT FILING DATE: 2003-07-25
; NUMBER OF SEQ ID NOS: 603
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 69
; LENGTH: 948
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-10-470-048B-69

Query Match 100.0%; Score 52; DB 17; Length 948;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SPEEDTEEDK 10
Db 696 SPEEDTEEDK 705

Search completed: October 22, 2005, 12:39:43
Job time : 58.25 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 22, 2005, 06:10:10 ; Search time 11.45 Seconds
(without alignments)
84.032 Million cell updates/sec

Title: US-10-731-238-66

Perfect score: 52
Sequence: 1 SFEDTEEDK 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	52	100.0	940	2 S19702	fibronectin-binding
2	52	100.0	961	2 G90053	hypothetical prote
3	52	100.0	1018	2 A32192	fibronectin-binding
4	52	100.0	1038	2 H90053	hypothetical prote
5	38	73.1	397	2 AC2110	hypothetical prote
6	38	73.1	653	2 T15665	hypothetical prote
7	38	73.1	1074	2 T01906	hypothetical prote
8	37	71.2	115	2 B72355	hypothetical prote
9	37	71.2	335	2 A54458	GI progression neg
10	37	71.2	339	2 C84653	hypothetical prote
11	37	71.2	467	2 F90989	sensor protein for
12	37	71.2	467	2 C84420	hypothetical prote
13	37	71.2	467	2 A85835	sensor protein (fo
14	37	71.2	467	2 E64974	sensory kinase Bae
15	37	71.2	771	2 T13618	hypothetical prote
16	37	71.2	1355	2 S40022	spalt protein - fr
17	36	69.2	340	2 B86778	ketol-acid reducto
18	36	69.2	344	1 S35140	probable ketol-aci
19	36	69.2	389	2 T51355	membrane protein l
20	36	69.2	423	2 H86195	hypothetical prote
21	36	69.2	435	2 A49387	replication origin
22	36	69.2	451	2 T20798	hypothetical prote
23	36	69.2	458	2 B96643	hypothetical prote
24	36	69.2	503	2 T00901	hypothetical prote
25	36	69.2	505	2 S68518	tub protein, brain
26	36	69.2	665	2 B71609	hypothetical prote
27	36	69.2	1558	2 B71603	RSA-H3 antigen PF
28	36	69.2	1879	2 T19481	hypothetical prote
29	35	67.3	69	2 T31027	hypothetical prote

30	35	67.3	149	2 S49527
31	35	67.3	157	2 AF3315
32	35	67.3	186	2 P81689
33	35	67.3	229	2 U01932
34	35	67.3	261	2 T02107
35	35	67.3	374	2 A59273
36	35	67.3	398	2 S21883
37	35	67.3	400	2 A71490
38	35	67.3	452	2 T50238
39	35	67.3	502	2 T14286
40	35	67.3	509	2 S08059
41	35	67.3	516	2 H82145
42	35	67.3	626	1 NBHUIA
43	35	67.3	689	4 S10392
44	35	67.3	783	2 A48998
45	35	67.3	1192	2 A71623

ALIGNMENTS

RESULT 1

S19702
fibronectin-binding protein B - Staphylococcus aureus
C/Species: Staphylococcus aureus
C/Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
R/Accession: S19702
R/Accession: K./Signae, C.; Mueller, H.P.; Lindberg, M.
Eur. J. Biochem. 202, 1041-1048, 1991
A/Title: Two different genes encode fibronectin binding proteins in Staphylococcus aureus
A/Reference number: S19702, PMID:9211475, PMID:1837266
A/Accession: S19702
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-940 <JOE>
A/Cross-references: UNIPROT:Q53682; EMBL:X62992; NID:949040; PIDD:CAA44726.1; PID:95815;
C/Keywords: fibronectin binding

Query Match 100.0%; Score 52; DB 2; Length 940;
Best Local Similarity 100.0%; Pred. No. 0.84;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SFEDTEEDK 10
DB 688 SFEDTEEDK 697

RESULT 2

G90053
hypothetical protein fmbB [imported] - Staphylococcus aureus (strain N315)
C/Species: Staphylococcus aureus
C/Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C./Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
A/Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.
A/Reference number: A89758; PMID:21311952; PMID:11418146
A/Accession: G90053
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-961 <KUR>
A/Cross-references: UNIPROT:Q99RD3; GB:BA000018; PID:913702452; PIDD:BA843593.1; GSPDB:
A/Experimental source: strain N315
C/Genetics:
A/Genes: fmbB

Query Match 100.0%; Score 52; DB 2; Length 961;
Best Local Similarity 100.0%; Pred. No. 0.86;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SFEDTEEDK 10

|||||
Db 699 SPEEDTEEDK 708

RESULT 3

A32192
fibronectin-binding protein - Staphylococcus aureus
C:Species: Staphylococcus aureus
C:Date: 31-Jul-1989 #sequence_revision 31-Jul-1989 #text_change 16-Feb-1997
C:Accession: A32192
R:Signaas, C.; Raucsi, G.; Jonsson, K.; Lindgren, P.E.; Anantharamiah, G.M.; Hoeoek, W
Proc. Natl. Acad. Sci. U.S.A. 86, 699-703, 1989
A:Title: Nucleotide sequence of the gene for a fibronectin-binding protein from Staphylo
A:Reference number: A32192; MUID:8908898; PMID:2521391
A:Accession: A32192
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1018 <SIG>
A:Cross-references: GB:J04151
C:Keywords: fibronectin binding

Query Match 100.0%; Score 52; DB 2; Length 1018;
Best Local Similarity 100.0%; Pred. No. 0.91;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SPEEDTEEDK 10
|||||
Db 752 SPEEDTEEDK 761

RESULT 4

H90053
hypothetical protein fmb [imported] - Staphylococcus aureus (strain N315)
C:Species: Staphylococcus aureus
C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C:Accession: H90053
R:Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Gui, L.; Oguc
ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kato, C.; Sekimizu, K.;
C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hirataesu, K.
Lancet 357, 1225-1240, 2001
A:Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.
A:Reference number: A89758; MUID:21311952; PMID:11418146
A:Accession: H90053
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1038 <KUR>
A:Cross-references: UNIPROT:Q99RD2; GB:BA000018; PID:G13702453; PIDN:BA843594.1; GSPDB:G
A:Experimental source: strain N315
C:Genetics:
A:Gene: fmb

Query Match 100.0%; Score 52; DB 2; Length 1038
Best Local Similarity 100.0%; Pred. No. 0.93;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SPEEDTEEDK 10
|||||
Db 748 SPEEDTEEDK 757

RESULT 5

AC2110
hypothetical protein alr2434 [imported] - Nostoc sp. (strain PCC 7120)
C:Species: Nostoc sp. PCC 7120
A:Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C:Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004
C:Accession: AC2110
R:Kamaki, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iritaghi
Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S
DNA Res. 8, 205-213, 2001
A:Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana
A:Reference number: AB1807; MUID:21595285; PMID:11759840
A:Accession: AC2110

A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-397 <KUR>
A:Cross-references: UNIPROT:Q8YUB8; GB:BA000019; PIDN:BA874133.1; PID:G17131526; GSPDB:G
A:Experimental source: strain PCC 7120
C:Genetics:
A:Gene: alr2434
C:Superfamily: Methanobacterium thermoautotrophicum conserved hypothetical protein MTH76

Query Match 73.1%; Score 38; DB 2; Length 397;
Best Local Similarity 77.8%; Pred. No. 68;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 FEEDTEEDK 10
|||||
Db 195 FEEDTEEDK 203

RESULT 6

T15665
hypothetical protein C27F2.1 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C:Accession: T15665
R:Kirsten, J.
submitted to the EMBL Data Library, November 1995
A:Description: The sequence of C. elegans cosmid C27F2.
A:Reference number: T15665
A:Accession: T15665
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-653 <KIR>
A:Cross-references: UNIPROT:Q18263; EMBL:U40419; NID:G1065504; PID:G1065511; PIDN:AAA014

C:Genetics:
A:Gene: CESP:C27F2.1
A:introns: 12/2; 97/3; 138/3; 171/1; 261/3; 302/1; 349/2; 373/3; 398/1; 434/2; 536/2; 56
C:Superfamily: Caenorhabditis elegans hypothetical protein C27F2.1

Query Match 73.1%; Score 38; DB 2; Length 653;
Best Local Similarity 77.8%; Pred. No. 1.2e+02;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 FEEDTEEDK 10
|||||
Db 66 FEEDTEEDK 74

RESULT 7

T01906
hypothetical protein T12H20.3 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 26-Feb-1999 #sequence_revision 26-Feb-1999 #text_change 09-Jul-2004
C:Accession: T01906
R:Colton, M.; Graves, T.; Sutterer, C.; Modde, T.
submitted to the EMBL Data Library, July 1998
A:Description: The sequence of A. thaliana T12H20.
A:Reference number: Z14453
A:Accession: T01906
A:Status: translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-1074 <COR>
A:Cross-references: UNIPROT:O82491; EMBL:AF080119; NID:G3600029; PID:G3600033
A:Experimental source: cultivar Columbia
C:Genetics:
A:Map position: 4
A:Note: T12H20.3

Query Match 73.1%; Score 38; DB 2; Length 1074;
Best Local Similarity 70.0%; Pred. No. 2e+02; 1; Indels 0; Gaps 0;
Matches 7; Conservative 2; Mismatches 1; Indels 0;

QY 1 SPEEDTEEDK 10
|||||

DB 459 SFEDEBEER 468

RESULT 8

B72355 hypothetical protein TM0606 - Thermotoga maritima (strain MSB8)

C/Species: Thermotoga maritima

C/Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004

C/Accession: B72355

C/Map position: 2

A/Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.

A/Reference number: A84420; MUID:20083487; PMID:10617197

A/Accession: C84653

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-339 <STO>

A/Cross-references: GB:AE002093; NID:g3643600; PIDD:AAAC42247.1; GSPDB:GN00139

C/Genetics: A/Map position: 2

Query Match 71.2%; Score 37; DB 2; Length 339;

Best Local Similarity 100.0%; Pred. No. 84;

Matches 5; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

DB 249 TVEDTDEDR 258

QY 1 SFEDEBEER 10

DB 249 TVEDTDEDR 258

QY 1 SFEDEBEER 10

DB 249 TVEDTDEDR 258

QY 1 SFEDEBEER 10

DB 249 TVEDTDEDR 258

QY 1 SFEDEBEER 10

DB 249 TVEDTDEDR 258

QY 1 SFEDEBEER 10

DB 249 TVEDTDEDR 258

QY 1 SFEDEBEER 10

DB 249 TVEDTDEDR 258

QY 1 SFEDEBEER 10

DB 249 TVEDTDEDR 258

QY 1 SFEDEBEER 10

DB 249 TVEDTDEDR 258

QY 1 SFEDEBEER 10

DB 249 TVEDTDEDR 258

QY 1 SFEDEBEER 10

DB 249 TVEDTDEDR 258

QY 1 SFEDEBEER 10

DB 249 TVEDTDEDR 258

QY 1 SFEDEBEER 10

DB 249 TVEDTDEDR 258

QY 1 SFEDEBEER 10

DB 249 TVEDTDEDR 258

QY 1 SFEDEBEER 10

QY 3 EEDTEEDK 10
 |||||
 Db 458 EEDVEEDK 465

RESULT 13

sensor protein (for Baer) [imported] - Escherichia coli (strain O157:H7, substrain EDL93)
 C:Species: Escherichia coli
 C:Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
 C:Accession: A85835
 R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.U.; Mayhew
 Miller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamocostas, K.; Apodaca,
 Nature 409, 529-533, 2001
 A:Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
 A:Reference number: A85480; MUID:21074935; PMID:11206551
 A:Accession: A85835
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-467 <STO>
 A:Cross-references: UNIPROT:Q8X712; GB:AB005174; NID:g12516284; PIDN:AAG57141.1; GSPDB:G
 A:Experimental source: strain O157:H7, substrain EDL933
 C:Genetics:
 A:Gene: baes

Query Match 71.2%; Score 37; DB 2; Length 467;
 Best Local Similarity 70.0%; Pred. No. 1.2e+02;
 Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 SPEEDTEEDK 10
 |||||
 Db 84 SPEHDNSEDK 93

RESULT 14

E64974
 sensory kinase Baes (EC 2.7.3.-) - Escherichia coli (strain K-12)
 M:Alternate names: signal transduction protein
 C:Species: Escherichia coli
 C:Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 09-Jul-2004
 C:Accession: E64974; JX0282
 R:Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Co
 A.; Rose, D.J.; Mau, B.; Shao, Y.
 Science 277, 1453-1462, 1997
 A:Title: The complete genome sequence of Escherichia coli K-12.
 A:Reference number: A64720; MUID:9742617; PMID:9278503
 A:Accession: E64974
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-467 <BLAT>
 A:Cross-references: UNIPROT:P30847; GB:AB000297; GB:U00096; NID:g1788382; PIDN:AAC75139.
 A:Experimental source: strain K-12, substrain MG1655
 R:Nagasawa, S.; Ishige, K.; Mizuno, T.
 J. Biochem. 114, 350-357, 1993
 A:Title: Novel members of the two-component signal transduction genes in Escherichia coli
 A:Reference number: JX0282; MUID:94110256; PMID:8282725
 A:Accession: JX0282
 A:Molecule type: DNA
 A:Residues: 1-413; 'VPAT', 'VPA', 422-467 <NAG>
 A:Cross-references: GB:D14054; NID:g216530; PIDN:BAA03140.1; PID:g1003646; PID:g216532
 C:Genetics:
 A:Gene: baes
 C:Keywords: autophosphorylation; phosphohistidine; phosphoprotein; phosphotransferase; s
 F:12-32/Domain: transmembrane #status predicted <TM1>
 F:168-186/Domain: transmembrane #status predicted <TM2>
 F:219-458/Domain: sensor histidine kinase homology <SHK>
 F:250/Binding site: phosphate (His) (covalent) (by autophosphorylation) #status predicted

Query Match 71.2%; Score 37; DB 2; Length 467;
 Best Local Similarity 70.0%; Pred. No. 1.2e+02;
 Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 SPEEDTEEDK 10
 |||||
 Db 84 SPEHDNSEDK 93

RESULT 15

hypothetical protein 8D8.4 - fruit fly (Drosophila melanogaster)
 T13618
 C:Species: Drosophila melanogaster
 C:Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 09-Jul-2004
 C:Accession: T13618
 R:Papagianmakis, G.; Spanos, L.; Cox, S.; Siden-Kiamos, I.; Louis, C.
 submitted to the EMBL Data Library, April 1999
 A:Description: Sequencing the distal X chromosome of Drosophila melanogaster.
 A:Reference number: Z17695
 A:Accession: T13618
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-771 <PAP>
 A:Cross-references: UNIPROT:O46307; EMBL:AL022018; NID:e1273253; PID:e1254565; PIDN:CA1
 C:Genetics:
 A:Cross-references: FlyBase:FBgn0024367
 A:Note: EG:8D8.4

Query Match 71.2%; Score 37; DB 2; Length 771;
 Best Local Similarity 70.0%; Pred. No. 2e+02;
 Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 SPEEDTEEDK 10
 |||||
 Db 367 SPEEDTPSDE 376

Search completed: October 22, 2005, 08:04:21
 Job time : 13.45 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 22, 2005, 06:06:36 ; Search time 55.85 Seconds
(without alignments)
91.688 Million cell updates/sec

Title: US-10-731-238-66

Perfect score: 52

Sequence: 1 SFEEDTEEDK 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1613378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1613378

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : UniProt_03: *
1: uniprot_sprot: *
2: uniprot_trembl: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	52	100.0	152	2 Q9AEP9	Q9AEP9 staphylococ
2	52	100.0	940	2 Q53682	Q53682 staphylococ
3	52	100.0	943	2 Q8NUT8	Q8NUT8 staphylococ
4	52	100.0	957	2 Q6G6H4	Q6G6H4 staphylococ
5	52	100.0	961	2 Q99RD3	Q99RD3 staphylococ
6	52	100.0	961	2 Q7A3J8	Q7A3J8 staphylococ
7	52	100.0	965	2 Q6GDU5	Q6GDU5 staphylococ
8	52	100.0	1015	2 Q8NUT7	Q8NUT7 staphylococ
9	52	100.0	1015	2 Q6G6H3	Q6G6H3 staphylococ
10	52	100.0	1038	1 FNBA STANU	P14738 staphylococ
11	52	100.0	1038	2 Q99RD2	Q99RD2 staphylococ
12	52	100.0	1038	2 Q7A3J7	Q7A3J7 staphylococ
13	43	82.7	502	2 Q8NFC6	Q8NFC6 homo sapien
14	40	76.9	145	2 Q95BJ9	Q95BJ9 digitaria s
15	40	76.9	146	2 Q95BJ2	Q95BJ2 digitaria r
16	40	76.9	150	2 Q95BT7	Q95BT7 digitaria c
17	40	76.9	170	2 Q95BT0	Q95BT0 digitaria i
18	39	75.0	441	1 LR17 HUMAN	Q8A6Y2 homo sapien
19	39	75.0	885	2 Q9GNC0	Q9GNC0 digitaria s
20	39	75.0	885	2 Q9VNX1	Q9VNX1 digitaria s
21	39	75.0	912	2 Q759E8	Q759E8 aabuya goss
22	38	73.1	189	2 Q9VWX2	Q9VWX2 digitaria s
23	38	73.1	200	2 Q8NRY2	Q8NRY2 corynebacte
24	38	73.1	260	2 Q7K2E7	Q7K2E7 digitaria s
25	38	73.1	271	2 Q81PL4	Q81PL4 digitaria s
26	38	73.1	349	2 Q7RJ10	Q7RJ10 plasmodium
27	38	73.1	393	2 Q93CJ1	Q93CJ1 anabaena va
28	38	73.1	397	2 Q8YUB8	Q8YUB8 anabaena sp
29	38	73.1	410	2 Q64K83	Q64K83 ixodes mmo
30	38	73.1	411	2 Q64K85	Q64K85 ixodes affi
31	38	73.1	413	2 Q64K75	Q64K75 ixodes rici

ALIGNMENTS

32	38	73.1	413	2 Q64K78	Q64K78 ixodes paci
33	38	73.1	413	2 Q64K84	Q64K84 ixodes jeil
34	38	73.1	597	2 Q81960	Q81960 corallina p
35	38	73.1	682	2 Q18263	Q18263 caenorhabdi
36	38	73.1	720	2 Q8X1Y0	Q8X1Y0 clostridium
37	38	73.1	984	2 Q7SDA9	Q7SDA9 neurospora
38	38	73.1	1074	2 Q82491	Q82491 arabidopsis
39	38	73.1	1129	2 Q82491	Q82491 homo sapien
40	38	73.1	1213	2 Q6C8W7	Q6C8W7 yarrowia ii
41	38	73.1	1510	2 Q6BHA4	Q6BHA4 debaryomyce
42	38	73.1	1675	2 Q7RHM8	Q7RHM8 plasmodium
43	38	73.1	2006	2 Q81D10	Q81D10 plasmodium
44	38	73.1	3504	2 Q81L45	Q81L45 plasmodium
45	38	73.1	5074	2 Q7RQY0	Q7RQY0 plasmodium

RESULT 1

ID	Q9AEP9	PRELIMINARY;	PRT;	152 AA.
AC	Q9AEP9;			
DT	01-JUN-2001 (Tremblrel. 17, Created)			
DT	01-JUN-2001 (Tremblrel. 17, Last sequence update)			
DT	01-DEC-2001 (Tremblrel. 19, Last annotation update)			
DE	Fibronectin-binding protein (Fragment).			
GN	Name=fnb;			
OS	Staphylococcus aureus.			
OC	Bacteria; Firmicutes; Bacillales; Staphylococcus.			
OX	NCBI_TaxID=1280;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=CMRSA-1;			
RX	MEDLINE=21246681; PubMed=11349044;			
RX	DOI=10.1128/IAI.69.6.3791-3799.2001;			
RA	Rice K., Huesca M., Vaz D., McGavin M.J.;			
RT	"variance in fibronectin binding and fnb locus polymorphisms in			
RT	Staphylococcus aureus: identification of antigenic variation in a			
RT	fibronectin binding protein adhesin of the epidemic CMRSA-1 strain of			
RT	methicillin-resistant S. aureus."			
RL	Infect. Immun. 69:3791-3799(2001).			
DR	EMBL: AY029184; AAK31588.1; -			
FT	NON_TER			
FT	NON_TER			
SQ	SEQUENCE 152 AA; 17193 MW; CFA3913C2B11C025 CRC64;			
Query Match 100.0%; Score 52; DB 2; Length 152;				
Best Local Similarity 100.0%; Pred. No. 1.1;				
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;				
QY	1 SFEEDTEEDK 10			
Db				
	7 SFEEDTEEDK 16			
RESULT 2				
ID	Q53682	PRELIMINARY;	PRT;	940 AA.
AC	Q53682;			
DT	01-NOV-1996 (Tremblrel. 01, Created)			
DT	01-NOV-1996 (Tremblrel. 01, Last sequence update)			
DT	01-MAR-2004 (Tremblrel. 26, Last annotation update)			
DE	Fibronectin binding protein B.			
GN	Name=fnb;			
OS	Staphylococcus aureus.			
OC	Bacteria; Firmicutes; Bacillales; Staphylococcus.			
OX	NCBI_TaxID=1280;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=8325-4;			
RX	MEDLINE=92111475; PubMed=1837266;			
RA	Jonsson K., Sigmas C., Muller H.P., Lindberg M.;			

```

RT      "Two different genes encode fibronectin binding proteins in
RT      Staphylococcus aureus. The complete nucleotide sequence and
RT      characterization of the second gene."
RT      Eur. J. Biochem. 202;1041-1048 (1991).
CC      -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC      an amide bond (By similarity).
DR      EMBL: X62992; CAA44726.1; -.
DR      PIR: S19702; S19702.
DR      HSSP: Q53653; 1N67.
DR      GO: GO:0009986; C:cell surface; IEA.
DR      GO: GO:0005618; C:cell wall; IEA.
DR      GO: GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR      GO: GO:0016020; C:membrane; IEA.
DR      GO: GO:0007155; P:cell adhesion; IEA.
DR      InterPro: IPR008966; Adhes_Bact.
DR      InterPro: IPR004237; Fn_bind.
DR      InterPro: IPR005877; Gpos_YsIRK.
DR      InterPro: IPR001899; Gram_pos_anchor.
DR      Pfam: PF02986; Fn_bind; 2.
DR      Pfam: PF00746; Gram_pos_anchor; 1.
DR      Pfam: PF04650; YsIRK_signal; 1.
DR      TIGRFAMs: TIGR01167; LPXTG_anchor; 1.
DR      TIGRFAMs: TIGR01168; YsIRK_signal; 1.
DR      PROSITE: PS50847; GRAM_POS_ANCHORING; 1.
DR      Cell wall, Peptidoglycan-anchor.
DR      KW      SEQUENCE 940 AA; 10355 MW; E35FBBCA907AE345 CRC64;
SQ      SEQUENCE 940 AA; 10355 MW; E35FBBCA907AE345 CRC64;

Query Match      100.0%; Score 52; DB 2; Length 940
Best Local Similarity 100.0%; Pred. No. 7.3;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 SPEEDTEEDK 10
DB      688 SPEEDTEEDK 697

RESULT 3
ID      Q8NU08      PRELIMINARY;      PRT;      943 AA.
AC      Q8NU08;
DT      01-OCT-2002 (TReMBLrel. 22, Created)
DT      01-OCT-2002 (TReMBLrel. 22, Last sequence update)
DT      01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE      FnbB protein.
GN      Name=fnbB; Ordered locusNames=WM2420;
OS      Staphylococcus aureus (strain WM2).
OC      Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX      NCBI_TaxID=196620;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN=WM2;
RX      MEDLINE=22040717; PubMed=12044378; DOI=10.1016/S0140-6736(00)08713-5;
RX      Baba T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Ogunchi A.,
RX      Nagai Y., Iwama N., Amano K., Naimi T., Kuroda H., Cui L.,
RX      Yamanoto K., Hiramatsu K.;
RA      Genome and virulence determinants of high virulence community-
RT      acquired MRSA."
RL      Lancet 359;1819-1827 (2002).
CC      -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC      an amide bond (By similarity).
DR      EMBL: AP004830; BAB96285.1; -.
DR      HSSP: Q53653; 1N67.
DR      GO: GO:0009986; C:cell surface; IEA.
DR      GO: GO:0005618; C:cell wall; IEA.
DR      GO: GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR      GO: GO:0016020; C:membrane; IEA.
DR      GO: GO:0007155; P:cell adhesion; IEA.
DR      InterPro: IPR008966; Adhes_Bact.
DR      InterPro: IPR004237; Fn_bind.
DR      InterPro: IPR005877; Gpos_YsIRK.
DR      InterPro: IPR001899; Gram_pos_anchor.
DR      Pfam: PF02986; Fn_bind; 1.
DR      Pfam: PF00746; Gram_pos_anchor; 1.

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DR      Pfam: PF04650; YsIRK_signal; 1.
DR      TIGRFAMs: TIGR01167; LPXTG_anchor; 1.
DR      TIGRFAMs: TIGR01168; YsIRK_signal; 1.
DR      PROSITE: PS50847; GRAM_POS_ANCHORING; 1.
DR      Cell wall, Peptide proteome; Peptidoglycan-anchor.
DR      KW      SEQUENCE 943 AA; 104537 MW; DABA5F31947E1B6A CRC64;
SQ      SEQUENCE 957 AA; 105980 MW; 28F8BA7FFDF3EAF CRC64;

Query Match      100.0%; Score 52; DB 2; Length 943;
Best Local Similarity 100.0%; Pred. No. 7.3;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 SPEEDTEEDK 10
DB      695 SPEEDTEEDK 704

RESULT 4
ID      Q6G6H4      PRELIMINARY;      PRT;      957 AA.
AC      Q6G6H4;
DT      05-JUL-2004 (TReMBLrel. 27, Created)
DT      05-JUL-2004 (TReMBLrel. 27, Last sequence update)
DT      05-JUL-2004 (TReMBLrel. 27, Last annotation update)
DE      Fibronectin-binding protein.
GN      Name=fnbB; Ordered locusNames=SMS2387;
OS      Staphylococcus aureus (strain MSSA476).
OC      Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX      NCBI_TaxID=282459;
RN      [1]
RP      SEQUENCE FROM N.A.
RX      PubMed=15213324; DOI=10.1073/pnas.0402521101;
RX      Holden M.T.G., Fell E.J., Lindsey J.A., Peacock S.J., Day N.P.J.,
RX      Enright M.C., Foster T.J., Moore C.E., Hurst L., Atkin R., Barron A.,
RX      Baason N., Bentley S.D., Chillingworth C., Chillingworth T.,
RX      Churcher C., Clark L., Cotton C., Cronin A., Doggett J., Dowd L.,
RX      Felwell T., Hance Z., Harris B., Hauser H., Holroyd S., Jagsle K.,
RX      James K.D., Leonard N., Line A., Mayes R., Moule S., Mungall K.,
RX      Ormond D., Quail M.A., Rabinowitch E., Rutherford K.M., Sanders M.,
RX      Sharp S., Simmonds M., Stevens K., Whitehead S., Barrall B.G.,
RX      Spratt B.G., Parkhill J.;
RA      "Complete genomes of two clinical Staphylococcus aureus strains:
RT      evidence for the rapid evolution of virulence and drug resistance."
RL      Proc. Natl. Acad. Sci. U.S.A. 101:9786-9791 (2004).
CC      -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC      an amide bond (By similarity).
DR      EMBL: BX571857; CAG44201.1; -.
DR      GO: GO:0009986; C:cell surface; IEA.
DR      GO: GO:0005618; C:cell wall; IEA.
DR      GO: GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR      GO: GO:0016020; C:membrane; IEA.
DR      GO: GO:0007155; P:cell adhesion; IEA.
DR      InterPro: IPR008966; Adhes_Bact.
DR      InterPro: IPR004237; Fn_bind.
DR      InterPro: IPR005877; Gpos_YsIRK.
DR      InterPro: IPR001899; Gram_pos_anchor.
DR      Pfam: PF02986; Fn_bind; 1.
DR      Pfam: PF00746; Gram_pos_anchor; 1.
DR      Pfam: PF04650; YsIRK_signal; 1.
DR      TIGRFAMs: TIGR01167; LPXTG_anchor; 1.
DR      TIGRFAMs: TIGR01168; YsIRK_signal; 1.
DR      PROSITE: PS50847; GRAM_POS_ANCHORING; 1.
DR      Cell wall, Complete proteome; Peptidoglycan-anchor.
DR      KW      SEQUENCE 957 AA; 105980 MW; 28F8BA7FFDF3EAF CRC64;
SQ      SEQUENCE 957 AA; 105980 MW; 28F8BA7FFDF3EAF CRC64;

Query Match      100.0%; Score 52; DB 2; Length 957;
Best Local Similarity 100.0%; Pred. No. 7.5;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 SPEEDTEEDK 10
DB      695 SPEEDTEEDK 704

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RESULT 5
O99RD3 PRELIMINARY; PRT; 961 AA.
ID O99RD3;
AC O99RD3;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE Fibronectin-binding protein homolog.
GN Name=fnb3; OrderedLocuNames=SAV2502;
OS Staphylococcus aureus (strain Mu50 / ATCC 700699).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=158878;
RN (1)
RP SEQUENCE FROM N.A.
RC MEDLINE=Mu50 / ATCC 700699;
RX MEDLINE=21311952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2;
RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Iian J.-O., Ito T.,
RA Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,
RA Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
RA Sekimizu K., Hiramatsu H., Kuhara S., Goto S., Yabuuchi J.,
RA Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
RA Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
RA "Whole genome sequencing of methicillin-resistant Staphylococcus
RT aureus."
RT Lancet 357:1225-1240(2001).
CC -1 SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC an amide bond (By similarity).
DR EMBL: AP003365; BAB58664.1; -.
DR FIR; G90053; G90053.
DR HSSP; Q53653; 1N67.
DR DR GO:0009986; C:cell surface; IEA.
DR DR GO:0005618; C:cell wall; IEA.
DR DR GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR DR GO:0016020; C:membrane; IEA.
DR DR GO:0007155; P:cell adhesion; IEA.
DR DR InterPro: IPR008966; Adhes_bact.
DR DR InterPro: IPR004237; Fn_bind.
DR DR InterPro: IPR005877; Gpos_YsIRK.
DR DR InterPro: IPR001899; Gram_pos_anchor.
DR DR Pfam: PF02986; Fn_bind_1.
DR DR Pfam: PF00746; Gram_pos_anchor; 1.
DR DR Pfam: PF04650; YsIRK_signal; 1.
DR DR TIGRfams: TIGR01167; LPXTG_anchor; 1.
DR DR TIGRfams: TIGR01168; YsIRK_signal; 1.
DR DR PROSITE: PSS0847; GRAM_POS_ANCHORING; 1.
DR DR Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ SEQUENCE 961 AA; 106010 MW; 364940F884EA4101 CRC64;

Query Match 100.0%; Score 52; DB 2; Length 961;
Best Local Similarity 100.0%; Pred.No. 7.5;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 SPEEDTEEDK 10
DB 699 SPEEDTEEDK 708

RESULT 6
O7A3J8 PRELIMINARY; PRT; 961 AA.
ID O7A3J8;
AC O7A3J8;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE FmbB protein.
GN Name=fnb3; OrderedLocuNames=SA2290;
OS Staphylococcus aureus (strain N315).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=158879;
RN (1)
RP SEQUENCE FROM N.A.
RX MEDLINE=21311952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2;
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RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Iian J.-O., Ito T.,
RA Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,
RA Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
RA Sekimizu K., Hiramatsu H., Kuhara S., Goto S., Yabuuchi J.,
RA Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
RA Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
RA "Whole genome sequencing of methicillin-resistant Staphylococcus
RT aureus."
RT Lancet 357:1225-1240(2001).
CC -1 SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC an amide bond (By similarity).
DR EMBL: AP003337; BAB43593.1; -.
DR DR GO:0009986; C:cell surface; IEA.
DR DR GO:0005618; C:cell wall; IEA.
DR DR GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR DR GO:0016020; C:membrane; IEA.
DR DR GO:0007155; P:cell adhesion; IEA.
DR DR InterPro: IPR008966; Adhes_bact.
DR DR InterPro: IPR004237; Fn_bind.
DR DR InterPro: IPR005877; Gpos_YsIRK.
DR DR InterPro: IPR001899; Gram_pos_anchor.
DR DR Pfam: PF02986; Fn_bind_1.
DR DR Pfam: PF00746; Gram_pos_anchor; 1.
DR DR Pfam: PF04650; YsIRK_signal; 1.
DR DR TIGRfams: TIGR01167; LPXTG_anchor; 1.
DR DR TIGRfams: TIGR01168; YsIRK_signal; 1.
DR DR PROSITE: PSS0847; GRAM_POS_ANCHORING; 1.
DR DR Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ SEQUENCE 961 AA; 106010 MW; 364940F884EA4101 CRC64;

Query Match 100.0%; Score 52; DB 2; Length 961;
Best Local Similarity 100.0%; Pred.No. 7.5;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 SPEEDTEEDK 10
DB 699 SPEEDTEEDK 708

RESULT 7
O6GDUS PRELIMINARY; PRT; 965 AA.
ID O6GDUS;
AC O6GDUS;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE Fibronectin-binding protein.
GN Name=fnbA; OrderedLocuNames=SA2580;
OS Staphylococcus aureus (strain MRS4252).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=282458;
RN (1)
RP SEQUENCE FROM N.A.
RX PubMed=15213324; DOI=10.1073/pnas.0402521101;
RA Holden M.T.G., Fell E.J., Lindsey J.A., Peacock S.J., Day N.P.J.,
RA Enright M.C., Foster T.J., Moore C.E., Hurst L., Atkin R., Barron A.,
RA Bason N., Bentley S.D., Chillingworth C., Chillingworth T.,
RA Churcher C., Clark L., Cotton C., Cronin A., Doggett J., Dowd L.,
RA Felwell T., Hance Z., Harris B., Hauser H., Holtroyd S., Jørgels K.,
RA James K.D., Lennard N., Line A., Mayes R., Moule S., Mungall K.,
RA Ormond D., Quail M.A., Rabinowitsch E., Rutherford K.M., Sanders M.,
RA Sharp S., Simmonds M., Stevens K., Whitehead S., Barrett B.G.,
RA Spratt B.G., Parkhill J.;
RA "Complete genomes of two clinical Staphylococcus aureus strains:
RT evidence for the rapid evolution of virulence and drug resistance.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:9786-9791(2004).
CC -1 SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC an amide bond (By similarity).
DR EMBL: BX571856; CAG41560.1; -.
DR DR GO:0009986; C:cell surface; IEA.
DR DR GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR DR GO:0016020; C:membrane; IEA.
```

DR GO:0007155; P:cell adhesion; IEA.
 DR InterPro: IPR008966; Adhes_bact.
 DR InterPro: IPR004237; Fn_bind.
 DR InterPro: IPR005877; Gpos_YsIRK.
 DR InterPro: IPR001899; Gram_pos_anchor.
 DR Pfam: PF02986; Fn_bind; 1.
 DR Pfam: PF00746; Gram_pos_anchor; 1.
 DR Pfam: PF04650; YsIRK_signal; 1.
 DR TIGRPFAMs: TIGR01167; LPXTG_anchor; 1.
 DR TIGRPFAMs: TIGR01168; YsIRK_signal; 1.
 DR PROSITE: PS50847; GRAM_POS_ANCHORING; 1.
 DR Cell wall; Complete proteome; Peptidoglycan-anchor.
 KW SEQUENCE 965 AA; 105691 MW; 2982E132164D0551 CRC64;

Query Match 100.0%; Score 52; DB 2; Length 965.
 Best Local Similarity 100.0%; Pred. No. 7.5;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SPEEDTEEDK 10
 Db 753 SPEEDTEEDK 764

RESULT 8

Q8NUU7 PRELIMINARY; PRT; 1015 AA.

AC Q8NUU7; 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Fnb protein.
 GN Name=fnb; Ordered locus names=MW2421;
 OS Staphylococcus aureus (strain MW2).
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 OX NCBI_TaxID=196620;
 [1]
 RN SEQUENCE FROM N.A.
 RC STRAIN=MW2;
 RX MEDLINE=22040717; PubMed=12044378; DOI=10.1016/S0140-6736(03)08713-5;
 RA Baba T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Oguchi A.,
 RA Nagai Y., Iwama N., Amano K., Naimi T., Kuroda H., Cui L.,
 RA Yamamoto K., Hiramatsu K.;
 RT "Genome and virulence determinants of high virulence commu...ty-
 RT acquired MRSA";
 RL Lancet 359:1819-1827(2002).
 CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
 CC an amide bond (By similarity).
 DR EMBL: AF004830; BAB96286.1; -;
 DR GO: GO:0009986; C:cell surface; IEA.
 DR GO: GO:0005618; C:cell wall; IEA.
 DR GO: GO:0009275; C:cell wall (benu Gram-positive Bacteria); IEA.
 DR GO: GO:0016020; C:membrane; IEA.
 DR GO: GO:0007155; P:cell adhesion; IEA.
 DR InterPro: IPR008966; Adhes_bact.
 DR InterPro: IPR004237; Fn_bind.
 DR InterPro: IPR005877; Gpos_YsIRK.
 DR InterPro: IPR001899; Gram_pos_anchor.
 DR Pfam: PF02986; Fn_bind; 1.
 DR Pfam: PF00746; Gram_pos_anchor; 1.
 DR Pfam: PF04650; YsIRK_signal; 1.
 DR TIGRPFAMs: TIGR01167; LPXTG_anchor; 1.
 DR TIGRPFAMs: TIGR01168; YsIRK_signal; 1.
 DR PROSITE: PS50847; GRAM_POS_ANCHORING; 1.
 KW Cell wall; Complete proteome; Peptidoglycan-anchor.
 SQ SEQUENCE 1015 AA; 111145 MW; D0F9281BB64D44D2 CRC64;

Query Match 100.0%; Score 52; DB 2; Length 1015;
 Best Local Similarity 100.0%; Pred. No. 7.9;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SPEEDTEEDK 10
 Db 753 SPEEDTEEDK 762

RESULT 9

ID Q6G6H3 PRELIMINARY; PRT; 1015 AA.

AC Q6G6H3; 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Fibronectin-binding protein.
 GN Ordered locus names=SA2398;
 OS Staphylococcus aureus (strain MSSA476).
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 OX NCBI_TaxID=282459;
 [1]

RP SEQUENCE FROM N.A.
 RX PubMed=15213324; DOI=10.1073/pnas.0402521101;
 RA Holden M.T.G., Fell E.J., Lindsay J.A., Peacock S.J., Day N.P.J.,
 RA Enright M.C., Foster T.J., Moore C.E., Hurst L., Atkin R., Barron A.,
 RA Bason N., Bentley S.D., Chillingworth C., Chillingworth T.,
 RA Churcher C., Clark L., Cronin A., Doggett J., Dowd L.,
 RA Fellwell T., Hance Z., Harris B., Hauser H., Holroyd S., Jagels K.,
 RA James K.D., Lennard N., Line A., Mayes R., Moule S., Mungall K.,
 RA Ormond D., Quail M.A., Rabinowitch E., Rutherford K.M., Sanders M.,
 RA Sharp S., Simmonds M., Stevens K., Whitehead S., Barrett B.G.,
 RA Spratt B.G., Parkhill J.;
 RT "Complete genomes of two clinical Staphylococcus aureus strains:
 RT evidence for the rapid evolution of virulence and drug resistance.";
 RL Proc. Natl. Acad. Sci. U.S.A. 101:9786-9791(2004).
 CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
 CC an amide bond (By similarity).
 DR EMBL: BX571857; CAG44202.1; -;
 DR GO: GO:0009986; C:cell surface; IEA.
 DR GO: GO:0005618; C:cell wall; IEA.
 DR GO: GO:0009275; C:cell wall (benu Gram-positive Bacteria); IEA.
 DR GO: GO:0016020; C:membrane; IEA.
 DR GO: GO:0007155; P:cell adhesion; IEA.
 DR InterPro: IPR008966; Adhes_bact.
 DR InterPro: IPR004237; Fn_bind.
 DR InterPro: IPR005877; Gpos_YsIRK.
 DR InterPro: IPR001899; Gram_pos_anchor.
 DR Pfam: PF02986; Fn_bind; 1.
 DR Pfam: PF00746; Gram_pos_anchor; 1.
 DR Pfam: PF04650; YsIRK_signal; 1.
 DR TIGRPFAMs: TIGR01167; LPXTG_anchor; 1.
 DR TIGRPFAMs: TIGR01168; YsIRK_signal; 1.
 DR PROSITE: PS50847; GRAM_POS_ANCHORING; 1.
 KW Cell wall; Complete proteome; Peptidoglycan-anchor.
 SQ SEQUENCE 1015 AA; 111145 MW; D0F9281BB64D44D2 CRC64;

Query Match 100.0%; Score 52; DB 2; Length 1015;
 Best Local Similarity 100.0%; Pred. No. 7.9;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SPEEDTEEDK 10
 Db 753 SPEEDTEEDK 762

RESULT 10

FNBA STAAU STANDARD; PRT; 1018 AA.

AC P14738; 01-APR-1990 (rel. 14, Created)
 DT 01-APR-1990 (rel. 14, Last sequence update)
 DT 25-OCT-2004 (rel. 45, Last annotation update)
 DE Fibronectin-binding protein precursor (FBNP).
 GN Name=fnbA;
 OS Staphylococcus aureus.
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 OX NCBI_TaxID=1280;
 [1]
 RN SEQUENCE FROM N.A.

RC STRAIN=NCTC 8325-4;
 RX MEDLINE=89098998; PubMed=2521391;
 RA Signes C., Raucsi G., Joensen K., Lindgren P.-E.,
 RA Anantharamaiah G.M., Hoeck M., Lindberg M.;
 RT "Nucleotide sequence of the gene for a fibronectin-binding protein
 from *Staphylococcus aureus*: use of this peptide sequence in the
 RT synthesis of biologically active peptides";
 RL Proc. Natl. Acad. Sci. U.S.A. 86:699-703(1989).
 CC -1- FUNCTION: The ability of bacteria to bind fibronectin has been
 CC proposed as a virulence factor enabling bacteria to colonize wound
 CC tissues and blood clots. Binding of plasma fibronectin to the
 CC bacterial surface might block adhesion receptors on *S. aureus*, thus
 CC representing an important defense mechanism against tissue
 CC invasion.
 CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
 CC an amide bond (Potential).
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; J04151; AAA26632.1; -
 CC InterPro: IPR004237; Fn_bind.
 CC InterPro: IPR005877; Gpos_YsIRK.
 CC InterPro: IPR001899; Gram_pos_anchor.
 CC Pfam; PF00746; Gram_pos_anchor; 1.
 CC Pfam; PF04650; YsIRK_signal; 1.
 CC TRIGRAMS; TIGR01167; LPXTG_anchor; 1.
 CC TRIGRAMS; TIGR01168; YsIRK_signal; 1.
 CC PROSITE; PSS0847; GRAM_POS_ANCHORING; 1.
 CC Cell adhesion; Cell wall; Peptidoglycan-anchor; Repeat; Signal;
 KW virulence.
 FT SIGNAL 1 36
 FT CHAIN 37 985
 FT PROPEP 986 1018
 FT REPEAT 545 574
 FT REPEAT 575 604
 FT DOMAIN 745 878
 FT REPEAT 745 782
 FT REPEAT 783 820
 FT REPEAT 821 859
 FT REPEAT 860 878
 FT DOMAIN 879 948
 FT REPEAT 879 892
 FT REPEAT 893 906
 FT REPEAT 907 920
 FT REPEAT 921 934
 FT REPEAT 935 948
 FT SITE 982 986
 FT MOD_RES 985 985
 SQ SEQUENCE 1018 AA; 111780 MW; 58175E0020E81F1F CRC64;
 Query Match 100.0%; Score 52; DB 1; Length 1018;
 Best Local Similarity 100.0%; Pred. No. 8;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 SPEEDTEBDK 10
 DB 752 SPEEDTEBDK 761
 RESULT 11
 ID 099RD2 PRELIMINARY; PRT; 1038 AA.
 AC 099RD2;
 DT 01-JUN-2001 (TREMBlrel. 17, Created)

DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
 DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
 DE Fibronectin-binding protein homolog.
 GN Name=fnb; OrderedLocNames=SAV2503;
 OS *Staphylococcus aureus* (strain Mu50 / ATCC 700699).
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 OX NCBI_TaxId=158878;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=MU50 / ATCC 700699;
 RX MEDLINE=21311952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2;
 RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
 RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Iian J.-Q., Ito T.,
 RA Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,
 RA Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
 RA Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
 RA Hattori M., Ogasawara N., Hayashi H., Hiramoto K.;
 RT "Whole genome sequencing of methicillin-resistant *Staphylococcus*
 RT *aureus*."; Lancet 357:1225-1240(2001).
 RL Lancel 357:1225-1240(2001).
 CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
 CC an amide bond (By similarity).
 CC EMBL; AP003365; BAB58665.1; -
 CC PIR; H90053; H90053.
 CC GO; GO:0009986; Cell surface; IEA.
 CC GO; GO:0005618; Cell wall; IEA.
 CC GO; GO:0009275; Cell wall (sensu Gram-positive Bacteria); IEA.
 CC GO; GO:0016020; Membrane; IEA.
 CC GO; GO:0007155; P-cell adhesion; IEA.
 CC InterPro: IPR008966; Adhes_bact.
 CC InterPro: IPR004237; Fn_bind.
 CC InterPro: IPR005877; Gpos_YsIRK.
 CC InterPro: IPR001899; Gram_pos_anchor.
 CC Pfam; PF02986; Fn_bind; 1.
 CC Pfam; PF00746; Gram_pos_anchor; 1.
 CC Pfam; PF04650; YsIRK_signal; 1.
 CC TRIGRAMS; TIGR01167; LPXTG_anchor; 1.
 CC TRIGRAMS; TIGR01168; YsIRK_signal; 1.
 CC PROSITE; PSS0847; GRAM_POS_ANCHORING; 1.
 CC Cell wall; Complete proteome; Peptidoglycan-anchor.
 SQ SEQUENCE 1038 AA; 113618 MW; 666B6BF2BFEB12 CRC64;
 Query Match 100.0%; Score 52; DB 2; Length 1038;
 Best Local Similarity 100.0%; Pred. No. 8.1;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 SPEEDTEBDK 10
 DB 748 SPEEDTEBDK 757
 RESULT 12
 ID 07A3J7 PRELIMINARY; PRT; 1038 AA.
 AC 07A3J7;
 DT 05-JUL-2004 (TREMBlrel. 27, Created)
 DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
 DE Fnb protein.
 GN Name=fnb; OrderedLocNames=SA2291;
 OS *Staphylococcus aureus* (strain N15).
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 OX NCBI_TaxId=158879;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21311952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2;
 RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
 RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Iian J.-Q., Ito T.,
 RA Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,
 RA Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
 RA Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,

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RA Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
RT "Whole genome sequencing of methicillin-resistant Staphylococcus
RL aureus."
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC an amide bond (By similarity).
DR EMBL: AP003137; BAB43594.1; -.
DR GO: GO:0009986; C:cell surface; IEA.
DR GO: GO:0005618; C:cell wall; IEA.
DR GO: GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO: GO:0016020; C:membrane; IEA.
DR GO: GO:007155; P:cell adhesion; IEA.
DR InterPro: IPR008966; Adhes_bact.
DR InterPro: IPR004237; Fn_bind.
DR InterPro: IPR005877; Gpob_Ysirk.
DR InterPro: IPR001899; Gram_pos_anchor.
DR Pfam: PF02986; Fn_bind; 1.
DR Pfam: PF04650; Ysirk_signal; 1.
DR TIGRfam: TIGR01167; Lpxg_anchor; 1.
DR TIGRfam: TIGR01168; Ysirk_signal; 1.
DR PROSITE: PS00847; GRAM_POS_ANCHORING; 1.
KW Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ SEQUENCE 1038 AA; 113618 MW; 666BF6BF2BFEB312 CRC64;

Query Match
Best Local Similarity 100.0%; Score 52; DB 2; Length 1038;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SPEEDTEED 10
Db 748 SPEEDTEED 757

RESULT 13
ID Q8NFC6 PRELIMINARY; PRT; 502 AA.
AC Q8NFC6;
DT 01-OCT-2002 (Tremblrel. 22, Created)
DT 01-OCT-2002 (Tremblrel. 22, Last sequence update)
DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Ovary;
RL Guo J.H., Yu L.;
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF528529; AM94279.1; -.
KW Hypothetical protein.
SQ SEQUENCE 502 AA; 55115 MW; C77D17CCA720FA04 CRC64;

Query Match
Best Local Similarity 82.7%; Score 43; DB 2; Length 502;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SPEEDTEED 9
Db 418 SPEEDTEED 426

RESULT 14
ID Q95B19 PRELIMINARY; PRT; 145 AA.
AC Q95B19;
DT 01-DEC-2001 (Tremblrel. 19, Created)
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
DT 01-JUN-2003 (Tremblrel. 24, Last annotation update)
DE DNA-directed RNA polymerase beta' subunit 2 (Fragment).
GN Name=rpoc2;

```

```

OS Digitaria setigera.
OC Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC PACCAD clade; Panicoideae; Paniceae; Digitaria.
OX NCBI_TaxID=158097;
RN [1]
RP SEQUENCE FROM N.A.
RT Duval M.R., Noll J.D., Minn A.H.;
RT "Phylogenetics of Paniceae (Poaceae).";
RL Am. J. Bot. 88:1988-1992 (2001).
DR EMBL: AF372171; AAL25750.1; -.
DR GO: GO:0009507; C:chloroplast; IEA.
DR GO: GO:0003899; F:DNA-directed RNA polymerase activity; IEA.
KW Chloroplast; DNA-directed RNA polymerase.
FT NON_TER 1 145
FT NON_TER 1 145
SQ SEQUENCE 145 AA; 17593 MW; B5097AEFE6959E0F CRC64;

Query Match
Best Local Similarity 76.9%; Score 40; DB 2; Length 145;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SPEEDTEED 9
Db 133 TREEDSEED 141

RESULT 15
ID Q95B2 PRELIMINARY; PRT; 146 AA.
AC Q95B2;
DT 01-DEC-2001 (Tremblrel. 19, Created)
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
DT 01-JUN-2003 (Tremblrel. 24, Last annotation update)
DE DNA-directed RNA polymerase beta' subunit 2 (Fragment).
GN Name=rpoc2;
OS Digitaria radicata.
OC Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC PACCAD clade; Panicoideae; Paniceae; Digitaria.
OX NCBI_TaxID=158096;
RN [1]
RP SEQUENCE FROM N.A.
RT Duval M.R., Noll J.D., Minn A.H.;
RT "Phylogenetics of Paniceae (Poaceae).";
RL Am. J. Bot. 88:1988-1992 (2001).
DR EMBL: AF372168; AAL25747.1; -.
DR GO: GO:0009507; C:chloroplast; IEA.
DR GO: GO:0003899; F:DNA-directed RNA polymerase activity; IEA.
KW Chloroplast; DNA-directed RNA polymerase.
FT NON_TER 1 146
FT NON_TER 1 146
SQ SEQUENCE 146 AA; 17687 MW; 58149361BFA0BE67 CRC64;

Query Match
Best Local Similarity 76.9%; Score 40; DB 2; Length 146;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SPEEDTEED 9
Db 133 TREEDSEED 141

```

Search completed: October 22, 2005, 08:00:26
Job time : 57.85 secs

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OM protein - protein search, using sw model

Run on: October 25, 2005, 20:21:18 ; Search time 63.2 Seconds
(without alignments)
61.196 Million cell updates/sec

Title: US-10-731-238-67

Perfect score: 54

Sequence: 1 EDTEEDKPK 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

1: Geneseq_16Dec04:*
2: geneseqp1980s:*
3: geneseqp1990s:*
4: geneseqp2000s:*
5: geneseqp2001s:*
6: geneseqp2002s:*
7: geneseqp2003as:*
8: geneseqp2003bs:*
9: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	54	100.0	10	2 AAW65723	AAW65723 Fibronec
2	54	100.0	14	2 AAW65761	AAW65761 Peptide #
3	54	100.0	38	1 AAP80660	AAP80660 Protein w
4	54	100.0	38	1 AAP82116	AAP82116 Fibronec
5	54	100.0	38	2 AAW65662	AAW65662 Fibronec
6	54	100.0	38	2 AAW65691	AAW65691 Fibronec
7	54	100.0	38	2 AAW65699	AAW65699 Fibronec
8	54	100.0	38	2 AAW65661	AAW65661 Fibronec
9	54	100.0	39	2 AAW65712	AAW65712 Fibronec
10	54	100.0	39	2 AAW65713	AAW65713 Fibronec
11	54	100.0	130	2 AAW65806	AAW65806 Fibronec
12	54	100.0	130	2 AAW65807	AAW65807 Fibronec
13	54	100.0	130	2 AAW65808	AAW65808 Fibronec
14	54	100.0	130	2 AAW65809	AAW65809 Fibronec
15	54	100.0	134	2 AAW65808	AAW65808 Fibronec
16	54	100.0	134	2 AAW65808	AAW65808 Fibronec
17	54	100.0	134	2 AAW65808	AAW65808 Fibronec
18	54	100.0	139	2 AAW65808	AAW65808 Fibronec
19	54	100.0	174	2 AAW65808	AAW65808 Fibronec
20	54	100.0	174	2 AAW65808	AAW65808 Fibronec
21	54	100.0	181	2 AAW65808	AAW65808 Fibronec
22	54	100.0	181	2 AAW65808	AAW65808 Fibronec
23	54	100.0	559	2 AAW65808	AAW65808 Fibronec
24	54	100.0	767	4 AAW65808	AAW65808 Fibronec
25	54	100.0	767	4 AAW65808	AAW65808 Fibronec

26	54	100.0	940	2 AAR07070	AAR07070 Fibronec
27	54	100.0	940	6 ABJ19111	ABJ19111 Pathogen
28	54	100.0	948	6 ADA89470	ADA89470 Staphyloc
29	54	100.0	948	6 ABJ18923	ABJ18923 Pathogen
30	54	100.0	948	6 ABW72536	ABW72536 Staphyloc
31	54	100.0	961	6 ABU15854	ABU15854 Protein e
32	54	100.0	978	6 AAU33960	AAU33960 Staphyloc
33	54	100.0	1001	4 AAU37093	AAU37093 Staphyloc
34	54	100.0	1018	1 AAW82115	AAW82115 Fibronec
35	54	100.0	1018	4 AAW37245	AAW37245 Staphyloc
36	54	100.0	1018	4 AAU34301	AAU34301 Staphyloc
37	54	100.0	1018	6 ABJ18922	ABJ18922 Pathogen
38	54	100.0	1018	6 ABW72537	ABW72537 Staphyloc
39	54	100.0	1027	2 AAW89806	AAW89806 Staphyloc
40	54	100.0	1038	6 ABU15903	ABU15903 Protein e
41	54	100.0	1038	6 AAW65658	AAW65658 Fibronec
42	50	92.6	10	2 AAW65718	AAW65718 Fibronec
43	50	92.6	30	4 AAW82164	AAW82164 Peptide f
44	50	92.6	30	7 ADC69221	ADC69221 Fibronec
45	50	92.6	31	7 ADC69222	ADC69222 Fibronec

ALIGNMENTS

RESULT 1
ID AAW65723 standard; peptide; 10 AA.
XX

AC AAW65723;
XX

DT 16-OCT-1998 (first entry)
XX

DE Fibronec binding protein-derived peptide #67.
XX

XX microbial surface components recognising adhesive matrix molecule;
XX MSCRAMM: fibronec; fibronec-binding protein; antibody; epitope;
KW antibiotic; bacterial infection; antibiotic-resistant strain.

XX Synthetic.
OS Staphylococcus aureus.

XX WO9831369-A2.
XX

XX 23-JUL-1998.
XX

XX 21-JAN-1998; 98WO-US001222.
XX

XX 21-JAN-1997; 97US-0036139P.
XX

XX (TEXA) UNIV TEXAS A & M SYSTEM.
XX

XX Hoeoek M, Patti JM, House-Pompeo KL, Speziale P, Joh D;
XX McGavin MJ;
XX WPI; 1998-413816/35.

XX Antibody that binds to fibronec-binding protein, preventing its
XX binding to fibronec - used to treat or prevent bacterial infection,
XX especially by Staphylococci and Streptococci.

XX Example 9; Page 110; 201pp; English.

The invention relates to antibodies that bind to a fibronec-binding domain of a fibronec-binding protein, and inhibit binding of the protein to fibronec. Also claimed are: (1) isolated peptides of a fibronec-binding protein that do not bind to fibronec; (2) fusion protein containing at least one peptide of a fibronec-binding protein linked to a second amino acid sequence; (3) nucleic acid encoding the isolated peptide of (1). Antibodies, the isolated peptides of (1) and the nucleic acids are all useful for immunisation (active or passive) and (by inhibiting binding of bacteria to fibronec) for preventing or treating infection in humans or other animals, particularly by staphylococci or

CC streptococci, e.g. meningitis, otitis media, pneumonia, endocarditis,
 CC mastitis in cattle, abortion in horses and many others. Since the
 CC antibodies block binding of bacteria, they should be effective against
 CC antibiotic-resistant strains, and may replace antibiotic therapy or
 CC increase its effectiveness. Sequences AAW65719-41 and AAW65658 represent
 CC peptides which were synthesised to span the D1 motif and the N-terminal
 CC 18 amino acids of D2, with each peptide overlapping by eight amino acids
 CC with the previous sequence
 XX
 SQ Sequence 10 AA;

Query Match 100.0%; Score 54; DB 2; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.032;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EEDTEEDKPK 10
 |||||
 DB 1 EEDTEEDKPK 10

RESULT 2
 ID AAW65761 standard; peptide; 14 AA.

XX AAW65761;
 XX
 DT 16-OCT-1998 (first entry)
 XX
 DE Peptide #105.
 XX
 KM microbial surface components recognising adhesive matrix molecule;
 KM MSCRAMM; fibronectin-binding protein; antibody; epitope;
 KM antibiotic; bacterial infection; antibiotic-resistant strain.

OS Synthetic.
 OS Staphylococcus aureus.

XX MO9631369-A2.

XX 23-JUL-1998.

XX 21-JAN-1998; 98WO-US001222.

XX 21-JAN-1997; 97US-0036139P.

XX (TEXA) UNIV TEXAS A & M SYSTEM.

XX Hoeoek M, Patcl JM, House-Pompeo KL, Speziale P, Joh D;
 PI McGavin MJ;

XX WPI; 1998-413816/35.

XX Antibody that binds to fibronectin-binding protein, preventing its
 PT binding to fibronectin - used to treat or prevent bacterial infection,
 PT especially by Staphylococci and Streptococci.
 XX

PS Disclosure; Page 173; 201pp; English.

XX The invention relates to antibodies that bind to a fibronectin-binding
 CC domain of a fibronectin-binding protein, and inhibit peptides of the
 CC protein to fibronectin. Also claimed are: (1) isolated peptides of a
 CC fibronectin-binding protein that do not bind to fibronectin; (2) fusion
 CC protein containing at least one peptide of a fibronectin-binding protein
 CC linked to a second amino acid sequence; (3) nucleic acid encoding the
 CC isolated peptide of (1). Antibodies, the isolated peptides of (1) and the
 CC nucleic acids are all useful for immunisation (active or passive) and (by
 CC inhibiting binding of bacteria to fibronectin) for preventing or treating
 CC infection in humans or other animals, particularly by staphylococci or
 CC streptococci, e.g. meningitis, otitis media, pneumonia, endocarditis,
 CC mastitis in cattle, abortion in horses and many others. Since the
 CC antibodies block binding of bacteria, they should be effective against
 CC antibiotic-resistant strains, and may replace antibiotic therapy or
 CC increase its effectiveness. The present sequence is shown in the

CC specification
 XX
 SQ Sequence 14 AA;

Query Match 100.0%; Score 54; DB 2; Length 14;
 Best Local Similarity 100.0%; Pred. No. 0.044;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EEDTEEDKPK 10
 |||||
 DB 3 EEDTEEDKPK 12

RESULT 3
 ID AAP80660 standard; protein; 38 AA.

XX AAP80660;
 XX
 DT 25-MAR-2003 (revised)
 DT 07-OCT-1990 (first entry)

DE Protein with fibronectin binding ability.

KM Hybrid DNA molecule; fibronectin binding; mastitis; ruminants;
 KM wound infection.

OS Staphylococcus aureus.

XX EP294349-A.

XX 07-DEC-1988.

XX 30-MAY-1988; 88EP-00850188.

XX 01-JUN-1987; 87SE-00002272.

XX (ALFA) ALFA LAVAL AGRIC INT AB.

XX Lindberg MK, Signas LC, Wadstrom TM, Froman G;

XX WPI; 1988-347978/49.

XX N-PSDB; AAN81097.

XX Hybrid DNA encoding Staphylococcus aureus fibronectin binding protein -
 PT useful for immunisation and topical application to prevent staphylococcal
 PT infections.
 XX

PS Claim 11; Page 12; 23pp; English.

XX The peptide has fibronectin binding ability. It is useful for immunising
 CC ruminants against staphylococcal mastitis, pref. when used at 0.5-5
 CC micrograms/kg, using 3 doses given at 1-3 week intervals; for topical
 CC application to prevent wound infection, using an isotonic saline soln. of
 CC concn. 25-250 micrograms/ml; and, when immobilised on a carrier, for
 CC diagnosing staphylococcal infections. (Updated on 25-MAR-2003 to correct
 CC PF field.) (Updated on 25-MAR-2003 to correct PA field.)
 XX

SQ Sequence 38 AA;

Query Match 100.0%; Score 54; DB 1; Length 38;
 Best Local Similarity 100.0%; Pred. No. 0.12;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EEDTEEDKPK 10
 |||||
 DB 10 EEDTEEDKPK 19

RESULT 4
 ID AAP82116 standard; protein; 38 AA.

XX

AC AAP2116;
 XX
 XX 25-MAR-2003 (revised)
 DT 05-JAN-1990 (first entry)
 XX
 XX
 DE Fibronectin binding protein.
 XX
 KW Fibronectin binding protein; *S. aureus*; immunisation; mastitis; ruminants;
 KM wound infection; diagnosis.
 XX
 XX Staphylococcus aureus.
 OS
 XX
 PN EP294349-A.
 XX
 PD 07-DEC-1988.
 XX
 PF 30-MAY-1988; 88EP-00850188.
 XX
 PR 01-JUN-1987; 87SE-00002272.
 XX
 PA (ALPA) ALPA LAVAL AGRIC INT AB.
 XX
 PI Lindberg MK, Signas LC, Wadstrom TM, Froman G;
 DR WPI; 1988-347978/49.
 XX
 DR N-PSDB; AAN82054.
 XX
 PT Hybrid DNA encoding Staphylococcus aureus fibronectin binding protein -
 PT useful for immunisation and topical application to prevent staphylococcal
 PT infections.
 PS
 PS Claim 11; Page 12; 23pp; English.
 XX
 CC The *S. aureus* fibronectin binding protein may be included in a hybrid
 CC protein. The protein may be used to immunise ruminants against
 CC staphylococcal mastitis, pref. when given at 0.5-5 microg/kg, using 3
 CC doses at 1-3 week intervals; and for topical applicm. to prevent wound
 CC infection, pref. using isotonic saline soln. of concn. 25-250 microg/mg.
 CC The DNA encoding the binding protein and the hybrid protein may be
 CC immobilised on a carrier and used to diagnose staphylococcal infections.
 CC (Updated on 25-MAR-2003 to correct PA field.)
 CC
 SQ Sequence 38 AA;
 XX
 XX
 Query Match 100.0%; Score 54; DB 1; Length 38;
 Best Local Similarity 100.0%; Pred. No. 0.12;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 EEDTEEDKPK 10
 DB 10 EEDTEEDKPK 19
 XX
 XX
 RESULT 5
 ID AAW65662
 XX AAW65662 standard; peptide; 38 AA.
 AC
 XX AAW65662;
 DT 16-OCT-1998 (first entry)
 XX
 DE Fibronectin binding protein-derived peptide #6.
 XX
 KM microbial surface components recognising adhesive matrix molecule;
 KM MSCRAMM; fibronectin; fibronectin-binding protein; antibody; epitope;
 KM antibiotic; bacterial infection; antibiotic-resistant strain.
 XX
 OS Synthetic.
 OS Staphylococcus aureus.
 PN W09831389-A2.
 XX
 PD 23-JUL-1998.

XX
 PF 21-JAN-1998; 98WO-US001222.
 XX
 PR 21-JAN-1997; 97US-0036139P.
 XX
 PA (TEXA) UNIV TEXAS A & M SYSTEM.
 XX
 PI Hoeoek M, Patti JM, House-Pompeo KL, Speciale P, Joh D;
 PI McGavin MJ;
 DR WPI; 1998-413816/35.
 XX
 PT Antibody that binds to fibronectin-binding protein, preventing its
 PT binding to fibronectin - used to treat or prevent bacterial infection,
 PT especially by Staphylococci and Streptococci.
 PS
 PS Example 2; Page 92; 201pp; English.
 XX
 CC The invention relates to antibodies that bind to a fibronectin-binding
 CC domain of a fibronectin-binding protein, and inhibit binding of the
 CC protein to fibronectin. Also claimed are: (1) isolated peptides of a
 CC fibronectin-binding protein that do not bind to fibronectin; (2) fusion
 CC protein containing at least one peptide of a fibronectin-binding protein
 CC linked to a second amino acid sequence; (3) nucleic acid encoding the
 CC isolated peptide of (1). Antibodies, the isolated peptides of (1) and the
 CC nucleic acids are all useful for immunisation (active or passive) and (by
 CC inhibiting binding of bacteria to fibronectin) for preventing or treating
 CC infection in humans or other animals, particularly by staphylococci or
 CC streptococci, e.g. meningitis, otitis media, pneumonia, endocarditis,
 CC mastitis in cattle, abortion in horses and many others. Since the
 CC antibodies block binding of bacteria, they should be effective against
 CC antibiotic-resistant strains, and may replace antibiotic therapy or
 CC increase its effectiveness. Sequences AAW65659-68 represent synthetic
 CC epitopes from the fibronectin binding domains DU and DI-D4 of the *S.*
 CC aureus fnbA gene
 XX
 SQ Sequence 38 AA;
 XX
 XX
 Query Match 100.0%; Score 54; DB 2; Length 38;
 Best Local Similarity 100.0%; Pred. No. 0.12;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 EEDTEEDKPK 10
 DB 9 EEDTEEDKPK 18
 XX
 XX
 RESULT 6
 ID AAW65691
 XX AAW65691 standard; peptide; 38 AA.
 AC
 XX AAW65691;
 DT 16-OCT-1998 (first entry)
 XX
 DE Fibronectin binding protein-derived peptide #35.
 XX
 KM microbial surface components recognising adhesive matrix molecule;
 KM MSCRAMM; fibronectin; fibronectin-binding protein; antibody; epitope;
 KM antibiotic; bacterial infection; antibiotic-resistant strain.
 XX
 OS Synthetic.
 OS Staphylococcus aureus.
 PN W09831389-A2.
 XX
 PD 23-JUL-1998.
 XX
 PF 21-JAN-1998; 98WO-US001222.
 XX
 PR 21-JAN-1997; 97US-0036139P.
 XX
 PA (TEXA) UNIV TEXAS A & M SYSTEM.

XX Hoecek M, Patti JM, House-Pompeo KL, Speziale P, Joh D;
 PI Mcgavin MJ;
 XX WPI; 1998-413816/35.
 XX
 XX Antibody that binds to fibronectin-binding protein, preventing its
 PT binding to fibronectin - used to treat or prevent bacterial infection,
 PT especially by Staphylococci and Streptococci.
 XX
 XX Example 8; Page 101; 201pp; English.
 XX
 XX The invention relates to antibodies that bind to a fibronectin-binding
 CC domain of a fibronectin-binding protein, and inhibit binding of the
 CC protein to fibronectin. Also claimed are: (1) isolated peptides of a
 CC fibronectin-binding protein that do not bind to fibronectin; (2) fusion
 CC protein containing at least one peptide of a fibronectin-binding protein
 CC linked to a second amino acid sequence; (3) nucleic acid encoding the
 CC isolated peptide of (1). Antibodies, the isolated peptides of (1) and the
 CC nucleic acids are all useful for immunisation (active or passive) and (by
 CC inhibiting binding of bacteria to fibronectin) for preventing or treating
 CC infection in humans or other animals, particularly by staphylococci or
 CC streptococci, e.g. meningitis, otitis media, pneumonia, endocarditis,
 CC mastitis in cattle, abortion in horses and many others. Since the
 CC antibodies block binding of bacteria, they should be effective against
 CC antibiotic-resistant strains, and may replace antibiotic therapy or
 CC increase its effectiveness. Sequences AAW65691-700 represent a series of
 CC synthetic peptides based on the D1 region of S. aureus fibronectin
 CC binding protein A. They were synthesised to contain mutations
 XX
 SQ Sequence 38 AA;

Query Match 100.0%; Score 54; DB 2; Length 38;
 Best Local Similarity 100.0%; Pred. No. 0.12;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 EEDTEEDKPK 10
 |||||
 DB 9 EEDTEEDKPK 18

RESULT 7
 AAW65699
 ID AAW65699 standard; peptide; 38 AA.
 XX
 AC AAW65699;
 XX
 DT 16-OCT-1998 (first entry)
 XX
 DE Fibronectin binding protein-derived peptide #43.
 XX
 XX microbial surface components recognising adhesive matrix molecule;
 KW MSCRAMM; fibronectin; fibronectin-binding protein; antibody; epitope;
 KW antibiotic; bacterial infection; antibiotic-resistant strain..
 XX
 OS Synthetic.
 OS Staphylococcus aureus.
 OS
 PN WO9831389-A2.
 XX
 PD 23-JUL-1998.
 XX
 PF 21-JAN-1998; 98WO-US001222.
 XX
 PR 21-JAN-1997; 97US-0036139P.
 XX
 PA (TEXA) UNIV TEXAS A & M SYSTEM.
 XX
 PI Hoecek M, Patti JM, House-Pompeo KL, Speziale P, Joh D;
 PI Mcgavin MJ;
 XX
 DR WPI; 1998-413816/35.
 XX

PT Antibody that binds to fibronectin-binding protein, preventing its
 PT binding to fibronectin - used to treat or prevent bacterial infection,
 PT especially by Staphylococci and Streptococci.
 XX
 XX Example 8; Page 102; 201pp; English.
 XX
 XX The invention relates to antibodies that bind to a fibronectin-binding
 CC domain of a fibronectin-binding protein, and inhibit binding of the
 CC protein to fibronectin. Also claimed are: (1) isolated peptides of a
 CC fibronectin-binding protein that do not bind to fibronectin; (2) fusion
 CC protein containing at least one peptide of a fibronectin-binding protein
 CC linked to a second amino acid sequence; (3) nucleic acid encoding the
 CC isolated peptide of (1). Antibodies, the isolated peptides of (1) and the
 CC nucleic acids are all useful for immunisation (active or passive) and (by
 CC inhibiting binding of bacteria to fibronectin) for preventing or treating
 CC infection in humans or other animals, particularly by staphylococci or
 CC streptococci, e.g. meningitis, otitis media, pneumonia, endocarditis,
 CC mastitis in cattle, abortion in horses and many others. Since the
 CC antibodies block binding of bacteria, they should be effective against
 CC antibiotic-resistant strains, and may replace antibiotic therapy or
 CC increase its effectiveness. Sequences AAW65691-700 represent a series of
 CC synthetic peptides based on the D1 region of S. aureus fibronectin
 CC binding protein A. They were synthesised to contain mutations
 XX
 SQ Sequence 38 AA;

Query Match 100.0%; Score 54; DB 2; Length 38;
 Best Local Similarity 100.0%; Pred. No. 0.12;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 EEDTEEDKPK 10
 |||||
 DB 9 EEDTEEDKPK 18

RESULT 8
 AAW65661
 ID AAW65661 standard; peptide; 38 AA.
 XX
 AC AAW65661;
 XX
 DT 16-OCT-1998 (first entry)
 XX
 DE Fibronectin binding protein-derived peptide #5.
 XX
 XX microbial surface components recognising adhesive matrix molecule;
 KW MSCRAMM; fibronectin; fibronectin-binding protein; antibody; epitope;
 KW antibiotic; bacterial infection; antibiotic-resistant strain..
 XX
 OS Synthetic.
 OS Staphylococcus aureus.
 OS
 PN WO9831389-A2.
 XX
 PD 23-JUL-1998.
 XX
 PF 21-JAN-1998; 98WO-US001222.
 XX
 PR 21-JAN-1997; 97US-0036139P.
 XX
 PA (TEXA) UNIV TEXAS A & M SYSTEM.
 XX
 PI Hoecek M, Patti JM, House-Pompeo KL, Speziale P, Joh D;
 PI Mcgavin MJ;
 XX
 DR WPI; 1998-413816/35.
 XX
 XX Antibody that binds to fibronectin-binding protein, preventing its
 PT binding to fibronectin - used to treat or prevent bacterial infection,
 PT especially by Staphylococci and Streptococci.
 XX
 XX Example 2; Page 92; 201pp; English.
 XX

CC The invention relates to antibodies that bind to a fibronectin-binding
 CC domain of a fibronectin-binding protein, and inhibit binding of the
 CC protein to fibronectin. Also claimed are: (1) isolated peptides of a
 CC fibronectin-binding protein that do not bind to fibronectin; (2) fusion
 CC protein containing at least one peptide of a fibronectin-binding protein
 CC linked to a second amino acid sequence; (3) nucleic acid encoding the
 CC isolated peptide of (1). Antibodies, the isolated peptides of (1) and the
 CC nucleic acids are all useful for immunisation (active or passive) and (by
 CC inhibiting binding of bacteria to fibronectin) for preventing or treating
 CC infection in humans or other animals, particularly by staphylococci or
 CC streptococci, e.g. meningitis, otitis media, pneumonia, endocarditis,
 CC mastitis in cattle, abortion in horses and many others. Since the
 CC antibodies block binding of bacteria, they should be effective against
 CC antibiotic-resistant strains, and may replace antibiotic therapy or
 CC increase its effectiveness. Sequences AAW65659-68 represent synthetic
 CC epitopes from the fibronectin binding domains DU and DI-D4 of the S.
 CC aureus fnbA gene

XX Sequence 38 AA;

Query Match 100.0%; Score 54; DB 2; Length 38;

Best Local Similarity 100.0%; Pred. No. 0.12;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EEDTEEDKPK 10
 |||||
 DB 9 EEDTEEDKPK 18

RESULT 9

AAW65712 standard; peptide; 39 AA.

XX AAW65712;

DT 16-OCT-1998 (first entry)

XX Fibronectin binding protein-derived peptide #56.

XX microbial surface components recognising adhesive matrix molecule;

KW MSCRAMM; fibronectin; fibronectin-binding protein; antibody; epitope;

XX antibiotic; bacterial infection; antibiotic-resistant strain.

OS Synthetic.

XX Staphylococcus aureus.

PN WO9831389-A2.

PD 23-JUL-1998.

PF 21-JAN-1998; 98WO-US001222.

PR 21-JAN-1997; 97US-0036139P.

PA (TEXA) UNIV TEXAS A & M SYSTEM.

XX Hoeck M, Patti JM, House-Pompeo KL, Speziale P, Joh D;

PI Mcgavyn MJ;

DR WPI; 1998-413816/35.

XX Antibody that binds to fibronectin-binding protein, preventing its

PT binding to fibronectin - used to treat or prevent bacterial infection,

XX especially by staphylococci and streptococci.

PS Example 8; Page 104; 201pp; English.

XX The invention relates to antibodies that bind to a fibronectin-binding

CC domain of a fibronectin-binding protein, and inhibit binding of the

CC protein to fibronectin. Also claimed are: (1) isolated peptides of a

CC fibronectin-binding protein that do not bind to fibronectin; (2) fusion

CC protein containing at least one peptide of a fibronectin-binding protein

CC linked to a second amino acid sequence; (3) nucleic acid encoding the

CC isolated peptide of (1). Antibodies, the isolated peptides of (1) and the
 CC nucleic acids are all useful for immunisation (active or passive) and (by
 CC inhibiting binding of bacteria to fibronectin) for preventing or treating
 CC infection in humans or other animals, particularly by staphylococci or
 CC streptococci, e.g. meningitis, otitis media, pneumonia, endocarditis,
 CC mastitis in cattle, abortion in horses and many others. Since the
 CC antibodies block binding of bacteria, they should be effective against
 CC antibiotic-resistant strains, and may replace antibiotic therapy or
 CC increase its effectiveness. The present sequence is shown in the
 CC specification

XX Sequence 39 AA;

Query Match 100.0%; Score 54; DB 2; Length 39;

Best Local Similarity 100.0%; Pred. No. 0.12;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EEDTEEDKPK 10
 |||||
 DB 9 EEDTEEDKPK 18

RESULT 10

AAW65713 standard; peptide; 39 AA.

XX AAW65713;

DT 16-OCT-1998 (first entry)

XX Fibronectin binding protein-derived peptide #57.

XX microbial surface components recognising adhesive matrix molecule;

KW MSCRAMM; fibronectin; fibronectin-binding protein; antibody; epitope;

XX antibiotic; bacterial infection; antibiotic-resistant strain.

OS Synthetic.

XX Staphylococcus aureus.

PN WO9831389-A2.

PD 23-JUL-1998.

PF 21-JAN-1998; 98WO-US001222.

PR 21-JAN-1997; 97US-0036139P.

PA (TEXA) UNIV TEXAS A & M SYSTEM.

XX Hoeck M, Patti JM, House-Pompeo KL, Speziale P, Joh D;

PI Mcgavyn MJ;

DR WPI; 1998-413816/35.

XX Antibody that binds to fibronectin-binding protein, preventing its

PT binding to fibronectin - used to treat or prevent bacterial infection,

XX especially by staphylococci and streptococci.

PS Example 8; Page 104; 201pp; English.

XX The invention relates to antibodies that bind to a fibronectin-binding

CC domain of a fibronectin-binding protein, and inhibit binding of the

CC protein to fibronectin. Also claimed are: (1) isolated peptides of a

CC fibronectin-binding protein that do not bind to fibronectin; (2) fusion

CC protein containing at least one peptide of a fibronectin-binding protein

CC linked to a second amino acid sequence; (3) nucleic acid encoding the

CC isolated peptide of (1). Antibodies, the isolated peptides of (1) and the

CC nucleic acids are all useful for immunisation (active or passive) and (by

CC inhibiting binding of bacteria to fibronectin) for preventing or treating

CC infection in humans or other animals, particularly by staphylococci or

CC streptococci, e.g. meningitis, otitis media, pneumonia, endocarditis,

CC mastitis in cattle, abortion in horses and many others. Since the

CC antibodies block binding of bacteria, they should be effective against

CC antibiotic-resistant strains, and may replace antibiotic therapy or
 CC increase its effectiveness. The present sequence is shown in the
 CC specification
 CC
 XX
 SQ Sequence 39 AA;

Query Match 100.0%; Score 54; DB 2; Length 39;
 Best Local Similarity 100.0%; Pred. No. 0.12;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EEDTEEDKPK 10
 |||||
 Db 9 EEDTEEDKPK 18

RESULT 11
 AAR58806
 ID AAR58806 standard; protein; 130 AA.
 XX
 AC AAR58806;

DT 25-MAR-2003 (revised)
 DT 30-MAR-1995 (first entry)

DE Fibronectin binding domain D1-D4 (709-838 (P838T)).

KM Fibronectin binding protein; Fbp; fibronectin binding domain;
 KM monoclonal antibody; MAb; adhesion; Gram-positive bacterium; bacteremia;
 KM Escherichia coli.

OS Staphylococcus aureus.

PN WO9418327-A1.

PD 18-AUG-1994.

PF 04-FEB-1994; 94WO-GB000215.

PR 05-FEB-1993; 93GB-00002289.

PR 20-OCT-1993; 93GB-00021592.

PA (SMTK) SMITHKLINE BEECHAM PLC.

PI Burnham MKR, Chopra I, Critchley IA, Knowles DJC;

DR WPI; 1994-279748/34.

PT Fibronectin binding protein and monoclonal antibodies specific for Fbp -
 PT useful to prevent adherence of Gram-positive bacteria to indwelling
 PT devices or wounds.

PS Disclosure; Page 30; 40pp; English.

CC Polypeptides corresponding to residues G709-T886 plus PRIVATE, G709-
 CC P838 (P838T) and G709-P838 (AAR58805-07, respectively) of S. aureus J2385
 CC (NCIMB 40532) Fbp type A fibronectin binding domain D1-D4 region
 CC (AAR58808) were expressed in E. coli BL21 (DE4) and used to raise MAbs
 CC specific for Fbp. (Updated on 25-MAR-2003 to correct PN field.)

XX Sequence 130 AA;

Query Match 100.0%; Score 54; DB 2; Length 130;
 Best Local Similarity 100.0%; Pred. No. 0.39;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EEDTEEDKPK 10
 |||||
 Db 10 EEDTEEDKPK 19

RESULT 12
 AAR58807
 ID AAR58807 standard; protein; 130 AA.

XX AAR58807;

DT 25-MAR-2003 (revised)
 DT 30-MAR-1995 (first entry)

DE Fibronectin binding domain D1-D4 (709-838).

KM Fibronectin binding protein; Fbp; fibronectin binding domain;
 KM monoclonal antibody; MAb; adhesion; Gram-positive bacterium; bacteremia;
 KM Escherichia coli.

OS Staphylococcus aureus.

PN WO9418327-A1.

PD 18-AUG-1994.

PF 04-FEB-1994; 94WO-GB000215.

PR 05-FEB-1993; 93GB-00002289.

PR 20-OCT-1993; 93GB-00021592.

PA (SMTK) SMITHKLINE BEECHAM PLC.

PI Burnham MKR, Chopra I, Critchley IA, Knowles DJC;

DR WPI; 1994-279748/34.

PT Fibronectin binding protein and monoclonal antibodies specific for Fbp -
 PT useful to prevent adherence of Gram-positive bacteria to indwelling
 PT devices or wounds.

PS Disclosure; Page 30; 40pp; English.

CC Polypeptides corresponding to residues G709-T886 plus PRIVATE, G709-
 CC P838 (P838T) and G709-P838 (AAR58805-07, respectively) of S. aureus J2385
 CC (NCIMB 40532) Fbp type A fibronectin binding domain D1-D4 region
 CC (AAR58808) were expressed in E. coli BL21 (DE4) and used to raise MAbs
 CC specific for Fbp. (Updated on 25-MAR-2003 to correct PN field.)

XX Sequence 130 AA;

Query Match 100.0%; Score 54; DB 2; Length 130;
 Best Local Similarity 100.0%; Pred. No. 0.39;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EEDTEEDKPK 10
 |||||
 Db 10 EEDTEEDKPK 19

RESULT 13

AAR91202
 ID AAR91202 standard; peptide; 130 AA.

AC AAR91202;

DT 13-NOV-1996 (first entry)

DE D1-D4 fibronectin binding domains.

KM Fibronectin; oral hygiene; gingivitis; gum disease; adhesion;
 KM periodontitis; oral pathogen; caries; calculus; candidiasis; oral surgery;
 KM tissue regeneration; irrigation; toothpaste; dentifrice; mouthwash;
 KM lozenge.

OS Staphylococcus aureus.

PN WO9604003-A1.

PD 15-FEB-1996.

XX

PF 18-JUL-1995; 95WO-EP002825.
 XX
 PR 05-AUG-1994; 94GB-00015902.
 XX
 PA (SMIK) SMITHKLINE BEECHAM PLC.
 XX
 PI Barnett P, Critchley IA, Dodd I;
 XX
 DR WPI; 1996-129122/13.
 XX
 PT Prevention of adherence of oral pathogens in the oral cavity, partic.
 PT tooth surfaces - by application of a fibronectin binding protein or
 XX polypeptide or a monoclonal antibody or fragment against it.
 PS
 XX Claim 5; Page 32; 41pp; English.
 CC Adherence of oral pathogens, particularly to tooth surfaces, can be
 CC prevented by application of a fibronectin binding protein or polypeptide.
 CC The fibronectin binding protein or polypeptide is useful in the
 CC manufacture of oral hygiene compositions, eg. toothpaste, liquid
 CC dentifrice, mouthwash or lozenge. They are useful to prevent the plaque-
 CC related development of carious lesions, gingivitis, calculus or
 CC periodontal disease and to combat oral cavity infections, e.g.
 CC candidiasis. They may also be useful in oral surgery e.g. in guided
 CC tissue regeneration procedures to prevent subsequent bacterial infection,
 CC and for irrigation of periodontal pockets. This sequence corresponds to
 CC amino acids 709-838 of the D1-D4 fibronectin binding domain of
 CC Staphylococcus aureus
 XX
 SQ Sequence 130 AA;
 XX
 Query Match 100.0%; Score 54; DB 2; Length 130;
 Best Local Similarity 100.0%; Pred. No. 0.39;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 EEDTEEDKPK 10
 DB 10 EEDTEEDKPK 19
 XX
 RESULT 14
 ID AAR91201 standard; peptide; 130 AA.
 XX
 AC AAR91201;
 XX
 DT 13-NOV-1996 (first entry)
 XX
 DE D1-D4 fibronectin binding domains.
 XX
 KM Fibronectin; oral hygiene; gingivitis; gum disease; adhesion;
 KM periodontitis; oral pathogens; caries; calculus; candidiasis; oral surgery;
 KM tissue regeneration; irrigation; toothpaste; dentifrice; mouthwash;
 KM lozenge.
 KW
 XX
 XX Staphylococcus aureus.
 XX
 OS
 XX
 PN WO9604003-A1.
 XX
 PD 15-FEB-1996.
 XX
 PF 18-JUL-1995; 95WO-EP002825.
 XX
 PR 05-AUG-1994; 94GB-00015902.
 XX
 PA (SMIK) SMITHKLINE BEECHAM PLC.
 XX
 PI Barnett P, Critchley IA, Dodd I;
 XX
 DR WPI; 1996-129122/13.
 XX
 PT Prevention of adherence of oral pathogens in the oral cavity, partic.
 PT tooth surfaces - by application of a fibronectin binding protein or

PT polypeptide or a monoclonal antibody or fragment against it.
 XX
 XX Claim 5; Page 31-32; 41pp; English.
 XX
 PS
 XX Adherence of oral pathogens, particularly to tooth surfaces, can be
 CC prevented by application of a fibronectin binding protein or polypeptide.
 CC The fibronectin binding protein or polypeptide is useful in the
 CC manufacture of oral hygiene compositions, eg. toothpaste, liquid
 CC dentifrice, mouthwash or lozenge. They are useful to prevent the plaque-
 CC related development of carious lesions, gingivitis, calculus or
 CC periodontal disease and to combat oral cavity infections, e.g.
 CC candidiasis. They may also be useful in oral surgery e.g. in guided
 CC tissue regeneration procedures to prevent subsequent bacterial infection,
 CC and for irrigation of periodontal pockets. This sequence corresponds to
 CC amino acids 709-838 of the D1-D4 fibronectin binding domain of
 CC Staphylococcus aureus with a P838T substitution
 XX
 SQ Sequence 130 AA;
 XX
 Query Match 100.0%; Score 54; DB 2; Length 130;
 Best Local Similarity 100.0%; Pred. No. 0.39;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 EEDTEEDKPK 10
 DB 10 EEDTEEDKPK 19
 XX
 RESULT 15
 ID AAY29089 standard; protein; 134 AA.
 XX
 AC AAY29089;
 XX
 DT 28-SEP-1999 (first entry)
 XX
 DE Cloned fibronectin binding protein binding domain (FnBAB) sequence.
 XX
 KM Bovine herpes virus-2; BHV-2; cytokine; immune response; immunogen; IL;
 KM interleukin; colony stimulating factor; CSF; interferon; IFN; TNF;
 KM tumour necrosis factor; recombinant virus; vaccine; mucosal disease;
 KM mastitis; breast cancer; stress-induced disease; binding domain; FnBAB;
 KM fibronectin binding protein.
 KW
 XX
 XX Staphylococcus aureus.
 XX
 OS
 XX
 PN WO916892-A1.
 XX
 PD 08-APR-1999.
 XX
 PF 29-SEP-1998; 98WO-GB002927.
 XX
 PR 29-SEP-1997; 97GB-00020633.
 XX
 PA (UYBR-) UNIV BRISTOL.
 XX
 PI Bradley AJ, Duffas WP;
 XX
 DR WPI; 1999-255101/21.
 XX
 DR N-PSDB; AAX91506.
 XX
 PF New bovine herpes virus-2 vectors.
 XX
 PS Example 2; Fig 8A-B; 130pp; English.
 XX
 CC The invention provides bovine herpes virus-2 (BHV-2) based vectors that
 CC comprise at least one cytokine-encoding DNA sequence. The expression of
 CC cytokines in mammals can up-regulate immune responses to the immunogens.
 CC The cytokine is selected from interleukins (IL), colony stimulating
 CC factors (CSF), interferons (IFN) and tumour necrosis factors (TNF). The
 CC BHV-2 based vector or recombinant virus can be used as vaccines. They can
 CC be used for preventing or treating a mucosal disease in a subject, e.g.
 CC ruminants, cattle, sheep, goats, dogs, cats, horses, or man, particularly

CC mastitis in cows or breast cancers in humans. They can also be used for
 CC preventing or treating a stress-induced disease. The present sequence
 CC represents a S. aureus fibronectin binding protein binding domain
 CC sequence FNBA8, the gene cloned for use in this invention. The gene has
 CC 97.8 percent identity when compared to the previously published sequences
 CC FNBA and FNBB
 CC
 XX

SQ Sequence 134 AA;

Query Match 100.0%; Score 54; DB 2; Length 134;

Best Local Similarity 100.0%; Pred. No. 0.4; Mismatches 0; Indels 0; Gaps 0;

Matches 10; Conservative 0; Indels 0; Gaps 0;
 QY 1 EEDTEEDKPK 10
 |||||
 DB 10 EEDTEEDKPK 19

Search completed: October 25, 2005, 20:58:41
 Job time : 63.2 secs

(ojdso) xua/2 egn' cu/1
 Tm's

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 22, 2005, 05:46:56 ; Search time 17.3 Seconds
(without alignments)
43.150 Million cell updates/sec

Title: US-10-731-238-67

Perfect score: 54
Sequence: 1 EEDTERDKPK 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA: *
1: /cgn2_6/ptodata/1/1aa/5A.COMB.pep.*
2: /cgn2_6/ptodata/1/1aa/5B.COMB.pep.*
3: /cgn2_6/ptodata/1/1aa/6A.COMB.pep.*
4: /cgn2_6/ptodata/1/1aa/6B.COMB.pep.*
5: /cgn2_6/ptodata/1/1aa/PTCUS.COMB.pep.*
6: /cgn2_6/ptodata/1/1aa/backfile1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	54	100.0	10	4	US-09-010-317-67
2	54	100.0	14	4	US-09-010-317-105
3	54	100.0	38	1	US-08-234-622A-2
4	54	100.0	38	1	US-08-729-767-3
5	54	100.0	38	4	US-09-010-317-5
6	54	100.0	38	4	US-09-010-317-6
7	54	100.0	38	4	US-09-010-317-35
8	54	100.0	38	4	US-09-010-317-43
9	54	100.0	39	4	US-09-010-317-56
10	54	100.0	39	4	US-09-010-317-57
11	54	100.0	114	1	US-08-259-000-3
12	54	100.0	130	2	US-08-459-135A-7
13	54	100.0	130	2	US-08-459-135A-8
14	54	100.0	130	2	US-08-495-559-7
15	54	100.0	130	3	US-08-495-559-8
16	54	100.0	139	3	US-08-856-253-8
17	54	100.0	174	2	US-08-459-135A-10
18	54	100.0	174	2	US-08-459-135A-13
19	54	100.0	174	3	US-08-495-559-10
20	54	100.0	174	3	US-08-495-559-13
21	54	100.0	176	3	US-08-495-559-6
22	54	100.0	178	2	US-08-459-135A-12
23	54	100.0	178	3	US-08-495-559-12
24	54	100.0	181	2	US-08-459-135A-6
25	54	100.0	559	4	US-08-956-171E-5251
26	54	100.0	559	4	US-08-781-986A-5251
27	54	100.0	1027	4	US-08-956-171E-5254

28	54	100.0	1027	4	US-08-781-986A-5254	Sequence 5254, Ap
29	50	92.6	10	4	US-09-010-317-2	Sequence 2, Appl
30	50	92.6	12	4	US-09-010-317-62	Sequence 62, Appl
31	50	92.6	38	1	US-08-234-622A-3	Sequence 3, Appl
32	50	92.6	38	1	US-08-729-767-4	Sequence 4, Appl
33	50	92.6	38	1	US-09-010-317-7	Sequence 7, Appl
34	50	92.6	38	4	US-09-010-317-8	Sequence 8, Appl
35	50	92.6	38	4	US-09-010-317-45	Sequence 45, Appl
36	50	92.6	38	4	US-09-010-317-49	Sequence 49, Appl
37	49	90.7	38	4	US-09-010-317-36	Sequence 36, Appl
38	48	88.9	38	4	US-09-010-317-37	Sequence 37, Appl
39	48	88.9	38	4	US-09-010-317-39	Sequence 39, Appl
40	48	88.9	38	4	US-09-010-317-40	Sequence 40, Appl
41	48	88.9	38	4	US-09-010-317-41	Sequence 41, Appl
42	47	87.0	38	4	US-09-010-317-38	Sequence 38, Appl
43	47	87.0	38	4	US-09-010-317-42	Sequence 42, Appl
44	45	83.3	38	4	US-09-010-317-46	Sequence 46, Appl
45	44	81.5	10	4	US-09-010-317-68	Sequence 68, Appl

ALIGNMENTS

RESULT 1
US-09-010-317-67
; Sequence 67, Application US/09010317
; Patent No. 6685943
; GENERAL INFORMATION:
; APPLICANT: Hook, Magnus
; APPLICANT: Patti, Joseph M.
; APPLICANT: House-Pompeo, Karen L.
; APPLICANT: Speziale, Pietro
; APPLICANT: Joti, Danny
; APPLICANT: Mcgavin, Martin J.
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
; TITLE OF INVENTION: AND METHODS OF USE
; NUMBER OF SEQUENCES: 105
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: TX
; COUNTRY: USA
; ZIP: 77210-4433
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/010,317
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/036,139
; FILING DATE: 21-JAN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Hidler, David W.
; REGISTRATION NUMBER: 41,071
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 512-418-3000
; TELEFAX: 512-474-7577
; INFORMATION FOR SEQ ID NO: 67:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; US-09-010-317-67
Query Match 100.0%; Score 54; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0065;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EEDTEEDKPK 10
|||||

Db 1 EEDTEEDKPK 10

RESULT 2

US-09-010-317-105

/ Sequence 105, Application US/09010317

/ Patent No. 6685943

/ GENERAL INFORMATION:

/ APPLICANT: Hook, Magnus

/ APPLICANT: Patti, Joseph M.

/ APPLICANT: House-Pompeo, Karen L.

/ APPLICANT: Speziale, Pietro

/ APPLICANT: McGavin, Martin J.

/ TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS

/ TITLE OF INVENTION: AND METHODS OF USE

/ NUMBER OF SEQUENCES: 105

/ CORRESPONDENCE ADDRESS:

/ ADDRESSEE: Arnold, White & Durkee

/ STREET: P.O. Box 4433

/ CITY: Houston

/ STATE: TX

/ COUNTRY: USA

/ ZIP: 77210-4433

/ COMPUTER READABLE FORM:

/ MEDIUM TYPE: Floppy disk

/ OPERATING SYSTEM: PC-DOS/MS-DOS

/ SOFTWARE: Patentin Releasee #1.0, Version #1.30

/ CURRENT APPLICATION DATA:

/ APPLICATION NUMBER: US/09/010,317

/ FILING DATE:

/ CLASSIFICATION:

/ PRIOR APPLICATION DATA:

/ APPLICATION NUMBER: US 60/036,139

/ FILING DATE: 21-JAN-1997

/ ATTORNEY/AGENT INFORMATION:

/ NAME: Hibler, David W.

/ REGISTRATION NUMBER: 41,071

/ TELECOMMUNICATION INFORMATION:

/ TELEPHONE: 512-418-3000

/ TELEFAX: 512-474-7577

/ INFORMATION FOR SEQ ID NO: 105:

/ SEQUENCE CHARACTERISTICS:

/ LENGTH: 14 amino acids

/ TYPE: amino acid

/ STRANDEDNESS:

/ TOPOLOGY: linear

US-09-010-317-105

Query Match 100.0%; Score 54; DB 4; Length 14;

Best Local Similarity 100.0%; Pred. No. 0.0091;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EEDTEEDKPK 10
|||||

Db 3 EEDTEEDKPK 12

RESULT 3

US-08-234-622A-2

/ Sequence 2, Application US/08234622A

/ Patent No. 5440014

/ GENERAL INFORMATION:

/ APPLICANT: Hook, Magnus

/ APPLICANT: MCGAVIN, Martin

/ APPLICANT: RAUCCI, Giuseppe

/ TITLE OF INVENTION: A FIBRONECTIN BINDING PEPTIDE

/ NUMBER OF SEQUENCES: 4

/ CORRESPONDENCE ADDRESS:

/ ADDRESSEE: Burns, Doane, Swecker & Machis

/ STREET: P.O. Box 1404

/ CITY: Alexandria

/ STATE: Virginia

/ COUNTRY: United States

/ ZIP: 22313-1404

/ COMPUTER READABLE FORM:

/ MEDIUM TYPE: Floppy disk

/ OPERATING SYSTEM: PC-DOS/MS-DOS

/ SOFTWARE: Patentin Releasee #1.0, Version #1.30

/ CURRENT APPLICATION DATA:

/ APPLICATION NUMBER: US/08/234,622A

/ FILING DATE: 28-APR-1994

/ CLASSIFICATION: 530

/ PRIOR APPLICATION DATA:

/ APPLICATION NUMBER: SE 9002617-0

/ FILING DATE: 10-AUG-1990

/ PRIOR APPLICATION DATA:

/ APPLICATION NUMBER: WO PCT/SE91/00534

/ FILING DATE: 09-AUG-1991

/ ATTORNEY/AGENT INFORMATION:

/ NAME: Meuth, Donna M

/ REGISTRATION NUMBER: 36,607

/ REFERENCE/DOCKET NUMBER: 012885-044

/ TELECOMMUNICATION INFORMATION:

/ TELEPHONE: (703) 836-6620

/ TELEFAX: (703) 836-2021

/ INFORMATION FOR SEQ ID NO: 2:

/ SEQUENCE CHARACTERISTICS:

/ LENGTH: 38 amino acids

/ TYPE: amino acid

/ STRANDEDNESS: single

/ TOPOLOGY: linear

/ MOLECULE TYPE: peptide

US-08-234-622A-2

Query Match 100.0%; Score 54; DB 1; Length 38;

Best Local Similarity 100.0%; Pred. No. 0.025;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EEDTEEDKPK 10
|||||

Db 9 EEDTEEDKPK 18

RESULT 4

US-08-729-767-3

/ Sequence 3, Application US/08729767

/ Patent No. 5770702

/ GENERAL INFORMATION:

/ APPLICANT: Hook, Magnus

/ APPLICANT: LINDBERG, Martin Kjell

/ APPLICANT: SIGMAS, Lars Christer

/ APPLICANT: WADSTROM, Torkel Mikael

/ APPLICANT: FROMAN, Gunnar

/ TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN AS WELL AS

/ TITLE OF INVENTION: ITS PREPARATION

/ NUMBER OF SEQUENCES: 6

/ CORRESPONDENCE ADDRESS:

/ ADDRESSEE: Burns, Doane, Swecker & Machis, L.L.P.

/ STREET: P.O. Box 1404

/ CITY: Alexandria

/ STATE: Virginia

/ COUNTRY: United States

/ ZIP: 22313-1404

/ COMPUTER READABLE FORM:

/ MEDIUM TYPE: Floppy disk

/ OPERATING SYSTEM: PC-DOS/MS-DOS

/ SOFTWARE: Patentin Releasee #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/729,767
FILING DATE: 07-OCT-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/259,000
FILING DATE: 13-JUN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/007,817
FILING DATE: 22-JAN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/201,028
FILING DATE: 01-JUN-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: SE 8702272-9
FILING DATE: 01-JUN-1987
ATTORNEY/AGENT INFORMATION:
NAME: McGowan, Malcolm K.
REGISTRATION NUMBER: 39,300
REFERENCE/DOCKET NUMBER: 012889-036
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-729-767-3

Query Match 100.0%; Score 54; DB 1; Length 38;
Best Local Similarity 100.0%; Pred. No. 0.025;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EEDTEEDKPK 10
DB 10 EEDTEEDKPK 19

RESULT 5
US-09-010-317-5
Sequence 5, Application US/09010317
Patent No. 6685943
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
APPLICANT: Patti, Joseph M.
APPLICANT: House-Pompeo, Karen L.
APPLICANT: Speziale, Pietro
APPLICANT: Joh, Danny
APPLICANT: McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
TITLE OF INVENTION: AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/036,139

FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TANK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-09-010-317-5

Query Match 100.0%; Score 54; DB 4; Length 38;
Best Local Similarity 100.0%; Pred. No. 0.025;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EEDTEEDKPK 10
DB 9 EEDTEEDKPK 18

RESULT 6
US-09-010-317-6
Sequence 6, Application US/09010317
Patent No. 6685943
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
APPLICANT: Patti, Joseph M.
APPLICANT: House-Pompeo, Karen L.
APPLICANT: Speziale, Pietro
APPLICANT: Joh, Danny
APPLICANT: McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
TITLE OF INVENTION: AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TANK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-09-010-317-6

Query Match 100.0%; Score 54; DB 4; Length 38;
Best Local Similarity 100.0%; Pred. No. 0.025;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EEDTEDKPK 10
| | | | | | | | | |
Db 9 EEDTEDKPK 18

RESULT 7

US-09-010-317-35
; Sequence 35, Application US/09010317
; Patent No. 6685943
; GENERAL INFORMATION:
; APPLICANT: Hook, Magnus
; APPLICANT: Patti, Joseph M.
; APPLICANT: House-Pompeo, Karen L.
; APPLICANT: Speziale, Pietro
; APPLICANT: Joh, Danny
; APPLICANT: McGavin, Martin J.
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
; NUMBER OF SEQUENCES: 105
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: TX
; COUNTRY: USA
; ZIP: 77210-4433
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/010,317
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/036,139
; FILING DATE: 21-JAN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Hibler, David W.
; REGISTRATION NUMBER: 41,071
; REFERENCE/DOCKET NUMBER: TANK:189
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 512-418-3000
; TELEFAX: 512-474-7577
; INFORMATION FOR SEQ ID NO: 35:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 38 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
US-09-010-317-35

Query Match 100.0%; Score 54; DB 4; Length 38;
Best Local Similarity 100.0%; Pred. No. 0.025;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EEDTEDKPK 10
| | | | | | | | | |
Db 9 EEDTEDKPK 18

RESULT 8

US-09-010-317-43
; Sequence 43, Application US/09010317
; Patent No. 6685943
; GENERAL INFORMATION:
; APPLICANT: Hook, Magnus
; APPLICANT: Patti, Joseph M.

; APPLICANT: House-Pompeo, Karen L.

; APPLICANT: Speziale, Pietro

; APPLICANT: Joh, Danny

; APPLICANT: McGavin, Martin J.

; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS

; NUMBER OF SEQUENCES: 105

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Arnold, White & Durkee

; STREET: P.O. Box 4433

; CITY: Houston

; STATE: TX

; COUNTRY: USA

; ZIP: 77210-4433

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/010,317

; FILING DATE:

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 60/036,139

; FILING DATE: 21-JAN-1997

; ATTORNEY/AGENT INFORMATION:

; NAME: Hibler, David W.

; REGISTRATION NUMBER: 41,071

; REFERENCE/DOCKET NUMBER: TANK:189

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 512-418-3000

; TELEFAX: 512-474-7577

; INFORMATION FOR SEQ ID NO: 43:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 38 amino acids

; TYPE: amino acid

; STRANDEDNESS:

; TOPOLOGY: linear
US-09-010-317-43

Query Match 100.0%; Score 54; DB 4; Length 38;
Best Local Similarity 100.0%; Pred. No. 0.025;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EEDTEDKPK 10
| | | | | | | | | |
Db 9 EEDTEDKPK 18

RESULT 9

US-09-010-317-56
; Sequence 56, Application US/09010317
; Patent No. 6685943
; GENERAL INFORMATION:
; APPLICANT: Hook, Magnus
; APPLICANT: Patti, Joseph M.
; APPLICANT: House-Pompeo, Karen L.
; APPLICANT: Speziale, Pietro
; APPLICANT: Joh, Danny
; APPLICANT: McGavin, Martin J.
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
; NUMBER OF SEQUENCES: 105
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: TX
; COUNTRY: USA
; ZIP: 77210-4433
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk

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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAMK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 56:
SEQUENCE CHARACTERISTICS:
LENGTH: 39 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-09-010-317-56

Query Match      100.0%; Score 54; DB 4; Length 39;
Best Local Similarity 100.0%; Pred. No. 0.026;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 EEDTEEDKPK 10
Db      9 EEDTEEDKPK 18

RESULT 10
US-09-010-317-57
Sequence 57, Application US/09010317
Patent No. 6685943
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
APPLICANT: Patti, Joseph M.
APPLICANT: House-Pompeo, Karen L.
APPLICANT: Speciale, Pietro
APPLICANT: Joh, Danny
APPLICANT: McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
TITLE OF INVENTION: AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESSES:
ADDRESSER: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAMK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
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TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 57:
SEQUENCE CHARACTERISTICS:
LENGTH: 39 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-09-010-317-57

Query Match      100.0%; Score 54; DB 4; Length 39;
Best Local Similarity 100.0%; Pred. No. 0.026;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 EEDTEEDKPK 10
Db      9 EEDTEEDKPK 18

RESULT 11
US-08-259-000-3
Sequence 3, Application US/08259000
Patent No. 5571514
GENERAL INFORMATION:
APPLICANT: HOOK, Magnus
APPLICANT: LINDBERG, Martin Kjell
APPLICANT: SIGMAs, Lars Christer
APPLICANT: WADSTROM, Torkel Mikael
APPLICANT: FROMAN, Gunnar
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN AS WELL AS
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESSES:
ADDRESSER: Burns, Doane, Swecker & Mathis
STREET: P.O. Box 1404
CITY: Alexandria
STATE: Virginia
COUNTRY: United States
ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/259,000
FILING DATE: 13-JUN-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: SE 8702272-9
FILING DATE: 01-JUN-1987
ATTORNEY/AGENT INFORMATION:
NAME: Meuth, Donna M
REGISTRATION NUMBER: 36,607
REFERENCE/DOCKET NUMBER: 012885-062
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 114 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-259-000-3

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Best Local Similarity 100.0%; Pred. No. 0.078;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 EEDTEEDKPK 10
Db      10 EEDTEEDKPK 19
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RESULT 12
US-08-459-135A-7
Sequence 7, Application US/08459135A
Patent No. 5955078
GENERAL INFORMATION:
APPLICANT: BURHAM, Martin Karl Russel
APPLICANT: CHOPRA, Ian
APPLICANT: CRITCHLEY, Ian Alfred
APPLICANT: KNOWLES, David Justin Charles
TITLE OF INVENTION: FIBROECTIN BINDING PROTEIN: MONOCLONAL ANTIBODY AND THEIR US
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
STATE: PA
COUNTRY: U.S.A.
ZIP: 19406-0939
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: Fastseq, Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/459,135A
FILING DATE: 02-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB/94/00215
FILING DATE: 04-Feb-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Gimml, Edward R
REGISTRATION NUMBER: 38,891
REFERENCE/DOCKET NUMBER: P30591C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-4478
TELEFAX: 610-270-5090
TELEX:
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 130 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-459-135A-7

Query Match 100.0%; Score 54; DB 2; Length 130;
Best Local Similarity 100.0%; Pred. No. 0.089; 0; Indels 0; Gaps 0;
Matches 10; Conservative 0; Mismatches 0;

QY 1 EEDTEEDKPK 10
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DB 10 EEDTEEDKPK 19

RESULT 13
US-08-459-135A-8
Sequence 8, Application US/08459135A
Patent No. 5955078
GENERAL INFORMATION:
APPLICANT: BURHAM, Martin Karl Russel
APPLICANT: CHOPRA, Ian
APPLICANT: CRITCHLEY, Ian Alfred
APPLICANT: KNOWLES, David Justin Charles
TITLE OF INVENTION: FIBROECTIN BINDING PROTEIN: MONOCLONAL ANTIBODY AND THEIR US
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia

STATE: PA
COUNTRY: U.S.A.
ZIP: 19406-0939
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: Fastseq, Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/459,135A
FILING DATE: 02-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB/94/00215
FILING DATE: 04-Feb-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Gimml, Edward R
REGISTRATION NUMBER: 38,891
REFERENCE/DOCKET NUMBER: P30591C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-4478
TELEFAX: 610-270-5090
TELEX:
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 130 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-459-135A-8

Query Match 100.0%; Score 54; DB 2; Length 130;
Best Local Similarity 100.0%; Pred. No. 0.089; 0; Indels 0; Gaps 0;
Matches 10; Conservative 0; Mismatches 0;

QY 1 EEDTEEDKPK 10
| | | | | | | | | |
DB 10 EEDTEEDKPK 19

RESULT 14
US-08-495-559-7
Sequence 7, Application US/08495559A
Patent No. 6054572
GENERAL INFORMATION:
APPLICANT: BURHAM, Martin Karl Russel
APPLICANT: CHOPRA, Ian
APPLICANT: CRITCHLEY, Ian Alfred
APPLICANT: KNOWLES, David Justin Charles
TITLE OF INVENTION: ANTIBODY AND THEIR USE IN PREVENTING BACTERIAL ADHESION
FILE REFERENCE: P30591
CURRENT APPLICATION NUMBER: US/08/495,559A
CURRENT FILING DATE: 1995-08-03
EARLIER APPLICATION NUMBER: GB 9302289.5
EARLIER FILING DATE: 1993-02-05
EARLIER APPLICATION NUMBER: GB 9321592.9
EARLIER FILING DATE: 1993-10-20
NUMBER OF SEQ ID NOS: 13
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 7
LENGTH: 130
TYPE: PRT
ORGANISM: Staphylococcus aureus
US-08-495-559-7

Query Match 100.0%; Score 54; DB 3; Length 130;
Best Local Similarity 100.0%; Pred. No. 0.089; 0; Indels 0; Gaps 0;
Matches 10; Conservative 0; Mismatches 0;

QY 1 EEDTEEDKPK 10
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Db 10 EEDTEEDKPK 19

RESULT 15
US-08-495-559-8
; Sequence 8, Application US/08495559A
; Patent No. 6054572
; GENERAL INFORMATION:
; APPLICANT: BURMAN, Martin Karl Russel
; APPLICANT: CHOPRA, Ian
; APPLICANT: CRITCHLEY, Ian Alfred
; APPLICANT: KNOWLES, David Justin Charles
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN: MONOCLONAL
; TITLE OF INVENTION: ANTIBODY AND THEIR USE IN PREVENTING BACTERIAL ADHESION
; FILE REFERENCE: P30591
; CURRENT APPLICATION NUMBER: US/08/495,559A
; CURRENT FILING DATE: 1995-08-03
; EARLIER APPLICATION NUMBER: GB 9302289.5
; EARLIER FILING DATE: 1993-02-05
; EARLIER APPLICATION NUMBER: GB 9321592.9
; EARLIER FILING DATE: 1993-10-20
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 8
; LENGTH: 130
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-08-495-559-8

Query Match 100.0%; Score 54; DB 3; Length 130;
Best Local Similarity 100.0%; Pred. No. 0.089;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EEDTEEDKPK 10
10 EEDTEEDKPK 19

Search completed: October 22, 2005, 07:41:40
Job time : 17.35 secs

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GenCore version 5.1.6
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OM protein - protein search, using SW model

Run on: October 22, 2005, 12:09:40 ; Search time 57.25 Seconds
(without alignments)
72.924 Million cell updates/sec

Title: US-10-731-238-67

Perfect score: 54

Sequence: 1 EBDTERDKPK 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1862951 seqs, 417491010 residues

Total number of hits satisfying chosen parameters: 1862951

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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13: /cgnt2_6/prodata/2/pubpaa/US10_PUBCOMB.pep.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	54	100.0	14	18	US-10-731-238-105
3	54	100.0	38	18	US-10-731-238-5
4	54	100.0	38	18	US-10-731-238-6
5	54	100.0	38	18	US-10-731-238-35
6	54	100.0	38	18	US-10-731-238-43
7	54	100.0	39	18	US-10-731-238-56
8	54	100.0	39	18	US-10-731-238-57
9	54	100.0	139	9	US-09-813-820-8
10	54	100.0	388	8	US-08-901-062-1
11	54	100.0	559	8	US-08-781-986A-5251

12	54	100.0	559	15	US-10-329-624-5251	Sequence 5251, Ap
13	54	100.0	767	9	US-09-815-242-5899	Sequence 5899, Ap
14	54	100.0	767	9	US-09-815-242-13140	Sequence 13140, A
15	54	100.0	940	17	US-10-470-048B-424	Sequence 424, App
16	54	100.0	948	17	US-10-470-048B-69	Sequence 69, Appl
17	54	100.0	961	15	US-10-282-122A-43778	Sequence 43778, A
18	54	100.0	978	9	US-09-815-242-5456	Sequence 5456, Ap
19	54	100.0	1001	9	US-09-815-242-12686	Sequence 12686, A
20	54	100.0	1018	9	US-09-815-242-5797	Sequence 5797, Ap
21	54	100.0	1018	9	US-09-815-242-12838	Sequence 12838, A
22	54	100.0	1018	9	US-10-470-048B-68	Sequence 68, Appl
23	54	100.0	1027	8	US-08-781-986A-5254	Sequence 5254, Ap
24	54	100.0	1027	15	US-10-329-624-5254	Sequence 5254, Ap
25	54	100.0	1038	15	US-10-282-122A-43827	Sequence 43827, A
26	50	92.6	10	18	US-10-731-238-2	Sequence 2, Appl
27	50	92.6	12	18	US-10-731-238-62	Sequence 62, Appl
28	50	92.6	30	14	US-10-287-821-1	Sequence 1, Appl
29	50	92.6	31	14	US-10-287-821-2	Sequence 2, Appl
30	50	92.6	38	18	US-10-731-238-7	Sequence 7, Appl
31	50	92.6	38	18	US-10-731-238-8	Sequence 8, Appl
32	50	92.6	38	18	US-10-731-238-45	Sequence 45, Appl
33	50	92.6	38	18	US-10-731-238-49	Sequence 49, Appl
34	49	90.7	38	18	US-10-731-238-36	Sequence 36, Appl
35	48	88.9	38	18	US-10-731-238-37	Sequence 37, Appl
36	48	88.9	38	18	US-10-731-238-39	Sequence 39, Appl
37	48	88.9	38	18	US-10-731-238-40	Sequence 40, Appl
38	48	88.9	38	18	US-10-731-238-41	Sequence 41, Appl
39	47	87.0	38	18	US-10-731-238-38	Sequence 38, Appl
40	47	87.0	38	18	US-10-731-238-42	Sequence 42, Appl
41	45	83.3	38	18	US-10-731-238-46	Sequence 46, Appl
42	45	83.3	1832	14	US-10-128-714-8298	Sequence 8298, Ap
43	44	81.5	10	18	US-10-731-238-68	Sequence 68, Appl
44	44	81.5	38	18	US-10-731-238-44	Sequence 44, Appl
45	44	81.5	38	18	US-10-731-238-47	Sequence 47, Appl

ALIGNMENTS

RESULT 1
US-10-731-238-67
Sequence 67, Application US/1071238
Publication No US20050123552A1
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
Patli, Joseph M.
House-Pompeo, Karen L.
Speziale, Pietro
Joh, Danny
McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/731.238
FILING DATE: 10-Dec-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/010.317
FILING DATE: 21-Jan-1998
APPLICATION NUMBER: US 60/036.139


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;
; FILING DATE: 21-JAN-1997
; ATTORNEY/AGENT INFORMATION:
;   NAME: Hibler, David W.
;   REGISTRATION NUMBER: 41,071
;   REFERENCE/DOCKET NUMBER: TAMK:189
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE: 512-418-3000
;     TELEFAX: 512-474-7577
; INFORMATION FOR SEQ ID NO: 67:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH: 10 amino acids
;     TYPE: amino acid
;     STRANDEDNESS: <Unknown>
;     TOPOLOGY: linear
;   SEQUENCE DESCRIPTION: SEQ ID NO: 67:
US-10-731-238-67

Query Match      100.0%; Score 54; DB 18; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.05;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 EEDTEEDKPK 10
        |||
        1 EEDTEEDKPK 10

Db

RESULT 2
US-10-731-238-105
; Sequence 105, Application US/10731238
; Publication No. US20050123552A1
; GENERAL INFORMATION:
;   APPLICANT: Hook, Magnus
;     Patti, Joseph M.
;     House-Pompeo, Karen L.
;     Speziale, Pietro
;     Joh, Danny
;     McGavin, Martin J.
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
;
; NUMBER OF SEQUENCES: 105
; CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Arnold, White & Durkee
;   STREET: P.O. Box 4433
;   CITY: Houston
;   STATE: TX
;   COUNTRY: USA
;   ZIP: 77210-4433
; COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/10/731,238
;   FILING DATE: 10-Dec-2003
;   CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US/09/010,317
;   FILING DATE: 21-Jan-1998
;   REFERENCE/DOCKET NUMBER: TAMK:189
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE: 512-418-3000
;     TELEFAX: 512-474-7577
; INFORMATION FOR SEQ ID NO: 105:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH: 14 amino acids
;     TYPE: amino acid
;     STRANDEDNESS: <Unknown>

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;
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 105:
US-10-731-238-105

Query Match      100.0%; Score 54; DB 18; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.071;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 EEDTEEDKPK 10
        |||
        3 EEDTEEDKPK 12

Db

RESULT 3
US-10-731-238-5
; Sequence 5, Application US/10731238
; Publication No. US20050123552A1
; GENERAL INFORMATION:
;   APPLICANT: Hook, Magnus
;     Patti, Joseph M.
;     House-Pompeo, Karen L.
;     Speziale, Pietro
;     Joh, Danny
;     McGavin, Martin J.
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
;
; NUMBER OF SEQUENCES: 105
; CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Arnold, White & Durkee
;   STREET: P.O. Box 4433
;   CITY: Houston
;   STATE: TX
;   COUNTRY: USA
;   ZIP: 77210-4433
; COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/10/731,238
;   FILING DATE: 10-Dec-2003
;   CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US/09/010,317
;   FILING DATE: 21-Jan-1998
;   REFERENCE/DOCKET NUMBER: TAMK:189
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE: 512-418-3000
;     TELEFAX: 512-474-7577
; INFORMATION FOR SEQ ID NO: 5:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH: 38 amino acids
;     TYPE: amino acid
;     STRANDEDNESS: <Unknown>
;     TOPOLOGY: linear
;   SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-10-731-238-5

Query Match      100.0%; Score 54; DB 18; Length 38;
Best Local Similarity 100.0%; Pred. No. 0.2;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 EEDTEEDKPK 10
        |||
        9 EEDTEEDKPK 18

Db

```

```
RESULT 4
US-10-731-238-6
; Sequence 6, Application US/10731238
; Publication No. US20050123552A1
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
; Patti, Joseph M.
; House-Pompeo, Karen L.
; Speziale, Pietro
; Joh, Danny
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSER: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/731,238
FILING DATE: 10-Dec-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE: 21-Jan-1998
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAMK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-10-731-238-6
Query Match 100.0%; Score 54; DB 18; Length 38;
Best Local Similarity 100.0%; Pred. No. 0.2;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 EEDTEEDPK 10
Db 9 EEDTEEDPK 18
RESULT 5
US-10-731-238-35
; Sequence 35, Application US/10731238
; Publication No. US20050123552A1
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
; Patti, Joseph M.
; House-Pompeo, Karen L.
; Speziale, Pietro
; Joh, Danny
; McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
AND METHODS OF USE
```

```
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSER: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/731,238
FILING DATE: 10-Dec-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE: 21-Jan-1998
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAMK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 35:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 35:
US-10-731-238-35
Query Match 100.0%; Score 54; DB 18; Length 38;
Best Local Similarity 100.0%; Pred. No. 0.2;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 EEDTEEDPK 10
Db 9 EEDTEEDPK 18
RESULT 6
US-10-731-238-43
; Sequence 43, Application US/10731238
; Publication No. US20050123552A1
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
; Patti, Joseph M.
; House-Pompeo, Karen L.
; Speziale, Pietro
; Joh, Danny
; McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSER: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
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;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/731,238
; FILING DATE: 10-Dec-2003
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/010,317
; FILING DATE: 21-Jan-1998
; APPLICATION NUMBER: US 60/036,139
; FILING DATE: 21-Jan-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Hibler, David W.
; REGISTRATION NUMBER: 41,071
; REFERENCE/DOCKET NUMBER: TAMK:189
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 512-418-3000
; TELEFAX: 512-474-7577
; INFORMATION FOR SEQ ID NO: 43:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 38 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
;
; SEQUENCE DESCRIPTION: SEQ ID NO: 43:
US-10-731-238-43

Query Match      100.0%; Score 54; DB 18; Length 38,
Best Local Similarity 100.0%; Pred. No. 0.2;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 EEDTEEDKPK 10
        |||||
        9 EEDTEEDKPK 18

RESULT 7
US-10-731-238-56
; Sequence 56, Application US/10731238
; Publication No. US20050123552A1
; GENERAL INFORMATION:
; APPLICANT: Hook, Magnus
; Patti, Joseph M.
; House-Pompeo, Karen L.
; Speziale, Pietro
; John, Danny
;
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
;
; NUMBER OF SEQUENCES: 105
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: TX
; COUNTRY: USA
; ZIP: 77210-4433
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/731,238
; FILING DATE: 10-Dec-2003
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/010,317
; FILING DATE: 21-Jan-1998
; APPLICATION NUMBER: US 60/036,139
; FILING DATE: 21-Jan-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Hibler, David W.
; REGISTRATION NUMBER: 41,071
; REFERENCE/DOCKET NUMBER: TAMK:189
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 512-418-3000
; TELEFAX: 512-474-7577
; INFORMATION FOR SEQ ID NO: 57:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 39 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
;
; SEQUENCE DESCRIPTION: SEQ ID NO: 57:
US-10-731-238-57

Query Match      100.0%; Score 54; DB 18; Length 39,
Best Local Similarity 100.0%; Pred. No. 0.2;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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;
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 512-418-3000
; TELEFAX: 512-474-7577
; INFORMATION FOR SEQ ID NO: 56:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 39 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
;
; SEQUENCE DESCRIPTION: SEQ ID NO: 56:
US-10-731-238-56

Query Match      100.0%; Score 54; DB 18; Length 39,
Best Local Similarity 100.0%; Pred. No. 0.2;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 EEDTEEDKPK 10
        |||||
        9 EEDTEEDKPK 18

RESULT 8
US-10-731-238-57
; Sequence 57, Application US/10731238
; Publication No. US20050123552A1
; GENERAL INFORMATION:
; APPLICANT: Hook, Magnus
; Patti, Joseph M.
; House-Pompeo, Karen L.
; Speziale, Pietro
; John, Danny
; McGavin, Martin J.
;
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
;
; NUMBER OF SEQUENCES: 105
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: TX
; COUNTRY: USA
; ZIP: 77210-4433
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/731,238
; FILING DATE: 10-Dec-2003
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/010,317
; FILING DATE: 21-Jan-1998
; APPLICATION NUMBER: US 60/036,139
; FILING DATE: 21-Jan-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Hibler, David W.
; REGISTRATION NUMBER: 41,071
; REFERENCE/DOCKET NUMBER: TAMK:189
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 512-418-3000
; TELEFAX: 512-474-7577
; INFORMATION FOR SEQ ID NO: 57:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 39 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
;
; SEQUENCE DESCRIPTION: SEQ ID NO: 57:
US-10-731-238-57

Query Match      100.0%; Score 54; DB 18; Length 39,
```

NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: HALE AND DORR LLP
STREET: 60 State Street
CITY: Boston
STATE: MA
COUNTRY: United States Of America

```

;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy
; COMPUTER: IBM PC COMP

```

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30

APPLICATON NUMBER: US/08/901.0622

CLASSIFICATION: 424
FILING DATE: 25-JUL-1997

ATTORNEY/AGENT INFORMATION:

NAME: Baker, Hollie L.
REGISTRATION NUMBER: 31,321

TELECOMMUNICATION INFORMATION:

TELEPHONE: (617) 526-6000
TELEFAX: (617) 526-5000

INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:

LENGTH: 388 amino acids
TYPE: amino acid

STRANDEDNESS: single
TOPOLOGY: linear

MOLECULE TYPE: protein
HYBOTHEICAL: NO

ANTI-SENSE: NO

Customer Match 1005-08-301-062-1

Query Match	Best Local Similarity
10	10

Matches 10; conservation 10

QY 1 BEDIEDKPK 10
|||||
|||||

DB 273 EBDTEBDKPK 282

RESULT 11

US-08-781-986A-5251
; Sequence 5251, Application US/08781986A

Publication No. US20030054436
; GENERAL INFORMATION:
;

APPLICANT: Charles Kunsch
TITLE OF INVENTION: Staphylococcus aureus Polymuclleides and Sequences

```

;
NUMBER OF SEQUENCES: 5255
;
CORRESPONDENCE ADDRESS:
;

```

ADDRESSEE: Human Genome Science
STREET: 9410 West Avenue

;
;
CITY: Rockville
STATE: Maryland
;

COUNTRY: USA
ZIP: 20850

```

;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
;

```

```
COMPUTER: HP Vectra
OPERATING SYSTEM: MS
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```

; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
;

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APPLICATION NUMBER:
FILING DATE:

CLASSIFICATION: 435
PRIOR APPLICATION DATA

APPLI CATION NUMBER:
FILING DATE:

ATTORNEY/AGENT INFORMATION:
NAME: Benson, Bob

```
;
;   REGISTRATION NUMBER: 30,446
;   REFERENCE/DOCKET NUMBER: PB248PP
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: (301) 309-8504
;   TELEFAX: (301) 309-8512
;   INFORMATION FOR SEQ ID NO: 5251:
;   SEQUENCE CHARACTERISTICS:
;       LENGTH: 559 amino acids
;       TYPE: amino acid
;       STRANDEDNESS: single
;       TOPOLOGY: linear
;   MOLECULE TYPE: protein
;   US-08-781-986A-5251

Query Match          100.0%; Score 54; DB 8; Length 559;
Best Local Similarity 100.0%; Pred. No. 3.2;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 EEDTEEDKPK 10
        |||||
Db      309 EEDTEEDKPK 318

RESULT 12
US-10-329-624-5251
; Sequence 5251, Application US/10329624
; Publication No. US20040043037A1
; GENERAL INFORMATION:
;   APPLICANT: Charles Kunsch
;       Gil H. Choi
;       Patrick S. Dillon
;       Craig A. Rosen
;       Steven C. Barash
;       Michael R. Farnon
;   TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
;   NUMBER OF SEQUENCES: 5256
;   CORRESPONDENCE ADDRESS:
;       ADDRESSER: Human Genome Sciences, Inc.
;       STREET: 9410 Key West Avenue
;       CITY: Rockville
;       STATE: Maryland
;       COUNTRY: USA
;       ZIP: 20850
;   COMPUTER READABLE FORM:
;       MEDIUM TYPE: Diskette, 3.50 inch, 1.4MB storage
;       COMPUTER: HP Vectra 486/33
;       OPERATING SYSTEM: MSDOS version 6.2
;       SOFTWARE: ASCII Text
;   CURRENT APPLICATION DATA:
;       APPLICATION NUMBER: US/10/329,624
;       FILING DATE: 27-Dec-2002
;   PRIOR APPLICATION DATA:
;       APPLICATION NUMBER: 08/956,171
;       FILING DATE: October 20, 1997
;       APPLICATION NUMBER: 60/009,861
;       FILING DATE: January 5, 1996
;       APPLICATION NUMBER: 08/781,986
;       FILING DATE: January 3, 1997
;   ATTORNEY/AGENT INFORMATION:
;       NAME: Mark J. Hyman
;       REGISTRATION NUMBER: 46,789
;       REFERENCE/DOCKET NUMBER: PB248P1D1
;   TELECOMMUNICATION INFORMATION:
;       TELEPHONE: (240) 314-1224
;       TELEFAX: (301) 309-8439
;   INFORMATION FOR SEQ ID NO: 5251:
;   SEQUENCE CHARACTERISTICS:
;       LENGTH: 559 amino acids
;       TYPE: amino acid
;       STRANDEDNESS: single
;       TOPOLOGY: linear
;   MOLECULE TYPE: protein
;   SEQUENCE DESCRIPTION: SEQ ID NO: 5251:
```

```
US-10-329-624-5251

Query Match          100.0%; Score 54; DB 15; Length 559;
Best Local Similarity 100.0%; Pred. No. 3.2;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 EEDTEEDKPK 10
        |||||
Db      309 EEDTEEDKPK 318

RESULT 13
US-09-815-242-5899
; Sequence 5899, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
;   APPLICANT: Haselbeck, Robert
;   APPLICANT: Ohlsen, Karl L.
;   APPLICANT: Zyskind, Judith W.
;   APPLICANT: Wall, Daniel
;   APPLICANT: Trawick, John D.
;   APPLICANT: Carr, Grant J.
;   APPLICANT: Yamamoto, Robert T.
;   APPLICANT: Xu, H. Howard
;   TITLE OF INVENTION: Identification of Essential Genes in
;   FILE REFERENCE: ELITRA-011A
;   CURRENT APPLICATION NUMBER: US/09/815,242
;   CURRENT FILING DATE: 2001-03-21
;   PRIOR APPLICATION NUMBER: 60/191,078
;   PRIOR FILING DATE: 2000-03-21
;   PRIOR APPLICATION NUMBER: 60/206,848
;   PRIOR FILING DATE: 2000-05-23
;   PRIOR APPLICATION NUMBER: 60/207,727
;   PRIOR FILING DATE: 2000-05-26
;   PRIOR APPLICATION NUMBER: 60/242,578
;   PRIOR FILING DATE: 2000-10-23
;   PRIOR APPLICATION NUMBER: 60/253,625
;   PRIOR FILING DATE: 2000-11-27
;   PRIOR APPLICATION NUMBER: 60/257,931
;   PRIOR FILING DATE: 2000-12-22
;   PRIOR APPLICATION NUMBER: 60/269,308
;   PRIOR FILING DATE: 2001-02-16
;   NUMBER OF SEQ ID NOS: 14110
;   SOFTWARE: FastSeq for Windows Version 4.0
;   SEQ ID NO 5899
;   LENGTH: 767
;   TYPE: PRT
;   ORGANISM: Staphylococcus aureus
;   US-09-815-242-5899

Query Match          100.0%; Score 54; DB 9; Length 767;
Best Local Similarity 100.0%; Pred. No. 4.4;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 EEDTEEDKPK 10
        |||||
Db      690 EEDTEEDKPK 699

RESULT 14
US-09-815-242-13140
; Sequence 13140, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
;   APPLICANT: Haselbeck, Robert
;   APPLICANT: Ohlsen, Karl L.
;   APPLICANT: Zyskind, Judith W.
;   APPLICANT: Wall, Daniel
;   APPLICANT: Trawick, John D.
;   APPLICANT: Carr, Grant J.
;   APPLICANT: Yamamoto, Robert T.
;   APPLICANT: Xu, H. Howard
```

```

; TITLE OF INVENTION: Identification of Essential Genes in
; FILE OF INVENTION: Prokaryotes
; FILE REFERENCE: ELITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 1410
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13140
; LENGTH: 767
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-09-815-242-13140

```

```

Query Match          100.0%; Score 54; DB 9; Length 767;
Best Local Similarity 100.0%; Pred. No. 4.4;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      1 EEDTEEDKPK 10
      |||||
Db      690 EEDTEEDKPK 699

```

```

RESULT 15
US-10-470-048B-424
; Sequence 424, Application US/10470048B
; Publication No. US20050037444A1
; GENERAL INFORMATION:
; APPLICANT: METRIKE ET AL.
; TITLE OF INVENTION: A METHOD FOR IDENTIFICATION, ISOLATION AND PRODUCTION OF
; FILE REFERENCE: SONM:035US
; CURRENT APPLICATION NUMBER: US/10/470,048B
; CURRENT FILING DATE: 2003-07-25
; NUMBER OF SEQ ID NOS: 603
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 424
; LENGTH: 940
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-10-470-048B-424

```

```

Query Match          100.0%; Score 54; DB 17; Length 940;
Best Local Similarity 100.0%; Pred. No. 5.4;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 EEDTEEDKPK 10
      |||||
Db      690 EEDTEEDKPK 699

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Search completed: October 22, 2005, 12:39:43
Job time : 57.25 secs

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The Page Blank (uspto)

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 22, 2005, 06:10:10 ; Search time 11.45 Seconds
(without alignments)
84.032 Million cell updates/sec

Title: US-10-731-238-67

Perfect score: 54
Sequence: 1 EEDTEEDKPK 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR 79:*

1: p1r1:*

2: p1r2:*

3: p1r3:*

4: p1r4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query %	Length	DB	ID	Description
1	54	100.0	940	2	S19702	fibronectin-binding
2	54	100.0	961	2	G90053	hypothetical prote
3	54	100.0	1018	2	A32192	fibronectin-binding
4	54	100.0	1038	2	H90053	hypothetical prote
5	42	77.8	56	2	S74259	tropoinin T 3, fast
6	42	77.8	67	2	S48650	tropoinin T 1, fast
7	42	77.8	258	2	I53021	tropoinin T - human
8	42	77.8	517	1	A39038	1-caldesmon, nonmu
9	42	77.8	771	1	A33430	h-caldesmon - chic
10	41	75.9	51	2	I66796	fetal tropoinin T 3
11	41	75.9	56	2	I53073	fetal tropoinin T 2
12	41	75.9	371	2	A55302	probable transcript
13	40	74.1	689	4	S30392	hypothetical RTVL-
14	39	72.2	239	2	B69946	phage-related term
15	39	72.2	268	2	P00199	glycinin A5A483 pr
16	39	72.2	537	2	B46535	interleukin 2 rece
17	39	72.2	560	2	S11004	glycinin G4 precu
18	39	72.2	562	1	FMSYGS	glycinin chain A5A
19	39	72.2	562	2	S20946	glycinin G4 precu
20	39	72.2	563	2	S54802	glycinin A5A483 ch
21	39	72.2	976	2	S40597	processing endop
22	38	70.4	236	2	P00806	glycinin A3B4 - so
23	38	70.4	238	2	P00809	glycinin A3B4 (pla
24	38	70.4	243	2	P00807	glycinin A3B4 - so
25	38	70.4	251	2	P00808	glycinin A3B4 (pla
26	38	70.4	273	2	C88429	protein ceh-43 lim
27	38	70.4	282	2	S43577	C88A5.4 protein (c
28	38	70.4	516	1	FMSYGS	glycinin G5 precu
29	38	70.4	539	2	T16400	hypothetical prote

30	38	70.4	548	2	T27542	hypothetical prote
31	38	70.4	687	2	T30958	hypothetical prote
32	38	70.4	845	2	A45659	neurofilament trip
33	38	70.4	849	2	S00030	neurofilament trip
34	38	70.4	952	2	S64473	translation initia
35	38	70.4	1579	2	T10516	type II DNA topois
36	37	68.5	212	2	T29480	hypothetical prote
37	37	68.5	234	2	B44459	tropoinin T, fast s
38	37	68.5	250	2	T02392	hypothetical prote
39	37	68.5	250	2	C85040	hypothetical prote
40	37	68.5	271	2	T04666	hypothetical prote
41	37	68.5	316	2	T11021	hypothetical prote
42	37	68.5	335	2	A54458	G1 progression neg
43	37	68.5	339	1	MDBPCP	N-acetylmutamoyl-L
44	37	68.5	444	2	T26229	hypothetical prote
45	37	68.5	467	2	C84420	hypothetical prote

ALIGNMENTS

RESULT 1

S19702

fibronectin-binding protein B - Staphylococcus aureus

C/Species: Staphylococcus aureus

C/Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004

C/Accession: S19702

R/Joensson, K.; Signaes, C.; Mueller, H.P.; Lindberg, M.

Eur. J. Biochem. 202, 1041-1048, 1991

A/Title: Two different genes encode fibronectin binding proteins in Staphylococcus aure

A/Reference number: S19702, PMID:92111475, PMID:1837266

A/Accession: S19702

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-940 <JOB>

A/Cross-references: UNIPROT:Q53682; EMBL:X62992; NID:949040; PIDN:CAA44726.1; PID:95815

C/Keywords: fibronectin binding

Query Match

Score 54; DB 2; Length 940;

Best Local Similarity 100.0%; Pred. No. 0.38;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EEDTEEDKPK 10

DB 690 EEDTEEDKPK 699

RESULT 2

hypothetical protein fnbB [imported] - Staphylococcus aureus (strain N315)

C/Species: Staphylococcus aureus

C/Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004

C/Accession: G90053

R/Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Ogu

ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaio, C.; Sekimizu, K.;

C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.

Lancet 357, 1225-1240, 2001

A/Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.

A/Reference number: AB9758; PMID:21311952; PMID:11418146

A/Accession: G90053

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-961 <KUR>

A/Cross-references: UNIPROT:Q99RD3; GB:BA000018; PID:913702452; PIDN:BA43593.1; GSPDB:

A/Experimental source: strain N315

C/Genetics:

A/Genes: fnbB

Query Match

Score 54; DB 2; Length 961;

Best Local Similarity 100.0%; Pred. No. 0.39;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EEDTEEDKPK 10

|||||
DB 701 EEDTEDKPK 710

RESULT 3

A2192
fibronectin-binding protein - Staphylococcus aureus
C:Species: Staphylococcus aureus
C:Date: 31-Jul-1989 #sequence_revision 31-Jul-1989 #text_change 16-Feb-1997
C:Accession: A32192
R:Signaes, C.; Rautci, G.; Jonsson, K.; Lindgren, P.E.; Anantharamiah, G.M.; Hoeck, W
Proc. Natl. Acad. Sci. U.S.A. 86, 699-703, 1989
A:Title: Nucleotide sequence of the gene for a fibronectin-binding protein from Staphyloc
A:Reference number: A32192; MUID:89038998; PMID:2521391
A:Accession: A32192
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1018 <SIG>
A:Cross-references: GB:J04151
C:Keywords: fibronectin binding

Query Match 100.0%; Score 54; DB 2; Length 1013;
Best Local Similarity 100.0%; Pred. No. 0.41;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EEDTEDKPK 10
|||||
DB 754 EEDTEDKPK 763

RESULT 4

H90053
hypothetical protein fnb [imported] - Staphylococcus aureus (strain N315)
C:Species: Staphylococcus aureus
C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C:Accession: H90053
R:Kurda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguc
ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.;
C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
A:Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.
A:Reference number: A89758; MUID:21311952; PMID:11418146
A:Accession: H90053
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1038 <KUR>
A:Cross-references: UNIPROT:Q99RD2; GB:BA000018; PID:G13702453; PIDN:BA843594.1; GSPDB:G
A:Experimental source: strain N315
C:Genetics:
A:Gene: fnb

Query Match 100.0%; Score 54; DB 2; Length 1038.
Best Local Similarity 100.0%; Pred. No. 0.42;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EEDTEDKPK 10
|||||
DB 750 EEDTEDKPK 759

RESULT 5

S74259
tropoin T 3, fast skeletal muscle, fetal - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 13-Mar-1997 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
C:Accession: S74259
R:Briggs, M.M.; Maready, M.; Schmidt, J.M.; Schachar, F.
FEBS Lett. 350, 37-40, 1994
A:Title: Identification of a fetal exon in the human fast Troponin T gene.
A:Reference number: S48660; MUID:94341369; PMID:8062920
A:Accession: S74259
A:Molecule type: mRNA
A:Residues: 1-56 <BRI>

A:Cross-references: UNIPROT:P45378; EMBL:U14642; NID:G557025; PIDN:AAA50360.1; PID:G5570
C:Superfamily: troponin T
C:Keywords: alternative splicing; phosphoprotein; skeletal muscle

Query Match 77.8%; Score 42; DB 2; Length 56;
Best Local Similarity 70.0%; Pred. No. 2;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 EEDTEDKPK 10
|||||
DB 31 EEDAEKPKR 40

RESULT 6

S48660
tropoin T 1, fast skeletal muscle, fetal - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 07-May-1995 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
C:Accession: S48660
R:Briggs, M.M.; Maready, M.; Schmidt, J.M.; Schachar, F.
FEBS Lett. 350, 37-40, 1994
A:Title: Identification of a fetal exon in the human fast Troponin T gene.
A:Reference number: S48660; MUID:94341369; PMID:8062920
A:Accession: S48660
A:Molecule type: mRNA
A:Residues: 1-67 <BRI>
A:Cross-references: UNIPROT:P45378; EMBL:U14641; NID:G557023; PIDN:AAA50359.1; PID:G5570
C:Superfamily: troponin T
C:Keywords: alternative splicing; phosphoprotein; skeletal muscle

Query Match 77.8%; Score 42; DB 2; Length 67;
Best Local Similarity 70.0%; Pred. No. 2.4;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 EEDTEDKPK 10
|||||
DB 42 EEDAEKPKR 51

RESULT 7

I53021
tropoin T - human
C:Species: Homo sapiens (man)
C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C:Accession: I53021
R:Wu, Q.L.; Jha, P.K.; Raychowdhury, M.K.; Du, Y.; Leavis, P.C.; Sarkar, S.
DNA Cell Biol. 13, 217-233, 1994
A:Title: Isolation and characterization of human fast skeletal beta troponin T cDNA: Com
A:Reference number: I53021; MUID:94226695; PMID:8172653
A:Accession: I53021
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-258 <RES>
A:Cross-references: UNIPROT:P45378; GB:M21984; NID:G508854; PIDN:AAA6777.1; PID:G508855
C:Genetics:
A:Gene: GDB:TNNNT3
A:Cross-references: GDB:350952; OMIM:600692
A:Map position: 11p15.5-11p15.5
C:Superfamily: troponin T

Query Match 77.8%; Score 42; DB 2; Length 258;
Best Local Similarity 70.0%; Pred. No. 9.8;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 EEDTEDKPK 10
|||||
DB 31 EEDAEKPKR 40

RESULT 8

A39038
1-caldesmon, nonmuscle - chicken
N:Alternate names: caldesmon, nonmuscle

C/Species: Gallus gallus (chicken)
 C/Date: 31-Jul-1991 #sequence_revision 27-Jun-1994 #text_change 22-Jun-1999
 C/Accession: A33038
 R/Hayashi, K.; Fujio, Y.; Kato, I.; Sobue, K.
 J. Biol. Chem. 266, 355-361, 1991
 A/Title: Structural and functional relationships between h- and l-caldesmons.
 A/Reference number: A33038; PMID:91093148; PMID:1824698
 A/Accession: A33038
 A/Molecule type: mRNA
 A/Residues: 1-517 <HAV>
 A/Cross-references: GB:M80620; GB:M8015; NID:g212242; PIDN:AAA48936.1; PID:g212243
 A/Experimental source: brain
 C/Comment: The binding of caldesmon to F-actin is modulated by calcium and calmodulin.
 C/Comment: Two calmodulin molecules can bind to nonoverlapping domains of each caldesmon
 C/Superfamily: caldesmon
 C/Keywords: actin binding; calmodulin binding; phosphoprotein
 F/342,427,463/Binding site: phosphate (Ser) (covalent) #status predicted
 F/333,456/Binding site: phosphate (Thr) (covalent) #status predicted

Query Match 77.8%; Score 42; DB 1; Length 517;
 Best Local Similarity 70.0%; Pred. No. 20;
 Matches 7; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 EBDTEBDKPK 10
 DB 174 EKDESEKPK 183

RESULT 9
 A33430
 h-caldesmon - chicken
 N/Alternate names: caldesmon, smooth muscle, calmodulin- and actin-binding protein
 C/Species: Gallus gallus (chicken)
 C/Date: 27-Feb-1990 #sequence_revision 27-Jun-1994 #text_change 09-Jul-2004
 C/Accession: A33430; A32642; A32445; A41064; A60461; PC2003; PX0022
 R/Hayashi, K.; Kanda, K.; Kimizuka, F.; Kato, I.; Sobue, K.
 Biochem. Biophys. Res. Commun. 164, 503-511, 1989
 A/Title: Primary structure and functional expression of h-caldesmon complementary DNA.
 A/Reference number: A33430; PMID:90026426; PMID:2803315
 A/Accession: A33430
 A/Molecule type: mRNA
 A/Residues: 1-771 <HAV>
 A/Cross-references: UNIPROT:P12957; GB:M28417; NID:g211895; PIDN:AAA48810.1; PID:g211896
 A/Experimental source: gizzard
 A/Note: Part of this sequence was confirmed by protein sequencing
 R/Bryan, J.; Imai, M.; Lee, R.; Moore, P.; Cook, R.G.; Lin, W.G.
 J. Biol. Chem. 264, 13873-13879, 1989
 A/Title: Cloning and expression of a smooth muscle caldesmon.
 A/Reference number: A32642; PMID:89340480; PMID:2760048
 A/Accession: A32642
 A/Molecule type: mRNA
 A/Residues: 1-318,334-771 <BRY>
 A/Cross-references: GB:J04668; NID:g212656; PIDN:AAA49067.1; PID:g212657
 A/Note: the authors translated the codon GAA for residue 743 as Leu
 A/Note: this alternative splice form is a high molecular weight caldesmon (h-caldesmon)
 R/Hayashi, K.; Yamada, S.; Kanda, K.; Kimizuka, F.; Kato, I.; Sobue, K.
 Biochem. Biophys. Res. Commun. 161, 38-45, 1989
 A/Title: 35kDa fragment of h-caldesmon conserves two consensus sequences of the tropomyosin
 A/Reference number: A32445; PMID:89273666; PMID:2730665
 A/Accession: A32445
 A/Molecule type: mRNA
 A/Residues: 466-771 <HA2>
 A/Cross-references: GB:M26684; NID:g211897; PIDN:AAA48811.1; PID:g211898
 R/Mak, A.S.; Carpenter, M.; Smillie, L.B.; Wang, J.H.
 J. Biol. Chem. 266, 19971-19975, 1991
 A/Title: Phosphorylation of caldesmon by p34(cdc2) kinase. Identification of phosphoryla
 A/Reference number: A41064; PMID:92041815; PMID:1939059
 A/Accession: A41064
 A/Molecule type: protein
 A/Residues: 597-600:678-696:711-721 <MAK>
 R/Wang, C.L.A.; Wang, L.W.C.; Lu, R.C.
 Biochem. Biophys. Res. Commun. 162, 746-752, 1989
 A/Title: Caldesmon has two calmodulin-binding domains.

A/Reference number: A60461; PMID:89334885; PMID:2757638
 A/Accession: A60461
 A/Molecule type: protein
 A/Residues: 2-17,'X',19-38,466-485 <MAN>
 R/Haruna, M.; Hayashi, K.; Yano, H.; Takeuchi, O.; Sobue, K.
 Biochem. Biophys. Res. Commun. 197, 145-153, 1993
 A/Title: Common structural and expressional properties of vertebrate caldesmon genes.
 A/Reference number: PC2003; PMID:94071934; PMID:8250919
 A/Accession: PC2003
 A/Molecule type: DNA
 A/Residues: 74-419 <HAR>
 R/Takagi, T.; Yazawa, M.; Ueno, T.; Suzuki, S.; Yagi, K.
 J. Biochem. 106, 778-783, 1989
 A/Title: Amino acid sequence studies on cyanogen bromide peptides of chicken caldesmon
 A/Reference number: PX0022; PMID:90130380; PMID:2613684
 A/Accession: PX0022
 A/Molecule type: protein
 A/Residues: 462-477,'D',479-563:674-762,'A',763-771 <TAK>
 C/Comment: This protein plays a vital role in the regulation of smooth muscle and nonmu
 C/Comment: The binding of caldesmon to F-actin is modulated by calcium and calmodulin.
 C/Comment: Two calmodulin molecules can bind to nonoverlapping domains of each caldesmo
 C/Superfamily: caldesmon
 C/Keywords: actin binding; alternative splicing; calmodulin binding; cytoskeleton; muscl
 F/1-771/Product: h-caldesmon #status predicted <HMA7>
 F/1-318,334-771/Product: h-caldesmon, alternative splice form #status predicted <LMA7>
 F/266-390/Region: 13-residue repeats
 F/511-582/Region: tropomyosin binding
 F/622-636/Region: tropomyosin binding
 F/597,682,717/Binding site: phosphate (Ser) (covalent) (by cdc2 kinase) #status experimenta
 F/688,711/Binding site: phosphate (Thr) (covalent) (by cdc2 kinase) #status experimenta

Query Match 77.8%; Score 42; DB 1; Length 771;
 Best Local Similarity 70.0%; Pred. No. 30;
 Matches 7; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 EBDTEBDKPK 10
 DB 182 EKDESEKPK 191

RESULT 10
 I66796
 fetal tropoin T 3 - rat (fragment)
 C/Species: Rattus norvegicus (Norway rat)
 C/Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 09-Jul-2004
 C/Accession: I66796
 R/Briggs, M.M.; Schachat, F.
 Dev. Biol. 158, 503-509, 1993
 A/Title: Origin of fetal tropoin T: Developmentally regulated splicing of a new exon i
 A/Reference number: I53073; PMID:93345743; PMID:8344466
 A/Accession: I66796
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: mRNA
 A/Residues: 1-51 <RES>
 A/Cross-references: UNIPROT:Q62619; EMBL:U04980; NID:g440820; PIDN:AAA16033.1; PID:g440
 C/Superfamily: tropoin T

Query Match 75.9%; Score 41; DB 2; Length 51;
 Best Local Similarity 70.0%; Pred. No. 27;
 Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 EBDTEBDKPK 10
 DB 36 EBDTEBDKPK 45

RESULT 11
 I53073
 fetal tropoin T 2 - rat (fragment)
 C/Species: Rattus norvegicus (Norway rat)
 C/Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 09-Jul-2004
 C/Accession: I53073
 R/Briggs, M.M.; Schachat, F.

Dev. Biol. 158, 503-509, 1993
A>Title: Origin of fecal tropomyosin T: Developmentally regulated splicing of a new exon in
A:Reference number: 153073; MUID:93345743; PMID:8344466
A:Accession: 153073
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-56 <RES>
A:Cross-references: UNIPROT:Q62618; EMBL:U04979; NID:g440818; P1DN:AAA16032.1; PID:g4408
C:Superfamily: tropomyosin T

Query Match 75.9%; Score 41; DB 2; Length 56;
Best Local Similarity 70.0%; Pred. No. 3;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 EEDTEDEKPK 10
Db 41 EEDTEDEKPK 50

RESULT 12
A53302
Probable transcription factor regulin - mouse
C:Species: Mus musculus (house mouse)
C:Date: 08-Jul-1995 #sequence_revision 03-Aug-1995 #text_change 35-Nov-1999
C:Accession: A53302
R:Gibby, T.G.; Mantel, P.L.; Rosali, R.; Crean, C.D.
J. Biol. Chem. 269, 29515-29519, 1994
A>Title: Requiem: a novel zinc finger gene essential for apoptosis in myeloid cells.
A:Reference number: A53302; MUID:95050794; PMID:7961935
A:Accession: A53302
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-371 <GAB>
A:Cross-references: GB:U10435; NID:G606660; P1DN:AAA64637.1; PID:G606661

Query Match 75.9%; Score 41; DB 2; Length 371;
Best Local Similarity 70.0%; Pred. No. 21;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 EEDTEDEKPK 10
Db 149 DEDTEDEKPK 158

RESULT 13
S30392
hypothetical RTVL-H3 promoter region/phospholipase A2 homolog PLA2L fusion protein (clon
C:Species: Homo sapiens (man)
C:Date: 16-Apr-1999 #sequence_revision 16-Apr-1999 #text_change 0-Apr-2000
C:Accession: S30392; S28508
R:Feuchter-Murthy, A.E.; Freeman, J.D.; Mager, D.L.
Nucleic Acids Res. 21, 135-143, 1993
A>Title: Splicing of a human endogenous retrovirus to a novel phcepholipase A2 related g
A:Reference number: S30392; MUID:93181166; PMID:8382789
A:Accession: S30392
A:Molecule type: mRNA
A:Residues: 1-689 <FEU1>
A:Cross-references: EMBL:214310; GB:SS5809; NID:G59976
A:Experimental source: human teratocarcinoma cell line NTera2D1
R:Feuchter-Murthy, A.E.; Freeman, J.D.; Mager, D.L.
submitted to the EMBL Data Library, August 1992
A:Reference number: S28508
A:Accession: S28508
A:Molecule type: mRNA
A:Residues: 1-390, 'P', 392-689 <FEU2>
A:Cross-references: EMBL:214310; GB:SS5809; NID:G59976; P1DN:CAA76662.1; PID:G59977
C:Genetics:
A:Gene: GDB:PLA2L
A:Cross-references: GDB:133794; OMIM:601658
A:Map position: 8q24-Bqter
C:Keywords: fusion protein
F:1-49/Region: retrovirus-like H3 promoter region derived
F:50-689/Region: human phospholipase A2 homolog PLA2L derived

Query Match 74.1%; Score 40; DB 4; Length 689;
Best Local Similarity 70.0%; Pred. No. 58;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 EEDTEDEKPK 10
Db 655 EEDTEDEPKQ 664

RESULT 14
B69946
phage-related terminase small subunit homolog ygas - Bacillus subtilis
C:Species: Bacillus subtilis
C:Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
C:Accession: B69946
R:Kunet, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berter
C.; Bron, S.; Brouillet, S.; Brusch, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Cho
A.; Ehrlich, S.D.; Emerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.
Nature 390, 249-256, 1997
A:Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Funo, S.; Galizzi, A.; Galler
leeh, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holtsappel, S.; Hosono, S.; Hullo, M.F.
Koetter, P.; Koningsstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois
A:Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel
Y, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle
Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadale, Y.; Sato, T.; Scanlon
A:Authors: Schleich, S.; Schroeder, R.; Scoffone, F.; Sekiguchi, J.; Sekowaka, A.; Seror
deutch, M.; Tanakoshi, A.; Tanaka, T.; Terpeira, P.; Tognoni, A.; Tosato, V.; Uchiyama,
T.; Whetters, P.; Wipac, A.; Yamamoto, H.; Yamane, K.; Yasunoto, K.; Yata, K.; Yoshida, K.
A:Authors: Yoshikawa, H.F.; Zumestein, E.; Yoshikawa, H.; Danchin, A.
A>Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.
A:Reference number: A69580; MUID:98044033; PMID:9384377
A:Accession: B69946
A>Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-239 <KUN>
A:Cross-references: UNIPROT:P45915; GB:Z99117; GB:AL009126; NID:G2634966; P1DN:CAB14561.
A:Experimental source: strain 168
C:Genetics:
A:Gene: ygas

Query Match 72.2%; Score 39; DB 2; Length 239;
Best Local Similarity 68.9%; Pred. No. 29;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 EEDTEDEKPK 9
Db 218 EELTEDEKPK 226

RESULT 15
P00199
glycinin A5A4B3 precursor - soybean (fragment)
C:Species: Glycine max (soybean)
C:Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 09-Jul-2004
C:Accession: P00199
R:Scallion, B.; Thanh, V.H.; Floener, L.A.; Nielsen, N.C.
Theor. Appl. Genet. 70, 510-519, 1991
A>Title: Identification and characterization of DNA clones encoding group-II glycinin su
A:Reference number: P00199
A:Accession: P00199
A:Molecule type: DNA
A:Residues: 1-268 <SCA>
A:Cross-references: UNIPROT:Q43452; UNIPROT:Q95B11
A:Experimental source: embryo, strain CX635-1-1-1
C:Superfamily: glycinin
C:Keywords: seed, storage protein

Query Match 72.2%; Score 39; DB 2; Length 268;
Best Local Similarity 60.0%; Pred. No. 32;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 EEDTEDEKPK 10

Db :||:||||:
18 DEDEDEDEKPR 27

Search completed: October 22, 2005, 08:04:22
Job time : 12.45 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 22, 2005, 06:06:36 ; Search time 55.85 Seconds
(without alignments)

91.688 Million cell updates/sec

Title: US-10-731-238-67

Perfect score: 54
Sequence: 1 EEDTEEDKPK 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1613378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1613378

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-Processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database : UniProt_03: *
1: uniprot_sprot: *
2: uniprot_trembl: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	54	100.0	152	2 Q9AEP9	Q9AEP9 staphylococ
2	54	100.0	940	2 Q53682	Q53682 staphylococ
3	54	100.0	943	2 Q8NUT8	Q8NUT8 staphylococ
4	54	100.0	957	2 Q6G6H4	Q6G6H4 staphylococ
5	54	100.0	961	2 Q99RD3	Q99RD3 staphylococ
6	54	100.0	961	2 Q7A3J8	Q7A3J8 staphylococ
7	54	100.0	965	2 Q6GDU5	Q6GDU5 staphylococ
8	54	100.0	1015	2 Q8NUT7	Q8NUT7 staphylococ
9	54	100.0	1015	2 Q6G6H3	Q6G6H3 staphylococ
10	54	100.0	1038	1 FNBA STAU	P14738 staphylococ
11	54	100.0	1038	2 Q99RD2	Q99RD2 staphylococ
12	54	100.0	1038	2 Q7A3J7	Q7A3J7 staphylococ
13	45	83.3	569	2 Q8SR48	Q8SR48 encephalito
14	45	83.3	1213	2 Q6C8W7	Q6C8W7 Yarrowia 11
15	44	81.5	164	2 Q7RT09	Q7RT09 plasmodium
16	43	79.6	310	2 Q8CBA4	Q8CBA4 mus musculu
17	43	79.6	311	2 Q8SY78	Q8SY78 staphylococ
18	43	79.6	311	2 Q9VIO6	Q9VIO6 dirosophila
19	43	79.6	1055	1 UB25 MOUSE	P57080 mus musculu
20	43	79.6	1087	1 UB25 HUMAN	Q9UHP3 homo sapien
21	42	77.8	429	1 TRT3 HUMAN	P45378 homo sapien
22	42	77.8	429	2 Q8TPG9	Q8TPG9 methanobarc
23	42	77.8	504	1 AMPA CHLIE	Q8KJ74 chlorobium
24	42	77.8	513	2 Q6ZKJ9	Q6ZKJ9 cryza sativ
25	42	77.8	771	1 CALD CHICK	P12957 gallus gall
26	41	75.9	51	2 Q62619	Q62619 ractus norv
27	41	75.9	56	2 Q62618	Q62618 ractus norv
28	41	75.9	242	2 Q9CLV3	Q9CLV3 pasteurilla
29	41	75.9	271	1 TRT3 MOUSE	Q9QZ47 mus musculu
30	41	75.9	310	2 Q8R563	Q8R563 mus musculu
31	41	75.9	315	2 Q8OW78	Q8OW78 mus musculu

ALIGNMENTS

32	41	75.9	356	1 DPF3 MOUSE	P58269 mus musculu
33	41	75.9	359	2 Q64T22	Q64T22 bacteroides
34	41	75.9	378	2 Q8CAD8	Q8CAD8 mus musculu
35	41	75.9	467	2 Q8H8X6	Q8H8X6 cryza sativ
36	41	75.9	572	2 Q7YZ17	Q7YZ17 scypha sp.
37	41	75.9	586	2 Q6QJ78	Q6QJ78 zea mays
38	41	75.9	727	2 Q86KB4	Q86KB4 dictyostell
39	41	75.9	798	2 Q6BKH3	Q6BKH3 debaromyce
40	41	75.9	826	2 Q6C855	Q6C855 yarrowia 11
41	41	75.9	1300	2 Q7QBM6	Q7QBM6 anopheles g
42	40	74.1	224	1 DPF3 HUMAN	Q92784 homo sapien
43	40	74.1	235	2 Q6QAN3	Q6QAN3 megachile r
44	40	74.1	259	2 Q9F187	Q9F187 arabidopsis
45	40	74.1	278	2 Q7ZW15	Q7ZW15 brachydanio

RESULT 1

Q9AEP9	PRELIMINARY;	PRT;	152 AA.
AC Q9AEP9;			
DT 01-JUN-2001 (TEMBLrel. 17, Created)			
DT 01-JUN-2001 (TEMBLrel. 17, Last sequence update)			
DT 01-DEC-2001 (TEMBLrel. 19, Last annotation update)			
DE Fibronectin-binding protein (Fragment).			
GN Name=fnb;			
OS Staphylococcus aureus.			
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.			
OX NCBI_TaxId=1280;			
RN [1]			
RP SEQUENCE FROM N.A.			
RC STRAIN=CMRSA-1;			
RX MEDLINE=21246681; PubMed=11349044;			
RY DOI=10.1128/IAI.69.6.3791-3799.2001;			
RA Rice K., Huesca M., Vaz D., McGavin M.J.;			
RT "Variance in fibronectin binding and fnb locus polymorphisms in			
RT Staphylococcus aureus: identification of antigenic variation in a			
RT fibronectin binding protein adhesin of the epidemic CMRSA-1 strain of			
RT methicillin-resistant S. aureus."			
RL Infect. Immun. 69:3791-3799(2001).			
DR EMBL: AY029184; AAK31586.1; -.			
FT NON_TER			
FT 152			
FT NON_TER			
SQ SEQUENCE 152 AA; 17193 MW; CFA3913C2B11C025 CRC64;			
Query Match	100.0%;	Score 54; DB 2; Length 152;	
Best Local Similarity	100.0%;	Pred. No. 0.92;	
Matches	10; Conservative	0; Mismatches	0; Indels
0; Gaps	0;		
QY	1 EEDTEEDKPK 10		
Db	9 EEDTEEDKPK 18		
RESULT 2			
ID Q53682	PRELIMINARY;	PRT;	940 AA.
AC Q53682;			
DT 01-NOV-1996 (TEMBLrel. 01, Created)			
DT 01-NOV-1996 (TEMBLrel. 01, Last sequence update)			
DT 01-MAR-2004 (TEMBLrel. 26, Last annotation update)			
DE Fibronectin binding protein B.			
GN Name=fnbB;			
OS Staphylococcus aureus.			
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.			
OX NCBI_TaxId=1280;			
RN [1]			
RP SEQUENCE FROM N.A.			
RC STRAIN=8325-4;			
RX MEDLINE=92111475; PubMed=1837266;			
RA Jonsson K., Sigmas C., Muller H.P., Lindberg M.;			

RT "Two different genes encode fibronectin binding proteins in
 RT Staphylococcus aureus. The complete nucleotide sequence and
 RT characterization of the second gene";
 RL Eur. J. Biochem. 202:1041-1048 (1991).
 CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
 CC an amide bond (By similarity).
 DR EMBL: X62992; CAA44726.1; -.
 DR PIR: S19702; S19702.
 DR HSSP: Q53553; 1N67.
 DR GO: GO:0009986; C:cell surface; IEA.
 DR GO: GO:0005618; C:cell wall; IEA.
 DR GO: GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
 DR GO: GO:0016020; C:membrane; IEA.
 DR GO: GO:0007155; P:cell adhesion; IEA.
 DR InterPro: IPR008966; Adhes_bact.
 DR InterPro: IPR004237; Fn_bind.
 DR InterPro: IPR005877; Gpos_YsIRK.
 DR Pfam: PF02986; Gram_pos_anchor.
 DR Pfam: PF02986; Gram_pos_anchor; 1.
 DR Pfam: PF04650; YsIRK_signal; 1.
 DR TIGRPFAM: TIGR01167; LpxTG_anchor; 1.
 DR TIGRPFAM: TIGR01168; YsIRK_signal; 1.
 DR PROSITE: PS50847; GRAM_POS_ANCHORING; 1.
 DR Cell wall; Peptidoglycan-anchor.
 KW SEQUENCE 940 AA; 103555 MW; E35FBBCA907AE345 CRC64;

Query Match 100.0%; Score 54; DB 2; Length 940
 Best Local Similarity 100.0%; Pred. No. 5.9;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EEDTEEDKPK 10
 DB 690 EEDTEEDKPK 699

RESULT 3
 Q8NU08 PRELIMINARY; PRT; 943 AA.
 ID Q8NU08
 AC Q8NU08
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE FnbB protein.
 GN Name=fnbB; Ordered locus names=MM420;
 OS Staphylococcus aureus (strain MW2).
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 OX NCBI_TaxID=196620;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=MM2;
 RX MEDLINE=22040717; PubMed=12044378; DOI=10.1016/S0140-6736(02)08713-5;
 RA Baba T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Ogunshi A.,
 RA Nagai Y., Iwama N., Asano K., Naimi T., Kuroda H., Cui L.,
 RA Yamamoto K., Hiramatsu K.;
 RT "Genome and virulence determinants of high virulence commun. ty-
 RT acquired MRSA";
 RL Lancet 359:1819-1827 (2002).
 CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
 CC an amide bond (By similarity).
 DR EMBL: AF004830; BAB9685.1; -.
 DR HSSP: Q53553; 1N67.
 DR GO: GO:0009986; C:cell surface; IEA.
 DR GO: GO:0005618; C:cell wall; IEA.
 DR GO: GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
 DR GO: GO:0016020; C:membrane; IEA.
 DR GO: GO:0007155; P:cell adhesion; IEA.
 DR InterPro: IPR008966; Adhes_bact.
 DR InterPro: IPR004237; Fn_bind.
 DR InterPro: IPR005877; Gpos_YsIRK.
 DR Pfam: PF02986; Gram_pos_anchor.
 DR Pfam: PF02986; Gram_pos_anchor; 1.

DR Pfam: PF04650; YsIRK_signal; 1.
 DR TIGRPFAM: TIGR01167; LpxTG_anchor; 1.
 DR TIGRPFAM: TIGR01168; YsIRK_signal; 1.
 DR PROSITE: PS50847; GRAM_POS_ANCHORING; 1.
 DR Cell wall; Complete proteome; Peptidoglycan-anchor.
 KW SEQUENCE 943 AA; 104537 MW; DA8A5F31947B1BA CRC64;

Query Match 100.0%; Score 54; DB 2; Length 943;
 Best Local Similarity 100.0%; Pred. No. 5.9;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EEDTEEDKPK 10
 DB 697 EEDTEEDKPK 706

RESULT 4
 Q6G6H4 PRELIMINARY; PRT; 957 AA.
 ID Q6G6H4
 AC Q6G6H4
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DE Fibronectin-binding protein.
 GN Name=fnbB; Ordered locus names=SA52387;
 OS Staphylococcus aureus (strain MSSA476).
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 OX NCBI_TaxID=282459;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX PubMed=15213324; DOI=10.1073/pnas.0402521101;
 RA Holden M.T.G., Fell B.J., Lindsey J.A., Peacock S.J., Day N.P.J.,
 RA Enright M.C., Foster T.J., Moore C.E., Hurst L., Atkin R., Barron A.,
 RA Bason N., Bentley S.D., Chillingworth C., Chillingworth T.,
 RA Churcher C., Clark L., Cotton C., Cronin A., Doggett J., Dowd L.,
 RA Felwell T., Hance Z., Harris B., Hauser H., Holtroyd S., Jagsis K.,
 RA James K.D., Leonard N., Line A., Mayes R., Moule S., Mungall K.,
 RA Ormond D., Quail M.A., Rabinowitch E., Rutherford K.M., Sanders M.,
 RA Sharp S., Simmonds M., Stevens K., Whitehead S., Barrett B.G.,
 RA Spratt B.G., Parkhill J.;
 RT "Complete genomes of two clinical Staphylococcus aureus strains:
 RT evidence for the rapid evolution of virulence and drug resistance";
 RL Proc. Natl. Acad. Sci. U.S.A. 101:9786-9791 (2004).
 CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
 CC an amide bond (By similarity).

DR EMBL: BX571857; CAG44201.1; -.
 DR GO: GO:0009986; C:cell surface; IEA.
 DR GO: GO:0005618; C:cell wall; IEA.
 DR GO: GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
 DR GO: GO:0016020; C:membrane; IEA.
 DR GO: GO:0007155; P:cell adhesion; IEA.
 DR InterPro: IPR008966; Adhes_bact.
 DR InterPro: IPR004237; Fn_bind.
 DR InterPro: IPR005877; Gpos_YsIRK.
 DR InterPro: IPR001899; Gram_pos_anchor.
 DR Pfam: PF02986; Fn_bind; 1.
 DR Pfam: PF02986; Gram_pos_anchor; 1.
 DR Pfam: PF04650; YsIRK_signal; 1.
 DR TIGRPFAM: TIGR01167; LpxTG_anchor; 1.
 DR TIGRPFAM: TIGR01168; YsIRK_signal; 1.
 DR PROSITE: PS50847; GRAM_POS_ANCHORING; 1.
 DR Cell wall; Complete proteome; Peptidoglycan-anchor.
 KW SEQUENCE 957 AA; 105980 MW; 28F8BA7FFDFP3BAF CRC64;

Query Match 100.0%; Score 54; DB 2; Length 957;
 Best Local Similarity 100.0%; Pred. No. 6;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EEDTEEDKPK 10
 DB 697 EEDTEEDKPK 706

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RESULT 5
099RD3 PRELIMINARY; PRT; 961 AA.
AC 099RD3;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE Fibronectin-binding protein homolog.
GN Name=fnbB; OrderedLocNames=SAV2502;
OS Staphylococcus aureus (strain M50 / ATCC 700699).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=158878;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=M50 / ATCC 700699;
RX MEDLINE=21311952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2;
RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Iian J.-Q., Ito T.,
RA Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,
RA Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
RA Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
RA Kanemitsu K., Hiraoka S., Goto S., Yabuzaki J.,
RA Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
RA Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.,
RT "Whole genome sequencing of methicillin-resistant Staphylococcus
RT aureus."
RL Lancet 357:1225-1240(2001).
CC -1 SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC an amide bond (By similarity).
EMBL: AP003365; BAB5664.1; -.
DR HSP; G90053; G90053.
DR HSP; G90053; G90053.
DR GO; GO:0009986; C:cell surface; IEA.
DR GO; GO:0005618; C:cell wall; IEA.
DR GO; GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0007155; P:cell adhesion; IEA.
DR InterPro; IPR008966; Adhes_bact.
DR InterPro; IPR004237; Fn_bind.
DR InterPro; IPR005877; Gpos_YsIRK.
DR InterPro; IPR001899; Gram_pos_anchor.
DR Pfam; PF02986; Fn_bind_1.
DR Pfam; PF00746; Gram_pos_anchor; 1.
DR Pfam; PF04650; YsIRK_signal; 1.
DR TIGRfams; TIGR01167; LPXTG_anchor; 1.
DR TIGRfams; TIGR01168; YsIRK_signal; 1.
DR PROSITE; PS50847; GRAM_POS_ANCHORING; 1.
KM Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ SEQUENCE 961 AA; 106010 MW; 364940F884EA4101 CRC64;

Query Match 100.0%; Score 54; DB 2; Length 961;
Best Local Similarity 100.0%; Pred. No. 6;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Iian J.-Q., Ito T.,
RA Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,
RA Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
RA Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
RA Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
RA Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.,
RT "Whole genome sequencing of methicillin-resistant Staphylococcus
RT aureus."
RL Lancet 357:1225-1240(2001).
CC -1 SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC an amide bond (By similarity).
EMBL: AP003365; BAB43593.1; -.
DR GO; GO:0009986; C:cell surface; IEA.
DR GO; GO:0005618; C:cell wall; IEA.
DR GO; GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0007155; P:cell adhesion; IEA.
DR InterPro; IPR008966; Adhes_bact.
DR InterPro; IPR004237; Fn_bind.
DR InterPro; IPR005877; Gpos_YsIRK.
DR InterPro; IPR001899; Gram_pos_anchor.
DR Pfam; PF02986; Fn_bind_1.
DR Pfam; PF00746; Gram_pos_anchor; 1.
DR Pfam; PF04650; YsIRK_signal; 1.
DR TIGRfams; TIGR01167; LPXTG_anchor; 1.
DR TIGRfams; TIGR01168; YsIRK_signal; 1.
DR PROSITE; PS50847; GRAM_POS_ANCHORING; 1.
KM Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ SEQUENCE 961 AA; 106010 MW; 364940F884EA4101 CRC64;

Query Match 100.0%; Score 54; DB 2; Length 961;
Best Local Similarity 100.0%; Pred. No. 6;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 6
07A3J8 PRELIMINARY; PRT; 961 AA.
ID 07A3J8;
AC 07A3J8;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE FmbB protein.
GN Name=fmbB; OrderedLocNames=SA2290;
OS Staphylococcus aureus (strain N315).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=158879;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=21311952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2;

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DR GO:0007155; P:cell adhesion; IEA.
 DR InterPro: IPR008966; Adhes_bact.
 DR InterPro: IPR004237; Fn_bind.
 DR InterPro: IPR005877; Gpos_YsIRK.
 DR InterPro: IPR001899; Gram_pos_anchor.
 DR Pfam: PF02986; Fn_bind; 1.
 DR Pfam: PF00746; Gram_pos_anchor; 1.
 DR TIGRPFAM: TIGR01167; LPXTG_anchor; 1.
 DR TIGRPFAM: TIGR01168; YsIRK_signal; 1.
 DR PROSITE: PS50847; GRAM_POS_ANCHORING; 1.
 DR Cell wall; Complete proteome; Peptidoglycan-anchor.
 SQ SEQUENCE 965 AA; 105691 MW; 2982E132164D0551 CRC64;

Query Match 100.0%; Score 54; DB 2; Length 965;
 Best Local Similarity 100.0%; Pred. No. 6.1;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 EEDTEEDKPK 10
 |||||
 Db 757 EEDTEEDKPK 766

RESULT 8
 08NUU7 PRELIMINARY; PRT; 1015 AA.

AC 08NUU7; 01-OCT-2002 (TRENBLrel. 22, Created)
 DT 01-OCT-2002 (TRENBLrel. 22, Last sequence update)
 DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
 DE Fnb protein.
 GN Name=fnb: OrderedLocustNames=MW2421;
 OS Staphylococcus aureus (strain MW2)
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 OX NCBI_TaxId=196620;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=MW2;
 RX MEDLINE=22040717; PubMed=12044378; DOI=10.1016/S0140-6736(02)08713-5;
 RA Baba T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Oguchi A.,
 RA Nagai Y., Iwama N., Asano K., Naimi T., Kuroda H., Cui L.,
 RA Yamamoto K., Hiramatsu K.;
 RT "Genome and virulence determinants of high virulence community-
 acquired MRSA.";
 RL Lancet 359:1819-1827(2002).
 CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
 an amide bond (By similarity).
 CC EMBL; APO04830; BAB96286.1; -;
 DR GO: GO:0009986; C:cell surface; IEA.
 DR GO: GO:0005618; C:cell wall; IEA.
 DR GO: GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
 DR GO: GO:0016020; C:membrane; IEA.
 DR GO: GO:0007155; P:cell adhesion; IEA.
 DR InterPro: IPR008966; Adhes_bact.
 DR InterPro: IPR004237; Fn_bind.
 DR InterPro: IPR005877; Gpos_YsIRK.
 DR InterPro: IPR001899; Gram_pos_anchor.
 DR Pfam: PF02986; Fn_bind; 1.
 DR Pfam: PF00746; Gram_pos_anchor; 1.
 DR Pfam: PF04650; YsIRK_signal; 1.
 DR TIGRPFAM: TIGR01167; LPXTG_anchor; 1.
 DR TIGRPFAM: TIGR01168; YsIRK_signal; 1.
 DR PROSITE: PS50847; GRAM_POS_ANCHORING; 1.
 DR Cell wall; Complete proteome; Peptidoglycan-anchor.
 SQ SEQUENCE 1015 AA; 111145 MW; D0F9281BB64D44D2 CRC64;

Query Match 100.0%; Score 54; DB 2; Length 1015;
 Best Local Similarity 100.0%; Pred. No. 6.4;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 EEDTEEDKPK 10
 |||||
 Db 755 EEDTEEDKPK 764

RESULT 9
 06G6H3 PRELIMINARY; PRT; 1015 AA.
 ID 06G6H3;
 AC 06G6H3; 05-JUL-2004 (TRENBLrel. 27, Created)
 DT 05-JUL-2004 (TRENBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TRENBLrel. 27, Last annotation update)
 DE Fibronectin-binding protein.
 GN OrderedLocustNames=SA52398;
 OS Staphylococcus aureus (strain MSSA476).
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 OX NCBI_TaxId=282459;
 RN [1]

RP SEQUENCE FROM N.A.
 RX PubMed=15213324; DOI=10.1073/pnas.0402521101;
 RA Holden M.T.G., Fell E.U., Lindsay J.A., Peacock S.J., Day N.P.J.,
 RA Enright M.C., Foster T.J., Moore C.E., Hurst L., Atkin R., Barron A.,
 RA Bason N., Bentley S.D., Chillingworth C., Chillingworth T.,
 RA Churcher C., Clark L., Corton C., Cronin A., Doggett J., Dowd L.,
 RA Felwell T., Hance Z., Harris B., Hauser H., Holroyd S., Jagsels K.,
 RA James K.D., Lennard N., Line A., Mayes R., Moule S., Mungall K.,
 RA Ormond D., Quail M.A., Rabinowitch E., Rutherford K.M., Sanders M.,
 RA Sharp S., Simmonds M., Stevens K., Whitehead S., Barrett B.G.,
 RA Spratt B.G., Parkhill J.;
 RT "Complete genomes of two clinical Staphylococcus aureus strains:
 evidence for the rapid evolution of virulence and drug resistance.";
 RL Proc. Natl. Acad. Sci. U.S.A. 101:9786-9791(2004).
 CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
 an amide bond (By similarity).
 CC EMBL; BX571857; CAG44202.1; -;
 DR GO: GO:0009986; C:cell surface; IEA.
 DR GO: GO:0005618; C:cell wall; IEA.
 DR GO: GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
 DR GO: GO:0016020; C:membrane; IEA.
 DR GO: GO:0007155; P:cell adhesion; IEA.
 DR InterPro: IPR008966; Adhes_bact.
 DR InterPro: IPR004237; Fn_bind.
 DR InterPro: IPR005877; Gpos_YsIRK.
 DR InterPro: IPR001899; Gram_pos_anchor.
 DR Pfam: PF02986; Fn_bind; 1.
 DR Pfam: PF00746; Gram_pos_anchor; 1.
 DR Pfam: PF04650; YsIRK_signal; 1.
 DR TIGRPFAM: TIGR01167; LPXTG_anchor; 1.
 DR TIGRPFAM: TIGR01168; YsIRK_signal; 1.
 DR PROSITE: PS50847; GRAM_POS_ANCHORING; 1.
 DR Cell wall; Complete proteome; Peptidoglycan-anchor.
 SQ SEQUENCE 1015 AA; 111145 MW; D0F9281BB64D44D2 CRC64;

Query Match 100.0%; Score 54; DB 2; Length 1015;
 Best Local Similarity 100.0%; Pred. No. 6.4;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 EEDTEEDKPK 10
 |||||
 Db 755 EEDTEEDKPK 764

RESULT 10
 FNBA STAAU STANDARD; PRT; 1018 AA.
 ID FNBA STAAU
 AC P14738; 01-APR-1990 (rel. 14, Created)
 DT 01-APR-1990 (rel. 14, Last sequence update)
 DT 25-OCT-2004 (rel. 45, Last annotation update)
 DE Fibronectin-binding protein precursor (FNBP).
 GN Name=fnbp;
 OS Staphylococcus aureus.
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 OX NCBI_TaxId=1280;
 RN [1]
 RP SEQUENCE FROM N.A.

CC STRAIN=NTC 8325-4;
 RX MEDLINE=89089898; PubMed=2521391;
 RA Signaes C., Raucel G., Joensen K., Lindgren P.-E.,
 RA Anantharamiah G.M., Hoeek M., Lindberg M.,
 RT "Nucleotide sequence of the gene for a fibronectin-binding protein
 from *Staphylococcus aureus*: use of this peptide sequence in the
 RT synthesis of biologically active peptides."
 CC Proc. Natl. Acad. Sci. U.S.A. 86:699-703(1989).
 CC -1- FUNCTION: The ability of bacteria to bind fibronectin has been
 CC proposed as a virulence factor enabling bacteria to colonize wound
 CC tissues and blood clots. Binding of plasma fibronectin to the
 CC bacterial surface might block adhesion receptors on *S. aureus*, thus
 CC representing an important defense mechanism against tissue
 CC invasion.
 CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
 CC an amide bond (Potential).
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
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 CC or send an email to license@sib-sib.ch).
 CC -----
 CC EMBL, J04151; AAA26632.1; -
 CC InterPro: IPR004237; Fn bind.
 CC InterPro: IPR005877; Gpos YSIRK.
 CC InterPro: IPR001899; Gram_pos_anchor.
 CC Pfam: PF02986; Fn_bind; 1.
 CC Pfam: PF00746; Gram_pos_anchor; 1.
 CC DR TIGRPFAM: TIGR01167; LPXTG_anchor; 1.
 CC DR TIGRPFAM: TIGR01168; YSIRK_anchor; 1.
 CC DR PROSITE: PS50847; GRAM_POS_ANCHORING; 1.
 CC Cell adhesion; Cell wall; Peptidoglycan-anchor; Repeat; Signal;
 CC virulence.
 CC KW SIGNAL 1 36
 CC FT CHAIN 37 985
 CC FT PROPEP 986 1018
 CC FT REPEAT 545 574
 CC FT REPEAT 575 604
 CC FT DOMAIN 745 878
 CC FT REPEAT 745 782
 CC FT REPEAT 783 820
 CC FT REPEAT 821 859
 CC FT REPEAT 860 878
 CC FT DOMAIN 879 948
 CC FT REPEAT 879 892
 CC FT REPEAT 893 906
 CC FT REPEAT 907 920
 CC FT REPEAT 921 934
 CC FT REPEAT 935 948
 CC FT SITE 982 986
 CC MOD_RES 985 985
 CC SO SEQUENCE 1018 AA, 111780 MW, 5817550020881FIF CRC64;
 CC
 CC Query Match 100.0%; Score 54; DB 1; Length 1018;
 CC Best Local Similarity 100.0%; Pred. No. 6.4;
 CC Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DT 01-JUN-2001 (TREMBLrel. 17, last sequence update)
 DT 01-MAR-2004 (TREMBLrel. 26, last annotation update)
 DT Fibronectin-binding protein homolog.
 GN Name=fnb; OrderedLocustNames=SAV2503;
 OS *Staphylococcus aureus* (strain Mu50 / ATCC 700699).
 OC Bacteria; Firmicutes; Bacillales; *Staphylococcus*.
 OX NCBI_TaxID=158878;
 RP SEQUENCE FROM N.A.
 RP STRAIN=Mu50 / ATCC 700699;
 RX MEDLINE=2111952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2;
 RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
 RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Iino T.,
 RA Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,
 RA Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
 RA Kanehisa M., Yamashita A., Kuhara S., Goto S., Yabuzaki J.,
 RA Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.,
 RT "Whole genome sequencing of methicillin-resistant *Staphylococcus*
 RT *aureus*."
 CC Lancet 357:1225-1240(2001).
 CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
 CC an amide bond (By similarity).
 CC EMBL, AF003365; BAB58665.1; -
 CC PIR, H90053; H90053.
 CC DR GO: GO:0009986; C:cell surface; IEA.
 CC DR GO: GO:0005618; C:cell wall; IEA.
 CC DR GO: GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
 CC DR GO: GO:0016020; C:membrane; IEA.
 CC DR GO: GO:0007155; P:cell adhesion; IEA.
 CC DR InterPro: IPR008966; Adhes_bact.
 CC DR InterPro: IPR004237; Fn_bind.
 CC DR InterPro: IPR005877; Gpos_YSIRK.
 CC DR InterPro: IPR001899; Gram_pos_anchor.
 CC Pfam: PF02986; Fn_bind; 1.
 CC Pfam: PF00746; Gram_pos_anchor; 1.
 CC DR TIGRPFAM: TIGR01167; LPXTG_anchor; 1.
 CC DR TIGRPFAM: TIGR01168; YSIRK_anchor; 1.
 CC DR PROSITE: PS50847; GRAM_POS_ANCHORING; 1.
 CC KW Cell wall; Complete proteome; Peptidoglycan-anchor.
 CC SO SEQUENCE 1038 AA, 113618 MW, 666BF6BF2BF8B12 CRC64;
 CC
 CC Query Match 100.0%; Score 54; DB 2; Length 1038;
 CC Best Local Similarity 100.0%; Pred. No. 6.5;
 CC Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DT 07A3J7 PRELIMINARY; PRT; 1038 AA.
 AC 07A3J7;
 DT 05-JUL-2004 (TREMBLrel. 27, last sequence update)
 DT 05-JUL-2004 (TREMBLrel. 27, last sequence update)
 DT 05-JUN-2004 (TREMBLrel. 27, last annotation update)
 DE Pnb protein.
 GN Name=fnb; OrderedLocustNames=SA2291;
 OS *Staphylococcus aureus* (strain N315).
 OC Bacteria; Firmicutes; Bacillales; *Staphylococcus*.
 OX NCBI_TaxID=158879;
 RN [1]
 RP SEQUENCE FROM N.A.
 RP MEDLINE=21311952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2;
 RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
 RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Iino T.,
 RA Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,
 RA Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
 RA Sekimizu K., Hiramatsu K., Kuhara S., Goto S., Yabuzaki J.,
 RA Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,

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RA Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
RT "Whole genome sequencing of methicillin-resistant Staphylococcus
RL aureus."
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC an amide bond (By similarity).
DR EMBL: AP003137; BAB43594.1; -.
DR GO: GO:0009986; C:cell surface; IEA.
DR GO: GO:0005618; C:cell wall; IEA.
DR GO: GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO: GO:0016020; C:membrane; IEA.
DR GO: GO:007155; P:cell adhesion; IEA.
DR InterPro: IPR008966; Adhes_bact.
DR InterPro: IPR004237; Fn_bind.
DR InterPro: IPR005877; Gpos_YSTRK.
DR InterPro: IPR001899; Gram_pos_anchor.
DR Pfam: PF02986; Fn_bind_1.
DR Pfam: PF00746; Gram_pos_anchor_1.
DR Pfam: PF04650; YSTRK_signal_1.
DR TIGRfam: TIGR01167; LpxTG_anchor_1.
DR TIGRfam: TIGR01168; YSTRK_signal_1.
DR PROSITE: PS50847; GRAM_POS_ANCHORING; 1.
DR Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ SEQUENCE 1038 AA; 113618 MW; 6668F6B72BFEB12 CRC64;

Query Match 100.0%; Score 54; DB 2; Length 1038;
Best Local Similarity 100.0%; Pred. No. 6.5;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EEDTEEDKPK 10
    |||||
Db 750 EEDTEEDKPK 759

RESULT 13
QSR48 PRELIMINARY; PRT; 569 AA.
AC QSR48;
DC 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE TRANSLATION INITIATION FACTOR EIF-2B EPSILON SUBUNIT.
GN Name=ECU10.0700;
OS Encephalitozoon cuniculi GB-M1.
OC Eukaryota; Fungi; Microsporidia; Unikaryoniidae; Encephalitozoon.
OX NCBI_TaxID=284813;
[1]
RN SEQUENCE FROM N.A.
RP STRAIN=GB-M1;
RC MEDLINE=21576510; PubMed=11719806; DOI=10.1038/35106579;
RX Katinka M.D., Duprat S., Cornillot E., Metenier G., Thamarat F.,
RA Prenier G., Barbe V., Peyretailade E., Broctier P., Winkler P.,
RA Delbac F., El Alaoui H., Peyret P., Saurin W., Gouy M.,
RA Weisenbach J., Vivares C.P.;
RT "Genome sequence and gene compaction of the eukaryote parasite
RT Encephalitozoon cuniculi."
RL Nature 414:450-453 (2001).
[2]
RN SEQUENCE FROM N.A.
RP STRAIN=GB-M1;
RC Genoscope;
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AL590449; CAD25789.1; -.
DR GO: GO:0003743; P:translation initiation factor activity; IEA.
KW Initiation factor.
SQ SEQUENCE 569 AA; 65302 MW; 220BC49ABFEB2C4B CRC64;

Query Match 83.3%; Score 45; DB 2; Length 569;
Best Local Similarity 80.0%; Pred. No. 88;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 EEDTEEDKPK 10
    |||||

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Db 414 DEDEEDKPK 423

RESULT 14
Q6C8W7 PRELIMINARY; PRT; 1213 AA.
AC Q6C8W7;
DC 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Similar to tr|Q06132 Saccharomyces cerevisiae YLR336C SGD1 involved in
DE HOG pathway.
DE ORFName=YAL10D16313g;
OS Yarrowia lipolytica CLIB99.
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Dipodascaceae; Yarrowia.
OX NCBI_TaxID=284591;
[1]
RN SEQUENCE FROM N.A.
RP STRAIN=CLIB99;
RC Genolevures;
RA Dujon B., Sherman D., Fischer G., Durrens P., Casaregola S.,
RA Lafontaine I., de Montigny J., Marcq C., Neveglise C., Talla E.,
RA Goffard N., Frangeul L., Aigle M., Anthouard V., Babour A., Barbe V.,
RA Barnay S., Blanchin S., Beckerich J.M., Beyne E., Bleykasten C.,
RA Boisarme A., Boyer J., Catolico L., Confanioleri F., de Darvar A.,
RA Despons L., Fabre E., Fairhead C., Ferry-Dumazet H., Groppi A.,
RA Hantraye F., Hennequin C., Jauniaux N., Joyet P., Kachouri R.,
RA Kerrest A., Koszul R., Lemaire M., Lesur I., Ma L., Muller H.,
RA Nicoud J.M., Nikolski M., Oztas S., Ozler-Kalogeropoulos O.,
RA Pellens S., Potier S., Richard G.F., Straub M.L., Suleau A.,
RA Swennene D., Tekala F., Wesolowski-Louvel M., Westhof E., Wirth B.,
RA Zeniou-Meyer M., Zivanovic I., Bolotin-Pukhara M., Thierry A.,
RA Bouchier C., Caudron B., Scarpelli C., Gaillardin C., Weisenbach J.,
RA Winkler P., Souciet J.L.;
RT "Genome evolution in yeasts."
RL Nature 430:35-44(2004).
[2]
RN SEQUENCE FROM N.A.
RP STRAIN=CLIB99;
RC Genoscope;
RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL: CR382130; CAG81086.1; -.
DR GO: GO:0003723; F:RNA binding; IEA.
DR GO: GO:0006412; P:protein biosynthesis; IEA.
DR InterPro: IPR008398; AKM.
DR InterPro: IPR002048; EF-hand.
DR InterPro: IPR003890; IF_eIF4G.
DR InterPro: IPR001351; Luciferase_like.
DR Pfam: PF02847; MA3; 1.
DR Pfam: PF02854; MIF4G; 1.
DR SMART: SM00544; MA3; 1.
DR SMART: SM00543; MIF4G; 1.
DR PROSITE: PS00018; EF_HAND; UNKNOWN 1.
SQ SEQUENCE 1213 AA; 137023 MW; A55AFB9140E50B CRC64;

Query Match 83.3%; Score 45; DB 2; Length 1213;
Best Local Similarity 88.9%; Pred. No. 1.9e+02;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EEDTEEDKPK 9
    |||||
Db 198 EEDTEEDKPK 206

RESULT 15
Q7RT09 PRELIMINARY; PRT; 164 AA.
AC Q7RT09;
DC 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)

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DE Hypochemical protein.
GN Name=PY00192;
OS Plasmodium yoelii yoelii.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=73239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=17XNL;
RX PubMed=12368865; DOI=10.1038/nature01099;
RA Carlton J.M., Anguoli S.V., Suh B.B., Kool J.T.W., Perrea M.,
RA Silva J.C., Ermolaeva M.D., Allen J.B., Selengut J.D., Koo H.L.,
RA Peterson J.D., Pop M., Kosack D.S., Shumway M.F., Bidwell S.L.,
RA Shallom S.V., van Aken S.E., Riedmiller S.B., Feldblyum T.V.,
RA Cho J.K., Quackenbush J., Sedegah M., Shoabli A., Cummings L.M.,
RA Florens L., Yates F.R. III, Raine J.D., Sinden R.E., Harris M.A.,
RA Cunningham D.A., Preiser P.R., Bergman L.W., Vaidya A.B.,
RA van Lin L.H., Jase C.J., Waters A.P., Smith H.O., White O.R.,
RA Salzberg S.L., Venter J.C., Fraser C.M., Hoffman S.L., Gardner M.J.,
RA Carucci D.U.;
RT "Genome sequence and comparative analysis of the model rodent malaria
RT parasite Plasmodium yoelii yoelii."
RL Nature 419:512-519(2002).
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
CC EMBL: AABL0100051; EAA21296.1; -.
CC InterPro: IPR001876; Znf_RanGDP.
DR PROSITE: PS01358; ZF_RANBP2_1; 1.
DR PROSITE: PS50199; ZF_RANBP2_2; 1.
KW Hypochemical protein.
SQ SEQUENCE 164 AA; 18693 MW; 5630EDDE606DB6B1 CRC64;

Query Match 81.5%; Score 44; DB 2; Length 164;
Best Local Similarity 80.0%; Pred. No. 35;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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Search completed: October 22, 2005, 08:00:28
Job time : 57.85 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 25, 2005, 20:21:18 ; Search time 63.2 Seconds
(without alignments)
61.196 Million cell updates/sec

Title: US-10-731-238-68

Perfect score: 56

Sequence: 1 DTEDKPKYE 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seque, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_16Dec04:*

1: geneseqp1980s:*\n2: geneseqp1990s:*\n3: geneseqp2000s:*\n4: geneseqp2001s:*\n5: geneseqp2002s:*\n6: geneseqp2003as:*\n7: geneseqp2003bs:*\n8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	56	100.0	10	2	AAW65724 Fibronec
2	56	100.0	14	2	AAW65761 Peptide #
3	56	100.0	38	1	AAW65761 Peptide #
4	56	100.0	38	1	AAW65761 Peptide #
5	56	100.0	38	2	AAW65692 Fibronec
6	56	100.0	38	2	AAW65662 Fibronec
7	56	100.0	38	2	AAW65700 Fibronec
8	56	100.0	38	2	AAW65691 Fibronec
9	56	100.0	38	2	AAW65699 Fibronec
10	56	100.0	38	2	AAW65661 Fibronec
11	56	100.0	38	2	AAW65693 Fibronec
12	56	100.0	38	2	AAW65712 Fibronec
13	56	100.0	38	2	AAW65713 Fibronec
14	56	100.0	38	2	AAW65713 Fibronec
15	56	100.0	38	2	AAW65713 Fibronec
16	56	100.0	38	2	AAW65713 Fibronec
17	56	100.0	38	2	AAW65713 Fibronec
18	56	100.0	38	2	AAW65713 Fibronec
19	56	100.0	38	2	AAW65713 Fibronec
20	56	100.0	38	2	AAW65713 Fibronec
21	56	100.0	38	2	AAW65713 Fibronec
22	56	100.0	38	2	AAW65713 Fibronec
23	56	100.0	38	2	AAW65713 Fibronec
24	56	100.0	38	2	AAW65713 Fibronec
25	56	100.0	38	2	AAW65713 Fibronec

ALIGNMENTS

26	56	100.0	559	2	AAW69803	AAW69803 Staphyloc
27	56	100.0	767	4	AAU34403	AAU34403 Staphyloc
28	56	100.0	767	4	AAU37547	AAU37547 Staphyloc
29	56	100.0	940	2	AAW07070	AAW07070 Fibronec
30	56	100.0	940	6	ABU19111	ABU19111 Pathogen
31	56	100.0	948	6	ADA89470	ADA89470 Staphyloc
32	56	100.0	948	6	ABU18923	ABU18923 Pathogen
33	56	100.0	948	6	ABW72536	ABW72536 Staphyloc
34	56	100.0	961	6	ABU15854	ABU15854 Protein e
35	56	100.0	978	4	AAU33960	AAU33960 Staphyloc
36	56	100.0	1001	4	AAU37093	AAU37093 Staphyloc
37	56	100.0	1018	4	AAW62115	AAW62115 Fibronec
38	56	100.0	1018	4	AAU37245	AAU37245 Staphyloc
39	56	100.0	1018	4	AAU34301	AAU34301 Staphyloc
40	56	100.0	1018	6	ABU18922	ABU18922 Pathogen
41	56	100.0	1018	6	ABW72537	ABW72537 Staphyloc
42	56	100.0	1027	2	AAW69806	AAW69806 Staphyloc
43	56	100.0	1038	6	ABU15903	ABU15903 Protein e
44	52	92.9	30	4	AAW82164	AAW82164 Peptide f
45	52	92.9	30	7	ADC69221	ADC69221 Fibronec

RESULT 1
AAW65724 standard; peptide, 10 AA.

AAW65724:

16-OCT-1998 (first entry)

Fibronec binding protein-derived peptide #68.

microbial surface components recognising adhesive matrix molecule;

MSCRAM; fibronec; fibronec-binding protein; antibody; epitope;

antibiotic; bacterial infection; antibiotic-resistant strain.

Synthetic.

Staphylococcus aureus.

W09831389-A2.

21-JAN-1998; 98WO-US001222.

21-JAN-1997; 97US-0036139P.

(TEXA) UNIV TEXAS A & M SYSTEM.

Hoeok M, Patti JM, House-Pompeo KL, Speziale P, Joh D;

Mogavin MJ;

WPI; 1998-413816/35.

Antibody that binds to fibronec-binding protein, preventing its

binding to fibronec - used to treat or prevent bacterial infection,

especially by Staphylococci and Streptococci.

Example 9; Page 110; 20pp; English.

The invention relates to antibodies that bind to a fibronec-binding domain of a fibronec-binding protein, and inhibit binding of the protein to a fibronec. Also claimed are: (1) isolated peptides of a fibronec-binding protein that do not bind to fibronec; (2) fusion protein containing at least one peptide of a fibronec-binding protein linked to a second amino acid sequence; (3) nucleic acid encoding the isolated peptide of (1). Antibodies, the isolated peptides of (1) and the nucleic acids are all useful for immunisation (active or passive) and (by inhibiting binding of bacteria to fibronec) for preventing or treating infection in humans or other animals, particularly by staphylococci or

CC streptococci, e.g. meningitis, otitis media, pneumonia, endocarditis,
 CC mastitis in cattle, abortion in horses and many others. Since the
 CC antibodies block binding of bacteria, they should be effective against
 CC antibiotic-resistant strains, and may replace antibiotic therapy or
 CC increase its effectiveness. Sequences AAW65719-41 and AAW65658 represent
 CC peptides which were synthesised to span the D1 motif and the N-terminal
 CC 18 amino acids of D2, with each peptide overlapping by eight amino acids
 CC with the previous sequence

XX Sequence 10 AA;

Query Match 100.0%; Score 56; DB 2; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.012;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DTEEDKPKYE 10
 |||||
 DB 1 DTEEDKPKYE 10

RESULT 2
 ID AAW65761 standard; peptide; 14 AA.

AC AAW65761;
 XX
 XX 16-OCT-1998 (first entry)
 DT
 XX Peptide #105.
 DE
 XX microbial surface components recognising adhesive matrix molecule;
 KM MSCRAMM; fibronectin-binding protein; antibody; epitope;
 KM antibiotic; bacterial infection; antibiotic-resistant strain.
 XX
 OS Synthetic.
 OS Staphylococcus aureus.

XX
 XX WO9831389-A2.
 PN
 XX 23-JUL-1998.
 PD
 XX 21-JAN-1998; 98WO-US001222.
 PF
 XX 21-JAN-1997; 97US-0036139P.
 PR
 XX (TEXA) UNIV TEXAS A & M SYSTEM.
 PA
 XX Hoeoek M, Patli JM, House-Pompeo KL, Speziale P, Jol D;
 PI McGavin MJ;
 PI WPI; 1998-413816/35.

XX
 XX Antibody that binds to fibronectin-binding protein, preventing its
 PT binding to fibronectin - used to treat or prevent bacterial infection,
 PT especially by Staphylococci and Streptococci.
 PR
 XX Disclosure; Page 173; 201pp; English.

XX The invention relates to antibodies that bind to a fibronectin-binding
 CC domain of a fibronectin-binding protein, and inhibit binding of the
 CC protein to fibronectin. Also claimed are: (1) isolated peptides of a
 CC fibronectin-binding protein that do not bind to fibronectin; (2) fusion
 CC protein containing at least one peptide of a fibronectin-binding protein
 CC linked to a second amino acid sequence; (3) nucleic acid encoding the
 CC isolated peptide of (1). Antibodies, the isolated peptides of (1) and the
 CC nucleic acids are all useful for immunisation (active or passive) and (by
 CC inhibiting binding of bacteria to fibronectin) for preventing or treating
 CC infection in humans or other animals, particularly by staphylococci or
 CC streptococci, e.g. meningitis, otitis media, pneumonia, endocarditis,
 CC mastitis in cattle, abortion in horses and many others. Since the
 CC antibodies block binding of bacteria, they should be effective against
 CC antibiotic-resistant strains, and may replace antibiotic therapy or
 CC increase its effectiveness. The present sequence is shown in the

CC specification
 XX
 SQ Sequence 14 AA;

Query Match 100.0%; Score 56; DB 2; Length 14;
 Best Local Similarity 100.0%; Pred. No. 0.016;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DTEEDKPKYE 10
 |||||
 DB 5 DTEEDKPKYE 14

RESULT 3
 ID AAP80660 standard; protein; 38 AA.

AC AAP80660;
 XX
 XX 25-MAR-2003 (revised)
 DT 07-OCT-1990 (first entry)
 DT
 XX Protein with fibronectin binding ability.
 DE
 XX Hybrid DNA molecule; fibronectin binding; mastitis; ruminants;
 KM wound infection.
 KM
 XX Staphylococcus aureus.
 OS
 XX EP294349-A.
 PN
 XX 07-DEC-1988.
 PD
 XX 30-MAY-1988; 88EP-00850188.
 PF
 XX 01-JUN-1987; 87SE-00002272.
 PR
 XX (ALFA) ALFA LAVAL AGRIC INT AB.
 PA
 XX Lindberg MK, Signas LC, Wadstrom TM, Froman G;
 PI WPI; 1988-347978/49.
 DR
 XX N-PSDB; AAN81097.

XX
 XX Hybrid DNA encoding Staphylococcus aureus fibronectin binding protein -
 PT useful for immunisation and topical application to prevent staphylococcal
 PT infections.
 PT
 XX Claim 11; Page 12; 23pp; English.

XX The peptide has fibronectin binding ability. It is useful for immunising
 CC ruminants against staphylococcal mastitis, pref. when used at 0.5-5
 CC micrograms/kg, using 3 doses given at 1-3 week intervals; for topical
 CC application to prevent wound infection, using an isotonic saline soln. of
 CC concn. 25-250 micrograms/ml; and, when immobilised on a carrier, for
 CC diagnosing staphylococcal infections. (Updated on 25-MAR-2003 to correct
 CC PF field.) (Updated on 25-MAR-2003 to correct PA field.)

XX Sequence 38 AA;

Query Match 100.0%; Score 56; DB 1; Length 38;
 Best Local Similarity 100.0%; Pred. No. 0.044;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DTEEDKPKYE 10
 |||||
 DB 12 DTEEDKPKYE 21

RESULT 4
 ID AAP82116 standard; protein; 38 AA.

XX

AC AAP82116;
 XX
 XX 25-MAR-2003 (revised)
 DT 05-JAN-1990 (first entry)
 XX
 DE Fibronection binding protein.
 XX Fibronection binding protein; S.aureus; immunisation; mastitis; ruminants;
 KM wound infection; diagnosis.
 XX
 XX Staphylococcus aureus.
 OS
 XX EP294349-A.
 FN
 XX 07-DEC-1988.
 PD
 XX 30-MAY-1988; 88EP-00850188.
 PF
 XX 01-JUN-1987; 87SE-00002272.
 PR
 XX (ALFA) ALFA LAVAL AGRIC INT AB.
 PA
 XX Lindberg MK, Signas LC, Wedstrom TM, Froman G;
 PI
 XX MPI; 1988-347978/49.
 DR
 XX N-PSDB; AAN82054.
 DR
 XX Hybrid DNA encoding Staphylococcus aureus fibronection binding protein -
 PT useful for immunisation and topical application to prevent staphylococcal
 PT infections.
 PT
 XX Claim 11; Page 12; 23pp; English.
 PS
 XX The S.aureus fibronection binding protein may be included in a hybrid
 CC protein. The protein may be used to immunise ruminants against
 CC staphylococcal mastitis, pref. when given at 0.5-5 microg/kg, using 3
 CC doses at 1-3 week intervals; and for topical applicn. to prevent wound
 CC infection, pref. using isotonic saline soln. of concn. 25-250 microg/mg.
 CC The DNA encoding the binding protein and the hybrid protein may be
 CC immobilised on a carrier and used to diagnose staphylococcal infections.
 CC (updated on 25-MAR-2003 to correct PA field.)
 CC
 XX Sequence 38 AA;
 SQ
 QY
 DB 1 DTEEDKPKYE 10
 12 DTEEDKPKYE 21
 Query Match 100.0%; Score 56; DB 1; Length 38;
 Best Local Similarity 100.0%; Pred. No. 0.044;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 5
 AAW65692
 ID AAW65692 standard; peptide; 38 AA.
 AC
 XX AAW65692;
 AC
 XX 16-OCT-1998 (first entry)
 DT
 XX Fibronection binding protein-derived peptide #36.
 DE
 XX microbial surface components recognising adhesive matrix molecule;
 KM MSCRAMM; fibronection; fibronection-binding protein; antibody; epitope;
 KM antibiotic; bacterial infection; antibiotic-resistant strain.
 XX
 XX Synthetic.
 OS
 XX Staphylococcus aureus.
 OS
 XX WO9831389-A2.
 FN
 XX 23-JUL-1998.
 PD

XX
 PF 21-JAN-1998; 98WO-US001222.
 PR 21-JAN-1997; 97US-0036139P.
 XX
 XX (TEXA) UNIV TEXAS A & M SYSTEM.
 PA
 PI Hoeck M, Patli JM, House-Pompeo KL, Speciale P, Joh D;
 PI Mcgavin MJ;
 XX MPI; 1998-413816/35.
 DR
 XX Antibody that binds to fibronection-binding protein, preventing its
 PT binding to fibronection - used to treat or prevent bacterial infection,
 PT especially by Staphylococci and Streptococci.
 PT
 XX Example 8; Page 101; 201pp; English.
 PS
 XX The invention relates to antibodies that bind to a fibronection-binding
 CC domain of a fibronection-binding protein, and inhibit binding of the
 CC protein to fibronection. Also claimed are: (1) isolated peptides of a
 CC fibronection-binding protein that do not bind to fibronection; (2) fusion
 CC protein containing at least one peptide of a fibronection-binding protein
 CC linked to a second amino acid sequence; (3) nucleic acid encoding the
 CC isolated peptide of (1). Antibodies, the isolated peptides of (1) and (by
 CC nucleic acids are all useful for immunisation (active or passive) and (by
 CC inhibiting binding of bacteria to fibronection) for preventing or treating
 CC infection in humans or other animals, particularly by staphylococci or
 CC streptococci, e.g. meningitis, otitis media, pneumonia, endocarditis,
 CC mastitis in cattle, abortion in horses and many others. Since the
 CC antibodies block binding of bacteria, they should be effective against
 CC antibiotic-resistant strains, and may replace antibiotic therapy or
 CC increase its effectiveness. Sequences AAW65691-700 represent a series of
 CC synthetic peptides based on the DI region of S. aureus fibronection
 CC binding protein A. They were synthesised to contain mutations
 CC
 XX Sequence 38 AA;
 SQ
 QY
 DB 1 DTEEDKPKYE 10
 11 DTEEDKPKYE 20
 Query Match 100.0%; Score 56; DB 2; Length 38;
 Best Local Similarity 100.0%; Pred. No. 0.044;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 6
 AAW65662
 ID AAW65662 standard; peptide; 38 AA.
 AC
 XX AAW65662;
 AC
 XX 16-OCT-1998 (first entry)
 DT
 XX Fibronection binding protein-derived peptide #6.
 DE
 XX microbial surface components recognising adhesive matrix molecule;
 KM MSCRAMM; fibronection; fibronection-binding protein; antibody; epitope;
 KM antibiotic; bacterial infection; antibiotic-resistant strain.
 XX
 XX Synthetic.
 OS
 XX Staphylococcus aureus.
 OS
 XX WO9831389-A2.
 FN
 XX 23-JUL-1998.
 PD
 XX 21-JAN-1998; 98WO-US001222.
 PF
 XX 21-JAN-1997; 97US-0036139P.
 PR
 XX (TEXA) UNIV TEXAS A & M SYSTEM.
 PA


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XX
PI Hoeoek M, Patti JM, House-Pompeo KL, Speziale P, Joh L;
PI Mcgavin MJ;
XX
DR WPI; 1998-413816/35.
XX
PT Antibody that binds to fibronectin-binding protein, preventing its
PT binding to fibronectin - used to treat or prevent bacterial infection,
PT especially by Staphylococci and Streptococci.
XX
PS Example 2; Page 92; 201pp; English.
XX
CC The invention relates to antibodies that bind to a fibronectin-binding
CC domain of a fibronectin-binding protein, and inhibit binding of the
CC protein to fibronectin. Also claimed are: (1) isolated peptides of a
CC fibronectin-binding protein that do not bind to fibronectin; (2) fusion
CC protein containing at least one peptide of a fibronectin-binding protein
CC linked to a second amino acid sequence; (3) nucleic acid encoding the
CC isolated peptide of (1). Antibodies, the isolated peptides of (1) and the
CC nucleic acids are all useful for immunisation (active or passive) and (by
CC inhibiting binding of bacteria to fibronectin) for preventing or treating
CC infection in humans or other animals, particularly by staphylococci or
CC streptococci, e.g. meningitis, otitis media, pneumonia, endocarditis,
CC mastitis in cattle, abortion in horses and many others. Since the
CC antibodies block binding of bacteria, they should be effective against
CC antibiotic-resistant strains, and may replace antibiotic therapy or
CC increase its effectiveness. Sequences AAW65659-68 represent synthetic
CC epitopes from the fibronectin binding domains DU and DI-D4 of the S.
CC aureus fnbA gene
XX
SQ Sequence 38 AA;
XX
Query Match 100.0%; Score 56; DB 2; Length 38;
Best Local Similarity 100.0%; Pred. No. 0.044;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 DTEEDKPKYE 10
DB 11 DTEEDKPKYE 20
XX
RESULT 7
AAW65700
ID AAW65700 standard; peptide; 38 AA.
XX
AC AAW65700;
XX
DT 16-OCT-1998 (first entry)
XX
DE Fibronectin binding protein-derived peptide #44.
XX
KW microbial surface components recognising adhesive matrix molecule;
KW MSCRAMM; fibronectin; fibronectin-binding protein; antibody; epitope;
KW antibiotic; bacterial infection; antibiotic-resistant strain.
XX
OS Synthetic.
OS Staphylococcus aureus.
XX
PN WO9831389-A2.
XX
PD 23-JUL-1998.
XX
PF 21-JAN-1998; 98WO-US001222.
XX
PR 21-JAN-1997; 97US-0036139P.
XX
PA (TEXA ) UNIV TEXAS A & M SYSTEM.
XX
PI Hoeoek M, Patti JM, House-Pompeo KL, Speziale P, Joh D;
XX
PI Mcgavin MJ;
XX
DR WPI; 1998-413816/35.
XX

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PT Antibody that binds to fibronectin-binding protein, preventing its
PT binding to fibronectin - used to treat or prevent bacterial infection,
PT especially by Staphylococci and Streptococci.
XX
PS Example 8; Page 102; 201pp; English.
XX
CC The invention relates to antibodies that bind to a fibronectin-binding
CC domain of a fibronectin-binding protein, and inhibit binding of the
CC protein to fibronectin. Also claimed are: (1) isolated peptides of a
CC fibronectin-binding protein that do not bind to fibronectin; (2) fusion
CC protein containing at least one peptide of a fibronectin-binding protein
CC linked to a second amino acid sequence; (3) nucleic acid encoding the
CC isolated peptide of (1). Antibodies, the isolated peptides of (1) and the
CC nucleic acids are all useful for immunisation (active or passive) and (by
CC inhibiting binding of bacteria to fibronectin) for preventing or treating
CC infection in humans or other animals, particularly by staphylococci or
CC streptococci, e.g. meningitis, otitis media, pneumonia, endocarditis,
CC mastitis in cattle, abortion in horses and many others. Since the
CC antibodies block binding of bacteria, they should be effective against
CC antibiotic-resistant strains, and may replace antibiotic therapy or
CC increase its effectiveness. Sequences AAW65691-700 represent a series of
CC synthetic peptides based on the DI region of S. aureus fibronectin
CC binding protein A. They were synthesised to contain mutations
XX
SQ Sequence 38 AA;
XX
Query Match 100.0%; Score 56; DB 2; Length 38;
Best Local Similarity 100.0%; Pred. No. 0.044;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 DTEEDKPKYE 10
DB 11 DTEEDKPKYE 20
XX
RESULT 8
AAW65691
ID AAW65691 standard; peptide; 38 AA.
XX
AC AAW65691;
XX
DT 16-OCT-1998 (first entry)
XX
DE Fibronectin binding protein-derived peptide #35.
XX
KW microbial surface components recognising adhesive matrix molecule;
KW MSCRAMM; fibronectin; fibronectin-binding protein; antibody; epitope;
KW antibiotic; bacterial infection; antibiotic-resistant strain.
XX
OS Synthetic.
OS Staphylococcus aureus.
XX
PN WO9831389-A2.
XX
PD 23-JUL-1998.
XX
PF 21-JAN-1998; 98WO-US001222.
XX
PR 21-JAN-1997; 97US-0036139P.
XX
PA (TEXA ) UNIV TEXAS A & M SYSTEM.
XX
PI Hoeoek M, Patti JM, House-Pompeo KL, Speziale P, Joh D;
XX
PI Mcgavin MJ;
XX
DR WPI; 1998-413816/35.
XX
PT Antibody that binds to fibronectin-binding protein, preventing its
PT binding to fibronectin - used to treat or prevent bacterial infection,
PT especially by Staphylococci and Streptococci.
XX
PS Example 8; Page 101; 201pp; English.
XX

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CC The invention relates to antibodies that bind to a fibronectin-binding
 CC domain of a fibronectin-binding protein, and inhibit binding of the
 CC protein to fibronectin. Also claimed are: (1) isolated peptides of a
 CC fibronectin-binding protein that do not bind to fibronectin; (2) fusion
 CC protein containing at least one peptide of a fibronectin-binding protein
 CC linked to a second amino acid sequence; (3) nucleic acid encoding the
 CC isolated peptide of (1). Antibodies, the isolated peptides of (1) and the
 CC nucleic acids are all useful for immunisation (active or passive) and (by
 CC inhibiting binding of bacteria to fibronectin) for preventing or treating
 CC infection in humans or other animals, particularly by staphylococci or
 CC streptococci, e.g. meningitis, otitis media, pneumonia, endocarditis,
 CC mastitis in cattle, abortion in horses and many others. Since the
 CC antibodies block binding of bacteria, they should be effective against
 CC antibiotic-resistant strains, and may replace antibiotic therapy or
 CC increase its effectiveness. Sequences AAW65691-700 represent a series of
 CC synthetic peptides based on the D1 region of *S. aureus* fibronectin
 CC binding protein A. They were synthesised to contain mutations

XX Sequence 38 AA;

SO Query Match 100.0%; Score 56; DB 2; Length 38;
 Best Local Similarity 100.0%; Pred. No. 0.044;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DTEDKPKYE 10
 |||||
 DB 11 DTEDKPKYE 20

RESULT 9
 AAW65699
 ID AAW65699 standard; peptide; 38 AA.

XX AAW65699;
 DT 16-OCT-1998 (first entry)

XX Fibronectin binding protein-derived peptide #43.

XX microbial surface components recognising adhesive matrix molecule;
 KM MSCRAMM; fibronectin; fibronectin-binding protein; antibody; epitope;
 XX antibiotic; bacterial infection; antibiotic-resistant strain.

OS Synthetic.
 OS Staphylococcus aureus.

XX WO9831389-A2.

XX 23-JUL-1998.

XX 21-JAN-1998; 98WO-US001222.

XX 21-JAN-1997; 97US-0036139P.

XX (TEXA) UNIV TEXAS A & M SYSTEM.

XX Hoeek M, Patti JM, House-Pompeo KL, Speziale P, Joh D;
 PI McGavin MJ;

XX WPI; 1998-413816/35.

XX Antibody that binds to fibronectin-binding protein, preventing its
 PT binding to fibronectin - used to treat or prevent bacterial infection,
 PT especially by Staphylococci and Streptococci.

XX Example 8; Page 102; 201pp; English.

XX The invention relates to antibodies that bind to a fibronectin-binding
 CC domain of a fibronectin-binding protein, and inhibit binding of the
 CC protein to fibronectin. Also claimed are: (1) isolated peptides of a
 CC fibronectin-binding protein that do not bind to fibronectin; (2) fusion
 CC protein containing at least one peptide of a fibronectin-binding protein
 CC linked to a second amino acid sequence; (3) nucleic acid encoding the

CC isolated peptide of (1). Antibodies, the isolated peptides of (1) and the
 CC nucleic acids are all useful for immunisation (active or passive) and (by
 CC inhibiting binding of bacteria to fibronectin) for preventing or treating
 CC infection in humans or other animals, particularly by staphylococci or
 CC streptococci, e.g. meningitis, otitis media, pneumonia, endocarditis,
 CC mastitis in cattle, abortion in horses and many others. Since the
 CC antibodies block binding of bacteria, they should be effective against
 CC antibiotic-resistant strains, and may replace antibiotic therapy or
 CC increase its effectiveness. Sequences AAW65691-700 represent a series of
 CC synthetic peptides based on the D1 region of *S. aureus* fibronectin
 CC binding protein A. They were synthesised to contain mutations

XX Sequence 38 AA;

SO Query Match 100.0%; Score 56; DB 2; Length 38;
 Best Local Similarity 100.0%; Pred. No. 0.044;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DTEDKPKYE 10
 |||||
 DB 11 DTEDKPKYE 20

RESULT 10
 AAW65661
 ID AAW65661 standard; peptide; 38 AA.

XX AAW65661;

DT 16-OCT-1998 (first entry)

XX Fibronectin binding protein-derived peptide #5.

XX microbial surface components recognising adhesive matrix molecule;
 KM MSCRAMM; fibronectin; fibronectin-binding protein; antibody; epitope;
 XX antibiotic; bacterial infection; antibiotic-resistant strain.

OS Synthetic.
 OS Staphylococcus aureus.

XX WO9831389-A2.

XX 23-JUL-1998.

XX 21-JAN-1998; 98WO-US001222.

XX 21-JAN-1997; 97US-0036139P.

XX (TEXA) UNIV TEXAS A & M SYSTEM.

XX Hoeek M, Patti JM, House-Pompeo KL, Speziale P, Joh D;
 PI McGavin MJ;

XX WPI; 1998-413816/35.

XX Antibody that binds to fibronectin-binding protein, preventing its
 PT binding to fibronectin - used to treat or prevent bacterial infection,
 PT especially by Staphylococci and Streptococci.

XX Example 2; Page 92; 201pp; English.

XX The invention relates to antibodies that bind to a fibronectin-binding
 CC domain of a fibronectin-binding protein, and inhibit binding of the
 CC protein to fibronectin. Also claimed are: (1) isolated peptides of a
 CC fibronectin-binding protein that do not bind to fibronectin; (2) fusion
 CC protein containing at least one peptide of a fibronectin-binding protein
 CC linked to a second amino acid sequence; (3) nucleic acid encoding the
 CC isolated peptide of (1). Antibodies, the isolated peptides of (1) and the
 CC nucleic acids are all useful for immunisation (active or passive) and (by
 CC inhibiting binding of bacteria to fibronectin) for preventing or treating
 CC infection in humans or other animals, particularly by staphylococci or
 CC streptococci, e.g. meningitis, otitis media, pneumonia, endocarditis,
 CC mastitis in cattle, abortion in horses and many others. Since the

CC antibodies block binding of bacteria, they should be effective against
 CC antibiotic-resistant strains, and may replace antibiotic therapy or
 CC increase its effectiveness. Sequences AAM65693-68 represent synthetic
 CC epitopes from the fibronectin binding domains DU and DI-D4 of the S.
 CC aureus fmbA gene
 CC
 XX

SQ Sequence 38 AA;

Query Match 100.0%; Score 56; DB 2; Length 38;
 Best Local Similarity 100.0%; Pred. No. 0.044;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DTEEDKPKYE 10
 |||||
 11 DTEEDKPKYE 20

RESULT 11

ID AAM65693 standard; peptide; 38 AA.

XX AAM65693;

DT 16-OCT-1998 (first entry)

XX Fibronectin binding protein-derived peptide #37.

KW microbial surface components recognising adhesive matrix molecule;

KW MSCRAMM; fibronectin; fibronectin-binding protein; antibody; epitope;

KW antibiotic; bacterial infection; antibiotic-resistant strain.

XX Synthetic.

OS Staphylococcus aureus.

XX WO9831389-A2.

XX 23-JUL-1998.

XX 21-JAN-1998; 98WO-US001222.

XX 21-JAN-1997; 97US-0036139P.

XX (TEXA) UNIV TEXAS A & M SYSTEM.

PI Hoeoek M, Patti JM, House-Pompeo KL, Speziale P, Joh D;
 PI McGavin MJ;

XX WPI; 1998-413816/35.

PT Antibody that binds to fibronectin-binding protein, preventing its
 PT binding to fibronectin - used to treat or prevent bacterial infection,
 PT especially by Staphylococci and Streptococci.

XX Example 8; Page 102; 201pp; English.

CC The invention relates to antibodies that bind to a fibronectin-binding
 CC domain of a fibronectin-binding protein, and inhibit binding of the
 CC protein to fibronectin. Also claimed are: (1) isolated peptides of a
 CC fibronectin-binding protein that do not bind to fibronectin; (2) fusion
 CC protein containing at least one peptide of a fibronectin-binding protein
 CC linked to a second amino acid sequence; (3) nucleic acid encoding the
 CC isolated peptide of (1). Antibodies, the isolated peptides of (1) and the
 CC nucleic acids are all useful for immunisation (active or passive) and (by
 CC inhibiting binding of bacteria to fibronectin) for preventing or treating
 CC infection in humans or other animals, particularly by staphylococci or
 CC streptococci, e.g. meningitis, otitis media, pneumonia, endocarditis,
 CC mastitis in cattle, abortion in horses and many others. Since the
 CC antibodies block binding of bacteria, they should be effective against
 CC antibiotic-resistant strains, and may replace antibiotic therapy or
 CC increase its effectiveness. Sequences AAM65691-700 represent a series of
 CC synthetic peptides based on the DI region of S. aureus fibronectin
 CC binding protein A. They were synthesised to contain mutations

SQ Sequence 38 AA;

Query Match 100.0%; Score 56; DB 2; Length 38;
 Best Local Similarity 100.0%; Pred. No. 0.044;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DTEEDKPKYE 10
 |||||
 11 DTEEDKPKYE 20

RESULT 12

ID AAM65712 standard; peptide; 39 AA.

XX AAM65712;

DT 16-OCT-1998 (first entry)

XX Fibronectin binding protein-derived peptide #56.

KW microbial surface components recognising adhesive matrix molecule;

KW MSCRAMM; fibronectin; fibronectin-binding protein; antibody; epitope;

KW antibiotic; bacterial infection; antibiotic-resistant strain.

XX Synthetic.

OS Staphylococcus aureus.

XX WO9831389-A2.

XX 23-JUL-1998.

XX 21-JAN-1998; 98WO-US001222.

XX 21-JAN-1997; 97US-0036139P.

XX (TEXA) UNIV TEXAS A & M SYSTEM.

PI Hoeoek M, Patti JM, House-Pompeo KL, Speziale P, Joh D;
 PI McGavin MJ;

XX WPI; 1998-413816/35.

PT Antibody that binds to fibronectin-binding protein, preventing its
 PT binding to fibronectin - used to treat or prevent bacterial infection,
 PT especially by Staphylococci and Streptococci.

XX Example 8; Page 104; 201pp; English.

CC The invention relates to antibodies that bind to a fibronectin-binding
 CC domain of a fibronectin-binding protein, and inhibit binding of the
 CC protein to fibronectin. Also claimed are: (1) isolated peptides of a
 CC fibronectin-binding protein that do not bind to fibronectin; (2) fusion
 CC protein containing at least one peptide of a fibronectin-binding protein
 CC linked to a second amino acid sequence; (3) nucleic acid encoding the
 CC isolated peptide of (1). Antibodies, the isolated peptides of (1) and the
 CC nucleic acids are all useful for immunisation (active or passive) and (by
 CC inhibiting binding of bacteria to fibronectin) for preventing or treating
 CC infection in humans or other animals, particularly by staphylococci or
 CC streptococci, e.g. meningitis, otitis media, pneumonia, endocarditis,
 CC mastitis in cattle, abortion in horses and many others. Since the
 CC antibodies block binding of bacteria, they should be effective against
 CC antibiotic-resistant strains, and may replace antibiotic therapy or
 CC increase its effectiveness. The present sequence is shown in the
 CC specification

SQ Sequence 39 AA;

Query Match 100.0%; Score 56; DB 2; Length 39;
 Best Local Similarity 100.0%; Pred. No. 0.045;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DTEEDKPKYE 10

Db 11 DTEEDKPKYE 20

RESULT 13
ID AAM65713 standard; peptide; 39 AA.

XX AAM65713;
XX
DT 16-OCT-1998 (first entry)

DE Fibronectin binding protein-derived peptide #57.

XX microbial surface components recognising adhesive matrix molecule;
XX MSCRAMM; fibronectin; fibronectin-binding protein; antibody; epitope;
XX antibiotic; bacterial infection; antibiotic-resistant strain.

OS Synthetic.
OS Staphylococcus aureus.

XX MO981389-A2.

XX 23-JUL-1998.

XX 21-JAN-1998; 98MO-US001222.

XX 21-JAN-1997; 97US-0036139P.

XX (TEXA) UNIV TEXAS A & M SYSTEM.

XX Hoeek M; Patil JM, House-Pompeo KL, Speciale P, Joh D;
XX Mcgavin MJ;

XX WPI; 1998-413816/35.

XX Antibody that binds to fibronectin-binding protein, preventing its
PT binding to fibronectin - used to treat or prevent bacterial infection,
PT especially by Staphylococci and Streptococci.

XX Example 8; Page 104; 201pp; English.

XX The invention relates to antibodies that bind to a fibronectin-binding
CC domain of a fibronectin-binding protein, and inhibit binding of the
CC protein to fibronectin. Also claimed are: (1) isolated peptides of a
CC fibronectin-binding protein that do not bind to fibronectin; (2) fusion
CC protein containing at least one peptide of a fibronectin-binding protein
CC linked to a second amino acid sequence; (3) nucleic acid encoding the
CC isolated peptide of (1). Antibodies, the isolated peptides of (1) and the
CC nucleic acids are all useful for immunisation (active or passive) and (by
CC inhibiting binding of bacteria to fibronectin) for preventing or treating
CC infection in humans or other animals, particularly by staphylococci or
CC streptococci, e.g. meningitis, otitis media, pneumonia, endocarditis,
CC mastitis in cattle, abortion in horses and many others. Since the
CC antibodies in block binding of bacteria, they should be effective against
CC antibiotic-resistant strains, and may replace antibiotic therapy or
CC increase its effectiveness. The present sequence is shown in the
CC specification

XX Sequence 39 AA;

Query Match 100.0%; Score 56; DB 2; Length 39;

Best Local Similarity 100.0%; Pred. No. 0.045;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 DTEEDKPKYE 10
DB 11 DTEEDKPKYE 20

RESULT 14
AAR58806
ID AAR58806 standard; protein; 130 AA.

XX AAR58806;

XX 25-MAR-2003 (revised)
DT 30-MAR-1995 (first entry)

DE Fibronectin binding domain D1-D4 (709-838 (P838T)).

XX Fibronectin binding protein; Fbp; fibronectin binding domain;
XX monoclonal antibody; Mab; adhesion; Gram-positive bacterium; bacteraemia;
XX Escherichia coli.

XX Staphylococcus aureus.

XX MO9418327-A1.

XX 18-AUG-1994.

XX 04-FEB-1994; 94MO-GB000215.

XX 05-FEB-1993; 93GB-00002289.

XX 20-OCT-1993; 93GB-00021592.

XX (SMIK) SMITHKLINE BEECHAM PLC.

XX Burnham MKR, Chopra I, Critchley IA, Knowles DJC;

XX WPI; 1994-279748/34.

XX Fibronectin binding protein and monoclonal antibodies specific for Fbp -
PT useful to prevent adherence of Gram-positive bacteria to indwelling
PT devices or wounds.

XX Disclosure; Page 30; 40pp; English.

XX Polypeptides corresponding to residues G709-T886 plus PPIVPT, G709-
CC P838(P838T) and G709-P838 (AAR58805-07, respectively) of S. aureus J2385
CC (NCIMB 40532) Fbp type A fibronectin binding domain D1-D4 region
CC (AAR58808) were expressed in E. coli B21 (DB4) and used to raise MAbs
CC specific for Fbp. (Updated on 25-MAR-2003 to correct PN field.)

XX Sequence 130 AA;

Query Match 100.0%; Score 56; DB 2; Length 130;
Best Local Similarity 100.0%; Pred. No. 0.15;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 DTEEDKPKYE 10
DB 12 DTEEDKPKYE 21

RESULT 15

ID AAR58807 standard; protein; 130 AA.

XX AAR58807;

XX 25-MAR-2003 (revised)
DT 30-MAR-1995 (first entry)

DE Fibronectin binding domain D1-D4 (709-838).

XX Fibronectin binding protein; Fbp; fibronectin binding domain;
XX monoclonal antibody; Mab; adhesion; Gram-positive bacterium; bacteraemia;
XX Escherichia coli.

XX Staphylococcus aureus.

XX MO9418327-A1.

XX 18-AUG-1994.

PF 04-FEB-1994; 94WO-GB000215.
 XX
 PR 05-FEB-1993; 93GB-00002289.
 PR 20-OCT-1993; 93GB-00021592.
 XX
 PA (SMIK) SMITHKLINE BEECHAM PLC.
 XX
 PI Burnham MKR, Chopra I, Critchley IA, Knowles DJC;
 XX
 DR WPI; 1994-279748/34.
 XX
 PT Fibronectin binding protein and monoclonal antibodies specific for Fbp -
 PT useful to prevent adherence of Gram-positive bacteria to intwelling
 PT devices or wounds.
 XX
 PS Disclosure; Page 30; 40pp; English.
 XX
 CC Polypeptides corresponding to residues G709-T886 plus PPIVPT, G709-
 CC P838(P838T) and G709-P838 (AAR58805-07, respectively) of S. aureus J2385
 CC (NCIMB 40532) Fbp type A fibronectin binding domain D1-D4 region
 CC (AAR58808) were expressed in E. coli BL21(DE4) and used to raise MAb
 CC specific for Fbp. (Updated on 25-MAR-2003 to correct PN field.)
 XX
 SQ Sequence 130 AA;

Query Match 100.0%; Score 56; DB 2; Length 130;
 Best Local Similarity 100.0%; Pred. NO. 0.15; 0; Indels 0; Gaps 0;
 Matches 10; Conservative 0; Mismatches 0;

QY 1 DTEDDKPKYE 10
 |||||
 Db 12 DTEDDKPKYE 21

Search completed: October 25, 2005, 20:58:42
 Job time : 64.2 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 22, 2005, 05:46:56 ; Search time 17.3 Seconds
(without alignments)
43.150 Million cell updates/sec

Title: US-10-731-238-68

Sequence: 1 DTEBDKPKYE 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*

- 1: /cgn2_6/prodata/1/iaa/5A_COMB.pep:*
- 2: /cgn2_6/prodata/1/iaa/5B_COMB.pep:*
- 3: /cgn2_6/prodata/1/iaa/6A_COMB.pep:*
- 4: /cgn2_6/prodata/1/iaa/6B_COMB.pep:*
- 5: /cgn2_6/prodata/1/iaa/PC/TUS_COMB.pep:*
- 6: /cgn2_6/prodata/1/iaa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	56	100.0	10	4	US-09-010-317-68
2	56	100.0	14	4	US-09-010-317-105
3	56	100.0	38	1	US-08-234-622A-2
4	56	100.0	38	1	US-08-729-767-3
5	56	100.0	38	4	US-09-010-317-5
6	56	100.0	38	4	US-09-010-317-6
7	56	100.0	38	4	US-09-010-317-35
8	56	100.0	38	4	US-09-010-317-36
9	56	100.0	38	4	US-09-010-317-37
10	56	100.0	38	4	US-09-010-317-43
11	56	100.0	38	4	US-09-010-317-44
12	56	100.0	39	4	US-09-010-317-56
13	56	100.0	39	4	US-09-010-317-57
14	56	100.0	114	1	US-08-259-000-3
15	56	100.0	130	2	US-08-459-135A-7
16	56	100.0	130	2	US-08-459-135A-8
17	56	100.0	130	3	US-08-495-559-7
18	56	100.0	130	3	US-08-495-559-8
19	56	100.0	139	3	US-08-856-253-8
20	56	100.0	174	2	US-08-459-135A-10
21	56	100.0	174	2	US-08-459-135A-13
22	56	100.0	174	3	US-08-495-559-10
23	56	100.0	174	3	US-08-495-559-13
24	56	100.0	176	3	US-08-495-559-6
25	56	100.0	178	3	US-08-459-135A-12
26	56	100.0	178	3	US-08-495-559-12
27	56	100.0	181	2	US-08-459-135A-6

ALIGNMENTS

28	56	100.0	559	4	US-08-956-171E-5251	Sequence 5251, Ap
29	56	100.0	559	4	US-08-781-986A-5251	Sequence 5251, Ap
30	56	100.0	1027	4	US-08-956-171E-5254	Sequence 5254, Ap
31	56	100.0	1027	4	US-08-781-986A-5254	Sequence 5254, Ap
32	52	92.9	38	1	US-08-234-622A-3	Sequence 3, Appl1
33	52	92.9	38	1	US-08-729-767-4	Sequence 4, Appl1
34	52	92.9	38	4	US-09-010-317-7	Sequence 7, Appl1
35	52	92.9	38	4	US-09-010-317-8	Sequence 8, Appl1
36	52	92.9	38	4	US-09-010-317-45	Sequence 45, Appl1
37	52	92.9	38	4	US-09-010-317-46	Sequence 46, Appl1
38	52	92.9	38	4	US-09-010-317-47	Sequence 47, Appl1
39	52	92.9	38	4	US-09-010-317-49	Sequence 49, Appl1
40	52	92.9	38	4	US-09-010-317-50	Sequence 50, Appl1
41	50	89.3	38	4	US-09-010-317-38	Sequence 38, Appl1
42	50	89.3	38	4	US-09-010-317-39	Sequence 39, Appl1
43	50	89.3	38	4	US-09-010-317-40	Sequence 40, Appl1
44	50	89.3	38	4	US-09-010-317-41	Sequence 41, Appl1
45	49	87.5	38	4	US-09-010-317-42	Sequence 42, Appl1

RESULT 1
US-09-010-317-68
Sequence 68, Application US/09010317
Patent No. 6685943
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
APPLICANT: Patti, Joseph M.
APPLICANT: House-Pompeo, Karen L.
APPLICANT: Speciale, Pietro
APPLICANT: John, Danny
APPLICANT: McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
TITLE OF INVENTION: AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSER: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAMK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 68:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: Linear
US-09-010-317-68
Query Match 100.0%; Score 56; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0024;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DTEBDKPKYE 10
|||||

Db 1 DTEBDKPKYE 10

RESULT 2

US-09-010-317-105

/ Sequence 105, Application US/09010317
/ Patent No. 6685943

/ GENERAL INFORMATION:

/ APPLICANT: Hook, Magnus

/ APPLICANT: Patti, Joseph M.

/ APPLICANT: House-Pompeo, Karen L.

/ APPLICANT: Speziale, Pietro

/ APPLICANT: McGavin, Martin J.

/ TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS

/ NUMBER OF SEQUENCES: 105

/ CORRESPONDENCE ADDRESS:

/ ADDRESSEE: Arnold, White & Durkee

/ STREET: P.O. Box 4433

/ CITY: Houston

/ STATE: TX USA

/ COUNTRY: USA

/ ZIP: 77210-4433

/ COMPUTER READABLE FORM:

/ MEDIUM TYPE: Floppy disk

/ COMPUTER: IBM PC compatible

/ OPERATING SYSTEM: PC-DOS/MS-DOS

/ SOFTWARE: Patentin Release #1.0, Version #1.30

/ CURRENT APPLICATION DATA:

/ APPLICATION NUMBER: US/09/010,317

/ FILING DATE:

/ CLASSIFICATION:

/ PRIOR APPLICATION DATA:

/ APPLICATION NUMBER: US 60/036,139

/ FILING DATE: 21-JAN-1997

/ ATTORNEY/AGENT INFORMATION:

/ NAME: Hibler, David W.

/ REGISTRATION NUMBER: 41,071

/ TELECOMMUNICATION INFORMATION:

/ TELEPHONE: 512-418-3000

/ TELEFAX: 512-474-7577

/ INFORMATION FOR SEQ ID NO: 105:

/ SEQUENCE CHARACTERISTICS:

/ LENGTH: 14 amino acids

/ TYPE: amino acid

/ STRANDEDNESS:

/ TOPOLOGY: linear

/ US-09-010-317-105

QY 1 DTEBDKPKYE 10
|||||

Db 5 DTEBDKPKYE 14

RESULT 3

US-08-234-622A-2

/ Sequence 2, Application US/08234622A

/ Patent No. 5440014

/ GENERAL INFORMATION:

/ APPLICANT: HOOK, Magnus

/ APPLICANT: MCGAVIN, Martin

/ APPLICANT: RAUCCI, Giuseppe

/ TITLE OF INVENTION: A FIBRONECTIN BINDING PEPTIDE

/ NUMBER OF SEQUENCES: 4

/ CORRESPONDENCE ADDRESS:

/ ADDRESSEE: Burns, Doane, Swecker & Mathis

/ STREET: P.O. Box 1404

/ CITY: Alexandria

/ STATE: Virginia

/ COUNTRY: United States

/ ZIP: 22313-1404

/ COMPUTER READABLE FORM:

/ MEDIUM TYPE: Floppy disk

/ COMPUTER: IBM PC compatible

/ OPERATING SYSTEM: PC-DOS/MS-DOS

/ SOFTWARE: Patentin Release #1.0, Version #1.30

/ CURRENT APPLICATION DATA:

/ APPLICATION NUMBER: US/08/234,622A

/ FILING DATE: 28-APR-1994

/ CLASSIFICATION: 530

/ PRIOR APPLICATION DATA:

/ APPLICATION NUMBER: SE 9002617-0

/ FILING DATE: 10-AUG-1990

/ PRIOR APPLICATION DATA:

/ APPLICATION NUMBER: WO PCT/SE91/00534

/ FILING DATE: 09-AUG-1991

/ ATTORNEY/AGENT INFORMATION:

/ NAME: Meuth, Donna M

/ REGISTRATION NUMBER: 36,607

/ TELECOMMUNICATION INFORMATION:

/ TELEPHONE: (703) 836-6620

/ TELEFAX: (703) 836-2021

/ INFORMATION FOR SEQ ID NO: 2:

/ SEQUENCE CHARACTERISTICS:

/ LENGTH: 38 amino acids

/ TYPE: amino acid

/ STRANDEDNESS: single

/ TOPOLOGY: linear

/ MOLECULE TYPE: peptide

/ US-08-234-622A-2

QY 1 DTEBDKPKYE 10
|||||

Db 11 DTEBDKPKYE 20

RESULT 4

US-08-729-767-3

/ Sequence 3, Application US/08729767

/ Patent No. 5770702

/ GENERAL INFORMATION:

/ APPLICANT: HOOK, Magnus

/ APPLICANT: LINDBERG, Martin Kjell

/ APPLICANT: SIGNAS, Lars Christer

/ APPLICANT: MADSTROM, Torkel Mikael

/ APPLICANT: FROMAN, Gunnar

/ TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN AS WELL AS

/ NUMBER OF SEQUENCES: 6

/ CORRESPONDENCE ADDRESS:

/ ADDRESSEE: Burns, Doane, Swecker & Mathis, L.L.P.

/ STREET: P.O. Box 1404

/ CITY: Alexandria

/ STATE: Virginia

/ COUNTRY: United States

/ ZIP: 22313-1404

/ COMPUTER READABLE FORM:

/ MEDIUM TYPE: Floppy disk

/ COMPUTER: IBM PC compatible

/ OPERATING SYSTEM: PC-DOS/MS-DOS

/ SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/729,767
FILING DATE: 07-OCT-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/259,000
FILING DATE: 13-JUN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/007,817
FILING DATE: 22-JAN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/201,028
FILING DATE: 01-JUN-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: SE 8702272-9
FILING DATE: 01-JUN-1987
ATTORNEY/AGENT INFORMATION:
NAME: McGowan, Malcolm K.
REGISTRATION NUMBER: 39,300
REFERENCE/DOCKET NUMBER: 012889-036
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ. ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-729-767-3

Query Match 100.0%; Score 56; DB 1; Length 38;
Best local Similarity 100.0%; Pred. No. 0.0091;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DTEDPKPYE 10
|||||
Db 12 DTEDPKPYE 21

RESULT 5
US-09-010-317-5
Sequence 5, Application US/09010317
Patent No. 6685943
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
APPLICANT: Patti, Joseph M.
APPLICANT: House-Pompeo, Karen L.
APPLICANT: Speziale, Pietro
APPLICANT: Joh, Danny
APPLICANT: McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
TITLE OF INVENTION: AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: PC-DOS/MS-DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/036,139

FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TANK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ. ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-09-010-317-5

Query Match 100.0%; Score 56; DB 4; Length 38;
Best local Similarity 100.0%; Pred. No. 0.0091;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DTEDPKPYE 10
|||||
Db 11 DTEDPKPYE 20

RESULT 6
US-09-010-317-6
Sequence 6, Application US/09010317
Patent No. 6685943
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
APPLICANT: Patti, Joseph M.
APPLICANT: House-Pompeo, Karen L.
APPLICANT: Speziale, Pietro
APPLICANT: Joh, Danny
APPLICANT: McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
TITLE OF INVENTION: AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: PC-DOS/MS-DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TANK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ. ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-09-010-317-6

Query Match 100.0%; Score 56; DB 4; Length 38;
Best Local Similarity 100.0%; Pred. No. 0.0091;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DTEEDPKPYE 10
| | | | | | | | | |
DB 11 DTEEDPKPYE 20

RESULT 7
US-09-010-317-35
; Sequence 35, Application US/09010317
; Patent No. 6685943

; GENERAL INFORMATION:
; APPLICANT: Hook, Magnus
; APPLICANT: Patti, Joseph M.
; APPLICANT: House-Pompeo, Karen L.
; APPLICANT: Speziale, Pietro
; APPLICANT: Job, Danny
; APPLICANT: McGavin, Martin J.
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
; TITLE OF INVENTION: AND METHODS OF USE
; NUMBER OF SEQUENCES: 105
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: TX
; COUNTRY: USA
; ZIP: 77210-4433
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/010,317
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/036,139
; FILING DATE: 21-JAN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Hibler, David W.
; REGISTRATION NUMBER: 41,071
; REFERENCE/DOCKET NUMBER: TANK:189
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 512-418-3000
; TELEFAX: 512-474-7577
; INFORMATION FOR SEQ. ID NO: 35:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 38 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
US-09-010-317-35

Query Match 100.0%; Score 56; DB 4; Length 38;
Best Local Similarity 100.0%; Pred. No. 0.0091;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DTEEDPKPYE 10
| | | | | | | | | |
DB 11 DTEEDPKPYE 20

RESULT 8
US-09-010-317-36
; Sequence 36, Application US/09010317
; Patent No. 6685943

; GENERAL INFORMATION:
; APPLICANT: Hook, Magnus
; APPLICANT: Patti, Joseph M.

; APPLICANT: House-Pompeo, Karen L.
; APPLICANT: Speziale, Pietro
; APPLICANT: Job, Danny
; APPLICANT: McGavin, Martin J.
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
; TITLE OF INVENTION: AND METHODS OF USE
; NUMBER OF SEQUENCES: 105
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: TX
; COUNTRY: USA
; ZIP: 77210-4433

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/010,317
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/036,139
; FILING DATE: 21-JAN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Hibler, David W.
; REGISTRATION NUMBER: 41,071
; REFERENCE/DOCKET NUMBER: TANK:189
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 512-418-3000
; TELEFAX: 512-474-7577
; INFORMATION FOR SEQ. ID NO: 36:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 38 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
US-09-010-317-36

Query Match 100.0%; Score 56; DB 4; Length 38;
Best Local Similarity 100.0%; Pred. No. 0.0091;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DTEEDPKPYE 10
| | | | | | | | | |
DB 11 DTEEDPKPYE 20

RESULT 9
US-09-010-317-37
; Sequence 37, Application US/09010317
; Patent No. 6685943

; GENERAL INFORMATION:
; APPLICANT: Hook, Magnus
; APPLICANT: Patti, Joseph M.
; APPLICANT: House-Pompeo, Karen L.
; APPLICANT: Speziale, Pietro
; APPLICANT: Job, Danny
; APPLICANT: McGavin, Martin J.
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
; TITLE OF INVENTION: AND METHODS OF USE
; NUMBER OF SEQUENCES: 105
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: TX
; COUNTRY: USA
; ZIP: 77210-4433
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAMK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 37:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-09-010-317-37
Query Match 100.0%; Score 56; DB 4; Length 38;
Best local Similarity 100.0%; Pred. No. 0.0091;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 DTEEDKPKYE 10
Db 11 DTEEDKPKYE 20
RESULT 10
US-09-010-317-43
Sequence 43, Application US/09010317
Patent No. 6685943
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
APPLICANT: Patti, Joseph M.
APPLICANT: House-Pompeo, Karen L.
APPLICANT: Speziale, Pietro
APPLICANT: Joh, Danny
APPLICANT: McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
TITLE OF INVENTION: AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAMK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000

TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 43:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-09-010-317-43
Query Match 100.0%; Score 56; DB 4; Length 38;
Best local Similarity 100.0%; Pred. No. 0.0091;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 DTEEDKPKYE 10
Db 11 DTEEDKPKYE 20
RESULT 11
US-09-010-317-44
Sequence 44, Application US/09010317
Patent No. 6685943
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
APPLICANT: Patti, Joseph M.
APPLICANT: House-Pompeo, Karen L.
APPLICANT: Speziale, Pietro
APPLICANT: Joh, Danny
APPLICANT: McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
TITLE OF INVENTION: AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAMK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 44:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-09-010-317-44
Query Match 100.0%; Score 56; DB 4; Length 38;
Best local Similarity 100.0%; Pred. No. 0.0091;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 DTEEDKPKYE 10
Db 11 DTEEDKPKYE 20

RESULT 12
US-09-010-817-56
; Sequence 56, Application US/09010317
; Patent No. 6685943
; GENERAL INFORMATION:
; APPLICANT: Hook, Magnus
; APPLICANT: Patti, Joseph M.
; APPLICANT: House-Pompeo, Karen L.
; APPLICANT: Speziale, Pietro
; APPLICANT: McGavin, Martin J.
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
; TITLE OF INVENTION: AND METHODS OF USE
; NUMBER OF SEQUENCES: 105
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: TX
; COUNTRY: USA
; ZIP: 77210-4433
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/010,317
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/036,139
; FILING DATE: 21-JAN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Hibler, David W.
; REGISTRATION NUMBER: 41,071
; REFERENCE/DOCKET NUMBER: TANK:189
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 512-418-3000
; TELEFAX: 512-474-7577
; INFORMATION FOR SEQ ID NO: 56:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 39 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
US-09-010-317-56
Query Match 100.0%; Score 56; DB 4; Length 39;
Best Local Similarity 100.0%; Pred. No. 0.0094;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 DTEEDKPKYE 10
Db 11 DTEEDKPKYE 20
RESULT 13
US-09-010-317-57
; Sequence 57, Application US/09010317
; Patent No. 6685943
; GENERAL INFORMATION:
; APPLICANT: Hook, Magnus
; APPLICANT: Patti, Joseph M.
; APPLICANT: House-Pompeo, Karen L.
; APPLICANT: Speziale, Pietro
; APPLICANT: McGavin, Martin J.
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
; TITLE OF INVENTION: AND METHODS OF USE
; NUMBER OF SEQUENCES: 105

; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: TX
; COUNTRY: USA
; ZIP: 77210-4433
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/010,317
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/036,139
; FILING DATE: 21-JAN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Hibler, David W.
; REGISTRATION NUMBER: 41,071
; REFERENCE/DOCKET NUMBER: TANK:189
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 512-418-3000
; TELEFAX: 512-474-7577
; INFORMATION FOR SEQ ID NO: 57:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 39 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
US-09-010-317-57
Query Match 100.0%; Score 56; DB 4; Length 39;
Best Local Similarity 100.0%; Pred. No. 0.0094;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 DTEEDKPKYE 10
Db 11 DTEEDKPKYE 20
RESULT 14
US-08-259-000-3
; Sequence 3, Application US/08259000
; Patent No. 5571514
; GENERAL INFORMATION:
; APPLICANT: HOOK, Magnus
; APPLICANT: LINDBERG, Martin Kjell
; APPLICANT: SIGNAS, Lars Christer
; APPLICANT: WADSTROM, Torkel Mikael
; APPLICANT: FROMAN, Gunnar
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN AS WELL AS
; TITLE OF INVENTION: ITS PREPARATION
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Doane, Swecker & Mathis
; STREET: P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/259,000
; FILING DATE: 13-JUN-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:

APPLICATION NUMBER: SE 8702272-9
FILING DATE: 01-JUN-1987
ATTORNEY/AGENT INFORMATION:
NAME: Meuth, Donna M
REGISTRATION NUMBER: 36,607
REFERENCE/DOCKET NUMBER: 012885-062
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 114 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-259-000-3

Query Match 100.0%; Score 56; DB 1; Length 114;
Best Local Similarity 100.0%; Pred. No. 0.028;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DTEDDKPKYE 10
Db 12 DTEDDKPKYE 21

RESULT 15

US-08-459-135A-7
Sequence 7, Application US/08459135A
Patent No. 5955078
GENERAL INFORMATION:
APPLICANT: BURHAM, Martin Karl Russel
APPLICANT: CHOPRA, Ian
APPLICANT: CRITCHLEY, Ian Alfred
APPLICANT: KNOWLES, David Justin Charles
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN: MONOCLONAL ANTIBODY AND THEIR US
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESSES:
ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
STATE: PA
COUNTRY: U.S.A.
ZIP: 19406-0939
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: Fastseq, Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/459,135A
FILING DATE: 02-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB/94/00215
FILING DATE: 04-Feb-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Gimmil, Edward R
REGISTRATION NUMBER: 38,891
REFERENCE/DOCKET NUMBER: P30591C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-4478
TELEFAX: 610-270-5090
TELEX:
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 130 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-459-135A-7

Query Match 100.0%; Score 56; DB 2; Length 130;
Best Local Similarity 100.0%; Pred. No. 0.032;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DTEDDKPKYE 10
Db 12 DTEDDKPKYE 21

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Job time : 17.35 secs

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OM protein - protein search, using sw model

Run on: October 22, 2005, 12:09:40 ; Search time 57.25 Seconds
(without alignments)
72.924 Million cell updates/sec

Title: US-10-731-238-68

Perfect score: 56
Sequence: 1 DTEEDPKYKE 10

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Gapop 10.0 , Gapext 0.5

Searched: 1862951 seqs, 417491010 residues

Total number of hits satisfying chosen parameters: 1862951

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA:*

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22: /cgn2_6/prodata/2/pubppaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	56	100.0	10	US-10-731-238-68	Sequence 68, Appl1
2	56	100.0	14	US-10-731-238-105	Sequence 105, Appl1
3	56	100.0	38	US-10-731-238-5	Sequence 5, Appl1
4	56	100.0	38	US-10-731-238-6	Sequence 6, Appl1
5	56	100.0	38	US-10-731-238-35	Sequence 35, Appl1
6	56	100.0	38	US-10-731-238-36	Sequence 36, Appl1
7	56	100.0	38	US-10-731-238-37	Sequence 37, Appl1
8	56	100.0	38	US-10-731-238-43	Sequence 43, Appl1
9	56	100.0	38	US-10-731-238-44	Sequence 44, Appl1
10	56	100.0	39	US-10-731-238-56	Sequence 56, Appl1
11	56	100.0	39	US-10-731-238-57	Sequence 57, Appl1

12 56 100.0 139 9 US-09-813-820-8 Sequence 8, Appl1
13 56 100.0 388 8 US-08-901-062-1 Sequence 1, Appl1
14 56 100.0 559 8 US-08-781-986A-5251 Sequence 5251, Ap
15 56 100.0 559 15 US-10-329-624-5251 Sequence 5251, Ap
16 56 100.0 767 9 US-09-815-242-5899 Sequence 5899, Ap
17 56 100.0 767 9 US-09-815-242-13140 Sequence 13140, A
18 56 100.0 940 17 US-10-470-048B-424 Sequence 424, App
19 56 100.0 948 17 US-10-470-048B-69 Sequence 43778, A
20 56 100.0 961 15 US-10-287-122A-43778 Sequence 43778, A
21 56 100.0 978 9 US-09-815-242-5456 Sequence 5456, Ap
22 56 100.0 1001 9 US-09-815-242-14686 Sequence 12686, A
23 56 100.0 1018 9 US-09-815-242-5797 Sequence 5797, Ap
24 56 100.0 1018 9 US-09-815-242-12838 Sequence 12838, A
25 56 100.0 1018 17 US-10-470-048B-68 Sequence 68, Appl1
26 56 100.0 1027 8 US-08-781-986A-5254 Sequence 5254, Ap
27 56 100.0 1027 15 US-10-329-624-5254 Sequence 5254, Ap
28 56 100.0 1038 15 US-10-287-122A-43827 Sequence 43827, A
29 52 92.9 30 14 US-10-287-821-1 Sequence 1, Appl1
30 52 92.9 31 14 US-10-287-821-2 Sequence 2, Appl1
31 52 92.9 38 18 US-10-731-238-7 Sequence 7, Appl1
32 52 92.9 38 18 US-10-731-238-6 Sequence 8, Appl1
33 52 92.9 38 18 US-10-731-238-45 Sequence 45, Appl1
34 52 92.9 38 18 US-10-731-238-46 Sequence 46, Appl1
35 52 92.9 38 18 US-10-731-238-47 Sequence 47, Appl1
36 52 92.9 38 18 US-10-731-238-49 Sequence 49, Appl1
37 52 92.9 38 18 US-10-731-238-50 Sequence 50, Appl1
38 50 89.3 38 18 US-10-731-238-38 Sequence 38, Appl1
39 50 89.3 38 18 US-10-731-238-39 Sequence 39, Appl1
40 50 89.3 38 18 US-10-731-238-40 Sequence 40, Appl1
41 50 89.3 38 18 US-10-731-238-41 Sequence 41, Appl1
42 46 87.5 38 18 US-10-731-238-42 Sequence 42, Appl1
43 46 82.1 38 18 US-10-731-238-48 Sequence 48, Appl1
44 45 80.4 10 18 US-10-731-238-69 Sequence 69, Appl1
45 44 78.6 10 18 US-10-731-238-67 Sequence 67, Appl1

ALIGNMENTS

RESULT 1
US-10-731-238-68
; Sequence 68, Application US/10713238
; Publication No. US20050123552A1
; GENERAL INFORMATION:
; APPLICANT: Hook, Magnus
; Patti, Joseph M.
; House-Pompeo, Karen L.
; Speziale, Pietro
; Job, Danny
; McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/731,238
FILING DATE: 10-Dec-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE: 21-Jan-1998
APPLICATION NUMBER: US 60/036,139

```

; FILING DATE: 21-JAN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Hibler, David W.
; REGISTRATION NUMBER: 41,071
; REFERENCE/DOCKET NUMBER: TAMK:189
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 512-418-3000
; TELEFAX: 512-474-7577
; INFORMATION FOR SEQ ID NO: 68:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 68:
US-10-731-238-68

Query Match      100.0%; Score 56; DB 18; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.007;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 DTEEDKPKYE 10
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Db      1 DTEEDKPKYE 10

RESULT 2
US-10-731-238-105
; Sequence 105, Application US/10731238
; Publication No. US20050123552A1
; GENERAL INFORMATION:
; APPLICANT: Hook, Magnus
;          Patti, Joseph M.
;          House-Pompeo, Karen L.
;          Speziale, Pietro
;          John, Danny
;          McGavin, Martin J.
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
; AND METHODS OF USE
; NUMBER OF SEQUENCES: 105
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: TX
; COUNTRY: USA
; ZIP: 77210-4433
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/731,238
; FILING DATE: 10-Dec-2003
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/010,317
; FILING DATE: 21-Jan-1998
; APPLICATION NUMBER: US 60/036,139
; FILING DATE: 21-JAN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Hibler, David W.
; REGISTRATION NUMBER: 41,071
; REFERENCE/DOCKET NUMBER: TAMK:189
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 512-418-3000
; TELEFAX: 512-474-7577
; INFORMATION FOR SEQ ID NO: 105:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>

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; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 105:
US-10-731-238-105

Query Match      100.0%; Score 56; DB 18; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.01;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 DTEEDKPKYE 10
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Db      5 DTEEDKPKYE 14

RESULT 3
US-10-731-238-5
; Sequence 5, Application US/10731238
; Publication No. US20050123552A1
; GENERAL INFORMATION:
; APPLICANT: Hook, Magnus
;          Patti, Joseph M.
;          House-Pompeo, Karen L.
;          Speziale, Pietro
;          John, Danny
;          McGavin, Martin J.
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
; AND METHODS OF USE
; NUMBER OF SEQUENCES: 105
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: TX
; COUNTRY: USA
; ZIP: 77210-4433
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/731,238
; FILING DATE: 10-Dec-2003
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/010,317
; FILING DATE: 21-Jan-1998
; APPLICATION NUMBER: US 60/036,139
; FILING DATE: 21-JAN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Hibler, David W.
; REGISTRATION NUMBER: 41,071
; REFERENCE/DOCKET NUMBER: TAMK:189
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 512-418-3000
; TELEFAX: 512-474-7577
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 38 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-10-731-238-5

Query Match      100.0%; Score 56; DB 18; Length 38;
Best Local Similarity 100.0%; Pred. No. 0.028;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 DTEEDKPKYE 10
        |||||
Db      11 DTEEDKPKYE 20

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RESULT 4
US-10-731-238-6
; Sequence 6, Application US/10731238
; Publication No. US20050123552A1
; GENERAL INFORMATION:
; APPLICANT: Hook, Magnus
; Patti, Joseph M.
; House-Pompeo, Karen L.
; Speziale, Pietro
; John, Danny
; McGavin, Martin J.
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
; AND METHODS OF USE
; NUMBER OF SEQUENCES: 105
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: TX
; COUNTRY: USA
; ZIP: 77210-4433
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/731,238
; FILING DATE: 10-Dec-2003
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/010,317
; FILING DATE: 21-Jan-1998
; APPLICATION NUMBER: US 60/036,139
; FILING DATE: 21-JAN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Hibler, David W.
; REGISTRATION NUMBER: 41,071
; REFERENCE/DOCKET NUMBER: TAMK:189
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 512-418-3000
; TELEFAX: 512-474-7577
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 38 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-10-731-238-6
Query Match 100.0%; Score 56; DB 18; Length 38;
Best Local Similarity 100.0%; Pred. No. 0.028;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 DTEEDKPKYE 10
| | | | | | | | | |
| | | | | | | | | |
Db 11 DTEEDKPKYE 20
RESULT 5
US-10-731-238-35
; Sequence 35, Application US/10731238
; Publication No. US20050123552A1
; GENERAL INFORMATION:
; APPLICANT: Hook, Magnus
; Patti, Joseph M.
; House-Pompeo, Karen L.
; Speziale, Pietro
; John, Danny
; McGavin, Martin J.
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
; AND METHODS OF USE

NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/731,238
FILING DATE: 10-Dec-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE: 21-Jan-1998
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAMK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 35:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 35:
US-10-731-238-35
Query Match 100.0%; Score 56; DB 18; Length 38;
Best Local Similarity 100.0%; Pred. No. 0.028;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 DTEEDKPKYE 10
| | | | | | | | | |
| | | | | | | | | |
Db 11 DTEEDKPKYE 20
RESULT 6
US-10-731-238-36
; Sequence 36, Application US/10731238
; Publication No. US20050123552A1
; GENERAL INFORMATION:
; APPLICANT: Hook, Magnus
; Patti, Joseph M.
; House-Pompeo, Karen L.
; Speziale, Pietro
; John, Danny
; McGavin, Martin J.
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
; AND METHODS OF USE
; NUMBER OF SEQUENCES: 105
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: TX
; COUNTRY: USA
; ZIP: 77210-4433
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30


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;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/731,238
; FILING DATE: 10-Dec-2003
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/010,317
; FILING DATE: 21-Jan-1998
; APPLICATION NUMBER: US 60/036,139
; FILING DATE: 21-Jan-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Hibler, David W.
; REGISTRATION NUMBER: 41,071
; REFERENCE/DOCKET NUMBER: TAMK:189
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 512-418-3000
; TELEFAX: 512-474-7577
; INFORMATION FOR SEQ ID NO: 36:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 38 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 36:
US-10-731-238-36

Query Match      100.0%; Score 56; DB 18; Length 38;
Best Local Similarity 100.0%; Pred. No. 0.028;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 DTEEDKPKYE 10
        |||||
        11 DTEEDKPKYE 20

Db

RESULT 7
US-10-731-238-37
; Sequence 37, Application US/10731238
; Publication No. US20050123552A1
; GENERAL INFORMATION:
; APPLICANT: Hook, Magnus
;          Patti, Joseph M.
;          House-Pompeo, Karen L.
;          Speziale, Pietro
;          Joh, Danny
;          McGavin, Martin J.
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
; NUMBER OF SEQUENCES: 105
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: TX
; COUNTRY: USA
; ZIP: 77210-4433
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/731,238
; FILING DATE: 10-Dec-2003
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/010,317
; FILING DATE: 21-Jan-1998
; APPLICATION NUMBER: US 60/036,139
; FILING DATE: 21-Jan-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Hibler, David W.
; REGISTRATION NUMBER: 41,071
; REFERENCE/DOCKET NUMBER: TAMK:189
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 512-418-3000
; TELEFAX: 512-474-7577
; INFORMATION FOR SEQ ID NO: 37:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 38 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 37:
US-10-731-238-37

Query Match      100.0%; Score 56; DB 18; Length 38;
Best Local Similarity 100.0%; Pred. No. 0.028;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 DTEEDKPKYE 10
        |||||
        11 DTEEDKPKYE 20

Db

RESULT 8
US-10-731-238-43
; Sequence 43, Application US/10731238
; Publication No. US20050123552A1
; GENERAL INFORMATION:
; APPLICANT: Hook, Magnus
;          Patti, Joseph M.
;          House-Pompeo, Karen L.
;          Speziale, Pietro
;          Joh, Danny
;          McGavin, Martin J.
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
; NUMBER OF SEQUENCES: 105
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: TX
; COUNTRY: USA
; ZIP: 77210-4433
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/731,238
; FILING DATE: 10-Dec-2003
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/010,317
; FILING DATE: 21-Jan-1998
; APPLICATION NUMBER: US 60/036,139
; FILING DATE: 21-Jan-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Hibler, David W.
; REGISTRATION NUMBER: 41,071
; REFERENCE/DOCKET NUMBER: TAMK:189
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 512-418-3000
; TELEFAX: 512-474-7577
; INFORMATION FOR SEQ ID NO: 43:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 38 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 43:
US-10-731-238-43

Query Match      100.0%; Score 56; DB 18; Length 38;
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```

;
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 512-418-3000
; TELEFAX: 512-474-7577
; INFORMATION FOR SEQ ID NO: 37:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 38 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 37:
US-10-731-238-37

Query Match      100.0%; Score 56; DB 18; Length 38;
Best Local Similarity 100.0%; Pred. No. 0.028;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 DTEEDKPKYE 10
        |||||
        11 DTEEDKPKYE 20

Db

RESULT 8
US-10-731-238-43
; Sequence 43, Application US/10731238
; Publication No. US20050123552A1
; GENERAL INFORMATION:
; APPLICANT: Hook, Magnus
;          Patti, Joseph M.
;          House-Pompeo, Karen L.
;          Speziale, Pietro
;          Joh, Danny
;          McGavin, Martin J.
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
; NUMBER OF SEQUENCES: 105
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: TX
; COUNTRY: USA
; ZIP: 77210-4433
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/731,238
; FILING DATE: 10-Dec-2003
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/010,317
; FILING DATE: 21-Jan-1998
; APPLICATION NUMBER: US 60/036,139
; FILING DATE: 21-Jan-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Hibler, David W.
; REGISTRATION NUMBER: 41,071
; REFERENCE/DOCKET NUMBER: TAMK:189
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 512-418-3000
; TELEFAX: 512-474-7577
; INFORMATION FOR SEQ ID NO: 43:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 38 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 43:
US-10-731-238-43

Query Match      100.0%; Score 56; DB 18; Length 38;
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Best Local Similarity 100.0%; Pred. No. 0.028;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DTEEDKPKYE 10
Db 11 DTEEDKPKYE 20

RESULT 9

US-10-731-238-44

; Sequence 44; Application US/10731238

; Publication No. US20050123552A1

; GENERAL INFORMATION:

APPLICANT: Hook, Magnus

Pattl, Joseph M.

House-Pompeo, Karen L.

Speziale, Pietro

Joh, Danny

McGavin, Martin J.

TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS

AND METHODS OF USE

NUMBER OF SEQUENCES: 105

CORRESPONDENCE ADDRESS:

ADDRESSEE: Arnold, White & Durkee

STREET: P.O. Box 4433

CITY: Houston

STATE: TX

COUNTRY: USA

ZIP: 77210-4433

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/731,238

FILING DATE: 10-Dec-2003

CLASSIFICATION: <Unknown>

PRIORITY APPLICATION DATA:

APPLICATION NUMBER: US/09/010,317

FILING DATE: 21-Jan-1998

APPLICATION NUMBER: US 60/036,139

FILING DATE: 21-JAN-1997

ATTORNEY/AGENT INFORMATION:

NAME: Hibler, David W.

REGISTRATION NUMBER: 41,071

REFERENCE/DOCKET NUMBER: TAMK:189

TELECOMMUNICATION INFORMATION:

TELEPHONE: 512-418-3000

TELEFAX: 512-474-7577

INFORMATION FOR SEQ ID NO: 44:

SEQUENCE CHARACTERISTICS:

LENGTH: 38 amino acids

TYPE: amino acid

STRANDEDNESS: <Unknown>

TOPOLOGY: linear

SEQUENCE DESCRIPTION: SEQ ID NO: 44:

US-10-731-238-44

Query Match 100.0%; Score 56; DB 18; Length 38;

Best Local Similarity 100.0%; Pred. No. 0.028;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DTEEDKPKYE 10
Db 11 DTEEDKPKYE 20

RESULT 10

US-10-731-238-56

; Sequence 56; Application US/10731238

; Publication No. US20050123552A1

; GENERAL INFORMATION:

APPLICANT: Hook, Magnus

Pattl, Joseph M.

House-Pompeo, Karen L.

Speziale, Pietro

Joh, Danny

McGavin, Martin J.

TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS

AND METHODS OF USE

NUMBER OF SEQUENCES: 105

CORRESPONDENCE ADDRESS:

ADDRESSEE: Arnold, White & Durkee

STREET: P.O. Box 4433

CITY: Houston

STATE: TX

COUNTRY: USA

ZIP: 77210-4433

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/731,238

FILING DATE: 10-Dec-2003

CLASSIFICATION: <Unknown>

PRIORITY APPLICATION DATA:

APPLICATION NUMBER: US/09/010,317

FILING DATE: 21-Jan-1998

APPLICATION NUMBER: US 60/036,139

FILING DATE: 21-JAN-1997

ATTORNEY/AGENT INFORMATION:

NAME: Hibler, David W.

REGISTRATION NUMBER: 41,071

REFERENCE/DOCKET NUMBER: TAMK:189

TELECOMMUNICATION INFORMATION:

TELEPHONE: 512-418-3000

TELEFAX: 512-474-7577

INFORMATION FOR SEQ ID NO: 56:

SEQUENCE CHARACTERISTICS:

LENGTH: 39 amino acids

TYPE: amino acid

STRANDEDNESS: <Unknown>

TOPOLOGY: linear

SEQUENCE DESCRIPTION: SEQ ID NO: 56:

US-10-731-238-56

Query Match 100.0%; Score 56; DB 18; Length 39;

Best Local Similarity 100.0%; Pred. No. 0.029;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DTEEDKPKYE 10
Db 11 DTEEDKPKYE 20

RESULT 11

US-10-731-238-57

; Sequence 57; Application US/10731238

; Publication No. US20050123552A1

; GENERAL INFORMATION:

APPLICANT: Hook, Magnus

Pattl, Joseph M.

House-Pompeo, Karen L.

Speziale, Pietro

Joh, Danny

McGavin, Martin J.

TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS

AND METHODS OF USE

NUMBER OF SEQUENCES: 105

CORRESPONDENCE ADDRESS:

ADDRESSEE: Arnold, White & Durkee

STREET: P.O. Box 4433

CITY: Houston

STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/731,238
FILING DATE: 10-Dec-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE: 21-Jan-1998
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAMK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 57:
SEQUENCE CHARACTERISTICS:
LENGTH: 39 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 57:
US-10-731-238-57
Query Match 100.0%; Score 56; DB 18; Length 39;
Best Local Similarity 100.0%; Pred. No. 0.029;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 DTEBDKPKYE 10
DB 11 DTEBDKPKYE 20
RESULT 12
US-09-813-820-8
Sequence 8, Application US/09813820
Patent No. US20020102262A1
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
Pacti, Joseph M.
House-Pompeo, Karen
Sthanam, Narayana
Symersky, Jindrich
TITLE OF INVENTION: COLLAGEN BINDING PROTEIN COMPOSITIONS
AND METHODS OF USE
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: Texas
COUNTRY: U.S.
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/813,820
FILING DATE: 22-Mar-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/856,253

FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Kitchell, Barbara S.
REGISTRATION NUMBER: 33,928
REFERENCE/DOCKET NUMBER: TAMK:193
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
TELEFAX: (512) 474-7577
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 139 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-09-813-820-8
Query Match 100.0%; Score 56; DB 9; Length 139;
Best Local Similarity 100.0%; Pred. No. 0.11;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 DTEBDKPKYE 10
DB 26 DTEBDKPKYE 35

RESULT 13
US-08-901-062-1
Sequence 1, Application US/08901062
Publication No. US20020025324A1
GENERAL INFORMATION:
APPLICANT: SEALS, JONATHAN R.
TITLE OF INVENTION: RECOMBINANT BIVALENT BACTERIAL VACCINE
FOR THE PREVENTION OF MASTITIS
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: HALE AND DORR LLP
STREET: 60 State Street
CITY: Boston
STATE: MA
COUNTRY: United States Of America
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/901,062
FILING DATE: 25-JUL-1997
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Baker, Hollie L.
REGISTRATION NUMBER: 31,321
REFERENCE/DOCKET NUMBER: 106941.153
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 526-6000
TELEFAX: (617) 526-5000
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 388 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-901-062-1

Query Match 100.0%; Score 56; DB 8; Length 388;
Best Local Similarity 100.0%; Pred. No. 0.31;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DTEEDKPKYE 10
|||||
DB 275 DTEEDKPKYE 284

RESULT 14

US-08-781-986A-5251
; Sequence 5251, Application US/08781986A
; Publication No. US20030054436A1
; GENERAL INFORMATION:
; APPLICANT: Charles Kunsch
; TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
; NUMBER OF SEQUENCES: 5255
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4MB storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/781,986A
; FILING DATE:
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Benson, Bob
; REGISTRATION NUMBER: 30,446
; REFERENCE/DOCKET NUMBER: PB248PP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 5251:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 559 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-781-986A-5251

Query Match 100.0%; Score 56; DB 8; Length 559;
Best Local Similarity 100.0%; Pred. No. 0.45;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 DTEEDKPKYE 10
|||||
DB 311 DTEEDKPKYE 320

RESULT 15

US-10-329-624-5251
; Sequence 5251, Application US/10329624
; Publication No. US20040043037A1
; GENERAL INFORMATION:
; APPLICANT: Charles Kunsch
; GIL H. Choi
; Patrick S. Dillon
; Craig A. Rosen
; Steven C. Barash
; Michael R. Fannon
; TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
; NUMBER OF SEQUENCES: 5256
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue

CITY: Rockville
STATE: Maryland
COUNTRY: USA
ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4MB storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/329,624
; FILING DATE: 27-Dec-2002
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: 08/956,171
; FILING DATE: October 20, 1997
; APPLICATION NUMBER: 60/009,861
; FILING DATE: January 5, 1996
; APPLICATION NUMBER: 08/781,986
; FILING DATE: January 3, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Mark J. Hyman
; REGISTRATION NUMBER: 46,789
; REFERENCE/DOCKET NUMBER: PB248P1D1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (240) 314-1224
; TELEFAX: (301) 309-8439
; INFORMATION FOR SEQ ID NO: 5251:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 559 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 5251:
US-10-329-624-5251

Query Match 100.0%; Score 56; DB 15; Length 559;
Best Local Similarity 100.0%; Pred. No. 0.45;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 DTEEDKPKYE 10
|||||
DB 311 DTEEDKPKYE 320

Search completed: October 22, 2005, 12:39:43
Job time : 57.25 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 22, 2005, 06:10:10 ; Search time 11.45 Seconds
(without alignments)
84.032 Million cell updates/sec

Title: US-10-731-238-68

Perfect score: 56

Sequence: 1 DTEEDKPKYE 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	56	100.0	940	2 S19702	fibronectin-binding
2	56	100.0	961	2 G90053	hypothetical prote
3	56	100.0	1018	2 A32192	fibronectin-binding
4	56	100.0	1038	2 H90053	hypothetical prote
5	42	75.0	448	2 S39348	26S ATP/ubiquitin-
6	41	73.2	2957	2 T33152	hypothetical prote
7	40	71.4	890	2 S44150	coat protein - str
8	38	67.9	193	2 S44791	superoxide dismuta
9	37	66.1	601	2 T04777	hypothetical prote
10	36.5	65.2	700	2 T24092	hypothetical prote
11	36.5	65.2	783	2 F88808	protein R09510.3
12	36	64.3	217	2 B96557	unknown protein, 8
13	36	64.3	471	2 T48743	probable 26S ATP/u
14	36	64.3	517	1 A39038	l-caldesmon, nonmu
15	36	64.3	526	2 T21811	hypothetical prote
16	36	64.3	595	2 T52152	probable membrane
17	36	64.3	702	2 T20019	hypothetical prote
18	36	64.3	771	1 A33430	h-caldesmon - chic
19	35	62.5	240	2 T25191	hypothetical prote
20	35	62.5	241	2 T25799	hypothetical prote
21	35	62.5	275	2 C99858	conserved hypotet
22	35	62.5	339	1 N0BPCP	N-acetylmutamoyl-L
23	35	62.5	388	2 B87600	carbamoyl-phosphat
24	35	62.5	407	2 S27794	hypothetical flagella
25	35	62.5	419	2 G75062	probable flagella
26	35	62.5	548	2 T27542	hypothetical prote
27	35	62.5	554	2 T25437	hypothetical prote
28	35	62.5	615	2 A53069	cold-shock dead-bo
29	35	62.5	615	2 F98217	inducible ATP-inde

30	35	62.5	627	2 T04562	hypothetical prote
31	35	62.5	638	2 F70444	threonine-CRNA lig
32	35	62.5	640	2 G72339	threonine-CRNA lig
33	35	62.5	712	2 T25438	hypothetical prote
34	35	62.5	843	2 S44868	kinesin heavy chain
35	35	62.5	1009	2 T47327	hypothetical prote
36	35	62.5	1192	2 A71623	probable secreted
37	34	60.7	99	2 J00038	nonhistone chromos
38	34	60.7	136	2 D71030	hypothetical prote
39	34	60.7	185	2 T26703	hypothetical prote
40	34	60.7	216	2 F96657	hypothetical prote
41	34	60.7	229	2 E90195	conserved hypotet
42	34	60.7	240	2 B84606	probable ATP synth
43	34	60.7	271	2 T04665	hypothetical prote
44	34	60.7	273	2 C08429	protein cel-43 (lm
45	34	60.7	274	2 T04619	hypothetical prote

ALIGNMENTS

RESULT 1

S19702

fibronectin-binding protein B - Staphylococcus aureus

C:Species: Staphylococcus aureus

C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004

C:Accession: S19702

R:Joensuu, K.; Signaes, C.; Mueller, H.P.; Lindberg, M.

Bur. J. Biochem. 202, 1041-1048, 1991

A:Title: Two different genes encode fibronectin binding proteins in Staphylococcus aure

A:Reference number: S19702, PMID:92111475, PMID:1837266

A:Accession: S19702

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-940 <JOE>

A:Cross-references: UNIPROT:O53682; EMBL:X62992; NID:949040; PIDN:CAA44726.1; PID:95815

C:Keywords: fibronectin binding

Query Match

Best Local Similarity 100.0%; Score 56; DB 2; Length 940;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 692 DTEEDKPKYE 701

QY 1 DTEEDKPKYE 10

|||||

Db 692 DTEEDKPKYE 701

QY 1 DTEEDKPKYE 10

|||||

Db 692 DTEEDKPKYE 701

QY 1 DTEEDKPKYE 10

|||||

Db 692 DTEEDKPKYE 701

QY 1 DTEEDKPKYE 10

RESULT 2

hypothetical protein fnbB (imported) - Staphylococcus aureus (strain N315)

C:Species: Staphylococcus aureus

C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004

C:Accession: G90053

R:Kuroda, M.; Ohba, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Ogu

ma, A.; Mutantani, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.

C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.

Lancet 357, 1225-1240, 2001

A:Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.

A:Reference number: A89758; PMID:21311952; PMID:11418146

A:Accession: G90053

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-961 <KUR>

A:Cross-references: UNIPROT:Q99RD3; GB:BA000018; PID:G13702452; PIDN:BA043593.1; GSPDB:

A:Experimental source: strain N315

C:Genetics:

A:Gene: fnbB

Query Match

Best Local Similarity 100.0%; Score 56; DB 2; Length 961;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 DTEEDKPKYE 10

QY 1 DTEEDKPKYE 10

|||||

Db 1 DTEEDKPKYE 10

QY 1 DTEEDKPKYE 10

|||||

Db 1 DTEEDKPKYE 10

QY 1 DTEEDKPKYE 10

|||||

Db 1 DTEEDKPKYE 10

|||||
Db 703 DTEEDKPKYE 712

RESULT 3

A32192
C:Species: Staphylococcus aureus
C:Date: 31-Jul-1989 #sequence_revision 31-Jul-1989 #text_change 16-Feb-1997
A:Accession: A32192
R:Signaee: C.; Raucel, G.; Jonsson, K.; Lindgren, P.E.; Anantharamaiah, G.M.; Hoecek, W
Proc. Natl. Acad. Sci. U.S.A. 86, 699-703, 1989
A:Title: Nucleotide sequence of the gene for a fibronectin-binding protein from Staphylo
A:Reference number: A32192; PMID:8908998; PMID:2521391
A:Accession: A32192
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1018 <SIG>
A:Cross-references: GB:J04151
C:Keywords: fibronectin binding

Query Match 100.0%; Score 56; DB 2; Length 1013;
Best Local Similarity 100.0%; Pred. No. 0.055;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DTEEDKPKYE 10
|||||
Db 756 DTEEDKPKYE 765

RESULT 4

H90053
hypothetical protein fnb (imported) - Staphylococcus aureus (strain N315)
C:Species: Staphylococcus aureus
C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
A:Accession: H90053
R:Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguc
ma, A.; Mizutani-Ul, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Iatco, C.; Sekimizu, K.;
C.; Shiba, T.; Hatton, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
A:Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.
A:Reference number: A89758; PMID:21311952; PMID:11418146
A:Accession: H90053
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1038 <KUR>
A:Cross-references: UNIPROT:Q99RD2; GB:BA000018; PID:g13702453; PIDN:BAB3594.1; GSPDB:G
A:Experimental source: strain N315
C:Genetics:
A:Gene: fnb

Query Match 100.0%; Score 56; DB 2; Length 1038;
Best Local Similarity 100.0%; Pred. No. 0.057;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DTEEDKPKYE 10
|||||
Db 752 DTEEDKPKYE 761

RESULT 5

S39348
266 ATP/ubiquitin-dependent proteinase chain S4 - fission yeast Schizosaccharomyces pom
C:Species: Schizosaccharomyces pombe
C:Date: 18-Feb-1994 #sequence_revision 23-Feb-1996 #text_change (9-Jul-2004
A:Accession: S39348; T40421
R:Gordon, C.; McGurk, G.; Dillon, P.; Rosen, C.; Hastie, N.D.
Nature 366, 355-357, 1993
A:Title: Defective mitosis due to a mutation in the gene for a fission yeast 26S protease
A:Reference number: S39348; PMID:94067321; PMID:8247731
A:Accession: S39348
A:Status: nucleic acid sequence not shown
A:Molecule type: DNA

A:Residues: 1-448 <GOR>
A:Cross-references: UNIPROT:P36612; EMBL:Z29366; NID:G442507; PIDN:CAA82554.1; PID:G4425
R:McDougal, R.C.; Rajandream, M.A.; Bartell, B.G.; Brown, S.; Hartle, D.
submitted to the EMBL Data Library, October 1999
A:Reference number: Z21927
A:Accession: T40421
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-448 <MCD>
A:Cross-references: EMBL:AL121863; PIDN:CA58406.1; GSPDB:GN00067; SPDB:SPBC4.07C
A:Experimental source: strain 972h-; cosmid c4
C:Genetics:
A:Gene: SPBC4.07C
A:Map position: 2
A:Introns: 1/3

C:Superfamily: ATP-dependent 26S proteinase; FtsH/SEC18/CDC48-type ATP-binding domain ho
C:Keywords: ATP; nucleotide binding; nucleus; P-loop
F:205-416/Domain: FtsH/SEC18/CDC48-type ATP-binding domain homology <VATP>
F:232-239/Region: nucleotide-binding motif A (P-loop)

Query Match 75.0%; Score 42; DB 2; Length 448;
Best Local Similarity 70.0%; Pred. No. 7.9;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 DTEEDKPKYE 10
|:|||||
Db 23 DQKDKPKYE 32

RESULT 6

T33152
hypothetical protein T04D1.4 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
A:Accession: T33152
R:Davidson, S.; Woldmann, P.
submitted to the EMBL Data Library, May 1998
A:Description: The sequence of C. elegans cosmid T04D1.
A:Reference number: Z21292
A:Accession: T33152
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-2957 <DAV>
A:Cross-references: UNIPROT:O61845; EMBL:AF067617; PIDN:AA17559.1; GSPDB:GN00019; CESP
C:Genetics:
A:Gene: CESP.T04D1.4
A:Map position: 1
A:Introns: 122/3; 293/3; 515/3; 1205/2; 1577/1; 2221/3; 2776/1; 2864/3

Query Match 73.2%; Score 41; DB 2; Length 2957;
Best Local Similarity 87.5%; Pred. No. 89;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 EEDKPKYE 10
|||||
Db 673 EEDKPKYE 680

RESULT 7

S44150
coat protein - strawberry latent ringspot virus
C:Species: strawberry latent ringspot virus
C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
A:Accession: S44150
R:Kreiah, S.; Strunk, G.; Cooper, J.I.
submitted to the EMBL Data Library, February 1994
A:Description: Sequence analysis and location of capsid proteins within RNA-2 of strawbe
A:Reference number: S44150
A:Accession: S44150
A:Status: preliminary
A:Molecule type: genomic RNA
A:Residues: 1-890 <KRE>

A:Cross-references: UNIPROT:Q88171; EMBL:X77466
C:Superfamily: strawberry latent ringspot virus coat protein

Query Match 71.4%; Score 40; DB 2; Length 890;
Best Local Similarity 66.7%; Pred. No. 38;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 DTEEDKPKY 9
DB 11 DTDEEPRKY 19

RESULT 8
A44791

superoxide dismutase (EC 1.15.1.1) (Fe/Mn) - Coxiiella burnetii

C:Species: Coxiiella burnetii
C>Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 09-Jul-2004

C:Accession: A44791; S12141
R:Heinzen, R.A.; Frazier, M.E.; Mallavia, L.P.

Infect. Immun. 60, 3814-3823, 1992

A:Title: Coxiiella burnetii superoxide dismutase gene: cloning, sequencing, and expression

A:Reference number: A44791; MUID:92363582; PMID:1500190

A:Accession: A44791

A:Molecule type: DNA

A:Residues: 1-193 <HEI1>

A:Cross-references: UNIPROT:P19685; GB:M74242; NID:g145001; PIDN:AAA23311.1; PID:g145002

A:Note: sequence extracted from NCBI backbone (NCBIN:111011, NCBIP:111012)

Nucleic Acids Res. 18, 6437, 1990

A:Title: Nucleotide sequence of Coxiiella burnetii superoxide dismutase.

A:Reference number: S12141; MUID:91057143; PMID:2243797

A:Accession: S12141

A:Molecule type: DNA

A:Residues: 1-193 <HEI2>

A:Cross-references: EMBL:X54627; NID:g40405; PIDN:CAA38444.1; PID:g40406

C:Function:

A:Description: catalyzes the dismutation of 2 molecules of peroxide radical to dioxygen

C:Superfamily: superoxide dismutase (Mn)

C:Keywords: iron; manganese; metalloprotein; oxidoreductase

F:27,74,157,161/Binding site: iron/manganese (His, His, Asp, His) #status predicted

Query Match 67.9%; Score 38; DB 2; Length 193;
Best Local Similarity 66.7%; Pred. No. 17;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 DTEEDKPKY 9
DB 166 DTNRDRPKY 174

RESULT 9
T04747

hypothetical protein T16H5.20 - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)

C>Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004

C:Accession: T04747

R:Bayan, M.; De Haan, M.; Maarse, A.C.; Grievell, L.A.; Bancroft, I.; Mewes, H.W.; Mayer,

submitted to the Protein Sequence Database, June 1998

A:Reference number: Z15383

A:Accession: T04747

A:Molecule type: DNA

A:Residues: 1-601 <BEV>

A:Cross-references: UNIPROT:O81848; EMBL:AL024486

A:Experimental source: cultivar Columbia; BAC clone T16H5

C:Genetics:

A:Map position: 4

A:Introns: 173/3; 420/1

Query Match 66.1%; Score 37; DB 2; Length 601;
Best Local Similarity 60.0%; Pred. No. 87;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 DTEEDKPKY 10
DB 90 DSSEKKPKY 99

RESULT 10
T24092

hypothetical protein R09E10.3 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004

C:Accession: T24092

R:Mathews, L.

submitted to the EMBL Data Library, March 1996

A:Reference number: Z19839

A:Accession: T24092

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-700 <WIL>

A:Cross-references: UNIPROT:Q21872; EMBL:Z70287; PIDN:CAA94298.2; GSPDB:GN00022; CESP:R

A:Experimental source: clone R09E10

C:Genetics:

A:Gene: CESP:R09E10.3

A:Map position: 4

A:Introns: 29/3; 87/3; 153/3; 202/1; 329/2; 395/2; 598/3; 646/3

C:Superfamily: human long-chain-fatty-acid-CoA ligase; acetate-CoA ligase homology

F:337-675/Domain: acetate-CoA ligase homology <ACLT>

Query Match 65.2%; Score 36.5; DB 2; Length 700;
Best Local Similarity 80.0%; Pred. No. 1.3e+02;
Matches 8; Conservative 1; Mismatches 0; Indels 1; Gaps 1;

QY 2 TEEDK-PKYE 10
DB 636 TEEDKPRYE 645

RESULT 11
F88808

protein R09E10.3 (imported) - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C>Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004

C:Accession: F88808

R:Anonymous, The C. elegans Sequencing Consortium.

Science 282, 2012-2018, 1998

A:Title: Genome sequence of the nematode C. elegans: a platform for investigating biolo

A:Reference number: A75000; MUID:99069613; PMID:9851916

A:Note: see websites genome.wustl.edu/gsc/C.elegans/ and www.sanger.ac.uk/Projects/C.e

A:Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; an

A:Accession: F88808

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-783 <STO>

A:Cross-references: UNIPROT:Q21872; GB:chr_IV; PIDN:CAA94298.1; PID:g3879082; GSPDB:GN0

C:Genetics:

A:Gene: R09E10.3

A:Map position: 4

C:Superfamily: human long-chain-fatty-acid-CoA ligase; acetate-CoA ligase homology

Query Match 65.2%; Score 36.5; DB 2; Length 783;
Best Local Similarity 80.0%; Pred. No. 1.4e+02;
Matches 8; Conservative 1; Mismatches 0; Indels 1; Gaps 1;

QY 2 TEEDK-PKYE 10
DB 719 TEEDKPRYE 728

RESULT 12
E96657

unknown protein, 83062-84229 (imported) - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)

C>Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004

C:Accession: E96657

R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewart, K.; Hansen, N.F.; Hughes, B.; Hitzar, L.
Nature 408, 816-820, 2000
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, E.; Khaykin, E.; Kim, C.C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Lueros, J.S.; Maiti, R.; Marziani, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, Ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A:Title: Sequence and analysis of chromosome 1 of the plant *Arabidopsis*.
A:Reference number: A86141; MUID:21016719; PMID:11130712
A:Accession: E96657
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-217 <STO>
A:Cross-references: UNIPROT:Q9CAM4; GB:AE005173; NID:G10092245; FIDN:AA012660.1; GSPDB:G
C:Genetics:
A:Gene: F16M19.9
A:Map position: 1

Query Match 64.3%; Score 36; DB 2; Length 217;
Best Local Similarity 85.7%; Pred. No. 45;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 EEDPKY 9
|:|:|:|
Db 36 EEDPKY 42

RESULT 13
T48743
probable 26S ATP/ubiquitin-dependent proteinase chain S4 [imported] - *Neurospora crassa*
N:Alternate names: protein 8D4.170
C:Species: *Neurospora crassa*
C>Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change C9-Jul-2004
C:Accession: T48743
R:Schulte, U.; Aign, V.; Hohesl, J.; Brandt, P.; Fartmann, B.; Holland, R.; Nyakatura, submitted to the Protein Sequence Database, April 2000
A:Reference number: Z24541
A:Accession: T48743
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-471 <SCH>
A:Cross-references: UNIPROT:Q9P723; EMBL:AL353819; GSPDB:GN00112; NCSP:8D4.170
A:Experimental source: comid contig 8D4; strain 74
C:Genetics:
A:Gene: NCSP:8D4.170
A:Map position: 2
A:Introns: 33/3; 303/3
C:Superfamily: ATP-dependent 26S proteinase; FtsH/SEC18/CDC48-type ATP-binding domain hc

Query Match 64.3%; Score 36; DB 2; Length 471;
Best Local Similarity 85.7%; Pred. No. 1e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 EEDPKY 10
|:|:|:|
Db 34 KDXPKY 40

RESULT 14
A39038
1-caldesmon, nonmuscle - chicken
N:Alternate names: caldesmon, nonmuscle
C:Species: *Gallus gallus* (chicken)
C>Date: 31-Jul-1991 #sequence_revision 27-Jun-1994 #text_change 22-Jun-1999
C:Accession: A39038
R:Hayashi, K.; Fujio, Y.; Kato, I.; Sobue, K.
J. Biol. Chem. 266, 355-361, 1991
A:Title: Structural and functional relationships between h- and l-caldesmons.
A:Reference number: A39038; MUID:91093148; PMID:1824698
A:Accession: A39038
A:Molecule type: mRNA

A:Residues: 1-517 <HAY>
A:Cross-references: GB:M60620; GB:M38015; NID:G212242; FIDN:AAA48936.1; PID:G212243
A:Experimental source: brain
C:Comment: The binding of caldesmon to F-actin is modulated by calcium and calmodulin.
C:Comment: Two calmodulin molecules can bind to nonoverlapping domains of each caldesmon
C:Superfamily: caldesmon
C:Keywords: actin binding; calmodulin binding; phosphoprotein
F:342,427,462/Binding site: phosphate (Ser) (covalent) #status predicted
F:433,456/Binding site: phosphate (Thr) (covalent) #status predicted

Query Match 64.3%; Score 36; DB 1; Length 517;
Best Local Similarity 75.0%; Pred. No. 1.1e+02;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DTEEDPKY 8
|:|:|:|
Db 176 DSEEDPKY 183

RESULT 15
T21811
hypothetical protein F35G12.12 - *Caenorhabditis elegans*
C:Species: *Caenorhabditis elegans*
C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T21811
R:Chui, C.
submitted to the EMBL Data Library, October 1994
A:Reference number: Z19473
A:Accession: T21811
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-526 <MTL>
A:Cross-references: UNIPROT:Q20058; EMBL:Z46242; FIDN:CAA6334.1; GSPDB:GN000021; CESP:F3
A:Experimental source: clone F35G12
C:Genetics:
A:Gene: CESP:F35G12.12
A:Map position: 3
A:Introns: 12/3; 46/2; 82/3; 176/3; 240/3; 260/1; 381/1
C:Superfamily: *Caenorhabditis elegans* hypothetical protein F35G12.12

Query Match 64.3%; Score 36; DB 2; Length 526;
Best Local Similarity 60.0%; Pred. No. 1.1e+02;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 DTEEDPKY 10
|:|:|:|
Db 465 DSEEDPKY 474

Search completed: October 22, 2005, 08:04:23
Job time : 12.45 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 22, 2005, 06:06:36 ; Search time 55.85 Seconds
(without alignments)
91.688 Million cell updates/sec

Title: US-10-731-238-68
Perfect score: 56
Sequence: 1 DTEDKPKYE 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Uniprot_03:*

1: uniprot_sprot:*

2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	56	100.0	152	2	Q9AEP9	Q9AEP9 staphylococ
2	56	100.0	940	2	Q53682	Q53682 staphylococ
3	56	100.0	943	2	Q8NU08	Q8NU08 staphylococ
4	56	100.0	957	2	Q6G6H4	Q6G6H4 staphylococ
5	56	100.0	961	2	Q9PRD3	Q9PRD3 staphylococ
6	56	100.0	961	2	Q7A3U8	Q7A3U8 staphylococ
7	56	100.0	965	2	Q6GDU5	Q6GDU5 staphylococ
8	56	100.0	1015	2	Q8NU07	Q8NU07 staphylococ
9	56	100.0	1015	2	Q6G6H3	Q6G6H3 staphylococ
10	56	100.0	1018	1	FNBA_STRAU	P14738 staphylococ
11	56	100.0	1038	2	Q9PRD2	Q9PRD2 staphylococ
12	56	100.0	1038	2	Q7A3U7	Q7A3U7 staphylococ
13	45	80.4	829	2	Q72CT7	Q72CT7 desulfovibr
14	43	76.8	619	2	Q6SU21	Q6SU21 manheimia
15	42	75.0	293	2	Q8GK03	Q8GK03 enterococcu
16	42	75.0	299	2	P71446	P71446 lactococcu
17	42	75.0	448	1	PR64_SCHPO	P36612 schizosacch
18	42	75.0	552	2	Q6S9B4	Q6S9B4 hexamita in
19	42	75.0	552	2	Q6S9B5	Q6S9B5 hexamita in
20	41	73.2	2957	2	Q61845	Q61845 caenorhabdi
21	40	71.4	274	2	Q8RNB7	Q8RNB7 bradyrhizob
22	40	71.4	340	2	Q6SV93	Q6SV93 rattus norv
23	40	71.4	517	2	Q7PNT2	Q7PNT2 anopheles g
24	40	71.4	890	2	Q8B171	Q8B171 strawberry
25	40	71.4	1028	2	Q6U7U3	Q6U7U3 crinipellis
26	39	69.6	253	2	Q80SFB	Q80SFB tomato infe
27	39	69.6	324	2	Q7R3H8	Q7R3H8 giardia lam
28	39	69.6	987	2	Q8SXJ5	Q8SXJ5 drosophila
29	39	69.6	997	2	Q9V9Q2	Q9V9Q2 drosophila
30	39	69.6	2689	2	Q7R8S7	Q7R8S7 plaesmodium
31	39	69.6	2720	2	Q6IMC6	Q6IMC6 plasmodium

32	38	67.9	172	2	Q9UVI8	Q9UVI8 candida alb
33	38	67.9	193	1	SODP_COXBU	P19685 coxiella bu
34	38	67.9	235	2	Q6GAN3	Q6GAN3 megachile r
35	38	67.9	433	2	Q6BV66	Q6BV66 debaryomyce
36	38	67.9	528	2	Q9LW16	Q9LW16 oryza sativ
37	38	67.9	539	2	Q96M38	Q96M38 homo sapien
38	38	67.9	569	2	Q8SR48	Q8SR48 encaphalito
39	38	67.9	600	2	Q6BZD5	Q6BZD5 debaryomyce
40	38	67.9	767	2	Q81YY4	Q81YY4 homo sapien
41	38	67.9	1075	2	Q6C2V2	Q6C2V2 yarrowia li
42	37	66.1	181	2	Q8AW33	Q8AW33 brachydanio
43	37	66.1	195	2	Q64N95	Q64N95 bacteroides
44	37	66.1	228	2	Q8G5E9	Q8G5E9 bifidobacte
45	37	66.1	252	2	Q82IK9	Q82IK9 streptomyce

ALIGNMENTS

RESULT 1

ID	Q9AEP9	PRELIMINARY;	PRT;	152 AA.
AC	Q9AEP9;			
DT	01-JUN-2001 (TREMBLrel. 17, Created)			
DT	01-JUN-2001 (TREMBLrel. 17, Last sequence update)			
DT	01-DEC-2001 (TREMBLrel. 19, Last annotation update)			
DE	Fibronectin-binding protein (Fragment).			
GN	Name=fnb;			
OS	Staphylococcus aureus.			
OC	Bacteria; Firmicutes; Bacillales; Staphylococcus.			
OX	NCBI_TaxID=1280;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=CMRSA-1;			
RX	MEDLINE=21246681; PubMed=11349044;			
RX	DOI=10.1128/IAI.69.6.3791-3799.2001;			
RA	Rice K., Huesca M., Vaz D., McGavin M.J.;			
RT	"Variance in fibronectin binding and fnb locus polymorphisms in			
RT	Staphylococcus aureus: identification of antigenic variation in a			
RT	fibronectin binding protein adhesin of the epidemic CMRSA-1 strain of			
RT	methicillin-resistant S. aureus.";			
RL	Infect. Immun. 69:3791-3799(2001).			
DR	EMBL: AY029184; AKK31588.1; -.			
FT	NON_TER			
FT	NON_TER			
SQ	SEQUENCE	152 AA;	17193 MW;	CFA3913C2B11C025 CRC64;

Query Match 100.0%; Score 56; DB 2; Length 152;
Best Local Similarity 100.0%; Pred. No. 0.096; 0; Mismatches 0; Indels 0; Gaps 0;
Matches 10; Conservative 0;

Qy 1 DTEDKPKYE 10
Db 11 DTEDKPKYE 20

RESULT 2

ID	Q53682	PRELIMINARY;	PRT;	940 AA.
AC	Q53682;			
DT	01-NOV-1996 (TREMBLrel. 01, Created)			
DT	01-NOV-1996 (TREMBLrel. 01, Last sequence update)			
DT	01-MAR-2004 (TREMBLrel. 26, Last annotation update)			
DE	Fibronectin binding protein B.			
GN	Name=fnbB;			
OS	Staphylococcus aureus.			
OC	Bacteria; Firmicutes; Bacillales; Staphylococcus.			
OX	NCBI_TaxID=1280;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=8325-4;			
RX	MEDLINE=92111475; PubMed=1837266;			
RA	Jonsson K., Signas C., Muller H.P., Lindberg M.;			

RT "Two different genes encode fibronectin binding proteins 11
RT Staphylococcus aureus. The complete nucleotide sequence and
RT characterization of the second gene."
RL Eur. J. Biochem. 202;1041-1048(1991).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC an amide bond (By similarity).
DR EMBL: X62992; CAA44726.1; -.
DR PIR: S19702; S19702.
DR HSP: O53653; IN67.
DR GO: GO:0009986; C:cell surface; IEA.
DR GO: GO:0005618; C:cell wall; IEA.
DR GO: GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO: GO:0016020; C:membrane; IEA.
DR GO: GO:0007155; P:cell adhesion; IEA.
DR InterPro: IPR008966; Adhes_bact.
DR InterPro: IPR004237; Fn_bind.
DR InterPro: IPR005877; Gpos_YsIRK.
DR Pfam: PF02986; Fn_bind; 2.
DR Pfam: PF04650; YsIRK_signal; 1.
DR TIGRfams: TIGR01167; LPTG_anchor; 1.
DR TIGRfams: TIGR01168; YsIRK_signal; 1.
DR PROSITE: PS50847; GRAM_POS_ANCHORING; 1.
KW Cell wall; Peptidoglycan-anchor.
SQ SEQUENCE 940 AA; 103555 MW; E35FBBCA907AE345 CRC64;

Query Match 100.0%; Score 56; DB 2; Length 940;
Best Local Similarity 100.0%; Pred. No. 0.63;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DTEEDKPKYE 10
Db 692 DTEEDKPKYE 701

RESULT 3
OSNU8 PRELIMINARY; PRT; 943 AA.
ID OSNU8
AC OSNU8;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Fnb protein.
GN Name=fnb; OrderedlocusNames=MM2420;
OS Staphylococcus aureus (strain MM2).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=196620;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MM2.
RX MEDLINE=22040717; PubMed12044378; DOI=10.1016/S0140-6736(0)08713-5;
RA Baba T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Oguchi A.,
RA Nagai Y., Iwama N., Asano K., Naimi T., Kuroda H., Cui L.,
RA Yamamoto K., Hiramatsu K.;
RT "Genome and virulence determinants of high virulence community-
RT acquired MRSA".
RT Lancet 359:1819-1827(2002).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC an amide bond (By similarity).
DR EMBL: AP004830; BAB96285.1; -.
DR HSP: O53653; IN67.
DR GO: GO:0009986; C:cell surface; IEA.
DR GO: GO:0005618; C:cell wall; IEA.
DR GO: GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO: GO:0016020; C:membrane; IEA.
DR GO: GO:0007155; P:cell adhesion; IEA.
DR InterPro: IPR008966; Adhes_bact.
DR InterPro: IPR004237; Fn_bind.
DR InterPro: IPR005877; Gpos_YsIRK.
DR Pfam: PF02986; Fn_bind; 1.
DR Pfam: PF00746; Gram_pos_anchor; 1.

DR Pfam: PF04650; YsIRK_signal; 1.
DR TIGRfams: TIGR01167; LPTG_anchor; 1.
DR TIGRfams: TIGR01168; YsIRK_signal; 1.
DR PROSITE: PS50847; GRAM_POS_ANCHORING; 1.
KW Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ SEQUENCE 943 AA; 104537 MW; DA8A5F31947B1B6A CRC64;

Query Match 100.0%; Score 56; DB 2; Length 943;
Best Local Similarity 100.0%; Pred. No. 0.63;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DTEEDKPKYE 10
Db 699 DTEEDKPKYE 708

RESULT 4
O6G6H4 PRELIMINARY; PRT; 957 AA.
ID O6G6H4
AC O6G6H4;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Fibronectin-binding protein.
GN Name=fnb; OrderedlocusNames=SA52387;
OS Staphylococcus aureus (strain MSSA476).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=282459;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed15213324; DOI=10.1073/pnas.0402521101;
RA Holden M.T.G., Fell E.J., Lindsey J.A., Peacock S.J., Day N.P.J.,
RA Enright M.C., Foster T.J., Moore C.E., Hurst L., Atkin R., Barron A.,
RA Baason N., Bentley S.D., Chillingworth C., Chillingworth T.,
RA Churcher C., Clark L., Cotton C., Cronin A., Doggett J., Dowd L.,
RA Felwell T., Hance Z., Harris B., Hauser H., Holtroyd S., Jagsis K.,
RA James K.D., Lennard N., Line A., Mayes R., Moule S., Mungall K.,
RA Ormond D., Quail M.A., Rabinowitch E., Rutherford K.M., Sanders M.,
RA Sharp S., Simmonds M., Stevens K., Whitehead S., Barrall B.G.,
RA Spratt B.G., Parkhill J.;
RT "Complete genomes of two clinical Staphylococcus aureus strains:
RT evidence for the rapid evolution of virulence and drug resistance".
RT Proc. Natl. Acad. Sci. U.S.A. 101:9786-9791(2004).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC an amide bond (By similarity).
DR EMBL: BX571857; CAG44201.1; -.
DR GO: GO:0009986; C:cell surface; IEA.
DR GO: GO:0005618; C:cell wall; IEA.
DR GO: GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO: GO:0016020; C:membrane; IEA.
DR GO: GO:0007155; P:cell adhesion; IEA.
DR InterPro: IPR008966; Adhes_bact.
DR InterPro: IPR004237; Fn_bind.
DR InterPro: IPR005877; Gpos_YsIRK.
DR InterPro: IPR001899; Gram_pos_anchor.
DR Pfam: PF02986; Fn_bind; 1.
DR Pfam: PF00746; Gram_pos_anchor; 1.
DR TIGRfams: TIGR01167; LPTG_anchor; 1.
DR TIGRfams: TIGR01168; YsIRK_signal; 1.
DR PROSITE: PS50847; GRAM_POS_ANCHORING; 1.
KW Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ SEQUENCE 957 AA; 105980 MW; 28F8BA7FFDF3EAF CRC64;

Query Match 100.0%; Score 56; DB 2; Length 957;
Best Local Similarity 100.0%; Pred. No. 0.64;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DTEEDKPKYE 10
Db 699 DTEEDKPKYE 708

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RESULT 5
ID 099RD3 PRELIMINARY; PRT; 961 AA.
AC 099RD3;
DT 01-JUN-2001 (TEMBLrel. 17, Created)
DT 01-JUN-2001 (TEMBLrel. 17, Last sequence update)
DE 01-JUN-2001 (TEMBLrel. 24, Last annotation update)
DE Fibronectin-binding protein homolog.
GN Name=fnbB; OrderedLocustNames=SAV2502;
OS Staphylococcus aureus (strain Mu50 / ATCC 700699).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=158878;
RN
RP SEQUENCE FROM N.A.
RC STRAIN=Mu50 / ATCC 700699;
RX MEDLINE=21311952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2;
RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Lian J.-Q., Ito T.,
RA Kanemori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,
RA Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
RA Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
RA Kanohia M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
RA Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
RT "Whole genome sequencing of methicillin-resistant Staphylococcus
RT aureus.";
RL Lancet 357:1225-1240(2001).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC an amide bond (By similarity).
DR EMBL: AP003365; BAB58664.1; -.
DR FIR; G90053; G90053.
DR HSSP; Q53653; IN67.
DR DR GO:0009986; C:cell surface; IEA.
DR GO:0005618; C:cell wall; IEA.
DR GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO:0016020; C:membrane; IEA.
DR GO:0007155; P:cell adhesion; IEA.
DR InterPro: IPR004237; Fn_bind.
DR InterPro: IPR005877; Gpos_YsIRK.
DR InterPro: IPR001899; Gram_pos_anchor.
DR Pfam: PF02986; Fn_bind; 1.
DR Pfam: PF00746; Gram_pos_anchor; 1.
DR Pfam: PF04650; YsIRK_signal; 1.
DR TIGRfams: TIGR01167; LPXTG_anchor; 1.
DR TIGRfams: TIGR01168; YsIRK_signal; 1.
DR PROSITE: PS50847; GRAM_POS_ANCHORING; 1.
KM Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ SEQUENCE 961 AA; 106010 MW; 364940F884EA4101 CRC64;

Query Match 100.0%; Score 56; DB 2; Length 961;
Best Local Similarity 100.0%; Pred. No. 0.65;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 6
ID 07A3J8 PRELIMINARY; PRT; 961 AA.
AC 07A3J8;
DT 05-JUL-2004 (TEMBLrel. 27, Created)
DT 05-JUL-2004 (TEMBLrel. 27, Last sequence update)
DE 05-JUL-2004 (TEMBLrel. 27, Last annotation update)
DE FnbB protein.
GN Name=fnbB; OrderedLocustNames=SA2290;
OS Staphylococcus aureus (strain NJ15).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=158879;
RN
RP SEQUENCE FROM N.A.
RX MEDLINE=21311952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2;

Query Match 100.0%; Score 56; DB 2; Length 961;
Best Local Similarity 100.0%; Pred. No. 0.65;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 7
ID 06GDU5 PRELIMINARY; PRT; 965 AA.
AC 06GDU5;
DT 05-JUL-2004 (TEMBLrel. 27, Created)
DT 05-JUL-2004 (TEMBLrel. 27, Last sequence update)
DE 05-JUL-2004 (TEMBLrel. 27, Last annotation update)
DE Fibronectin-binding protein.
GN Name=fnbA; OrderedLocustNames=SA2580;
OS Staphylococcus aureus (strain MSA252).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=282458;
RN
RP SEQUENCE FROM N.A.
RX PubMed=15213324; DOI=10.1073/pnas.0402521101;
RA Holden M.T.G., Fell B.J., Lindsey J.A., Peacock S.J., Day N.P.J.,
RA Enright M.C., Foster T.J., Moore C.E., Hurst L., Atkin R., Barron A.,
RA Bason N., Bentley S.D., Chillingworth C., Chillingworth T.,
RA Churcher C., Clark L., Cotton C., Cronin A., Doggett J., Dowd L.,
RA Felwell T., Hance Z., Harris B., Hauser H., Holtroyd S., Jagels K.,
RA James K.D., Lennard N., Line A., Mayes R., Moule S., Mungall K.,
RA Ormond D., Quail M.A., Rabbittowitch E., Rutherford K.M., Sanders M.,
RA Sharp S.G., Simmonds M., Stevens K., Whitehead S., Barrett B.G.;
RT "Complete genomes of two clinical Staphylococcus aureus strains:
RT evidence for the rapid evolution of virulence and drug resistance.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:9786-9791(2004).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC an amide bond (By similarity).
DR EMBL: BX571856; CAG41560.1; -.
DR GO:0009986; C:cell surface; IEA.
DR GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO:0016020; C:membrane; IEA.

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DR GO:0007155; P:cell adhesion; IEA.
DR InterPro: IPR008966; Adhes_Bact.
DR InterPro: IPR004237; Fn_bind.
DR InterPro: IPR005877; Gpos_YsIRK.
DR InterPro: IPR001899; Gram_pos_anchor.
DR Pfam: PF02986; Fn_bind; 1.
DR Pfam: PF00746; Gram_pos_anchor; 1.
DR Pfam: PF04650; YsIRK_signal; 1.
DR TIGRfams: TIGR01167; LpxTG_anchor; 1.
DR TIGRfams: TIGR01168; YsIRK_signal; 1.
DR PROSITE: PS50847; GRAM_POS_ANCHORING; 1.
DR Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ SEQUENCE 965 AA; 105691 MW; 2982E132164D0551 CRC64;

Query Match 100.0%; Score 56; DB 2; Length 965;
Best Local Similarity 100.0%; Pred. No. 0.65;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DTEEDPKPYE 10
Db 759 DTEEDPKPYE 768

RESULT 8
Q8NU7 PRELIMINARY; PRT; 1015 AA.
ID Q8NU7;
AC Q8NU7;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Pnb protein.
GN Name=fnb; OrderedlocusNames=MM2421;
OC Staphylococcus aureus (strain MM2).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxId=196620;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MM2.
RX MEDLINE=2040717; PubMed=12044378; DOI=10.1016/S0140-6736((2)08713-5;
RA Baba T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Oguchi A.,
RA Nagai Y., Iwana N., Asano K., Naimi T., Kuroda H., Cui L.,
RA Yamamoto K., Hiramatsu K.;
RT "Genome and virulence determinants of high virulence community-
acquired MRSA.";
RL Lancet 359:1819-1827(2002).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
an amide bond (By similarity).
DR EMBL: AF004830; BAB96286.1; -.
DR GO: GO:0009986; C:cell surface; IEA.
DR GO: GO:0005618; C:cell wall; IEA.
DR GO: GO:0003275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO: GO:0016020; C:membrane; IEA.
DR GO: GO:0007155; P:cell adhesion; IEA.
DR InterPro: IPR008966; Adhes_bact.
DR InterPro: IPR004237; Fn_bind.
DR InterPro: IPR005877; Gpos_YsIRK.
DR InterPro: IPR001899; Gram_pos_anchor.
DR Pfam: PF02986; Fn_bind; 1.
DR Pfam: PF00746; Gram_pos_anchor; 1.
DR Pfam: PF04650; YsIRK_signal; 1.
DR TIGRfams: TIGR01167; LpxTG_anchor; 1.
DR TIGRfams: TIGR01168; YsIRK_signal; 1.
DR PROSITE: PS50847; GRAM_POS_ANCHORING; 1.
DR Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ SEQUENCE 1015 AA; 111145 MW; D0F9281BB64D4D2 CRC64;

Query Match 100.0%; Score 56; DB 2; Length 1015;
Best Local Similarity 100.0%; Pred. No. 0.68;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DTEEDPKPYE 10
Db 757 DTEEDPKPYE 766

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RESULT 9
Q6G6H3 PRELIMINARY; PRT; 1015 AA.
ID Q6G6H3;
AC Q6G6H3;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Fibronectin-binding protein.
GN OrderedlocusNames=SAS238;
OC Staphylococcus aureus (strain MSSA476).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxId=282459;
RN [1]
RP SEQUENCE FROM N.A.
RC PubMed=15213324; DOI=10.1073/pnas.0402521101;
RX Holden M.T.G., Fell E.J., Lindsay J.A., Peacock S.J., Day N.P.J.,
RA Enright M.C., Foster T.J., Moore C.E., Hurst L., Atkin R., Barron A.,
RA Bason N., Bentley S.D., Chillingworth C., Chillingworth T.,
RA Churcher C., Clark L., Cronin A., Doggett J., Dowd L.,
RA Felwell T., Hance Z., Harris B., Hauser H., Holroyd S., Jazgale K.,
RA James K.D., Lennard N., Line A., Mayes R., Moule S., Mungall K.,
RA Ormond D., Quail M.A., Rabinovitch E., Rutherford K.M., Sanders M.,
RA Sharp S., Simmonds M., Stevens K., Whitehead S., Barrett B.G.,
RA Spratt B.G., Parhill J.;
RT "Complete genomes of two clinical Staphylococcus aureus strains:
evidence for the rapid evolution of virulence and drug resistance.";
RT Proc. Natl. Acad. Sci. U.S.A. 101:9786-9791(2004).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
an amide bond (By similarity).
DR EMBL: BX571857; CAG44202.1; -.
DR GO: GO:0009986; C:cell surface; IEA.
DR GO: GO:0005618; C:cell wall; IEA.
DR GO: GO:0003275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO: GO:0016020; C:membrane; IEA.
DR GO: GO:0007155; P:cell adhesion; IEA.
DR InterPro: IPR008966; Adhes_bact.
DR InterPro: IPR004237; Fn_bind.
DR InterPro: IPR005877; Gpos_YsIRK.
DR InterPro: IPR001899; Gram_pos_anchor.
DR Pfam: PF02986; Fn_bind; 1.
DR Pfam: PF00746; Gram_pos_anchor; 1.
DR Pfam: PF04650; YsIRK_signal; 1.
DR TIGRfams: TIGR01167; LpxTG_anchor; 1.
DR TIGRfams: TIGR01168; YsIRK_signal; 1.
DR PROSITE: PS50847; GRAM_POS_ANCHORING; 1.
DR Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ SEQUENCE 1015 AA; 111145 MW; D0F9281BB64D4D2 CRC64;

Query Match 100.0%; Score 56; DB 2; Length 1015;
Best Local Similarity 100.0%; Pred. No. 0.66;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DTEEDPKPYE 10
Db 757 DTEEDPKPYE 766

RESULT 10
FNBA STAAU STANDARD; PRT; 1018 AA.
ID FNBA STAAU;
AC P14738;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Fibronectin-binding protein precursor (FNBP).
GN Name=fnbA;
OC Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxId=1280;
RN [1]
RP SEQUENCE FROM N.A.

```

CC STRAIN=NCTC 8325-4;
 RX MEDLINE=8908998; PubMed=2521391;
 RA Signes C., Raucel G., Joenson K., Lindgren P.-E.,
 RA Anantharaman G.M., Hoeck M., Lindberg M.,
 RT "Nucleotide sequence of the gene for a fibronectin-binding protein
 from *Staphylococcus aureus*: use of this peptide sequence in the
 RT synthesis of biologically active peptides."
 RL Proc. Natl. Acad. Sci. U.S.A. 86:699-703(1989).
 CC -1- FUNCTION: The ability of bacteria to bind fibronectin has been
 CC proposed as a virulence factor enabling bacteria to colonize wound
 CC tissues and blood clots. Binding of plasma fibronectin to the
 CC bacterial surface might block adhesion receptors on *S. aureus*, thus
 CC representing an important defense mechanism against tissue
 CC invasion.
 CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
 CC an amide bond (Potential).
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
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 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; J04151; AAA26632.1; -
 DR InterPro: IPR004237; Fn bind.
 DR InterPro: IPR005877; Gpos YSIRK.
 DR InterPro: IPR001899; Gram_pos_anchor.
 DR Pfam; PF00746; Gram_pos_anchor; 1.
 DR Pfam; PF04650; YSIRK_signal; 1.
 DR TIGRPFAM; TIGR01167; LPXTG_anchor; 1.
 DR TIGRPFAM; TIGR01168; YSIRK_signal; 1.
 DR PROSITE; PSS0847; GRAM_POS_ANCHORING; 1.
 KW Cell adhesion; Cell wall; Peptidoglycan-anchor; Repeat; Signal;
 KW virulence.
 FT SIGNAL 1 36
 FT CHAIN 985
 FT PROPEP 37 1018
 FT REPEAT 545 574
 FT REPEAT 575 604
 FT DOMAIN 745 878
 FT REPEAT 745 782
 FT REPEAT 783 820
 FT REPEAT 821 859
 FT REPEAT 860 878
 FT DOMAIN 879 948
 FT REPEAT 879 892
 FT REPEAT 893 906
 FT REPEAT 907 920
 FT REPEAT 921 934
 FT REPEAT 935 948
 FT SITE 982 986
 FT MOD_RES 985 985
 SQ SEQUENCE 1018 AA; 111780 MW; 58175E0020E81F1F CRC64;
 Query Match 100.0%; Score 56; DB 1; Length 1018;
 Best Local Similarity 100.0%; Pred. No. 0.69;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DTEEDKPKYE 10
 DB 756 DTEEDKPKYE 765
 RESULT 11
 ID Q99RD2 PRELIMINARY; PRT; 1038 AA.
 AC Q99RD2;
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)

DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 GN Fibronectin-binding protein homolog.
 GN Name=fnb; OrderedLocNames=SAV2503;
 OC *Staphylococcus aureus* (strain Mu50 / ATCC 700699).
 OC Bacteria; Firmicutes; Bacillales; *Staphylococcus*.
 OX NCBI_TaxID=158878;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX STRAIN=Mus0 / ATCC 700699;
 RX MEDLINE=2111952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2;
 RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
 RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Lian J.-Q., Ito T.,
 RA Kanamori M., Matsunaru H., Maruyama A., Murakami H., Hosoyama A.,
 RA Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
 RA Kanehisa M., Yamashita A., Kuhara S., Goto S., Yabuzaki J.,
 RA Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.,
 RT "Whole genome sequencing of methicillin-resistant *Staphylococcus*
 RT *aureus*."
 RL Lancet 357:1225-1240(2001).
 CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
 CC an amide bond (By similarity).
 CC EMBL; AF003365; BAB58665.1; -
 DR PIR; H90053; H90053
 DR GO; GO:0009986; Cell surface; IEA.
 DR GO; GO:0005618; C:cell wall; IEA.
 DR GO; GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0007155; P:cell adhesion; IEA.
 DR InterPro: IPR008966; Adhes_bact.
 DR InterPro: IPR004237; Fn_bind.
 DR InterPro: IPR005877; Gpos YSIRK.
 DR InterPro: IPR001899; Gram_pos_anchor.
 DR Pfam; PF00746; Gram_pos_anchor; 1.
 DR Pfam; PF04650; YSIRK_signal; 1.
 DR TIGRPFAM; TIGR01167; LPXTG_anchor; 1.
 DR TIGRPFAM; TIGR01168; YSIRK_signal; 1.
 DR PROSITE; PSS0847; GRAM_POS_ANCHORING; 1.
 KW Cell wall; Complete proteome; Peptidoglycan-anchor.
 SQ SEQUENCE 1038 AA; 113618 MW; 666BF6BF2BFEB12 CRC64;
 Query Match 100.0%; Score 56; DB 2; Length 1038;
 Best Local Similarity 100.0%; Pred. No. 0.7;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DTEEDKPKYE 10
 DB 752 DTEEDKPKYE 761
 RESULT 12
 ID Q7A3J7 PRELIMINARY; PRT; 1038 AA.
 AC Q7A3J7;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Fnb protein.
 GN Name=fnb; OrderedLocNames=SA2291;
 OS *Staphylococcus aureus* (strain N315).
 OC Bacteria; Firmicutes; Bacillales; *Staphylococcus*.
 OX NCBI_TaxID=158879;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21311952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2;
 RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
 RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Lian J.-Q., Ito T.,
 RA Kanamori M., Matsunaru H., Maruyama A., Murakami H., Hosoyama A.,
 RA Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
 RA Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
 RA Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,

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RA Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
RT "Whole genome sequencing of methicillin-resistant Staphylococcus
RL Lancet 357:1225-1240(2001).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC an amide bond (By similarity).
DR EMBL: AP003137; BAB43594.1; -.
DR GO: GO:0009986; C:cell surface; IEA.
DR GO: GO:0005618; C:cell wall; IEA.
DR GO: GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO: GO:0016020; C:membrane; IEA.
DR GO: GO:0007155; P:cell adhesion; IEA.
DR InterPro: IPR008966; Adhes_bact.
DR InterPro: IPR004237; Fn_bind.
DR InterPro: IPR005877; Gpos_YsIRK.
DR InterPro: IPR001899; Gram_pos_anchor.
DR Pfam: PF02986; Fn_bind; 1.
DR Pfam: PF00746; Gram_pos_anchor; 1.
DR Pfam: PF04650; YsIRK_signal; 1.
DR TIGRPFAM: TIGR01167; LPXG_anchor; 1.
DR TIGRPFAM: TIGR01168; YsIRK_signal; 1.
DR PROSITE: PS50847; GRAM_POS_ANCHORING; 1.
DR Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ SEQUENCE 1038 AA; 113618 MW; 666BF6BF2BFEB312 CRC64;

Query Match 100.0%; Score 56; DB 2; Length 1038;
Best Local Similarity 100.0%; Pred. No. 0.7;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DTEBDKPKYE 10
Db 752 DTEBDKPKYE 761

RESULT 13
Q72CT7 PRELIMINARY; PRT; 829 AA.
ID 072CT7
AC 072CT7;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Leucyl-CRNA synthetase (EC 6.1.1.4).
GN Name=leus; OrderedLocNames=DVT1196;
OS Desulfovibrio vulgaris (strain Hildenborough / ATCC 29579 / NCIMB
OS 8303).
OC Bacteria; Proteobacteria; Deltaproteobacteria; Desulfovibrionales;
OC Desulfovibrionaceae; Desulfovibrio.
OX NCBI_TaxID=882;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=15077118; DOI=10.1038/nbt959;
RA Heidelberg J.F., Seshadri R., Haveman S.A., Heme C.L., Paulsen I.T.,
RA Kolonay J.F., Eisen J.A., Ward N.L., Mehe B.A., Brinkac L.M.,
RA Daugherty S.C., DeBoy R.T., Dodson R.D., Durkin A.S., Madupu R.,
RA Nelson W.C., Sullivan S.A., Fouts D.E., Haft D.H., Selengut J.,
RA Peterson J.D., Davidson T.M., Zafar N., Zhou L., Radune D.,
RA Dimitrov G., Hance M., Tran K., Khouri H.M., Gill J., Utterback T.R.,
RA Feldlyum T.V., Wall J.D., Vootdow G., Fraser C.M.;
RT "The genome sequence of the anaerobic, sulfate-reducing bacterium
RT Desulfovibrio vulgaris Hildenborough.";
RL Nat. Biotechnol. 22:554-559(2004).
DR EMBL: AB017313; AAS95674.1; -.
DR TIGR: DVT1196; -.
DR GO: GO:0005524; F:ATP binding; IEA.
DR GO: GO:0004823; P:leucine-CRNA ligase activity; IEA.
DR GO: GO:0006429; P:leucyl-CRNA aminoacylation; IEA.
DR InterPro: IPR002302; Leu-CRNAsynt1a.
DR InterPro: IPR002300; tRNA-synt_1a.
DR InterPro: IPR001412; tRNA-synt_1a.
DR InterPro: IPR009080; tRNA-synt_1a_bind.
DR InterPro: IPR009008; ValRS_1Iers_edit.
DR Pfam: PF00133; tRNA-synt_1; 1.
DR PRINTS: PR00985; TRNASYNTHLEU.

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DR TIGRPFAM: TIGR00396; leus_bact; 1.
DR PROSITE: PS00178; AA_TRNA_LIGASE_I; 1.
DR Complete proteome.
SQ SEQUENCE 829 AA; 93979 MW; 075C5C6BBD149142 CRC64;

Query Match 80.4%; Score 45; DB 2; Length 829;
Best Local Similarity 88.9%; Pred. No. 44;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 DTEBDKPKY 9
Db 25 DTEBDKPKY 33

RESULT 14
Q65U21 PRELIMINARY; PRT; 619 AA.
ID Q65U21
AC Q65U21;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE MdlB protein.
GN Name=mdlB; ORFNames=MS0932;
OS Mannheimia succiniciproducens MBE155E.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
OC Pasteurellaceae; Mannheimia.
OX NCBI_TaxID=221986;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=MBE155E;
RA Hong S.H., Kim J.S., Lee S.Y., In Y.H., Choi S.S., Rih J.-K.,
RA Kim C.H., Jeong H., Hur C.-G., Kim J.G.;
RT "The genome sequence of the capnophilic rumen bacterium Mannheimia
RT succiniciproducens.";
RL Nat. Biotechnol. 0:0-0(2004).
DR EMBL: AE016827; AA037539.1; -.
SQ SEQUENCE 619 AA; 68502 MW; 088CB21AF658F786 CRC64;

Query Match 76.8%; Score 43; DB 2; Length 619;
Best Local Similarity 80.0%; Pred. No. 71;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 DTEBDKPKYE 10
Db 362 DTEBDKPKYE 371

RESULT 15
Q8GK03 PRELIMINARY; PRT; 293 AA.
ID Q8GK03
AC Q8GK03;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE SfeI restriction endonuclease.
GN Name=sfeIR;
OS Enterococcus faecalis (Streptococcus faecalis).
OC Bacteria; Firmicutes; Lactobacillales; Enterococcaceae; Enterococcus.
OX NCBI_TaxID=1351;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=SE72;
RA Okhapkina S., Neresova N., Golikova L., Seregina E., Sosnovtsev S.,
RA Abdurashitov M., Degtyarev S.;
RT "Comparison of the homologous SfeI and LlaBI Restriction and
RT Modification Systems.";
RL Mol. Biol. 36:333-337(2002).
DR EMBL: AY151403; AAN71749.1; -.
DR GO: GO:0004519; F:endonuclease activity; IEA.
DR Endonuclease.
SQ SEQUENCE 293 AA; 34043 MW; F9E8463A8A0187B7 CRC64;

Query Match 75.0%; Score 42; DB 2; Length 293;

```

Best Local Similarity 80.0%; Pred. No. 49;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 DTEEDKKYE 10
| | | | |
Db 219 DLEEDKKYE 228

Search completed: October 22, 2005, 08:00:30
Job time : 57.85 secs

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OM protein - protein search, using sw model

Run on: October 25, 2005, 20:21:18 ; Search time 63.2 Seconds
(without alignments)
61.196 Million cell updates/sec

Title: US-10-731-238-69

Perfect score: 56

Sequence: 1 EEDKPYEKG 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

A_Geneseq_16Dec04: *
1: geneseqp1980s: *
2: geneseqp1990s: *
3: geneseqp2000s: *
4: geneseqp2001s: *
5: geneseqp2002s: *
6: geneseqp2003s: *
7: geneseqp2003bs: *
8: geneseqp2004s: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	56	100.0	10	2 AAW65725	AAW65725 Fibronec
2	56	100.0	38	1 AAP80660	AAP80660 Protein w
3	56	100.0	38	1 AAP82116	AAP82116 Fibronec
4	56	100.0	38	2 AAW65692	AAW65692 Fibronec
5	56	100.0	38	2 AAW65695	AAW65695 Fibronec
6	56	100.0	38	2 AAW65694	AAW65694 Fibronec
7	56	100.0	38	2 AAW65691	AAW65691 Fibronec
8	56	100.0	38	2 AAW65699	AAW65699 Fibronec
9	56	100.0	38	2 AAW65661	AAW65661 Fibronec
10	56	100.0	38	2 AAW65693	AAW65693 Fibronec
11	56	100.0	39	2 AAW65712	AAW65712 Fibronec
12	56	100.0	130	2 AAR58806	AAR58806 Fibronec
13	56	100.0	130	2 AAR58807	AAR58807 Fibronec
14	56	100.0	130	2 AAR91202	AAR91202 D1-D4 fib
15	56	100.0	130	2 AAR91201	AAR91201 D1-D4 fib
16	56	100.0	134	2 AAY29089	AAY29089 Cloned fi
17	56	100.0	134	2 AAY29088	AAY29088 S. aureus
18	56	100.0	134	2 AAY29087	AAY29087 S. aureus
19	56	100.0	139	2 AAW31556	AAW31556 Fibronec
20	56	100.0	174	2 AAR58808	AAR58808 Fdp fibro
21	56	100.0	174	2 AAR91203	AAR91203 D1-D4 fib
22	56	100.0	181	2 AAR58805	AAR58805 Fibronec
23	56	100.0	181	2 AAR91200	AAR91200 D1-D4 fib
24	56	100.0	559	2 AAW89803	AAW89803 Staphyloc
25	56	100.0	767	4 AAU34403	AAU34403 Staphyloc

26	56	100.0	767	4	AAU37547	AAU37547 Staphyloc
27	56	100.0	940	6	AAR07070	AAR07070 Fibronec
28	56	100.0	940	6	ABJ19111	ABJ19111 Pathogen
29	56	100.0	948	6	ADA89470	ADA89470 Staphyloc
30	56	100.0	948	6	ABJ18923	ABJ18923 Pathogen
31	56	100.0	948	6	ABW72536	ABW72536 Staphyloc
32	56	100.0	961	6	ABU15854	ABU15854 Protein e
33	56	100.0	978	4	AAU33960	AAU33960 Staphyloc
34	56	100.0	1001	4	AAU37093	AAU37093 Fibronec
35	56	100.0	1018	4	AAW82115	AAW82115 Fibronec
36	56	100.0	1018	4	AAU37245	AAU37245 Staphyloc
37	56	100.0	1018	4	AAU34301	AAU34301 Staphyloc
38	56	100.0	1018	6	ABJ18922	ABJ18922 Pathogen
39	56	100.0	1018	6	ABW72537	ABW72537 Staphyloc
40	56	100.0	1027	2	AAW89806	AAW89806 Staphyloc
41	56	100.0	1038	6	ABU15903	ABU15903 Protein e
42	52	92.9	30	4	AAW82164	AAW82164 Peptide f
43	52	92.9	30	7	ADC69221	ADC69221 Fibronec
44	52	92.9	31	7	ADC69222	ADC69222 Fibronec
45	51	91.1	38	2	AAW65696	AAW65696 Fibronec

ALIGNMENTS

RESULT 1
AAW65725
ID AAW65725 standard; peptide; 10 AA.

AC AAW65725;

DT 16-OCT-1998 (first entry)

XX Fibronec binding protein-derived peptide #69.

DE microbial surface components recognising adhesive matrix molecule;

KM MSCRAM; fibronec; fibronec-binding protein; antibody; epitope;

KW antibiotic; bacterial infection; antibiotic-resistant strain.

XX Synthetic.

OS Staphylococcus aureus.

PN W09831389-A2.

XX 23-JUL-1998.

PF 21-JAN-1998; 98MO-US001222.

PR 21-JAN-1997; 97US-0036139P.

XX (TEXA) UNIV TEXAS A & M SYSTEM.

XX Hoeoek M, Patti JM, House-Pompeo KL, Speciale P, Joh D;

PI McGavin MJ;

PT WPI; 1998-413816/35.

XX Antibody that binds to fibronec-binding protein, preventing its

XX binding to fibronec - used to treat or prevent bacterial infection,

XX especially by Staphylococci and Streptococci.

XX Example 9, Page 110; 201p; English.

XX The invention relates to antibodies that bind to a fibronec-binding

XX domain of a fibronec-binding protein, and inhibit binding of the

XX protein to fibronec. Also claimed are: (1) isolated peptides of a

XX fibronec-binding protein that do not bind to fibronec; (2) fusion

XX protein containing at least one peptide of a fibronec-binding protein

XX linked to a second amino acid sequence; (3) nucleic acid encoding the

XX isolated peptide of (1). Antibodies, the isolated peptides of (1) and the

XX nucleic acids are all useful for immunisation (active or passive) and (by

XX inhibiting binding of bacteria to fibronec) for preventing or treating

XX infection in humans or other animals, particularly by staphylococci or

CC streptococci, e.g. meningitis, otitis media, pneumonia, endocarditis,
 CC mastitis in cattle, abortion in horses and many others. Since the
 CC antibodies block binding of bacteria, they should be effective against
 CC antibiotic-resistant strains, and may replace antibiotic therapy or
 CC increase its effectiveness. Sequences AAW65719-41 and AAW65658 represent
 CC peptides which were synthesised to span the D1 motif and the N-terminal
 CC 18 amino acids of D2, with each peptide overlapping by eight amino acids
 CC with the previous sequence
 CC
 XX
 SQ Sequence 10 AA;

Query Match 100.0%; Score 56; DB 2; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.0049;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EEDKPKYEQG 10
 |||||
 Db 1 EEDKPKYEQG 10

RESULT 2
 AAP80660
 ID AAP80660 standard; protein; 38 AA.
 XX
 AC AAP80660;

XX 25-MAR-2003 (revised)
 DT 07-OCT-1990 (first entry)

DE Protein with fibronectin binding ability.

XX Hybrid DNA molecule; fibronectin binding; mastitis; ruminants;
 KM wound infection.

OS Staphylococcus aureus.

PN EP294349-A.

XX 07-DEC-1988.

XX 30-MAY-1988; 88EP-00850188.

XX 01-JUN-1987; 87SE-00002272.

XX (ALFA) ALFA LAVAL AGRIC INT AB.

PI Lindberg MK, Signas LC, Wadstrom TM, Froman G;

DR WPI; 1988-347978/49.

DR N-PSDB; AAW81097.

PT Hybrid DNA encoding Staphylococcus aureus fibronectin binding protein -
 PT useful for immunisation and topical application to prevent staphylococcal
 PT infections.

PS Claim 11; Page 12; 23pp; English.

XX The peptide has fibronectin binding ability. It is useful for immunising
 CC ruminants against staphylococcal mastitis, pref. when used at 0.5-5
 CC micrograms/kg, using 3 doses given at 1-3 week intervals; for topical
 CC application to prevent wound infection, using an isotonic saline soln. of
 CC concn. 25-250 micrograms/ml; and, when immobilised on a carrier, for
 CC diagnosing staphylococcal infections. (Updated on 25-MAR-2003 to correct
 CC PF field.) (Updated on 25-MAR-2003 to correct PA field.)
 CC
 XX

SQ Sequence 38 AA;

Query Match 100.0%; Score 56; DB 1; Length 38;
 Best Local Similarity 100.0%; Pred. No. 0.019;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EEDKPKYEQG 10
 |||||

Db 14 EEDKPKYEQG 23

RESULT 3
 AAP82116
 ID AAP82116 standard; protein; 38 AA.

XX AAP82116;

XX 25-MAR-2003 (revised)

DT 05-JAN-1990 (first entry)

DE Fibronectin binding protein.

XX Fibronectin binding protein; S.aureus; immunisation; mastitis; ruminants;
 KM wound infection; diagnosis.

OS Staphylococcus aureus.

PN EP294349-A.

XX 07-DEC-1988.

XX 30-MAY-1988; 88EP-00850188.

XX 01-JUN-1987; 87SE-00002272.

XX (ALFA) ALFA LAVAL AGRIC INT AB.

PI Lindberg MK, Signas LC, Wadstrom TM, Froman G;

DR WPI; 1988-347978/49.

DR N-PSDB; AAW82054.

PT Hybrid DNA encoding Staphylococcus aureus fibronectin binding protein -
 PT useful for immunisation and topical application to prevent staphylococcal
 PT infections.

PS Claim 11; Page 12; 23pp; English.

XX The S.aureus fibronectin binding protein may be included in a hybrid
 CC protein. The protein may be used to immunise ruminants against
 CC staphylococcal mastitis, pref. when given at 0.5-5 microg/kg, using 3
 CC doses at 1-3 week intervals; and for topical applicn. to prevent wound
 CC infection, pref. using isotonic saline soln. of concn. 25-250 microg/mg.
 CC The DNA encoding the binding protein and the hybrid protein may be
 CC immobilised on a carrier and used to diagnose staphylococcal infections.
 CC (Updated on 25-MAR-2003 to correct PA field.)
 CC
 XX

SQ Sequence 38 AA;

Query Match 100.0%; Score 56; DB 1; Length 38;
 Best Local Similarity 100.0%; Pred. No. 0.019;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EEDKPKYEQG 10
 |||||
 Db 14 EEDKPKYEQG 23

RESULT 4
 AAW65692
 ID AAW65692 standard; peptide; 38 AA.

XX AAW65692;

XX 16-OCT-1998 (first entry)

DE Fibronectin binding protein-derived peptide #36.

XX microbial surface components recognising adhesive matrix molecule;
 KM MSCRAMM; fibronectin; fibronectin-binding protein; antibody; epitope;
 KW antibiotic; bacterial infection; antibiotic-resistant strain.

```

XX OS Synthetic.
XX OS Staphylococcus aureus.
XX PN WO9831389-A2.
XX PD 23-JUL-1998.
XX PF 21-JAN-1998; 98WO-US001222.
XX PR 21-JAN-1997; 97US-0036139P.
XX (TEXA ) UNIV TEXAS A & M SYSTEM.
XX PA Hoeoek M, Patti JM, House-Pompeo KL, Speciale P, Joh D;
XX PI McGavin MJ;
XX DR WPI; 1998-413816/35.
XX PT Antibody that binds to fibronectin-binding protein, preventing its
XX PT binding to fibronectin - used to treat or prevent bacterial infection,
XX PT especially by Staphylococci and Streptococci.
XX PS Example 8; Page 101; 201pp; English.
XX CC The invention relates to antibodies that bind to a fibronectin-binding
XX CC domain of a fibronectin-binding protein, and inhibit binding of the
XX CC protein to fibronectin. Also claimed are: (1) isolated peptides of a
XX CC fibronectin-binding protein that do not bind to fibronectin; (2) fusion
XX CC protein containing at least one peptide of a fibronectin-binding protein
XX CC linked to a second amino acid sequence; (3) nucleic acid encoding the
XX CC isolated peptide of (1). Antibodies, the isolated peptides of (1) and (by
XX CC nucleic acids are all useful for immunisation (active or passive) and (by
XX CC inhibiting binding of bacteria to fibronectin) for preventing or treating
XX CC infection in humans or other animals, particularly by staphylococci or
XX CC streptococci, e.g. meningitis, otitis media, pneumonia, endocarditis,
XX CC mastitis in cattle, abortion in horses and many others. Since the
XX CC antibodies block binding of bacteria, they should be effective against
XX CC antibiotic-resistant strains, and may replace antibiotic therapy or
XX CC increase its effectiveness. Sequences AAW65691-700 represent a series of
XX CC synthetic peptides based on the D1 region of S. aureus fibronectin
XX CC binding protein A. They were synthesised to contain mutations
XX CC
XX SQ Sequence 38 AA:
XX
XX Query Match 100.0%; Score 56; DB 2; Length 38;
XX Best Local Similarity 100.0%; Pred. No. 0.019;
XX Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 EEDKPKYEQG 10
Db 13 EEDKPKYEQG 22

```

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RESULT 5
AAW65695
ID AAW65695 standard; peptide; 38 AA.
XX
XX AAW65695;
AC
XX
XX 16-OCT-1998 (first entry)
DT
XX
XX

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DE Fibronectin binding protein-derived peptide #39.
XX
XX microbial surface components recognising adhesive matrix molecule;
XX MSCRAMM; fibronectin; fibronectin-binding protein; antibody; epitope;
XX antibiotic; bacterial infection; antibiotic-resistant strain.
XX
XX Synthetic.
XX OS Staphylococcus aureus.
XX PN WO9831389-A2.
XX

```

```

PD 23-JUL-1998.
XX PF 21-JAN-1998; 98WO-US001222.
XX PR 21-JAN-1997; 97US-0036139P.
XX (TEXA ) UNIV TEXAS A & M SYSTEM.
XX PA Hoeoek M, Patti JM, House-Pompeo KL, Speciale P, Joh D;
XX PI McGavin MJ;
XX DR WPI; 1998-413816/35.
XX PT Antibody that binds to fibronectin-binding protein, preventing its
XX PT binding to fibronectin - used to treat or prevent bacterial infection,
XX PT especially by Staphylococci and Streptococci.
XX PS Example 8; Page 102; 201pp; English.
XX CC The invention relates to antibodies that bind to a fibronectin-binding
XX CC domain of a fibronectin-binding protein, and inhibit binding of the
XX CC protein to fibronectin. Also claimed are: (1) isolated peptides of a
XX CC fibronectin-binding protein that do not bind to fibronectin; (2) fusion
XX CC protein containing at least one peptide of a fibronectin-binding protein
XX CC linked to a second amino acid sequence; (3) nucleic acid encoding the
XX CC isolated peptide of (1). Antibodies, the isolated peptides of (1) and (by
XX CC nucleic acids are all useful for immunisation (active or passive) and (by
XX CC inhibiting binding of bacteria to fibronectin) for preventing or treating
XX CC infection in humans or other animals, particularly by staphylococci or
XX CC streptococci, e.g. meningitis, otitis media, pneumonia, endocarditis,
XX CC mastitis in cattle, abortion in horses and many others. Since the
XX CC antibodies block binding of bacteria, they should be effective against
XX CC antibiotic-resistant strains, and may replace antibiotic therapy or
XX CC increase its effectiveness. Sequences AAW65691-700 represent a series of
XX CC synthetic peptides based on the D1 region of S. aureus fibronectin
XX CC binding protein A. They were synthesised to contain mutations
XX CC
XX SQ Sequence 38 AA:
XX
XX Query Match 100.0%; Score 56; DB 2; Length 38;
XX Best Local Similarity 100.0%; Pred. No. 0.019;
XX Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 EEDKPKYEQG 10
Db 13 EEDKPKYEQG 22

```

```

RESULT 6
AAW65694
ID AAW65694 standard; peptide; 38 AA.
XX
XX AAW65694;
AC
XX
XX 16-OCT-1998 (first entry)
DT
XX
XX

```

```

DE Fibronectin binding protein-derived peptide #38.
XX
XX microbial surface components recognising adhesive matrix molecule;
XX MSCRAMM; fibronectin; fibronectin-binding protein; antibody; epitope;
XX antibiotic; bacterial infection; antibiotic-resistant strain.
XX
XX Synthetic.
XX OS Staphylococcus aureus.
XX PN WO9831389-A2.
XX PD 23-JUL-1998.
XX PF 21-JAN-1998; 98WO-US001222.
XX PR 21-JAN-1997; 97US-0036139P.
XX

```

PA (TEXA) UNIV TEXAS A & M SYSTEM.
 XX
 PT Hoeoek M, Patci JM, House-Pompeo KL, Speziale P, Joh D;
 PI Mcgavin MJ;
 DR WPI; 1998-413816/35.
 XX
 PT Antibody that binds to fibronectin-binding protein, preventing its
 PT binding to fibronectin - used to treat or prevent bacterial infection,
 PT especially by Staphylococci and Streptococci.
 XX
 PS Example 8; Page 102; 201pp; English.
 CC The invention relates to antibodies that bind to a fibronectin-binding
 CC domain of a fibronectin-binding protein, and inhibit binding of the
 CC protein to fibronectin. Also claimed are: (1) isolated peptides of a
 CC fibronectin-binding protein that do not bind to fibronectin; (2) fusion
 CC protein containing at least one peptide of a fibronectin-binding protein
 CC linked to a second amino acid sequence; (3) nucleic acid encoding the
 CC isolated peptide of (1). Antibodies, the isolated peptides of (1) and the
 CC nucleic acids are all useful for immunisation (active or passive) and (by
 CC inhibiting binding of bacteria to fibronectin) for preventing or treating
 CC infection in humans or other animals, particularly by staphylococci or
 CC streptococci, e.g. meningitis, otitis media, pneumonia, endocarditis,
 CC mastitis in cattle, abortion in horses and many others. Since the
 CC antibodies block binding of bacteria, they should be effective against
 CC antibiotic-resistant strains, and may replace antibiotic therapy or
 CC increase its effectiveness. Sequences AAW65691-700 represent a series of
 CC synthetic peptides based on the D1 region of S. aureus fibronectin
 CC binding protein A. They were synthesised to contain mutations
 XX
 SQ Sequence 38 AA;
 QY 1 EEDKPKYEEG 10
 |||||
 13 EEDKPKYEEG 22
 Db
 Query Match 100.0%; Score 56; DB 2; Length 38;
 Best Local Similarity 100.0%; Pred. No. 0.019;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 7
 AAW65691
 ID AAW65691 standard; peptide; 38 AA.
 XX
 AC AAW65691;
 XX
 DT 16-OCT-1998 (first entry)
 XX
 DE Fibronectin binding protein-derived peptide #35.
 XX
 KW microbial surface components recognising adhesive matrix molecule;
 KW MSCRAMM; fibronectin; fibronectin-binding protein; antibody; epitope;
 KW antibiotic; bacterial infection; antibiotic-resistant strain.
 XX
 OS Synthetic.
 OS Staphylococcus aureus.
 XX
 PN WO9831389-A2.
 XX
 PD 23-JUL-1998.
 XX
 PF 21-JAN-1998; 98WO-US001222.
 XX
 PR 21-JAN-1997; 97US-0036139P.
 XX
 PA (TEXA) UNIV TEXAS A & M SYSTEM.
 XX
 PI Hoeoek M, Patci JM, House-Pompeo KL, Speziale P, Joh D;
 PI Mcgavin MJ;
 XX
 DR WPI; 1998-413816/35.

XX
 PT Antibody that binds to fibronectin-binding protein, preventing its
 PT binding to fibronectin - used to treat or prevent bacterial infection,
 PT especially by Staphylococci and Streptococci.
 XX
 PS Example 8; Page 101; 201pp; English.
 CC The invention relates to antibodies that bind to a fibronectin-binding
 CC domain of a fibronectin-binding protein, and inhibit binding of the
 CC protein to fibronectin. Also claimed are: (1) isolated peptides of a
 CC fibronectin-binding protein that do not bind to fibronectin; (2) fusion
 CC protein containing at least one peptide of a fibronectin-binding protein
 CC linked to a second amino acid sequence; (3) nucleic acid encoding the
 CC isolated peptide of (1). Antibodies, the isolated peptides of (1) and the
 CC nucleic acids are all useful for immunisation (active or passive) and (by
 CC inhibiting binding of bacteria to fibronectin) for preventing or treating
 CC infection in humans or other animals, particularly by staphylococci or
 CC streptococci, e.g. meningitis, otitis media, pneumonia, endocarditis,
 CC mastitis in cattle, abortion in horses and many others. Since the
 CC antibodies block binding of bacteria, they should be effective against
 CC antibiotic-resistant strains, and may replace antibiotic therapy or
 CC increase its effectiveness. Sequences AAW65691-700 represent a series of
 CC synthetic peptides based on the D1 region of S. aureus fibronectin
 CC binding protein A. They were synthesised to contain mutations
 XX
 SQ Sequence 38 AA;
 QY 1 EEDKPKYEEG 10
 |||||
 13 EEDKPKYEEG 22
 Db
 Query Match 100.0%; Score 56; DB 2; Length 38;
 Best Local Similarity 100.0%; Pred. No. 0.019;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 8
 AAW65699
 ID AAW65699 standard; peptide; 38 AA.
 XX
 AC AAW65699;
 XX
 DT 16-OCT-1998 (first entry)
 XX
 DE Fibronectin binding protein-derived peptide #43.
 XX
 KW microbial surface components recognising adhesive matrix molecule;
 KW MSCRAMM; fibronectin; fibronectin-binding protein; antibody; epitope;
 KW antibiotic; bacterial infection; antibiotic-resistant strain.
 XX
 OS Synthetic.
 OS Staphylococcus aureus.
 XX
 PN WO9831389-A2.
 XX
 PD 23-JUL-1998.
 XX
 PF 21-JAN-1998; 98WO-US001222.
 XX
 PR 21-JAN-1997; 97US-0036139P.
 XX
 PA (TEXA) UNIV TEXAS A & M SYSTEM.
 XX
 PI Hoeoek M, Patci JM, House-Pompeo KL, Speziale P, Joh D;
 PI Mcgavin MJ;
 XX
 DR WPI; 1998-413816/35.
 XX
 PT Antibody that binds to fibronectin-binding protein, preventing its
 PT binding to fibronectin - used to treat or prevent bacterial infection,
 PT especially by Staphylococci and Streptococci.
 XX
 PS Example 8; Page 102; 201pp; English.

XX The invention relates to antibodies that bind to a fibronectin-binding
 CC domain of a fibronectin-binding protein, and inhibit binding of the
 CC protein to fibronectin. Also claimed are: (1) isolated peptides of a
 CC fibronectin-binding protein that do not bind to fibronectin; (2) fusion
 CC protein containing at least one peptide of a fibronectin-binding protein
 CC linked to a second amino acid sequence; (3) nucleic acid encoding the
 CC isolated peptide of (1). Antibodies, the isolated peptides of (1) and the
 CC nucleic acids are all useful for immunisation (active or passive) and (by
 CC inhibiting binding of bacteria to fibronectin) for preventing or treating
 CC infection in humans or other animals, particularly by staphylococci or
 CC streptococci, e.g. meningitis, otitis media, pneumonia, endocarditis,
 CC mastitis in cattle, abortion in horses and many others. Since the
 CC antibodies block binding of bacteria, they should be effective against
 CC antibiotic-resistant strains, and may replace antibiotic therapy or
 CC increase its effectiveness. Sequences AAW65691-700 represent a series of
 CC synthetic peptides based on the D1 region of *S. aureus* fibronectin
 CC binding protein A. They were synthesised to contain mutations

XX SQ Sequence 38 AA;

Query Match 100.0%; Score 56; DB 2; Length 38;
 Best Local Similarity 100.0%; Pred. No. 0.019;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EEDKPKYEEG 10
 |||||
 DB 13 EEDKPKYEEG 22

RESULT 9
 AAW65661 ID AAW65661 standard; peptide; 38 AA.

XX AAW65661;

XX 16-OCT-1998 (first entry)

XX Fibronectin binding protein-derived peptide #5.

XX microbial surface components recognising adhesive matrix molecule;
 KM MSCRAMM; fibronectin; fibronectin-binding protein; antibody; epitope;
 KM antibiotic; bacterial infection; antibiotic-resistant strain.

XX Synthetic.
 OS Staphylococcus aureus.

XX WO9831389-A2.

XX 23-JUL-1998.

XX 21-JAN-1998; 98WO-US001222.

XX 21-JAN-1997; 97US-0036139P.

XX (TEXA) UNIV TEXAS A & M SYSTEM.

XX Hoeoek M., Patli JM, House-Pompeo KL, Speziale P, Joh D;
 PI McGavin MJ;

XX WPI; 1998-413816/35.

XX Antibody that binds to fibronectin-binding protein, preventing its
 PT binding to fibronectin - used to treat or prevent bacterial infection,
 PT especially by Staphylococci and Streptococci.

XX Example 2; Page 92; 201pp; English.

XX The invention relates to antibodies that bind to a fibronectin-binding
 CC domain of a fibronectin-binding protein, and inhibit binding of the
 CC protein to fibronectin. Also claimed are: (1) isolated peptides of a
 CC fibronectin-binding protein that do not bind to fibronectin; (2) fusion
 CC protein containing at least one peptide of a fibronectin-binding protein

CC linked to a second amino acid sequence; (3) nucleic acid encoding the
 CC isolated peptide of (1). Antibodies, the isolated peptides of (1) and (by
 CC nucleic acids are all useful for immunisation (active or passive) and (by
 CC inhibiting binding of bacteria to fibronectin) for preventing or treating
 CC infection in humans or other animals, particularly by staphylococci or
 CC streptococci, e.g. meningitis, otitis media, pneumonia, endocarditis,
 CC mastitis in cattle, abortion in horses and many others. Since the
 CC antibodies block binding of bacteria, they should be effective against
 CC antibiotic-resistant strains, and may replace antibiotic therapy or
 CC increase its effectiveness. Sequences AAW6559-68 represent synthetic
 CC epitopes from the fibronectin binding domains DU and DI-D4 of the *S.*
 CC aureus fnbA gene

XX SQ Sequence 38 AA;

Query Match 100.0%; Score 56; DB 2; Length 38;
 Best Local Similarity 100.0%; Pred. No. 0.019;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EEDKPKYEEG 10
 |||||
 DB 13 EEDKPKYEEG 22

RESULT 10
 AAW65693 ID AAW65693 standard; peptide; 38 AA.

XX AAW65693;

XX 16-OCT-1998 (first entry)

XX Fibronectin binding protein-derived peptide #37.

XX microbial surface components recognising adhesive matrix molecule;
 KM MSCRAMM; fibronectin; fibronectin-binding protein; antibody; epitope;
 KM antibiotic; bacterial infection; antibiotic-resistant strain.

XX Synthetic.
 OS Staphylococcus aureus.

XX WO9831389-A2.

XX 23-JUL-1998.

XX 21-JAN-1998; 98WO-US001222.

XX 21-JAN-1997; 97US-0036139P.

XX (TEXA) UNIV TEXAS A & M SYSTEM.

XX Hoeoek M., Patli JM, House-Pompeo KL, Speziale P, Joh D;
 PI McGavin MJ;

XX WPI; 1998-413816/35.

XX Antibody that binds to fibronectin-binding protein, preventing its
 PT binding to fibronectin - used to treat or prevent bacterial infection,
 PT especially by Staphylococci and Streptococci.

XX Example 8; Page 102; 201pp; English.

XX The invention relates to antibodies that bind to a fibronectin-binding
 CC domain of a fibronectin-binding protein, and inhibit binding of the
 CC protein to fibronectin. Also claimed are: (1) isolated peptides of a
 CC fibronectin-binding protein that do not bind to fibronectin; (2) fusion
 CC protein containing at least one peptide of a fibronectin-binding protein
 CC linked to a second amino acid sequence; (3) nucleic acid encoding the
 CC isolated peptide of (1). Antibodies, the isolated peptides of (1) and the
 CC nucleic acids are all useful for immunisation (active or passive) and (by
 CC inhibiting binding of bacteria to fibronectin) for preventing or treating
 CC infection in humans or other animals, particularly by staphylococci or
 CC streptococci, e.g. meningitis, otitis media, pneumonia, endocarditis,

CC mastitis in cattle, abortion in horses and many others. Since the
 CC antibodies block binding of bacteria, they should be effective against
 CC antibiotic-resistant strains, and may replace antibiotic therapy or
 CC increase its effectiveness. Sequences AAM65691-700 represent a series of
 CC synthetic peptides based on the D1 region of *S. aureus* fibronectin
 CC binding protein A. They were synthesised to contain mutations

XX Sequence 38 AA:

Query Match 100.0%; Score 56; DB 2; Length 38;
 Best Local Similarity 100.0%; Pred. No. 0.019;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EEDKPKYEQG 10
 |||||
 DB 13 EEDKPKYEQG 22

RESULT 11

AAM65712
 ID AAM65712 standard; peptide; 39 AA.

XX AAM65712;

XX 16-OCT-1998 (first entry)

DE Fibronectin binding protein-derived peptide #56.

XX microbial surface components recognising adhesive matrix molecule;
 KW MSCRAMM; fibronectin; fibronectin-binding protein; antibody; epitope;
 KW antibiotic; bacterial infection; antibiotic-resistant strain.

XX Synthetic.

OS Staphylococcus aureus.

XX WO9831389-A2.

XX 23-JUL-1998.

XX 21-JAN-1998; 98WO-US001222.

XX 21-JAN-1997; 97US-0036139P.

XX (TEXA) UNIV TEXAS A & M SYSTEM.

PI Hoecek M, Patti JM, House-Pompeo XL, Speciale P, Joh D;
 PI McGavin MJ;

XX WPI; 1998-413816/35.

PT Antibody that binds to fibronectin-binding protein, preventing its
 PT binding to fibronectin - used to treat or prevent bacterial infection,
 PT especially by Staphylococci and Streptococci.

PS Example 8; Page 104; 201pp; English.

CC The invention relates to antibodies that bind to a fibronectin-binding
 CC domain of a fibronectin-binding protein, and inhibit binding of the
 CC protein to fibronectin. Also claimed are: (1) isolated peptides of a
 CC fibronectin-binding protein that do not bind to fibronectin; (2) fusion
 CC protein containing at least one peptide of a fibronectin-binding protein
 CC linked to a second amino acid sequence; (3) nucleic acid encoding the
 CC isolated peptide of (1). Antibodies, the isolated peptides of (1) and the
 CC nucleic acids are all useful for immunisation (active or passive) and (by
 CC inhibiting binding of bacteria to fibronectin) for preventing or treating
 CC infection in humans or other animals, particularly by staphylococci or
 CC streptococci, e.g. meningitis, otitis media, pneumonia, endocarditis,
 CC mastitis in cattle, abortion in horses and many others. Since the
 CC antibodies block binding of bacteria, they should be effective against
 CC antibiotic-resistant strains, and may replace antibiotic therapy or
 CC increase its effectiveness. The present sequence is shown in the
 CC specification

SQ Sequence 39 AA:

Query Match 100.0%; Score 56; DB 2; Length 39;
 Best Local Similarity 100.0%; Pred. No. 0.02;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EEDKPKYEQG 10
 |||||
 DB 13 EEDKPKYEQG 22

RESULT 12

AAR58806
 ID AAR58806 standard; protein; 130 AA.

XX AAR58806;

XX 25-MAR-2003 (revised)

DT 30-MAR-1995 (first entry)

DE Fibronectin binding domain D1-D4 (709-838 (P838T)).

XX Fibronectin binding protein; Fbp; fibronectin binding domain;
 KW monoclonal antibody; MAb; adhesion; Gram-positive bacterium; bacteremia;
 KW Escherichia coli.

OS Staphylococcus aureus.

XX WO9418327-A1.

XX 18-AUG-1994.

XX 04-FEB-1994; 94MO-GB000215.

XX 05-FEB-1993; 93GB-00002289.

XX 20-OCT-1993; 93GB-00021592.

XX (SMWK) SMITHKLINE BEECHAM PLC.

PI Burnham MKR, Chopra I, Critchley IA, Knowles DUC;

XX WPI; 1994-279748/34.

PT Fibronectin binding protein and monoclonal antibodies specific for Fbp -
 PT useful to prevent adherence of Gram-positive bacteria to indwelling
 PT devices or wounds.

PS Disclosure; Page 30; 40pp; English.

CC Polypeptides corresponding to residues 6709-T886 plus PPIVPT, 6709-
 CC P838(P838T) and 6709-P838 (AAR58805-07, respectively) of *S. aureus* J2385
 CC (NCIMB 40532) Fbp type A fibronectin binding domain D1-D4 region
 CC (AAR58808) were expressed in *E. coli* BL21 (DE4) and used to raise Mabs
 CC specific for Fbp. (Updated on 25-MAR-2003 to correct PN field.)

SQ Sequence 130 AA;

Query Match 100.0%; Score 56; DB 2; Length 130;
 Best Local Similarity 100.0%; Pred. No. 0.066;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EEDKPKYEQG 10
 |||||
 DB 14 EEDKPKYEQG 23

RESULT 13

AAR58807
 ID AAR58807 standard; protein; 130 AA.

XX AAR58807;

XX 25-MAR-2003 (revised)

DT 30-MAR-1995 (first entry)
 XX Fibronectin binding domain D1-D4 (709-838).
 DE Fibronectin binding protein; Fbp; fibronectin binding domain;
 XX monoclonal antibody; Mab; adhesion; Gram-positive bacterium; bacteremia;
 KW Escherichia coli.
 XX Staphylococcus aureus.
 OS
 XX WO9418327-A1.
 PN
 XX 18-AUG-1994.
 PD
 XX 04-FEB-1994; 94WO-GB000215.
 PF
 XX 05-FEB-1993; 93GB-00002289.
 PR 20-OCT-1993; 93GB-00021592.
 XX (SMK) SMITHKLINE BEECHAM PLC.
 PA Burnham MKR, Chopra I, Critchley IA, Knowles DJC;
 XX WPI; 1994-279748/34.
 DR
 XX Fibronectin binding protein and monoclonal antibodies specific for Fbp -
 PT useful to prevent adherence of Gram-positive bacteria to indwelling
 PT devices or wounds.
 PS Disclosure; Page 30; 40pp; English.
 XX Polypeptides corresponding to residues G709-T886 plus PPIVPT, G709-
 CC P838(P838T) and G709-P838 (AAR58805-07, respectively) of S. aureus J2385
 CC (NCIMB 40532) Fbp type A fibronectin binding domain D1-D4 region
 CC (AAR58808) were expressed in E. coli BL21(DE4) and used to raise MAb
 CC specific for Fbp. (Updated on 25-MAR-2003 to correct PN field.)
 CC
 XX Sequence 130 AA;
 SQ
 Query Match 100.0%; Score 56; DB 2; Length 130;
 Best Local Similarity 100.0%; Pred. No. 0.066;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 EEDKPKYEQG 10
 DB 14 EEDKPKYEQG 23
 RESULT 14
 AAR91202
 ID AAR91202 standard; peptide; 130 AA.
 XX
 AC AAR91202;
 XX
 DT 13-NOV-1996 (first entry)
 XX
 DE D1-D4 fibronectin binding domains.
 XX
 KW Fibronectin; oral hygiene; gingivitis; gum disease; adhesion;
 KW periodontitis; oral pathogen; caries; calculus; candidiasis; oral surgery;
 KW tissue regeneration; irrigation; toothpaste; dentifrice; mouthwash;
 KW lozenge.
 XX
 OS Staphylococcus aureus.
 XX
 PN WO9604003-A1.
 XX
 PD 15-FEB-1996.
 XX
 PF 18-JUL-1995; 95WO-EP002825.
 XX
 PR 05-AUG-1994; 94GB-00015902.
 XX

PA (SMK) SMITHKLINE BEECHAM PLC.
 XX
 PI Barnett P, Critchley IA, Dodd I;
 XX WPI; 1996-129122/13.
 DR
 XX Prevention of adherence of oral pathogens in the oral cavity, partic.
 PT tooth surfaces - by application of a fibronectin binding protein or
 PT polypeptide or a monoclonal antibody or fragment against it.
 XX
 PS Claim 5; Page 32; 41pp; English.
 XX
 CC Adherence of oral pathogens, particularly to tooth surfaces, can be
 CC prevented by application of a fibronectin binding protein or polypeptide.
 CC The fibronectin binding protein or polypeptide is useful in the
 CC manufacture of oral hygiene compositions, eg. toothpaste, liquid
 CC dentifrice, mouthwash or lozenge. They are useful to prevent the plaque-
 CC related development of carious lesions, gingivitis, calculus or
 CC periodontal disease and to combat oral cavity infections, e.g.
 CC candidiasis. They may also be useful in oral surgery e.g. in guided
 CC tissue regeneration procedures to prevent subsequent bacterial infection,
 CC and for irrigation of periodontal pockets. This sequence corresponds to
 CC amino acids 709-838 of the D1-D4 fibronectin binding domain of
 CC Staphylococcus aureus
 XX
 SQ Sequence 130 AA;
 Query Match 100.0%; Score 56; DB 2; Length 130;
 Best Local Similarity 100.0%; Pred. No. 0.066;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 EEDKPKYEQG 10
 DB 14 EEDKPKYEQG 23
 RESULT 15
 AAR91201
 ID AAR91201 standard; peptide; 130 AA.
 XX
 AC AAR91201;
 XX
 DT 13-NOV-1996 (first entry)
 XX
 DE D1-D4 fibronectin binding domains.
 XX
 KW Fibronectin; oral hygiene; gingivitis; gum disease; adhesion;
 KW periodontitis; oral pathogen; caries; calculus; candidiasis; oral surgery;
 KW tissue regeneration; irrigation; toothpaste; dentifrice; mouthwash;
 KW lozenge.
 XX
 OS Staphylococcus aureus.
 XX
 PN WO9604003-A1.
 XX
 PD 15-FEB-1996.
 XX
 PF 18-JUL-1995; 95WO-EP002825.
 XX
 PR 05-AUG-1994; 94GB-00015902.
 XX
 PA (SMK) SMITHKLINE BEECHAM PLC.
 XX
 PI Barnett P, Critchley IA, Dodd I;
 XX WPI; 1996-129122/13.
 DR
 XX Prevention of adherence of oral pathogens in the oral cavity, partic.
 PT tooth surfaces - by application of a fibronectin binding protein or
 PT polypeptide or a monoclonal antibody or fragment against it.
 XX
 PS Claim 5; Page 31-32; 41pp; English.
 XX

CC Adherence of oral pathogens, particularly to tooth surfaces, can be
CC prevented by application of a fibronectin binding protein or polypeptide.
CC The fibronectin binding protein or polypeptide is useful in the
CC manufacture of oral hygiene compositions, eg. toothpaste, liquid
CC dentifrice, mouthwash or lozenge. They are useful to prevent the plaque-
CC related development of carious lesions, gingivitis, calculus or
CC periodontal disease and to combat oral cavity infections, e.g.
CC candidiasis. They may also be useful in oral surgery e.g. in guided
CC tissue regeneration procedures to prevent subsequent bacterial infection,
CC and for irrigation of periodontal pockets. This sequence corresponds to
CC amino acids 709-838 of the D1-D4 fibronectin binding domain of
CC Staphylococcus aureus with a P838T substitution

XX Sequence 130 AA:

Query Match 100.0%; Score 56; DB 2; Length 130;
Best Local Similarity 100.0%; Pred. No. 0.066;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EEDKPKYEEG 10
|||
Db 14 EEDKPKYEEG 23

Search completed: October 25, 2005, 20:58:42
Job time : 63.2 secs

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OM protein - protein search, using sw model

Run on: October 22, 2005, 05:46:56 ; Search time 17.3 Seconds
(without alignments)
43.150 Million cell updates/sec

Title: US-10-731-238-69

Perfect score: 56

Sequence: 1 EEDKPYEQG 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

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Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA: *
1: /cgn2_6/prodata/1/aa/5A_COMB.pep: *
2: /cgn2_6/prodata/1/aa/5B_COMB.pep: *
3: /cgn2_6/prodata/1/aa/6A_COMB.pep: *
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5: /cgn2_6/prodata/1/aa/PCTUS_COMB.pep: *
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	56	100.0	10	US-09-010-317-69	Sequence 69, Appl
2	56	100.0	38	US-08-234-622A-2	Sequence 2, Appl
3	56	100.0	38	US-08-729-767-3	Sequence 3, Appl
4	56	100.0	38	US-09-010-317-5	Sequence 5, Appl
5	56	100.0	38	US-09-010-317-35	Sequence 35, Appl
6	56	100.0	38	US-09-010-317-36	Sequence 36, Appl
7	56	100.0	38	US-09-010-317-37	Sequence 37, Appl
8	56	100.0	38	US-09-010-317-38	Sequence 38, Appl
9	56	100.0	38	US-09-010-317-39	Sequence 39, Appl
10	56	100.0	38	US-09-010-317-43	Sequence 43, Appl
11	56	100.0	39	US-09-010-317-56	Sequence 56, Appl
12	56	100.0	114	US-08-259-000-3	Sequence 3, Appl
13	56	100.0	130	US-08-459-135A-7	Sequence 7, Appl
14	56	100.0	130	US-08-459-135A-8	Sequence 8, Appl
15	56	100.0	130	US-08-495-559-7	Sequence 7, Appl
16	56	100.0	130	US-08-495-559-8	Sequence 8, Appl
17	56	100.0	139	US-08-856-253-8	Sequence 8, Appl
18	56	100.0	174	US-08-459-135A-10	Sequence 10, Appl
19	56	100.0	174	US-08-459-135A-13	Sequence 13, Appl
20	56	100.0	174	US-08-495-559-10	Sequence 10, Appl
21	56	100.0	174	US-08-495-559-13	Sequence 13, Appl
22	56	100.0	176	US-08-495-559-6	Sequence 6, Appl
23	56	100.0	178	US-08-459-135A-12	Sequence 12, Appl
24	56	100.0	178	US-08-495-559-12	Sequence 12, Appl
25	56	100.0	181	US-08-459-135A-6	Sequence 6, Appl
26	56	100.0	559	US-08-956-171E-5251	Sequence 5251, Ap
27	56	100.0	559	US-08-781-986A-5251	Sequence 5251, Ap

28	56	100.0	1027	US-08-956-171E-5254	Sequence 5254, Ap
29	56	100.0	1027	US-08-781-986A-5254	Sequence 5254, Ap
30	51	91.1	38	US-09-010-317-40	Sequence 40, Appl
31	50	89.3	38	US-09-010-317-6	Sequence 6, Appl
32	50	89.3	38	US-09-010-317-41	Sequence 41, Appl
33	50	89.3	38	US-09-010-317-44	Sequence 44, Appl
34	50	89.3	39	US-09-010-317-57	Sequence 57, Appl
35	49	87.5	38	US-09-010-317-42	Sequence 42, Appl
36	47	83.9	38	US-08-234-622A-3	Sequence 3, Appl
37	47	83.9	38	US-08-729-767-4	Sequence 4, Appl
38	47	83.9	38	US-09-010-317-7	Sequence 7, Appl
39	47	83.9	38	US-09-010-317-45	Sequence 45, Appl
40	47	83.9	38	US-09-010-317-46	Sequence 46, Appl
41	47	83.9	38	US-09-010-317-47	Sequence 47, Appl
42	47	83.9	38	US-09-010-317-48	Sequence 48, Appl
43	47	83.9	38	US-09-010-317-49	Sequence 49, Appl
44	46	82.1	10	US-09-010-317-70	Sequence 70, Appl
45	45	80.4	10	US-09-010-317-68	Sequence 68, Appl

ALIGNMENTS

RESULT 1
US-09-010-317-69
; Sequence 69, Application US/09010317
; Patent No. 6685943
; GENERAL INFORMATION:
; APPLICANT: Hook, Magnus
; APPLICANT: Patti, Joseph M.
; APPLICANT: House-Pompeo, Karen L.
; APPLICANT: Speziale, Pietro
; APPLICANT: John, Danny
; APPLICANT: McQuinn, Martin J.
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
; TITLE OF INVENTION: AND METHODS OF USE
; NUMBER OF SEQUENCES: 105
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: TX
; COUNTRY: USA
; ZIP: 77210-4433
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/010,317
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/036,139
; FILING DATE: 21-JAN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Hilder, David W.
; REGISTRATION NUMBER: 41,071
; REFERENCE/DOCKET NUMBER: TAMK:169
; TELEPHONE: 512-418-3000
; TELEFAX: 512-474-7577
; INFORMATION FOR SEQ ID NO: 69:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; US-09-010-317-69
Query Match 100.0%; Score 56; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0014;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EEDKPYE0G 10
|||||

Db 1 EEDKPYE0G 10

RESULT 2
US-08-234-622A-2
; Sequence 2, Application US/08234622A
; Patent No. 5440014
; GENERAL INFORMATION:
; APPLICANT: HOOK, Magnus
; APPLICANT: MCGAVIN, Martin
; APPLICANT: RAUCCI, Giuseppe
; TITLE OF INVENTION: A FIBRONECTIN BINDING PEPTIDE
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Doane, Swecker & Mathis
; STREET: P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22113-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/234,622A
; FILING DATE: 28-APR-1994
; CLASSIFICATION: 330
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: SE 9002617-0
; FILING DATE: 10-AUG-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/SE91/00534
; FILING DATE: 09-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Meuth, Donna M
; REGISTRATION NUMBER: 36,607
; REFERENCE/DOCKET NUMBER: 012885-044
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 38 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-234-622A-2

Query Match 100.0%; Score 56; DB 1; Length 38;
Best Local Similarity 100.0%; Pred. No. 0.0054;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EEDKPYE0G 10
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Db 13 EEDKPYE0G 22

RESULT 3
US-08-729-767-3
; Sequence 3, Application US/08729767
; Patent No. 570702
; GENERAL INFORMATION:
; APPLICANT: HOOK, Magnus
; APPLICANT: LINDBERG, Martin Kjell
; APPLICANT: SIGNAS, Lars Christer
; APPLICANT: WADSTROM, Torkel Mikael

; APPLICANT: FROMAN, Gunnar
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN AS WELL AS
; TITLE OF INVENTION: ITS PREPARATION
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Doane, Swecker & Mathis, L.L.P.
; STREET: P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22113-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/729,767
; FILING DATE: 07-OCT-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/259,000
; FILING DATE: 13-JUN-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/007,817
; FILING DATE: 22-JAN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/201,028
; FILING DATE: 01-JUN-1988
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: SE 8702272-9
; FILING DATE: 01-JUN-1987
; ATTORNEY/AGENT INFORMATION:
; NAME: McGowan, Malcolm K.
; REGISTRATION NUMBER: 39,300
; REFERENCE/DOCKET NUMBER: 012889-036
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 38 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-729-767-3

Query Match 100.0%; Score 56; DB 1; Length 38;
Best Local Similarity 100.0%; Pred. No. 0.0054;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EEDKPYE0G 10
|||||

Db 14 EEDKPYE0G 23

RESULT 4
US-09-010-317-5
; Sequence 5, Application US/09010317
; Patent No. 6685943
; GENERAL INFORMATION:
; APPLICANT: Hook, Magnus
; APPLICANT: Patil, Joseph M.
; APPLICANT: House-Pompeo, Karen L.
; APPLICANT: Speciale, Pietro
; APPLICANT: Joh, Danny
; APPLICANT: McGavin, Martin J.
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
; TITLE OF INVENTION: AND METHODS OF USE
; NUMBER OF SEQUENCES: 105
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee

STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/036,139
ATTORNEY/AGENT INFORMATION:
NAME: Hibley, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAMK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-09-010-317-5
Query Match 100.0%; Score 56; DB 4; Length 38;
Best Local Similarity 100.0%; Pred. No. 0.0054;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 EEDKPYEKG 10
Db 13 EEDKPYEKG 22
RESULT 5
US-09-010-317-35
Sequence 35, Application US/09010317
Patent No. 6685943
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
APPLICANT: Patti, Joseph M.
APPLICANT: House-Pompeo, Karen L.
APPLICANT: Speziale, Pietro
APPLICANT: Joh, Danny
APPLICANT: McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
TITLE OF INVENTION: AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/036,139

FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibley, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAMK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 35:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-09-010-317-35
Query Match 100.0%; Score 56; DB 4; Length 38;
Best Local Similarity 100.0%; Pred. No. 0.0054;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 EEDKPYEKG 10
Db 13 EEDKPYEKG 22
RESULT 6
US-09-010-317-36
Sequence 36, Application US/09010317
Patent No. 6685943
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
APPLICANT: Patti, Joseph M.
APPLICANT: House-Pompeo, Karen L.
APPLICANT: Speziale, Pietro
APPLICANT: Joh, Danny
APPLICANT: McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
TITLE OF INVENTION: AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibley, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAMK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 36:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-09-010-317-36

Query Match 100.0%; Score 56; DB 4; Length 38;
Best Local Similarity 100.0%; Pred. No. 0.0054;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EEDKPYEEOG 10
13 EEDKPYEEOG 22

Db 13 EEDKPYEEOG 22

RESULT 7

US-09-010-317-37
; Sequence 37, Application US/09010317
; Patent No. 6685943
; GENERAL INFORMATION:
; APPLICANT: Hook, Magnus
; APPLICANT: Patti, Joseph M.
; APPLICANT: House-Pompeo, Karen L.
; APPLICANT: Speziale, Pietro
; APPLICANT: McGavin, Martin J.
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
; TITLE OF INVENTION: AND METHODS OF USE
; NUMBER OF SEQUENCES: 105
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: TX
; COUNTRY: USA
; ZIP: 77210-4433
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/010,317
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/036,139
; FILING DATE: 21-JAN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Hibler, David W.
; REGISTRATION NUMBER: 41,071
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 512-474-7577
; TELEFAX: 512-474-7577
; INFORMATION FOR SEQ ID NO: 37:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 38 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
US-09-010-317-37

Query Match 100.0%; Score 56; DB 4; Length 38;
Best Local Similarity 100.0%; Pred. No. 0.0054;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EEDKPYEEOG 10
13 EEDKPYEEOG 22

Db 13 EEDKPYEEOG 22

RESULT 8

US-09-010-317-38
; Sequence 38, Application US/09010317
; Patent No. 6685943
; GENERAL INFORMATION:
; APPLICANT: Hook, Magnus
; APPLICANT: Patti, Joseph M.

; APPLICANT: House-Pompeo, Karen L.
; APPLICANT: Speziale, Pietro
; APPLICANT: Joh, Danny
; APPLICANT: McGavin, Martin J.
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
; TITLE OF INVENTION: AND METHODS OF USE
; NUMBER OF SEQUENCES: 105
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: TX
; COUNTRY: USA
; ZIP: 77210-4433
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/010,317
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/036,139
; FILING DATE: 21-JAN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Hibler, David W.
; REGISTRATION NUMBER: 41,071
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 512-474-7577
; TELEFAX: 512-474-7577
; INFORMATION FOR SEQ ID NO: 38:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 38 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
US-09-010-317-38

Query Match 100.0%; Score 56; DB 4; Length 38;
Best Local Similarity 100.0%; Pred. No. 0.0054;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EEDKPYEEOG 10
13 EEDKPYEEOG 22

Db 13 EEDKPYEEOG 22

RESULT 9

US-09-010-317-39
; Sequence 39, Application US/09010317
; Patent No. 6685943
; GENERAL INFORMATION:
; APPLICANT: Hook, Magnus
; APPLICANT: Patti, Joseph M.
; APPLICANT: House-Pompeo, Karen L.
; APPLICANT: Speziale, Pietro
; APPLICANT: McGavin, Martin J.
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
; TITLE OF INVENTION: AND METHODS OF USE
; NUMBER OF SEQUENCES: 105
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: TX
; COUNTRY: USA
; ZIP: 77210-4433
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk

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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAMK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 39:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-09-010-317-39

Query Match          100.0%; Score 56; DB 4; Length 38;
Best Local Similarity 100.0%; Pred. No. 0.0054;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EEDKPKYEQG 10
Db 13 EEDKPKYEQG 22

RESULT 10
US-09-010-317-43
Sequence 43, Application US/09010317
Patent No. 6685943
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
APPLICANT: Patti, Joseph M.
APPLICANT: House-Pompeo, Karen L.
APPLICANT: Speziale, Pietro
APPLICANT: Joh, Danny
APPLICANT: McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
TITLE OF INVENTION: AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSER: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAMK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 56:
SEQUENCE CHARACTERISTICS:
LENGTH: 39 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-09-010-317-56

Query Match          100.0%; Score 56; DB 4; Length 39;
Best Local Similarity 100.0%; Pred. No. 0.0056;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 43:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-09-010-317-43

Query Match          100.0%; Score 56; DB 4; Length 38;
Best Local Similarity 100.0%; Pred. No. 0.0054;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EEDKPKYEQG 10
Db 13 EEDKPKYEQG 22

RESULT 11
US-09-010-317-56
Sequence 56, Application US/09010317
Patent No. 6685943
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
APPLICANT: Patti, Joseph M.
APPLICANT: House-Pompeo, Karen L.
APPLICANT: Speziale, Pietro
APPLICANT: Joh, Danny
APPLICANT: McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
TITLE OF INVENTION: AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSER: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAMK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 56:
SEQUENCE CHARACTERISTICS:
LENGTH: 39 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-09-010-317-56

Query Match          100.0%; Score 56; DB 4; Length 39;
Best Local Similarity 100.0%; Pred. No. 0.0056;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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RESULT 12
US-08-259-000-3
Sequence 3, Application US/08259000
Patent No. 5571514
GENERAL INFORMATION:
APPLICANT: HOOK, Magnus
APPLICANT: LINDERBERG, Martin Kjell
APPLICANT: SIGNAS, Lars Christer
APPLICANT: MADSTROM, Torkel Mikael
APPLICANT: FROMAN, Gunnar
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN AS WELL AS
TITLE OF INVENTION: ITS PREPARATION
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Burns, Doane, Swecker & Mathis
STREET: P.O. Box 1404
CITY: Alexandria
STATE: Virginia
COUNTRY: United States
ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/259,000
FILING DATE: 13-JUN-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: SE 8702272-9
FILING DATE: 01-JUN-1987
ATTORNEY/AGENT INFORMATION:
NAME: Meuth, Donna M
REGISTRATION NUMBER: 36,607
REFERENCE/DOCKET NUMBER: 012885-062
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-6620
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 114 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-259-000-3

Query Match 100.0%; Score 56; DB 1; Length 114;
Best Local Similarity 100.0%; Pred. No. 0.016;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EEDKPYEEOG 10
DB 14 EEDKPYEEOG 23

RESULT 13
US-08-459-135A-7
Sequence 7, Application US/08459135A
Patent No. 5955078
GENERAL INFORMATION:
APPLICANT: BURNHAM, Martin Karl Russel
APPLICANT: CHOPRA, Ian
APPLICANT: CRITCHLEY, Ian Alfred
APPLICANT: KNOWLES, David Justin Charles
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN: MONOCLONAL ANTIBODY AND THEIR US
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road

CITY: King of Prussia
STATE: PA
COUNTRY: U.S.A.
ZIP: 19406-0939
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: Fastseq, Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/459,135A
FILING DATE: 02-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB/94/00215
FILING DATE: 04-Feb-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Gimm, Edward R
REGISTRATION NUMBER: 38,891
REFERENCE/DOCKET NUMBER: P30591C2
TELEPHONE: 610-270-4478
TELEFAX: 610-270-5090
TELEX:
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 130 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-459-135A-7

Query Match 100.0%; Score 56; DB 2; Length 130;
Best Local Similarity 100.0%; Pred. No. 0.019;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EEDKPYEEOG 10
DB 14 EEDKPYEEOG 23

RESULT 14
US-08-459-135A-8
Sequence 8, Application US/08459135A
Patent No. 5955078
GENERAL INFORMATION:
APPLICANT: BURNHAM, Martin Karl Russel
APPLICANT: CHOPRA, Ian
APPLICANT: CRITCHLEY, Ian Alfred
APPLICANT: KNOWLES, David Justin Charles
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN: MONOCLONAL ANTIBODY AND THEIR US
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
STATE: PA
COUNTRY: U.S.A.
ZIP: 19406-0939
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: Fastseq, Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/459,135A
FILING DATE: 02-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB/94/00215
FILING DATE: 04-Feb-1994
CLASSIFICATION: 435

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; ATTORNEY/AGENT INFORMATION:
; NAME: Gimmil, Edward R
; REGISTRATION NUMBER: 38,891
; REFERENCE/DOCKET NUMBER: P30591C2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-270-4478
; TELEFAX: 610-270-5090
;
; TELEX:
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 130 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
;
US-08-459-135A-8

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Query Match          100.0%; Score 56; DB 2; Length 130;
Best Local Similarity 100.0%; Pred. No. 0.019;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      1 EEDKPKYEQG 10
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        14 EEDKPKYEQG 23

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RESULT 15
US-08-495-559-7
; Sequence 7, Application US/08495559A
; Patent No. 6054572
; GENERAL INFORMATION:
; APPLICANT: BURMAN, Martin Karl Russel
; APPLICANT: CHOPRA, Ian
; APPLICANT: CRITCHLEY, Ian Alfred
; APPLICANT: KNOWLES, David Justin Charles
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN: MONOCLONAL
; TITLE OF INVENTION: ANTIBODY AND THEIR USE IN PREVENTING BACTERIAL ADHESION
; FILE REFERENCE: P30591
; CURRENT APPLICATION NUMBER: US/08/495,559A
; CURRENT FILING DATE: 1995-08-03
; EARLIER APPLICATION NUMBER: GB 9302289.5
; EARLIER FILING DATE: 1993-02-05
; EARLIER APPLICATION NUMBER: GB 9321592.9
; EARLIER FILING DATE: 1993-10-20
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 7
; LENGTH: 130
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
;
US-08-495-559-7

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Query Match          100.0%; Score 56; DB 3; Length 130;
Best Local Similarity 100.0%; Pred. No. 0.019;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      1 EEDKPKYEQG 10
        |||||
        14 EEDKPKYEQG 23

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Job time : 18.35 secs

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GenCore version 5.1.6
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OM protein - protein search, using SW model

Run on: October 22, 2005, 12:09:40 ; Search time 57.25 Seconds
(without alignments)
72.924 Million cell updates/sec

Title: US-10-731-238-69

Perfect score: 56

Sequence: 1 BEDKPKYEQG 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1862951 seqs, 417491010 residues

Total number of hits satisfying chosen parameters: 1862951

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA.*

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3: /cgn2_6/ptodata/2/pubppa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/2/pubppa/US07_PUBCOMB.pep.*
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18: /cgn2_6/ptodata/2/pubppa/US10_PUBCOMB.pep.*
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22: /cgn2_6/ptodata/2/pubppa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	56	100.0	10	US-10-731-238-69	Sequence 69, Appl
2	56	100.0	38	US-10-731-238-5	Sequence 5, Appl
3	56	100.0	38	US-10-731-238-35	Sequence 35, Appl
4	56	100.0	38	US-10-731-238-36	Sequence 36, Appl
5	56	100.0	38	US-10-731-238-37	Sequence 37, Appl
6	56	100.0	38	US-10-731-238-38	Sequence 38, Appl
7	56	100.0	38	US-10-731-238-39	Sequence 39, Appl
8	56	100.0	38	US-10-731-238-43	Sequence 43, Appl
9	56	100.0	39	US-10-731-238-56	Sequence 56, Appl
10	56	100.0	139	US-09-813-820-8	Sequence 8, Appl
11	56	100.0	388	US-08-901-062-1	Sequence 1, Appl

12	56	100.0	559	8	US-08-781-986A-5251	Sequence 5251, Ap
13	56	100.0	559	15	US-10-329-624-5251	Sequence 5251, Ap
14	56	100.0	767	9	US-09-815-242-5899	Sequence 5899, Ap
15	56	100.0	767	9	US-09-815-242-13140	Sequence 13140, A
16	56	100.0	940	17	US-10-470-048B-424	Sequence 424, App
17	56	100.0	948	17	US-10-470-048B-69	Sequence 69, Appl
18	56	100.0	961	15	US-10-282-122A-43778	Sequence 43778, A
19	56	100.0	978	9	US-09-815-242-5456	Sequence 5456, Ap
20	56	100.0	1001	9	US-09-815-242-12686	Sequence 12686, A
21	56	100.0	1018	9	US-09-815-242-5797	Sequence 5797, Ap
22	56	100.0	1018	9	US-09-815-242-12838	Sequence 12838, A
23	56	100.0	1018	17	US-10-470-048B-68	Sequence 68, Appl
24	56	100.0	1027	8	US-08-781-986A-5254	Sequence 5254, Ap
25	56	100.0	1027	15	US-10-329-624-5254	Sequence 5254, Ap
26	56	100.0	1038	15	US-10-282-122A-43827	Sequence 43827, A
27	56	100.0	1038	15	US-10-282-122A-43827	Sequence 43827, A
28	52	92.9	30	14	US-10-287-821-1	Sequence 1, Appl
29	52	92.9	31	14	US-10-287-821-2	Sequence 2, Appl
30	51	91.1	38	18	US-10-731-238-40	Sequence 40, Appl
31	50	89.3	38	18	US-10-731-238-41	Sequence 41, Appl
32	50	89.3	38	18	US-10-731-238-41	Sequence 41, Appl
33	50	89.3	38	18	US-10-731-238-41	Sequence 41, Appl
34	50	89.3	38	18	US-10-731-238-41	Sequence 41, Appl
35	49	87.5	38	18	US-10-731-238-42	Sequence 42, Appl
36	47	83.9	38	18	US-10-731-238-45	Sequence 45, Appl
37	47	83.9	38	18	US-10-731-238-46	Sequence 46, Appl
38	47	83.9	38	18	US-10-731-238-47	Sequence 47, Appl
39	47	83.9	38	18	US-10-731-238-48	Sequence 48, Appl
40	47	83.9	38	18	US-10-731-238-49	Sequence 49, Appl
41	46	82.1	10	18	US-10-731-238-70	Sequence 70, Appl
42	45	80.4	10	18	US-10-731-238-105	Sequence 105, Appl
43	45	80.4	14	18	US-10-731-238-8	Sequence 8, Appl
44	41	73.2	38	18	US-10-731-238-8	Sequence 8, Appl
45	41	73.2	38	18	US-10-731-238-50	Sequence 50, Appl

ALIGNMENTS

RESULT 1
US-10-731-238-69
Sequence 69, Application US/10731238
Publication No. US20050123552A1
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
Pacifi, Joseph M.
House-Pompeo, Karen L.
Speziale, Pietro
Job, Danny
McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSER: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/731,238
FILING DATE: 10-Dec-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE: 21-Jan-1998
APPLICATION NUMBER: US 60/036,139

FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAMK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 69:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 69:
US-10-731-238-69

Query Match 100.0%; Score 56; DB 18; Length 10
Best Local Similarity 100.0%; Pred. No. 0.0049;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 BEDKPYE0G 10
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DB 1 BEDKPYE0G 10

RESULT 2
US-10-731-238-5
Sequence 5, Application US/10731238
Publication No. US20050123552A1
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
Patti, Joseph M.
House-Pompeo, Karen L.
Speziale, Pietro
Joh, Danny
McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/731,238
FILING DATE: 10-Dec-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE: 21-Jan-1998
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAMK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>

TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-10-731-238-5

Query Match 100.0%; Score 56; DB 18; Length 38;
Best Local Similarity 100.0%; Pred. No. 0.019;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 BEDKPYE0G 10
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DB 13 BEDKPYE0G 22

RESULT 3
US-10-731-238-35
Sequence 35, Application US/10731238
Publication No. US20050123552A1
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
Patti, Joseph M.
House-Pompeo, Karen L.
Speziale, Pietro
Joh, Danny
McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/731,238
FILING DATE: 10-Dec-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE: 21-Jan-1998
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAMK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 35:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 35:
US-10-731-238-35

Query Match 100.0%; Score 56; DB 18; Length 38;
Best Local Similarity 100.0%; Pred. No. 0.019;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 BEDKPYE0G 10
|||||

DB 13 BEDKPYE0G 22

RESULT 4
US-10-731-238-36
; Sequence 36, Application US/10731238
; Publication No. US20050123552A1
; GENERAL INFORMATION:
; APPLICANT: Hook, Magnus
; Patti, Joseph M.
; House-Pompeo, Karen L.
; Speciale, Pietro
; John, Danny
; McGavin, Martin J.
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
; NUMBER OF SEQUENCES: 105
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: TX
; COUNTRY: USA
; ZIP: 77210-4433
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/731,238
; FILING DATE: 10-Dec-2003
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/010,317
; FILING DATE: 21-Jan-1998
; APPLICATION NUMBER: US 60/036,139
; FILING DATE: 21-Jan-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Hibler, David W.
; REGISTRATION NUMBER: 41,071
; REFERENCE/DOCKET NUMBER: TAMK:189
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 512-418-3000
; TELEFAX: 512-474-7577
; INFORMATION FOR SEQ ID NO: 36:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 38 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 36:
US-10-731-238-36

Query Match 100.0%; Score 56; DB 18; Length 38;
Best Local Similarity 100.0%; Pred. No. 0.019; 0;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EEDKPKYEEG 10
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| | | | | | | | | |
Db 13 EEDKPKYEEG 22

RESULT 5
US-10-731-238-37
; Sequence 37, Application US/10731238
; Publication No. US20050123552A1
; GENERAL INFORMATION:
; APPLICANT: Hook, Magnus
; Patti, Joseph M.
; House-Pompeo, Karen L.
; Speciale, Pietro
; John, Danny
; McGavin, Martin J.
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
; AND METHODS OF USE

; NUMBER OF SEQUENCES: 105
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: TX
; COUNTRY: USA
; ZIP: 77210-4433
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/731,238
; FILING DATE: 10-Dec-2003
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/010,317
; FILING DATE: 21-Jan-1998
; APPLICATION NUMBER: US 60/036,139
; FILING DATE: 21-Jan-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Hibler, David W.
; REGISTRATION NUMBER: 41,071
; REFERENCE/DOCKET NUMBER: TAMK:189
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 512-418-3000
; TELEFAX: 512-474-7577
; INFORMATION FOR SEQ ID NO: 37:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 38 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 37:
US-10-731-238-37

Query Match 100.0%; Score 56; DB 18; Length 38;
Best Local Similarity 100.0%; Pred. No. 0.019;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EEDKPKYEEG 10
| | | | | | | | | |
| | | | | | | | | |
Db 13 EEDKPKYEEG 22

RESULT 6
US-10-731-238-38
; Sequence 38, Application US/10731238
; Publication No. US20050123552A1
; GENERAL INFORMATION:
; APPLICANT: Hook, Magnus
; Patti, Joseph M.
; House-Pompeo, Karen L.
; Speciale, Pietro
; John, Danny
; McGavin, Martin J.
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
; AND METHODS OF USE
; NUMBER OF SEQUENCES: 105
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: TX
; COUNTRY: USA
; ZIP: 77210-4433
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/731,238
FILING DATE: 10-Dec-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE: 21-Jan-1998
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-Jan-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAMK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 38:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 38:
US-10-731-238-38

Query Match 100.0%; Score 56; DB 18; Length 38;
Best Local Similarity 100.0%; Pred. No. 0.019;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EEDKPKYEQG 10
|||
DB 13 EEDKPKYEQG 22

RESULT 7
US-10-731-238-39
Sequence 39, Application US/10731238
Publication No. US20050123552A1
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
Patli, Joseph M.
House-Pompeo, Karen L.
Speziale, Pietro
Job, Danny
McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/731,238
FILING DATE: 10-Dec-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE: 21-Jan-1998
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-Jan-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAMK:189

TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 39:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 39:
US-10-731-238-39

Query Match 100.0%; Score 56; DB 18; Length 38;
Best Local Similarity 100.0%; Pred. No. 0.019;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EEDKPKYEQG 10
|||
DB 13 EEDKPKYEQG 22

RESULT 8
US-10-731-238-43
Sequence 43, Application US/10731238
Publication No. US20050123552A1
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
Patli, Joseph M.
House-Pompeo, Karen L.
Speziale, Pietro
Job, Danny
McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/731,238
FILING DATE: 10-Dec-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE: 21-Jan-1998
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-Jan-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAMK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 43:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 43:
US-10-731-238-43

Query Match 100.0%; Score 56; DB 18; Length 38;

Best Local Similarity 100.0%; Pred. No. 0.019;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EEDKPKYEG 10
|||
Db 13 EEDKPKYEG 22

RESULT 9

US-10-731-238-56

; Sequence 56, Application US/10731238

; Publication No. US20050123552A1

; GENERAL INFORMATION:

APPLICANT: Hook, Magnus

Pattl, Joseph M.

House-Pompeo, Karen L.

Speziale, Pietro

Job, Danny

McGavin, Martin J.

TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS

AND METHODS OF USE

NUMBER OF SEQUENCES: 105

CORRESPONDENCE ADDRESS:

ADDRESSEE: Arnold, White & Durkee

STREET: P.O. Box 4433

CITY: Houston

STATE: TX

COUNTRY: USA

ZIP: 77210-4433

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/731.238

FILING DATE: 10-Dec-2003

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/010.317

FILING DATE: 21-Jan-1998

APPLICATION NUMBER: US 60/036,139

FILING DATE: 21-JAN-1997

ATTORNEY/AGENT INFORMATION:

NAME: Hibler, David W.

REGISTRATION NUMBER: 41,071

REFERENCE/DOCKET NUMBER: TAMK.189

TELECOMMUNICATION INFORMATION:

TELEPHONE: 512-418-3000

TELEFAX: 512-474-7577

INFORMATION FOR SEQ ID NO: 56:

SEQUENCE CHARACTERISTICS:

LENGTH: 39 amino acids

TYPE: amino acid

STRANDEDNESS: <Unknown>

TOPOLOGY: linear

SEQUENCE DESCRIPTION: SEQ ID NO: 56:

US-10-731-238-56

Query Match 100.0%; Score 56; DB 18; Length 39;

Best Local Similarity 100.0%; Pred. No. 0.02;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EEDKPKYEG 10
|||
Db 13 EEDKPKYEG 22

APPLICANT: Hook, Magnus

Pattl, Joseph M.

House-Pompeo, Karen

Sthanam, Narayana

Symerksy, Jindrich

TITLE OF INVENTION: COLLAGEN BINDING PROTEIN COMPOSITIONS

AND METHODS OF USE

NUMBER OF SEQUENCES: 8

CORRESPONDENCE ADDRESS:

ADDRESSEE: Arnold, White & Durkee

STREET: P.O. Box 4433

CITY: Houston

STATE: Texas

COUNTRY: U.S.

ZIP: 77210

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/813,820

FILING DATE: 22-Mar-2001

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/856,253

FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: Kitchell, Barbara S.

REGISTRATION NUMBER: 33,928

REFERENCE/DOCKET NUMBER: TAMK.193

TELECOMMUNICATION INFORMATION:

TELEPHONE: (512) 418-3000

TELEFAX: (512) 474-7577

INFORMATION FOR SEQ ID NO: 8:

SEQUENCE CHARACTERISTICS:

LENGTH: 139 amino acids

TYPE: amino acid

STRANDEDNESS: <Unknown>

TOPOLOGY: linear

SEQUENCE DESCRIPTION: SEQ ID NO: 8:

US-09-813-820-8

Query Match 100.0%; Score 56; DB 9; Length 139;

Best Local Similarity 100.0%; Pred. No. 0.073; Indels 0; Gaps 0;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EEDKPKYEG 10
|||
Db 28 EEDKPKYEG 37

RESULT 11

US-08-901-062-1

; Sequence 1, Application US/08901062

; Publication No. US20020025324A1

; GENERAL INFORMATION:

APPLICANT: SEALS, JONATHAN R.

TITLE OF INVENTION: RECOMBINANT BIVALENT BACTERIAL VACCINE

FOR THE PREVENTION OF MASTITIS

NUMBER OF SEQUENCES: 2

CORRESPONDENCE ADDRESS:

ADDRESSEE: HALE AND DORR LLP

STREET: 60 State Street

CITY: Boston

STATE: MA

COUNTRY: United States Of America

ZIP: 02109

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/901,062
FILING DATE: 25-JUL-1997
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Baker, Hollie L.
REGISTRATION NUMBER: 31,321
REFERENCE/DOCKET NUMBER: 106941.153
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 526-6000
TELEFAX: (617) 526-5000
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 388 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-901-062-1

Query Match 100.0%; Score 56; DB 8; Length 388;
Best Local Similarity 100.0%; Pred. No. 0.21;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EEDKPKYEQG 10
DB 277 EEDKPKYEQG 286

RESULT 12
US-08-781-986A-5251
Sequence 5251, Application US/08781986A
Publication No. US20030054436A1
GENERAL INFORMATION:
APPLICANT: Charles Kunsch
TITLE OF INVENTION: Staphylococcus aureus polynucleotides and Sequences
NUMBER OF SEQUENCES: 5255
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COUNTRY: USA
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/781,986A
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Benson, Bob
REGISTRATION NUMBER: 30,446
REFERENCE/DOCKET NUMBER: PB248PP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 5251:
SEQUENCE CHARACTERISTICS:
LENGTH: 559 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-781-986A-5251

Query Match 100.0%; Score 56; DB 8; Length 559;
Best Local Similarity 100.0%; Pred. No. 0.3;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EEDKPKYEQG 10
DB 313 EEDKPKYEQG 322

RESULT 13
US-10-329-624-5251
Sequence 5251, Application US/10329624
Publication No. US20040043037A1
GENERAL INFORMATION:
APPLICANT: Charles Kunsch
Gill H. Choi
Patrick S. Dillon
Craig A. Rosen
Steven C. Barash
Michael R. Pannon
TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
NUMBER OF SEQUENCES: 5256
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COUNTRY: USA
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/329,624
FILING DATE: 27-Dec-2002
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/956,171
FILING DATE: October 20, 1997
APPLICATION NUMBER: 60/009,861
FILING DATE: January 5, 1996
APPLICATION NUMBER: 08/781,986
FILING DATE: January 3, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Mark J. Hyman
REGISTRATION NUMBER: 46,789
REFERENCE/DOCKET NUMBER: PB248P1D1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (240) 314-1224
TELEFAX: (301) 309-8439
INFORMATION FOR SEQ ID NO: 5251:
SEQUENCE CHARACTERISTICS:
LENGTH: 559 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 5251:
US-10-329-624-5251

Query Match 100.0%; Score 56; DB 15; Length 559;
Best Local Similarity 100.0%; Pred. No. 0.3;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EEDKPKYEQG 10
DB 313 EEDKPKYEQG 322

RESULT 14
US-09-815-242-5899

```

; Sequence 5899, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Karl L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; FILE REFERENCE: ELITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5899
; LENGTH: 767
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-09-815-242-5899

```

```

Query Match      100.0%; Score 56; DB 9; Length 767;
Best Local Similarity 100.0%; Pred. No. 0.42;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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```

QY      1 EEDKPKYEQG 10
      |||||
Db      694 EEDKPKYEQG 703

```

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RESULT 15
US-09-815-242-13140
; Sequence 13140, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Karl L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; FILE REFERENCE: ELITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23

```

```

; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13140
; LENGTH: 767
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-09-815-242-13140

```

```

Query Match      100.0%; Score 56; DB 9; Length 767;
Best Local Similarity 100.0%; Pred. No. 0.42;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      1 EEDKPKYEQG 10
      |||||
Db      694 EEDKPKYEQG 703

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Search completed: October 22, 2005, 12:39:43
Job time : 57.25 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 22, 2005, 06:10:10 ; Search time 11.45 Seconds
(without alignments)
84.032 Million cell updates/sec

Title: US-10-731-238-69

Perfect score: 56
Sequence: 1 EEDKPKYEQG 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	56	100.0	940	2	S19702	fibronectin-binding
2	56	100.0	961	2	G90053	hypothetical prote
3	56	100.0	1018	2	A32192	fibronectin-binding
4	56	100.0	1038	2	H90053	hypothetical prote
5	41	73.2	2957	2	T33152	hypothetical prote
6	37	66.1	365	2	F84033	germination (corte
7	37	66.1	448	2	S39348	26S ATP/ubiquitin-
8	36	64.3	217	2	E96657	unknown protein, 8
9	36	64.3	240	2	B84606	probable ATP synth
10	36	64.3	275	2	C89858	conserved hypotet
11	36	64.3	449	2	JC2381	virulence protein
12	36	64.3	456	2	D97662	virulence acvB pro
13	36	64.3	456	2	AG2886	agrobacterium chro
14	36	64.3	460	2	S06469	photosystem II chl
15	36	64.3	461	2	UT0322	photosystem II chl
16	36	64.3	461	2	S41480	photosystem II chl
17	36	64.3	461	2	S04025	photosystem II chl
18	36	64.3	461	2	T06936	photosystem II chl
19	36	64.3	471	2	T48743	probable 26S ATP/u
20	36	64.3	471	2	S78347	photosystem II chl
21	36	64.3	473	1	P2LV44	photosystem II chl
22	36	64.3	473	1	F2NT44	photosystem II chl
23	36	64.3	473	1	F2R244	photosystem II chl
24	36	64.3	473	1	F2SP44	photosystem II chl
25	36	64.3	473	2	UN0346	photosystem II chl
26	36	64.3	473	2	S03436	photosystem II chl
27	36	64.3	473	2	S58537	photosystem II chl
28	36	64.3	473	2	T07228	photosystem II chl
29	36	64.3	473	2	T07548	photosystem II chl

30	36	64.3	473	2	T08998	photosystem II pro
31	36	64.3	859	2	T01461	hypothetical prote
32	36	64.3	1589	2	C44766	defective chotin-
33	35	62.5	43	2	B83894	hypothetical prote
34	35	62.5	240	2	T25191	hypothetical prote
35	35	62.5	325	2	H70073	two-component sens
36	35	62.5	369	2	D72240	tRNA guanine trans
37	35	62.5	374	2	AG0387	queuing tRNA-ribos
38	35	62.5	379	2	H82284	queuing tRNA-ribos
39	35	62.5	382	2	H86643	queuing tRNA-ribos
40	35	62.5	388	2	B87600	cardamoyl-phosphat
41	35	62.5	401	1	TVVPMH	middle T antigen -
42	35	62.5	407	2	S27794	hypothetical 46.7K
43	35	62.5	419	2	G75062	probable flagella-
44	35	62.5	459	2	S42647	photosystem II chl
45	35	62.5	459	2	AD2342	photosystem II chl

ALIGNMENTS

RESULT 1

S19702

fibronectin-binding protein B - Staphylococcus aureus

C/Species: Staphylococcus aureus

C/Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #ext_change 09-Jul-2004

C/Accession: S19702

R/Joensen, K.; Signaes, C.; Mueller, H.P.; Lindberg, M.

Eur. J. Biochem. 202, 1041-1048, 1991

A/Title: Two different genes encode fibronectin binding proteins in Staphylococcus aure

A/Reference number: S19702; PMID:92111475; PMID:1837266

A/Accession: S19702

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-940 <JOB>

A/Cross-references: UNIPROT:Q53682; EMBL:X62992; NID:G49040; PIDN:CAA44726.1; PID:G5815

C/Keywords: fibronectin binding

Query Match

Best Local Similarity 100.0%; Score 56; DB 2; Length 940;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EEDKPKYEQG 10

DB 694 EEDKPKYEQG 703

RESULT 2

hypothetical protein fmbB [imported] - Staphylococcus aureus (strain N315)

C/Species: Staphylococcus aureus

C/Date: 10-May-2001 #sequence_revision 10-May-2001 #ext_change 09-Jul-2004

C/Accession: G90053

R/Kuroda, M.; Ohba, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Ogun

ma, A.; Mizutani, U.; Y., Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.

C./Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.

Lancet 357, 1225-1240, 2001

A/Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.

A/Reference number: AB9758; PMID:11418146

A/Accession: G90053

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-961 <KUR>

A/Cross-references: UNIPROT:Q99RD3; GB:BA000018; PID:G13702452; PIDN:BA43593.1; GSPDB:

A/Experimental source: strain N315

C/Genetics:

A/Gene: fmbB

Query Match

Best Local Similarity 100.0%; Score 56; DB 2; Length 961;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EEDKPKYEQG 10

Db 705 EBDKPYE0G 714

RESULT 3

A32192 fibronectin-binding protein - Staphylococcus aureus

C:Species: Staphylococcus aureus

C>Date: 31-Jul-1989 #sequence_revision 31-Jul-1989 #text_change 16-Feb-1997

C:Accession: A32192

R:Signaess, C.; Rautci, G.; Jonsenon, K.; Lindgren, P.E.; Anantharamiah, G.M.; Hoeoek, W

Proc. Natl. Acad. Sci. U.S.A. 86, 659-703, 1989

A:Title: Nucleotide sequence of the gene for a fibronectin-binding protein from Staphylo

A:Reference number: A32192; MUID:89088998; PMID:2521391

A:Accession: A32192

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-1018 <SIG>

A:Cross-references: GB:J04151

C:Keywords: fibronectin binding

Query Match 100.0%; Score 56; DB 2; Length 1011;
Best Local Similarity 100.0%; Pred. No. 0.04;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EBDKPYE0G 10
|||||
758 EBDKPYE0G 767

Db 758 EBDKPYE0G 767

RESULT 4

H90053 hypothetical protein fnb [imported] - Staphylococcus aureus (strain N315)

C:Species: Staphylococcus aureus

C>Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004

C:Accession: H90053

R:Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguo

ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.;

C.; Shiba, T.; Hatori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.

Lancet 357, 1225-1240, 2001

A:Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.

A:Reference number: A89758; MUID:21311952; PMID:11418146

A:Accession: H90053

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-1038 <KUR>

A:Cross-references: UNIPROT:Q99RD2; GB:BA000018; PID:G13702453; PIDN:BA843594.1; GSPDB:G

A:Experimental source: strain N315

C:Genetics:

A:Gene: fnb

Query Match 100.0%; Score 56; DB 2; Length 1038;
Best Local Similarity 100.0%; Pred. No. 0.041;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EBDKPYE0G 10
|||||
754 EBDKPYE0G 763

Db 754 EBDKPYE0G 763

RESULT 5

T33152 hypothetical protein T04D1.4 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C>Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 19-Jul-2004

C:Accession: T33152

R:Davidson, S.; Woldmann, P.

submitted to the EMBL Data Library, May 1998

A:Description: The sequence of C. elegans cosmid T04D1.

A:Reference number: Z21292

A:Accession: T33152

A:Status: preliminary

A:Molecule type: DNA

A:Cross-references: translated from GB/EMBL/DBJ

A:Gene: fnb

A:Accession: T33152

A:Status: preliminary

A:Molecule type: DNA

A:Cross-references: translated from GB/EMBL/DBJ

A:Gene: fnb

A:Accession: T33152

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-2957 <DAV>
A:Cross-references: UNIPROT:O61845; EMBL:AF067617; PIDN:AC17559.1; GSPDB:GN00019; CESP:
A:Experimental source: strain Bristol N2; clone T04D1
C:Genetics:
A:Gene: CESP:T04D1.4
A:Map position: 1
A:introns: 122/3; 293/3; 515/3; 1205/2; 1570/1; 2221/3; 2776/1; 2864/3

Query Match 73.2%; Score 41; DB 2; Length 2957;
Best Local Similarity 87.5%; Pred. No. 73;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EBDKPYE 8
|||||
673 EBDKPYE 680

RESULT 6

F84033 germination (cortex hydrolysis) and sporulation (stage II, multiple polar septa) germ [1

C:Species: Bacillus halodurans

C>Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004

C:Accession: F84033

R:Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, F.; Hira

Nucleic Acids Res. 28, 4317-4331, 2000

A:Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and

A:Reference number: A83650; MUID:20512582; PMID:11058132

A:Accession: F84033

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-365 <STO>

A:Cross-references: UNIPROT:Q9K8D6; GB:AP001517; GB:BA000004; NID:G10175500; PIDN:BA8067

A:Experimental source: strain C-125

C:Genetics:

A:Gene: germ

Query Match 66.1%; Score 37; DB 2; Length 365;
Best Local Similarity 75.0%; Pred. No. 43;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 3 DPKPYE0G 10
|||
285 DPKPYE0G 292

Db 285 DPKPYE0G 292

RESULT 7

S39348 26S ATP/ubiquitin-dependent proteinase chain S4 - fission yeast (Schizosaccharomyces pom

C:Species: Schizosaccharomyces pombe

C>Date: 18-Feb-1994 #sequence_revision 23-Feb-1996 #text_change 09-Jul-2004

C:Accession: S39348; T40421

R:Gordon, C.; McGurk, G.; Dillon, P.; Rosen, C.; Haecle, N.D.

Nature 366, 355-357, 1993

A:Title: Defective mitosis due to a mutation in the gene for a fission yeast 26S protease

A:Reference number: S39348; MUID:94067321; PMID:8247131

A:Accession: S39348

A:Status: nucleic acid sequence not shown

A:Molecule type: DNA

A:Residues: 1-448 <GOR>

A:Cross-references: UNIPROT:P36612; EMBL:Z29366; NID:G442507; PIDN:CA82554.1; PID:G4425

R:McDougall, R.C.; Rajadream, M.A.; Barrell, B.G.; Brown, S.; Hattie, D.

submitted to the EMBL Data Library, October 1999

A:Reference number: Z21927

A:Accession: T40421

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-448 <MCD>

A:Cross-references: EMBL:AL121863; PIDN:CAB58406.1; GSPDB:GN00067; SPDB:SPBC4.07C

A:Experimental source: strain 972h-, cosmid c4

C:Genetics:

A:Gene: SPBC4.07C

A:Map position: 2

A:introns: 1/3

A:Accession: T40421

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-448 <MCD>

A:Cross-references: EMBL:AL121863; PIDN:CAB58406.1; GSPDB:GN00067; SPDB:SPBC4.07C

A:Experimental source: strain 972h-, cosmid c4

C:Genetics:

A:Gene: SPBC4.07C

A:Map position: 2

A:introns: 1/3

A:Accession: T40421

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-448 <MCD>

A:Cross-references: EMBL:AL121863; PIDN:CAB58406.1; GSPDB:GN00067; SPDB:SPBC4.07C

A:Experimental source: strain 972h-, cosmid c4

C:Genetics:

A:Gene: SPBC4.07C

A:Map position: 2

A:introns: 1/3

C:Superfamily: ATP-dependent 26S proteinase; FtsH/SEC18/CDC48-type ATP-binding domain hc
C:Keywords: ATP; nucleotide binding; nucleus; P-loop
F:205-416/Domain: FtsH/SEC18/CDC48-type ATP-binding domain homology <VAR>
F:232-239/Region: nucleotide-binding motif A (P-loop)

Query Match 66.1%; Score 37; DB 2; Length 448;
Best Local Similarity 75.0%; Pred. No. 54;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 BEDPKRYE 8
DB 25 KDDPKRYE 32

RESULT 8
E96657
unknown protein: 83062-84229 [imported] - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004

C:Accession: E96657
R:Theologian, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;
ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000

A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luoro, J.S.; Maiti, R.; Marziani,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shim, P.; Southwick, A.M.; Sun, H.; Tallon,
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A>Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A:Reference number: A86141; MUID:21016719; PMID:11130712
A:Accession: E96657
A:Status: preliminary
A:Molecule type: DNA

A:Residues: 1-217 <STO>
A:Cross-references: UNIPROT:Q9SCM4; GB:AE005173; NID:G10092245; PIDD:AA612660.1; GSPDB:G
C:Genetics:
A:Gene: P16M19.9
A:Map position: 1

Query Match 64.3%; Score 36; DB 2; Length 217;
Best Local Similarity 85.7%; Pred. No. 38;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 BEDPKRYE 7
DB 36 EEDPKRYE 42

RESULT 9
B84606
probable ATP synthase [imported] - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
C:Accession: B84606

R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Bentol, M.I.; Town, C.D.; Fujii, C.Y.;
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.
eues, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.
Nature 402, 761-768, 1999

A>Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A:Reference number: A84420; MUID:20083487; PMID:10617197
A:Accession: B84606
A:Status: preliminary
A:Molecule type: DNA

A:Residues: 1240 <STO>
A:Cross-references: UNIPROT:Q9SU12; GB:AE002093; NID:G4417280; PIDD:AA620405.1; GSPDB:GN
C:Genetics:
A:Gene: AC2921870
A:Map position: 2

Query Match 64.3%; Score 36; DB 2; Length 240;
Best Local Similarity 66.7%; Pred. No. 42;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 BEDPKRYE 9
DB 184 KEDPKRYE 192

RESULT 10
C89858
conserved hypothetical protein SA0783 [imported] - Staphylococcus aureus (strain N315)

C:Species: Staphylococcus aureus
C>Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C:Accession: C89858

R:Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Ogun
ma, A.; Mizutani-U, Y.; Kobayashi, N.; Ogasawara, N.; Hayashi, H.; Hiratake, K.;
C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.;
Lancet 357, 1225-1240, 2001

A>Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.
A:Reference number: A89758; MUID:21111952; PMID:11418146
A:Accession: C89858
A:Status: preliminary
A:Molecule type: DNA

A:Residues: 1-275 <KUR>
A:Cross-references: UNIPROT:Q9YVF4; GB:BA000018; PIDD:G13700725; PIDD:BA842022.1; GSPDB:G
A:Experimental source: strain N315
C:Genetics:
A:Gene: SA0783

Query Match 64.3%; Score 36; DB 2; Length 275;
Best Local Similarity 85.7%; Pred. No. 49;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 DPKRYE 9
DB 136 DPKRYE 142

RESULT 11
JC2381
virulence protein acvB precursor - Agrobacterium tumefaciens

C:Species: Agrobacterium tumefaciens
C>Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 28-Jul-2003
C:Accession: JC2381; PC2236; B36922

R:Kang, H.W.; Mirawan, I.G.P.; Kojima, M.
Biosci. Biotechnol. Biochem. 58, 2024-2032, 1994
A>Title: Cellular localization and functional analysis of the protein encoded by the ch
A:Reference number: JC2381; MUID:95078508; PMID:7765595
A:Accession: JC2381
A:Molecule type: DNA

A:Residues: 1-449 <KAN>
A:Accession: PC2236
A:Molecule type: protein

A:Residues: 25-43 <KAN>
J. Bacteriol. 175, 3208-3212, 1993
R:Mirawan, I.G.; Kang, H.W.; Kojima, M.

A>Title: Isolation and characterization of a new chromosomal virulence gene of Agrobact
A:Reference number: A36922; MUID:9325972; PMID:8491736
A:Accession: B36922
A:Status: preliminary
A:Molecule type: DNA

A:Residues: 1-151, 'V', 153-284, 'FRSPVRSLSAMPGRIRKWRRAIPASSTPIARNGRMSF' <WIR>
A>Note: sequence extracted from NCBI backbone (NCBIN:132025, NCBIPI:132027)
A>Note: this sequence has been revised in reference JC2381
C:Genetics:
A:Gene: acv B

C:Superfamily: type IV secretory pathway, Vir component
F:1-24/Domain: signal sequence #status predicted <Sig>
F:25-449/Product: AcvB protein #status predicted <Mat>

Query Match 64.3%; Score 36; DB 2; Length 449;
Best Local Similarity 66.7%; Pred. No. 82;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Oy 2 BDKPYE0G 10
 Db 25 QDKPAYETG 33

RESULT 12

D97662

virulence acvB protein [imported] - Agrobacterium tumefaciens (strain C58, Cereon)

C:Species: Agrobacterium tumefaciens

C>Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 28-Jul-2003

C:Accession: D97662

R:Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, H.; Qurollo, B.; Goldman, A.; Liu, F.; Wollam, C.; Allinger, M.; Dougherty, D.; Scott, C.; Lappas, C.; Markelz, B.;

Science 294, 2233-2328, 2001

A>Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tumefaciens

A:Reference number: A97359; MUID:21608551; PMID:11743194

A:Accession: D97662

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-456 <KUR>

A:Cross-references: GB:AE007869; PIDN:AAK8253.1; PID:g15157711; GSPDB:GN00169

C:Genetics:

A:Gene: AGR_C_4582

A:Map position: circular chromosome

C:Superfamily: type IV secretory pathway, VirD component

Query Match 64.3%; Score 36; DB 2; Length 456;

Best Local Similarity 66.7%; Pred. No. 84;

Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Oy 2 BDKPYE0G 10
 Db 25 QDKPAYETG 33

RESULT 13

AG2886

agrobacterium chromosomal virulence protein B [imported] - Agrobacterium tumefaciens (st

C:Species: Agrobacterium tumefaciens

C>Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 28-Jul-2003

C:Accession: AG2886

R:Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, I.

erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kuyavhan, T.; Levy, R.; Li, M.; McClell

; Karp, P.; Romero, P.; Zhang, S.

Science 294, 2317-2323, 2001

A:Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,

ster, E.W.

A>Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.

A:Reference number: AB2577; MUID:21608550; PMID:11743193

A:Accession: AG2886

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-456 <KUR>

A:Cross-references: GB:AE008688; PIDN:AAL43509.1; PID:g17741017; GSPDB:GN00186

A:Experimental source: strain C58 (Dupont)

C:Genetics:

A:Gene: acvB

A:Map position: circular chromosome

C:Superfamily: type IV secretory pathway, VirD component

Query Match 64.3%; Score 36; DB 2; Length 456;

Best Local Similarity 66.7%; Pred. No. 84;

Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Oy 2 BDKPYE0G 10
 Db 25 QDKPAYETG 33

RESULT 14

S06469

photosystem II chlorophyll a-binding protein pSbc - Synechocystis sp. (strain PCC 6803)
 N:Alternate names: chlorophyll-binding protein, 43k, photosynthetic reaction center 44k

C:Species: Synechocystis sp.

A:Variety: PCC 6803

C>Date: 07-Jun-1990 #sequence_revision 19-Jan-1996 #text_change 20-Jun-2000

C:Accession: S06469; S07497; S02380; S74838

R:Chisholm, D.; Williams, J.G.K.

Plant Mol. Biol. 10, 293-301, 1988

A>Title: Nucleotide sequence of pSbc, the gene encoding the CP-43 chlorophyll a-binding

A:Reference number: S06469

A:Accession: S06469

A:Status: not compared with conceptual translation

A:Molecule type: DNA

A:Residues: 'MTLSLSLRFPSPV', 2-460 <CHI>

A:Cross-references: GB:M21538; NID:G340699; PIDN:AAA85378.1; PID:g1161272

A>Note: this sequence uses an incorrect initiation codon

R:Carpenner, S.D.; Charite, J.; Eggers, B.; Vernaa, W.F.J.

FEBS Lett. 260, 135-137, 1990

A>Title: The pSbc start codon in Synechocystis sp. PCC 6803.

A:Reference number: S07496; MUID:90127396; PMID:2105233

A:Accession: S07497

A:Molecule type: DNA

A:Residues: 1-7 <CAR>

A>Note: the authors definitely establish that the Met-1 GTG is the initiation codon and

R:Delzelkaine, V.A.; Bogorad, L.

EMBO J. 7, 333-338, 1988

A>Title: Molecular analysis of a mutant defective in photosynthetic oxygen evolution and

A:Reference number: S02379; MUID:88211542; PMID:3130247

A:Accession: S02380

A:Molecule type: DNA

A:Residues: 'MTLSLSLRFPSPV', 2-54, 'N', 56-149, 'I', 151-288 <DZE>

A:Cross-references: EMBL:X07018; NID:G48064; PIDN:CAA30071.1; PID:g48066

A>Note: the authors translated the codon CAT for residue 131 as Phe; this sequence uses

R:Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asanizu, E.; Nakamura, Y.; Miyajima, N.;

O. K.; Okumura, S.; Shimo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda

DNA Res. 3, 109-136, 1996

A>Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis

B.

A:Reference number: S74322; MUID:97061201; PMID:8905231

A:Accession: S74838

A:Status: nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 'MTLSLSLRFPSPV', 2-41, 'A', 43-460 <KAN>

A:Cross-references: EMBL:D90909; GB:AB001139; NID:g1652844; PIDN:BAAI7799.1; PID:g165288

A>Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996

A:Note: this sequence uses an incorrect initiation codon

C:Genetics:

A:Gene: pSbc

A:Start codon: GTG

C:Superfamily: photosystem II chlorophyll a-binding protein pSbc

C:Keywords: chlorophyll, membrane-associated complex; photosynthesis; photosystem II; th

Query Match 64.3%; Score 36; DB 2; Length 460;

Best Local Similarity 75.0%; Pred. No. 84;

Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Oy 3 DPKPYE0G 10
 Db 65 EKPWE0G 72

RESULT 15

JT0322

photosystem II chlorophyll a-binding protein pSbc - Synechococcus sp. (strain PCC 7942)

N:Alternate names: photosystem II protein Cpl3

C:Species: Synechococcus sp.

C>Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 09-Jul-2004

C:Accession: JT0322

R:Golden, S.S.; Stearns, G.W.

Gene 67, 85-96, 1988

A>Title: Nucleotide sequence and transcript analysis of three photosystem II genes from

A:Accession: JT0322

A:Reference number: JT0321; MUID:88329748; PMID:3138165

A:Molecule type: DNA

A:Residues: 1-461 <GOL>

A:Cross-references: UNIPROT:P11004; GB:M20814; NID:g154587; PIDN:AA27359.1; PID:g154589
C:Comment: The major membrane protein complexes of photosynthetic thylakoids from oxygen
the D1 and D2 which house all of the cofactors of the reaction center, and two subunits
C:Genetics:

A:Gene: psbC

C:Superfamily: photosystem II chlorophyll a-binding protein psbC

C:Keywords: chlorophyll; photosynthesis; photosystem II; thylakoid

Query Match

64.3%; Score 36; DB 2; Length 461;

Best Local Similarity 75.0%; Pred. No. 85;

Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 3 DKPKYEQG 10

: || || |

Db 66 EKPMYEQG 73

Search completed: October 22, 2005, 08:04:24
Job time : 12.45 secs

Handwritten text, possibly a signature or name, oriented diagonally.

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 22, 2005, 06:06:36 ; Search time 55.85 Seconds
(without alignment)
91.688 Million cell updates/sec

Title: US-10-731-238-69
Perfect score: 56
Sequence: 1 EEDKPKYEQG 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues
Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : uniprot_03:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	56	100.0	152	2	Q9AEP9
2	56	100.0	940	2	Q53682
3	56	100.0	943	2	Q8NUT8
4	56	100.0	957	2	Q6G6H4
5	56	100.0	961	2	Q9PRD3
6	56	100.0	961	2	Q7A3J8
7	56	100.0	965	2	Q6GD05
8	56	100.0	1015	2	Q8NUT7
9	56	100.0	1015	2	Q6G6H3
10	56	100.0	1018	1	FNBA_STPAU
11	56	100.0	1038	2	Q9PRD2
12	56	100.0	1038	2	Q7A3J7
13	56	100.0	552	2	Q6S9B4
14	42	75.0	552	2	Q6S9B5
15	42	75.0	697	2	Q7YZJ4
16	41	73.2	2957	2	Q61845
17	41	73.2	3166	2	Q9W320
18	41	73.2	228	2	Q8G5B9
19	40	71.4	242	2	Q9EX91
20	40	71.4	257	2	Q92MR6
21	40	71.4	462	2	Q7UBB4
22	39	69.6	196	2	Q703H1
23	39	69.6	458	2	Q8SGZ6
24	39	69.6	479	2	Q6CDI1
25	39	69.6	533	2	Q6ZFE6
26	39	69.6	553	2	Q7M8Y5
27	39	69.6	618	2	Q8S3U7
28	39	69.6	638	2	Q747S4
29	39	69.6	2689	2	Q7RES7
30	39	69.6	2720	2	Q6IMC6
31	38	67.9	215	2	Q8G8U1

32	38	67.9	293	2	Q8GKQ3	Q8GKQ3 enterococcus
33	38	67.9	299	2	P71446	P71446 lactococcus
34	38	67.9	330	2	Q7W87	Q7W87 meloidogyne
35	38	67.9	576	2	Q7S1R1	Q7S1R1 neurospora
36	38	67.9	765	2	Q7V2C8	Q7V2C8 prochloroco
37	38	67.9	1075	2	Q6C2V2	Q6C2V2 yarrowia 11
38	37	66.1	252	2	Q82IK9	Q82IK9 streptomyces
39	37	66.1	292	2	Q6Y7S1	Q6Y7S1 staphylococ
40	37	66.1	365	2	Q9K8D6	Q9K8D6 bacillus ha
41	37	66.1	399	2	Q8MPR8	Q8MPR8 caenorhabdi
42	37	66.1	401	2	Q7JP74	Q7JP74 treponema d
43	37	66.1	448	1	PRS4_SCHPO	P36612 schizosacch
44	37	66.1	459	2	Q9P7Z3	Q9P7Z3 neurospora
45	37	66.1	497	2	Q8MPR7	Q8MPR7 caenorhabdi

ALIGNMENTS

RESULT 1
Q9AEP9 ID Q9AEP9 PRELIMINARY; PRT; 152 AA.
AC Q9AEP9;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Fibronectin-binding protein (Fragment).
GN Name=fnb;
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1280;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=CMRSA-1;
RX MEDLINE=21246681; PubMed=11349044;
DOI=10.1128/IAI.69.6.3791-3799.2001;
RA Rice K., Huesca M., Vaz D., McGavin M.J.;
RT "Variance in fibronectin binding and fnb locus polymorphisms in
RT Staphylococcus aureus: identification of antigenic variation in a
RT fibronectin binding protein adhesin of the epidemic CMRSA-1 strain of
RT methicillin-resistant S. aureus.";
RT Infect. Immun. 69:3791-3799(2001).
DR EMBL; AY029184; MAK31588.1; -.
FT NON_TER
FT 152
SQ SEQUENCE 152 AA; 17193 MW; CFA3913CB11C025 CRC64;
Query Match 100.0%; Score 56; DB 2; Length 152;
Best Local Similarity 100.0%; Pred No. 0.022; 0; Indels 0; Gaps 0;
Matches 10; Conservative 0; Mismatches 0;
Qy 1 EEDKPKYEQG 10
Db 13 EEDKPKYEQG 22
RESULT 2
Q53682 ID Q53682 PRELIMINARY; PRT; 940 AA.
AC Q53682;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Fibronectin binding protein B.
GN Name=fnbB;
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1280;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=8325-4;
RX MEDLINE=92111475; PubMed=1837266;
Jonsen K., Sigas C., Muller H.P., Lindberg M.;

RT "Two different genes encode fibronectin binding proteins in
RT Staphylococcus aureus. The complete nucleotide sequence and
RL characterization of the second gene."
RL Bur. J. Biochem. 202:1041-1048(1991).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC an amide bond (By similarity).
DR EMBL: X62992; CAA44726.1; -.
DR PIR: S19702; S19702.
DR HSSP: O53653; 1N67.
DR GO: GO:0009986; C:cell surface; IEA.
DR GO: GO:0005618; C:cell wall; IEA.
DR GO: GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO: GO:0016020; C:membrane; IEA.
DR GO: GO:0007155; P:cell adhesion; IEA.
DR InterPro: IPR008966; Adhes_bact.
DR InterPro: IPR004237; Fn_bind.
DR InterPro: IPR005877; Gpos_YsIRK.
DR InterPro: IPR001899; Gram_pos_anchor.
DR Pfam: PF02986; Fn_bind; 2.
DR Pfam: PF00746; Gram_pos_anchor; 1.
DR Pfam: PF04650; YsIRK_signal; 1.
DR TIGRFAMs: TIGR01167; LPTXG_anchor; 1.
DR TIGRFAMs: TIGR01168; YsIRK_signal; 1.
DR PROSITE: PS50847; GRAM_POS_ANCHORING; 1.
DR Cell wall; Peptidoglycan-anchor.
KW SEQUENCE 940 AA; 103555 MW; E35FBBCA907AE345 CRC64;

Query Match 100.0%; Score 56; DB 2; Length 940
Best Local Similarity 100.0%; Pred. No. 0.17;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EEDKPYEQG 10
Db 694 EEDKPYEQG 703

RESULT 3
08NU8 PRELIMINARY; PRT; 943 AA.
AC 08NU8;
DT 01-OCT-2002 (TREMblrel. 22, Created)
DT 01-OCT-2002 (TREMblrel. 22, Last sequence update)
DT 01-OCT-2003 (TREMblrel. 25, Last annotation update)
DE FnbB protein.
GN Name=fnbB; OrderedLocustNames=MM2420;
OS Staphylococcus aureus (strain MM2).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=196620;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MM2.
RX MEDLINE=22040717; PubMed=12044378; DOI=10.1016/S0140-6736(02)08713-5;
RA Baba T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Oguchi A.,
RA Nagai Y., Iwama N., Asano K., Naito T., Kuroda H., Cui L.,
RA Yamamoto K., Hiramoto K.;
RT "Genome and virulence determinants of high virulence community-
RT acquired MRSA";
RL Lancet 359:1819-1827(2002).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC an amide bond (By similarity).
DR EMBL: AP004830; BAB96285.1; -.
DR HSSP: O53653; 1N67.
DR GO: GO:0009986; C:cell surface; IEA.
DR GO: GO:0005618; C:cell wall; IEA.
DR GO: GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO: GO:0016020; C:membrane; IEA.
DR GO: GO:0007155; P:cell adhesion; IEA.
DR InterPro: IPR008966; Adhes_bact.
DR InterPro: IPR004237; Fn_bind.
DR InterPro: IPR005877; Gpos_YsIRK.
DR InterPro: IPR001899; Gram_pos_anchor.
DR Pfam: PF02986; Fn_bind; 1.
DR Pfam: PF00746; Gram_pos_anchor; 1.

DR Pfam: PF04650; YsIRK_signal; 1.
DR TIGRFAMs: TIGR01167; LPTXG_anchor; 1.
DR TIGRFAMs: TIGR01168; YsIRK_signal; 1.
DR PROSITE: PS50847; GRAM_POS_ANCHORING; 1.
KW Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ SEQUENCE 943 AA; 104537 MW; DA8A5F31947B186A CRC64;

Query Match 100.0%; Score 56; DB 2; Length 943;
Best Local Similarity 100.0%; Pred. No. 0.17;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EEDKPYEQG 10
Db 701 EEDKPYEQG 710

RESULT 4
06G6H4 PRELIMINARY; PRT; 957 AA.
ID 06G6H4;
AC 06G6H4;
DT 05-JUL-2004 (TREMblrel. 27, Created)
DT 05-JUL-2004 (TREMblrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMblrel. 27, Last annotation update)
DE Fibronectin-binding protein.
GN Name=fnbB; OrderedLocustNames=SN52387;
OS Staphylococcus aureus (strain MSSA476).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=282459;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=15213324; DOI=10.1073/pnas.0402521101;
RA Holden M.T.G., Fell E.J., Lindsey J.A., Peacock S.J., Day N.P.J.,
RA Enright M.C., Foster T.J., Moore C.E., Hurst L., Atkin R., Barron A.,
RA Baeson N., Bentley S.D., Chillingworth C., Chillingworth T.,
RA Churcher C., Clark L., Cotton C., Cronin A., Doggett J., Dowd L.,
RA Felwell T., Hance Z., Harris B., Hauser H., Holroyd S., Jagers K.,
RA James K.D., Kennard N., Line A., Mayes R., Moule S., Mungall K.,
RA Ormond D., Quail M.A., Rabinowitch E., Rutherford K.M., Sanders M.,
RA Sharp S., Simmonds M., Stevens K., Whitehead S., Barrett B.G.,
RA Spratt B.G., Parkhill J.;
RT "Complete genomes of two clinical Staphylococcus aureus strains:
RT evidence for the rapid evolution of virulence and drug resistance."
RL Proc. Natl. Acad. Sci. U.S.A. 101:9786-9791(2004).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC an amide bond (By similarity).
DR EMBL: BX571857; CAG44201.1; -.
DR GO: GO:0009986; C:cell surface; IEA.
DR GO: GO:0005618; C:cell wall; IEA.
DR GO: GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO: GO:0016020; C:membrane; IEA.
DR GO: GO:0007155; P:cell adhesion; IEA.
DR InterPro: IPR008966; Adhes_bact.
DR InterPro: IPR004237; Fn_bind.
DR InterPro: IPR005877; Gpos_YsIRK.
DR InterPro: IPR001899; Gram_pos_anchor.
DR Pfam: PF02986; Fn_bind; 1.
DR Pfam: PF00746; Gram_pos_anchor; 1.
DR Pfam: PF04650; YsIRK_signal; 1.
DR TIGRFAMs: TIGR01167; LPTXG_anchor; 1.
DR TIGRFAMs: TIGR01168; YsIRK_signal; 1.
DR PROSITE: PS50847; GRAM_POS_ANCHORING; 1.
KW Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ SEQUENCE 957 AA; 105980 MW; 28F8BA7FFDF03EAF CRC64;

Query Match 100.0%; Score 56; DB 2; Length 957;
Best Local Similarity 100.0%; Pred. No. 0.18;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EEDKPYEQG 10
Db 701 EEDKPYEQG 710

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RESULT 5
Q99RD3      PRELIMINARY;      PRT;      961 AA.
ID          Q99RD3;
AC          Q99RD3;
DT          01-JUN-2001 (TrEMBLrel. 17, Created)
DT          01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT          01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE          Fibronectin-binding protein homolog.
GN          Name=fndB; OrderedLocustNames=SAV2502;
OS          Staphylococcus aureus (strain M50 / ATCC 700699).
OC          Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX          NCBI_Taxid=158878;
RN          [1]
RP          SEQUENCE FROM N.A.
RC          STRAIN=M50 / ATCC 700699;
RX          MEDLINE=21311952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2;
RA          Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
RA          Cui L., Oguchi A., Aoki K.-I., Nagai Y., Lian J.-Q., Ito T.,
RA          Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,
RA          Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
RA          Sekimizu K., Hiramata H., Kihara S., Goto S., Yabuzaki J.,
RA          Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
RA          Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
RT          "Whole genome sequencing of methicillin-resistant Staphylococcus
RT          aureus."
RL          Lancet 357:1225-1240(2001).
CC          -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC          an amide bond (By similarity).
EMBL; AF003365; BAB58664.1; -.
DR          PIR: G90053; G90053.
DR          HSSP: QS3653; 1N67.
DR          GO: GO:0009986; C:cell surface; IEA.
DR          GO: GO:0005618; C:cell wall; IEA.
DR          GO: GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR          GO: GO:0016020; C:membrane; IEA.
DR          GO: GO:0007155; P:cell adhesion; IEA.
DR          InterPro: IPR008966; Adhes_bact.
DR          InterPro: IPR004237; Fn_bind.
DR          InterPro: IPR005877; Gpos_YsIRK.
DR          Pfam: PF002986; Gram_pos_anchor.
DR          Pfam: PF00746; Gram_pos_anchor.
DR          Pfam: PF04650; YsIRK_signal; 1.
DR          TIGRfams: TIGR01167; LpxTG_anchor; 1.
DR          TIGRfams: TIGR01168; YsIRK_signal; 1.
DR          PROSITE: PSS0847; GRAM_POS_ANCHORING; 1.
KW          Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ          SEQUENCE 961 AA; 106010 MW; 364940F884EA4101 CRC64;

Query Match      100.0%; Score 56; DB 2; Length 961;
Best Local Similarity 100.0%; Pred. No. 0.18;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY          1 EEDKPYEEOG 10
DB          705 EEDKPYEEOG 714

RESULT 6
Q7A3J8      PRELIMINARY;      PRT;      961 AA.
ID          Q7A3J8;
AC          Q7A3J8;
DT          05-JUL-2004 (TrEMBLrel. 27, Created)
DT          05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT          05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE          RndB protein.
GN          Name=fndB; OrderedLocustNames=SA2290;
OS          Staphylococcus aureus (strain N315).
OC          Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX          NCBI_Taxid=158879;
RN          [1]
RP          SEQUENCE FROM N.A.
RC          MEDLINE=21311952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2;

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RA          Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
RA          Cui L., Oguchi A., Aoki K.-I., Nagai Y., Lian J.-Q., Ito T.,
RA          Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,
RA          Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
RA          Sekimizu K., Hiramata H., Kihara S., Goto S., Yabuzaki J.,
RA          Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
RA          Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
RT          "Whole genome sequencing of methicillin-resistant Staphylococcus
RT          aureus."
RL          Lancet 357:1225-1240(2001).
CC          -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC          an amide bond (By similarity).
EMBL; AF003137; BAB43593.1; -.
DR          GO: GO:0009986; C:cell surface; IEA.
DR          GO: GO:0005618; C:cell wall; IEA.
DR          GO: GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR          GO: GO:0016020; C:membrane; IEA.
DR          GO: GO:0007155; P:cell adhesion; IEA.
DR          InterPro: IPR008966; Adhes_bact.
DR          InterPro: IPR004237; Fn_bind.
DR          InterPro: IPR005877; Gpos_YsIRK.
DR          InterPro: IPR001899; Gram_pos_anchor.
DR          Pfam: PF02986; Fn_bind; 1.
DR          Pfam: PF00746; Gram_pos_anchor; 1.
DR          Pfam: PF04650; YsIRK_signal; 1.
DR          TIGRfams: TIGR01167; LpxTG_anchor; 1.
DR          TIGRfams: TIGR01168; YsIRK_signal; 1.
DR          PROSITE: PSS0847; GRAM_POS_ANCHORING; 1.
KW          Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ          SEQUENCE 961 AA; 106010 MW; 364940F884EA4101 CRC64;

Query Match      100.0%; Score 56; DB 2; Length 961;
Best Local Similarity 100.0%; Pred. No. 0.18;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY          1 EEDKPYEEOG 10
DB          705 EEDKPYEEOG 714

RESULT 7
Q6GDUS      PRELIMINARY;      PRT;      965 AA.
ID          Q6GDUS;
AC          Q6GDUS;
DT          05-JUL-2004 (TrEMBLrel. 27, Created)
DT          05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT          05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE          Fibronectin-binding protein.
GN          Name=fndB; OrderedLocustNames=SA2580;
OS          Staphylococcus aureus (strain M5A252).
OC          Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX          NCBI_Taxid=282458;
RN          [1]
RP          SEQUENCE FROM N.A.
RC          PubMed=15213324; DOI=10.1073/pnas.0402521101;
RX          Holden M.T.G., Fell E.J., Lindsay J.A., Peacock S.J., Day N.P.J.,
RX          Enright M.C., Foster T.U., Moore C.E., Hurst L., Atkin R., Barton A.,
RX          Bason N., Bentley S.D., Chillingworth C., Chillingworth T.,
RX          Churcher C., Clark L., Cronin A., Doggett J., Dowd L.,
RX          Feltham T., Hance Z., Harris B., Hauser H., Holtroyd S., Jagels K.,
RX          James K.D., Lennard N., Line A., Mayes R., Moule S., Mungall K.,
RX          Ormond D., Quail M.A., Rabinowitch E., Rutherford K.M., Sanders M.,
RX          Sharp S., Simmonds M., Stevens K., Whitehead S., Barrett B.G.,
RX          Spratt B.G., Parkhill J.;
RT          "Complete genomes of two clinical Staphylococcus aureus strains:
RT          evidence for the rapid evolution of virulence and drug resistance."
RL          Proc. Natl. Acad. Sci. U.S.A. 101:9786-9791(2004).
CC          -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC          an amide bond (By similarity).
EMBL; BX571856; CAG41560.1; -.
DR          GO: GO:0009986; C:cell surface; IEA.
DR          GO: GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR          GO: GO:0016020; C:membrane; IEA.

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DR GO:0007155; P:cell adhesion; IEA.
 DR InterPro; IPR008966; Adhes_bact.
 DR InterPro; IPR004237; Fn_bind.
 DR InterPro; IPR005877; Gpos_YsIRK.
 DR InterPro; IPR001899; Gram_pos_anchor.
 DR Pfam; PF02986; Fn_bind; 1.
 DR Pfam; PF00746; Gram_pos_anchor; 1.
 DR TIGRFAMs; TIGR01167; LpxTG_anchor; 1.
 DR TIGRFAMs; TIGR01168; YsIRK_signal; 1.
 DR PROSITE; PS50847; GRAM_POS_ANCHORING; 1.
 DR Cell wall; Complete proteome; Peptidoglycan-anchor.
 KW SEQUENCE 965 AA; 105691 MW; 2982E132164D051 CRC64;

Query Match 100.0%; Score 56; DB 2; Length 965;
 Best Local Similarity 100.0%; Pred. No. 0.18;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EEDKPYE0G 10
 Db 761 EEDKPYE0G 770

RESULT 8
 Q8NUU7 PRELIMINARY; PRT; 1015 AA.

AC Q8NUU7; 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, last annotation update)
 DE Fnb protein.
 GN Name=fnb; Ordered locus names=MM2421;
 OS Staphylococcus aureus (strain MM2).
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 NC NCBI_TaxID=196620;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=MM2.
 RX MEDLINE=22040717; PubMed=12044378; DOI=10.1016/S0140-6736(03)08713-5;
 RA Baba T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Oguishi A.,
 RA Nagai Y., Iwama N., Asano K., Naimi T., Kuroda H., Cui L.,
 RA Yamamoto K., Hiramoto K.;
 RT "Genome and virulence determinants of high virulence community-acquired MRSA";
 RL Lancet 359:1819-1827(2002).
 CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by an amide bond (By similarity).
 CC EMBL; AP004830; BAB96286.1; -;
 DR GO:GO:0009986; C:cell surface; IEA.
 DR GO:GO:0005618; C:cell wall; IEA.
 DR GO:GO:0009275; C:cell wall (benu Gram-positive Bacteria); IEA.
 DR GO:GO:0016020; C:membrane; IEA.
 DR GO:GO:0007155; P:cell adhesion; IEA.
 DR InterPro; IPR008966; Adhes_bact.
 DR InterPro; IPR004237; Fn_bind.
 DR InterPro; IPR005877; Gpos_YsIRK.
 DR InterPro; IPR001899; Gram_pos_anchor.
 DR Pfam; PF02986; Fn_bind; 1.
 DR Pfam; PF00746; Gram_pos_anchor; 1.
 DR TIGRFAMs; TIGR01167; LpxTG_anchor; 1.
 DR TIGRFAMs; TIGR01168; YsIRK_signal; 1.
 DR PROSITE; PS50847; GRAM_POS_ANCHORING; 1.
 DR Cell wall; Complete proteome; Peptidoglycan-anchor.
 KW SEQUENCE 1015 AA; 111145 MW; D0F9281BB64D4D2 CRC64;

Query Match 100.0%; Score 56; DB 2; Length 1015;
 Best Local Similarity 100.0%; Pred. No. 0.19;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EEDKPYE0G 10
 Db 759 EEDKPYE0G 768

RESULT 9
 Q6G6H3 PRELIMINARY; PRT; 1015 AA.
 AC Q6G6H3;
 ID Q6G6H3;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, last annotation update)
 DE Fibronectin-binding protein.
 GN Ordered locus names=SAS238;
 OS Staphylococcus aureus (strain MSSA476).
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 NC NCBI_TaxID=282459;
 RN [1]

RP SEQUENCE FROM N.A.
 RX PubMed=15213324; DOI=10.1073/pnas.040251101;
 RA Holden M.T.G., Fell E.J., Lindsay J.A., Peacock S.J., Day N.P.J.,
 RA Enright M.C., Foster T.J., Moore C.E., Hurst L., Atkin R., Barton A.,
 RA Bason N., Bentley S.D., Chillingworth C., Chillingworth T.,
 RA Churcher C., Clark L., Cronin A., Doggett J., Dowd L.,
 RA Felwell T., Hance Z., Harris B., Hauser H., Holroyd S., Jogle K.,
 RA James K.D., Kennard N., Line A., Mayes R., Moule S., Mungall K.,
 RA Ormond D., Quail M.A., Rabinovitch E., Rutherford K.M., Sanders M.,
 RA Sharp S., Simmonds M., Stevens K., Whitehead S., Barrett B.G.,
 RA Spratt B.G., Parkhill J.;
 RT "Complete genomes of two clinical Staphylococcus aureus strains: evidence for the rapid evolution of virulence and drug resistance."; Proc. Natl. Acad. Sci. U.S.A. 101:9786-9791(2004).
 CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by an amide bond (By similarity).
 CC EMBL; BX571857; CAG44202.1; -;
 DR GO:GO:0009986; C:cell surface; IEA.
 DR GO:GO:0005618; C:cell wall; IEA.
 DR GO:GO:0009275; C:cell wall (benu Gram-positive Bacteria); IEA.
 DR GO:GO:0016020; C:membrane; IEA.
 DR GO:GO:0007155; P:cell adhesion; IEA.
 DR InterPro; IPR008966; Adhes_bact.
 DR InterPro; IPR004237; Fn_bind.
 DR InterPro; IPR005877; Gpos_YsIRK.
 DR InterPro; IPR001899; Gram_pos_anchor.
 DR Pfam; PF02986; Fn_bind; 1.
 DR Pfam; PF00746; Gram_pos_anchor; 1.
 DR Pfam; PF04650; YsIRK_signal; 1.
 DR TIGRFAMs; TIGR01167; LpxTG_anchor; 1.
 DR TIGRFAMs; TIGR01168; YsIRK_signal; 1.
 DR PROSITE; PS50847; GRAM_POS_ANCHORING; 1.
 DR Cell wall; Complete proteome; Peptidoglycan-anchor.
 KW SEQUENCE 1015 AA; 111145 MW; D0F9281BB64D4D2 CRC64;

Query Match 100.0%; Score 56; DB 2; Length 1015;
 Best Local Similarity 100.0%; Pred. No. 0.19;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EEDKPYE0G 10
 Db 759 EEDKPYE0G 768

RESULT 10
 FNBA_STAAU STANDARD; PRT; 1018 AA.
 ID FNBA_STAAU
 AC P14738;
 DT 01-APR-1990 (Rel. 14, Created)
 DT 01-APR-1990 (Rel. 14, last sequence update)
 DT 25-OCT-2004 (Rel. 45, last annotation update)
 DE Fibronectin-binding protein precursor (FNBP).
 GN Name=fnbA;
 OS Staphylococcus aureus.
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 NC NCBI_TaxID=1280;
 RN [1]
 RP SEQUENCE FROM N.A.

RC STRAIN=NTC 8325-4;
 RX MEDLINE=89098998; PubMed=2521391;
 RA Signaes C., Raucel G., Joensson K., Lindgren P.-E.,
 RA Anantharamiah G.M., Hoeck M., Lindberg M.;
 RT "Nucleotide sequence of the gene for a fibronectin-binding protein
 from *Staphylococcus aureus*: use of this peptide sequence in the
 RT synthesis of biologically active peptides."
 RL Proc. Natl. Acad. Sci. U.S.A. 86:699-703(1989).
 CC -1- FUNCTION: The ability of bacteria to bind fibronectin has been
 CC proposed as a virulence factor enabling bacteria to colonize wound
 CC tissues and blood clots. Binding of plasma fibronectin to the
 CC bacterial surface might block adhesion receptors on *S. aureus*, thus
 CC representing an important defense mechanism against tissue
 CC invasion.
 CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
 CC an amide bond (potential).
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
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 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; J04151; AAA26632.1; -;
 DR InterPro: IPR004237; Fn_bind.
 DR InterPro: IPR005877; Gpos_YsIRK.
 DR InterPro: IPR001899; Gram_pos_anchor.
 DR Pfam; PF02986; Fn_bind; 1.
 DR Pfam; PF00746; Gram_pos_anchor; 1.
 DR Pfam; PF04650; YsIRK_signal; 1.
 DR TIGRPFAM; TIGR01167; LPXTG_anchor; 1.
 DR TIGRPFAM; TIGR01168; YsIRK_signal; 1.
 DR PROSITE; PSS0847; GRAM_POS_ANCHORING; 1.
 DR Cell adhesion; Cell wall; Peptidoglycan-anchor; Repeat; Signal;
 KW virulence;
 KM
 FT SIGNAL 1 36
 FT CHAIN 37 985
 FT PROPEP 986 1018
 FT REPEAT 545 574
 FT REPEAT 575 604
 FT DOMAIN 745 878
 FT REPEAT 745 782
 FT REPEAT 783 820
 FT REPEAT 821 859
 FT REPEAT 860 878
 FT DOMAIN 879 948
 FT REPEAT 879 892
 FT REPEAT 893 906
 FT REPEAT 907 920
 FT REPEAT 921 934
 FT REPEAT 935 948
 FT SITE 982 986
 FT MOD_RES 985 985
 FT SEQUENCE 1018 AA; 111780 MW; 58175E0020E81F1F CRC64;
 SQ
 Query Match 100.0%; Score 56; DB 1; Length 1018;
 Best Local Similarity 100.0%; Pred. No. 0.19;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DT 01-JUN-2001 (TrEMBLrel. 17, last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, last annotation update)
 DE Fibronectin-binding protein homolog.
 GN Name=fnb; OrderedLocustNames=SAV2503;
 OS *Staphylococcus aureus* (strain Mu50 / ATCC 700699).
 OC Bacteria; Firmicutes; Bacillales; *Staphylococcus*.
 OX NCBI_TaxId=158878;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Mu50 / ATCC 700699;
 RX MEDLINE=21111952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2;
 RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
 RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Lian J.-Q., Ito T.,
 RA Kanamori M., Matsunaru H., Maruyama A., Murakami H., Hosoyama A.,
 RA Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
 RA Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
 RA Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
 RA Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
 RT "Whole genome sequencing of methicillin-resistant *Staphylococcus*
 RT aureus."
 RL Lancet 357:1225-1240(2001).
 CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
 CC an amide bond (By similarity).
 CC EMBL; AP003365; BAB58665.1; -;
 DR PIR; H90053; H90053.
 DR GO; GO:0009986; C:cell surface; IEA.
 DR GO; GO:0005618; C:cell wall; IEA.
 DR GO; GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0007155; P:cell adhesion; IEA.
 DR InterPro: IPR008966; Adhes_bact.
 DR InterPro: IPR004237; Fn_bind.
 DR InterPro: IPR005877; Gpos_YsIRK.
 DR InterPro: IPR001899; Gram_pos_anchor.
 DR Pfam; PF02986; Fn_bind; 1.
 DR Pfam; PF00746; Gram_pos_anchor; 1.
 DR Pfam; PF04650; YsIRK_signal; 1.
 DR TIGRPFAM; TIGR01167; LPXTG_anchor; 1.
 DR TIGRPFAM; TIGR01168; YsIRK_signal; 1.
 DR PROSITE; PSS0847; GRAM_POS_ANCHORING; 1.
 KM Cell wall; Complete proteome; Peptidoglycan-anchor.
 SQ SEQUENCE 1038 AA; 113618 MW; 666BF6BF2BFEB12 CRC64;
 Query Match 100.0%; Score 56; DB 2; Length 1038;
 Best Local Similarity 100.0%; Pred. No. 0.19;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
RA Hattori M., Ogasawara N., Hayaishi H., Hiramatsu K.;  
RT "Whole genome sequencing of methicillin-resistant Staphylococcus  
RL aureus.";  
CC Lancelot 357;1225-1240(2001).  
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by  
CC an amide bond (By similarity).  
DR EMBL; AP003137; BAB43594.1; -.  
DR GO; GO:0009986; C:cell surface; IEA.  
DR GO; GO:0005618; C:cell wall; IEA.  
DR GO; GO:0003275; C:cell wall (sensu Gram-positive Bacteria); IEA.  
DR GO; GO:0016020; C:membrane; IEA.  
DR GO; GO:0007155; P:cell adhesion; IEA.  
DR InterPro; IPR008966; Adhes_bact.  
DR InterPro; IPR004237; Fn_bind.  
DR InterPro; IPR005877; Gpos_YSTRK.  
DR InterPro; IPR001899; Gram_pos_anchor.  
DR Pfam; PF02986; Fn_bind; 1.  
DR Pfam; PF00746; Gram_pos_anchor; 1.  
DR TIGRfam; TIGR01167; Lpxng_anchor; 1.  
DR TIGRfam; TIGR01168; YSTRK_signal; 1.  
DR TIGRfam; TIGR01169; YSTRK_signal; 1.  
DR PROSITE; PS50847; GRAM_POS_ANCHORING; 1.  
KW Cell wall; Complete proteome; Peptidoglycan-anchor.  
SQ SEQUENCE 1038 AA; 113618 MW; 666BF6BF2BFEB12 CRC64;  
  
Query Match 100.0%; Score 56; DB 2; Length 1038;  
Best Local Similarity 100.0%; Pred. No. 0.19; Mismatches 0; Indels 0; Gaps 0;  
Matches 10; Conservative 0;  
  
Oy 1 EEDKPKYEQ 10  
Db 754 EEDKPKYEQ 763  
  
RESULT 13  
O6S9B4 PRELIMINARY; PRT; 552 AA.  
ID O6S9B4  
AC O6S9B4;  
DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
DE Heat shock protein 90 (Fragment).  
GN Name=hsp90-2;  
OS Hexamita inflata.  
OC Eukaryota; Diplomonadida; Hexamitidae; Hexamitinae; Hexamita.  
OX NCBI_TaxID=28002;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=AZ-4;  
RX MEDLINE=22483903; PubMed=12595248; DOI=10.1016/S0022-2836(03)00057-3;  
RT Keeling P.J., Leander B.S.;  
RT "Characterization of a non-canonical genetic code in the oxymonad  
RT Strblomastix strix.";  
RT J. Mol. Biol. 326:1337-1349(2003).  
DR EMBL; AY462240; AAR26696.1; -.  
DR HSSP; P02829; IAH8.  
DR GO; GO:0005524; F:ATP binding; IEA.  
DR GO; GO:0051082; F:unfolded protein binding; IEA.  
DR GO; GO:0006457; P:protein folding; IEA.  
DR GO; GO:0006986; P:response to unfolded protein; IEA.  
DR InterPro; IPR009079; 4_helix_cytokine.  
DR InterPro; IPR003594; ATPbind_ATPase.  
DR InterPro; IPR001404; Hsp90.  
DR Pfam; PF02518; HATPase_c; 1.  
DR Pfam; PF00183; HSP90; 1.  
DR PRINTS; PR00775; HEATSHOCK90.  
DR SMART; SM00387; HATPase_c; 1.  
KW Heat shock.  
FT NON_TER 1  
FT NON_TER 552  
SQ SEQUENCE 552 AA; 63527 MW; 5E064DC55899D46 CRC64;  
  
Query Match 75.0%; Score 42; DB 2; Length 552;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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Best Local Similarity 88.9%; Pred. No. 40;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
Oy 1 EEDKPKYEQ 9  
Db 372 EEDKPKYEQ 380  
  
RESULT 14  
O6S9B5 PRELIMINARY; PRT; 552 AA.  
ID O6S9B5  
AC O6S9B5;  
DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
DE Heat shock protein 90 (Fragment).  
GN Name=hsp90-1;  
OS Hexamita inflata.  
OC Eukaryota; Diplomonadida; Hexamitidae; Hexamitinae; Hexamita.  
OX NCBI_TaxID=28002;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=AZ-4;  
RX MEDLINE=22483903; PubMed=12595248; DOI=10.1016/S0022-2836(03)00057-3;  
RT Keeling P.J., Leander B.S.;  
RT "Characterization of a non-canonical genetic code in the oxymonad  
RT Strblomastix strix.";  
RT J. Mol. Biol. 326:1337-1349(2003).  
DR EMBL; AY462239; AAR26695.1; -.  
DR HSSP; P02829; IAH8.  
DR GO; GO:0005524; F:ATP binding; IEA.  
DR GO; GO:0051082; F:unfolded protein binding; IEA.  
DR GO; GO:0006457; P:protein folding; IEA.  
DR GO; GO:0006986; P:response to unfolded protein; IEA.  
DR InterPro; IPR009079; 4_helix_cytokine.  
DR InterPro; IPR003594; ATPbind_ATPase.  
DR InterPro; IPR001404; Hsp90.  
DR Pfam; PF02518; HATPase_c; 1.  
DR Pfam; PF00183; HSP90; 1.  
DR PRINTS; PR00775; HEATSHOCK90.  
DR SMART; SM00387; HATPase_c; 1.  
KW Heat shock.  
FT NON_TER 1  
FT NON_TER 552  
SQ SEQUENCE 552 AA; 63640 MW; 5E1D5F5DE87DF3 CRC64;  
  
Query Match 75.0%; Score 42; DB 2; Length 552;  
Best Local Similarity 88.9%; Pred. No. 40;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
Oy 1 EEDKPKYEQ 9  
Db 372 EEDKPKYEQ 380  
  
RESULT 15  
O7YZJ4 PRELIMINARY; PRT; 697 AA.  
ID O7YZJ4  
AC O7YZJ4;  
DT 01-OCT-2003 (TrEMBLrel. 25, Created)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
DE 90-kDa heat-shock protein (Fragment).  
GN Name=hsp90;  
OS Monosiga brevicollis.  
OC Eukaryota; Choanoflagellida; Codonosigidae; Monosiga.  
OX NCBI_TaxID=81824;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=ATCC 50154;  
RX MEDLINE=22707964; PubMed=12823451;  
RT Rokas A., King N., Flinerty J., Carroll S.B.;  
RT "Conflicting phylogenetic signals at the base of the metazoan tree.";
```

RL Evol. Dev. 5:346-359(2003).
 DR EMBL; AY226081; AAP51213.1; -.
 DR HSP; P02829; 1USU.
 DR GO; GO:0005524; P:ATP binding; IEA.
 DR GO; GO:0051082; P:unfolded protein binding; IEA.
 DR GO; GO:0006457; P:protein folding; IEA.
 DR InterPro; IPR009079; 4_helix_cytokine.
 DR InterPro; IPR003594; ATPbind_Atpase.
 DR InterPro; IPR001404; Hsp90.
 DR Pfam; PF02518; HATPase_c; 1.
 DR Pfam; PF00183; HSP90; 1.
 DR SMART; SM00387; HATPase_c; 1.
 DR PROSITE; PS00298; HSP90; 1.
 FT NON_TER 1 1
 SQ SEQUENCE 697 AA; 79914 MW; 62DB6A5524126954 CRC64;

Query Match 75.0%; Score 42; DB 2; Length 697;
 Best Local Similarity 88.9%; Pred. No. 52;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 EEDKPKYEQ 9
 ||| |||
 Db 528 EEDKAKYEQ 536

Search completed: October 22, 2005, 08:00:32
 Job time : 57.85 secs

The Eye blank (uspio)

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 25, 2005, 20:21:18 ; Search time 63.2 Seconds
(without alignments)
61.196 Million cell updates/sec

Title: US-10-731-238-70

Perfect score: 58

Sequence: 1 DKPKYEGGCGN 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

1: A_Geneseq_16Dec04:*
2: geneseqp19808:*
3: geneseqp19908:*
4: geneseqp20008:*
5: geneseqp20018:*
6: geneseqp20028:*
7: geneseqp20038:*
8: geneseqp20048:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	58	100.0	10	2	AAW65726
2	58	100.0	30	4	AAW65726
3	58	100.0	30	7	ADCG9221
4	58	100.0	31	7	ADCG9222
5	58	100.0	38	1	AAW60660
6	58	100.0	38	1	AAW62116
7	58	100.0	38	2	AAW65692
8	58	100.0	38	2	AAW65695
9	58	100.0	38	2	AAW65696
10	58	100.0	38	2	AAW65697
11	58	100.0	38	2	AAW65694
12	58	100.0	38	2	AAW65691
13	58	100.0	38	2	AAW65661
14	58	100.0	38	2	AAW65693
15	58	100.0	39	2	AAW65712
16	58	100.0	130	2	AAW58806
17	58	100.0	130	2	AAW58807
18	58	100.0	130	2	AAW58807
19	58	100.0	130	2	AAW58807
20	58	100.0	134	2	AAW58808
21	58	100.0	134	2	AAW58808
22	58	100.0	134	2	AAW58808
23	58	100.0	139	2	AAW58808
24	58	100.0	174	2	AAW58808
25	58	100.0	174	2	AAW58808

26	58	100.0	181	2	AAW58805	AAW58805	Fibronect
27	58	100.0	181	2	AAW58805	AAW58805	Fibronect
28	58	100.0	559	2	AAW58803	AAW58803	Staphyloc
29	58	100.0	767	4	AAW58803	AAW58803	Staphyloc
30	58	100.0	767	4	AAW58803	AAW58803	Staphyloc
31	58	100.0	940	2	AAW58803	AAW58803	Staphyloc
32	58	100.0	940	2	AAW58803	AAW58803	Staphyloc
33	58	100.0	948	6	AAW58803	AAW58803	Staphyloc
34	58	100.0	948	6	AAW58803	AAW58803	Staphyloc
35	58	100.0	948	6	AAW58803	AAW58803	Staphyloc
36	58	100.0	961	6	AAW58803	AAW58803	Staphyloc
37	58	100.0	978	4	AAW58803	AAW58803	Staphyloc
38	58	100.0	1001	4	AAW58803	AAW58803	Staphyloc
39	58	100.0	1018	1	AAW58803	AAW58803	Staphyloc
40	58	100.0	1018	4	AAW58803	AAW58803	Staphyloc
41	58	100.0	1018	4	AAW58803	AAW58803	Staphyloc
42	58	100.0	1018	6	AAW58803	AAW58803	Staphyloc
43	58	100.0	1018	6	AAW58803	AAW58803	Staphyloc
44	58	100.0	1027	2	AAW58803	AAW58803	Staphyloc
45	58	100.0	1038	6	AAW58803	AAW58803	Staphyloc

ALIGNMENTS

RESULT 1
AAW65726 standard; peptide; 10 AA.
AAW65726; 16-OCT-1998 (first entry)
Fibronectin binding protein-derived peptide #70.
microbial surface components recognising adhesive matrix molecule;
MSCRAMM; fibronectin; fibronectin-binding protein; antibody; epitope;
antibiotic; bacterial infection; antibiotic-resistant strain.
Synthetic.
Staphylococcus aureus.
W09831389-A2.
23-JUL-1998.
21-JAN-1998; 98WO-US001222.
21-JAN-1997; 97US-0036139P.
(TEXA) UNIV TEXAS A & M SYSTEM.
Hoeok M, Patti JM, House-Pompeo KL, Speciale P, Joh D;
Megavlin MJ;
WPI, 1998-413816/35.
Antibody that binds to fibronectin-binding protein, preventing its
binding to fibronectin - used to treat or prevent bacterial infection,
especially by Staphylococci and Streptococci.
Example 9; Page 110; 20pp; English.
The invention relates to antibodies that bind to a fibronectin-binding
domain of a fibronectin-binding protein, and inhibit binding of the
protein to fibronectin. Also claimed are: (1) isolated peptides of a
fibronectin-binding protein that do not bind to fibronectin; (2) fusion
protein containing at least one peptide of a fibronectin-binding protein
linked to a second amino acid sequence; (3) nucleic acid encoding the
isolated peptide of (1). Antibodies, the isolated peptides of (1) and the
nucleic acids are all useful for immunisation (active or passive) and (by
inhibiting binding of bacteria to fibronectin) for preventing or treating
infection in humans or other animals, particularly by staphylococci or

XX	Fibronectin binding protein A; Fnbpa; fibronectin binding protein B;
KW	Fnbpb; antibody; staphylococcal infection; D2 peptide; fibronectin;
KX	antibacterial; immunostimulant.
XX	
OS	Synthetic.
OS	Staphylococcus aureus.
XX	
PN	US2003153022-A1.
XX	
XX	14-AUG-2003.
PD	
XX	
PF	05-NOV-2002; 2002US-00287821.
XX	
PR	05-NOV-2001; 2001US-0330964P.
XX	
PA	(PAT/) PATTI J M.
PA	(PATE/) PATEL P.
PA	(HALL/) HALL A.
PA	(DOMA/) DOMANSKI P.
PA	(SYRI/) SYRIBEYS P.
PA	(HUTC/) HUTCHINS J T.
PI	Patti JM, Patel P, Hall A, Domanski P, Syribey P, Hutchins JT;
XX	
DR	WPI; 2003-801749/75.
XX	
PT	Monoclonal antibody for treating or preventing staphylococcal infections
XX	binds specified fibronectin binding protein from Staphylococcus aureus.
XX	
PS	Claim 10; SEQ ID NO 2; 12pp; English.
XX	
CC	The invention relates to a new monoclonal antibody that binds fibronectin
CC	binding proteins from Staphylococcus aureus, including fibronectin
CC	binding protein A (Fnbpa) and fibronectin binding protein B (Fnbpb). The
CC	antibody is useful in treating, preventing or diagnosing staphylococcal
CC	infections in a human or animal. The antibody is capable of recognising
CC	Staphylococcus aureus with high affinity. It also inhibits binding of
CC	staphylococcal bacteria to fibronectin. This sequence represents a
CC	modified Fnbpb D2 peptide of the invention.
XX	
XX	
SQ	Sequence 31 AA;
XX	
Query Match	100.0%; Score 58; DB 7; Length 31;
Best Local Similarity	100.0%; Pred. No. 0.004;
Matches 10; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
Cy	1 DKPKYEGGCGN 10
Db	17 DKPKYEGGCGN 26
XX	
RESULT 5	
ID	AAFP80660 standard; protein; 38 AA.
XX	
AC	AAFP80660;
XX	
DT	25-MAR-2003 (revised)
DT	07-OCT-1990 (first entry)
XX	
DE	Protein with fibronectin binding ability.
XX	
KW	Hybrid DNA molecule; fibronectin binding; mastitis; ruminants;
XX	wound infection.
XX	
OS	Staphylococcus aureus.
XX	
PN	EP294349-A.
XX	
PD	07-DEC-1988.
XX	
PF	30-MAY-1988; 88EP-00850188.

```

XX 01-JUN-1987; 87SE-00002272.
XX (ALFA ) ALFA LAVAL AGRIC INT AB.
XX PA Lindberg MK, Signae LC, Wadstrom TM, Froman G;
XX PI WPI; 1988-347978/49.
XX DR N-PSDB; AAN81097.
XX PF Hybrid DNA encoding Staphylococcus aureus fibronectin binding protein -
XX PT useful for immunisation and topical application to prevent staphylococcal
XX infections.
XX PS Claim 11; Page 12; 23pp; English.
XX CC The peptide has fibronectin binding ability. It is useful for immunising
XX CC ruminants against staphylococcal mastitis, pref. when used at 0.5-5
XX CC micrograms/kg, using 3 doses given at 1-3 week intervals; for topical
XX CC application to prevent wound infection, using an isotonic saline soln. of
XX CC concn. 25-250 micrograms/ml; and, when immobilised on a carrier, for
XX CC diagnosing staphylococcal infections. (Updated on 25-MAR-2003 to correct
XX CC PF field.) (Updated on 25-MAR-2003 to correct PA field.)
XX SQ Sequence 38 AA;

Query Match 100.0%; Score 58; DB 1; Length 38;
Best Local Similarity 100.0%; Pred. NO. 0.005;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0

QY 1 DKPKYEGCGN 10
   |||||
   16 DKPKYEGCGN 25

RESULT 6
AAP82116
ID AAP82116 standard; protein; 38 AA.
XX AAP82116;
XX 25-MAR-2003 (revised)
XX DT 05-JAN-1990 (first entry)
XX DE Fibronectin binding protein.
XX KW Fibronectin binding protein; S.aureus; immunisation; mastitis; ruminants;
XX KW wound infection; diagnosis.
XX OS Staphylococcus aureus.
XX PN EP294349-A.
XX PD 07-DEC-1988.
XX PF 30-MAY-1988; 88EP-00850188.
XX PR 01-JUN-1987; 87SE-00002272.
XX PA (ALFA ) ALFA LAVAL AGRIC INT AB.
XX PI Lindberg MK, Signae LC, Wadstrom TM, Froman G;
XX DR WPI; 1988-347978/49.
XX DR N-PSDB; AAN82054.
XX PT Hybrid DNA encoding Staphylococcus aureus fibronectin binding protein -
XX PT useful for immunisation and topical application to prevent staphylococcal
XX PT infections.
XX PS Claim 11; Page 12; 23pp; English.
XX CC The S.aureus fibronectin binding protein may be included in a hybrid

```

CC protein. The protein may be used to immunise ruminants against
 CC staphylococcal mastitis, pref. when given at 0.5-5 microg/kg, using 3
 CC doses at 1-3 week intervals; and for topical applicn. to prevent wound
 CC infection, pref. using isotonic saline soln. of concn. 25-250 microg/mg.
 CC The DNA encoding the binding protein and the hybrid protein may be
 CC immobilised on a carrier and used to diagnose staphylococcal infections.
 CC (updated on 25-MAR-2003 to correct PA field.)
 XX
 SQ Sequence 38 AA;
 Query Match 100.0%; Score 58; DB 1; Length 38;
 Best Local Similarity 100.0%; Pred. No. 0.005;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DKPKYEOGNG 10
 |||||
 DB 16 DKPKYEOGNG 25
 RESULT 7
 AAW65692
 ID AAW65692 standard; peptide; 38 AA.
 XX
 AC AAW65692;
 XX
 DT 16-OCT-1998 (first entry)
 XX
 DE Fibronectin binding protein-derived peptide #36.
 XX
 XX microbial surface components recognising adhesive matrix molecule;
 KW MSCRAMM; fibronectin; fibronectin-binding protein; antibody; epitope;
 KW antibiotic; bacterial infection; antibiotic-resistant strain.
 XX
 OS Synthetic.
 OS Staphylococcus aureus.
 XX
 XX WO9831389-A2.
 XX
 PD 23-JUL-1998.
 XX
 PF 21-JAN-1998; 98WO-US001222.
 XX
 PR 21-JAN-1997; 97US-0036139P.
 XX
 PA (TEXA) UNIV TEXAS A & M SYSTEM.
 XX
 PI Hoecek M, Patti JM, House-Pompeo KL, Speziale P, Joh D.
 PI McGavin MJ;
 XX
 DR WPI, 1998-413816/35.
 XX
 PT Antibody that binds to fibronectin-binding protein, preventing its
 PT binding to fibronectin - used to treat or prevent bacterial infection,
 PT especially by Staphylococci and Streptococci.
 XX
 PS Example 8; Page 101; 201pp; English.
 XX
 XX The invention relates to antibodies that bind to a fibronectin-binding
 CC domain of a fibronectin-binding protein, and inhibit binding of the
 CC protein to fibronectin. Also claimed are: (1) isolated peptides of a
 CC fibronectin-binding protein that do not bind to fibronectin; (2) fusion
 CC protein containing at least one peptide of a fibronectin-binding protein
 CC linked to a second amino acid sequence; (3) nucleic acid encoding the
 CC isolated peptide of (1). Antibodies, the isolated peptides of (1) and the
 CC nucleic acids are all useful for immunisation (active or passive) and (by
 CC inhibiting binding of bacteria to fibronectin) for preventing or treating
 CC infection in humans or other animals, particularly by staphylococci or
 CC streptococci, e.g. meningitis, otitis media, pneumonia, endocarditis,
 CC mastitis in cattle, abortion in horses and many others. Since the
 CC antibodies block binding of bacteria, they should be effective against
 CC antibiotic-resistant strains, and may replace antibiotic therapy or
 CC increase its effectiveness. Sequences AAW65691-700 represent a series of
 CC synthetic peptides based on the DI region of S. aureus fibronectin

CC binding protein A. They were synthesised to contain mutations
 XX
 SQ Sequence 38 AA;
 Query Match 100.0%; Score 58; DB 2; Length 38;
 Best Local Similarity 100.0%; Pred. No. 0.005;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DKPKYEOGNG 10
 |||||
 DB 15 DKPKYEOGNG 24
 RESULT 8
 AAW65695
 ID AAW65695 standard; peptide; 38 AA.
 XX
 AC AAW65695;
 XX
 DT 16-OCT-1998 (first entry)
 XX
 DE Fibronectin binding protein-derived peptide #39.
 XX
 XX microbial surface components recognising adhesive matrix molecule;
 KW MSCRAMM; fibronectin; fibronectin-binding protein; antibody; epitope;
 KW antibiotic; bacterial infection; antibiotic-resistant strain.
 XX
 OS Synthetic.
 OS Staphylococcus aureus.
 XX
 XX WO9831389-A2.
 XX
 PD 23-JUL-1998.
 XX
 PF 21-JAN-1998; 98WO-US001222.
 XX
 PR 21-JAN-1997; 97US-0036139P.
 XX
 PA (TEXA) UNIV TEXAS A & M SYSTEM.
 XX
 PI Hoecek M, Patti JM, House-Pompeo KL, Speziale P, Joh D;
 PI McGavin MJ;
 XX
 DR WPI, 1998-413816/35.
 XX
 PT Antibody that binds to fibronectin-binding protein, preventing its
 PT binding to fibronectin - used to treat or prevent bacterial infection,
 PT especially by Staphylococci and Streptococci.
 XX
 PS Example 8; Page 102; 201pp; English.
 XX
 XX The invention relates to antibodies that bind to a fibronectin-binding
 CC domain of a fibronectin-binding protein, and inhibit binding of the
 CC protein to fibronectin. Also claimed are: (1) isolated peptides of a
 CC fibronectin-binding protein that do not bind to fibronectin; (2) fusion
 CC protein containing at least one peptide of a fibronectin-binding protein
 CC linked to a second amino acid sequence; (3) nucleic acid encoding the
 CC isolated peptide of (1). Antibodies, the isolated peptides of (1) and the
 CC nucleic acids are all useful for immunisation (active or passive) and (by
 CC inhibiting binding of bacteria to fibronectin) for preventing or treating
 CC infection in humans or other animals, particularly by staphylococci or
 CC streptococci, e.g. meningitis, otitis media, pneumonia, endocarditis,
 CC mastitis in cattle, abortion in horses and many others. Since the
 CC antibodies block binding of bacteria, they should be effective against
 CC antibiotic-resistant strains, and may replace antibiotic therapy or
 CC increase its effectiveness. Sequences AAW65691-700 represent a series of
 CC synthetic peptides based on the DI region of S. aureus fibronectin
 CC binding protein A. They were synthesised to contain mutations
 XX
 SQ Sequence 38 AA;
 Query Match 100.0%; Score 58; DB 2; Length 38;
 Best Local Similarity 100.0%; Pred. No. 0.005;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DKPKYEQGN 10
 |||||
 DB 15 DKPKYEQGN 24

RESULT 9
 AAM65696
 ID AAM65696 standard; peptide; 38 AA.

AC AAM65696;

DT 16-OCT-1998 (first entry)

XX Fibronectin binding protein-derived peptide #40.

XX microbial surface components recognising adhesive matrix molecule;
 KM MSCRAM; fibronectin; fibronectin-binding protein; antibody; epitope;
 KM antibiotic; bacterial infection; antibiotic-resistant strain.

OS Synthetic.

XX Staphylococcus aureus.

PN WO981389-A2.

XX 23-JUL-1998.

XX 21-JAN-1998; 98WO-US001222.

XX 21-JAN-1997; 97US-0036139P.

XX (TEXA) UNIV TEXAS A & M SYSTEM.

XX Hoeck M, Patti JM, House-Pompeo KL, Speziale P, Joh D;
 PI Mcgavin MJ;

XX WPI; 1998-413816/35.

XX Antibody that binds to fibronectin-binding protein, preventing its
 PT binding to fibronectin - used to treat or prevent bacterial infection,
 PT especially by Staphylococci and Streptococci.

XX Example 8; Page 102; 201pp; English.

XX The invention relates to antibodies that bind to a fibronectin-binding
 CC domain of a fibronectin-binding protein, and inhibit binding of the
 CC protein to fibronectin. Also claimed are: (1) isolated peptides of a
 CC fibronectin-binding protein that do not bind to fibronectin; (2) fusion
 CC protein containing at least one peptide of a fibronectin-binding protein
 CC linked to a second amino acid sequence; (3) nucleic acid encoding the
 CC isolated peptide of (1). Antibodies, the isolated peptides of (1) and the
 CC nucleic acids are all useful for immunisation (active or passive) and (by
 CC inhibiting binding of bacteria to fibronectin) for preventing or treating
 CC infection in humans or other animals, particularly by staphylococci or
 CC streptococci, e.g. meningitis, otitis media, pneumonia, endocarditis,
 CC mastitis in cattle, abortion in horses and many others. Since the
 CC antibodies block binding of bacteria, they should be effective against
 CC antibiotic-resistant strains, and may replace antibiotic therapy or
 CC increase its effectiveness. Sequences AAM65691-700 represent a series of
 CC synthetic peptides based on the DI region of S. aureus fibronectin
 CC binding protein A. They were synthesised to contain mutations

XX Sequence 38 AA;

Query Match 100.0%; Score 58; DB 2; Length 38;

Best Local Similarity 100.0%; Pred. No. 0.005;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DKPKYEQGN 10
 |||||
 DB 15 DKPKYEQGN 24

RESULT 10

AAM65697
 ID AAM65697 standard; peptide; 38 AA.

AC AAM65697;

DT 16-OCT-1998 (first entry)

XX Fibronectin binding protein-derived peptide #41.

XX microbial surface components recognising adhesive matrix molecule;
 KM MSCRAM; fibronectin; fibronectin-binding protein; antibody; epitope;
 KM antibiotic; bacterial infection; antibiotic-resistant strain.

OS Synthetic.

XX Staphylococcus aureus.

PN WO981389-A2.

XX 23-JUL-1998.

XX 21-JAN-1998; 98WO-US001222.

XX 21-JAN-1997; 97US-0036139P.

XX (TEXA) UNIV TEXAS A & M SYSTEM.

XX Hoeck M, Patti JM, House-Pompeo KL, Speziale P, Joh D;
 PI Mcgavin MJ;

XX WPI; 1998-413816/35.

XX Antibody that binds to fibronectin-binding protein, preventing its
 PT binding to fibronectin - used to treat or prevent bacterial infection,
 PT especially by Staphylococci and Streptococci.

XX Example 8; Page 102; 201pp; English.

XX The invention relates to antibodies that bind to a fibronectin-binding
 CC domain of a fibronectin-binding protein, and inhibit binding of the
 CC protein to fibronectin. Also claimed are: (1) isolated peptides of a
 CC fibronectin-binding protein that do not bind to fibronectin; (2) fusion
 CC protein containing at least one peptide of a fibronectin-binding protein
 CC linked to a second amino acid sequence; (3) nucleic acid encoding the
 CC isolated peptide of (1). Antibodies, the isolated peptides of (1) and the
 CC nucleic acids are all useful for immunisation (active or passive) and (by
 CC inhibiting binding of bacteria to fibronectin) for preventing or treating
 CC infection in humans or other animals, particularly by staphylococci or
 CC streptococci, e.g. meningitis, otitis media, pneumonia, endocarditis,
 CC mastitis in cattle, abortion in horses and many others. Since the
 CC antibodies block binding of bacteria, they should be effective against
 CC antibiotic-resistant strains, and may replace antibiotic therapy or
 CC increase its effectiveness. Sequences AAM65691-700 represent a series of
 CC synthetic peptides based on the DI region of S. aureus fibronectin
 CC binding protein A. They were synthesised to contain mutations

XX Sequence 38 AA;

Query Match 100.0%; Score 58; DB 2; Length 38;

Best Local Similarity 100.0%; Pred. No. 0.005;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DKPKYEQGN 10
 |||||
 DB 15 DKPKYEQGN 24

RESULT 11

AAM65694
 ID AAM65694 standard; peptide; 38 AA.

AC AAM65694;

```

XX 16-OCT-1998 (first entry)
DT
XX Fibronectin binding protein-derived peptide #38.
DE
XX microbial surface components recognising adhesive matrix molecule;
XX MSCRAMM; fibronectin; fibronectin-binding protein; antibody; epitope;
KW antibiotic; bacterial infection; antibiotic-resistant strain.
XX
XX Synthetic.
OS Staphylococcus aureus.
XX
XX WO9831389-A2.
XX
XX 23-JUL-1998.
XX
XX 21-JAN-1998; 98WO-US001222.
XX
XX 21-JAN-1997; 97US-0036139P.
XX
XX (TEXA ) UNIV TEXAS A & M SYSTEM.
XX
XX Hoecek M, Patti JM, House-Pompeo KU, Speziale P, Joh D;
XX McGavin MJ;
XX
XX WPI; 1998-413816/35.
XX
XX Antibody that binds to fibronectin-binding protein, preventing its
XX binding to fibronectin - used to treat or prevent bacterial infection,
XX especially by Staphylococci and Streptococci.
XX
XX Example 8; Page 102; 201pp; English.
XX
XX The invention relates to antibodies that bind to a fibronectin-binding
XX domain of a fibronectin-binding protein, and inhibit binding of the
XX protein to fibronectin. Also claimed are: (1) isolated peptides of a
XX fibronectin-binding protein that do not bind to fibronectin; (2) fusion
XX protein containing at least one peptide of a fibronectin-binding protein
XX linked to a second amino acid sequence; (3) nucleic acid encoding the
XX isolated peptide of (1). Antibodies, the isolated peptides of (1) and the
XX nucleic acids are all useful for immunisation (active or passive) and (by
XX inhibiting binding of bacteria to fibronectin) for preventing or treating
XX infection in humans or other animals, particularly by staphylococci or
XX streptococci, e.g. meningitis, otitis media, pneumonia, endocarditis,
XX mastitis in cattle, abortion in horses and many others. Since the
XX antibodies block binding of bacteria, they should be effective against
XX antibiotic-resistant strains, and may replace antibiotic therapy or
XX increase its effectiveness. Sequences AAW65691-700 represent a series of
XX synthetic peptides based on the DI region of S. aureus fibronectin
XX binding protein A. They were synthesised to contain mutations
XX
XX Sequence 38 AA:
SQ
XX
XX Query Match 100.0%; Score 58; DB 2; Length 38;
XX Best Local Similarity 100.0%; Pred. No. 0.005;
XX Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 DKPKYEOGNG 10
QY |||||
XX |||||
DB 15 DKPKYEOGNG 24
XX
XX
XX RESULT 12
XX AAW65691 standard; peptide; 38 AA.
XX
XX AAW65691;
XX
XX 16-OCT-1998 (first entry)
XX
XX Fibronectin binding protein-derived peptide #35.
XX
XX microbial surface components recognising adhesive matrix molecule;
XX MSCRAMM; fibronectin; fibronectin-binding protein; antibody; epitope;
XX antibiotic; bacterial infection; antibiotic-resistant strain.
XX
XX Synthetic.
OS Staphylococcus aureus.
XX
XX

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KW MSCRAMM; fibronectin; fibronectin-binding protein; antibody; epitope;
KW antibiotic; bacterial infection; antibiotic-resistant strain.
XX
XX Synthetic.
OS Staphylococcus aureus.
XX
XX WO9831389-A2.
XX
XX 23-JUL-1998.
XX
XX 21-JAN-1998; 98WO-US001222.
XX
XX 21-JAN-1997; 97US-0036139P.
XX
XX (TEXA ) UNIV TEXAS A & M SYSTEM.
XX
XX Hoecek M, Patti JM, House-Pompeo KU, Speziale P, Joh D;
XX McGavin MJ;
XX
XX WPI; 1998-413816/35.
XX
XX Antibody that binds to fibronectin-binding protein, preventing its
XX binding to fibronectin - used to treat or prevent bacterial infection,
XX especially by Staphylococci and Streptococci.
XX
XX Example 8; Page 101; 201pp; English.
XX
XX The invention relates to antibodies that bind to a fibronectin-binding
XX domain of a fibronectin-binding protein, and inhibit binding of the
XX protein to fibronectin. Also claimed are: (1) isolated peptides of a
XX fibronectin-binding protein that do not bind to fibronectin; (2) fusion
XX protein containing at least one peptide of a fibronectin-binding protein
XX linked to a second amino acid sequence; (3) nucleic acid encoding the
XX isolated peptide of (1). Antibodies, the isolated peptides of (1) and the
XX nucleic acids are all useful for immunisation (active or passive) and (by
XX inhibiting binding of bacteria to fibronectin) for preventing or treating
XX infection in humans or other animals, particularly by staphylococci or
XX streptococci, e.g. meningitis, otitis media, pneumonia, endocarditis,
XX mastitis in cattle, abortion in horses and many others. Since the
XX antibodies block binding of bacteria, they should be effective against
XX antibiotic-resistant strains, and may replace antibiotic therapy or
XX increase its effectiveness. Sequences AAW65691-700 represent a series of
XX synthetic peptides based on the DI region of S. aureus fibronectin
XX binding protein A. They were synthesised to contain mutations
XX
XX Sequence 38 AA:
SQ
XX
XX Query Match 100.0%; Score 58; DB 2; Length 38;
XX Best Local Similarity 100.0%; Pred. No. 0.005;
XX Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 DKPKYEOGNG 10
QY |||||
XX |||||
DB 15 DKPKYEOGNG 24
XX
XX
XX RESULT 13
XX AAW65661 standard; peptide; 38 AA.
XX
XX AAW65661;
XX
XX 16-OCT-1998 (first entry)
XX
XX Fibronectin binding protein-derived peptide #5.
XX
XX microbial surface components recognising adhesive matrix molecule;
XX MSCRAMM; fibronectin; fibronectin-binding protein; antibody; epitope;
XX antibiotic; bacterial infection; antibiotic-resistant strain.
XX
XX Synthetic.
OS Staphylococcus aureus.
XX
XX

```

PN W09831389-A2.
 XX 23-JUL-1998.
 PD 21-JAN-1998; 98WO-US001222.
 XX 21-JAN-1997; 97US-0036139P.
 PR (TEXA) UNIV TEXAS A & M SYSTEM.
 PA Hoeek M, Patti JM, House-Pompeo KL, Speziale P, Joh D;
 PI Mcgavin MJ;
 DR WPI; 1998-413816/35.
 XX Antibody that binds to fibronectin-binding protein, preventing its
 PT binding to fibronectin - used to treat or prevent bacterial infection,
 PR especially by Staphylococci and Streptococci.
 XX Example 2; Page 92; 201pp; English.
 PS The invention relates to antibodies that bind to a fibronectin-binding
 CC domain of a fibronectin-binding protein, and inhibit binding of the
 CC protein to fibronectin. Also claimed are: (1) isolated peptides of a
 CC fibronectin-binding protein that do not bind to fibronectin; (2) fusion
 CC protein containing at least one peptide of a fibronectin-binding protein
 CC linked to a second amino acid sequence; (3) nucleic acid encoding the
 CC isolated peptide of (1). Antibodies, the isolated peptides of (1) and the
 CC nucleic acids are all useful for immunisation (active or passive) and (by
 CC inhibiting binding of bacteria to fibronectin) for preventing or treating
 CC infection in humans or other animals, particularly by staphylococci or
 CC streptococci, e.g. meningitis, otitis media, pneumonia, endocarditis,
 CC mastitis in cattle, abortion in horses and many others. Since the
 CC antibodies block binding of bacteria, they should be effective against
 CC antibiotic-resistant strains, and may replace antibiotic therapy or
 CC increase its effectiveness. Sequences AAW65691-68 represent synthetic
 CC epitopes from the fibronectin binding domains DU and DI-D4 of the S.
 CC aureus fnbA gene
 XX SQ Sequence 38 AA:
 QY 1 DKPKYEOGGN 10
 DB 15 DKPKYEOGGN 24
 Query Match 100.0%; Score 58; DB 2; Length 38;
 Best Local Similarity 100.0%; Pred. No. 0.005;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 14
 AAW65693
 ID AAW65693 standard; peptide; 38 AA.
 XX AAW65693;
 AC 16-OCT-1998 (first entry)
 DT 16-OCT-1998 (first entry)
 XX Fibronectin binding protein-derived peptide #37.
 DE microbial surface components recognising adhesive matrix molecule;
 XX MSCRAMM; fibronectin; fibronectin-binding protein; antibody; epitope;
 KM antibiotic; bacterial infection; antibiotic-resistant strain.
 XX OS Synthetic.
 OS Staphylococcus aureus.
 XX W09831389-A2.
 PN 23-JUL-1998.
 PD 21-JAN-1998; 98WO-US001222.
 XX 21-JAN-1998; 98WO-US001222.

PR 21-JAN-1997; 97US-0036139P.
 XX (TEXA) UNIV TEXAS A & M SYSTEM.
 PA Hoeek M, Patti JM, House-Pompeo KL, Speziale P, Joh D;
 PI Mcgavin MJ;
 DR WPI; 1998-413816/35.
 XX Antibody that binds to fibronectin-binding protein, preventing its
 PT binding to fibronectin - used to treat or prevent bacterial infection,
 PR especially by Staphylococci and Streptococci.
 XX Example 8; Page 102; 201pp; English.
 PS The invention relates to antibodies that bind to a fibronectin-binding
 CC domain of a fibronectin-binding protein, and inhibit binding of the
 CC protein to fibronectin. Also claimed are: (1) isolated peptides of a
 CC fibronectin-binding protein that do not bind to fibronectin; (2) fusion
 CC protein containing at least one peptide of a fibronectin-binding protein
 CC linked to a second amino acid sequence; (3) nucleic acid encoding the
 CC isolated peptide of (1). Antibodies, the isolated peptides of (1) and the
 CC nucleic acids are all useful for immunisation (active or passive) and (by
 CC inhibiting binding of bacteria to fibronectin) for preventing or treating
 CC infection in humans or other animals, particularly by staphylococci or
 CC streptococci, e.g. meningitis, otitis media, pneumonia, endocarditis,
 CC mastitis in cattle, abortion in horses and many others. Since the
 CC antibodies block binding of bacteria, they should be effective against
 CC antibiotic-resistant strains, and may replace antibiotic therapy or
 CC increase its effectiveness. Sequences AAW65691-700 represent a series of
 CC synthetic peptides based on the DI region of S. aureus fibronectin
 CC binding protein A. They were synthesised to contain mutations
 XX SQ Sequence 38 AA:
 QY 1 DKPKYEOGGN 10
 DB 15 DKPKYEOGGN 24
 Query Match 100.0%; Score 58; DB 2; Length 38;
 Best Local Similarity 100.0%; Pred. No. 0.005;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 15
 AAW65712
 ID AAW65712 standard; peptide; 39 AA.
 XX AAW65712;
 AC 16-OCT-1998 (first entry)
 DT 16-OCT-1998 (first entry)
 XX Fibronectin binding protein-derived peptide #56.
 DE microbial surface components recognising adhesive matrix molecule;
 XX MSCRAMM; fibronectin; fibronectin-binding protein; antibody; epitope;
 KM antibiotic; bacterial infection; antibiotic-resistant strain.
 XX OS Synthetic.
 OS Staphylococcus aureus.
 XX W09831389-A2.
 PN 23-JUL-1998.
 PD 21-JAN-1998; 98WO-US001222.
 XX 21-JAN-1998; 98WO-US001222.
 XX 21-JAN-1997; 97US-0036139P.
 PR (TEXA) UNIV TEXAS A & M SYSTEM.
 PA Hoeek M, Patti JM, House-Pompeo KL, Speziale P, Joh D;
 PI Mcgavin MJ;

XX
DR WPI, 1998-413816/35.

XX Antibody that binds to fibronectin-binding protein, preventing its
PR binding to fibronectin - used to treat or prevent bacterial infection,
PR especially by Staphylococci and Streptococci.

XX
PS Example 8, Page 104, 201pp; English.

CC The invention relates to antibodies that bind to a fibronectin-binding
CC domain of a fibronectin-binding protein, and inhibit binding of the
CC protein to fibronectin. Also claimed are: (1) isolated peptides of a
CC fibronectin-binding protein that do not bind to fibronectin; (2) fusion
CC protein containing at least one peptide of a fibronectin-binding protein
CC linked to a second amino acid sequence; (3) nucleic acid encoding the
CC isolated peptide of (1). Antibodies, the isolated peptides of: (1) and the
CC nucleic acids are all useful for immunisation (active or passive) and (by
CC inhibiting binding of bacteria to fibronectin) for preventing or treating
CC infection in humans or other animals, particularly by staphylococci or
CC streptococci, e.g. meningitis, otitis media, pneumonia, endocarditis,
CC mastitis in cattle, abortion in horses and many others. Since the
CC antibodies block binding of bacteria, they should be effective against
CC antibiotic-resistant strains, and may replace antibiotic therapy or
CC increase its effectiveness. The present sequence is shown in the
CC specification

XX
SQ Sequence 39 AA;

Query Match 100.0%; Score 58; DB 2; Length 39;

Best Local Similarity 100.0%; Pred. No. 0.0051;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 DKPKYEGGN 10
Db 15 DKPKYEGGN 24

Search completed: October 25, 2005, 20:58:42
Job time : 63.2 secs

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OM protein - protein search, using sw model

Run on: October 22, 2005, 05:46:56 ; Search time 17.3 Seconds
(without alignments)
43.150 Million cell updates/sec

Title: US-10-731-238-70

Perfect score: 58

Sequence: 1 DKPKYEGGSGN 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-Processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA: *
1: /cgn2_6/prodata/1/iaa/5A_COMB.pep: *
2: /cgn2_6/prodata/1/iaa/5B_COMB.pep: *
3: /cgn2_6/prodata/1/iaa/6A_COMB.pep: *
4: /cgn2_6/prodata/1/iaa/6B_COMB.pep: *
5: /cgn2_6/prodata/1/iaa/PCITUS_COMB.pep: *
6: /cgn2_6/prodata/1/iaa/backfillseq.pep: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	58	100.0	10	4	US-09-010-317-70
2	58	100.0	38	1	US-08-234-622A-2
3	58	100.0	38	1	US-08-729-767-3
4	58	100.0	38	4	US-09-010-317-5
5	58	100.0	38	4	US-09-010-317-35
6	58	100.0	38	4	US-09-010-317-36
7	58	100.0	38	4	US-09-010-317-37
8	58	100.0	38	4	US-09-010-317-38
9	58	100.0	38	4	US-09-010-317-39
10	58	100.0	38	4	US-09-010-317-40
11	58	100.0	38	4	US-09-010-317-41
12	58	100.0	39	4	US-09-010-317-56
13	58	100.0	114	1	US-08-259-000-3
14	58	100.0	110	2	US-08-459-135A-7
15	58	100.0	130	2	US-08-459-135A-8
16	58	100.0	130	3	US-08-495-559-7
17	58	100.0	130	3	US-08-495-559-8
18	58	100.0	139	3	US-08-856-253-8
19	58	100.0	174	2	US-08-459-135A-10
20	58	100.0	174	2	US-08-459-135A-13
21	58	100.0	174	3	US-08-495-559-10
22	58	100.0	174	3	US-08-495-559-13
23	58	100.0	176	3	US-08-495-559-6
24	58	100.0	178	3	US-08-459-135A-12
25	58	100.0	178	3	US-08-459-135A-12
26	58	100.0	181	2	US-08-459-135A-6
27	58	100.0	559	4	US-08-956-171E-5251

28	58	100.0	559	4	US-08-781-986A-5251	Sequence 5251, Ap
29	58	100.0	1027	4	US-08-956-171E-5254	Sequence 5254, Ap
30	58	100.0	1027	4	US-08-781-986A-5254	Sequence 5254, Ap
31	53	91.4	38	1	US-08-234-622A-3	Sequence 3, Appl
32	53	91.4	38	1	US-08-729-767-4	Sequence 4, Appl
33	53	91.4	38	4	US-09-010-317-7	Sequence 7, Appl
34	53	91.4	38	4	US-09-010-317-45	Sequence 45, Appl
35	53	91.4	38	4	US-09-010-317-46	Sequence 46, Appl
36	53	91.4	38	4	US-09-010-317-47	Sequence 47, Appl
37	53	91.4	38	4	US-09-010-317-48	Sequence 48, Appl
38	52	89.7	38	4	US-09-010-317-42	Sequence 42, Appl
39	50	86.2	38	4	US-09-010-317-6	Sequence 6, Appl
40	50	86.2	38	4	US-09-010-317-43	Sequence 43, Appl
41	50	86.2	39	4	US-09-010-317-57	Sequence 57, Appl
42	47	81.0	10	4	US-09-010-317-71	Sequence 71, Appl
43	46	79.3	10	4	US-09-010-317-69	Sequence 69, Appl
44	45	77.6	38	4	US-09-010-317-8	Sequence 8, Appl
45	45	77.6	38	4	US-09-010-317-49	Sequence 49, Appl

ALIGNMENTS

RESULT 1
US-09-010-317-70
Sequence 70, Application US/09010317
Patent No. 6685943
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
APPLICANT: Patil, Joseph M.
APPLICANT: House-Pompeo, Karen L.
APPLICANT: Speziale, Pietro
APPLICANT: John, Danny
APPLICANT: McGeavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
TITLE OF INVENTION: AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAMK:189
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEO ID NO: 70:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-09-010-317-70
Query Match 100.0%; Score 58; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.00022;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DKPKYEGGN 10
|||||

Db 1 DKPKYEGGN 10

RESULT 2

US-08-234-622A-2
; Sequence 2, Application US/08234622A

; Patent No. 5440014

; GENERAL INFORMATION:

; APPLICANT: HOOK, Magnus

; APPLICANT: MCGAVIN, Martin

; APPLICANT: RAUCCI, Giuseppe

; TITLE OF INVENTION: A FIBRONECTIN BINDING PEPTIDE

; NUMBER OF SEQUENCES: 4

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Burns, Doane, Swecker & Mathis

; STREET: P.O. Box 1404

; CITY: Alexandria

; STATE: Virginia

; COUNTRY: United States

; ZIP: 22113-1404

; COMPUTER READABLE FORM:

; MEDIUM TYPE: floppy disk

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/234,622A

; FILING DATE: 28-APR-1994

; CLASSIFICATION: 530

; PRIORITY APPLICATION DATA:

; APPLICATION NUMBER: SE 9002617-0

; FILING DATE: 10-AUG-1990

; PRIORITY APPLICATION DATA:

; APPLICATION NUMBER: WO PCT/SE91/00534

; FILING DATE: 09-AUG-1991

; ATTORNEY/AGENT INFORMATION:

; NAME: Meuth, Donna M

; REGISTRATION NUMBER: 36,607

; REFERENCE/DOCKET NUMBER: 012885-044

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (703) 836-6620

; TELEFAX: (703) 836-2021

; INFORMATION FOR SEQ ID NO: 2:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 38 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

US-08-234-622A-2

Query Match 100.0%; Score 58; DB 1; Length 38;

Best Local Similarity 100.0%; Pred. No. 0.0009;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DKPKYEGGN 10
|||||

Db 15 DKPKYEGGN 24

RESULT 3

US-08-729-767-3
; Sequence 3, Application US/08729767

; Patent No. 5770702

; GENERAL INFORMATION:

; APPLICANT: HOOK, Magnus

; APPLICANT: LINDBERG, Martin Kjell

; APPLICANT: SIGNAS, Lars Christer

; APPLICANT: WADSTROM, Torkel Mikael

; APPLICANT: FROMAN, Gunnar

; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN AS WELL AS

; TITLE OF INVENTION: ITS PREPARATION

; NUMBER OF SEQUENCES: 6

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Burns, Doane, Swecker & Mathis, L.L.P.

; STREET: P.O. Box 1404

; CITY: Alexandria

; STATE: Virginia

; COUNTRY: United States

; ZIP: 22113-1404

; COMPUTER READABLE FORM:

; MEDIUM TYPE: floppy disk

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/729,767

; FILING DATE: 07-OCT-1996

; CLASSIFICATION: 435

; PRIORITY APPLICATION DATA:

; APPLICATION NUMBER: US 08/259,000

; FILING DATE: 13-JUN-1994

; PRIORITY APPLICATION DATA:

; APPLICATION NUMBER: US 08/007,817

; FILING DATE: 22-JAN-1993

; PRIORITY APPLICATION DATA:

; APPLICATION NUMBER: US 07/201,028

; FILING DATE: 01-JUN-1988

; PRIORITY APPLICATION DATA:

; APPLICATION NUMBER: SE 8702272-9

; FILING DATE: 01-JUN-1987

; ATTORNEY/AGENT INFORMATION:

; NAME: McGowan, Malcolm R.

; REGISTRATION NUMBER: 39,300

; REFERENCE/DOCKET NUMBER: 012889-036

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (703) 836-6620

; TELEFAX: (703) 836-2021

; INFORMATION FOR SEQ ID NO: 3:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 38 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: protein

US-08-729-767-3

Query Match 100.0%; Score 58; DB 1; Length 38;

Best Local Similarity 100.0%; Pred. No. 0.0009;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DKPKYEGGN 10
|||||

Db 16 DKPKYEGGN 25

RESULT 4

US-09-010-317-5
; Sequence 5, Application US/09010317

; Patent No. 6685943

; GENERAL INFORMATION:

; APPLICANT: Hook, Magnus

; APPLICANT: Patti, Joseph M.

; APPLICANT: House-Pompeo, Karen L.

; APPLICANT: Speciale, Pietro

; APPLICANT: Joh, Danny

; APPLICANT: McGavin, Martin J.

; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS

; NUMBER OF SEQUENCES: 105

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Arnold, White & Durkee

STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAMK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-09-010-317-5

Query Match 100.0%; Score 58; DB 4; Length 38;
Best Local Similarity 100.0%; Pred. No. 0.0009;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DKPKYEQGN 10
|||
Db 15 DKPKYEQGN 24

RESULT 5
US-09-010-317-35
Sequence 35, Application US/09010317
Patent No. 6685943
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
APPLICANT: Patti, Joseph M.
APPLICANT: House-Pompeo, Karen L.
APPLICANT: Speziale, Pietro
APPLICANT: Joh, Danny
APPLICANT: McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
TITLE OF INVENTION: AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/036,139

FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAMK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 35:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-09-010-317-35

Query Match 100.0%; Score 58; DB 4; Length 38;
Best Local Similarity 100.0%; Pred. No. 0.0009;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DKPKYEQGN 10
|||
Db 15 DKPKYEQGN 24

RESULT 6
US-09-010-317-36
Sequence 36, Application US/09010317
Patent No. 6685943
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
APPLICANT: Patti, Joseph M.
APPLICANT: House-Pompeo, Karen L.
APPLICANT: Speziale, Pietro
APPLICANT: Joh, Danny
APPLICANT: McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
TITLE OF INVENTION: AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAMK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 36:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-09-010-317-36

Query Match 100.0%; Score 58; DB 4; Length 38;
Best Local Similarity 100.0%; Pred. No. 0.0009;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DKPKYEQGN 10
|||
DB 15 DKPKYEQGN 24

RESULT 7

US-09-010-317-37
; Sequence 37, Application US/09010317
; Patent No. 6685943
; GENERAL INFORMATION:
; APPLICANT: Hook, Magnus
; APPLICANT: Patti, Joseph M.
; APPLICANT: House-Pompeo, Karen L.
; APPLICANT: Speziale, Pietro
; APPLICANT: Joh, Danny
; APPLICANT: McGavin, Martin J.
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
; TITLE OF INVENTION: AND METHODS OF USE
; NUMBER OF SEQUENCES: 105
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: TX
; COUNTRY: USA
; ZIP: 77210-4433
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/010,317
; FILING DATE:
; STRANDEDNESS:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/036,139
; FILING DATE: 21-JAN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Hibler, David W.
; REGISTRATION NUMBER: 41,071
; REFERENCE/DOCKET NUMBER: TANK:189
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 512-474-7577
; TELEFAX: 512-474-7577
; INFORMATION FOR SEQ ID NO: 37:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 38 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
US-09-010-317-37

Query Match 100.0%; Score 58; DB 4; Length 38;
Best Local Similarity 100.0%; Pred. No. 0.0009;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DKPKYEQGN 10
|||
DB 15 DKPKYEQGN 24

RESULT 8

US-09-010-317-38
; Sequence 36, Application US/09010317
; Patent No. 6685943
; GENERAL INFORMATION:
; APPLICANT: Hook, Magnus
; APPLICANT: Patti, Joseph M.

; APPLICANT: House-Pompeo, Karen L.
; APPLICANT: Speziale, Pietro
; APPLICANT: Joh, Danny
; APPLICANT: McGavin, Martin J.
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
; TITLE OF INVENTION: AND METHODS OF USE
; NUMBER OF SEQUENCES: 105
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: TX
; COUNTRY: USA
; ZIP: 77210-4433
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/010,317
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/036,139
; FILING DATE: 21-JAN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Hibler, David W.
; REGISTRATION NUMBER: 41,071
; REFERENCE/DOCKET NUMBER: TANK:189
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 512-474-7577
; TELEFAX: 512-474-7577
; INFORMATION FOR SEQ ID NO: 38:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 38 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
US-09-010-317-38

Query Match 100.0%; Score 58; DB 4; Length 38;
Best Local Similarity 100.0%; Pred. No. 0.0009;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DKPKYEQGN 10
|||
DB 15 DKPKYEQGN 24

RESULT 9

US-09-010-317-39
; Sequence 39, Application US/09010317
; Patent No. 6685943
; GENERAL INFORMATION:
; APPLICANT: Hook, Magnus
; APPLICANT: Patti, Joseph M.
; APPLICANT: House-Pompeo, Karen L.
; APPLICANT: Speziale, Pietro
; APPLICANT: Joh, Danny
; APPLICANT: McGavin, Martin J.
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
; TITLE OF INVENTION: AND METHODS OF USE
; NUMBER OF SEQUENCES: 105
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: TX
; COUNTRY: USA
; ZIP: 77210-4433
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TANK:189
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 39:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-09-010-317-39

Query Match 100.0%; Score 58; DB 4; Length 38;
Best Local Similarity 100.0%; Pred. No. 0.0009;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DKPKYEQGN 10
DB 15 DKPKYEQGN 24

RESULT 10
US-09-010-317-40
Sequence 40, Application US/09010317
Patent No. 6685943
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
APPLICANT: Patti, Joseph M.
APPLICANT: House-Pompeo, Karen L.
APPLICANT: Speziale, Pietro
APPLICANT: Joh, Danny
APPLICANT: McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
TITLE OF INVENTION: AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TANK:189
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 41:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-09-010-317-41

TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 40:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-09-010-317-40

Query Match 100.0%; Score 58; DB 4; Length 38;
Best Local Similarity 100.0%; Pred. No. 0.0009;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DKPKYEQGN 10
DB 15 DKPKYEQGN 24

RESULT 11
US-09-010-317-41
Sequence 41, Application US/09010317
Patent No. 6685943
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
APPLICANT: Patti, Joseph M.
APPLICANT: House-Pompeo, Karen L.
APPLICANT: Speziale, Pietro
APPLICANT: Joh, Danny
APPLICANT: McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
TITLE OF INVENTION: AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TANK:189
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 41:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-09-010-317-41

Query Match 100.0%; Score 58; DB 4; Length 38;
Best Local Similarity 100.0%; Pred. No. 0.0009;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DKPKYEQGN 10
DB 15 DKPKYEQGN 24

RESULT 12
US-09-010-317-56
Sequence 56, Application US/09010317
Patent No. 6685943
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
APPLICANT: Patti, Joseph M.
APPLICANT: House-Pompeo, Karen L.
APPLICANT: Speziale, Pietro
APPLICANT: Joh, Danny
APPLICANT: McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITION:
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P. O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hblbler, David W.
REGISTRATION NUMBER: 41,071
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 56:
SEQUENCE CHARACTERISTICS:
LENGTH: 39 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-09-010-317-56

Query Match 100.0%; Score 58; DB 4; Length 39;
Best Local Similarity 100.0%; Pred. No. 0.00092;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DKPKYEOGNN 10
|||
Db 15 DKPKYEOGNN 24

RESULT 13
US-08-259-000-3
Sequence 3, Application US/08259000
Patent No. 5571514
GENERAL INFORMATION:
APPLICANT: HOOK, Magnus
APPLICANT: LINDBERG, Martin Kjell
APPLICANT: SIGNAS, Lars Christer
APPLICANT: WADSTROM, Torkel Mikael
APPLICANT: FROMAN, Gunnar
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN AS WELL AS
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:

ADDRESSEE: Burns, Doane, Swecker & Mathis
STREET: P. O. Box 1404
CITY: Alexandria
STATE: Virginia
COUNTRY: United States
ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/259,000
FILING DATE: 13-JUN-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: SE 8702272-9
FILING DATE: 01-JUN-1987
ATTORNEY/AGENT INFORMATION:
NAME: Meuth, Donna M
REGISTRATION NUMBER: 36,607
REFERENCE/DOCKET NUMBER: 012885-062
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 114 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-259-000-3

Query Match 100.0%; Score 58; DB 1; Length 114;
Best Local Similarity 100.0%; Pred. No. 0.0029;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DKPKYEOGNN 10
|||
Db 16 DKPKYEOGNN 25

RESULT 14
US-08-459-135A-7
Sequence 7, Application US/08459135A
Patent No. 595078
GENERAL INFORMATION:
APPLICANT: BURNHAM, Martin Karl Russel
APPLICANT: CHOPRA, Ian
APPLICANT: CRITCHLEY, Ian Alfred
APPLICANT: KNOWLES, David Justin Charles
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN: MONOCLONAL ANTIBODY AND THEIR US
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
STATE: PA
COUNTRY: U.S.A.
ZIP: 19406-0939
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: Fastseq, Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/459,135A
FILING DATE: 02-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB/94/00215
FILING DATE: 04-Feb-1994

CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Gimmil, Edward R
REGISTRATION NUMBER: 38,891
REFERENCE/DOCKET NUMBER: P30591C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-4478
TELEFAX: 610-270-5090
TELEX:
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 130 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-459-135A-7

Query Match 100.0%; Score 58; DB 2; length 130;
Best Local Similarity 100.0%; Pred. No. 0.0033;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DKPKYEQGN 10
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Db 16 DKPKYEQGN 25

RESULT 15
US-08-459-135A-8
Sequence 8, Application US/08459135A
Patent No. 5955078
GENERAL INFORMATION:
APPLICANT: BURHAM, Martin Karl Russel
APPLICANT: CHOPRA, Ian
APPLICANT: CRITCHLEY, Ian Alfred
APPLICANT: KNOWLES, David Justin Charles
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN: MONOCLONAL ANTIBODY AND THEIR US
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
STATE: PA
COUNTRY: U.S.A.
ZIP: 19406-0939
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: Fastseq, Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/459,135A
FILING DATE: 02-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB/94/00215
FILING DATE: 04-Feb-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Gimmil, Edward R
REGISTRATION NUMBER: 38,891
REFERENCE/DOCKET NUMBER: P30591C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-4478
TELEFAX: 610-270-5090
TELEX:
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 130 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-459-135A-8

Query Match 100.0%; Score 58; DB 2; length 130;
Best Local Similarity 100.0%; Pred. No. 0.0033;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DKPKYEQGN 10
|||
Db 16 DKPKYEQGN 25

Search completed: October 22, 2005, 07:41:41
Job time : 17.35 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 22, 2005, 12:09:40 ; Search time 57.25 Seconds
(without alignments)
72.924 Million cell updates/sec

Title: US-10-731-238-70

Perfect score: 58
Sequence: 1 DKPKYEGGCGN 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1862951 seqs, 417491010 residues

Total number of hits satisfying chosen parameters: 1862951

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-Processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications: AA:*

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22: /cgn2_6/prodata/2/pubppaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	58	100.0	10	US-10-731-238-70	Sequence 70, Appl
2	58	100.0	10	US-10-287-821-1	Sequence 1, Appl
3	58	100.0	31	US-10-287-821-2	Sequence 2, Appl
4	58	100.0	38	US-10-731-238-5	Sequence 5, Appl
5	58	100.0	38	US-10-731-238-35	Sequence 35, Appl
6	58	100.0	38	US-10-731-238-36	Sequence 36, Appl
7	58	100.0	38	US-10-731-238-37	Sequence 37, Appl
8	58	100.0	38	US-10-731-238-38	Sequence 38, Appl
9	58	100.0	38	US-10-731-238-39	Sequence 39, Appl
10	58	100.0	38	US-10-731-238-40	Sequence 40, Appl
11	58	100.0	38	US-10-731-238-41	Sequence 41, Appl

12	58	100.0	39	US-10-731-238-56	Sequence 56, Appl
13	58	100.0	139	US-09-813-820-8	Sequence 8, Appl
14	58	100.0	388	US-08-901-062-1	Sequence 1, Appl
15	58	100.0	559	US-08-781-986A-5251	Sequence 5251, Ap
16	58	100.0	559	US-10-329-624-5251	Sequence 5899, Ap
17	58	100.0	767	US-09-815-242-5699	Sequence 13140, A
18	58	100.0	767	US-09-815-242-13140	Sequence 424, Ap
19	58	100.0	948	US-10-470-048B-424	Sequence 69, Appl
20	58	100.0	948	US-10-470-048B-69	Sequence 43778, A
21	58	100.0	961	US-10-282-122A-43778	Sequence 5456, Ap
22	58	100.0	978	US-09-815-242-5456	Sequence 12666, A
23	58	100.0	1001	US-09-815-242-15686	Sequence 5797, Ap
24	58	100.0	1018	US-09-815-242-5797	Sequence 12838, A
25	58	100.0	1018	US-09-815-242-12838	Sequence 68, Appl
26	58	100.0	1018	US-10-470-048B-69	Sequence 5254, Ap
27	58	100.0	1027	US-08-781-986A-5254	Sequence 52827, A
28	58	100.0	1027	US-10-329-624-5254	Sequence 43827, A
29	58	100.0	1038	US-10-282-122A-43827	Sequence 45, Appl
30	53	91.4	38	US-10-731-238-45	Sequence 46, Appl
31	53	91.4	38	US-10-731-238-45	Sequence 47, Appl
32	53	91.4	38	US-10-731-238-46	Sequence 48, Appl
33	53	91.4	38	US-10-731-238-47	Sequence 49, Appl
34	53	91.4	38	US-10-731-238-48	Sequence 50, Appl
35	52	89.7	38	US-10-731-238-42	Sequence 51, Appl
36	50	86.2	38	US-10-731-238-6	Sequence 52, Appl
37	50	86.2	38	US-10-731-238-43	Sequence 53, Appl
38	50	86.2	39	US-10-731-238-45	Sequence 54, Appl
39	47	81.0	10	US-10-731-238-71	Sequence 55, Appl
40	46	79.3	10	US-10-731-238-69	Sequence 56, Appl
41	45	77.6	38	US-10-731-238-8	Sequence 57, Appl
42	45	77.6	38	US-10-731-238-8	Sequence 58, Appl
43	42	72.4	38	US-10-731-238-49	Sequence 59, Appl
44	41	70.7	36	US-10-731-238-44	Sequence 60, Appl
45	38	65.5	276	US-10-099-278-15	Sequence 15, Appl

ALIGNMENTS

RESULT 1

US-10-731-238-70

Sequence 70, Application US/0731238

Publication No. US20050123552A1

GENERAL INFORMATION:

APPLICANT: Hook, Magnus

Patel, Joseph M.

House-Pompeo, Karen L.

Speziale, Pietro

Joh, Danny

McGavin, Martin J.

TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS

NUMBER OF SEQUENCES: 105

CORRESPONDENCE ADDRESS:

ADDRESSEE: Arnold, White & Durkee

STREET: P.O. Box 4433

CITY: Houston

STATE: TX

COUNTRY: USA

ZIP: 77210-4433

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/731.238

FILING DATE: 10-Dec-2003

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/010.317

FILING DATE: 21-Jan-1998

APPLICATION NUMBER: US 60/036.139


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; FILING DATE: 21-JAN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Hibler, David W.
; REGISTRATION NUMBER: 41,071
; REFERENCE/DOCKET NUMBER: TAMK.189
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 512-418-3000
; TELEFAX: 512-474-7577
; INFORMATION FOR SEQ ID NO: 70:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 70:
US-10-731-238-70

Query Match 100.0%; Score 58; DB 18; Length 10
Best Local Similarity 100.0%; Pred. No. 0.0011;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DKPKYEGGNN 10
|||
|||
Db 1 DKPKYEGGNN 10

RESULT 2
US-10-287-821-1
; Sequence 1, Application US/10287821
; Publication No. US20030153022A1
; GENERAL INFORMATION:
; APPLICANT: PATTI, Joseph M.
; TITLE OF INVENTION: MONOCLONAL ANTIBODIES TO THE FIBRONECTIN BINDING PROTEIN.
; FILE REFERENCE: P074270S01/BAS
; CURRENT APPLICATION NUMBER: US/10/287,821
; CURRENT FILING DATE: 2002-11-05
; PRIOR APPLICATION NUMBER: 60/330,964
; PRIOR FILING DATE: 2001-11-05
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 30
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-10-287-821-1

Query Match 100.0%; Score 58; DB 14; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.0033;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DKPKYEGGNN 10
|||
|||
Db 16 DKPKYEGGNN 25

RESULT 3
US-10-287-821-2
; Sequence 2, Application US/10287821
; Publication No. US20030153022A1
; GENERAL INFORMATION:
; APPLICANT: PATTI, Joseph M.
; TITLE OF INVENTION: MONOCLONAL ANTIBODIES TO THE FIBRONECTIN BINDING PROTEIN.
; FILE REFERENCE: P074270S01/BAS
; CURRENT APPLICATION NUMBER: US/10/287,821
; CURRENT FILING DATE: 2002-11-05
; PRIOR APPLICATION NUMBER: 60/330,964
; PRIOR FILING DATE: 2001-11-05
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 31
; TYPE: PRT
; ORGANISM: Staphylococcus aureus

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US-10-287-821-2
Query Match      100.0%; Score 58; DB 14; Length 31;
Best Local Similarity 100.0%; Pred. No. 0.0034;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY          1 DPKRYEOGNN 10
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Db           17 DPKRYEOGNN 26

RESULT 4
US-10-731-238-5
Sequence 5, Application US/10731238
Publication No. US20050123552A1
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
Patti, Joseph M.
House-Pompeo, Karen L.
Speziale, Pietro
Joh, Danny
McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/731,238
FILING DATE: 10-Dec-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE: 21-Jan-1998
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TMK.189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-10-731-238-5

Query Match      100.0%; Score 58; DB 18; Length 38;
Best Local Similarity 100.0%; Pred. No. 0.0041;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY          1 DPKRYEOGNN 10
            |||||
Db           15 DPKRYEOGNN 24
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Sequence 35, Application US/10731238
Publication No. US20050123552A1
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
Patti, Joseph M.
House-Pompeo, Karen L.
Speziale, Pietro
John, Danny
McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/731,238
FILING DATE: 10-Dec-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE: 21-Jan-1998
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAMK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 35:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 35:
US-10-731-238-35
Query Match 100.0%; Score 58; DB 18; Length 38;
Best Local Similarity 100.0%; Pred. No. 0.0041;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 DKPKYEQGN 10
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Db 15 DKPKYEQGN 24
RESULT 6
US-10-731-238-36
Sequence 36, Application US/10731238
Publication No. US20050123552A1
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
Patti, Joseph M.
House-Pompeo, Karen L.
Speziale, Pietro
John, Danny
McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:

ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/731,238
FILING DATE: 10-Dec-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE: 21-Jan-1998
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAMK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 36:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 36:
US-10-731-238-36
Query Match 100.0%; Score 58; DB 18; Length 38;
Best Local Similarity 100.0%; Pred. No. 0.0041;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 DKPKYEQGN 10
| | | | | | | | | |
Db 15 DKPKYEQGN 24
RESULT 7
US-10-731-238-37
Sequence 37, Application US/10731238
Publication No. US20050123552A1
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
Patti, Joseph M.
House-Pompeo, Karen L.
Speziale, Pietro
John, Danny
McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/731,238

Qy 1 DKPKYEGGN 10
 |||||
 Db 15 DKPKYEGGN 24

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RESULT 10
US-10-731-238-40
; Sequence 40, Application US/10731238
; Publication No. US20050123552A1
; GENERAL INFORMATION:
; APPLICANT: Hook, Magnus
; Patti, Joseph M.
; House-Pompeo, Karen L.
; Speziale, Pietro
; Joh, Danny
; McGavin, Martin J.
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
; AND METHODS OF USE
; NUMBER OF SEQUENCES: 105
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: TX
; COUNTRY: USA
; ZIP: 77210-4433
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/731,238
; FILING DATE: 10-Dec-2003
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/010,317
; FILING DATE: 21-Jan-1998
; APPLICATION NUMBER: US 60/036,139
; FILING DATE: 21-Jan-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Hibler, David W.
; REGISTRATION NUMBER: 41,071
; REFERENCE/DOCKET NUMBER: TAMK:189
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 512-418-3000
; TELEFAX: 512-474-7577
; INFORMATION FOR SEQ ID NO: 40:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 38 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 40:
US-10-731-238-40

Query Match 100.0%; Score 58; DB 18; Length 38;
Best Local Similarity 100.0%; Pred. No. 0.0041;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DKPKYEGGN 10
|||||
Db 15 DKPKYEGGN 24

RESULT 11
US-10-731-238-41
; Sequence 41, Application US/10731238
; Publication No. US20050123552A1
; GENERAL INFORMATION:
; APPLICANT: Hook, Magnus
; Patti, Joseph M.

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```

; House-Pompeo, Karen L.
; Speziale, Pietro
; Joh, Danny
; McGavin, Martin J.
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
; AND METHODS OF USE
; NUMBER OF SEQUENCES: 105
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: TX
; COUNTRY: USA
; ZIP: 77210-4433
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/731,238
; FILING DATE: 10-Dec-2003
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/010,317
; FILING DATE: 21-Jan-1998
; APPLICATION NUMBER: US 60/036,139
; FILING DATE: 21-Jan-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Hibler, David W.
; REGISTRATION NUMBER: 41,071
; REFERENCE/DOCKET NUMBER: TAMK:189
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 512-418-3000
; TELEFAX: 512-474-7577
; INFORMATION FOR SEQ ID NO: 41:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 38 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 41:
US-10-731-238-41

Query Match 100.0%; Score 58; DB 18; Length 38;
Best Local Similarity 100.0%; Pred. No. 0.0041;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DKPKYEGGN 10
|||||
Db 15 DKPKYEGGN 24

RESULT 12
US-10-731-238-56
; Sequence 56, Application US/10731238
; Publication No. US20050123552A1
; GENERAL INFORMATION:
; APPLICANT: Hook, Magnus
; Patti, Joseph M.
; House-Pompeo, Karen L.
; Speziale, Pietro
; Joh, Danny
; McGavin, Martin J.
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
; AND METHODS OF USE
; NUMBER OF SEQUENCES: 105
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: TX
; COUNTRY: USA

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ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/731,238
FILING DATE: 10-Dec-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE: 21-Jan-1998
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-Jan-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hildier, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAMK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 56:
SEQUENCE CHARACTERISTICS:
LENGTH: 39 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 56:
US-10-731-238-56

Query Match 100.0%; Score 58; DB 18; Length 39;
Best Local Similarity 100.0%; Pred. No. 0.0042;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DKPKYEOGNG 10
| | | | | | | | | |
Db 15 DKPKYEOGNG 24

RESULT 13
US-09-813-820-8
Sequence 8, Application US/09813820
Patent No. US20020102262A1
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
Pacifi, Joseph M.
House-Pompeo, Karen
Stranam, Narayana
Symersky, Jindrich
TITLE OF INVENTION: COLLAGEN BINDING PROTEIN COMPOSITIONS
AND METHODS OF USE
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: Texas
COUNTRY: U.S.
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/813,820
FILING DATE: 22-Mar-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/856,253
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:

NAME: Kitchell, Barbara S.
REGISTRATION NUMBER: 33,928
REFERENCE/DOCKET NUMBER: TAMK:193
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
TELEFAX: (512) 474-7577
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 139 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-09-813-820-8

Query Match 100.0%; Score 58; DB 9; Length 139;
Best Local Similarity 100.0%; Pred. No. 0.015;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DKPKYEOGNG 10
| | | | | | | | | |
Db 30 DKPKYEOGNG 39

RESULT 14
US-08-901-062-1
Sequence 1, Application US/08901062
Publication No. US20020025324A1
GENERAL INFORMATION:
APPLICANT: SEALS, JONATHAN R.
TITLE OF INVENTION: RECOMBINANT BIVALENT BACTERIAL VACCINE
FOR THE PREVENTION OF MASTITIS
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: HALE AND DORR LLP
STREET: 60 State Street
CITY: Boston
STATE: MA
COUNTRY: United States Of America
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/901,062
CLASSIFICATION: 424
FILING DATE: 25-JUL-1997
NAME: Baker, Hollie L.
ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 31,321
REFERENCE/DOCKET NUMBER: 106941.153
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 526-6000
TELEFAX: (617) 526-5000
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 388 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-901-062-1

Query Match 100.0%; Score 58; DB 8; Length 388;
Best Local Similarity 100.0%; Pred. No. 0.043;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DKPKYEOGNG 10
| | | | | | | | | |

Db 279 DKPKYEOGN 288

RESULT 15

US-08-781-986A-5251

; Sequence 5251, Application US/08781986A
; Publication No. US20030054436A1

GENERAL INFORMATION:

APPLICANT: Charles Kunsch

TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences

NUMBER OF SEQUENCES: 5255

CORRESPONDENCE ADDRESS:

ADDRESSEE: Human Genome Sciences, Inc.

STREET: 9410 Key West Avenue

CITY: Rockville

STATE: Maryland

COUNTRY: USA

ZIP: 20850

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage

COMPUTER: HP Vectra 486/33

OPERATING SYSTEM: MSDOS version 6.2

SOFTWARE: ASCII Text

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/781,986A

FILING DATE:

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Benson, Bob

REGISTRATION NUMBER: 30,446

REFERENCE/DOCKET NUMBER: PB248PP

TELECOMMUNICATION INFORMATION:

TELEPHONE: (301) 309-8504

TELEFAX: (301) 309-8512

INFORMATION FOR SEQ ID NO: 5251:

SEQUENCE CHARACTERISTICS:

LENGTH: 559 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-781-986A-5251

Query Match 100.0%; Score 58; DB 8; Length 559;
Best Local Similarity 100.0%; Pred. No. 0.063;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DKPKYEOGN 10
|||
Db 315 DKPKYEOGN 324

Search completed: October 22, 2005, 12:39:44
Job time : 58.25 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 22, 2005, 06:10:10 ; Search time 11.45 Seconds
(without alignments)
84.032 Million cell updates/sec

Title: US-10-731-238-70

Perfect score: 58
Sequence: 1 DKPKYEOGCGN 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : PIR 79:*

1: pirl:*

2: pirl2:*

3: pirl3:*

4: pirl4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	58	100.0	940	2	S19702	fibronectin-binding
2	58	100.0	961	2	G90053	hypothetical prote
3	58	100.0	1018	2	A32192	fibronectin-binding
4	58	100.0	1038	2	H90053	hypothetical prote
5	38	65.5	538	2	H87347	hypothetical prote
6	37	63.8	365	2	F84033	germination (corte
7	37	63.8	432	2	C97258	sugar-binding peri
8	37	63.8	1196	2	S65245	translation elonga
9	36	62.1	189	2	F83973	hypothetical prote
10	36	62.1	275	2	C89858	conserved hypoch
11	36	62.1	308	1	J01401	glutathione syntha
12	36	62.1	369	2	S72240	tRNA guanine trans
13	36	62.1	460	2	S06469	photosystem II chl
14	36	62.1	461	2	JT0322	photosystem II chl
15	36	62.1	461	2	S41480	photosystem II chl
16	36	62.1	461	2	S04025	photosystem II chl
17	36	62.1	461	2	T06936	photosystem II chl
18	36	62.1	471	2	S78347	photosystem II chl
19	36	62.1	473	1	F2LV44	photosystem II chl
20	36	62.1	473	1	F2NT44	photosystem II chl
21	36	62.1	473	1	F2RZ44	photosystem II chl
22	36	62.1	473	1	F2SP44	photosystem II chl
23	36	62.1	473	1	JN0346	photosystem II chl
24	36	62.1	473	2	S03436	photosystem II chl
25	36	62.1	473	2	S58537	photosystem II chl
26	36	62.1	473	2	T07238	photosystem II chl
27	36	62.1	473	2	T07548	photosystem II chl
28	36	62.1	473	2	T08998	photosystem II chl
29	36	62.1	476	2	S63445	hypothetical prote

30	36	62.1	539	2	B49855	heat shock protein
31	36	62.1	2108	2	H70819	probable polyketid
32	35	60.3	110	1	S43192	ribosomal protein
33	35	60.3	327	2	A44168	homeotic protein D
34	35	60.3	388	2	B87600	cardamomyl-phosphat
35	35	60.3	448	2	S39348	26S ATP/ubiquitin-
36	35	60.3	459	2	S42647	photosystem II chl
37	35	60.3	459	2	AD2342	photosystem II CP4
38	35	60.3	471	2	T48743	probable 26S ATP/u
39	35	60.3	473	1	F2RK4C	photosystem II chl
40	35	60.3	487	2	S73277	photosystem II chl
41	35	60.3	522	2	G02533	occludin - human
42	35	60.3	615	2	A83069	cold-shock dead-bo
43	35	60.3	615	2	F98217	inducible ATP- inde
44	35	60.3	788	2	T30510	viral enhancing fa
45	35	60.3	932	2	T39716	translation initia

ALIGNMENTS

RESULT 1

S19702

fibronectin-binding protein B - Staphylococcus aureus

C/Species: Staphylococcus aureus

C/Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #ext_change 09-Jul-2004

C/Accession: S19702

R/Joensson, K.; Signaes, C.; Mueller, H.P.; Lindberg, M.

Eur. J. Biochem. 202, 1041-1048, 1991

A/Title: Two different genes encode fibronectin binding proteins in Staphylococcus aure

A/Reference number: S19702; PMID:92111475; PMID:1837266

A/Accession: S19702

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-940 <JOE>

A/Cross-references: UNIPROT:Q53682; EMBL:X62992; NID:G49040; PIDN:CAA44726.1; PID:G5815

C/Keywords: fibronectin binding

Query Match 100.0%; Score 58; DB 2; Length 940;
Best Local Similarity 100.0%; Pred. No. 0.0076;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 2

G90053

hypothetical protein fmbB [imported] - Staphylococcus aureus (strain N315)

C/Species: Staphylococcus aureus

C/Date: 10-May-2001 #sequence_revision 10-May-2001 #ext_change 09-Jul-2004

C/Accession: G90053

R/Kuroda, M.; Ohba, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Ogu

ma, A.; Mizutani, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaio, C.; Sekimizu, K.

C./Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.

Lancet 357, 1225-1240, 2001

A/Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.

A/Reference number: A89758; PMID:21311952; PMID:11418146

A/Accession: G90053

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-961 <KUR>

A/Cross-references: UNIPROT:Q99RD3; GB:BA000018; PID:G13702452; PIDN:BA43593.1; GSPDB:

A/Experimental source: strain N315

C/Genetics:

A/Gene: fmbB

Query Match 100.0%; Score 58; DB 2; Length 961;
Best Local Similarity 100.0%; Pred. No. 0.0078;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 707 DKPKYEGGN 716

RESULT 3

A32192
fibronectin-binding protein - Staphylococcus aureus
C:Species: Staphylococcus aureus
C:Date: 31-Jul-1989 #sequence_revision 31-Jul-1989 #text_change 16-Feb-1997
C:Accession: A32192
R:Signaet, C.; Raucci, G.; Jonsson, K.; Lindgren, P.E.; Anantharamiah, G.M.; Hoeoek, W
Proc. Natl. Acad. Sci. U.S.A. 86, 699-703, 1989
A:Title: Nucleotide sequence of the gene for a fibronectin-binding protein from Staphylococcus aureus
A:Reference number: A32192; MUID:8908998; PMID:2521391
A:Accession: A32192
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1018 <SIG>
A:Cross-references: GB:J04151
C:Keywords: fibronectin binding

Query Match 100.0%; Score 58; DB 2; Length 1013;
Best Local Similarity 100.0%; Pred. No. 0.0083;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DKPKYEGGN 10
Db 760 DKPKYEGGN 769

RESULT 4

H90053
hypothetical protein fnb [imported] - Staphylococcus aureus (strain N315)
C:Species: Staphylococcus aureus
C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C:Accession: H90053
R:Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguc
ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Gato, C.; Sekimizu, K.;
C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hirama, S.; K.
Lancet 357, 1225-1240, 2001
A:Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.
A:Reference number: A89758; MUID:21311952; PMID:11418146
A:Accession: H90053
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1038 <KUR>
A:Cross-references: UNIPROT:Q99RD2; GB:BA000018; PID:G13702453; PIDN:BA843594.1; GSPDB:G
A:Experimental source: strain N315
C:Genetics:
A:Gene: fnb

Query Match 100.0%; Score 58; DB 2; Length 1031;
Best Local Similarity 100.0%; Pred. No. 0.0085;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DKPKYEGGN 10
Db 756 DKPKYEGGN 765

RESULT 5

H87347
hypothetical protein CC0795 [imported] - Caulobacter crescentus
C:Species: Caulobacter crescentus
C:Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004
C:Accession: H87347
R:Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Jisen, J.; Heidelberg, J.
B.; Laub, M.T.; Deboy, R.T.; Dodson, R.J.; Durkin, A.S.; Ginn, M.L.; Haft, D.H.; Kolon
n, J.; Esmolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A:Title: Complete Genome Sequence of Caulobacter crescentus.
A:Reference number: A87249; MUID:21173698; PMID:11259647
A:Accession: H87347

A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-538 <STO>
A:Cross-references: UNIPROT:Q9AA16; GB:AE005673; NID:G13422038; PIDN:AAK22780.1; GSPDB:G
C:Genetics:
A:Gene: CC0795
C:Superfamily: alpha-L-fucosidase

Query Match 65.5%; Score 38; DB 2; Length 538;
Best Local Similarity 66.7%; Pred. No. 29;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 DKPKYEGGN 9
Db 364 DKPKYEGGN 372

RESULT 6

F84033
germination (cortex hydrolysis) and sporulation (stage II, multiple polar septal) germ [i
C:Species: Bacillus halodurans
C:Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004
C:Accession: F84033
R:Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, F.; Hira
Nucleic Acids Res. 28, 4317-4331, 2000
A:Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and
A:Reference number: A83650; MUID:20512582; PMID:11058132
A:Accession: F84033
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-365 <STO>
A:Cross-references: UNIPROT:Q9KBD6; GB:AP001517; GB:BA000004; NID:G10175500; PIDN:BA8067
A:Experimental source: strain C-125
C:Genetics:
A:Gene: germ

Query Match 63.8%; Score 37; DB 2; Length 365;
Best Local Similarity 75.0%; Pred. No. 30;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 DKPKYEGGN 8
Db 285 DKPKYEGGN 292

RESULT 7

C97258
sugar-binding periplasmic protein [imported] - Clostridium acetobutylicum
C:Species: Clostridium acetobutylicum
C:Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 09-Jul-2004
C:Accession: C97258
R:Molling, J.; Breton, G.; Onelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee,
J.; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.
J. Bacteriol. 183, 4823-4838, 2001
A:Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Clo
A:Reference number: A96900; MUID:21359325; PMID:21359325
A:Accession: C97258
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-432 <KUR>
A:Cross-references: UNIPROT:Q97F41; GB:AE001437; PIDN:AAK80854.1; PID:G15025961; GSPDB:G
A:Experimental source: Clostridium acetobutylicum ATCC824
C:Genetics:
A:Gene: CAC2912

Query Match 63.8%; Score 37; DB 2; Length 432;
Best Local Similarity 75.0%; Pred. No. 36;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 DKPKYEGGN 10
Db 297 DKPKYEGGN 304

RESULT 8

translacton elongation factor eEF-3 homolog YPL226w - yeast (*Saccharomyces cerevisiae*)

S65245

N:Alternate names: protein P1445

C:Species: *Saccharomyces cerevisiae*

C>Date: 10-Dec-1994 #sequence_revision 31-May-1996 #text_change 16-Aug-2004

C:Accession: S65245; S65251; S61708

R:Rieger, M.; Mueller-Auer, S.; Schaefer, M.

submitted to the Protein Sequence Database, May 1996

A:Reference number: S65202

A:Accession: S65245

A:Molecule type: DNA

A:Residues: 1-1196 <RIB>

A:Cross-references: UNIPROT:Q08972; EMBL:Z73582; NID:g1370467; PIDN:CAA97941.1; PID:e247

A:Experimental source: strain S288C (AB972)

R:Ruttenstarz, L.A.; Vissers, S.

submitted to the Protein Sequence Database, May 1996

A:Reference number: S65251

A:Accession: S65251

A:Molecule type: DNA

A:Residues: 1-358 <URR>

A:Cross-references: EMBL:Z73582; MIPS:YPL226w

A:Experimental source: strain S288C (AB972)

R:Ruttenstarz, L.A.

submitted to the EMBL Data Library, December 1995

A:Reference number: S61699

A:Accession: S61708

A:Molecule type: DNA

A:Residues: 1-358 <URR>

A:Cross-references: EMBL:X94561; NID:g1181252; PIDN:CAA64261.1; PID:e217943; PID:g118126

C:Genetics:

A:Gene: SGD:NEW1

A:Cross-references: SGD:S0006147

A:Map position: 16L

C:Superfamily: ATP-binding cassette homology; chromobox homology

C:Keywords: ATP; nucleotide binding; P-loop

F:587-761/Domain: ATP-binding cassette homology <ABC1>

F:604-611/Region: nucleotide-binding motif A (P-loop)

F:829-1105/Domain: ATP-binding cassette homology <ABC2>

F:846-855/Region: nucleotide-binding motif A (P-loop)

F:942-979/Domain: chromobox homology <CBH>

QY 1 DKPKYEGGN 10

DB 1116 DQSKFEDGDN 1125

Query Match 63.8%; Score 37; DB 2; Length 1196;

Best Local Similarity 60.0%; Pred. No. 1.1e+02;

Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

RESULT 9

hypothetical protein BH2590 [imported] - *Bacillus halodurans* (strain C-125)

C:Species: *Bacillus halodurans*

C>Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004

C:Accession: F83973

R:Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, F.; Hirai

Nucleic Acids Res. 28, 4317-4331, 2000

A:Title: Complete genome sequence of the alkaliphilic bacterium *Bacillus halodurans* and

A:Reference number: AB3650; MUID:20512582; PMID:11058132

A:Accession: F83973

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-189 <STO>

A:Cross-references: UNIPROT:Q9X905; GB:BA001516; GB:BA000004; NID:g10175192; PIDN:BA063

C:Genetics:

A:Experimental source: strain C-125

A:Gene: BH2590

Query Match 62.1%; Score 36; DB 2; Length 189;

Best Local Similarity 85.7%; Pred. No. 23;

Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY

4 KYEGGN 10

DB 181 KYEGGN 187

RESULT 10

conserved hypothetical protein SA0783 [imported] - *Staphylococcus aureus* (strain N315)

C:Species: *Staphylococcus aureus*

C>Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004

C:Accession: C89858

R:Kurita, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Gui, L.; Oguc

ma, A.; Mizutani-U, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.;

C.; Shida, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiratsugu, K.

Lancet 357, 1225-1240, 2001

A:Title: Whole genome sequencing of methicillin-resistant *Staphylococcus aureus*.

A:Reference number: AB9758; MUID:21311952; PMID:11418146

A:Accession: C89858

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-275 <KUR>

A:Cross-references: UNIPROT:Q9YVF4; GB:BA000018; PID:g13700725; PIDN:BA842022.1; GSPDB:C

A:Experimental source: strain N315

C:Genetics:

A:Gene: SA0783

Query Match 62.1%; Score 36; DB 2; Length 275;

Best Local Similarity 85.7%; Pred. No. 34;

Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DKPKYEQ 7

DB 136 DKPKYEQ 142

RESULT 11

glutathione synthase (EC 6.3.2.3) - *Anaplasma centrale*

N:Alternate names: glutathione synthetase

C:Species: *Anaplasma centrale*

C>Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 09-Jul-2004

C:Accession: JQ1401

R:Peterson, J.M.; Dalrymple, B.P.; Jorgensen, W.K.

Biochem. Biophys. Res. Commun. 182, 1040-1046, 1992

A:Title: Sequence of a putative glutathione synthetase II gene and flanking regions from

A:Reference number: JQ1401; MUID:92171906; PMID:1540152

A:Accession: JQ1401

A:Molecule type: DNA

A:Residues: 1-308 <PET>

A:Cross-references: UNIPROT:P35667; GB:M80425; NID:g142168; PIDN:AAA22064.1; PID:g14217

A:Note: the authors translated the initiation codon GTG for residue 1 as Val

C:Comment: This enzyme catalyzes the formation of glutathione by condensing gamma-gluta

C:Genetics:

A:Gene: gsh II

A:Start codon: GTG

C:Superfamily: *Escherichia coli* glutathione synthase

C:Keywords: ATP; glutathione biosynthesis; ligase

Query Match 62.1%; Score 36; DB 1; Length 308;

Best Local Similarity 66.7%; Pred. No. 39;

Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 KPKYEGGN 10

DB 152 KPKYDYGDN 160

RESULT 12

trNA guanine transglycosylase - *Thermotoga maritima* (strain MSB8)

D72240

C.Species: Thermotoga maritima
 C.Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change (9-Jul-2004
 C.Accession: D72240
 C.Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwin, M.L.; Dodson, J.J.; Haft, D.H.; Hickey
 Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.
 C.M.
 Nature 399, 323-329, 1999
 A>Title: Evidence for lateral gene transfer between Archaea and bacteria from genome seq
 A.Reference number: A72200; MUID:99287316; PMID:10360571
 A.Accession: D72240
 A.Status: preliminary
 A.Molecule type: DNA
 A.Residues: 1-369 <ARN>
 A.Cross-references: UNIPROT:Q9X1P7; GB:AE001801; GB:AE000512; NII:g4982114; PIDN:AA03662
 A.Experimental source: strain MSB8
 C.Genetics:
 A.Gene: TML561
 C.Superfamily: queuine tRNA-ribosyltransferase

Query Match 62.1%; Score 36; DB 2; Length 369;
 Best Local Similarity 66.7%; Pred. No. 47;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 DKPXYEQG 9
 |||:||||
 Db 235 DKPXYFMG 243

RESULT 13
 S06469
 photosystem II chlorophyll a-binding protein pbsc - Synechocystis sp. (strain PCC 6803)
 N.Alternate names: chlorophyll-binding protein, 43K; photosynthetic reaction center 44K
 C.Species: Synechocystis sp.
 A.Variety: PCC 6803
 C.Date: 07-Jun-1990 #sequence_revision 19-Jan-1996 #text_change 20-Jun-2000
 C.Accession: S06469; S07497; S02380; S74838
 R.Chisholm, D.; Williams, J.G.K.
 Plant Mol. Biol. 10, 293-301, 1988
 A>Title: Nucleotide sequence of pbsc, the gene encoding the CP-43 chlorophyll a-binding
 A.Reference number: S06469
 A.Accession: S06469
 A.Status: not compared with conceptual translation
 A.Molecule type: DNA
 A.Residues: 'MKTLSLRSPV', 2-460 <CHI>
 A.Cross-references: GB:M21538; NID:9340699; PIDN:AAA5378.1; PID:91161272
 A.Note: this sequence uses an incorrect initiation codon
 R.Carpenter, S.D.; Charite, J.; Eggers, B.; Vermaas, W.F.J.
 FEBS Lett. 260, 135-137, 1990
 A>Title: The pbsc start codon in Synechocystis sp. PCC 6803.
 A.Reference number: S07496; MUID:90127396; PMID:2105233
 A.Accession: S07497
 A.Molecule type: DNA
 A.Residues: 1-7 <CAR>
 A.Note: the authors definitely establish that the Met-1 GTG is the initiation codon and
 R.Dzelzkalns, V.A.; Bogorad, L.
 EMBO J. 7, 333-338, 1988
 A>Title: Molecular analysis of a mutant defective in photosynthetic oxygen evolution and
 A.Reference number: S02379; MUID:88211542; PMID:3130247
 A.Accession: S02380
 A.Molecule type: DNA
 A.Residues: 'MKTLSLRSPV', 2-54, 'N', 56-149, 'I', 151-288 <DZE>
 A.Cross-references: EMBL:X07018; NID:948064; PIDN:CA30071.1; PID:948066
 A.Note: the authors translated the codon CAT for residue 131 as Phe; this sequence uses
 R.Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.;
 O. K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda
 DNA Res. 3, 109-136, 1996
 A>Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis
 S.
 A.Reference number: S74322; MUID:97061201; PMID:8905231
 A.Accession: S74838
 A.Status: nucleic acid sequence not shown; translation not shown;
 A.Molecule type: DNA
 A.Residues: 'MKTLSLRSPV', 2-41, 'A', 43-460 <KAN>

A.Cross-references: EMBL:D90909; GB:AB001339; NID:91652844; PIDN:BA17799.1; PID:9165288
 A.Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
 A.Note: this sequence uses an incorrect initiation codon
 C.Genetics:
 A.Gene: pbsc
 A.Start codon: GTG
 C.Superfamily: photosystem II chlorophyll a-binding protein pbsc
 C.Keywords: chlorophyll; membrane-associated complex; photosynthesis; photosystem II; th

Query Match 62.1%; Score 36; DB 2; Length 460;
 Best Local Similarity 75.0%; Pred. No. 60;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 DKPXYEQG 8
 |||:||||
 Db 65 EKPXYEQG 72

RESULT 14
 J70322
 photosystem II chlorophyll a-binding protein pbsc - Synechococcus sp. (strain PCC 7942)
 N.Alternate names: photosystem II protein CP43
 C.Species: Synechococcus sp.
 C.Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 09-Jul-2004
 C.Accession: J70322
 R.Golden, S.S.; Stearns, G.W.
 Gene 67, 85-96, 1988
 A>Title: Nucleotide sequence and transcript analysis of three photosystem II genes from
 A.Reference number: J70321; MUID:88329748; PMID:3138165
 A.Accession: J70322
 A.Molecule type: DNA
 A.Residues: 1-461 <GOL>
 A.Cross-references: UNIPROT:P11004; GB:M20814; NID:9154587; PIDN:AA27359.1; PID:9154589
 C.Comment: The major membrane protein complexes of photosynthetic thylakoids from oxygen
 his D1 and D2 which house all of the cofactors of the reaction center, and two subunits
 C.Genetics:
 A.Gene: pbsc
 C.Superfamily: photosystem II chlorophyll a-binding protein pbsc
 C.Keywords: chlorophyll; photosynthesis; photosystem II; thylakoid

Query Match 62.1%; Score 36; DB 2; Length 461;
 Best Local Similarity 75.0%; Pred. No. 60;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 DKPXYEQG 8
 |||:||||
 Db 66 EKPXYEQG 73

RESULT 15
 S41480
 photosystem II chlorophyll a-binding protein pbsc - Chlamydomonas eugametos chloroplast
 C.Species: Chlamydomonas eugametos
 C.Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Jul-2004
 C.Accession: S41480
 R.Cole, M.J.J.; Lemieux, C.; Turmel, M.
 submitted to the EMBL Data Library, May 1993
 A>Description: Identification of self-splicing group I introns in the chloroplast pbsc g
 of Chlamydomonas moewusii.
 A.Reference number: S41480
 A.Accession: S41480
 A.Molecule type: DNA
 A.Residues: 1-461 <CON>
 A.Cross-references: UNIPROT:O08684; EMBL:M90639; NID:9289948; PIDN:AAA84148.1; PID:92899
 C.Genetics:
 A.Gene: pbsc
 A.Genome: chloroplast
 A.Start codon: GTG
 A.Introns: 181/3; 294/3
 C.Superfamily: photosystem II chlorophyll a-binding protein pbsc
 C.Keywords: chlorophyll; chloroplast; membrane-associated complex; photosynthesis; phot

Query Match 62.1%; Score 36; DB 2; Length 461;

Best Local Similarity 75.0%; Pred. No. 60;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
Oy 1 DKPKYEQG 8
: |||||
Db 66 EKPMYEQG 73

Search completed: October 22, 2005, 08:04:24
Job time : 11.45 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 22, 2005, 06:06:36 ; Search time 55.85 Seconds
(without alignments)
91.688 Million cell updates/sec

Title: US-10-731-238-70
Perfect score: 58
Sequence: 1 DKPKYEGGNN 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_03:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	58	100.0	152	2 Q9AEP9	Q9AEP9 staphylococ
2	58	100.0	940	2 Q53682	Q53682 staphylococ
3	58	100.0	943	2 Q8NU08	Q8NU08 staphylococ
4	58	100.0	957	2 Q6G6H4	Q6G6H4 staphylococ
5	58	100.0	961	2 Q99RD3	Q99RD3 staphylococ
6	58	100.0	961	2 Q7A3U8	Q7A3U8 staphylococ
7	58	100.0	965	2 Q6GDU5	Q6GDU5 staphylococ
8	58	100.0	1015	2 Q8NU07	Q8NU07 staphylococ
9	58	100.0	1015	2 Q6G6H3	Q6G6H3 staphylococ
10	58	100.0	1018	1 FNBA STAU	P14738 staphylococ
11	58	100.0	1038	2 Q99RD2	Q99RD2 staphylococ
12	58	100.0	1038	2 Q7A3U7	Q7A3U7 staphylococ
13	45	77.6	215	2 Q8G8U1	Q8G8U1 uncultured
14	43	74.1	194	2 Q7KWL2	Q7KWL2 dictyostel
15	42	72.4	2992	2 Q7RXD7	Q7RXD7 neurospora
16	40	69.0	462	2 Q7UB84	Q7UB84 eynechococ
17	40	69.0	1133	2 Q71954	Q71954 bovine vira
18	39	67.2	458	2 Q85G26	Q85G26 cyanidiosch
19	38	65.5	168	2 Q6Y4S7	Q6Y4S7 bovine vira
20	38	65.5	383	2 Q939R5	Q939R5 bacillus th
21	38	65.5	538	2 Q9AAL6	Q9AAL6 caulobacter
22	38	65.5	655	2 Q75914	Q75914 aabysa goss
23	38	65.5	676	2 Q7RNV6	Q7RNV6 plasmodium
24	37	63.8	247	2 Q7W773	Q7W773 bordetella
25	37	63.8	247	2 Q7W1D8	Q7W1D8 bordetella
26	37	63.8	340	2 Q7OKC9	Q7OKC9 anopheles g
27	37	63.8	365	2 Q9K8D6	Q9K8D6 bacillus ha
28	37	63.8	381	2 Q7XXO8	Q7XXO8 oryza sativ
29	37	63.8	416	2 Q8LJ06	Q8LJ06 musa acumin
30	37	63.8	416	2 Q8GUR0	Q8GUR0 musa acumin
31	37	63.8	432	2 Q97F41	Q97F41 clostridium

32	37	63.8	479	2 Q6CDJ1	Q6CDJ1 yarrowia li
33	37	63.8	505	2 Q9VFN2	Q9VFN2 drosophila
34	37	63.8	530	2 Q6ZCR7	Q6ZCR7 oryza sativ
35	37	63.8	548	2 Q6PPF3	Q6PPF3 rattus norv
36	37	63.8	552	1 USIC_HUMAN	USIC_HUMAN
37	37	63.8	597	2 Q95QR5	Q95QR5 caenorhabd
38	37	63.8	618	2 Q8S3U7	Q8S3U7 chlamydomon
39	37	63.8	860	2 Q23916	Q23916 dictyostel
40	37	63.8	905	2 Q8A284	Q8A284 bacteroides
41	37	63.8	1196	2 Q08972	Q08972 saccharomyc
42	37	63.8	1967	2 Q7RHF3	Q7RHF3 plasmodium
43	36	62.1	128	2 Q8HTU6	Q8HTU6 utricularia
44	36	62.1	128	2 Q8HTU7	Q8HTU7 utricularia
45	36	62.1	128	2 Q8HTU8	Q8HTU8 utricularia

ALIGNMENTS

RESULT 1

ID Q9AEP9 PRELIMINARY; PRT; 152 AA.
AC Q9AEP9;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Fibronectin-binding protein (Fragment).
GN Name=fnb;
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1280;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CMRSA-1;
RX MEDLINE=2124681; PubMed=11349044;
RX DOI=10.1128/IAI.69.6.3791-3799.2001;
RA Rice K., Huesca M., Vaz D., McGavin M.J.;
RT "variance in fibronectin binding and fnb locus polymorphisms in
RT Staphylococcus aureus: identification of antigenic variation in a
RT fibronectin binding protein adhesin of the epidemic CMRSA-1 strain of
RT methicillin-resistant S. aureus.";
RT Infect. Immun. 69:3791-3799(2001).
DR EMBL: AY029184; AAK31588.1; -
FT NON_TER 1
FT NON_TER 152
SQ SEQUENCE 152 AA; 17193 MW; CFA3913C2B11C025 CRC64;

Query Match 100.0%; Score 58; DB 2; Length 152;
Best Local Similarity 100.0%; Pred. No. 0.0046;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DKPKYEGGNN 10
Db 15 DKPKYEGGNN 24

RESULT 2

ID Q53682 PRELIMINARY; PRT; 940 AA.
AC Q53682;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Fibronectin binding protein B.
GN Name=fnbB;
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1280;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=8325-4;
RX MEDLINE=9211475; PubMed=1837266;
RA Jonsson K., Sigfus C., Muller H.P., Lindberg M.;

```
RT "Two different genes encode fibronectin binding proteins in
RT Staphylococcus aureus. The complete nucleotide sequence and
RT characterization of the second gene."
RL Eur. J. Biochem. 202;1041-1048(1991).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC an amide bond (By similarity).
DR EMBL: X62992; CAA44726.1; -.
DR PIR: S19702; S19702.
DR HSP: O53653; 1N67.
DR GO: GO:0009986; C:cell surface; IEA.
DR GO: GO:0005618; C:cell wall; IEA.
DR GO: GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO: GO:0016020; C:membrane; IEA.
DR GO: GO:0007155; P:cell adhesion; IEA.
DR InterPro: IPR008966; Adhes_bact.
DR InterPro: IPR004237; Fn_bind.
DR InterPro: IPR005877; Gpos_YsIRK.
DR Pfam: PF02986; Fn_bind; 2.
DR Pfam: PF00746; Gram_pos_anchor; 1.
DR TIGRfams: TIGR01167; LpxTG_anchor; 1.
DR TIGRfams: TIGR01168; YsIRK_signal; 1.
DR PROSITE: PS50847; GRAM_POS_ANCHORING; 1.
KW Cell wall; Peptidoglycan-anchor.
SQ SEQUENCE 940 AA; 10355 MW; E35FBBCA907AE345 CRC64;

Query Match 100.0%; Score 58; DB 2; Length 940;
Best Local Similarity 100.0%; Pred. No. 0.036;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DKPKYEGGN 10
DB 696 DKPKYEGGN 705

RESULT 3
OQNU8 PRELIMINARY; PRT; 943 AA.
ID OQNU8
AC OQNU8;
DT 01-OCT-2002 (TREMBlrel. 22, Created)
DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Pnb protein.
GN Name=fnb; OrderedlocusNames=MM2420;
OS Staphylococcus aureus (strain MM2).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=196620;
RN [1]
RP STRAIN=MM2.
RC MEDLINE=22040717; PubMed=12044378; DOI=10.1016/S0140-6736(02)08713-5;
RX Baba T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Oguchi A.,
RA Nagai Y., Iwama N., Asano K., Naimi T., Kuroda H., Cui L.,
RA Yamamoto K., Hiramoto K.;
RA "Genome and virulence determinants of high virulence community-
RT acquired MRSA."
RT Lancet 359;1819-1827(2002).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC an amide bond (By similarity).
DR EMBL: AP004830; BAB96285.1; -.
DR HSP: O53653; 1N67.
DR GO: GO:0009986; C:cell surface; IEA.
DR GO: GO:0005618; C:cell wall; IEA.
DR GO: GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO: GO:0016020; C:membrane; IEA.
DR GO: GO:0007155; P:cell adhesion; IEA.
DR InterPro: IPR008966; Adhes_bact.
DR InterPro: IPR004237; Fn_bind.
DR InterPro: IPR005877; Gpos_YsIRK.
DR Pfam: PF02986; Fn_bind; 1.
DR Pfam: PF00746; Gram_pos_anchor; 1.
SQ SEQUENCE 957 AA; 105980 MW; 28F8BA7FFDF3EAF CRC64;
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DR Pfam: PF04650; YsIRK_signal; 1.
DR TIGRfams: TIGR01167; LpxTG_anchor; 1.
DR TIGRfams: TIGR01168; YsIRK_signal; 1.
DR PROSITE: PS50847; GRAM_POS_ANCHORING; 1.
KW Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ SEQUENCE 943 AA; 104537 MW; DA8A5F31947B1B6A CRC64;

Query Match 100.0%; Score 58; DB 2; Length 943;
Best Local Similarity 100.0%; Pred. No. 0.037;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY 1 DKPKYEGGN 10
DB 703 DKPKYEGGN 712
```

```
RESULT 4
OQ6G4 PRELIMINARY; PRT; 957 AA.
ID OQ6G4
AC OQ6G4;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE Fibronectin-binding protein.
GN Name=fnb; OrderedlocusNames=SAS2387;
OS Staphylococcus aureus (strain MSSA476).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=282459;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=15213324; DOI=10.1073/pnas.0402521101;
RA Holden M.T.G., Fell E.J., Lindsay J.A., Peacock S.J., Day N.P.J.,
RA Enright M.C., Foster T.J., Moore C.E., Hurst L., Atkin R., Barron A.,
RA Baeson N., Bentley S.D., Chillingworth C., Chillingworth T.,
RA Churcher C., Clark L., Cotton C., Cronin A., Doggett J., Dowd L.,
RA Feltham D., Fennell N., Harris B., Hauser H., Holtby S., Jorgensen K.,
RA James K.D., Leonard N., Line A., Mayes R., Moule S., Mungall K.,
RA Ormond D., Quail M.A., Rabinowitch E., Rutherford K.M., Sanders M.,
RA Sharp S., Simmonds M., Stevens K., Whitehead S., Barrall B.G.,
RA Spratt B.G., Parkhill J.;
RT "Complete genomes of two clinical Staphylococcus aureus strains:
RT evidence for the rapid evolution of virulence and drug resistance."
RT Proc. Natl. Acad. Sci. U.S.A. 101;9786-9791(2004).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC an amide bond (By similarity).
DR EMBL: EX571857; CAG44201.1; -.
DR GO: GO:0009986; C:cell surface; IEA.
DR GO: GO:0005618; C:cell wall; IEA.
DR GO: GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO: GO:0016020; C:membrane; IEA.
DR GO: GO:0007155; P:cell adhesion; IEA.
DR InterPro: IPR008966; Adhes_bact.
DR InterPro: IPR004237; Fn_bind.
DR InterPro: IPR005877; Gpos_YsIRK.
DR InterPro: IPR001899; Gram_pos_anchor.
DR Pfam: PF02986; Fn_bind; 1.
DR Pfam: PF00746; Gram_pos_anchor; 1.
DR TIGRfams: TIGR01167; LpxTG_anchor; 1.
DR TIGRfams: TIGR01168; YsIRK_signal; 1.
DR PROSITE: PS50847; GRAM_POS_ANCHORING; 1.
KW Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ SEQUENCE 957 AA; 105980 MW; 28F8BA7FFDF3EAF CRC64;

Query Match 100.0%; Score 58; DB 2; Length 957;
Best Local Similarity 100.0%; Pred. No. 0.037;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY 1 DKPKYEGGN 10
DB 703 DKPKYEGGN 712
```

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RESULT 5
O99RD3 PRELIMINARY; PRT; 961 AA.
ID O99RD3;
AC O99RD3;
DT 01-JUN-2001 (TEMBLrel. 17, Created)
DT 01-JUN-2001 (TEMBLrel. 17, Last sequence update)
DT 01-JUN-2003 (TEMBLrel. 24, Last annotation update)
DE Fibronectin-binding protein homolog.
GN Name=fnbB; OrderedLocustNames=SAV2502;
OS Staphylococcus aureus (strain M50 / ATCC 700699).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=158878;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=M50 / ATCC 700699;
RX MEDLINE=21311952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2;
RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Lian J.-O., Ito T.,
RA Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,
RA Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
RA Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
RA Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
RA Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
RT "Whole genome sequencing of methicillin-resistant Staphylococcus
RT aureus."
RT Lancet 357:1225-1240(2001).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC an amide bond (By similarity).
EMBL: AP003137; BAB3593.1; -.
DR GO: 0009986; C:cell surface; IEA.
DR GO: 0005618; C:cell wall; IEA.
DR GO: 0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO: 0016020; C:membrane; IEA.
DR GO: 0007155; P:cell adhesion; IEA.
DR InterPro: IPR008966; F:fn_bind.
DR InterPro: IPR005877; Gpos_YsIRK.
DR InterPro: IPR001899; Gram_pos_anchor.
DR Pfam: PF02986; Fm_bind_1.
DR Pfam: PF00746; Gram_pos_anchor; 1.
DR Pfam: PF04650; YsIRK_signal; 1.
DR TIGRfams: TIGR01167; LPXTG_anchor; 1.
DR TIGRfams: TIGR01168; YsIRK_signal; 1.
DR PROSITE: PS50847; GRAM_POS_ANCHORING; 1.
KW Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ SEQUENCE 961 AA; 106010 MW; 364940F884EA4101 CRC64;

Query Match 100.0%; Score 58; DB 2; Length 961;
Best Local Similarity 100.0%; Pred. No. 0.037;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DKPKYEQGN 10
Db 707 DKPKYEQGN 716

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RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Lian J.-O., Ito T.,
RA Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,
RA Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
RA Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
RA Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
RA Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
RT "Whole genome sequencing of methicillin-resistant Staphylococcus
RT aureus."
RT Lancet 357:1225-1240(2001).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC an amide bond (By similarity).
EMBL: AP003137; BAB3593.1; -.
DR GO: 0009986; C:cell surface; IEA.
DR GO: 0005618; C:cell wall; IEA.
DR GO: 0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO: 0016020; C:membrane; IEA.
DR GO: 0007155; P:cell adhesion; IEA.
DR InterPro: IPR008966; F:fn_bind.
DR InterPro: IPR005877; Gpos_YsIRK.
DR InterPro: IPR001899; Gram_pos_anchor.
DR Pfam: PF02986; Fm_bind_1.
DR Pfam: PF00746; Gram_pos_anchor; 1.
DR Pfam: PF04650; YsIRK_signal; 1.
DR TIGRfams: TIGR01167; LPXTG_anchor; 1.
DR TIGRfams: TIGR01168; YsIRK_signal; 1.
DR PROSITE: PS50847; GRAM_POS_ANCHORING; 1.
KW Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ SEQUENCE 961 AA; 106010 MW; 364940F884EA4101 CRC64;

Query Match 100.0%; Score 58; DB 2; Length 961;
Best Local Similarity 100.0%; Pred. No. 0.037;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DKPKYEQGN 10
Db 707 DKPKYEQGN 716

RESULT 7
O6GDUS PRELIMINARY; PRT; 965 AA.
ID O6GDUS;
AC O6GDUS;
DT 05-JUL-2004 (TEMBLrel. 27, Created)
DT 05-JUL-2004 (TEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TEMBLrel. 27, Last annotation update)
DE Fibronectin-binding protein.
GN Name=fnbA; OrderedLocustNames=SA2580;
OS Staphylococcus aureus (strain MRSA252).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=282458;
RN (1)
RP SEQUENCE FROM N.A.
RX PubMed=1521324; DOI=10.1073/pnas.0402521101;
RA Holden M.T.G., Fell E.J., Lindsey J.A., Peacock S.J., Day N.P.J.,
RA Enright M.C., Foster T.J., Moore C.B., Hurst L., Actin R., Barron A.,
RA Bason N., Bentley S.D., Chillingworth C., Chillingworth T.,
RA Churcher C., Clark L., Cotton C., Cronin A., Doggett J., Dowd L.,
RA Felwell T., Hance Z., Harris B., Hauser H., Holtroyd S., Jørgensen K.,
RA James K.D., Lennard N., Line A., Mayes R., Moule S., Mungall K.,
RA Ormond D., Quail M.A., Rabinowitch E., Rutherford K.M., Sanders M.,
RA Sharp S., Simmonds M., Stevens K., Whitehead S., Barrett B.G.,
RA Spratt B.G., Parkhill J.;
RT "Complete genomes of two clinical Staphylococcus aureus strains:
RT evidence for the rapid evolution of virulence and drug resistance."
RT Proc. Natl. Acad. Sci. U.S.A. 101:9786-9791(2004).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC an amide bond (By similarity).
EMBL: BX571856; CAG41560.1; -.
DR GO: 0009986; C:cell surface; IEA.
DR GO: 0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO: 0016020; C:membrane; IEA.

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DR GO:0007155; P:cell adhesion; IEA.
DR InterPro: IPR008966; Adhes.bact.
DR InterPro: IPR004237; Fn_bind.
DR InterPro: IPR005877; Gpos_YsIRK.
DR Pfam: PF02986; Fn_bind; 1.
DR Pfam: PF00746; Gram_pos_anchor; 1.
DR Pfam: PF04650; YsIRK_signal; 1.
DR TIGRFAMs: TIGR01167; LPXTG_anchor; 1.
DR TIGRFAMs: TIGR01168; YsIRK_signal; 1.
DR PROSITE: PS00847; GRAM_POS_ANCHORING; 1.
DR Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ SEQUENCE 965 AA; 105691 MW; 29828132164D0551 CRC64;

Query Match 100.0%; Score 58; DB 2; Length 965;
Best Local Similarity 100.0%; Pred. No. 0.038;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DKPKYEGGN 10
Db 761 DKPKYEGGN 772

RESULT 8
ID Q8NU7; PRELIMINARY; PRT; 1015 AA.
AC Q8NU7;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Fnb protein.
GN Name=fnb; OrderedLocustNames=MM2421;
OS Staphylococcus aureus (strain MM2).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=196620;
[1]
RP SEQUENCE FROM N.A.
RC MEDLINE=22040717; PubMed=12044378; DOI=10.1016/S0140-6736(02)08713-5;
RA Baba T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Oguchi A.,
RA Nagai Y., Iwana N., Asano K., Naito T., Kuroda H., Cui L.,
RA Yamamoto K., Hiramatsu K.;
RT "Genome and virulence determinants of high virulence community-
acquired MRSA";
RL Lancet 359:1819-1827(2002).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
an amide bond (By similarity).
EMBL: AF004830; BAB96286.1; -.
DR GO:0009986; C:cell surface; IEA.
DR GO:0005618; C:cell wall; IEA.
DR GO:0016020; C:membrane; IEA.
DR GO:0009275; C:cell wall (sensu Gram-positive Bacteria) IEA.
DR GO:0016020; C:membrane; IEA.
DR InterPro: IPR008966; Adhes.bact.
DR InterPro: IPR004237; Fn_bind.
DR InterPro: IPR005877; Gpos_YsIRK.
DR InterPro: IPR001899; Gram_pos_anchor.
DR Pfam: PF02986; Fn_bind; 1.
DR Pfam: PF00746; Gram_pos_anchor; 1.
DR Pfam: PF04650; YsIRK_signal; 1.
DR TIGRFAMs: TIGR01167; LPXTG_anchor; 1.
DR TIGRFAMs: TIGR01168; YsIRK_signal; 1.
DR PROSITE: PS00847; GRAM_POS_ANCHORING; 1.
DR Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ SEQUENCE 1015 AA; 111145 MW; D0F9281BB64D4D2 CRC64;

Query Match 100.0%; Score 58; DB 2; Length 1015;
Best Local Similarity 100.0%; Pred. No. 0.04;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DKPKYEGGN 10
Db 761 DKPKYEGGN 770
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RESULT 9
ID Q6G6H3; PRELIMINARY; PRT; 1015 AA.
AC Q6G6H3;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Fibronectin-binding protein.
GN OrderedLocustNames=SAS238;
OS Staphylococcus aureus (strain MSSA476).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=282459;
[1]
RP SEQUENCE FROM N.A.
RX PubMed=15213324; DOI=10.1073/pnas.0402521101;
RA Holden M.T.G., Fell E.J., Lindsay J.A., Peacock S.J., Day N.P.J.,
RA Enright M.C., Foster T.J., Moore C.E., Hurst L., Atkin R., Barton A.,
RA Bason N., Bentley S.D., Chillingworth C., Chillingworth T.,
RA Churcher C., Clark L., Corton C., Cronin A., Doggett J., Dowd L.,
RA Felwell T., Hance Z., Harris B., Hauser H., Holroyd S., Jagsall K.,
RA James K.D., Leonard N., Line A., Mays R., Mole S., Mungall K.,
RA Ormond D., Quail M.A., Rabinowitch E., Rutherford K.M., Sanders M.,
RA Sharp S., Simmonds M., Stevens K., Whitehead S., Barrett B.G.,
RA Spratt B.G., Parhill J.;
RT "Complete genomes of two clinical Staphylococcus aureus strains:
evidence for the rapid evolution of virulence and drug resistance.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:9786-9791(2004).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
an amide bond (By similarity).
EMBL: BX571857; CAG44202.1; -.
DR GO:0009986; C:cell surface; IEA.
DR GO:0005618; C:cell wall; IEA.
DR GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO:0016020; C:membrane; IEA.
DR GO:0007155; P:cell adhesion; IEA.
DR InterPro: IPR008966; Adhes.bact.
DR InterPro: IPR004237; Fn_bind.
DR InterPro: IPR005877; Gpos_YsIRK.
DR InterPro: IPR001899; Gram_pos_anchor.
DR Pfam: PF02986; Fn_bind; 1.
DR Pfam: PF00746; Gram_pos_anchor; 1.
DR Pfam: PF04650; YsIRK_signal; 1.
DR TIGRFAMs: TIGR01167; LPXTG_anchor; 1.
DR TIGRFAMs: TIGR01168; YsIRK_signal; 1.
DR PROSITE: PS00847; GRAM_POS_ANCHORING; 1.
DR Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ SEQUENCE 1015 AA; 111145 MW; D0F9281BB64D4D2 CRC64;

Query Match 100.0%; Score 58; DB 2; Length 1015;
Best Local Similarity 100.0%; Pred. No. 0.04;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DKPKYEGGN 10
Db 761 DKPKYEGGN 770

RESULT 10
ID FNBA_STAAU STANDARD; PRT; 1018 AA.
AC FNBA_STAAU;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Fibronectin-binding protein precursor (FMBP).
GN Name=fmbp;
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1280;
[1]
RP SEQUENCE FROM N.A.
```

RC STRAIN=NCITC 8325-4;
 RX MEDLINE=8908989; PubMed=2521391;
 RA Signaes C., Raucet G., Joensson K., Lindgren P.-E.,
 RA Anantharamiah G.M., Hoeseck M., Lindberg M.,
 RT "Nucleotide sequence of the gene for a fibronectin-binding protein
 from *Staphylococcus aureus*: use of this peptide sequence in the
 RT synthesis of biologically active peptides."
 RL Proc. Natl. Acad. Sci. U.S.A. 86:699-703(1989).
 CC -1- FUNCTION: The ability of bacteria to bind fibronectin has been
 CC proposed as a virulence factor enabling bacteria to colonize wound
 CC tissues and blood clots. Binding of plasma fibronectin to the
 CC bacterial surface might block adhesion receptors on *S. aureus*, thus
 CC representing an important defense mechanism against tissue
 CC invasion.
 CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
 CC an amide bond (Potential).
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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 CC use by non-profit institutions as long as its content is in no way
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL, J04151; AAA26632.1; -;
 DR InterPro: IPR004237; Fn bind.
 DR InterPro: IPR005877; Gpos YSIRK.
 DR InterPro: IPR001899; Gram_pos_anchor.
 DR Pfam: PF02986; Fn_bind; 1.
 DR Pfam: PF00746; Gram_pos_anchor; 1.
 DR Pfam: PF04650; YSIRK signal; 1.
 DR TIGRPFAM: TIGR01167; LPXTG anchor; 1.
 DR TIGRPFAM: TIGR01168; YSIRK signal; 1.
 DR PROSITE: PS50847; GRAM_POS_ANCHORING; 1.
 DR Cell adhesion; Cell wall; Peptidoglycan-anchor; Repeat; Signal;
 DR Virulence.
 KW SIGNAL.
 FT 1 36
 FT CHAIN 1 36
 FT PROPEP 985 1018
 FT REPEAT 545 574
 FT REPEAT 575 604
 FT DOMAIN 745 878
 FT REPEAT 745 782
 FT REPEAT 783 820
 FT REPEAT 821 859
 FT REPEAT 860 878
 FT DOMAIN 879 948
 FT REPEAT 879 892
 FT REPEAT 893 906
 FT REPEAT 907 920
 FT REPEAT 921 934
 FT REPEAT 935 948
 FT SITE 982 986
 FT MOD_RES 985 985
 SQ SEQUENCE 1018 AA; 111780 MW; 58175E0020E81F1F CRC64;
 Query Match 100.0%; Score 58; DB 1; Length 1018;
 Best Local Similarity 100.0%; Pred. No. 0.04;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DT 01-JUN-2001 (TrEMBLrel. 17, last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, last annotation update)
 GN Fibronectin-binding protein homolog.
 DE Name=fnb; OrderedLocustNames=SAV2503;
 OS *Staphylococcus aureus* (strain Mu50 / ATCC 700699).
 CC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 OX NCBI_TaxID=158878;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Mu50 / ATCC 700699;
 RX MEDLINE=21311952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2;
 RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
 RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Iian J.-Q., Ito T.,
 RA Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,
 RA Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
 RA Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
 RA Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
 RT "Whole genome sequencing of methicillin-resistant *Staphylococcus*
 RT *aureus*."
 RL Lancet 357:1225-1240(2001).
 CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
 CC an amide bond (By similarity).
 CC EMBL, AP003365; BAB58665.1; -;
 DR PIR: H90053; H90053.
 DR GO: GO:0009986; C:cell surface; IEA.
 DR GO: GO:0005618; C:cell wall; IEA.
 DR GO: GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
 DR GO: GO:0016020; C:membrane; IEA.
 DR GO: GO:0007155; P:cell adhesion; IEA.
 DR InterPro: IPR008966; Adhes bact.
 DR InterPro: IPR004237; Fn_bind.
 DR InterPro: IPR005877; Gpos YSIRK.
 DR InterPro: IPR001899; Gram_pos_anchor.
 DR Pfam: PF02986; Fn_bind; 1.
 DR Pfam: PF00746; Gram_pos_anchor; 1.
 DR Pfam: PF04650; YSIRK signal; 1.
 DR TIGRPFAM: TIGR01167; LPXTG anchor; 1.
 DR TIGRPFAM: TIGR01168; YSIRK signal; 1.
 DR PROSITE: PS50847; GRAM_POS_ANCHORING; 1.
 DR Cell wall; Complete proteome; Peptidoglycan-anchor.
 SQ SEQUENCE 1038 AA; 113618 MW; 666BF6BF2BFEB12 CRC64;
 Query Match 100.0%; Score 58; DB 2; Length 1038;
 Best Local Similarity 100.0%; Pred. No. 0.041; 0; Indels 0; Gaps 0;
 Matches 10; Conservative 0; Mismatches 0;
 QY 1 DKPKEQGN 10
 DB 756 DKPKEQGN 765
 RESULT 12
 ID 07A3J7 PRELIMINARY; PRT; 1038 AA.
 AC 07A3J7;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, last annotation update)
 DE Fnb protein.
 GN Name=fnb; OrderedLocustNames=SA2291;
 OS *Staphylococcus aureus* (strain N315).
 CC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 OX NCBI_TaxID=158879;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC MEDLINE=21311952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2;
 RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
 RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Iian J.-Q., Ito T.,
 RA Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,
 RA Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
 RA Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
 RA Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,

RA Hatori M., Ogasawara N., Hayaishi H., Hiramatsu K.;
 RT "Whole genome sequencing of methicillin-resistant *Staphylococcus*
 RT aureus.";
 RL Lancet 357:1225-1240(2001).
 CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
 CC an amide bond (By similarity).
 DR EMBL: AP003137; BAB43594.1; -;
 DR GO: GO:0009986; C:cell surface; IEA.
 DR GO: GO:0005618; C:cell wall; IEA.
 DR GO: GO:0009275; C:cell wall (benu Gram-positive Bacteria); IEA.
 DR GO: GO:0016020; C:membrane; IEA.
 DR GO: GO:0007155; P:cell adhesion; IEA.
 DR InterPro: IPR008966; Adhes_bact.
 DR InterPro: IPR005877; Gpos_YsIRK.
 DR InterPro: IPR001899; Gram_pos_anchor.
 DR Pfam: PF02986; Fn_bind; 1.
 DR Pfam: PF04650; Gram_pos_anchor; 1.
 DR Pfam: PF04650; YsIRK_signal; 1.
 DR TIGRfam: TIGR01167; LPXG_anchor; 1.
 DR TIGRfam: TIGR01168; YsIRK_signal; 1.
 DR PROSITE: PS50847; GRAM_POS_ANCHORING; 1.
 KW Cell wall; Complete proteome; Peptidoglycan-anchor.
 SQ SEQUENCE 1038 AA; 113618 MW; 666BF6BF2BFEB12 CRC64;

Query Match 100.0%; Score 58; DB 2; Length 103;
 Best Local Similarity 100.0%; Pred. No. 0.04;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DKPKYEOGNG 10
 |||||
 Db 756 DKPKYEOGNG 765

RESULT 13
 ID 08G8J1 PRELIMINARY; PRT; 215 AA.
 AC 08G8J1;
 DT 01-MAR-2003 (TREMblrel. 23, Created)
 DT 01-MAR-2003 (TREMblrel. 23, Last sequence update)
 DT 05-JUL-2004 (TREMblrel. 27, Last annotation update)
 DE Putative dissimilatory membrane-bound nitrate reductase
 DE (Fragment).
 GN Name=narg;
 OS uncultured bacterium.
 OC Bacteria; environmental samples.
 OX NCBI_Taxid=77133;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22338274; PubMed=2450836;
 RX DOI=10.1128/AEM.68.12.6121-6128.2002;
 RA Philippot L., Piuhi S., Martin-Laurent F., Hallet S., Gernon J.C.;
 RT "Molecular analysis of the nitrate-reducing community from unplanted
 RT and maize-planted soils.";
 DR EMBL: AY113751; AAC62192.1; -;
 DR EMBL: AY113751; AAC62232.1; -;
 DR HSSP: P09152; 1Q16.
 DR GO: GO:0016491; F:oxidoreductase activity; IEA.
 FT NON TER 1 1
 FT NON TER 215 215
 SQ SEQUENCE 215 AA; 24573 MW; A6ACC98CF4C6118 CRC64;

Query Match 77.6%; Score 45; DB 2; Length 215;
 Best Local Similarity 70.0%; Pred. No. 2.3;
 Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 1 DKPKYEOGNG 10
 |||||
 Db 58 DKPKYEOGNG 67

RESULT 14

O7KWL2
 ID 07KWL2 PRELIMINARY; PRT; 194 AA.
 AC 07KWL2;
 DT 05-JUL-2004 (TREMblrel. 27, Created)
 DT 05-JUL-2004 (TREMblrel. 27, Last sequence update)
 DT 05-JUL-2004 (TREMblrel. 27, Last annotation update)
 DE Hypothetical protein.
 OS Dictyostelium discoideum (Slime mold).
 OC Eukaryota; Mycetozoa; Dictyostelidae; Dictyostelium.
 OX NCBI_Taxid=44689;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=AX4;
 RX MEDLINE=22092622; PubMed=12097910; DOI=10.1038/nature00847;
 RA Glockner G., Eichinger L., Szafarski K., Pachter J., Dear P.,
 RA Lehmann R., Baumgart C., Parra G., April J.F., Guigo R., Kumpf K.,
 RA Tunggal B., Cox E., Quail M.A., Platzer M., Rosenthal A., Noegel A.A.;
 RT "Sequence and analysis of chromosome 2 of *Dictyostelium discoideum*.";
 RL Nature 418:79-85(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=AX4;
 RA Baumgart C.;
 RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AC117076; AAS38869.1; -;
 DR InterPro: IPR007527; Znf_SWIM.
 DR Pfam: PF04434; SWIM; 1.
 KW Hypothetical protein.
 SQ SEQUENCE 194 AA; 22353 MW; 2310D5758B0C37A2 CRC64;

Query Match 74.1%; Score 43; DB 2; Length 194;
 Best Local Similarity 60.0%; Pred. No. 5.1;
 Matches 6; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

OY 1 DKPKYEOGNG 10
 |||||
 Db 166 DEPKYEOGNG 175

RESULT 15
 ID 07RXD7 PRELIMINARY; PRT; 2992 AA.
 AC 07RXD7;
 DT 01-MAR-2004 (TREMblrel. 26, Created)
 DT 01-MAR-2004 (TREMblrel. 26, Last sequence update)
 DT 01-MAR-2004 (TREMblrel. 26, Last annotation update)
 DE Predicted protein.
 GN Name=NCU05047.1;
 OS Neurospora crassa.
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
 OC Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.
 OX NCBI_Taxid=5141;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=OR74A;
 RA Galagan J.E., Calvo S.E., Borkovich K.A., Selker E.U., Read N.D.,
 RA Jaffe D., Fitzhugh W., Ma L.-J., Smirnov S., Purcell S., Reiman B.,
 RA Ekins T., Engels R., Wang S., Nielsen C.B., Butler J., Endrizzi M.,
 RA Qui D., Ianakiev P., Pedersen D., Nelson M., Washburne M.,
 RA Selitrenikoff C.P., Kinsey J.A., Braun E.L., Zelter A., Schulte U.,
 RA Kothe G.O., Jedd G., Mewes W., Staben C., Marcotte E., Greenberg D.,
 RA Roy A., Foley K., Naylor J., Thomann N., Barrett R., Gnerre S.,
 RA Kamal M., Kamysasellis M., Mauceli E., Bielke C., Rudd S., Frisman D.,
 RA Kryzofova S., Rasmussen C., Metzberg R.L., Perkins D.D., Kroken S.,
 RA Cogoni C., Macino G., Catchside D., Li W., Pratt R.J., Osmant S.A.,
 RA Desouza C.C., Glass L., Orbach M.J., Berglund J., Voelker R.,
 RA Yarden O., Plamann M., Seiler S., Dunlap J., Radford A., Aramayo R.,
 RA Natvig D.O., Alex L.A., Mannhaupt G., Ebbold D.J., Freitag M.,
 RA Paulsen I., Sachs M.S., Lander E.S., Nussbaum C., Birren B.;
 RT "The Genome Sequence of the Filamentous Fungus *Neurospora crassa*.";
 RL Nature 0:0-0(2003).
 CC -1- SIMILARITY: Belongs to the cytochrome b5 family.
 CC -1- CAUTION: The sequence shown here is derived from an

CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
preliminary data.
CC EMBL; AABX01000748; EAA27185.1; -.
DR InterPro; IPR001199; Cyt_B5.
DR InterPro; IPR006025; Pept_M_zn_BS.
DR Pfam; PF00173; Cyt-b5; 1.
DR PROSITE; PS00191; CYTOCHROME_B5_1; UNKNOWN_1.
DR PROSITE; PS50255; CYTOCHROME_B5_2; 1.
DR PROSITE; PS00142; ZINC_PROTEASE; UNKNOWN_1.
KW Heme.
SQ SEQUENCE 2992 AA; 334971 MW; 45D47CEF43563713 CRC64;
Query Match 72.4%; Score 42; DB 2; Length 2992;
Best Local Similarity 70.0%; Pred. No. 1.8e+02;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
Qy 1 DKPKYEQGGN 10
||:||||
Db 1861 DEPEQEGGN 1870

Search completed: October 22, 2005, 08:00:34
Job time : 57.85 secs

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OM protein - protein search, using sw model

Run on: October 25, 2005, 20:21:18 ; Search time 63.2 Seconds
(without alignments)
61.196 Million cell updates/sec

Title: US-10-731-238-71
Perfect score: 55
Sequence: 1 PXYEQGNIV 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: Genesegp16dec04: *
2: genesegp1808: *
3: genesegp1908: *
4: genesegp2000: *
5: genesegp2001: *
6: genesegp2002: *
7: genesegp2003: *
8: genesegp2004: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	55	100.0	38	2	AAW65692 Fibronect
2	55	100.0	38	2	AAW65695 Fibronect
3	55	100.0	38	2	AAW65696 Fibronect
4	55	100.0	38	2	AAW65697 Fibronect
5	55	100.0	38	2	AAW65694 Fibronect
6	55	100.0	38	2	AAW65691 Fibronect
7	55	100.0	38	2	AAW65661 Fibronect
8	55	100.0	38	2	AAW65693 Fibronect
9	55	100.0	38	2	AAW65698 Fibronect
10	55	100.0	39	2	AAW65712 Fibronect
11	55	100.0	113	2	AAW65937 Fibronect
12	55	100.0	130	2	AAW65806 Fibronect
13	55	100.0	130	2	AAW65807 Fibronect
14	55	100.0	130	2	AAW65808 Fbp fibro
15	55	100.0	130	2	AAW65809 Fbp fibro
16	55	100.0	134	2	AAW65808 S. aureus
17	55	100.0	134	2	AAW65808 S. aureus
18	55	100.0	134	2	AAW65808 S. aureus
19	55	100.0	139	2	AAW65808 S. aureus
20	55	100.0	164	2	AAW65808 S. aureus
21	55	100.0	174	2	AAW65808 S. aureus
22	55	100.0	174	2	AAW65808 S. aureus
23	55	100.0	181	2	AAW65808 S. aureus
24	55	100.0	181	2	AAW65808 S. aureus
25	55	100.0	559	2	AAW65808 S. aureus

26	55	100.0	767	4	AAU34403 Staphyloc
27	55	100.0	767	4	AAU37547 Staphyloc
28	55	100.0	940	2	AAU37547 Staphyloc
29	55	100.0	940	6	AAU37547 Staphyloc
30	55	100.0	948	6	AAU37547 Staphyloc
31	55	100.0	948	6	AAU37547 Staphyloc
32	55	100.0	948	6	AAU37547 Staphyloc
33	55	100.0	948	6	AAU37547 Staphyloc
34	55	100.0	978	4	AAU37547 Staphyloc
35	55	100.0	1001	4	AAU37547 Staphyloc
36	55	100.0	1018	1	AAU37547 Staphyloc
37	55	100.0	1018	4	AAU37547 Staphyloc
38	55	100.0	1018	4	AAU37547 Staphyloc
39	55	100.0	1018	6	AAU37547 Staphyloc
40	55	100.0	1018	6	AAU37547 Staphyloc
41	55	100.0	1027	2	AAU37547 Staphyloc
42	55	100.0	1038	4	AAU37547 Staphyloc
43	55	100.0	1038	4	AAU37547 Staphyloc
44	55	100.0	1038	4	AAU37547 Staphyloc
45	55	100.0	1038	4	AAU37547 Staphyloc

ALIGNMENTS

RESULT 1
AAW65692 standard; peptide; 38 AA.

AAW65692;

16-OCT-1998 (first entry)

Fibronectin binding protein-derived peptide #36.

microbial surface components recognising adhesive matrix molecule;

MSCRAMM; fibronectin; fibronectin-binding protein; antibody; epitope;

antibiotic; bacterial infection; antibiotic-resistant strain.

Synthetic.

Staphylococcus aureus.

MO981389-A2.

23-JUL-1998.

21-JAN-1998; 98WO-US001222.

21-JAN-1997; 97US-0036139P.

(TEXA) UNIV TEXAS A & M SYSTEM.

Hoeck M, Patti JM, House-Pompeo KL, Speziale P, Joh D;

Megavir MJ;

WPI; 1998-413816/35.

Example 8; Page 101; 201P; English.

The invention relates to antibodies that bind to a fibronectin-binding

domain of a fibronectin-binding protein, and inhibit binding of the

protein to a fibronectin. Also claimed are: (1) isolated peptides of a

protein containing at least one peptide of a fibronectin-binding

protein linked to a second amino acid sequence; (2) nucleic acid encoding the

isolated peptide of (1). Antibodies, the isolated peptides of (1) and the

nucleic acids are all useful for immunisation (active or passive) and (by

inhibiting binding of bacteria to fibronectin) for preventing or treating

infection in humans or other animals, particularly by staphylococci or

```
CC streptococci, e.g. meningitis, otitis media, pneumonia, endocarditis,
CC mastitis in cattle, abortion in horses and many others. Since the
CC antibodies block binding of bacteria, they should be effective against
CC antibiotic-resistant strains, and may replace antibiotic therapy or
CC increase its effectiveness. Sequences AAW65691-700 represent a series of
CC synthetic peptides based on the D1 region of S. aureus fibronectin
CC binding protein A. They were synthesised to contain mutations
XX
SQ Sequence 38 AA;

Query Match      100.0%; Score 55; DB 2; Length 38;
Best Local Similarity 100.0%; Pred. No. 0.014;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PKYEOGGNIV 10
   |||||
DB 17 PKYEOGGNIV 26

RESULT 2
AAW65695
ID AAW65695 standard; peptide, 38 AA.
XX
AC AAW65695;
XX
DT 16-OCT-1998 (first entry)
XX
DE Fibronectin binding protein-derived peptide #39.
XX
KW microbial surface components recognising adhesive matrix molecule;
KW MSCRAMM; fibronectin; fibronectin-binding protein; antibody; epitope;
KW antibiotic; bacterial infection; antibiotic-resistant strain.
XX
OS Synthetic.
OS Staphylococcus aureus.
XX
PN WO9831389-A2.
XX
PD 23-JUL-1998.
XX
PF 21-JAN-1998; 98WO-US001222.
XX
PR 21-JAN-1997; 97US-0036139P.
XX
PA (TEXA ) UNIV TEXAS A & M SYSTEM.
XX
PI Hoeek M, Patti JM, House-Pompeo KL, Speziale P, Joh D;
XX
PI McGavin MJ;
XX
DR WPI, 1998-413816/35.
XX
PT Antibody that binds to fibronectin-binding protein, preventing its
XX
PT binding to fibronectin - used to treat or prevent bacterial infection,
XX
PT especially by Staphylococci and Streptococci.
XX
PS Example 8; Page 102; 201pp; English.
XX
CC The invention relates to antibodies that bind to a fibronectin-binding
CC domain of a fibronectin-binding protein, and inhibit binding of the
CC protein to fibronectin. Also claimed are: (1) isolated peptides of a
CC fibronectin-binding protein that do not bind to fibronectin; (2) fusion
CC protein containing at least one peptide of a fibronectin-binding protein
CC linked to a second amino acid sequence; (3) nucleic acid encoding the
CC isolated peptide of (1). Antibodies, the isolated peptides of (1) and the
CC nucleic acids are all useful for immunisation (active or passive) and (by
CC inhibiting binding of bacteria to fibronectin) for preventing or treating
CC infection in humans or other animals, particularly by staphylococci or
CC streptococci, e.g. meningitis, otitis media, pneumonia, endocarditis,
CC mastitis in cattle, abortion in horses and many others. Since the
CC antibodies block binding of bacteria, they should be effective against
CC antibiotic-resistant strains, and may replace antibiotic therapy or
CC increase its effectiveness. Sequences AAW65691-700 represent a series of
CC synthetic peptides based on the D1 region of S. aureus fibronectin
XX
```

```
CC binding protein A. They were synthesised to contain mutations
XX
SQ Sequence 38 AA;

Query Match      100.0%; Score 55; DB 2; Length 38;
Best Local Similarity 100.0%; Pred. No. 0.014;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PKYEOGGNIV 10
   |||||
DB 17 PKYEOGGNIV 26

RESULT 3
AAW65696
ID AAW65696 standard; peptide, 38 AA.
XX
AC AAW65696;
XX
DT 16-OCT-1998 (first entry)
XX
DE Fibronectin binding protein-derived peptide #40.
XX
KW microbial surface components recognising adhesive matrix molecule;
KW MSCRAMM; fibronectin; fibronectin-binding protein; antibody; epitope;
KW antibiotic; bacterial infection; antibiotic-resistant strain.
XX
OS Synthetic.
OS Staphylococcus aureus.
XX
PN WO9831389-A2.
XX
PD 23-JUL-1998.
XX
PF 21-JAN-1998; 98WO-US001222.
XX
PR 21-JAN-1997; 97US-0036139P.
XX
PA (TEXA ) UNIV TEXAS A & M SYSTEM.
XX
PI Hoeek M, Patti JM, House-Pompeo KL, Speziale P, Joh D;
XX
PI McGavin MJ;
XX
DR WPI, 1998-413816/35.
XX
PT Antibody that binds to fibronectin-binding protein, preventing its
XX
PT binding to fibronectin - used to treat or prevent bacterial infection,
XX
PT especially by Staphylococci and Streptococci.
XX
PS Example 8; Page 102; 201pp; English.
XX
CC The invention relates to antibodies that bind to a fibronectin-binding
CC domain of a fibronectin-binding protein, and inhibit binding of the
CC protein to fibronectin. Also claimed are: (1) isolated peptides of a
CC fibronectin-binding protein that do not bind to fibronectin; (2) fusion
CC protein containing at least one peptide of a fibronectin-binding protein
CC linked to a second amino acid sequence; (3) nucleic acid encoding the
CC isolated peptide of (1). Antibodies, the isolated peptides of (1) and the
CC nucleic acids are all useful for immunisation (active or passive) and (by
CC inhibiting binding of bacteria to fibronectin) for preventing or treating
CC infection in humans or other animals, particularly by staphylococci or
CC streptococci, e.g. meningitis, otitis media, pneumonia, endocarditis,
CC mastitis in cattle, abortion in horses and many others. Since the
CC antibodies block binding of bacteria, they should be effective against
CC antibiotic-resistant strains, and may replace antibiotic therapy or
CC increase its effectiveness. Sequences AAW65691-700 represent a series of
CC synthetic peptides based on the D1 region of S. aureus fibronectin
CC binding protein A. They were synthesised to contain mutations
XX
SQ Sequence 38 AA;

Query Match      100.0%; Score 55; DB 2; Length 38;
Best Local Similarity 100.0%; Pred. No. 0.014;
```

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PKYEGGNTIV 10
 |||||
 DB 17 PKYEGGNTIV 26

RESULT 4

AAW65697 standard; peptide; 38 AA.

AC AAW65697;

DT 16-OCT-1998 (first entry)

DE Fibronectin binding protein-derived peptide #41.

XX microbial surface components recognising adhesive matrix molecule;

KW MSCRAM; fibronectin; fibronectin-binding protein; antibody; epitope;

XX antibiotic; bacterial infection; antibiotic-resistant strain.

OS Synthetic.

PN Staphylococcus aureus.

XX WO9831389-A2.

PD 23-JUL-1998.

PF 21-JAN-1998; 98WO-US001222.

XX 21-JAN-1997; 97US-0036139P.

PA (TEXA) UNIV TEXAS A & M SYSTEM.

PI Hoeek M, Patti JM, House-Pompeo KL, Speziale P, Joh D;

PT Mcgavin MJ;

PS WPI; 1998-413816/35.

XX Antibody that binds to fibronectin-binding protein, preventing its

PT binding to fibronectin - used to treat or prevent bacterial infection,

XX especially by Staphylococci and Streptococci.

XX Example 8; Page 102; 201pp; English.

CC The invention relates to antibodies that bind to a fibronectin-binding

CC domain of a fibronectin-binding protein, and inhibit binding of the

CC protein to fibronectin. Also claimed are: (1) isolated peptides of a

CC fibronectin-binding protein that do not bind to fibronectin; (2) fusion

CC protein containing at least one peptide of a fibronectin-binding protein

CC linked to a second amino acid sequence; (3) nucleic acid encoding the

CC isolated peptide of (1). Antibodies, the isolated peptides of (1) and the

CC nucleic acids are all useful for immunisation (active or passive) and (by

CC inhibiting binding of bacteria to fibronectin) for preventing or treating

CC infection in humans or other animals, particularly by staphylococci or

CC streptococci, e.g. meningitis, otitis media, pneumonia, endocarditis,

CC mastitis in cattle, abortion in horses and many others. Since the

CC antibodies block binding of bacteria, they should be effective against

CC antibiotic-resistant strains, and may replace antibiotic therapy or

CC increase its effectiveness. Sequences AAW65691-700 represent a series of

CC synthetic peptides based on the DI region of S. aureus fibronectin

CC binding protein A. They were synthesised to contain mutations

XX Sequence 38 AA;

SO

Query Match 100.0%; Score 55; DB 2; Length 38;

Best Local Similarity 100.0%; Pred. No. 0.014;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PKYEGGNTIV 10
 |||||
 DB 17 PKYEGGNTIV 26

RESULT 5
 AAW65694 standard; peptide; 38 AA.

AC AAW65694;

DT 16-OCT-1998 (first entry)

DE Fibronectin binding protein-derived peptide #38.

XX microbial surface components recognising adhesive matrix molecule;

KW MSCRAM; fibronectin; fibronectin-binding protein; antibody; epitope;

XX antibiotic; bacterial infection; antibiotic-resistant strain.

OS Synthetic.

PN Staphylococcus aureus.

XX WO9831389-A2.

PD 23-JUL-1998.

PF 21-JAN-1998; 98WO-US001222.

XX 21-JAN-1997; 97US-0036139P.

PA (TEXA) UNIV TEXAS A & M SYSTEM.

PI Hoeek M, Patti JM, House-Pompeo KL, Speziale P, Joh D;

PT Mcgavin MJ;

PS WPI; 1998-413816/35.

XX Antibody that binds to fibronectin-binding protein, preventing its

PT binding to fibronectin - used to treat or prevent bacterial infection,

XX especially by Staphylococci and Streptococci.

XX Example 8; Page 102; 201pp; English.

CC The invention relates to antibodies that bind to a fibronectin-binding

CC domain of a fibronectin-binding protein, and inhibit binding of the

CC protein to fibronectin. Also claimed are: (1) isolated peptides of a

CC fibronectin-binding protein that do not bind to fibronectin; (2) fusion

CC protein containing at least one peptide of a fibronectin-binding protein

CC linked to a second amino acid sequence; (3) nucleic acid encoding the

CC isolated peptide of (1). Antibodies, the isolated peptides of (1) and the

CC nucleic acids are all useful for immunisation (active or passive) and (by

CC inhibiting binding of bacteria to fibronectin) for preventing or treating

CC infection in humans or other animals, particularly by staphylococci or

CC streptococci, e.g. meningitis, otitis media, pneumonia, endocarditis,

CC mastitis in cattle, abortion in horses and many others. Since the

CC antibodies block binding of bacteria, they should be effective against

CC antibiotic-resistant strains, and may replace antibiotic therapy or

CC increase its effectiveness. Sequences AAW65691-700 represent a series of

CC synthetic peptides based on the DI region of S. aureus fibronectin

CC binding protein A. They were synthesised to contain mutations

XX Sequence 38 AA;

SO

Query Match 100.0%; Score 55; DB 2; Length 38;

Best Local Similarity 100.0%; Pred. No. 0.014;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PKYEGGNTIV 10
 |||||
 DB 17 PKYEGGNTIV 26

RESULT 6
 AAW65691 standard; peptide; 38 AA.

AC AAW65691;


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XX 16-OCT-1998 (first entry)
XX Fibronectin binding protein-derived peptide #35.
XX microbial surface components recognising adhesive matrix molecule;
XX MSCRAMM; fibronectin; fibronectin-binding protein; antibody; epitope;
XX antibiotic; bacterial infection; antibiotic-resistant strain.
XX Synthetic.
XX Staphylococcus aureus.
XX MO9831389-A2.
XX 23-JUL-1998.
XX 21-JAN-1998; 98WO-US001222.
XX 21-JAN-1997; 97US-0036139P.
XX (TEXA ) UNIV TEXAS A & M SYSTEM.
XX Hosoeck M, Patti JM, House-Pompeo KL, Speciale P, Joh D:
XX McGavin MJ;
XX WPI; 1998-413816/35.
XX Antibody that binds to fibronectin-binding protein, preventing its
XX binding to fibronectin - used to treat or prevent bacteria infection,
XX especially by Staphylococci and Streptococci.
XX Example 8; Page 101, 201pp; English.
XX The invention relates to antibodies that bind to a fibronectin-binding
XX domain of a fibronectin-binding protein, and inhibit binding of the
XX protein to fibronectin. Also claimed are: (1) isolated peptides of a
XX fibronectin-binding protein that do not bind to fibronectin; (2) fusion
XX protein containing at least one peptide of a fibronectin-binding protein
XX linked to a second amino acid sequence; (3) nucleic acid encoding the
XX isolated peptide of (1). Antibodies, the isolated peptides of (1) and the
XX nucleic acids are all useful for immunisation (active or passive) and (by
XX inhibiting binding of bacteria to fibronectin) for preventing or treating
XX infection in humans or other animals, particularly by staphylococci or
XX streptococci, e.g. meningitis, otitis media, pneumonia, endocarditis,
XX mastitis in cattle, abortion in horses and many others. Since the
XX antibodies block binding of bacteria, they should be effective against
XX antibiotic-resistant strains, and may replace antibiotic therapy or
XX increase its effectiveness. Sequences AAM65591-700 represent a series of
XX synthetic peptides based on the D1 region of S. aureus fibronectin
XX binding protein A. They were synthesised to contain mutations
XX
XX Sequence 38 AA;
SQ
XX
XX Query Match 100.0%; Score 55; DB 2; Length 38;
XX Best Local Similarity 100.0%; Pred. No. 0.014;
XX Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0
XX
XX 1 PKYEGGNIIV 10
XX |||||
XX 17 PKYEGGNIIV 26
XX
XX RESULT 7
XX ID AAM65561 standard; peptide; 38 AA.
XX AAM65561;
XX
XX 16-OCT-1998 (first entry)
XX Fibronectin binding protein-derived peptide #5.
XX microbial surface components recognising adhesive matrix molecule;

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KW MSCRAMM; fibronectin; fibronectin-binding protein; antibody; epitope;
KM antibiotic; bacterial infection; antibiotic-resistant strain.
XX
XX Synthetic.
OS Staphylococcus aureus.
XX
XX MO9831389-A2.
XX
XX 23-JUL-1998.
XX
XX PD
XX PF 21-JAN-1998; 98WO-US001222.
XX PE
XX PR 21-JAN-1997; 97US-0036139P.
XX
XX (TEXA ) UNIV TEXAS A & M SYSTEM.
PA
PI Hoeoek M, Patti JM, House-Pompeo KL, Speciale P, Joh D;
PI McGavin MJ;
XX
XX WPI; 1998-413816/35.
XX
XX Antibody that binds to fibronectin-binding protein, preventing its
XX binding to fibronectin - used to treat or prevent bacterial infection,
XX especially by Staphylococci and Streptococci.
XX
XX Example 2: Page 92; 201pp; English.
XX
XX The invention relates to antibodies that bind to a fibronectin-binding
XX domain of a fibronectin-binding protein, and inhibit binding of the
XX protein to fibronectin. Also claimed are: (1) isolated peptides of a
XX fibronectin-binding protein that do not bind to fibronectin; (2) fusion
XX protein containing at least one peptide of a fibronectin-binding protein
XX linked to a second amino acid sequence; (3) nucleic acid encoding the
XX isolated peptide of (1). Antibodies, the isolated peptides of (1) and the
XX nucleic acids are all useful for immunisation (active or passive) and (by
XX inhibiting binding of bacteria to fibronectin) for preventing or treating
XX infection in humans or other animals, particularly by staphylococci or
XX streptococci, e.g. meningitis, otitis media, pneumonia, endocarditis,
XX mastitis in cattle, abortion in horses and many others. Since the
XX antibodies block binding of bacteria, they should be effective against
XX antibiotic-resistant strains, and may replace antibiotic therapy or
XX increase its effectiveness. Sequences AAM65659-68 represent synthetic
XX epitopes from the fibronectin binding domains DU and D1-D4 of the S.
XX aureus fnbA gene
XX
XX Sequence 38 AA;
SQ
XX
XX Query Match 100.0%; Score 55; DB 2; Length 38;
XX Best Local Similarity 100.0%; Pred. No. 0.014;
XX Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 PKYEOGNIV 10
XX |||||
XX DB 17 PKYEOGNIV 26
XX
XX RESULT 8
XX ID AAM65693 standard; peptide; 38 AA.
XX AC AAM65693;
XX
XX 16-OCT-1998 (first entry)
XX
XX Fibronectin binding protein-derived peptide #37.
XX
XX microbial surface components recognising adhesive matrix molecule;
XX MSCRAMM; fibronectin; fibronectin-binding protein; antibody; epitope;
XX antibiotic; bacterial infection; antibiotic-resistant strain.
XX
XX Synthetic.
XX OS Staphylococcus aureus.
XX

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PN WO9831389-A2.
 XX 23-JUL-1998.
 PD 21-JAN-1998; 98WO-US001222.
 XX PF 21-JAN-1997; 97US-0036139P.
 XX (TEXA) UNIV TEXAS A & M SYSTEM.
 XX Hoeoek M, Patti JM, House-Pompeo KL, Speciale P, Joh D;
 PI Mcgavin MJ;
 DR WPI; 1998-413816/35.
 XX Antibody that binds to fibronectin-binding protein, preventing its
 PT binding to fibronectin - used to treat or prevent bacterial infection,
 PT especially by Staphylococci and Streptococci.
 XX Example 8; Page 102; 201pp; English.
 XX The invention relates to antibodies that bind to a fibronectin-binding
 CC domain of a fibronectin-binding protein, and inhibit binding of the
 CC protein to fibronectin. Also claimed are: (1) isolated peptides of a
 CC fibronectin-binding protein that do not bind to fibronectin; (2) fusion
 CC protein containing at least one peptide of a fibronectin-binding protein
 CC linked to a second amino acid sequence; (3) nucleic acid encoding the
 CC isolated peptide of (1). Antibodies, the isolated peptides of (1) and (by
 CC nucleic acids are all useful for immunisation (active or passive) and (by
 CC inhibiting binding of bacteria to fibronectin) for preventing or treating
 CC infection in humans or other animals, particularly by staphylococci or
 CC streptococci, e.g. meningitis, otitis media, pneumonia, endocarditis,
 CC mastitis in cattle, abortion in horses and many others. Since the
 CC antibodies block binding of bacteria, they should be effective against
 CC antibiotic-resistant strains, and may replace antibiotic therapy or
 CC increase its effectiveness. Sequences AAM65691-700 represent a series of
 CC synthetic peptides based on the D1 region of S. aureus fibronectin
 CC binding protein A. They were synthesised to contain mutations
 XX
 SQ Sequence 38 AA:
 Query Match 100.0%; Score 55; DB 2; Length 38;
 Best Local Similarity 100.0%; Pred. No. 0.014;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 PKYEGGNTIV 10
 DB 17 PKYEGGNTIV 26
 RESULT 9
 AAM65698 standard; peptide; 38 AA.
 ID AAM65698
 AC AAM65698;
 XX 16-OCT-1998 (first entry)
 DT 16-OCT-1998 (first entry)
 XX Fibronectin binding protein-derived peptide #42.
 DE Fibronectin binding protein-derived peptide #42.
 XX microbial surface components recognising adhesive matrix molecule;
 KM MSCRAMM; fibronectin; fibronectin-binding protein; antibody; epitope;
 KM antibiotic; bacterial infection; antibiotic-resistant strain.
 XX Synthetic.
 OS Staphylococcus aureus.
 XX WO9831389-A2.
 XX 23-JUL-1998.
 PD 21-JAN-1997; 97US-0036139P.
 XX (TEXA) UNIV TEXAS A & M SYSTEM.
 XX Hoeoek M, Patti JM, House-Pompeo KL, Speciale P, Joh D;
 PI Mcgavin MJ;

PR 21-JAN-1997; 97US-0036139P.
 XX (TEXA) UNIV TEXAS A & M SYSTEM.
 XX Hoeoek M, Patti JM, House-Pompeo KL, Speciale P, Joh D;
 PI Mcgavin MJ;
 XX WPI; 1998-413816/35.
 DR Antibody that binds to fibronectin-binding protein, preventing its
 PT binding to fibronectin - used to treat or prevent bacterial infection,
 PT especially by Staphylococci and Streptococci.
 XX Example 8; Page 102; 201pp; English.
 XX The invention relates to antibodies that bind to a fibronectin-binding
 CC domain of a fibronectin-binding protein, and inhibit binding of the
 CC protein to fibronectin. Also claimed are: (1) isolated peptides of a
 CC fibronectin-binding protein that do not bind to fibronectin; (2) fusion
 CC protein containing at least one peptide of a fibronectin-binding protein
 CC linked to a second amino acid sequence; (3) nucleic acid encoding the
 CC isolated peptide of (1). Antibodies, the isolated peptides of (1) and (by
 CC nucleic acids are all useful for immunisation (active or passive) and (by
 CC inhibiting binding of bacteria to fibronectin) for preventing or treating
 CC infection in humans or other animals, particularly by staphylococci or
 CC streptococci, e.g. meningitis, otitis media, pneumonia, endocarditis,
 CC mastitis in cattle, abortion in horses and many others. Since the
 CC antibodies block binding of bacteria, they should be effective against
 CC antibiotic-resistant strains, and may replace antibiotic therapy or
 CC increase its effectiveness. Sequences AAM65691-700 represent a series of
 CC synthetic peptides based on the D1 region of S. aureus fibronectin
 CC binding protein A. They were synthesised to contain mutations
 XX
 SQ Sequence 38 AA:
 Query Match 100.0%; Score 55; DB 2; Length 38;
 Best Local Similarity 100.0%; Pred. No. 0.014;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 PKYEGGNTIV 10
 DB 17 PKYEGGNTIV 26
 RESULT 10
 AAM65712 standard; peptide; 39 AA.
 ID AAM65712
 AC AAM65712;
 XX 16-OCT-1998 (first entry)
 DT 16-OCT-1998 (first entry)
 XX Fibronectin binding protein-derived peptide #56.
 DE Fibronectin binding protein-derived peptide #56.
 XX microbial surface components recognising adhesive matrix molecule;
 KM MSCRAMM; fibronectin; fibronectin-binding protein; antibody; epitope;
 KM antibiotic; bacterial infection; antibiotic-resistant strain.
 XX Synthetic.
 OS Staphylococcus aureus.
 XX WO9831389-A2.
 XX 23-JUL-1998.
 PD 21-JAN-1997; 97US-0036139P.
 XX (TEXA) UNIV TEXAS A & M SYSTEM.
 XX Hoeoek M, Patti JM, House-Pompeo KL, Speciale P, Joh D;
 PI Mcgavin MJ;

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XX
DR WPI; 1998-413816/35.
XX
XX Antibody that binds to fibronectin-binding protein, preventing its
PT binding to fibronectin - used to treat or prevent bacterial infection,
PT especially by Staphylococci and Streptococci.
XX
XX Example 8; Page 104; 201pp; English.
XX
XX The invention relates to antibodies that bind to a fibronectin-binding
CC domain of a fibronectin-binding protein, and inhibit binding of the
CC protein to fibronectin. Also claimed are: (1) isolated peptides of a
CC fibronectin-binding protein that do not bind to fibronectin; (2) fusion
CC protein containing at least one peptide of a fibronectin-binding protein
CC linked to a second amino acid sequence; (3) nucleic acid encoding the
CC isolated peptide of (1). Antibodies, the isolated peptides of (1) and the
CC nucleic acids are all useful for immunisation (active or passive) and (by
CC inhibiting binding of bacteria to fibronectin) for preventing or treating
CC infection in humans or other animals, particularly by staphylococci or
CC streptococci, e.g. meningitis, otitis media, pneumonia, endocarditis,
CC mastitis in cattle, abortion in horses and many others. Since the
CC antibodies block binding of bacteria, they should be effective against
CC antibiotic-resistant strains, and may replace antibiotic therapy or
CC increase its effectiveness. The present sequence is shown in the
CC specification.
XX
SQ Sequence 39 AA;
XX
Query Match 100.0%; Score 55; DB 2; Length 39;
Best Local Similarity 100.0%; Pred. No. 0.014;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 PKYEGGNIV 10
DB 17 PKYEGGNIV 26

```

```

PA (SMK ) SMITHKLINE BEECHAM PLC.
XX
XX Critchley IA, Dodd I, Barnett P, Mcday DL;
XX
XX WPI; 1996-129397/13.
XX
XX Polypeptide(s) derived from Staphylococcus aureus fibronectin binding
PT protein - inhibit binding of bacteria to extracellular matrix proteins,
PT for combating infection at the site of wounds and surgical implants, and
PT in oral hygiene.
XX
XX Claim 6; Page 24; 35pp; English.
XX
XX AAR90937-R90942 represent D3D4 polypeptides. These sequences correspond
CC to fragments of the Staphylococcus aureus fibronectin binding protein
CC (Fbp). This sequence corresponds to residues 18-130 of S.aureus J2385
CC Fbp, and also contains the D2 region, and a portion of the D1 region.
CC These sequences, and monoclonal antibodies against them can be used to
CC combat infection at the site of wounds, surgical implants and other in-
CC dwelling devices (such as catheters), and as adherent agents in oral
CC hygiene. They can also be used in the manufacture of a medicament for the
CC prevention of adhesion of bacteria to extracellular matrix proteins
CC present on in-dwelling devices or in wounds, or of oral pathogens to
CC similar proteins on surfaces in the oral cavity.
XX
SQ Sequence 113 AA;
XX
Query Match 100.0%; Score 55; DB 2; Length 113;
Best Local Similarity 100.0%; Pred. No. 0.044;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 PKYEGGNIV 10
DB 1 PKYEGGNIV 10

```

```

RESULT 11
AAR90937
ID AAR90937 standard; peptide; 113 AA.
XX
XX AAR90937;
AC XX
XX 23-SEP-1996 (first entry)
DT XX
XX D3D4 polypeptide #1.
DE XX
XX Fibronectin binding protein; Fbp; S.aureus J2385; monoclonal antibody;
KW infection; surgical implant; adherent agent; hygiene; adhesion;
KM extracellular matrix protein; oral pathogen; oral cavity.
XX
XX Staphylococcus aureus.
OS
XX
XX Key Location/Qualifiers
FH Region 1..21
FT Region /note= "D1 region fragment"
FT Region 22..59
FT Region /note= "D2 region"
FT Region 60..98
FT Region /note= "D3 region"
FT Region 99..113
FT Region /note= "D4 region"
FT Misc-difference 113
FT /note= "P113T"
XX
XX WO9604381-A1.
XX
XX 15-FEB-1996.
PD
XX
XX 28-JUL-1995; 95WO-EP003040.
PF
XX
XX 05-AUG-1994; 94GB-00015900.
PR
XX

```

```

RESULT 12
AAR58806
ID AAR58806 standard; protein; 130 AA.
XX
XX AAR58806;
AC XX
XX 25-MAR-2003 (revised)
DT XX
XX 30-MAR-1995 (first entry)
DT XX
XX Fibronectin binding domain D1-D4(709-838(P838T)).
DE XX
XX Fibronectin binding protein; Fbp; fibronectin binding domain;
KW monoclonal antibody; MAb; adhesion; Gram-positive bacterium; bacteremia;
KM Escherichia coli.
XX
XX Staphylococcus aureus.
OS
XX
XX WO9418327-A1.
XX
XX 18-AUG-1994.
PD
XX
XX 04-FEB-1994; 94WO-GB000215.
PF
XX
XX 05-FEB-1993; 93GB-00002289.
PR
XX
XX 20-OCT-1993; 93GB-00021592.
PR
XX
XX (SMK ) SMITHKLINE BEECHAM PLC.
XX
XX Burnham MKR, Chopra I, Critchley IA, Knowles DC;
XX
XX WPI; 1994-279748/34.
XX
XX Fibronectin binding protein and monoclonal antibodies specific for Fbp -
PT useful to prevent adherence of Gram-positive bacteria to indwelling
PT devices or wounds.
XX
XX Disclosure; Page 30; 40pp; English.
PS

```

XX Polypeptides corresponding to residues G709-T886 plus PPIVPT, G709-
 CC P838(P838T) and G709-P838 (AAR58805-07, respectively) of S. aureus J2385
 CC (NCIMB 40532) Fbp type A fibronectin binding domain D1-D4 region
 CC (AAR58808) were expressed in E. coli BL21(DE4) and used to raise MAbs
 CC specific for Fbp. (Updated on 25-MAR-2003 to correct PN field.)
 XX
 SQ Sequence 130 AA;
 Query Match 100.0%; Score 55; DB 2; Length 130;
 Best Local Similarity 100.0%; Pred. No. 0.051;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 PKYEGGNIV 10
 DB 18 PKYEGGNIV 27

RESULT 13
 AAR58807 standard; protein; 130 AA.
 XX
 AC AAR58807;
 XX
 DT 25-MAR-2003 (revised)
 DT 30-MAR-1995 (first entry)
 XX
 DE Fibronectin binding domain D1-D4 (709-838).
 XX
 KW Fibronectin binding protein; Fbp; fibronectin binding domain;
 KW monoclonal antibody; Mab; adhesion; Gram-positive bacterium; Dactereamia;
 KW Escherichia coli.
 XX
 OS Staphylococcus aureus.
 XX
 PN WO9418327-A1.
 XX
 PD 18-AUG-1994.
 XX
 PF 04-FEB-1994; 94WO-GB000215.
 XX
 PR 05-FEB-1993; 93GB-00002289.
 PR 20-OCT-1993; 93GB-00021592.
 XX
 PA (SMIK) SMITHKLINE BEECHAM PLC.
 XX
 PI Burnham MKR, Chopra I, Critchley IA, Knowles DJC;
 XX
 DR WPI; 1994-279748/34.
 XX
 PT Fibronectin binding protein and monoclonal antibodies specific for Fbp -
 PT useful to prevent adherence of Gram-positive bacteria to indwelling
 PT devices or wounds.
 XX
 PS Disclosure; Page 30; 40pp; English.
 XX
 CC Polypeptides corresponding to residues G709-T886 plus PPIVPT, G709-
 CC P838(P838T) and G709-P838 (AAR58805-07, respectively) of S. aureus J2385
 CC (NCIMB 40532) Fbp type A fibronectin binding domain D1-D4 region
 CC (AAR58808) were expressed in E. coli BL21(DE4) and used to raise MAbs
 CC specific for Fbp. (Updated on 25-MAR-2003 to correct PN field.)
 XX
 SQ Sequence 130 AA;
 Query Match 100.0%; Score 55; DB 2; Length 130;
 Best Local Similarity 100.0%; Pred. No. 0.051;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 PKYEGGNIV 10
 DB 18 PKYEGGNIV 27

RESULT 14
 AAR91202 standard; peptide; 130 AA.
 ID AAR91202
 XX
 AC AAR91202;
 XX
 DT 13-NOV-1996 (first entry)
 XX
 DE D1-D4 fibronectin binding domains.
 XX
 KW Fibronectin; oral hygiene; gingivitis; gum disease; adhesion;
 KW periodontitis; oral pathogen; caries; calculus; candidiasis; oral surgery;
 KW tissue regeneration; irrigation; toothpaste; dentifrice; mouthwash;
 KW lozenge.
 XX
 OS Staphylococcus aureus.
 XX
 PN WO9604003-A1.
 XX
 PD 15-FEB-1996.
 XX
 PF 18-JUL-1995; 95WO-EP002825.
 XX
 PR 05-AUG-1994; 94GB-00015902.
 XX
 PA (SMIK) SMITHKLINE BEECHAM PLC.
 XX
 PI Barnett P, Critchley IA, Dodd I;
 XX
 DR WPI; 1996-129122/13.
 XX
 PT Prevention of adherence of oral pathogens in the oral cavity, partic.
 PT tooth surfaces - by application of a fibronectin binding protein or
 PT polypeptide or a monoclonal antibody or fragment against it.
 XX
 PS Claim 5; Page 32; 41pp; English.
 XX
 CC Adherence of oral pathogens, particularly to tooth surfaces, can be
 CC prevented by application of a fibronectin binding protein or polypeptide.
 CC The fibronectin binding protein or polypeptide is useful in the
 CC manufacture of oral hygiene compositions, eg. toothpaste, liquid
 CC dentifrice, mouthwash or lozenge. They are useful to prevent the plaque-
 CC related development of carious lesions, gingivitis, calculus or
 CC periodontal disease and to combat oral cavity infections, eg.
 CC candidiasis. They may also be useful in oral surgery e.g. in guided
 CC tissue regeneration procedures to prevent subsequent bacterial infection,
 CC and for irrigation of periodontal pockets. This sequence corresponds to
 CC amino acids 709-838 of the D1-D4 fibronectin binding domain of
 CC Staphylococcus aureus
 XX
 SQ Sequence 130 AA;
 Query Match 100.0%; Score 55; DB 2; Length 130;
 Best Local Similarity 100.0%; Pred. No. 0.051;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 PKYEGGNIV 10
 DB 18 PKYEGGNIV 27

RESULT 15
 AAR91201 standard; peptide; 130 AA.
 ID AAR91201
 XX
 AC AAR91201;
 XX
 DT 13-NOV-1996 (first entry)
 XX
 DE D1-D4 fibronectin binding domains.
 XX
 KW Fibronectin; oral hygiene; gingivitis; gum disease; adhesion;
 KW periodontitis; oral pathogen; caries; calculus; candidiasis; oral surgery;

```

KM tissue regeneration; irrigation; toothpaste; dentifrice; mouthwash;
KW lozenge.
XX
XX Staphylococcus aureus.
OS
XX WO9604003-A1.
PN
XX 15-FEB-1996.
PD
XX 18-JUL-1995; 95WO-EP002825.
PF
XX 05-AUG-1994; 94GB-00015902.
PR
XX
XX (SMK ) SMITHKLINE BEECHAM PLC.
PA
XX Barnett P, Critchley IA, Dodd I;
PI
XX WPI; 1996-129122/13.
DR
XX
XX Prevention of adherence of oral pathogens in the oral cavity, partic.
PT tooth surfaces - by application of a fibronectin binding protein or
PT polypeptide or a monoclonal antibody or fragment against it.
PS
XX Claim 5; Page 31-32; 41pp; English.
XX
CC Adherence of oral pathogens, particularly to tooth surfaces, can be
CC prevented by application of a fibronectin binding protein or polypeptide.
CC The fibronectin binding protein or polypeptide is useful in the
CC manufacture of oral hygiene compositions, eg. toothpaste, liquid
CC dentifrice, mouthwash or lozenge. They are useful to prevent the plaque-
CC related development of carious lesions, gingivitis, calculus or
CC periodontal disease and to combat oral cavity infections, e.g.
CC candidiasis. They may also be useful in oral surgery e.g. in guided
CC tissue regeneration procedures to prevent subsequent bacterial infection,
CC and for irrigation of periodontal pockets. This sequence corresponds to
CC amino acids 709-838 of the D1-D4 fibronectin binding domain of
CC Staphylococcus aureus with a P838T substitution
XX
SQ Sequence 130 AA;

```

Query Match 100.0%; Score 55; DB 2; Length 130;
 Best Local Similarity 100.0%; Pred. No. 0.051;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 PKYEOGNTV 10
   |||||
Db 18 PKYEOGNTV 27

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Search completed: October 25, 2005, 20:58:42
 Job time : 63.2 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 22, 2005, 05:46:56 ; Search time 17.3 Seconds
(without alignments)
43.150 Million cell updates/sec

Title: US-10-731-238-71

Perfect score: 55
Sequence: 1 PKYEGGNGIV 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-Processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
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2: /cgn2_6/prodata/1/iaa/5B_COMB.pep:*
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6: /cgn2_6/prodata/1/iaa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	55	100.0	10	4	US-09-010-317-71	Sequence 71, Appl
2	55	100.0	38	1	US-08-234-622A-2	Sequence 2, Appl
3	55	100.0	38	1	US-08-729-767-3	Sequence 3, Appl
4	55	100.0	38	4	US-09-010-317-5	Sequence 5, Appl
5	55	100.0	38	4	US-09-010-317-35	Sequence 35, Appl
6	55	100.0	38	4	US-09-010-317-36	Sequence 36, Appl
7	55	100.0	38	4	US-09-010-317-37	Sequence 37, Appl
8	55	100.0	38	4	US-09-010-317-38	Sequence 38, Appl
9	55	100.0	38	4	US-09-010-317-39	Sequence 39, Appl
10	55	100.0	38	4	US-09-010-317-40	Sequence 40, Appl
11	55	100.0	38	4	US-09-010-317-41	Sequence 41, Appl
12	55	100.0	38	4	US-09-010-317-42	Sequence 42, Appl
13	55	100.0	39	4	US-09-010-317-56	Sequence 56, Appl
14	55	100.0	114	1	US-08-259-000-3	Sequence 3, Appl
15	55	100.0	110	2	US-08-459-135A-7	Sequence 7, Appl
16	55	100.0	130	2	US-08-459-135A-8	Sequence 8, Appl
17	55	100.0	130	2	US-08-495-559-7	Sequence 7, Appl
18	55	100.0	130	3	US-08-495-559-8	Sequence 8, Appl
19	55	100.0	139	3	US-08-866-253-8	Sequence 8, Appl
20	55	100.0	174	2	US-08-459-135A-10	Sequence 10, Appl
21	55	100.0	174	2	US-08-459-135A-13	Sequence 13, Appl
22	55	100.0	174	3	US-08-495-559-10	Sequence 10, Appl
23	55	100.0	174	3	US-08-495-559-13	Sequence 13, Appl
24	55	100.0	176	3	US-08-495-559-6	Sequence 6, Appl
25	55	100.0	178	2	US-08-459-135A-12	Sequence 12, Appl
26	55	100.0	178	3	US-08-495-559-12	Sequence 12, Appl
27	55	100.0	181	2	US-08-459-135A-6	Sequence 6, Appl

28	55	100.0	559	4	US-08-956-171E-5251	Sequence 5251, Ap
29	55	100.0	559	4	US-08-781-986A-5251	Sequence 5251, Ap
30	55	100.0	1027	4	US-08-956-171E-5254	Sequence 5254, Ap
31	55	100.0	1027	4	US-08-781-986A-5254	Sequence 5254, Ap
32	49	89.1	38	1	US-08-234-622A-3	Sequence 3, Appl
33	49	89.1	38	1	US-08-729-767-4	Sequence 7, Appl
34	49	89.1	38	4	US-09-010-317-7	Sequence 4, Appl
35	49	89.1	38	4	US-09-010-317-45	Sequence 45, Appl
36	49	89.1	38	4	US-09-010-317-46	Sequence 46, Appl
37	49	89.1	38	4	US-09-010-317-47	Sequence 47, Appl
38	49	89.1	38	4	US-09-010-317-48	Sequence 48, Appl
39	47	85.5	10	4	US-09-010-317-70	Sequence 70, Appl
40	47	85.5	38	4	US-09-010-317-6	Sequence 6, Appl
41	47	85.5	38	4	US-09-010-317-43	Sequence 43, Appl
42	47	85.5	39	4	US-09-010-317-57	Sequence 57, Appl
43	47	85.5	10	4	US-09-010-317-72	Sequence 72, Appl
44	42	76.4	36	4	US-09-010-317-58	Sequence 58, Appl
45	41	74.5	38	4	US-09-010-317-8	Sequence 8, Appl

ALIGNMENTS

RESULT 1
US-09-010-317-71
; Sequence 71, Application US/09010317
; Patent No. 6685943
; GENERAL INFORMATION:
; APPLICANT: Hook, Magnus
; APPLICANT: Pattil, Joseph M.
; APPLICANT: House-Pompeo, Karen L.
; APPLICANT: Speziale, Pietro
; APPLICANT: Uch, Danny
; APPLICANT: McGeavin, Martin J.
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
; NUMBER OF INVENTIONS: AND METHODS OF USE
; NUMBER OF SEQUENCES: 105
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: TX
; COUNTRY: USA
; ZIP: 77210-4433
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/010,317
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/036,139
; FILING DATE: 21-JAN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Hibler, David W.
; REGISTRATION NUMBER: 41,071
; REFERENCE/DOCKET NUMBER: TAMK:189
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 512-418-3000
; TELEFAX: 512-474-7577
; INFORMATION FOR SEQ ID NO: 71:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; US-09-010-317-71
Query Match 100.0%; Score 55; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.00037;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PKYEGGNIV 10
|||||

DB 1 PKYEGGNIV 10

RESULT 2

US-08-234-622A-2
; Sequence 2, Application US/08234622A
; Patent No. 5440014
; GENERAL INFORMATION:
; APPLICANT: HOOK, Magnus
; APPLICANT: MCGAVIN, Martin
; APPLICANT: RAUCCI, Giuseppe
; TITLE OF INVENTION: A FIBRONECTIN BINDING PEPTIDE
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Doane, Swecker & Mathis
; STREET: P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/234,622A
; FILING DATE: 28-APR-1994
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: SE 9002617-0
; FILING DATE: 10-AUG-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/SE91/00534
; FILING DATE: 09-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Meuth, Donna M
; REGISTRATION NUMBER: 36,607
; REFERENCE/DOCKET NUMBER: 012885-044
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 38 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-234-622A-2

Query Match 100.0%; Score 55; DB 1; Length 38;
Best Local Similarity 100.0%; Pred. No. 0.0017;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PKYEGGNIV 10
|||||

DB 17 PKYEGGNIV 26

RESULT 3

US-08-729-767-3
; Sequence 3, Application US/08729767
; Patent No. 5770702
; GENERAL INFORMATION:
; APPLICANT: HOOK, Magnus
; APPLICANT: LINDBERG, Martin Kjell
; APPLICANT: SIGNAS, Lars Christer
; APPLICANT: WADSTROM, Torckel Mikael

; APPLICANT: FROMAN, Gunnar
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN AS WELL AS
; TITLE OF INVENTION: ITS PREPARATION
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Doane, Swecker & Mathis, L.L.P.
; STREET: P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/729,767
; FILING DATE: 07-OCT-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/259,000
; FILING DATE: 13-JUN-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/007,817
; FILING DATE: 22-JAN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/201,028
; FILING DATE: 01-JUN-1988
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: SE 8702272-9
; FILING DATE: 01-JUN-1987
; ATTORNEY/AGENT INFORMATION:
; NAME: McGowan, Malcolm K.
; REGISTRATION NUMBER: 39,300
; REFERENCE/DOCKET NUMBER: 012889-036
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 38 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-729-767-3

Query Match 100.0%; Score 55; DB 1; Length 38;
Best Local Similarity 100.0%; Pred. No. 0.0017;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PKYEGGNIV 10
|||||

DB 18 PKYEGGNIV 27

RESULT 4

US-09-010-317-5
; Sequence 5, Application US/09010317
; Patent No. 6685943
; GENERAL INFORMATION:
; APPLICANT: Hook, Magnus
; APPLICANT: Patti, Joseph M.
; APPLICANT: House-Pompeo, Karen L.
; APPLICANT: Speciale, Pietro
; APPLICANT: Joh, Danny
; APPLICANT: McGavin, Martin J.
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
; TITLE OF INVENTION: AND METHODS OF USE
; NUMBER OF SEQUENCES: 105
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee

STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/036,139
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAMK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-09-010-317-5

Query Match 100.0%; Score 55; DB 4; Length 38;
Best Local Similarity 100.0%; Pred. No. 0.0017;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PKYEOGGNTV 10
|||||
Db 17 PKYEOGGNTV 26

RESULT 5
US-09-010-317-35
Sequence 35, Application US/09010317
Patent No. 6685943
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
APPLICANT: Patti, Joseph M.
APPLICANT: House-Pompeo, Karen L.
APPLICANT: Speziale, Pietro
APPLICANT: Joh, Danny
APPLICANT: McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
TITLE OF INVENTION: AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/036,139

FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAMK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 35:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-09-010-317-35

Query Match 100.0%; Score 55; DB 4; Length 38;
Best Local Similarity 100.0%; Pred. No. 0.0017;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PKYEOGGNTV 10
|||||
Db 17 PKYEOGGNTV 26

RESULT 6
US-09-010-317-36
Sequence 36, Application US/09010317
Patent No. 6685943
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
APPLICANT: Patti, Joseph M.
APPLICANT: House-Pompeo, Karen L.
APPLICANT: Speziale, Pietro
APPLICANT: Joh, Danny
APPLICANT: McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
TITLE OF INVENTION: AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAMK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 36:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-09-010-317-36

Query Match 100.0%; Score 55; DB 4; Length 38;
Best Local Similarity 100.0%; Pred. No. 0.0017;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PKYEOGGNIV 10
| | | | | | | |
Db 17 PKYEOGGNIV 26

RESULT 7

US-09-010-317-37
; Sequence 37, Application US/09010317
; Patent No. 6685943
; GENERAL INFORMATION:
; APPLICANT: Hook, Magnus
; APPLICANT: Patti, Joseph M.
; APPLICANT: House-Pompeo, Karen L.
; APPLICANT: Speziale, Pietro
; APPLICANT: Joh, Danny
; APPLICANT: McGavin, Martin J.
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
; NUMBER OF SEQUENCES: 105
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: TX
; COUNTRY: USA
; ZIP: 77210-4433
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/010,317
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/036,139
; FILING DATE: 21-JAN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Hibler, David W.
; REGISTRATION NUMBER: 41,071
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 512-418-3000
; TELEFAX: 512-474-7577
; INFORMATION FOR SEQ ID NO: 37:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 38 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
US-09-010-317-37

Query Match 100.0%; Score 55; DB 4; Length 38;
Best Local Similarity 100.0%; Pred. No. 0.0017;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PKYEOGGNIV 10
| | | | | | | |
Db 17 PKYEOGGNIV 26

RESULT 8

US-09-010-317-38
; Sequence 38, Application US/09010317
; Patent No. 6685943
; GENERAL INFORMATION:
; APPLICANT: Hook, Magnus
; APPLICANT: Patti, Joseph M.

APPLICANT: House-Pompeo, Karen L.
APPLICANT: Speziale, Pietro
APPLICANT: Joh, Danny
APPLICANT: McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TANK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 38:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-09-010-317-38

Query Match 100.0%; Score 55; DB 4; Length 38;
Best Local Similarity 100.0%; Pred. No. 0.0017;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PKYEOGGNIV 10
| | | | | | | |
Db 17 PKYEOGGNIV 26

RESULT 9

US-09-010-317-39
; Sequence 39, Application US/09010317
; Patent No. 6685943
; GENERAL INFORMATION:
; APPLICANT: Hook, Magnus
; APPLICANT: Patti, Joseph M.
; APPLICANT: House-Pompeo, Karen L.
; APPLICANT: Speziale, Pietro
; APPLICANT: Joh, Danny
; APPLICANT: McGavin, Martin J.
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
; NUMBER OF SEQUENCES: 105
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: TX
; COUNTRY: USA
; ZIP: 77210-4433
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAMK:189
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 39:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-09-010-317-39

Query Match 100.0%; Score 55; DB 4; Length 38;
Best Local Similarity 100.0%; Pred. No. 0.0017;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PKYEOGGNTV 10
DB 17 PKYEOGGNTV 26

RESULT 10
US-09-010-317-40
Sequence 40, Application US/09010317
Patent No. 6685943
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
APPLICANT: Patti, Joseph M.
APPLICANT: House-Pompeo, Karen L.
APPLICANT: Speziale, Pietro
APPLICANT: Joh, Danny
APPLICANT: McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
TITLE OF INVENTION: AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSER: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAMK:189
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577

TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 40:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-09-010-317-40

Query Match 100.0%; Score 55; DB 4; Length 38;
Best Local Similarity 100.0%; Pred. No. 0.0017;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PKYEOGGNTV 10
DB 17 PKYEOGGNTV 26

RESULT 11
US-09-010-317-41
Sequence 41, Application US/09010317
Patent No. 6685943
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
APPLICANT: Patti, Joseph M.
APPLICANT: House-Pompeo, Karen L.
APPLICANT: Speziale, Pietro
APPLICANT: Joh, Danny
APPLICANT: McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
TITLE OF INVENTION: AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSER: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAMK:189
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 41:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-09-010-317-41

Query Match 100.0%; Score 55; DB 4; Length 38;
Best Local Similarity 100.0%; Pred. No. 0.0017;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PKYEOGGNTV 10
DB 17 PKYEOGGNTV 26

RESULT 12
US-09-010-317-42
Sequence 42, Application US/09010317
Patent No. 6685943
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
APPLICANT: Patti, Joseph M.
APPLICANT: House-Pompeo, Karen L.
APPLICANT: Speziale, Pietro
APPLICANT: Joh, Danny
APPLICANT: McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
TITLE OF INVENTION: AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE:
STRANDEDNESS:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TANK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 42:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-09-010-317-42

Query Match 100.0%; Score 55; DB 4; Length 38;
Best Local Similarity 100.0%; Pred. No. 0.0017;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PKYEGGNIV 10
DB 17 PKYEGGNIV 26

RESULT 13
US-09-010-317-56
Sequence 56, Application US/09010317
Patent No. 6685943
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
APPLICANT: Patti, Joseph M.
APPLICANT: House-Pompeo, Karen L.
APPLICANT: Speziale, Pietro
APPLICANT: Joh, Danny
APPLICANT: McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
TITLE OF INVENTION: AND METHODS OF USE
NUMBER OF SEQUENCES: 105

CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE:
STRANDEDNESS:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TANK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 56:
SEQUENCE CHARACTERISTICS:
LENGTH: 39 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-09-010-317-56

Query Match 100.0%; Score 55; DB 4; Length 39;
Best Local Similarity 100.0%; Pred. No. 0.0017;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PKYEGGNIV 10
DB 17 PKYEGGNIV 26

RESULT 14
US-08-259-000-3
Sequence 3, Application US/08259000
Patent No. 5571514
GENERAL INFORMATION:
APPLICANT: HOOK, Magnus
APPLICANT: LINDBERG, Martin Kjeil
APPLICANT: SIGMANS, Lars Christer
APPLICANT: WADSTROM, Torkel Mikael
APPLICANT: FROMAN, Gunnar
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN AS WELL AS
ITS PREPARATION
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Burns, Doane, Swecker & Mathis
STREET: P.O. Box 1404
CITY: Alexandria
STATE: Virginia
COUNTRY: United States
ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/259,000
FILING DATE: 13-JUN-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:

APPLICATION NUMBER: SE 8702272-9
FILING DATE: 01-JUN-1987
ATTORNEY/AGENT INFORMATION:
NAME: Meuth, Donna M
REGISTRATION NUMBER: 36,607
REFERENCE/DOCKET NUMBER: 012885-062
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 114 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-259-000-3

Query Match 100.0%; Score 55; DB 1; Length 114;
Best Local Similarity 100.0%; Pred. No. 0.0057;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PRTYEGGNIV 10
|||||
Db 18 PRTYEGGNIV 27

RESULT 15

US-08-459-135A-7
Sequence 7, Application US/08459135A
Patent No. 5955078
GENERAL INFORMATION:
APPLICANT: BURHAM, Martin Karl Russel
APPLICANT: CHOPRA, Ian
APPLICANT: CRITCHLEY, Ian Alfred
APPLICANT: KNOWLES, David Justin Charles
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN: MONOCLONAL ANTIBODY AND THEIR US
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
STATE: PA
COUNTRY: U.S.A.
ZIP: 19406-0939
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: Fastseq, Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/459,135A
FILING DATE: 02-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB/94/00215
FILING DATE: 04-Feb-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Gimmil, Edward R
REGISTRATION NUMBER: 38,891
REFERENCE/DOCKET NUMBER: P30591C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-4478
TELEFAX: 610-270-5090
TELEX:
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 130 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-459-135A-7

Query Match 100.0%; Score 55; DB 2; Length 130;
Best Local Similarity 100.0%; Pred. No. 0.0066;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PRTYEGGNIV 10
|||||
Db 18 PRTYEGGNIV 27

Search completed: October 22, 2005, 07:41:41
Job time : 17.35 secs

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Wed Oct 26 15:02:52 2005

Ltd.

GenCore version 5.1

Co

Copyright (c) 1993 - 2005 Arch time 57.25 Seconds

without alignment updates/sec

OM protein - protein search, using bw mgt

October 22, 2005, 17

Run on: US-10-731-238-71

Title: score: 1 PKYP717491010 residues

Perfect score: 1 PKYP717491010 residues

Sequence: 1 PKYP717491010 residues

Scoring table: 2000000000

Searched: Num Match 0%

Minimum Match 100%

Total: 45 summaries

Published Applications AA: *

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2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
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5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep.*
7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
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17: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep.*
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19: /cgn2_6/ptodata/2/pubpaa/US11_PUBCOMB.pep.*
20: /cgn2_6/ptodata/2/pubpaa/US11_PUBCOMB.pep.*
21: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
22: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	55	100.0	10	18	US-10-731-238-71	Sequence 71, Appl
2	55	100.0	38	18	US-10-731-238-5	Sequence 5, Appl
3	55	100.0	38	18	US-10-731-238-35	Sequence 35, Appl
4	55	100.0	38	18	US-10-731-238-36	Sequence 36, Appl
5	55	100.0	38	18	US-10-731-238-37	Sequence 37, Appl
6	55	100.0	38	18	US-10-731-238-38	Sequence 38, Appl
7	55	100.0	38	18	US-10-731-238-39	Sequence 39, Appl
8	55	100.0	38	18	US-10-731-238-40	Sequence 40, Appl
9	55	100.0	38	18	US-10-731-238-41	Sequence 41, Appl
10	55	100.0	38	18	US-10-731-238-42	Sequence 42, Appl
11	55	100.0	39	18	US-10-731-238-56	Sequence 56, Appl

12	55	100.0	139	9	US-09-813-820-8	Sequence 8, Appl
13	55	100.0	388	8	US-08-901-062-1	Sequence 1, Appl
14	55	100.0	559	8	US-08-781-986A-5251	Sequence 5251, Ap
15	55	100.0	559	15	US-10-329-624-5251	Sequence 5251, Ap
16	55	100.0	767	9	US-09-815-242-5899	Sequence 5899, Ap
17	55	100.0	767	9	US-09-815-242-5899	Sequence 13140, A
18	55	100.0	940	17	US-10-470-0488-424	Sequence 424, Ap
19	55	100.0	948	17	US-10-470-0488-69	Sequence 43778, A
20	55	100.0	961	15	US-10-282-122A-43778	Sequence 5456, Ap
21	55	100.0	978	9	US-09-815-242-5456	Sequence 12686, A
22	55	100.0	1001	9	US-09-815-242-5456	Sequence 5787, A
23	55	100.0	1018	9	US-09-815-242-5797	Sequence 12838, A
24	55	100.0	1018	9	US-09-815-242-12838	Sequence 684, Ap
25	55	100.0	1018	17	US-10-470-0488-68	Sequence 5254, Ap
26	55	100.0	1027	8	US-08-781-986A-5254	Sequence 5254, Ap
27	55	100.0	1027	15	US-10-329-624-5254	Sequence 43827, A
28	55	100.0	1038	15	US-10-282-122A-43827	Sequence 1, Appl
29	54	98.2	30	14	US-10-287-821-1	Sequence 2, Appl
30	54	98.2	31	14	US-10-287-821-2	Sequence 7, Appl
31	49	89.1	38	18	US-10-731-238-45	Sequence 45, Appl
32	49	89.1	38	18	US-10-731-238-46	Sequence 47, Appl
33	49	89.1	38	18	US-10-731-238-47	Sequence 48, Appl
34	49	89.1	38	18	US-10-731-238-48	Sequence 49, Appl
35	49	89.1	38	18	US-10-731-238-49	Sequence 50, Appl
36	47	85.5	38	18	US-10-731-238-50	Sequence 51, Appl
37	47	85.5	38	18	US-10-731-238-51	Sequence 52, Appl
38	47	85.5	38	18	US-10-731-238-52	Sequence 53, Appl
39	47	85.5	38	18	US-10-731-238-53	Sequence 54, Appl
40	43	78.2	10	18	US-10-731-238-57	Sequence 57, Appl
41	42	76.4	36	18	US-10-731-238-58	Sequence 58, Appl
42	41	74.5	38	18	US-10-731-238-59	Sequence 59, Appl
43	41	74.5	38	18	US-10-731-238-60	Sequence 60, Appl
44	40	72.7	591	15	US-10-282-122A-5313	Sequence 5313, A
45	39	70.9	38	18	US-10-731-238-44	Sequence 44, Appl

ALIGNMENTS

RESULT 1
US-10-731-238-71
Sequence 71, Application US/10731238
Publication No. US20050123552A1
GENERAL INFORMATION:
APPLICANT: HOOK, Magnus
Patel, Joseph M.
House-Pompeo, Karen L.
Speziale, Pietro
Job, Danny
McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSER: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Releasee #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/731,238
FILING DATE: 10-Dec-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE: 21-Jan-1998
APPLICATION NUMBER: US 60/036,139

FILED DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TANK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 71:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 71:
US-10-731-238-71

Query Match 100.0%; Score 55; DB 18; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0019;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PKYEGGNIV 10
DB 1 PKYEGGNIV 10

RESULT 2
US-10-731-238-5
Sequence 5, Application US/10731238
Publication No. US20050123552A1
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
Patel, Joseph M.
House-Pompeo, Karen L.
Speziale, Pietro
Joh, Danny
McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
TYPE: Floppy disk
PRIOR ART: IBM PC compatible
APPLICATION SYSTEM: PC-DOS/MS-DOS
APPLICATION Release #1.0, Version #1.30
FILING DATA:
FILING DATE: 21-JAN-1997
APPLICATION NUMBER: US 60/036,139
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TANK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>

TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-10-731-238-5

Query Match 100.0%; Score 55; DB 18; Length 38;
Best Local Similarity 100.0%; Pred. No. 0.0078;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PKYEGGNIV 10
DB 17 PKYEGGNIV 26

RESULT 3
US-10-731-238-35
Sequence 35, Application US/10731238
Publication No. US20050123552A1
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
Patel, Joseph M.
House-Pompeo, Karen L.
Speziale, Pietro
Joh, Danny
McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
TYPE: Floppy disk
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10731,238
FILING DATE: 10-Dec-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE: 21-Jan-1998
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TANK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 35:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 35:
US-10-731-238-35

Query Match 100.0%; Score 55; DB 18; Length 38;
Best Local Similarity 100.0%; Pred. No. 0.0078;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PKYEGGNIV 10
DB 17 PKYEGGNIV 26

RESULT 4
US-10-731-238-36
; Sequence 36, Application US/10731238
; Publication No. US20050123552A1
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
Patti, Joseph M.
House-Pompeo, Karen L.
Speciale, Pietro
John, Danny
McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/731,238
FILING DATE: 10-Dec-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE: 21-Jan-1998
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAMK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 36:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 36:
US-10-731-238-36
Query Match 100.0%; Score 55; DB 18; Length 38;
Best Local Similarity: 100.0%; Pred. No. 0.0078;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 PKYEGGNIV 10
DB 17 PKYEGGNIV 26
RESULT 5
US-10-731-238-37
; Sequence 37, Application US/10731238
; Publication No. US20050123552A1
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
Patti, Joseph M.
House-Pompeo, Karen L.
Speciale, Pietro
John, Danny
McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
AND METHODS OF USE

NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/731,238
FILING DATE: 10-Dec-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE: 21-Jan-1998
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAMK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 37:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 37:
US-10-731-238-37
Query Match 100.0%; Score 55; DB 18; Length 38;
Best Local Similarity: 100.0%; Pred. No. 0.0078;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 PKYEGGNIV 10
DB 17 PKYEGGNIV 26
RESULT 6
US-10-731-238-38
; Sequence 38, Application US/10731238
; Publication No. US20050123552A1
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
Patti, Joseph M.
House-Pompeo, Karen L.
Speciale, Pietro
John, Danny
McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30


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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/731,238
; FILING DATE: 10-Dec-2003
; CLASSIFICATION: <Unknown>
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/010,317
; FILING DATE: 21-Jan-1998
; APPLICATION NUMBER: US 60/036,139
; FILING DATE: 21-JAN-1997
;
; ATTORNEY/AGENT INFORMATION:
; NAME: Hibler, David W.
; REGISTRATION NUMBER: 41,071
; REFERENCE/DOCKET NUMBER: TAMK:189
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 512-418-3000
; TELEFAX: 512-474-7577
;
; INFORMATION FOR SEQ ID NO: 38:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 38 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
;
; SEQUENCE DESCRIPTION: SEQ ID NO: 38:
US-10-731-238-38

Query Match      100.0%; Score 55; DB 18; Length 38;
Beet Local Similarity 100.0%; Pred. No. 0.0078;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 PKEEGGNIV 10
        |||||
        17 PKEEGGNIV 26

Db

RESULT 7
US-10-731-238-39
; Sequence 39, Application US/10731238
; Publication No. US20050123552A1
; GENERAL INFORMATION:
; APPLICANT: Hook, Magnus
;          Patti, Joseph M.
;          House-Pompeo, Karen L.
;          Speziale, Pietro
;          Joh, Danny
;
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
; AND METHODS OF USE
;
; NUMBER OF SEQUENCES: 105
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: TX
; COUNTRY: USA
; ZIP: 77210-4433
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/731,238
; FILING DATE: 10-Dec-2003
; CLASSIFICATION: <Unknown>
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/010,317
; FILING DATE: 21-Jan-1998
; APPLICATION NUMBER: US 60/036,139
; FILING DATE: 21-JAN-1997
;
; ATTORNEY/AGENT INFORMATION:
; NAME: Hibler, David W.
; REGISTRATION NUMBER: 41,071
; REFERENCE/DOCKET NUMBER: TAMK:189
```

```

;
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 512-418-3000
; TELEFAX: 512-474-7577
;
; INFORMATION FOR SEQ ID NO: 39:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 38 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
;
; SEQUENCE DESCRIPTION: SEQ ID NO: 39:
US-10-731-238-39

Query Match      100.0%; Score 55; DB 18; Length 38;
Beet Local Similarity 100.0%; Pred. No. 0.0078;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 PKEEGGNIV 10
        |||||
        17 PKEEGGNIV 26

Db

RESULT 8
US-10-731-238-40
; Sequence 40, Application US/10731238
; Publication No. US20050123552A1
; GENERAL INFORMATION:
; APPLICANT: Hook, Magnus
;          Patti, Joseph M.
;          House-Pompeo, Karen L.
;          Speziale, Pietro
;          Joh, Danny
;          McGavin, Martin J.
;
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
; AND METHODS OF USE
;
; NUMBER OF SEQUENCES: 105
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: TX
; COUNTRY: USA
; ZIP: 77210-4433
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/731,238
; FILING DATE: 10-Dec-2003
; CLASSIFICATION: <Unknown>
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/010,317
; FILING DATE: 21-Jan-1998
; APPLICATION NUMBER: US 60/036,139
; FILING DATE: 21-JAN-1997
;
; ATTORNEY/AGENT INFORMATION:
; NAME: Hibler, David W.
; REGISTRATION NUMBER: 41,071
; REFERENCE/DOCKET NUMBER: TAMK:189
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 512-418-3000
; TELEFAX: 512-474-7577
;
; INFORMATION FOR SEQ ID NO: 40:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 38 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
;
; SEQUENCE DESCRIPTION: SEQ ID NO: 40:
US-10-731-238-40

Query Match      100.0%; Score 55; DB 18; Length 38;
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Best Local Similarity 100.0%; Pred. No. 0.0078;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PKYEGGNIV 10
|||||
17 PKYEGGNIV 26

Db

RESULT 9
US-10-731-238-41
; Sequence 41, Application US/10731238
; Publication No. US20050123552A1
; GENERAL INFORMATION:
; APPLICANT: Hook, Magnus
; Patti, Joseph M.
; House-Pompeo, Karen L.
; Speziale, Pietro
; Joh, Danny
; McGavin, Martin J.
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
; AND METHODS OF USE
; NUMBER OF SEQUENCES: 105
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: TX
; COUNTRY: USA
; ZIP: 77210-4433
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/731,238
; FILING DATE: 10-Dec-2003
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/010,317
; FILING DATE: 21-Jan-1998
; APPLICATION NUMBER: US 60/036,139
; FILING DATE: 21-JAN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Hibler, David W.
; REGISTRATION NUMBER: 41,071
; REFERENCE/DOCKET NUMBER: TAMK:189
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 512-418-3000
; TELEFAX: 512-474-7577
; INFORMATION FOR SEQ ID NO: 41:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 38 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 41:
US-10-731-238-41

Query Match 100.0%; Score 55; DB 18; Length 38;
Best Local Similarity 100.0%; Pred. No. 0.0078;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PKYEGGNIV 10
|||||
17 PKYEGGNIV 26

Db

RESULT 10
US-10-731-238-42
; Sequence 42, Application US/10731238
; Publication No. US20050123552A1
; GENERAL INFORMATION:

APPLICANT: Hook, Magnus
Patti, Joseph M.
House-Pompeo, Karen L.
Speziale, Pietro
Joh, Danny
McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/731,238
FILING DATE: 10-Dec-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE: 21-Jan-1998
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAMK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 42:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 42:
US-10-731-238-42

Query Match 100.0%; Score 55; DB 18; Length 38;
Best Local Similarity 100.0%; Pred. No. 0.0078;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PKYEGGNIV 10
|||||
17 PKYEGGNIV 26

Db

RESULT 11
US-10-731-238-56
; Sequence 56, Application US/10731238
; Publication No. US20050123552A1
; GENERAL INFORMATION:
; APPLICANT: Hook, Magnus
; Patti, Joseph M.
; House-Pompeo, Karen L.
; Speziale, Pietro
; Joh, Danny
; McGavin, Martin J.
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
; AND METHODS OF USE
; NUMBER OF SEQUENCES: 105
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston

STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/731,238
FILING DATE: 10-Dec-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE: 21-Jan-1998
APPLICATION NUMBER: US 60/036,139
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAMK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 56:
SEQUENCE CHARACTERISTICS:
LENGTH: 39 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 56:
US-10-731-238-56

Query Match 100.0%; Score 55; DB 18; Length 33;
Best Local Similarity 100.0%; Pred. No. 0.008;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PRYEOGQNV 10
Db 17 PRYEOGQNV 26

RESULT 12
US-09-813-820-8
Sequence 8, Application US/09813820
Patent No. US20020102262X1
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
Patti, Joseph M.
House-Pompeo, Karen
Shanani, Narayana
Symetery, Jindrich
TITLE OF INVENTION: COLLAGEN BINDING PROTEIN COMPOSITIONS
AND METHODS OF USE
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: Texas
COUNTRY: U.S.
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/813,820
FILING DATE: 22-Mar-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/856,253

FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Kitchell, Barbara S.
REGISTRATION NUMBER: 33,928
REFERENCE/DOCKET NUMBER: TAMK:193
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
TELEFAX: (512) 474-7577
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 139 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-09-813-820-8

Query Match 100.0%; Score 55; DB 9; Length 139;
Best Local Similarity 100.0%; Pred. No. 0.03;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PRYEOGQNV 10
Db 32 PRYEOGQNV 41

RESULT 13
US-08-901-062-1
Sequence 1, Application US/08901062
Publication No. US2002025324A1
GENERAL INFORMATION:
APPLICANT: SEALS, JONATHAN R.
TITLE OF INVENTION: RECOMBINANT BIVALENT BACTERIAL VACCINE
FOR THE PREVENTION OF MASTITIS
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: HALE AND DORR LLP
STREET: 60 State Street
CITY: Boston
STATE: MA
COUNTRY: United States Of America
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/901,062
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Baker, Hollie L.
REGISTRATION NUMBER: 31,321
REFERENCE/DOCKET NUMBER: 106941.153
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 526-6000
TELEFAX: (617) 526-5000
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 388 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-901-062-1

Query Match 100.0%; Score 55; DB 8; Length 388;
Best Local Similarity 100.0%; Pred. No. 0.089;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PKYEOGNIV 10
DB 281 PKYEOGNIV 290

RESULT 14

US-08-781-986A-5251
Sequence 5251, Application US/08781986A
Publication No. US20030054436A1
GENERAL INFORMATION:
APPLICANT: Charles Kunesh
TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
NUMBER OF SEQUENCES: 5255
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COUNTRY: USA
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4MB storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/781,986A
FILING DATE:
PRIORITY APPLICATION DATA:
PRIORITY APPLICATION NUMBER: 435
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Benson, Bob
REGISTRATION NUMBER: 30,446
REFERENCE/DOCKET NUMBER: PB248PP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 5251:
SEQUENCE CHARACTERISTICS:
LENGTH: 559 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-781-986A-5251

Query Match 100.0%; Score 55; DB 8; Length 559;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 PKYEOGNIV 10
DB 317 PKYEOGNIV 326

RESULT 15

US-10-329-624-5251
Sequence 5251, Application US/10329624
Publication No. US20040043037A1
GENERAL INFORMATION:
APPLICANT: Charles Kunesh
TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
NUMBER OF SEQUENCES: 5256
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue

CITY: Rockville
STATE: Maryland
COUNTRY: USA
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4MB storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/329,624
FILING DATE: 27-Dec-2002
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 08/956,171
FILING DATE: October 20, 1997
APPLICATION NUMBER: 60/009,861
FILING DATE: January 5, 1996
APPLICATION NUMBER: 08/781,986
FILING DATE: January 3, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Mark J. Hyman
REGISTRATION NUMBER: 46,789
REFERENCE/DOCKET NUMBER: PB248P1D1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (240) 314-1224
TELEFAX: (301) 309-8439
INFORMATION FOR SEQ ID NO: 5251:
SEQUENCE CHARACTERISTICS:
LENGTH: 559 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 5251:
US-10-329-624-5251

Query Match 100.0%; Score 55; DB 15; Length 559;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 PKYEOGNIV 10
DB 317 PKYEOGNIV 326

Search completed: October 22, 2005, 12:39:44
Job time : 57.25 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 22, 2005, 06:10:10 ; Search time 11.45 Seconds
(without alignments)
84.032 Million cell updates/sec

Title: US-10-731-238-71

Perfect score: 55

Sequence: 1 PKYEGGNIV 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 segs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	55	100.0	940	2	S19702 fibronectin-bindin
2	55	100.0	961	2	G90053 hypothetical prote
3	55	100.0	1018	2	A32192 fibronectin-bindin
4	55	100.0	1038	2	H90053 hypothetical prote
5	38	69.1	62	2	H89941 hypothetical prote
6	38	69.1	189	2	F83973 hypothetical prote
7	38	69.1	329	2	H72421 hypothetical prote
8	38	69.1	788	2	T30510 viral enhancing fa
9	37	67.3	228	2	G69493 conserved hypochet
10	37	67.3	352	1	K1BBD2 chymidine kinase
11	37	67.3	352	1	K1BBD4 chymidine kinase
12	37	67.3	352	2	T42582 chymidine kinase
13	37	67.3	352	4	S25497 chymidine kinase
14	37	67.3	432	2	C97258 sugar-binding perit
15	37	67.3	432	2	E96649 hypothetical prote
16	37	67.3	553	2	T46964 thiosulfate-oxidiz
17	36	65.5	110	1	S43192 ribosomal protein
18	36	65.5	111	2	S76083 hypothetical prote
19	36	65.5	215	2	H72290 conserved hypochet
20	36	65.5	244	2	B70422 hypothetical prote
21	35	63.6	128	2	E70168 flagellar protein
22	35	63.6	145	2	E70168 periplasmic chaper
23	35	63.6	208	2	D83318 homeotic protein D
24	35	63.6	327	2	A44168 integrase/recombin
25	35	63.6	344	2	T03499 hypothetical prote
26	35	63.6	470	2	A87298 hypothetical prote
27	34	61.8	95	2	C83832 N-hydroxyarylamine
28	34	61.8	254	2	C70032 hypothetical prote
29	34	61.8	283	2	T20367

30	34	61.8	306	2	JC7249 anterior fat body
31	34	61.8	336	1	PRSASK glutamyl endopepti
32	34	61.8	357	2	S21758 glutamic acid-spec
33	34	61.8	392	2	H81408 probable periplasm
34	34	61.8	397	2	D64096 galactokinase (EC
35	34	61.8	397	2	B69361 galactokinase (EC
36	34	61.8	397	2	G97335 subtilisin-like se
37	34	61.8	404	2	T20055 hypothetical prote
38	34	61.8	522	2	G02533 occudin - human
39	34	61.8	586	1	S47452 probable serine/ch
40	34	61.8	624	2	T42247 polypeptide N-acet
41	34	61.8	666	2	H75295 transketolase - De
42	34	61.8	682	2	T15092 hypothetical prote
43	34	61.8	719	2	JC1200 alpha-glucosidase
44	34	61.8	1165	2	D72496 hypothetical prote
45	33	60.0	98	2	AE2219 hypothetical prote

ALIGNMENTS

RESULT 1

S19702 fibronectin-binding protein B - Staphylococcus aureus

C/Species: Staphylococcus aureus

C/Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004

C/Accession: S19702

R/Joensen, K.; Signaes, C.; Mueller, H.P.; Lindberg, M.

Eur. J. Biochem. 202, 1041-1048, 1991

A/Title: Two different genes encode fibronectin binding proteins in Staphylococcus aurei

A/Reference number: S19702; MUID:92111475; PMID:1837266

A/Accession: S19702

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-940 <JOE>

A/Cross-references: UNIPROT:Q53682; EMBL:X62992; NID:G49040; PIDN:CAA44726.1; PID:G5815

C/Keyword: fibronectin binding

Query Match

Best Local Similarity 100.0%; Score 55; DB 2; Length 940;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PKYEGGNIV 10
DB 698 PKYEGGNIV 707

RESULT 2

G90053 hypothetical protein fnbB [imported] - Staphylococcus aureus (strain N315)

C/Species: Staphylococcus aureus

C/Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004

C/Accession: G90053

R/Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Ogu

ma, A.; Mizutani, U.; Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kato, C.; Sekimizu, K.

C.; Shib, T.; Hattori, M.; Ogasawara, N.; Hayaishi, H.; Hiramatsu, K.

Lancet 357, 1225-1240, 2001

A/Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.

A/Reference number: A89758; MUID:21311952; PMID:1148146

A/Accession: G90053

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-961 <KUR>

A/Cross-references: UNIPROT:Q99RD3; GB:BA000018; PID:G13702452; PIDN:BA843593.1; GSPDB:

A/Experimental source: strain N315

C/Genetic:

A/Gene: fnbB

Query Match 100.0%; Score 55; DB 2; Length 961;
Best Local Similarity 100.0%; Pred. No. 0.038; Indels 0; Gaps 0;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PKYEGGNIV 10

Db 709 PKYEOGNTV 718
|||||

RESULT 3

A32192
fibronectin-binding protein - Staphylococcus aureus
C:Species: Staphylococcus aureus
C:Date: 31-Jul-1989 #sequence_revision 31-Jul-1989 #text_change 16-Feb-1997
C:Accession: A32192
R:Signaess, C.; Raucel, G.; Joenson, K.; Lindgren, P.E.; Anantharamaiah, G.M.; Hoecek, W
Proc. Natl. Acad. Sci. U.S.A. 86, 699-703, 1989
A:Title: Nucleotide sequence of the gene for a fibronectin-binding protein from Staphylo
A:Reference number: A32192; MUID:89098998; PMID:2521391
A:Accession: A32192
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1018 <SIG>
A:Cross-references: GB:J04151
C:Keywords: fibronectin binding

Query Match 100.0%; Score 55; DB 2; Length 1118;
Best Local Similarity 100.0%; Pred. No. 0.04;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PKYEOGNTV 10
|||||

Db 762 PKYEOGNTV 771

RESULT 4

H90053
hypothetical protein fnb [imported] - Staphylococcus aureus (strain N315)
C:Species: Staphylococcus aureus
C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C:Accession: H90053
R:Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Ogu
ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.;
C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
A:Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.
A:Reference number: A89758; MUID:21311952; PMID:11418146
A:Accession: H90053
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1038 <KOR>
A:Cross-references: UNIPROT:Q99RD2; GB:BA000018; PID:G13702453; PIDN:BA843594.1; GSPDB:G
A:Experimental source: strain N315
C:Genetics:
A:Gene: fnb

Query Match 100.0%; Score 55; DB 2; Length 1038;
Best Local Similarity 100.0%; Pred. No. 0.041;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PKYEOGNTV 10
|||||

Db 758 PKYEOGNTV 767

RESULT 5

H89941
hypothetical protein SA1429 [imported] - Staphylococcus aureus (strain N315)
C:Species: Staphylococcus aureus
C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C:Accession: H89941
R:Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Ogu
ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.;
C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
A:Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.
A:Reference number: A89758; MUID:21311952; PMID:11418146
A:Accession: H89941

A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-62 <KTR>
A:Cross-references: UNIPROT:Q99TP8; GB:BA000018; PID:G13701399; PIDN:BA842693.1; GSPDB:G
A:Experimental source: strain N315
C:Genetics:
A:Gene: SA1429

Query Match 69.1%; Score 38; DB 2; Length 62;
Best Local Similarity 87.5%; Pred. No. 3.4;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 YEEOGNTV 10
|||||

Db 2 YEEOGNTV 9

RESULT 6

F83973
hypothetical protein BH2590 [imported] - Bacillus halodurans (strain C-125)
C:Species: Bacillus halodurans
C:Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004
C:Accession: F83973
R:Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, F.; Hira
Nucleic Acids Res. 28, 4317-4331, 2000
A:Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and
A:Reference number: A83650; MUID:20512582; PMID:11058132
A:Accession: F83973
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-189 <STO>
A:Cross-references: UNIPROT:Q9K9Q5; GB:AP001516; GB:BA000004; NID:G10175192; PIDN:BA8063
A:Experimental source: strain C-125
C:Genetics:
A:Gene: BH2590
C:Superfamily: Escherichia coli hypothetical 21.7K protein (ftsY-nika intergenic region)

Query Match 69.1%; Score 38; DB 2; Length 189;
Best Local Similarity 75.0%; Pred. No. 11;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 KYEOGNTV 9
|||||

Db 181 KYEOGNTV 188

RESULT 7

H72421
hypothetical protein TM0080 - Thermotoga maritima (strain MSB8)
C:Species: Thermotoga maritima
C:Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
C:Accession: H72421
R:Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwin, M.L.; Dodson, R.J.; Haft, D.H.; Hickey
Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.;
C.M.
Nature 399, 323-329, 1999
A:Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome seq
A:Reference number: A72200; MUID:99287316; PMID:10360571
A:Accession: H72421
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-329 <ARN>
A:Cross-references: UNIPROT:Q9WXT5; GB:AE001694; GB:AE000512; NID:G4980558; PIDN:AMJ3517
A:Experimental source: strain MSB8
C:Genetics:
A:Gene: TM0080

Query Match 69.1%; Score 38; DB 2; Length 329;
Best Local Similarity 50.0%; Pred. No. 20;
Matches 5; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 1 PKYEOGNTV 10
|:::|

DB 17 PRH08GNTL 26

RESULT 8

T30510

Viral enhancing factor 2 - Lymantria dispar nuclear polyhedrosis virus

C/Species: Lymantria dispar nuclear polyhedrosis virus, LdMNPV

C/Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004

C/Accession: T30510

R/Kuzio, J.; Pearson, M.N.; Harwood, S.H.; Funk, C.J.; Evans, J.T.; Slavicek, J.M.; Rohu

Virolology 253, 17-34, 1999

A/Title: Sequence and analysis of the genome of a baculovirus pathogenic for Lymantria d

A/Reference number: Z20836; MUID:99124785; PMID:9687315

A/Accession: T30510

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: DNA

A/Residues: 1-788 <KUZ>

A/Cross-references: UNIPROT:Q9YMG8; EMBL:AF081810; PIDD:AACT0346.1

Query Match 69.1%; Score 38; DB 2; Length 788;

Best Local Similarity 66.7%; Pred. No. 51;

Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

DB 114 PLYE0GNTV 122

RESULT 9

G69493

Conserved hypothetical protein AFI952 - Archaeoglobus fulgidus

C/Species: Archaeoglobus fulgidus

C/Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004

C/Accession: G69493

R/Kleek, H.P.; Claydon, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson

; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kalkness, E.F.

Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.

Nature 390, 364-370, 1997

A/Authors: Utebach, T.; Cotton, M.D.; Spriggs, T.; Artach, P.; Kaine, B.P.; Sykes, S.

Smith, H.O.; Moese, C.R.; Venter, J.C.

A/Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archae

A/Accession: G69493

A/Reference number: A69250; MUID:98049343; PMID:9389475

A/Status: preliminary; nucleic acid sequence not shown; translation not shown

A/Molecule type: DNA

A/Residues: 1-238 <RLE>

A/Cross-references: UNIPROT:Q208327; GB:AE000968; GB:AE000782; NID:G2689291; PIDD:AA8930

Query Match 67.3%; Score 37; DB 2; Length 238;

Best Local Similarity 60.0%; Pred. No. 22;

Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

DB 2 PKYE0GNTV 11

RESULT 10

K18ED2

Thymidine kinase (EC 2.7.1.21) - equine herpesvirus 1

C/Species: equine herpesvirus 1

C/Date: 30-Sep-1992 #sequence_revision 30-Sep-1992 #text_change 09-Jul-2004

C/Accession: S01995; D36799; S55498; A56627

R/Robertson, G.R.; Whalley, J.M.

Nucleic Acids Res. 16, 11303-11317, 1988

A/Title: Evolution of the herpes thymidine kinase: identification and comparison of the

A/Reference number: S01993; MUID:89083562; PMID:2849761

A/Accession: S01995

A/Molecule type: DNA

A/Residues: 1-352 <ROB>

A/Cross-references: UNIPROT:P09100; EMBL:X13209; NID:G59229; PIDD:CAA31599.1; PID:G59232

R/Telford, E.A.R.; Watson, M.S.; McBride, K.; Davison, A.J.

submitted to Genbank, March 1992

A/Description: The DNA sequence of equine herpesvirus-1.

A/Reference number: A36805

A/Accession: D36799

A/Molecule type: DNA

A/Residues: 1-352 <TEL>

A/Cross-references: GB:M8664; NID:G330791; PIDD:AB02474.1; PID:G330831

A/Experimental source: strain AD4P

R/Corrochano, L.M.; Madueno, F.; Field, H.J.; de la Fuente, R.

submitted to the EMBL Data Library, August 1992

A/Description: DNA sequence analysis of thymidine kinase defective mutants of equine her

A/Reference number: S25496

A/Accession: S25498

A/Molecule type: DNA

A/Residues: 1-352 <COR>

A/Cross-references: EMBL:X67961; NID:G59233; PIDD:CAA48144.1; PID:G59214

R/Telford, E.A.R.; Watson, M.S.; McBride, K.; Davison, A.J.

Virolology 189, 304-316, 1992

A/Title: The DNA sequence of equine herpesvirus-1.

A/Reference number: A41831; MUID:92295566; PMID:131606

A/Contents: annotation; possible protein-coding frames

A/Note: neither amino acid nor nucleotide sequence is given

R/Robertson, G.R.; Scott, N.A.; Miller, J.M.; Sabine, W.; Zheng, M.; Bell, C.W.; Whalley

DNA Seq. 1, 241-249, 1991

A/Title: Sequence characteristics of a gene in equine herpesvirus 1 homologous to glycof

A/Reference number: A56627; MUID:92216126; PMID:1666854

A/Accession: A56627

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 337-352 <RO2>

A/Cross-references: GB:S93400; NID:G59229

A/Experimental source: strain HVS 25A

A/Note: sequence extracted from NCBI backbone (NCBIN:93400, NCBI:P.93440)

C/Function: catalyzes the reversible phosphorylation of thymidine by ATP to produce t

C/Superfamily: herpesvirus thymidine kinase; herpesvirus thymidine kinase homology

C/Keywords: ATP; DNA biosynthesis; nucleotide binding; P-loop; phosphotransferase

F/25-310/Domain: herpesvirus thymidine kinase homology <HTK>

F/32-39/Region: nucleotide-binding motif A (P-loop)

F/34-138/Region: nucleotide-binding motif B

F/38/Binding site: ATP (Lys) #status predicted

Query Match 67.3%; Score 37; DB 1; Length 352;

Best Local Similarity 70.0%; Pred. No. 33;

Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

DB 171 PRE0GNTV 180

RESULT 11

K18ED4

Thymidine kinase (EC 2.7.1.21) - equine herpesvirus 4 (strain 1942)

C/Species: equine herpesvirus 4

C/Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 09-Jul-2004

C/Accession: A36657

R/Nicolson, L.; Cullinane, A.A.; Onions, D.E.

J. Gen. Virol. 71, 1801-1805, 1990

A/Title: The nucleotide sequence of the equine herpesvirus 4 thymidine kinase gene.

A/Reference number: A36657; MUID:90362067; PMID:2391500

A/Accession: A36657

A/Molecule type: DNA

A/Residues: 1-352 <NIC>

A/Cross-references: UNIPROT:P24425; GB:D14486; GB:D00684; NID:G221820; PIDD:BA03378.1;

C/Superfamily: herpesvirus thymidine kinase; herpesvirus thymidine kinase homology

C/Keywords: ATP; DNA biosynthesis; nucleotide binding; P-loop; phosphotransferase

F/25-310/Domain: herpesvirus thymidine kinase homology <HTK>

F/32-39/Region: nucleotide-binding motif A (P-loop)

F/32-39/Region: nucleotide-binding motif B

F/38/Binding site: ATP (Lys) #status predicted

Query Match 67.3%; Score 37; DB 1; Length 352;

Best Local Similarity 70.0%; Pred. No. 33;


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Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 1 PKYEGGNIV 10
   |:|||||
Db 171 PREPOGGNIV 180

RESULT 12
T42582
thymidine kinase (EC 2.7.1.21) - equine herpesvirus 4 (strain NS80567)
C:Species: equine herpesvirus 4
A:Variety: strain NS80567
C>Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 09-Jul-2004
C:Accession: T42582
R:Telord, B.A.; Watson, M.S.; Perry, J.; Cullinane, A.A.; Davison, A.J.
J. Gen. Virol. 79, 1197-1203, 1998
A:Title: The DNA sequence of equine herpesvirus-4.
A:Reference number: 222173; MUID:98264497; PMID:9603335
A:Accession: T42582
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-352 <TEL>
A:Cross-references: UNIPROT:Q39280; EMBL:AF030027; NID:92605953; PID:AC59555.1; PID:G2
A:Experimental source: strain NS80567
C:Genetics:
C:Superfamily: herpesvirus thymidine kinase; herpesvirus thymidine kinase homology
C:Keywords: ATP; DNA biosynthesis; P-loop; phosphotransferase

Query Match
Best Local Similarity 67.3%; Score 37; DB 2; Length 352;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 1 PKYEGGNIV 10
   |:|||||
Db 171 PREPOGGNIV 180

RESULT 13
S25497
thymidine kinase (EC 2.7.1.21) mutant PR3 - equine herpesvirus 1
C:Species: equine herpesvirus 1
C>Date: 09-Jun-1994 #sequence_revision 17-Mar-1997 #text_change 09-Jul-2004
C:Accession: S25497
R:Corrochano, L.M.; Madueno, F.; Field, H.J.; de la Fuente, R.
Submitted to the EMBL Data Library, August 1992
A:Description: DNA sequence analysis of thymidine kinase defective mutants of equine her
A:Reference number: S25496
A:Accession: S25497
A:Molecule type: DNA
A:Residues: 1-352 <COR>
A:Cross-references: UNIPROT:Q66596; EMBL:X67962; NID:G59211; PID:CAA48145.1; PID:G59212
C:Keywords: ATP; phosphotransferase

Query Match
Best Local Similarity 67.3%; Score 37; DB 4; Length 352;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 1 PKYEGGNIV 10
   |:|||||
Db 171 PREPOGGNIV 180

RESULT 14
C97258
sugar-binding periplasmic protein [imported] - Clostridium acetobutylicum
C:Species: Clostridium acetobutylicum
C>Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 09-Jul-2004
C:Accession: C97258
R:Nolling, U.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee,
J.; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.
J. Bacteriol. 183, 4823-4838, 2001
A:Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Cld
```

```
A:Reference number: A96900; MUID:21359325; PMID:21359325
A:Accession: C97258
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-432 <KUR>
A:Cross-references: UNIPROT:Q97941; GB:AE001437; PID:AAK0854.1; PID:G15025961; GSPDB:G
A:Experimental source: Clostridium acetobutylicum ATCC824
C:Genetics:
A:Gene: CAC2912

Query Match
Best Local Similarity 67.3%; Score 37; DB 2; Length 432;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 PKYEGGN 8
   |:|||||
Db 297 PAPEGGN 304

RESULT 15
E96649
hypothetical protein F19K23.21 [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C:Accession: E96649
R:Theologis, A.; Becker, J.R.; Palm, C.J.; Federpiehl, N.A.; Kaul, S.; White, O.; Alonso,
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;
ansen, N.F.; Hughes, B.; Huitar, L.
Nature 408, 816-820, 2000
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Malt, R.; Marziani,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A:Reference number: A6141; MUID:21016719; PMID:11130712
A:Accession: E96649
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-433 <STO>
A:Cross-references: UNIPROT:O04593; GB:AE005173; NID:92160151; PID:AA60773.1; GSPDB:GN
C:Genetics:
A:Gene: F19K23.21
A:Map position: 1
C:Superfamily: oryzasin; saposin repeat homology

Query Match
Best Local Similarity 67.3%; Score 37; DB 2; Length 433;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 1 PKYEGGNIV 10
   |:|||||
Db 235 PKSEGGNIV 244
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Search completed: October 22, 2005, 08:04:26
Job time : 13.45 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 22, 2005, 06:06:36 ; Search time 55.85 Seconds
(without alignments)
91.688 Million cell updates/sec

Title: US-10-731-238-71
Perfect score: 55
Sequence: 1 PKYEOGNTIV 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : UniProt_03 : *
1: uniprot_sprot : *
2: uniprot_trembl : *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	55	100.0	152	2	Q9AEP9	Q9AEP9 staphylococ
2	55	100.0	940	2	Q53682	Q53682 staphylococ
3	55	100.0	943	2	Q8NU08	Q8NU08 staphylococ
4	55	100.0	957	2	Q6G6H4	Q6G6H4 staphylococ
5	55	100.0	961	2	Q99RD3	Q99RD3 staphylococ
6	55	100.0	961	2	Q7A3J8	Q7A3J8 staphylococ
7	55	100.0	1015	2	Q8NU07	Q8NU07 staphylococ
8	55	100.0	1015	2	Q6G6H3	Q6G6H3 staphylococ
9	55	100.0	1018	1	FNBA_STNAU	FNBA_STNAU staphylococ
10	55	100.0	1038	2	Q99RD2	Q99RD2 staphylococ
11	55	100.0	1038	2	Q7A3J7	Q7A3J7 staphylococ
12	54	98.2	965	2	Q6GDU5	Q6GDU5 staphylococ
13	42	76.4	676	2	Q7RNV6	Q7RNV6 plasmodium
14	40	72.7	103	2	Q6FRR9	Q6FRR9 candida gla
15	40	72.7	189	2	Q6BVY8	Q6BVY8 debaromyce
16	40	72.7	591	2	Q8KMW4	Q8KMW4 clostridium
17	39	70.9	606	2	Q7QBT6	Q7QBT6 anopheles g
18	38	69.1	62	2	Q99TP8	Q99TP8 staphylococ
19	38	69.1	62	2	Q7A5A8	Q7A5A8 staphylococ
20	38	69.1	189	2	Q9K9Q5	Q9K9Q5 bacillus ha
21	38	69.1	229	2	Q8NM97	Q8NM97 staphylococ
22	38	69.1	229	2	Q6G8W7	Q6G8W7 staphylococ
23	38	69.1	329	2	Q9KWT5	Q9KWT5 thermotoga
24	38	69.1	383	2	Q939R5	Q939R5 bacillus th
25	38	69.1	699	2	Q7NNS3	Q7NNS3 gloeobacter
26	38	69.1	743	2	Q75G15	Q75G15 oryza sativ
27	38	69.1	788	2	Q9YMG8	Q9YMG8 lymantria d
28	37	67.3	238	2	Q283Z7	Q283Z7 chaeoglob
29	37	67.3	247	2	Q7W773	Q7W773 bordetella
30	37	67.3	247	2	Q7W1J8	Q7W1J8 bordetella
31	37	67.3	340	2	Q7QKC9	Q7QKC9 anopheles g

32	37	67.3	352	1	KITH_EHVLB	P09100 equine herp
33	37	67.3	352	1	KITH_EHVA	P24425 equine herp
34	37	67.3	352	2	O392S0	O39280 equid herpe
35	37	67.3	352	2	O66596	O66596 equid herpe
36	37	67.3	352	2	O66673	O66673 equid herpe
37	37	67.3	413	2	Q9M026	Q9M026 arabidopsis
38	37	67.3	432	2	Q97F41	Q97F41 clostridium
39	37	67.3	433	2	O04593	O04593 arabidopsis
40	37	67.3	513	2	Q8VYL3	Q8VYL3 arabidopsis
41	37	67.3	563	2	Q939U0	Q939U0 rhodovulum
42	37	67.3	563	2	Q89PG5	Q89PG5 bradyrhizob
43	37	67.3	564	2	P72177	P72177 paracoccus
44	37	67.3	572	2	Q8XUD8	Q8XUD8 ralsstonia s
45	37	67.3	583	2	Q9W145	Q9W145 drosophila

ALIGNMENTS

```

RESULT 1
Q9AEP9 ID Q9AEP9 PRELIMINARY; PRT; 152 AA.
AC Q9AEP9;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Fibronectin-binding protein (Fragment).
GN Name=fnb;
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1280;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=2146681; PubMed=11349044;
RX DOI=10.1128/IAI.69.6.3791-3799.2001;
RA Rice K., Huesca M., Vaz D., McGavin M.J.;
RT "Variance in fibronectin binding and fnb locus polymorphisms in a
RT Staphylococcus aureus: identification of antigenic variation in a
RT fibronectin binding protein adhesin of the epidemic CMRSA-1 strain of
RT methicillin-resistant S. aureus."
RL Infect. Immun. 69:3791-3799(2001).
DR EMBL; AY029184; AK31588.1; -.
FT NON_TER
FT 152
SQ SEQUENCE 152 AA; 17193 MW; CFA3913CB11C025 CRC64;

Query Match 100.0%; Score 55; DB 2; Length 152;
Best Local Similarity 100.0%; Pred. No. 0.014; Mismatches 0; Indels 0; Gaps 0;
Matches 10; Conservative 0;

Qy 1 PKYEOGNTIV 10
Db 17 PKYEOGNTIV 26

RESULT 2
Q53682 ID Q53682 PRELIMINARY; PRT; 940 AA.
AC Q53682;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Fibronectin binding protein B.
GN Name=fnbB;
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1280;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=8325-4;
RX MEDLINE=92111475; PubMed=1837266;
RA Jonsson K., Sigmas C., Muller H.P., Lindberg M.;

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RT      "Two different genes encode fibronectin binding proteins in
RT      Staphylococcus aureus. The complete nucleotide sequence and
RT      characterization of the second gene."
RT      Eur. J. Biochem. 202;1041-1048(1991).
CC      -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC      an amide bond (By similarity).
DR      EMBL: X62992; CAA44726.1; -.
DR      PIR: S19702; S19702.
DR      HSP: Q53653; I1N67.
DR      GO: GO:0009986; C:cell surface; IEA.
DR      GO: GO:0005618; C:cell wall; IEA.
DR      GO: GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR      GO: GO:0016020; C:membrane; IEA.
DR      GO: GO:0007155; P:cell adhesion; IEA.
DR      InterPro: IPR008966; Adhes_bact.
DR      InterPro: IPR004237; Fn_bind.
DR      InterPro: IPR005877; Gpos_YsIRK.
DR      Pfam: PF02986; Fn_bind_2; Gram_pos_anchor.
DR      Pfam: PF00746; Gram_pos_anchor; 1.
DR      Pfam: PF04650; YsIRK_signal; 1.
DR      TIGRFAMs: TIGR01167; LPTXG_anchor; 1.
DR      TIGRFAMs: TIGR01168; YsIRK_signal; 1.
DR      PROSITE: PS50847; GRAM_POS_ANCHORING; 1.
KW      Cell wall; Peptidoglycan-anchor.
SQ      SEQUENCE 940 AA; 10355 MW; E35FBBCA907AE345 CRC64;

Query Match      100.0%; Score 55; DB 2; Length 940;
Best Local Similarity 100.0%; Pred. No. 0.11;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 PKYEOGNIV 10
      |||||
Db      698 PKYEOGNIV 707

RESULT 3
ID      Q8NU08      PRELIMINARY;      PRT;      943 AA.
AC      Q8NU08;
DT      01-OCT-2002 (TREMBlrel. 22, Created)
DT      01-OCT-2002 (TREMBlrel. 22, Last sequence update)
DT      01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE      FnbB protein.
GN      Name=fnbB; OrderedLocustNames=fnbB2420;
OS      Staphylococcus aureus (strain MW2).
OC      Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX      NCBI_TaxId=196620;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN=MW2;
RC      MEDLINE=22040717; PubMed=12044378; DOI=10.1016/S0140-6736(02)08713-5;
RA      Baba T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Oguchi A.,
RA      Nagai Y., Iwano N., Amano K., Naito T., Kuroda H., Cui L.,
RA      Yamamoto K., Hiramoto K.;
RT      "Genome and virulence determinants of high virulence community-
RT      acquired MRSA."
RT      Lancet 359;1819-1827(2002).
CC      -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC      an amide bond (By similarity).
DR      EMBL: AP004830; BAB96285.1; -.
DR      HSP: Q53653; I1N67.
DR      GO: GO:0009986; C:cell surface; IEA.
DR      GO: GO:0005618; C:cell wall; IEA.
DR      GO: GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR      GO: GO:0016020; C:membrane; IEA.
DR      GO: GO:0007155; P:cell adhesion; IEA.
DR      InterPro: IPR008966; Adhes_bact.
DR      InterPro: IPR004237; Fn_bind.
DR      InterPro: IPR005877; Gpos_YsIRK.
DR      Pfam: PF02986; Fn_bind_1.
DR      Pfam: PF00746; Gram_pos_anchor; 1.

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DR      Pfam: PF04650; YsIRK_signal; 1.
DR      TIGRFAMs: TIGR01167; LPTXG_anchor; 1.
DR      TIGRFAMs: TIGR01168; YsIRK_signal; 1.
DR      PROSITE: PS50847; GRAM_POS_ANCHORING; 1.
KW      Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ      SEQUENCE 943 AA; 104537 MW; DA8A5F3194E1B6A CRC64;

Query Match      100.0%; Score 55; DB 2; Length 943;
Best Local Similarity 100.0%; Pred. No. 0.11;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 PKYEOGNIV 10
      |||||
Db      705 PKYEOGNIV 714

RESULT 4
ID      Q6G6H4      PRELIMINARY;      PRT;      957 AA.
AC      Q6G6H4;
DT      05-JUL-2004 (TREMBlrel. 27, Created)
DT      05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT      05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE      Fibronectin-binding protein.
GN      Name=fnbB; OrderedLocustNames=fnbB2387;
OS      Staphylococcus aureus (strain MSSA476).
OC      Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX      NCBI_TaxId=282459;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      PubMed=15213324; DOI=10.1073/pnas.0402521101;
RA      Holden M.T.G., Fell E.J., Lindsey J.A., Peacock S.J., Day N.P.J.,
RA      Enright M.C., Foster T.J., Moore C.E., Hurst L., Atkin R., Barron A.,
RA      Bason N., Bentley S.D., Chillingworth C., Chillingworth T.,
RA      Churcher C., Clark L., Cotton C., Cronin A., Doggett J., Dowd L.,
RA      Felwell T., Hance Z., Harris B., Hauser H., Holroyd S., Jagsels K.,
RA      James K.D., Leonard N., Line A., Mayes R., Moule S., Mungall K.,
RA      Ormond D., Quail M.A., Rabinowitch E., Rutherford K.M., Sanders M.,
RA      Sharp S., Simmonds M., Stevens K., Whitehead S., Barrett B.G.,
RA      Spratt B.G., Parkhill J.;
RT      "Complete genomes of two clinical Staphylococcus aureus strains:
RT      evidence for the rapid evolution of virulence and drug resistance."
RT      Proc. Natl. Acad. Sci. U.S.A. 101;9786-9791(2004).
CC      -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC      an amide bond (By similarity).
DR      EMBL: BX571857; CAG4201.1; -.
DR      GO: GO:0009986; C:cell surface; IEA.
DR      GO: GO:0005618; C:cell wall; IEA.
DR      GO: GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR      GO: GO:0016020; C:membrane; IEA.
DR      GO: GO:0007155; P:cell adhesion; IEA.
DR      InterPro: IPR008966; Adhes_bact.
DR      InterPro: IPR004237; Fn_bind.
DR      InterPro: IPR005877; Gpos_YsIRK.
DR      InterPro: IPR001899; Gram_pos_anchor.
DR      Pfam: PF02986; Fn_bind_1.
DR      Pfam: PF00746; Gram_pos_anchor; 1.
DR      Pfam: PF04650; YsIRK_signal; 1.
DR      TIGRFAMs: TIGR01167; LPTXG_anchor; 1.
DR      TIGRFAMs: TIGR01168; YsIRK_signal; 1.
DR      PROSITE: PS50847; GRAM_POS_ANCHORING; 1.
KW      Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ      SEQUENCE 957 AA; 105980 MW; 28F8BA7FFDFP3BEAF CRC64;

Query Match      100.0%; Score 55; DB 2; Length 957;
Best Local Similarity 100.0%; Pred. No. 0.11;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 PKYEOGNIV 10
      |||||
Db      705 PKYEOGNIV 714

```

RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
RA Cui L., Oguchi H., Aoki K.-I., Nagai Y., Iian J.-O., Ito T.,
RA Kanamori M., Matsunaru H., Maruyama A., Murakami H., Hoooyama A.,
RA Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
RA Sekitaniizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
RA Kanehisa M., Yamanishi A., Oshima K., Furuya K., Yoshino C., Shiba T.,
RA Hattori M., Ogasawara N., Hayashi H., Hiratacu K.,
RT "Whole genome sequencing of methicillin-resistant *Staphylococcus*
RT aureus".
RL Lancel 357:1225-1240(2001).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC an amide bond (By similarity).
DR EMBL: AP003137; BAB3593.1; -.
DR GO: GO:0009986; C:cell surface; IEA.
DR GO: GO:0005618; C:cell wall; IEA.
DR GO: GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO: GO:0016020; C:membrane; IEA.
DR GO: GO:0007155; P:cell adhesion; IEA.
DR InterPro: IPR008966; Adhes_bact.
DR InterPro: IPR004237; Fn_bind.
DR InterPro: IPR005877; Gpos_YsIRK.
DR InterPro: IPR001899; Gram_pos_anchor.
DR Pfam: PF02986; Fn_bind_1.
DR Pfam: PF00746; Gram_pos_anchor; 1.
DR Pfam: PF04650; YsIRK_signal; 1.
DR TIGRFAMs: TIGR01167; LpxTG_anchor; 1.
DR TIGRFAMs: TIGR01168; YsIRK_signal; 1.
DR PROSITE: PS50847; GRAM_POS_ANCHORING; 1.
DR Cell wall, complete proteome; Peptidoglycan-anchor.
SQ SEQUENCE 961 AA; 106010 MW; 364940f0884EA4101 CRC64;

Query Match 100.0%; Score 55; DB 2; Length 961;
Best Local Similarity 100.0%; Pred. No. 0.11;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PKYEGGNIV 10
|||
Db 709 PKYEGGNIV 718

RESULT 7
Q8NUU7 PRELIMINARY; PRT; 1015 AA.
ID Q8NUU7
AC Q8NUU7;
DT 01-OCT-2002 (TREMBlrel. 22, Created)
DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Fnd protein.
GN Name=fnd; OrderedLocustNames=MW2421;
OS *Staphylococcus aureus* (strain MW2).
OC Bacteria; Firmicutes; Bacillales; *Staphylococcus*.
OX NCBI_TaxId=196620;
[1]
RN SEQUENCE FROM N.A.
RP STRAIN=MW2;
RC MEDLINE=22040717; PubMed=12044378; DOI=10.1016/S0140-6736(02)08713-5;
RA Baba T., Takuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Oguchi A.,
RA Nagai Y., Iwano N., Asano K., Naito T., Kuroda H., Cui L.,
RA Yamamoto K., Hiratacu K.,
RT "Genome and virulence determinants of high virulence community-
RT acquired MRSA".
RL Lancel 359:1819-1827(2002).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC an amide bond (By similarity).
DR EMBL: AP004830; BAB96286.1; -.
DR GO: GO:0009986; C:cell surface; IEA.
DR GO: GO:0005618; C:cell wall; IEA.
DR GO: GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO: GO:0016020; C:membrane; IEA.
DR GO: GO:0007155; P:cell adhesion; IEA.
DR InterPro: IPR008966; Adhes_bact.
DR InterPro: IPR004237; Fn_bind.
DR InterPro: IPR005877; Gpos_YsIRK.

DR InterPro: IPR001899; Gram_pos_anchor.
 DR Pfam: PF02986; Fn_bind; 1.
 DR Pfam: PF00746; Gram_pos_anchor; 1.
 DR Pfam: PF04650; YSIRK_signal; 1.
 DR TIGRFAMs: TIGR01167; LPXTG_anchor; 1.
 DR TIGRFAMs: TIGR01167; YSIRK_signal; 1.
 DR PROSITE: PS50847; GRAM_POS_ANCHORING; 1.
 DR Cell wall; Complete proteome; Peptidoglycan-anchor.
 KW SEQUENCE 1015 AA; 111145 MW; D0F9281BB64D442D CRC64;

Query Match 100.0%; Score 55; DB 2; Length 1015;
 Best Local Similarity 100.0%; Pred. No. 0.11;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PKYEOGGINV 10
 DB 763 PKYEOGGINV 772

RESULT 8
 ID Q6G6H3 PRELIMINARY; PRT; 1015 AA.
 AC Q6G6H3;
 DT 05-JUL-2004 (TREMBLrel. 27, Created)
 DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
 DE Fibronectin-binding protein.
 GN OrderedLocNames=SAS2388;
 OS Staphylococcus aureus (strain MSSA476).
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 OX NCBI_TaxID=282459;
 RX [1]

SEQUENCE FROM N.A.
 DR Published:15213324; DOI=10.1073/pnas.0402521101;
 RA Holden M.T.G., Fell E.J., Lindsay J.A., Peacock S.J., Day N.P.J.,
 Baeson N., Bentley S.D., Chillingworth T.,
 Churcher C., Clark L., Cotton C., Cronin A., Doggett J., Dowd L.,
 Felwell T., Hance Z., Harris B., Hauser H., Holtroyd S., Jagels K.,
 Jones K.D., Leonard N., Line A., Mayes R., Moule S., Mungall K.,
 Nd D., Quail M.A., Rabinowitch B., Rutherford K.M., Sanders M.,
 S.S., Simmonds M., Stevens K., Whitehead S., Barrett B.G.,
 DR J.G., Parkhill J.;
 DR Genomes of two clinical Staphylococcus aureus strains:
 DR GO: the rapid evolution of virulence and drug resistance.";
 DR GO: Cad. Sci. U.S.A. 101:9786-9791(2004).
 DR GO: GO:04 (By similarity).
 DR InterPro: IPR001899; Fn_bind; 1.
 DR InterPro: IPR001899; Fn_bind; 1.
 DR InterPro: IPR001899; Fn_bind; 1.
 DR InterPro: IPR001899; Fn_bind; 1.
 DR Pfam: PF02986; Fn_bind; 1.
 DR Pfam: PF00746; Gram_pos_anchor; 1.
 DR TIGRFAMs: TIGR01167; LPXTG_anchor; 1.
 DR TIGRFAMs: TIGR01167; YSIRK_signal; 1.
 DR PROSITE: PS50847; GRAM_POS_ANCHORING; 1.
 DR Cell wall; Complete proteome; Peptidoglycan-anchor.
 KW SEQUENCE 1015 AA; 111145 MW; D0F9281BB64D442D CRC64;

Query Match 100.0%; Score 55; DB 2; Length 1015;
 Best Local Similarity 100.0%; Pred. No. 0.11;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 763 PKYEOGGINV 772

RESULT 9
 ID FNBA_STPAU STANDARD; PRT; 1018 AA.
 AC FNBA_STPAU;
 DT 01-APR-1990 (Rel. 14, Created)
 DT 01-APR-1990 (Rel. 14, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Fibronectin-binding protein precursor (FNBP).
 GN Name=fnbp;
 OS Staphylococcus aureus.
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 OX NCBI_TaxID=1280;
 RX [1]

SEQUENCE FROM N.A.
 RC STRAIN=NTC 8325-4;
 RX MEDLINE=89098998; PubMed=2521391;
 RA Signaes C., Raucel G., Joensson K., Lindgren P.-E.,
 RA Anantharamaiah G.M., Hoeck M., Lindberg M.;
 RT "Nucleotide sequence of the gene for a fibronectin-binding protein
 from Staphylococcus aureus: use of this peptide sequence in the
 synthesis of biologically active peptides.";
 RL Proc. Natl. Acad. Sci. U.S.A. 86:699-703(1989).
 CC -! FUNCTION: The ability of bacteria to bind fibronectin has been
 proposed as a virulence factor enabling bacteria to colonize wound
 tissues and blood clots. Binding of plasma fibronectin to the
 bacterial surface might block adhesion receptors on S.aureus, thus
 representing an important defense mechanism against tissue
 invasion.
 CC -! SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
 an amide bond (potential).
 CC CC

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 CC -----

DR EMBL: J04151; AAA26632.1; -;
 DR InterPro: IPR004237; Fn_bind.
 DR InterPro: IPR005877; Gpos_YSIRK.
 DR InterPro: IPR001899; Gram_pos_anchor.
 DR Pfam: PF02986; Fn_bind; 1.
 DR Pfam: PF00746; Gram_pos_anchor; 1.
 DR TIGRFAMs: TIGR01167; LPXTG_anchor; 1.
 DR TIGRFAMs: TIGR01167; YSIRK_signal; 1.
 DR PROSITE: PS50847; GRAM_POS_ANCHORING; 1.
 DR Cell adhesion; Cell wall; Peptidoglycan-anchor; Repeat; Signal;
 KW Virulence.
 FT SIGNAL 1 36
 FT CHAIN 37 985
 FT PROPEP 986 1018
 FT REPEAT 545 574
 FT REPEAT 575 604
 FT DOMAIN 745 878
 FT REPEAT 745 782
 FT REPEAT 783 820
 FT REPEAT 821 859
 FT REPEAT 860 878
 FT DOMAIN 879 948
 FT REPEAT 879 892
 FT REPEAT 893 906
 FT REPEAT 907 920
 FT REPEAT 921 934
 FT REPEAT 935 948
 FT SITE 982 986
 FT MOD_RES 985 985
 FT
 Fibronectin-binding protein.
 Removed by sortase (potential).
 B-1.
 B-2.
 4 x approximate tandem repeats,
 fibronectin-binding domain.
 D-1.
 D-2.
 D-3.
 D-4 (incomplete).
 5 x tandem repeats, Pro-rich (WR).
 WR 1.
 WR 2.
 WR 3.
 WR 4.
 WR 5.
 LPXTG sorting signal (potential).
 Pentaglycyl murein peptidoglycan amidated

FT SEQUENCE 1018 AA; 111780 MW; 58175E0020E81FLF CRC64;
 SQ Query Match 100.0%; Score 55; DB 1; Length 1018;
 Best Local Similarity 100.0%; Pred. No. 0.11;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PKYEOGGINIV 10
 DB 762 PKYEOGGINIV 771

RESULT 10
 Q99RD2 PRELIMINARY; PRT; 1038 AA.
 ID Q99RD2;
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)
 DT 01-JUN-2004 (TrEMBLrel. 17, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Fibronectin-binding protein homolog.
 GN Name=fnb; OrderedlocusNames=SAV2503;
 OS Staphylococcus aureus (strain Mu50 / ATCC 700699).
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 OX NCBI_TaxId=158878;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=MU50 / ATCC 700699;
 RX MEDLINE=21311952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2;
 RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
 RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Iian J.-Q., Ito T.,
 RA Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,
 RA Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
 RA Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
 RA Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
 RA Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
 RT "Whole genome sequencing of methicillin-resistant Staphylococcus
 RT aureus."
 RL Lancet 357:1225-1240(2001).
 CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
 CC an amide bond (By similarity).
 DR EMBL: AB003365; BAB5865.1; -.
 DR PIR: H90053; H90053.
 DR GO: GO:0009986; C:cell surface; IEA.
 DR GO: GO:0005618; C:cell wall; IEA.
 DR GO: GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
 DR GO: GO:0016020; C:membrane; IEA.
 DR GO: GO:0007155; P:cell adhesion; IEA.
 DR InterPro: IPR008966; Adhes_bact.
 DR InterPro: IPR004237; GPos_YsIRK.
 DR InterPro: IPR005877; GPos_YsIRK.
 DR InterPro: IPR001899; Gram_pos_anchor.
 DR Pfam: PF02986; Fm_bind_1.
 DR Pfam: PF00746; Gram_pos_anchor; 1.
 DR Pfam: PF04650; YsIRK_signal; 1.
 DR TIGRfams: TIGR01167; LpXTG_anchor; 1.
 DR TIGRfams: TIGR01168; YsIRK_signal; 1.
 DR PROSITE: PSS0847; GRAM_POS_ANCHORING; 1.
 KW Cell wall; Complete proteome; Peptidoglycan-anchor.
 SQ SEQUENCE 1038 AA; 113618 MW; 666BF6BF2BFEB12 CRC64;

Query Match 100.0%; Score 55; DB 2; Length 1038;
 Best Local Similarity 100.0%; Pred. No. 0.12;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PKYEOGGINIV 10
 DB 758 PKYEOGGINIV 767

RESULT 11
 Q7A3J7 PRELIMINARY; PRT; 1038 AA.
 ID Q7A3J7
 AC Q7A3J7;

DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Fnb protein.
 GN Name=fnb; OrderedlocusNames=SA2291;
 OS Staphylococcus aureus (strain N315).
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 OX NCBI_TaxId=158879;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21311952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2;
 RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
 RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Iian J.-Q., Ito T.,
 RA Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,
 RA Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
 RA Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
 RA Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
 RA Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
 RT "Whole genome sequencing of methicillin-resistant Staphylococcus
 RT aureus."
 RL Lancet 357:1225-1240(2001).
 CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
 CC an amide bond (By similarity).
 DR EMBL: AP003137; BAB43594.1; -.
 DR GO: GO:0009986; C:cell surface; IEA.
 DR GO: GO:0005618; C:cell wall; IEA.
 DR GO: GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
 DR GO: GO:0016020; C:membrane; IEA.
 DR GO: GO:0007155; P:cell adhesion; IEA.
 DR InterPro: IPR008966; Adhes_bact.
 DR InterPro: IPR004237; Fm_bind.
 DR InterPro: IPR005877; GPos_YsIRK.
 DR InterPro: IPR001899; Gram_pos_anchor.
 DR Pfam: PF02986; Fm_bind_1.
 DR Pfam: PF00746; Gram_pos_anchor; 1.
 DR Pfam: PF04650; YsIRK_signal; 1.
 DR TIGRfams: TIGR01167; LpXTG_anchor; 1.
 DR TIGRfams: TIGR01168; YsIRK_signal; 1.
 DR PROSITE: PSS0847; GRAM_POS_ANCHORING; 1.
 KW Cell wall; Complete proteome; Peptidoglycan-anchor.
 SQ SEQUENCE 1038 AA; 113618 MW; 666BF6BF2BFEB12 CRC64;

Query Match 100.0%; Score 55; DB 2; Length 1038;
 Best Local Similarity 100.0%; Pred. No. 0.12;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PKYEOGGINIV 10
 DB 758 PKYEOGGINIV 767

RESULT 12
 Q6GDUS PRELIMINARY; PRT; 965 AA.
 ID Q6GDUS
 AC Q6GDUS;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Fibronectin-binding protein.
 GN Name=fnbA; OrderedlocusNames=SA2580;
 OS Staphylococcus aureus (strain MRSA252).
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 OX NCBI_TaxId=282458;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX PubMed=15213324; DOI=10.1073/pnas.0402521101;
 RA Holden M.T.G., Fell E.J., Lindsey J.A., Peacock S.J., Day N.P.J.,
 RA Enright M.C., Foster T.J., Moore C.E., Hurst L., Aktin R., Barron A.,
 RA Bason N., Bentley S.D., Chillingworth C., Chillingworth T.,
 RA Churcher C., Clark L., Cotton C., Cronin A., Doggett J., Dowd L.,
 RA Felwell T., Hance Z., Harris B., Hauser H., Holtroyd J., Jagsels K.,
 RA James K.D., Leonard N., Line A., Mayes R., Mungall K.,
 RA Ormond D., Quail M.A., Rabinowitsch E., Rutherford K.M., Sanders M.,

RA Sharp S., Simmonds M., Stevens K., Whitehead S., Barrett B.G.,
 RA Spratt B.G., Parkhill J.,
 RT "Complete genomes of two clinical *Staphylococcus aureus* strains:
 RT evidence for the rapid evolution of virulence and drug resistance."
 RL Proc. Natl. Acad. Sci. U.S.A. 101:9786-9791(2004).
 CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
 CC an amide bond (By similarity).
 DR EMBL: BK571856; CACG41560.1; -;
 DR GO: GO:0009986; C:cell surface; IEA.
 DR GO: GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
 DR GO: GO:0016020; C:membrane; IEA.
 DR GO: GO:0007155; P:cell adhesion; IEA.
 DR InterPro: IPR008966; Adhes. bact.
 DR InterPro: IPR004237; Fn_bind.
 DR InterPro: IPR005877; Gpoe_YsIRK.
 DR InterPro: IPR001899; Gram_pos_anchor.
 DR Pfam: PF02986; Fn_bind; 1.
 DR Pfam: PF00746; Gram_pos_anchor; 1.
 DR TIGRFAMs: TIGR01167; LPXG_anchor; 1.
 DR TIGRFAMs: TIGR01168; YsIRK_signal; 1.
 DR PROSITE: PS50847; GRAM_POS_ANCHORING; 1.
 DR Cell wall; Complete proteome; Peptidoglycan-anchor.
 SQ SEQUENCE 965 AA; 105691 MW; 2982E132164D0551 CRC64;

Query Match 98.2%; Score 54; DB 2; Length 965;
 Best Local Similarity 90.0%; Pred. No. 0.17;
 Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 PKYEOGNIV 10
 DB 765 PKYEOGNII 774
 |||||
 |||||

RESULT 13
 O7RNV6 PRELIMINARY; PRT; 676 AA.
 ID O7RNV6
 AC O7RNV6
 DT 01-MAR-2004 (TREMBlrel. 26, Created)
 DT 01-MAR-2004 (TREMBlrel. 26, Last sequence update)
 DE Hypothetical protein.
 GN Name=PY01709;
 OS Plasmodium yoelii yoelii.
 OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
 OX NCBI_TaxID=73239;
 RX SEQUENCE FROM N.A.
 RC STRAIN=17XNL;
 RA PubMed:1236865; DOI=10.1038/nature01099;
 RA Carlton J.M., Angluoli S.V., Suh B.B., Kooij T.W., Petrea M.,
 RA Silva J.C., Ermolaeva M.D., Allen J.E., Seliengut J.D., Koo H.L.,
 RA Peterson J.D., Pop M., Kosack D.S., Shumway M.F., Bidwell S.L.,
 RA Shallow S.J., van Aken S.E., Riedmuller S.B., Feldblyum T.V.,
 RA Cho J.K., Quackenbush J., Sedegah M., Shoib A., Cummings L.M.,
 RA Florens L., Yates F.R. III, Raine J.D., Sinden R.E., Harris M.A.,
 RA Cunningham D.A., Freilser P.R., Bergman L.W., Vaideya A.B.,
 RA van Lin L.H., Janse C.J., Waters A.P., Smith H.O., White O.R.,
 RA Salzberg S.L., Venter J.C., Fraser C.M., Hoffman S.L., Gardner M.J.,
 RA Carucci D.J.;
 RA "Genome sequence and comparative analysis of the model rodent malaria
 RT parasite *Plasmodium yoelii yoelii*.";
 RL Nature 419:512-519(2002).
 CC -1- SIMILARITY: Contains 1 RING-type zinc finger.
 CC -1- CAUTION: The sequence shown here is derived from an
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.
 DR EMBL: AABL01000462; EAA21073.1; -;
 DR GO: GO:0000151; C:ubiquitin ligase complex; IEA.
 DR GO: GO:0004842; F:ubiquitin-protein ligase activity; IEA.
 DR GO: GO:0008270; F:zinc ion binding; IEA.
 DR GO: GO:0016567; P:protein ubiquitination; IEA.
 DR InterPro: IPR001841; Znf_ring.

DR Pfam: PF00097; zF-C3HC4; 1.
 DR PROSITE: PS50089; ZF_RING_2; 1.
 KW Hypothetical protein; Metal-binding; Zinc; Zinc-finger.
 SQ SEQUENCE 676 AA; 79173 MW; 1AB74A2C72F5E55D0 CRC64;

Query Match 76.4%; Score 42; DB 2; Length 676;
 Best Local Similarity 88.9%; Pred. No. 27;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 PKYEOGNII 9
 DB 118 PKYEOGNII 126
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 |||||

RESULT 14
 O6FR9 PRELIMINARY; PRT; 103 AA.
 ID O6FR9
 AC O6FR9
 DT 05-JUL-2004 (TREMBlrel. 27, Created)
 DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
 DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
 DE Similar to tr|Q06011|Saccharomyces cerevisiae YLR390w ECM19.
 GN ORFNames=CAGL0064359;
 OS Candida glabrata CBS138.
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; mitosporic Saccharomycetales; Candida.
 OX NCBI_TaxID=284593;
 RN (1)
 RC SEQUENCE FROM N.A.
 RP STRAIN=CBS138;
 RG Genolevures;
 RA Dujon B., Sherman D., Fischer G., Durrens P., Casaregola S.,
 RA Lafontaine I., de Montigny J., Marck C., Neuvéglise C., Talla E.,
 RA Goffard N., Frangeul L., Aigle M., Anthouard V., Babour A., Barre V.,
 RA Barnay S., Blanchin S., Beckerich J.M., Beyne E., Bleykasten C.,
 RA Boisarme A., Boyer J., Catolico L., Confanetra F., de Daruvar A.,
 RA Despons L., Fabre E., Fairhead C., Ferry-Dumazet H., Groppi A.,
 RA Hantreya F., Hennequin C., Jauniaux N., Joyet P., Kachouri R.,
 RA Kerrest A., Kozul R., Lemaire M., Lesur I., Ma L., Muller H.,
 RA Nicoud J.M., Nikolski M., Oztas S., Ozier-Kalogeropoulos O.,
 RA Pellenz S., Pottier S., Richard G.F., Straub M.L., Suleau A.,
 RA Swenne D., Tekala F., Wesolowski-Louvel M., Westhof E., Wirth B.,
 RA Zenlou-Meyer M., Zivanovic I., Bojotin-Fukuhara M., Thierry A.,
 RA Bouchier C., Caudron B., Scarpelli C., Gallardin C., Weissenbach J.,
 RA Wincker P., Souciet J.L.;
 RT "Genome evolution in yeasts."
 RL Nature 430:35-44(2004).
 RL EMBL: CR380954; CAG60008.1; -;
 SQ SEQUENCE 103 AA; 10536 MW; B4C690F2C8B26F0 CRC64;

Query Match 72.7%; Score 40; DB 2; Length 103;
 Best Local Similarity 60.0%; Pred. No. 8.2;
 Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 1 PKYEOGNIV 10
 DB 48 PKYEDGNLV 57
 |||||
 |||||

RESULT 15
 O6BY8 PRELIMINARY; PRT; 189 AA.
 ID O6BY8
 AC O6BY8
 DT 25-OCT-2004 (TREMBlrel. 28, Created)
 DT 25-OCT-2004 (TREMBlrel. 28, Last sequence update)
 DT 25-OCT-2004 (TREMBlrel. 28, Last annotation update)
 DE Similar to CA4114|IPF7704 Candida albicans IPF7704 of unknown
 DE function.
 GN ORFNames=DEHAB15829;
 OS Debaryomyces hananell CBS767.
 OS Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Saccharomycetales; Debaryomyces.
 OX NCBI_TaxID=284592;

```

RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CBST767;
RG Genolevures;
RA Dujon B., Sherman D., Fischer G., Durrens P., Casaregola S., Talla E.,
RA Latourelle I., de Montigny J., Marck C., Neuvéglise C., Talla E.,
RA Goffard N., Frangoul L., Aigle M., Anthouard V., Babour A., Barbe V.,
RA Barnay S., Blanchin S., Beckerich J.M., Beyne E., Bleykasten C.,
RA Boisrame A., Boyer J., Catolico L., Confantolero F., de Daruvar A.,
RA Despons L., Fabre E., Fairhead C., Ferry-Dumazet H., Groppi A.,
RA Hantay F., Hennequin C., Jauriaux N., Joyet P., Kachouri R.,
RA Kerrest A., Koszul R., Lemaire M., Lesur I., Ma L., Muller H.,
RA Nicoud J.M., Nikolski M., Ozias S., Ozer-Kalogeropoulos O.,
RA Pellenz S., Potier S., Richard G.F., Straub M.L., Suleau A.,
RA Swenemene D., Tekala F., Wesolowski-Louvel M., Westhof E., Wirth B.,
RA Zenlou-Meyer M., Zivanovic I., Bolotin-Fukuhara M., Thierry A.,
RA Bouchier C., Caudron B., Scarpelli C., Gallardin C., Weisenbach J.,
RA Wincker P., Souciet J.L.;
RT "Genome evolution in yeasts.";
RL Nature 430:35-44(2004).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=CBST767;
RA Genoscope; (JUL-2004) to the EMBL/GenBank/DBJ databases.
RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; CR382134; CAG85645.1; -.
SQ SEQUENCE 189 AA; 22341 MW; 33881FCE4E78EA03 CRC64;

Query Match 72.7%; Score 40; DB 2; Length 189;
Best Local Similarity 60.0%; Pred. No. 16;
Matches 6; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 PKYEGGNTY 10
|.:|:|:|:|:|:|:
Db 31 PKYKGGNTL 40

```

Search completed: October 22, 2005, 08:00:35
 Job time : 56.85 secs

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OM protein - protein search, using sw model

Run on: October 25, 2005, 20:21:18 ; Search time 63.2 Seconds
(without alignments)
61.196 Million cell updates/sec

Title: US-10-731-238-72
Perfect score: 53
Sequence: 1 YEOGNIYDI 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:*

1: geneseqp1980s:*
2: geneseqp1900s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	53	100.0	10	2	AAW65728
2	53	100.0	38	2	AAW65692
3	53	100.0	38	2	AAW65695
4	53	100.0	38	2	AAW65696
5	53	100.0	38	2	AAW65697
6	53	100.0	38	2	AAW65694
7	53	100.0	38	2	AAW65691
8	53	100.0	38	2	AAW65661
9	53	100.0	38	2	AAW65698
10	53	100.0	38	2	AAW65712
11	53	100.0	39	2	AAW65712
12	53	100.0	113	2	AAW65698
13	53	100.0	130	2	AAW65698
14	53	100.0	130	2	AAW65698
15	53	100.0	130	2	AAW65698
16	53	100.0	130	2	AAW65698
17	53	100.0	134	2	AAW65698
18	53	100.0	134	2	AAW65698
19	53	100.0	134	2	AAW65698
20	53	100.0	139	2	AAW65698
21	53	100.0	162	2	AAW65698
22	53	100.0	164	2	AAW65698
23	53	100.0	174	2	AAW65698
24	53	100.0	174	2	AAW65698
25	53	100.0	181	2	AAW65698

26	53	100.0	181	2	AAW65728
27	53	100.0	559	2	AAW65728
28	53	100.0	767	4	AAW65728
29	53	100.0	767	4	AAW65728
30	53	100.0	940	2	AAW65728
31	53	100.0	940	2	AAW65728
32	53	100.0	948	6	AAW65728
33	53	100.0	948	6	AAW65728
34	53	100.0	948	6	AAW65728
35	53	100.0	961	6	AAW65728
36	53	100.0	978	4	AAW65728
37	53	100.0	1001	4	AAW65728
38	53	100.0	1018	1	AAW65728
39	53	100.0	1018	4	AAW65728
40	53	100.0	1018	4	AAW65728
41	53	100.0	1018	6	AAW65728
42	53	100.0	1018	6	AAW65728
43	53	100.0	1027	2	AAW65728
44	53	100.0	1038	6	AAW65728
45	52	98.1	30	4	AAW65728

ALIGNMENTS

RESULT 1
AAW65728 standard; peptide; 10 AA.
XX
AC AAW65728;
XX
DT 16-OCT-1998 (first entry)
XX
DE Fibrinectin binding protein-derived peptide #72.
XX
KW microbial surface components recognising adhesive matrix molecule;
KW MSCRAMM; fibrinectin; fibrinectin-binding protein; antibody; epitope;
KW antibiotic; bacterial infection; antibiotic-resistant strain.
XX
OS Synthetic.
OS Staphylococcus aureus.
XX
PN W09831389-A2.
XX
PD 23-JUL-1998.
XX
PF 21-JAN-1998; 98WO-US001222.
XX
PR 21-JAN-1997; 97US-0036139P.
XX
PA (TEXA) UNIV TEXAS A & M SYSTEM.
XX
PI Hoeoek M, Patti JW, House-Pompeo KL, Speziale P, Joh D;
PI McGavin MJ;
XX
DR WPI; 1998-413816/35.
XX
PT Antibody that binds to fibrinectin-binding protein, preventing its
PT binding to fibrinectin - used to treat or prevent bacterial infection,
PT especially by Staphylococci and Streptococci.
XX
PS Example 9, Page 110; 201pp; English.
XX
CC The invention relates to antibodies that bind to a fibrinectin-binding
CC domain of a fibrinectin-binding protein, and inhibit binding of the
CC protein to fibrinectin. Also claimed are: (1) isolated peptides of a
CC fibrinectin-binding protein that do not bind to fibrinectin; (2) fusion
CC protein containing at least one peptide of a fibrinectin-binding protein
CC linked to a second amino acid sequence; (3) nucleic acid encoding the
CC isolated peptide of (1). Antibodies, the isolated peptides of (1) and the
CC nucleic acids are all useful for immunisation (active or passive) and (by
CC inhibiting binding of bacteria to fibrinectin) for preventing or treating
CC infection in humans or other animals, particularly by staphylococci or

CC streptococci, e.g. meningitis, otitis media, pneumonia, endocarditis,
 CC mastitis in cattle, abortion in horses and many others. Since the
 CC antibodies block binding of bacteria, they should be effective against
 CC antibiotic-resistant strains, and may replace antibiotic therapy or
 CC increase its effectiveness. Sequences AAW65719-41 and AAW65658 represent
 CC peptides which were synthesised to span the D1 motif and the N-terminal
 CC 18 amino acids of D2, with each peptide overlapping by eight amino acids
 CC with the previous sequence
 XX
 SQ Sequence 10 AA;

Query Match 100.0%; Score 53; DB 2; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.0057;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YEOGGNIVDI 10
 |||||
 Db 1 YEOGGNIVDI 10

RESULT 2
 AAW65692
 ID AAW65692 standard; peptide; 38 AA.
 XX
 AC AAW65692;
 XX
 DT 16-OCT-1998 (first entry)

XX Fibronectin binding protein-derived peptide #36.

XX microbial surface components recognising adhesive matrix molecule;
 KM MSCRAMM; fibronectin; fibronectin-binding protein; antibody; epitope;
 KW antibiotic; bacterial infection; antibiotic-resistant strain.
 XX
 OS Synthetic.
 OS Staphylococcus aureus.

XX WO9831389-A2.

XX 23-JUL-1998.

XX 21-JAN-1998; 98WO-US001222.

XX 21-JAN-1997; 97US-0036139P.

XX (TEXA) UNIV TEXAS A & M SYSTEM.

XX Hoeoek M, Patti JM, House-Pompeo KL, Speziale P, Joh D;
 PI Mcgavin MJ;
 PT
 XX

DR WPI, 1998-413816/35.

XX Antibody that binds to fibronectin-binding protein, preventing its
 PT binding to fibronectin - used to treat or prevent bacterial infection,
 PT especially by Staphylococci and Streptococci.
 XX

XX Example 8; Page 101; 201pp; English.

XX The invention relates to antibodies that bind to a fibronectin-binding
 CC domain of a fibronectin-binding protein, and inhibit binding of the
 CC protein to fibronectin. Also claimed are: (1) isolated peptides of a
 CC fibronectin-binding protein that do not bind to fibronectin; (2) fusion
 CC protein containing at least one peptide of a fibronectin-binding protein
 CC linked to a second amino acid sequence; (3) nucleic acid encoding the
 CC isolated peptide of (1). Antibodies, the isolated peptides of (1) and the
 CC nucleic acids are all useful for immunisation (active or passive) and (by
 CC inhibiting binding of bacteria to fibronectin) for preventing or treating
 CC infection in humans or other animals, particularly by staphylococci or
 CC streptococci, e.g. meningitis, otitis media, pneumonia, endocarditis,
 CC mastitis in cattle, abortion in horses and many others. Since the
 CC antibodies block binding of bacteria, they should be effective against
 CC antibiotic-resistant strains, and may replace antibiotic therapy or
 CC increase its effectiveness. Sequences AAW65691-700 represent a series of

CC synthetic peptides based on the D1 region of S. aureus fibronectin
 CC binding protein A. They were synthesised to contain mutations
 XX
 SQ Sequence 38 AA;

Query Match 100.0%; Score 53; DB 2; Length 38;
 Best Local Similarity 100.0%; Pred. No. 0.026;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YEOGGNIVDI 10
 |||||
 Db 19 YEOGGNIVDI 28

RESULT 3
 AAW65695
 ID AAW65695 standard; peptide; 38 AA.
 XX
 AC AAW65695;
 XX
 DT 16-OCT-1998 (first entry)

XX Fibronectin binding protein-derived peptide #39.

XX microbial surface components recognising adhesive matrix molecule;
 KM MSCRAMM; fibronectin; fibronectin-binding protein; antibody; epitope;
 KW antibiotic; bacterial infection; antibiotic-resistant strain.
 XX
 OS Synthetic.
 OS Staphylococcus aureus.

XX WO9831389-A2.

XX 23-JUL-1998.

XX 21-JAN-1998; 98WO-US001222.

XX 21-JAN-1997; 97US-0036139P.

XX (TEXA) UNIV TEXAS A & M SYSTEM.

XX Hoeoek M, Patti JM, House-Pompeo KL, Speziale P, Joh D;
 PI Mcgavin MJ;
 PT
 XX

DR WPI, 1998-413816/35.

XX Antibody that binds to fibronectin-binding protein, preventing its
 PT binding to fibronectin - used to treat or prevent bacterial infection,
 PT especially by Staphylococci and Streptococci.
 XX

XX Example 8; Page 102; 201pp; English.

XX The invention relates to antibodies that bind to a fibronectin-binding
 CC domain of a fibronectin-binding protein, and inhibit binding of the
 CC protein to fibronectin. Also claimed are: (1) isolated peptides of a
 CC fibronectin-binding protein that do not bind to fibronectin; (2) fusion
 CC protein containing at least one peptide of a fibronectin-binding protein
 CC linked to a second amino acid sequence; (3) nucleic acid encoding the
 CC isolated peptide of (1). Antibodies, the isolated peptides of (1) and the
 CC nucleic acids are all useful for immunisation (active or passive) and (by
 CC inhibiting binding of bacteria to fibronectin) for preventing or treating
 CC infection in humans or other animals, particularly by staphylococci or
 CC streptococci, e.g. meningitis, otitis media, pneumonia, endocarditis,
 CC mastitis in cattle, abortion in horses and many others. Since the
 CC antibodies block binding of bacteria, they should be effective against
 CC antibiotic-resistant strains, and may replace antibiotic therapy or
 CC increase its effectiveness. Sequences AAW65691-700 represent a series of
 CC synthetic peptides based on the D1 region of S. aureus fibronectin
 CC binding protein A. They were synthesised to contain mutations
 XX
 SQ Sequence 38 AA;
 XX
 Query Match 100.0%; Score 53; DB 2; Length 38;


```

AC AAW65694;
XX
DT 16-OCT-1998 (first entry)
XX
DE Fibronectin binding protein-derived peptide #38.
XX
KW microbial surface components recognising adhesive matrix molecule;
KM MSCRAM; fibronectin; fibronectin-binding protein; antibody; epitope;
KM antibiotic; bacterial infection; antibiotic-resistant strain.
XX
OS Synthetic.
OS Staphylococcus aureus.
XX
PN WO9831389-A2.
XX
PD 23-JUL-1998.
XX
PF 21-JAN-1998; 98WO-US001222.
XX
PR 21-JAN-1997; 97US-0036139P.
XX
PA (TEXA ) UNIV TEXAS A & M SYSTEM.
XX
PI Hoeoek M, Patti JM, House-Pompeo KL, Speziale P, Joh D;
PI McGavin MJ;
XX
DR WPI; 1998-413816/35.
XX
PT Antibody that binds to fibronectin-binding protein, preventing its
PT binding to fibronectin - used to treat or prevent bacterial infection,
PT especially by Staphylococci and Streptococci.
XX
PS Example 8; Page 102; 201pp; English.
XX
XX The invention relates to antibodies that bind to a fibronectin-binding
CC domain of a fibronectin-binding protein, and inhibit binding of the
CC protein to fibronectin. Also claimed are: (1) isolated peptides of a
CC fibronectin-binding protein that do not bind to fibronectin; (2) fusion
CC protein containing at least one peptide of a fibronectin-binding protein
CC linked to a second amino acid sequence; (3) nucleic acid encoding the
CC isolated peptide of (1). Antibodies, the isolated peptides of (1) and the
CC nucleic acids are all useful for immunisation (active or passive) and (by
CC inhibiting binding of bacteria to fibronectin) for preventing or treating
CC infection in humans or other animals, particularly by staphylococci or
CC streptococci, e.g. meningitis, otitis media, pneumonia, endocarditis,
CC mastitis in cattle, abortion in horses and many others. Since the
CC antibodies block binding of bacteria, they should be effective against
CC antibiotic-resistant strains, and may replace antibiotic therapy or
CC increase its effectiveness. Sequences AAW65691-700 represent a series of
CC synthetic peptides based on the DI region of S. aureus fibronectin
CC binding protein A. They were synthesised to contain mutations
XX
SQ Sequence 38 AA;
XX
Query Match 100.0%; Score 53; DB 2; Length 38;
Best Local Similarity 100.0%; Pred. No. 0.026;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 YEOGGNIVDI 10
Db 19 YEOGGNIVDI 28

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KW microbial surface components recognising adhesive matrix molecule;
KM MSCRAM; fibronectin; fibronectin-binding protein; antibody; epitope;
KM antibiotic; bacterial infection; antibiotic-resistant strain.
XX
OS Synthetic.
OS Staphylococcus aureus.
XX
PN WO9831389-A2.
XX
PD 23-JUL-1998.
XX
PF 21-JAN-1998; 98WO-US001222.
XX
PR 21-JAN-1997; 97US-0036139P.
XX
PA (TEXA ) UNIV TEXAS A & M SYSTEM.
XX
PI Hoeoek M, Patti JM, House-Pompeo KL, Speziale P, Joh D;
PI McGavin MJ;
XX
DR WPI; 1998-413816/35.
XX
PT Antibody that binds to fibronectin-binding protein, preventing its
PT binding to fibronectin - used to treat or prevent bacterial infection,
PT especially by Staphylococci and Streptococci.
XX
PS Example 8; Page 101; 201pp; English.
XX
XX The invention relates to antibodies that bind to a fibronectin-binding
CC domain of a fibronectin-binding protein, and inhibit binding of the
CC protein to fibronectin. Also claimed are: (1) isolated peptides of a
CC fibronectin-binding protein that do not bind to fibronectin; (2) fusion
CC protein containing at least one peptide of a fibronectin-binding protein
CC linked to a second amino acid sequence; (3) nucleic acid encoding the
CC isolated peptide of (1). Antibodies, the isolated peptides of (1) and the
CC nucleic acids are all useful for immunisation (active or passive) and (by
CC inhibiting binding of bacteria to fibronectin) for preventing or treating
CC infection in humans or other animals, particularly by staphylococci or
CC streptococci, e.g. meningitis, otitis media, pneumonia, endocarditis,
CC mastitis in cattle, abortion in horses and many others. Since the
CC antibodies block binding of bacteria, they should be effective against
CC antibiotic-resistant strains, and may replace antibiotic therapy or
CC increase its effectiveness. Sequences AAW65691-700 represent a series of
CC synthetic peptides based on the DI region of S. aureus fibronectin
CC binding protein A. They were synthesised to contain mutations
XX
SQ Sequence 38 AA;
XX
Query Match 100.0%; Score 53; DB 2; Length 38;
Best Local Similarity 100.0%; Pred. No. 0.026;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 YEOGGNIVDI 10
Db 19 YEOGGNIVDI 28

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```

RESULT 7
AAW65691
ID AAW65691 standard; peptide; 38 AA.
XX
AC AAW65691;
XX
DT 16-OCT-1998 (first entry)
XX
DE Fibronectin binding protein-derived peptide #35.
XX

```

```

RESULT 8
AAW65661
ID AAW65661 standard; peptide; 38 AA.
XX
AC AAW65661;
XX
DT 16-OCT-1998 (first entry)
XX
DE Fibronectin binding protein-derived peptide #5.
XX
KW microbial surface components recognising adhesive matrix molecule;
KM MSCRAM; fibronectin; fibronectin-binding protein; antibody; epitope;
KM antibiotic; bacterial infection; antibiotic-resistant strain.
XX
OS Synthetic.
OS Staphylococcus aureus.

```

XX XX MO9831389-A2.
 PN XX 23-JUL-1998.
 XX XX
 PD XX
 PF 21-JAN-1998; 98WO-US001222.
 XX XX
 PR 21-JAN-1997; 97US-0036139P.
 XX XX
 PA (TEXA) UNIV TEXAS A & M SYSTEM.
 PI Hoeoek M, Patti JM, House-Pompeo KL, Speziale P, Joh D;
 PI Mcgavin MJ;
 DR WPI; 1998-413816/35.
 XX XX
 PT Antibody that binds to fibronectin-binding protein, preventing its
 PT binding to fibronectin - used to treat or prevent bacterial infection,
 PT especially by Staphylococci and Streptococci.
 PS Example 2; Page 92; 201pp; English.
 XX XX
 PS The invention relates to antibodies that bind to a fibronectin-binding
 CC domain of a fibronectin-binding protein, and inhibit binding of the
 CC protein to fibronectin. Also claimed are: (1) isolated peptides of a
 CC fibronectin-binding protein that do not bind to fibronectin; (2) fusion
 CC protein containing at least one peptide of a fibronectin-binding protein
 CC linked to a second amino acid sequence; (3) nucleic acid encoding the
 CC isolated peptide of (1). Antibodies, the isolated peptides of (1) and the
 CC nucleic acids are all useful for immunisation (active or passive) and (by
 CC inhibiting binding of bacteria to fibronectin) for preventing or treating
 CC infection in humans or other animals, particularly by staphylococci or
 CC streptococci, e.g. meningitis, otitis media, pneumonia, endocarditis,
 CC mastitis in cattle, abortion in horses and many others. Since the
 CC antibodies block binding of bacteria, they should be effective against
 CC antibiotic-resistant strains, and may replace antibiotic therapy or
 CC increase its effectiveness. Sequences AAM6569-68 represent synthetic
 CC epitopes from the fibronectin binding domains DU and D1-D4 of the S.
 CC aureus fmbA gene
 CC XX
 SQ Sequence 38 AA:
 Query Match 100.0%; Score 53; DB 2; Length 38;
 Best Local Similarity 100.0%; Pred. No. 0.026;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 YEOGGNIVDI 10
 |||||
 Db 19 YEOGGNIVDI 28
 RESULT 9
 AAM65693
 ID AAM65693 standard; peptide; 38 AA.
 XX AC AAM65693;
 XX DT 16-OCT-1998 (first entry)
 DE Fibronectin binding protein-derived peptide #37.
 XX XX
 KM microbial surface components recognising adhesive matrix molecule;
 KM MSCRAMM; fibronectin; fibronectin-binding protein; antibody; epitope;
 KM antibiotic; bacterial infection; antibiotic-resistant strain.
 XX OS Synthetic.
 OS Staphylococcus aureus.
 XX XX
 PN MO9831389-A2.
 PD XX
 PR 23-JUL-1998.
 PA (TEXA) UNIV TEXAS A & M SYSTEM.
 PI Hoeoek M, Patti JM, House-Pompeo KL, Speziale P, Joh D;
 PI Mcgavin MJ;
 DR WPI; 1998-413816/35.
 XX XX
 PT Antibody that binds to fibronectin-binding protein, preventing its
 PT binding to fibronectin - used to treat or prevent bacterial infection,
 PT especially by Staphylococci and Streptococci.
 PS Example 2; Page 92; 201pp; English.
 XX XX
 PS The invention relates to antibodies that bind to a fibronectin-binding
 CC domain of a fibronectin-binding protein, and inhibit binding of the
 CC protein to fibronectin. Also claimed are: (1) isolated peptides of a
 CC fibronectin-binding protein that do not bind to fibronectin; (2) fusion
 CC protein containing at least one peptide of a fibronectin-binding protein
 CC linked to a second amino acid sequence; (3) nucleic acid encoding the
 CC isolated peptide of (1). Antibodies, the isolated peptides of (1) and the
 CC nucleic acids are all useful for immunisation (active or passive) and (by
 CC inhibiting binding of bacteria to fibronectin) for preventing or treating
 CC infection in humans or other animals, particularly by staphylococci or
 CC streptococci, e.g. meningitis, otitis media, pneumonia, endocarditis,
 CC mastitis in cattle, abortion in horses and many others. Since the
 CC antibodies block binding of bacteria, they should be effective against
 CC antibiotic-resistant strains, and may replace antibiotic therapy or
 CC increase its effectiveness. Sequences AAM65691-700 represent a series of
 CC synthetic peptides based on the D1 region of S. aureus fibronectin
 CC binding protein A. They were synthesised to contain mutations
 CC XX
 SQ Sequence 38 AA:
 Query Match 100.0%; Score 53; DB 2; Length 38;
 Best Local Similarity 100.0%; Pred. No. 0.026;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 YEOGGNIVDI 10
 |||||
 Db 19 YEOGGNIVDI 28
 RESULT 10
 AAM65698
 ID AAM65698 standard; peptide; 38 AA.
 XX AC AAM65698;
 XX DT 16-OCT-1998 (first entry)
 DE Fibronectin binding protein-derived peptide #42.
 XX XX
 KM microbial surface components recognising adhesive matrix molecule;
 KM MSCRAMM; fibronectin; fibronectin-binding protein; antibody; epitope;
 KM antibiotic; bacterial infection; antibiotic-resistant strain.
 XX OS Synthetic.
 OS Staphylococcus aureus.
 XX XX
 PN MO9831389-A2.
 PD XX
 PR 23-JUL-1998.
 PA (TEXA) UNIV TEXAS A & M SYSTEM.
 PI Hoeoek M, Patti JM, House-Pompeo KL, Speziale P, Joh D;
 PI Mcgavin MJ;
 DR WPI; 1998-413816/35.
 XX XX
 PT Antibody that binds to fibronectin-binding protein, preventing its
 PT binding to fibronectin - used to treat or prevent bacterial infection,
 PT especially by Staphylococci and Streptococci.
 PS Example 8; Page 102; 201pp; English.
 XX XX
 PS The invention relates to antibodies that bind to a fibronectin-binding
 CC domain of a fibronectin-binding protein, and inhibit binding of the
 CC protein to fibronectin. Also claimed are: (1) isolated peptides of a
 CC fibronectin-binding protein that do not bind to fibronectin; (2) fusion
 CC protein containing at least one peptide of a fibronectin-binding protein
 CC linked to a second amino acid sequence; (3) nucleic acid encoding the
 CC isolated peptide of (1). Antibodies, the isolated peptides of (1) and the
 CC nucleic acids are all useful for immunisation (active or passive) and (by
 CC inhibiting binding of bacteria to fibronectin) for preventing or treating
 CC infection in humans or other animals, particularly by staphylococci or
 CC streptococci, e.g. meningitis, otitis media, pneumonia, endocarditis,
 CC mastitis in cattle, abortion in horses and many others. Since the
 CC antibodies block binding of bacteria, they should be effective against
 CC antibiotic-resistant strains, and may replace antibiotic therapy or
 CC increase its effectiveness. Sequences AAM65691-700 represent a series of
 CC synthetic peptides based on the D1 region of S. aureus fibronectin
 CC binding protein A. They were synthesised to contain mutations
 CC XX

XX XX 21-JAN-1997; 97US-0036139P.
 PR XX (TEXA) UNIV TEXAS A & M SYSTEM.
 PA XX
 PI Hoeoek M, Patti JM, House-Pompeo KL, Speziale P, Joh D;
 PI Mcgavin MJ;
 DR WPI; 1998-413816/35.
 XX XX
 PT Antibody that binds to fibronectin-binding protein, preventing its
 PT binding to fibronectin - used to treat or prevent bacterial infection,
 PT especially by Staphylococci and Streptococci.
 PS Example 8; Page 102; 201pp; English.
 XX XX
 PS The invention relates to antibodies that bind to a fibronectin-binding
 CC domain of a fibronectin-binding protein, and inhibit binding of the
 CC protein to fibronectin. Also claimed are: (1) isolated peptides of a
 CC fibronectin-binding protein that do not bind to fibronectin; (2) fusion
 CC protein containing at least one peptide of a fibronectin-binding protein
 CC linked to a second amino acid sequence; (3) nucleic acid encoding the
 CC isolated peptide of (1). Antibodies, the isolated peptides of (1) and the
 CC nucleic acids are all useful for immunisation (active or passive) and (by
 CC inhibiting binding of bacteria to fibronectin) for preventing or treating
 CC infection in humans or other animals, particularly by staphylococci or
 CC streptococci, e.g. meningitis, otitis media, pneumonia, endocarditis,
 CC mastitis in cattle, abortion in horses and many others. Since the
 CC antibodies block binding of bacteria, they should be effective against
 CC antibiotic-resistant strains, and may replace antibiotic therapy or
 CC increase its effectiveness. Sequences AAM65691-700 represent a series of
 CC synthetic peptides based on the D1 region of S. aureus fibronectin
 CC binding protein A. They were synthesised to contain mutations
 CC XX
 SQ Sequence 38 AA:
 Query Match 100.0%; Score 53; DB 2; Length 38;
 Best Local Similarity 100.0%; Pred. No. 0.026;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 YEOGGNIVDI 10
 |||||
 Db 19 YEOGGNIVDI 28
 RESULT 10
 AAM65698
 ID AAM65698 standard; peptide; 38 AA.
 XX AC AAM65698;
 XX DT 16-OCT-1998 (first entry)
 DE Fibronectin binding protein-derived peptide #42.
 XX XX
 KM microbial surface components recognising adhesive matrix molecule;
 KM MSCRAMM; fibronectin; fibronectin-binding protein; antibody; epitope;
 KM antibiotic; bacterial infection; antibiotic-resistant strain.
 XX OS Synthetic.
 OS Staphylococcus aureus.
 XX XX
 PN MO9831389-A2.
 PD XX
 PR 23-JUL-1998.
 PA (TEXA) UNIV TEXAS A & M SYSTEM.
 PI Hoeoek M, Patti JM, House-Pompeo KL, Speziale P, Joh D;
 PI Mcgavin MJ;
 DR WPI; 1998-413816/35.
 XX XX
 PT Antibody that binds to fibronectin-binding protein, preventing its
 PT binding to fibronectin - used to treat or prevent bacterial infection,
 PT especially by Staphylococci and Streptococci.
 PS Example 8; Page 102; 201pp; English.
 XX XX
 PS The invention relates to antibodies that bind to a fibronectin-binding
 CC domain of a fibronectin-binding protein, and inhibit binding of the
 CC protein to fibronectin. Also claimed are: (1) isolated peptides of a
 CC fibronectin-binding protein that do not bind to fibronectin; (2) fusion
 CC protein containing at least one peptide of a fibronectin-binding protein
 CC linked to a second amino acid sequence; (3) nucleic acid encoding the
 CC isolated peptide of (1). Antibodies, the isolated peptides of (1) and the
 CC nucleic acids are all useful for immunisation (active or passive) and (by
 CC inhibiting binding of bacteria to fibronectin) for preventing or treating
 CC infection in humans or other animals, particularly by staphylococci or
 CC streptococci, e.g. meningitis, otitis media, pneumonia, endocarditis,
 CC mastitis in cattle, abortion in horses and many others. Since the
 CC antibodies block binding of bacteria, they should be effective against
 CC antibiotic-resistant strains, and may replace antibiotic therapy or
 CC increase its effectiveness. Sequences AAM65691-700 represent a series of
 CC synthetic peptides based on the D1 region of S. aureus fibronectin
 CC binding protein A. They were synthesised to contain mutations
 CC XX

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PI  Mcgavin MJ;
XX
XX  WPI, 1998-413816/35.
XX
XX  Antibody that binds to fibronectin-binding protein, preventing its
XX  binding to fibronectin - used to treat or prevent bacterial infection,
XX  especially by Staphylococci and Streptococci.
XX
XX  Example 8; Page 102; 201pp; English.
XX
XX  The invention relates to antibodies that bind to a fibronectin-binding
XX  domain of a fibronectin-binding protein, and inhibit binding of the
XX  protein to fibronectin. Also claimed are: (1) isolated peptides of a
XX  fibronectin-binding protein that do not bind to fibronectin; (2) fusion
XX  protein containing at least one peptide of a fibronectin-binding protein
XX  linked to a second amino acid sequence; (3) nucleic acid encoding the
XX  isolated peptide of (1). Antibodies, the isolated peptides of (1) and the
XX  nucleic acids are all useful for immunisation (active or passive) and (b)
XX  inhibiting binding of bacteria to fibronectin) for preventing or treating
XX  infection in humans or other animals, particularly by staphylococci or
XX  streptococci, e.g. meningitis, otitis media, pneumonia, endocarditis,
XX  mastitis in cattle, abortion in horses and many others. Since the
XX  antibodies block binding of bacteria, they should be effective against
XX  antibiotic-resistant strains, and may replace antibiotic therapy or
XX  increase its effectiveness. Sequences AAM65691-700 represent a series of
XX  synthetic peptides based on the D1 region of S. aureus fibronectin
XX  binding protein A. They were synthesised to contain mutations
XX
XX  Sequence 38 AA;
XX
XX  Query Match          100.0%; Score 53; DB 2; Length 38;
XX  Best Local Similarity 100.0%; Pred. No. 0.026;
XX  Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY  1 YEQGGINVIDI 10
XX  |||||
XX  19 YEQGGINVIDI 28
XX
XX
XX  RESULT 11
XX  AAM65712
XX  AAM65712 standard; peptide; 39 AA.
XX
XX  AAM65712;
XX
XX  16-OCT-1998 (first entry)
XX
XX  Fibronectin binding protein-derived peptide #56.
XX
XX  microbial surface components recognising adhesive matrix molecule;
XX  MSCRAMM; fibronectin; fibronectin-binding protein; antibody; epitope;
XX  antibiotic; bacterial infection; antibiotic-resistant strain.
XX
XX  Synthetic.
XX  OS Staphylococcus aureus.
XX
XX  WO9831389-A2.
XX
XX  23-JUL-1998.
XX
XX  21-JAN-1998; 98WO-US001222.
XX
XX  21-JAN-1997; 97US-0036139P.
XX
XX  (TEXA ) UNITV TEXAS A & M SYSTEM.
XX
XX  Hoeoek M, Partl JM, House-Pompeo KL, Speciale P, Joh D;
XX  Mcgavin MJ;
XX
XX  WPI, 1998-413816/35.
XX
XX  Antibody that binds to fibronectin-binding protein, preventing its
XX  binding to fibronectin - used to treat or prevent bacterial infection,

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```

PT  especially by Staphylococci and Streptococci.
XX
XX  Example 8; Page 104; 201pp; English.
XX
XX  The invention relates to antibodies that bind to a fibronectin-binding
XX  domain of a fibronectin-binding protein, and inhibit binding of the
XX  protein to fibronectin. Also claimed are: (1) isolated peptides of a
XX  fibronectin-binding protein that do not bind to fibronectin; (2) fusion
XX  protein containing at least one peptide of a fibronectin-binding protein
XX  linked to a second amino acid sequence; (3) nucleic acid encoding the
XX  isolated peptide of (1). Antibodies, the isolated peptides of (1) and the
XX  nucleic acids are all useful for immunisation (active or passive) and (b)
XX  inhibiting binding of bacteria to fibronectin) for preventing or treating
XX  infection in humans or other animals, particularly by staphylococci or
XX  streptococci, e.g. meningitis, otitis media, pneumonia, endocarditis,
XX  mastitis in cattle, abortion in horses and many others. Since the
XX  antibodies block binding of bacteria, they should be effective against
XX  antibiotic-resistant strains, and may replace antibiotic therapy or
XX  increase its effectiveness. The present sequence is shown in the
XX  specification
XX
XX  Sequence 39 AA;
XX
XX  Query Match          100.0%; Score 53; DB 2; Length 39;
XX  Best Local Similarity 100.0%; Pred. No. 0.027;
XX  Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY  1 YEQGGINVIDI 10
XX  |||||
XX  19 YEQGGINVIDI 28
XX
XX
XX  RESULT 12
XX  AAR90937
XX  AAR90937 standard; peptide; 113 AA.
XX
XX  AAR90937;
XX
XX  23-SEP-1996 (first entry)
XX
XX  D3D4 polypeptide #1.
XX
XX  Fibronectin binding protein; Fbp; S.aureus J2385; monoclonal antibody;
XX  infection; surgical implant; antiadherent agent; hygiene; adhesion;
XX  extracellular matrix protein; oral pathogen; oral cavity.
XX
XX  Staphylococcus aureus.
XX
XX  OS
XX  FH Key
XX  FT Region 1..21 Location/Qualifiers
XX  FT /note= "D1 region fragment"
XX  FT Region 22..59
XX  FT /note= "D2 region"
XX  FT Region 60..98
XX  FT /note= "D3 region"
XX  FT Region 99..113
XX  FT /note= "D4 region"
XX  FT Misc-difference 113
XX  FT /note= "P113T"
XX
XX  WO9604381-A1.
XX
XX  15-FEB-1996.
XX
XX  28-JUL-1995; 95WO-BP003040.
XX
XX  05-AUG-1994; 94GB-00015900.
XX
XX  (SMIK ) SMITHKLINE BEECHAM PLC.
XX
XX  Critchley IA, Dodd I, Barnett P, Mcbay DL,
XX  WPI, 1996-129397/13.
XX
XX

```


XX	13-NOV-1996	(first entry)
DT		
XX	D1-D4 fibronectin binding domains.	
DE		
XX	Fibronectin; oral hygiene; gingivitis; gum disease; adhesion;	
KM	periodontitis; oral pathogens; caries; calculus; candidiasis; oral surgery;	
KM	tissue regeneration; irrigation; toothpaste; dentifrice; mouthwash;	
KM	lozenge.	
XX		
OS	Staphylococcus aureus.	
XX		
PN	MO9604003-A1.	
PD		
XX	15-FEB-1996.	
XX		
PF	18-JUL-1995; 95WO-EP002825.	
XX		
PR	05-AUG-1994; 94GB-00015902.	
XX		
PA	(SMIK) SMITHKLINE BEECHAM PLC.	
PI	Barnett P, Critchley IA, Dodd I;	
XX		
DR	WPI; 1996-129122/13.	
XX		
PT	Prevention of adherence of oral pathogens in the oral cavity, partic.	
PT	tooth surfaces - by application of a fibronectin binding protein or	
PT	polypeptide or a monoclonal antibody or fragment against it.	
XX		
PS	Claim 5; Page 32; 41pp; English.	
XX		
CC	Adherence of oral pathogens, particularly to tooth surfaces, can be	
CC	prevented by application of a fibronectin binding protein or polypeptide.	
CC	The fibronectin binding protein or polypeptide is useful in the	
CC	manufacture of oral hygiene compositions, eg. toothpaste, liquid	
CC	dentifrice, mouthwash or lozenge. They are useful to prevent the plaque-	
CC	related development of carious lesions, gingivitis, calculus or	
CC	periodontal disease and to combat oral cavity infections, e.g.	
CC	candidiasis. They may also be useful in oral surgery e.g. in guided	
CC	tissue regeneration procedures to prevent subsequent bacterial infection,	
CC	and for irrigation of periodontal pockets. This sequence corresponds to	
CC	amino acids 709-838 of the D1-D4 fibronectin binding domain of	
CC	Staphylococcus aureus	
XX		
SQ	Sequence 130 AA;	
Query Match	100.0%;	Score 53; DB 2; Length 130;
Best Local Similarity	100.0%;	Pred. No. 0.1;
Matches 10; Conservative	0;	Mismatches 0; Indels 0; Gaps 0
1 YE0GNIWDI 10		
20 YE0GNIWDI 29		

Search completed: October 25, 2005, 20:58:43
Job time : 64.2 BECS

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 22, 2005, 05:46:56 ; Search time 17.3 Seconds
(without alignments)
43.150 Million cell updates/sec

Title: US-10-731-238-72

Perfect score: 53

Sequence: 1 YEOGGINVIDI 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

Issued Patents AA:*

- 1: /cgn2_6/prodata/1/iaa/5A.COMB.pep:*
- 2: /cgn2_6/prodata/1/iaa/5B.COMB.pep:*
- 3: /cgn2_6/prodata/1/iaa/6A.COMB.pep:*
- 4: /cgn2_6/prodata/1/iaa/6B.COMB.pep:*
- 5: /cgn2_6/prodata/1/iaa/PCTUS.COMB.pep:*
- 6: /cgn2_6/prodata/1/iaa/backfillset.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	53	100.0	10	4	US-09-010-317-72
2	53	100.0	38	1	US-08-234-622A-2
3	53	100.0	38	1	US-08-729-767-3
4	53	100.0	38	4	US-09-010-317-5
5	53	100.0	38	4	US-09-010-317-35
6	53	100.0	38	4	US-09-010-317-36
7	53	100.0	38	4	US-09-010-317-37
8	53	100.0	38	4	US-09-010-317-38
9	53	100.0	38	4	US-09-010-317-39
10	53	100.0	38	4	US-09-010-317-40
11	53	100.0	38	4	US-09-010-317-41
12	53	100.0	38	4	US-09-010-317-42
13	53	100.0	39	4	US-08-259-000-3
14	53	100.0	114	1	US-08-259-000-3
15	53	100.0	130	2	US-08-459-135A-7
16	53	100.0	130	2	US-08-459-135A-8
17	53	100.0	130	2	US-08-459-135A-9
18	53	100.0	130	3	US-08-495-559-7
19	53	100.0	139	3	US-08-495-559-8
20	53	100.0	174	2	US-08-459-135A-10
21	53	100.0	174	2	US-08-459-135A-11
22	53	100.0	174	3	US-08-495-559-10
23	53	100.0	174	3	US-08-495-559-11
24	53	100.0	176	3	US-08-495-559-12
25	53	100.0	178	2	US-08-459-135A-12
26	53	100.0	178	3	US-08-495-559-12
27	53	100.0	181	2	US-08-459-135A-6

28	53	100.0	559	4	US-08-956-171E-5251	Sequence 5251, Ap
29	53	100.0	559	4	US-08-781-986A-5251	Sequence 5251, Ap
30	53	100.0	1027	4	US-08-956-171E-5254	Sequence 5254, Ap
31	53	100.0	1027	4	US-08-781-986A-5254	Sequence 5254, Ap
32	47	88.7	36	4	US-09-010-317-58	Sequence 58, Appl
33	47	88.7	36	1	US-08-234-622A-3	Sequence 3, Appl
34	47	88.7	38	1	US-08-729-767-4	Sequence 4, Appl
35	47	88.7	38	4	US-09-010-317-45	Sequence 7, Appl
36	47	88.7	38	4	US-09-010-317-46	Sequence 45, Appl
37	47	88.7	38	4	US-09-010-317-47	Sequence 46, Appl
38	47	88.7	38	4	US-09-010-317-48	Sequence 47, Appl
39	47	88.7	38	4	US-09-010-317-49	Sequence 48, Appl
40	45	84.9	38	4	US-09-010-317-6	Sequence 6, Appl
41	45	84.9	38	4	US-09-010-317-43	Sequence 43, Appl
42	45	84.9	39	4	US-09-010-317-57	Sequence 57, Appl
43	43	81.1	10	4	US-09-010-317-71	Sequence 71, Appl
44	41	77.4	10	4	US-09-010-317-73	Sequence 73, Appl
45	41	77.4	14	4	US-09-010-317-60	Sequence 60, Appl

ALIGNMENTS

RESULT 1
US-09-010-317-72
Sequence 72, Application US/09010317
Patent No. 6685943
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
APPLICANT: Patti, Joseph M.
APPLICANT: House-Pompeo, Karen L.
APPLICANT: Speziale, Pietro
APPLICANT: Jon, Danny
APPLICANT: McLaughlin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
TITLE OF INVENTION: AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Habler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAMK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 72:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-09-010-317-72
Query Match 100.0%; Score 53; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0012;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YE0GGNIVDI 10
|||||

Db 1 YE0GGNIVDI 10

RESULT 2
US-08-234-622A-2

; Sequence 2, Application US/08234622A
; Patent No. 5440014

; GENERAL INFORMATION:

; APPLICANT: HOOK, Magnus

; APPLICANT: MCGAVIN, Martin

; APPLICANT: RAUCCI, Giuseppe

; TITLE OF INVENTION: A FIBRONECTIN BINDING PEPTIDE

; NUMBER OF SEQUENCES: 4

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Burns, Doane, Swecker & Mathis

; STREET: P.O. Box 1404

; CITY: Alexandria

; STATE: Virginia

; COUNTRY: United States

; ZIP: 22133-1404

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/234,622A

; FILING DATE: 28-APR-1994

; CLASSIFICATION: 530

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: SE 9002617-0

; FILING DATE: 10-AUG-1990

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: WO PCT/SE91/00534

; FILING DATE: 09-AUG-1991

; ATTORNEY/AGENT INFORMATION:

; NAME: Meuth, Donna M

; REGISTRATION NUMBER: 36,607

; REFERENCE/DOCKET NUMBER: 012885-044

; TELEPHONE: (703) 836-6620

; TELEFAX: (703) 836-6620

; INFORMATION FOR SEQ ID NO: 2:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 38 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

; US-08-234-622A-2

Query Match 100.0%; Score 53; DB 1; Length 38;

Best Local Similarity 100.0%; Pred. No. 0.0051;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YE0GGNIVDI 10
|||||

Db 19 YE0GGNIVDI 28

RESULT 3

US-08-729-767-3

; Sequence 3, Application US/08729767

; Patent No. 5770702

; GENERAL INFORMATION:

; APPLICANT: HOOK, Magnus

; APPLICANT: LINDBERG, Martin Kjell

; APPLICANT: SIGNS, Lars Christer

; APPLICANT: WADSTROM, Torkei Mikael

; APPLICANT: FROMAN, Gunnar

; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN AS WELL AS

; ITS PREPARATION

; NUMBER OF SEQUENCES: 6

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Burns, Doane, Swecker & Mathis, L.L.P.

; STREET: P.O. Box 1404

; CITY: Alexandria

; STATE: Virginia

; COUNTRY: United States

; ZIP: 22133-1404

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/729,767

; FILING DATE: 07-OCT-1996

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/259,000

; FILING DATE: 13-JUN-1994

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/007,817

; FILING DATE: 22-JAN-1993

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/201,028

; FILING DATE: 01-JUN-1988

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: SE 8702272-9

; FILING DATE: 01-JUN-1987

; ATTORNEY/AGENT INFORMATION:

; NAME: McGowan, Malcolm K.

; REGISTRATION NUMBER: 39,300

; REFERENCE/DOCKET NUMBER: 012889-036

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (703) 836-6620

; TELEFAX: (703) 836-2021

; INFORMATION FOR SEQ ID NO: 3:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 38 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; US-08-729-767-3

Query Match 100.0%; Score 53; DB 1; Length 38;

Best Local Similarity 100.0%; Pred. No. 0.0051;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YE0GGNIVDI 10
|||||

Db 20 YE0GGNIVDI 29

RESULT 4

US-09-010-317-5

; Sequence 5, Application US/09010317

; Patent No. 6685943

; GENERAL INFORMATION:

; APPLICANT: HOOK, Magnus

; APPLICANT: Patil, Joseph M.

; APPLICANT: House-Pompeo, Karen L.

; APPLICANT: Speciale, Pietro

; APPLICANT: Joh, Danny

; APPLICANT: McGavin, Martin J.

; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS

; NUMBER OF SEQUENCES: 105

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Arnold, White & Durkee

STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TANK:189
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-09-010-317-5
Query Match 100.0%; Score 53; DB 4; Length 38;
Best local Similarity 100.0%; Pred. No. 0.0051;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 YEOGGINVIDI 10
Db 19 YEOGGINVIDI 28
RESULT 5
US-09-010-317-35
Sequence 35, Application US/09010317
Patent No. 6685943
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
APPLICANT: Patti, Joseph M.
APPLICANT: House-Pompeo, Karen L.
APPLICANT: Speziale, Pietro
APPLICANT: Joh, Danny
APPLICANT: McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
TITLE OF INVENTION: AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSER: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/036,139

FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TANK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 35:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-09-010-317-35
Query Match 100.0%; Score 53; DB 4; Length 38;
Best local Similarity 100.0%; Pred. No. 0.0051;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 YEOGGINVIDI 10
Db 19 YEOGGINVIDI 28
RESULT 6
US-09-010-317-36
Sequence 36, Application US/09010317
Patent No. 6685943
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
APPLICANT: Patti, Joseph M.
APPLICANT: House-Pompeo, Karen L.
APPLICANT: Speziale, Pietro
APPLICANT: Joh, Danny
APPLICANT: McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
TITLE OF INVENTION: AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSER: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TANK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 36:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-09-010-317-36

Query Match 100.0%; Score 53; DB 4; Length 38;
Best Local Similarity 100.0%; Pred. No. 0.0051;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YE0GGINVIDI 10
| | | | | | | | | |
| | | | | | | | | |
Db 19 YE0GGINVIDI 28

RESULT 7

US-09-010-317-37
; Sequence 37, Application US/09010317
; Patent No. 6685943
; GENERAL INFORMATION:
; APPLICANT: Hook, Magnus
; APPLICANT: Patti, Joseph M.
; APPLICANT: House-Pompeo, Karen L.
; APPLICANT: Speziale, Pietro
; APPLICANT: Joh, Danny
; APPLICANT: McGavin, Martin J.
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
; NUMBER OF SEQUENCES: 105
; TITLE OF INVENTION: AND METHODS OF USE
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: TX
; COUNTRY: USA
; ZIP: 77210-4433
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/010,317
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/036,139
; FILING DATE: 21-JAN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Hibler, David W.
; REGISTRATION NUMBER: 41,071
; REFERENCE/DOCKET NUMBER: TANK:189
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 512-418-3000
; TELEFAX: 512-474-7577
; INFORMATION FOR SEQ ID NO: 37:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 38 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
US-09-010-317-37

Query Match 100.0%; Score 53; DB 4; Length 38;
Best Local Similarity 100.0%; Pred. No. 0.0051;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YE0GGINVIDI 10
| | | | | | | | | |
| | | | | | | | | |
Db 19 YE0GGINVIDI 28

RESULT 8

US-09-010-317-38
; Sequence 38, Application US/09010317
; Patent No. 6685943
; GENERAL INFORMATION:
; APPLICANT: Hook, Magnus
; APPLICANT: Patti, Joseph M.

APPLICANT: House-Pompeo, Karen L.
APPLICANT: Speziale, Pietro
APPLICANT: Joh, Danny
APPLICANT: McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
NUMBER OF SEQUENCES: 105
TITLE OF INVENTION: AND METHODS OF USE
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TANK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 38:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-09-010-317-38

Query Match 100.0%; Score 53; DB 4; Length 38;
Best Local Similarity 100.0%; Pred. No. 0.0051;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YE0GGINVIDI 10
| | | | | | | | | |
| | | | | | | | | |
Db 19 YE0GGINVIDI 28

RESULT 9

US-09-010-317-39
; Sequence 39, Application US/09010317
; Patent No. 6685943
; GENERAL INFORMATION:
; APPLICANT: Hook, Magnus
; APPLICANT: Patti, Joseph M.
; APPLICANT: House-Pompeo, Karen L.
; APPLICANT: Speziale, Pietro
; APPLICANT: Joh, Danny
; APPLICANT: McGavin, Martin J.
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
; NUMBER OF SEQUENCES: 105
; TITLE OF INVENTION: AND METHODS OF USE
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: TX
; COUNTRY: USA
; ZIP: 77210-4433
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAMK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 39:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-09-010-317-39

Query Match 100.0%; Score 53; DB 4; Length 38;
Best Local Similarity 100.0%; Pred. No. 0.0051;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YE0GGNIVDI 10
DB 19 YE0GGNIVDI 28

RESULT 10
US-09-010-317-40
Sequence 40, Application US/09010317
Patent No. 6685943
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
APPLICANT: Patti, Joseph M.
APPLICANT: House-Pompeo, Karen L.
APPLICANT: Speziale, Pietro
APPLICANT: Joh, Danny
APPLICANT: McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
TITLE OF INVENTION: AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAMK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000

TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 40:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-09-010-317-40

Query Match 100.0%; Score 53; DB 4; Length 38;
Best Local Similarity 100.0%; Pred. No. 0.0051;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YE0GGNIVDI 10
DB 19 YE0GGNIVDI 28

RESULT 11
US-09-010-317-41
Sequence 41, Application US/09010317
Patent No. 6685943
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
APPLICANT: Patti, Joseph M.
APPLICANT: House-Pompeo, Karen L.
APPLICANT: Speziale, Pietro
APPLICANT: Joh, Danny
APPLICANT: McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
TITLE OF INVENTION: AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAMK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 41:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-09-010-317-41

Query Match 100.0%; Score 53; DB 4; Length 38;
Best Local Similarity 100.0%; Pred. No. 0.0051;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YE0GGNIVDI 10
DB 19 YE0GGNIVDI 28

RESULT 12
US-09-010-317-42
; Sequence 42, Application US/09010317
; Patent No. 6685943
; GENERAL INFORMATION:
; APPLICANT: Hook, Magnus
; APPLICANT: Patti, Joseph M.
; APPLICANT: House-Pompeo, Karen L.
; APPLICANT: Speziale, Pietro
; APPLICANT: Joh, Danny
; APPLICANT: McGavin, Martin J.
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
; TITLE OF INVENTION: AND METHODS OF USE
; NUMBER OF SEQUENCES: 105
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: TX
; COUNTRY: USA
; ZIP: 77210-4433
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/010,317
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/036,139
; FILING DATE: 21-JAN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Hibler, David W.
; REGISTRATION NUMBER: 41,071
; REFERENCE/DOCKET NUMBER: TANK:189
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 512-418-3000
; TELEFAX: 512-474-7577
; INFORMATION FOR SEQ ID NO: 42:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 38 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; US-09-010-317-42

Query Match 100.0%; Score 53; DB 4; Length 38;
Best Local Similarity 100.0%; Pred. No. 0.0051;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YE0GNIYDI 10
Db 19 YE0GNIYDI 28

RESULT 13
US-09-010-317-56
; Sequence 56, Application US/09010317
; Patent No. 6685943
; GENERAL INFORMATION:
; APPLICANT: Hook, Magnus
; APPLICANT: Patti, Joseph M.
; APPLICANT: House-Pompeo, Karen L.
; APPLICANT: Speziale, Pietro
; APPLICANT: Joh, Danny
; APPLICANT: McGavin, Martin J.
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
; TITLE OF INVENTION: AND METHODS OF USE
; NUMBER OF SEQUENCES: 105

CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: TX
; COUNTRY: USA
; ZIP: 77210-4433
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/010,317
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/036,139
; FILING DATE: 21-JAN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Hibler, David W.
; REGISTRATION NUMBER: 41,071
; REFERENCE/DOCKET NUMBER: TANK:189
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 512-418-3000
; TELEFAX: 512-474-7577
; INFORMATION FOR SEQ ID NO: 56:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 39 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; US-09-010-317-56

Query Match 100.0%; Score 53; DB 4; Length 39;
Best Local Similarity 100.0%; Pred. No. 0.0052;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YE0GNIYDI 10
Db 19 YE0GNIYDI 28

RESULT 14
US-08-259-000-3
; Sequence 3, Application US/08259000
; Patent No. 5571514
; GENERAL INFORMATION:
; APPLICANT: HOOK, Magnus
; APPLICANT: LINDBERG, Martin Kjell
; APPLICANT: SIGNS, Lars Christler
; APPLICANT: WADSTROM, Torkel Mikael
; APPLICANT: FROMAN, Gunnar
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN AS WELL AS
; TITLE OF INVENTION: ITS PREPARATION
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Doane, Swecker & Mathis
; STREET: P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22113-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/259,000
; FILING DATE: 13-JUN-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:

APPLICATION NUMBER: SE 8702272-9
FILING DATE: 01-JUN-1987
ATTORNEY/AGENT INFORMATION:
NAME: Meuth, Donna M
REGISTRATION NUMBER: 36,607
REFERENCE/DOCKET NUMBER: 012885-062
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 114 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-259-000-3

Query Match 100.0%; Score 53; DB 1; Length 114;
Best Local Similarity 100.0%; Pred. No. 0.017;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YE0GGNIVDI 10
|||||
DB 20 YE0GGNIVDI 29

RESULT 15

US-08-459-135A-7
Sequence 7, Application US/08459135A
Patent No. 5955078

GENERAL INFORMATION:

APPLICANT: BURHAM, Martin Karl Russel
APPLICANT: CHOPRA, Ian
APPLICANT: CRITCHLEY, Ian Alfred
APPLICANT: KNOWLES, David Justin Charles
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN: MONOCLONAL ANTIBODY AND THEIR US
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
STATE: PA
COUNTRY: U.S.A.
ZIP: 19406-0939

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: Fastseq, Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/459,135A
FILING DATE: 02-JUN-1995
CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/GB/94/00215
FILING DATE: 04-Feb-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Gimmil, Edward R
REGISTRATION NUMBER: 38,891
REFERENCE/DOCKET NUMBER: P30591C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-4478
TELEFAX: 610-270-5090

TELEX:

INFORMATION FOR SEQ ID NO: 7:

SEQUENCE CHARACTERISTICS:
LENGTH: 130 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-459-135A-7

Query Match 100.0%; Score 53; DB 2; Length 130;
Best Local Similarity 100.0%; Pred. No. 0.02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YE0GGNIVDI 10
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DB 20 YE0GGNIVDI 29

Search completed: October 22, 2005, 07:41:41
Job time : 17.35 secs

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OM protein - protein search, using sw model

Run on: October 22, 2005, 12:09:40 ; Search time 57.25 Seconds
(without alignments)
72.924 Million cell updates/sec

Title: US-10-731-238-72

Perfect score: 53

Sequence: 1 YEOGNIVDI 10

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 1862951 seqs, 417491010 residues
Total number of hits satisfying chosen parameters: 1862951

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

Published Applications, AA:*

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2: /cgn2_6/prodata/2/pubppaa/PCT_NEW_PUB.pep:*
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8: /cgn2_6/prodata/2/pubppaa/US08_PUBCOMB.pep:*
9: /cgn2_6/prodata/2/pubppaa/US09A_PUBCOMB.pep:*
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14: /cgn2_6/prodata/2/pubppaa/US10C_PUBCOMB.pep:*
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20: /cgn2_6/prodata/2/pubppaa/US11_NEW_PUB.pep:*
21: /cgn2_6/prodata/2/pubppaa/US60_NEW_PUB.pep:*
22: /cgn2_6/prodata/2/pubppaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by the result to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	53	100.0	10	US-10-731-238-72	Sequence 72, Appl1
2	53	100.0	38	US-10-731-238-5	Sequence 5, Appl1
3	53	100.0	38	US-10-731-238-35	Sequence 35, Appl1
4	53	100.0	38	US-10-731-238-36	Sequence 36, Appl1
5	53	100.0	38	US-10-731-238-37	Sequence 37, Appl1
6	53	100.0	38	US-10-731-238-38	Sequence 38, Appl1
7	53	100.0	38	US-10-731-238-39	Sequence 39, Appl1
8	53	100.0	38	US-10-731-238-40	Sequence 40, Appl1
9	53	100.0	38	US-10-731-238-41	Sequence 41, Appl1
10	53	100.0	38	US-10-731-238-42	Sequence 42, Appl1
11	53	100.0	39	US-10-731-238-56	Sequence 56, Appl1

12	53	100.0	139	9	US-09-813-820-8	Sequence 8, Appl1
13	53	100.0	388	8	US-08-901-062-1	Sequence 1, Appl1
14	53	100.0	559	8	US-08-781-966A-5251	Sequence 5251, Ap
15	53	100.0	559	15	US-10-329-624-5251	Sequence 5251, Ap
16	53	100.0	767	9	US-09-815-242-5899	Sequence 5899, Ap
17	53	100.0	767	9	US-09-815-242-13140	Sequence 13140, A
18	53	100.0	940	17	US-10-470-048B-424	Sequence 424, App
19	53	100.0	948	17	US-10-470-048B-69	Sequence 69, Appl1
20	53	100.0	961	15	US-10-282-122A-43778	Sequence 43778, A
21	53	100.0	978	9	US-09-815-242-5456	Sequence 5456, Ap
22	53	100.0	1001	9	US-09-815-242-14686	Sequence 12686, A
23	53	100.0	1018	9	US-09-815-242-5797	Sequence 5797, Ap
24	53	100.0	1018	9	US-09-815-242-12838	Sequence 12838, A
25	53	100.0	1018	17	US-10-470-048B-68	Sequence 68, Appl1
26	53	100.0	1027	8	US-08-781-966A-5254	Sequence 5254, Ap
27	53	100.0	1027	15	US-10-329-624-5254	Sequence 5254, Ap
28	53	100.0	1038	15	US-10-282-122A-43827	Sequence 43827, A
29	52	98.1	30	14	US-10-287-821-1	Sequence 1, Appl1
30	52	98.1	31	14	US-10-287-821-2	Sequence 2, Appl1
31	47	88.7	36	18	US-10-731-238-58	Sequence 58, Appl1
32	47	88.7	38	18	US-10-731-238-7	Sequence 7, Appl1
33	47	88.7	38	18	US-10-731-238-45	Sequence 45, Appl1
34	47	88.7	38	18	US-10-731-238-46	Sequence 46, Appl1
35	47	88.7	38	18	US-10-731-238-47	Sequence 47, Appl1
36	47	88.7	38	18	US-10-731-238-48	Sequence 48, Appl1
37	45	84.9	38	18	US-10-731-238-6	Sequence 6, Appl1
38	45	84.9	38	18	US-10-731-238-43	Sequence 43, Appl1
39	45	84.9	39	18	US-10-731-238-57	Sequence 57, Appl1
40	43	81.1	10	18	US-10-731-238-71	Sequence 71, Appl1
41	41	77.4	10	18	US-10-731-238-73	Sequence 73, Appl1
42	41	77.4	14	18	US-10-731-238-60	Sequence 60, Appl1
43	41	75.5	591	15	US-10-282-122A-53313	Sequence 53313, A
44	40	75.5	91	16	US-10-425-115-38463	Sequence 38463, A
45	39	73.6	36	18	US-10-731-238-59	Sequence 59, Appl1

ALIGNMENTS

RESULT 1
US-10-731-238-72
; Sequence 72, Application US/0731238
; Publication No. US20050123552A1
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
Patel, Joseph M.
House-Pompeo, Karen L.
Speziale, Pietro
John, Danny
McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 443
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/731,238
FILING DATE: 10-Dec-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE: 21-Jan-1998
APPLICATION NUMBER: US 60/036,139

FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAMK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 72:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 72:
US-10-731-238-72

Query Match 100.0%; Score 53; DB 18; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0086;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YE0GGNIVDI 10
Db 1 YE0GGNIVDI 10

RESULT 2
US-10-731-238-5
Sequence 5, Application US/10731238
Publication No. US20050123552A1
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
Patti, Joseph M.
House-Pompeo, Karen L.
Speziale, Pietro
John, Danny
McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/731,238
FILING DATE: 10-Dec-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE: 21-Jan-1998
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAMK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>

TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-10-731-238-5

Query Match 100.0%; Score 53; DB 18; Length 38;
Best Local Similarity 100.0%; Pred. No. 0.035;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YE0GGNIVDI 10
Db 19 YE0GGNIVDI 28

RESULT 3
US-10-731-238-35
Sequence 35, Application US/10731238
Publication No. US20050123552A1
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
Patti, Joseph M.
House-Pompeo, Karen L.
Speziale, Pietro
John, Danny
McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/731,238
FILING DATE: 10-Dec-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE: 21-Jan-1998
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAMK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 35:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 35:
US-10-731-238-35

Query Match 100.0%; Score 53; DB 18; Length 38;
Best Local Similarity 100.0%; Pred. No. 0.035;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YE0GGNIVDI 10
Db 19 YE0GGNIVDI 28

Db 1 KPSYQFGHNPVDFEEDTLPK 21

RESULT 15
US-09-010-317-33

; Sequence 33, Application US/09010317
; Patent No. 6685943

; GENERAL INFORMATION:

; APPLICANT: Hook, Magnus

; APPLICANT: Patti, Joseph M.

; APPLICANT: House-Pompeo, Karen L.

; APPLICANT: Speziale, Pietro

; APPLICANT: Joh, Danny

; APPLICANT: McGavin, Martin J.

; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS

; TITLE OF INVENTION: AND METHODS OF USE

; NUMBER OF SEQUENCES: 105

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Arnold, White & Durkee

; STREET: P.O. Box 4433

; CITY: Houston

; STATE: TX

; COUNTRY: USA

; ZIP: 77210-4433

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/010,317

; FILING DATE:

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 60/036,139

; FILING DATE: 21-JAN-1997

; ATTORNEY/AGENT INFORMATION:

; NAME: Hibler, David W.

; REGISTRATION NUMBER: 41,071

; REFERENCE/DOCKET NUMBER: TANK:189

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 512-418-3000

; TELEFAX: 512-474-7577

; INFORMATION FOR SEQ ID NO: 33:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 21 amino acids

; TYPE: amino acid

; STRANDEDNESS:

; TOPOLOGY: linear

; US-09-010-317-33

Query Match 87.5%; Score 105; DB 4; Length 21;

Best Local Similarity 95.0%; Pred. No. 7e-10; 1; Indels 0; Gaps 0;

Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Search completed: October 22, 2005, 03:51:14

Job time : 15.9358 secs

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1 KPSYQFGHNSVDFEEDTLPP 20

1 KPSYQFGHNSVDFEEDTLPP 20

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GenCore version 5.1.6
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OM protein - protein search, using SW model

Run on: October 22, 2005, 10:49:15 ; Search time 59.2367 Seconds
(without alignments)
148.005 Million cell updates/sec

Title: US-10-731-238-31

Perfect score: 120
Sequence: 1 KPSYQFGHNSVDFEEDTPPK 21

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1862951 seqs, 417491010 residues

Total number of hits satisfying chosen parameters: 1862951

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

Published Applications AA.*
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19: /cgn2_6/ptodata/2/pubpaa/US11A_PUBCOMB.pep.*
20: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep.*
21: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
22: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	120	100.0	21	18	US-10-731-238-31
2	110	91.7	21	18	US-10-731-238-9
3	110	91.7	37	20	US-11-066-697-1134
4	110	91.7	139	9	US-09-813-820-8
5	110	91.7	1018	9	US-09-815-242-5797
6	110	91.7	1018	9	US-09-815-242-12838
7	110	91.7	1018	17	US-10-470-048B-68
8	110	91.7	1027	15	US-08-781-986A-5254
9	110	91.7	1027	15	US-10-329-624-5254
10	107	89.2	961	15	US-10-282-122A-43778
11	107	89.2	978	9	US-09-815-242-5456

12	107	89.2	1001	9	US-09-815-242-12686	Sequence 12686, A
13	107	89.2	1038	15	US-10-282-122A-43827	Sequence 43827, A
14	105	87.5	21	18	US-10-731-238-14	Sequence 14, App1
15	105	87.5	21	18	US-10-731-238-16	Sequence 16, App1
16	105	87.5	21	18	US-10-731-238-23	Sequence 23, App1
17	105	87.5	21	18	US-10-731-238-33	Sequence 33, App1
18	104	86.7	21	18	US-10-731-238-18	Sequence 18, App1
19	104	86.7	21	18	US-10-731-238-24	Sequence 24, App1
20	104	86.7	21	18	US-10-731-238-27	Sequence 27, App1
21	104	86.7	21	18	US-10-731-238-28	Sequence 28, App1
22	104	86.7	21	18	US-10-731-238-30	Sequence 30, App1
23	103	85.8	21	18	US-10-731-238-25	Sequence 25, App1
24	103	85.8	21	18	US-10-731-238-29	Sequence 29, App1
25	103	85.8	388	8	US-08-901-062-1	Sequence 1, App1
26	103	85.8	559	8	US-08-781-986A-5251	Sequence 5251, Ap
27	103	85.8	559	15	US-10-329-624-5251	Sequence 5251, Ap
28	103	85.8	940	17	US-10-470-048B-424	Sequence 424, App1
29	103	85.8	948	17	US-10-470-048B-69	Sequence 69, App1
30	102	85.0	21	18	US-10-731-238-15	Sequence 15, App1
31	102	85.0	21	18	US-10-731-238-17	Sequence 17, App1
32	102	85.0	21	18	US-10-731-238-20	Sequence 20, App1
33	102	85.0	21	18	US-10-731-238-22	Sequence 22, App1
34	102	85.0	21	18	US-10-731-238-32	Sequence 32, App1
35	102	85.0	22	18	US-10-731-238-13	Sequence 13, App1
36	100	83.3	21	18	US-10-731-238-17	Sequence 17, App1
37	100	83.3	21	18	US-10-731-238-19	Sequence 19, App1
38	100	83.3	21	18	US-10-731-238-21	Sequence 21, App1
39	100	83.3	21	18	US-10-731-238-26	Sequence 26, App1
40	82	68.3	21	18	US-10-731-238-34	Sequence 34, App1
41	78	65.0	14	18	US-10-731-238-51	Sequence 51, App1
42	59	49.2	10	18	US-10-731-238-96	Sequence 96, App1
43	58	48.3	10	18	US-10-731-238-97	Sequence 97, App1
44	57	47.5	10	18	US-10-731-238-98	Sequence 98, App1
45	56	46.7	10	18	US-10-731-238-99	Sequence 99, App1

ALIGNMENTS

RESULT 1
US-10-731-238-31
Sequence 31, Application US/10731238
Publication No. US20050123552A1
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
Patli, Joseph M.
House-Pompeo, Karen L.
Speziale, Pietro
Job, Danny
McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSER: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/731,238
FILING DATE: 10-Dec-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE: 21-Jan-1998
APPLICATION NUMBER: US 60/036,139

FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAMK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 31:
US-10-731-238-31

Query Match 100.0%; Score 120; DB 18; Length 21;
Best Local Similarity 100.0%; Pred. No. 5,4e-11;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KPSYFGGHSVDFEEDTPK 21
DB 1 KPSYFGGHSVDFEEDTPK 21

RESULT 2
US-10-731-238-9
Sequence 9, Application US/10731238
Publication No. US20050123552A1
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
Pacti, Joseph M.
House-Pompeo, Karen L.
Speziale, Pietro
Joh, Danny
McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/731,238
FILING DATE: 10-Dec-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE: 21-Jan-1998
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAMK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>

TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 9:
US-10-731-238-9

Query Match 91.7%; Score 110; DB 18; Length 21;
Best Local Similarity 95.2%; Pred. No. 1.8e-09;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KPSYFGGHSVDFEEDTPK 21
DB 1 KPSYFGGHSVDFEEDTPK 21

RESULT 3
US-11-066-697-1134
Sequence 1134, Application US/11066697
Publication No. US20050187159A1
GENERAL INFORMATION:
APPLICANT: Bridon, Dominique P.
Ezzin, Alan M.
Milner, Peter G.
Holmes, Darren L.
APPLICANT: Thibaudau, Karen
TITLE OF INVENTION: PROTECTION OF ENDOGENOUS THERAPEUTIC PEPTIDES FROM
PEPTIDASE ACTIVITY THROUGH CONJUGATION TO BLOOD
TITLE OF INVENTION: COMPONENTS
FILE REFERENCE: 500862002301
CURRENT APPLICATION NUMBER: US/11/066,697
CURRENT FILING DATE: 2005-02-25
PRIOR APPLICATION NUMBER: 09/657,276
PRIOR FILING DATE: 2000-09-07
PRIOR APPLICATION NUMBER: 60/153,406
PRIOR FILING DATE: 1999-09-10
PRIOR APPLICATION NUMBER: 60/159,783
PRIOR FILING DATE: 1999-10-15
NUMBER OF SEQ ID NOS: 1617
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1134
LENGTH: 37
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-11-066-697-1134

Query Match 91.7%; Score 110; DB 20; Length 37;
Best Local Similarity 95.2%; Pred. No. 3.2e-09;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KPSYFGGHSVDFEEDTPK 21
DB 16 KPSYFGGHSVDFEEDTPK 36

RESULT 4
US-09-813-820-8
Sequence 8, Application US/09813820
Patent No. US20020102262A1
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
Pacti, Joseph M.
House-Pompeo, Karen
Shanam, Narayana
Symerky, Jindlich
TITLE OF INVENTION: COLLAGEN BINDING PROTEIN COMPOSITIONS
AND METHODS OF USE
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: Texas

```

; COUNTRY: U.S.
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION NUMBER: US/09/813,820
; APPLICATION NUMBER: 22-Mar-2001
; FILING DATE: 22-Mar-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/856,253
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Kitchell, Barbara S.
; REGISTRATION NUMBER: 33,928
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (512) 418-3000
; TELEFAX: (512) 474-7577
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 139 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-09-813-820-8

Query Match          91.7%; Score 110; DB 9; Length 139;
Best Local Similarity 95.2%; Pred. No. 1.3e-08;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Db 107 KPSYQFGHNSVDFEEDTPK 127

RESULT 5
US-09-815-242-5797
; Sequence 5797, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Karl L.
; APPLICANT: Zyekind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; FILE REFERENCE: ELITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version 4.0
; FILE REFERENCE: SOINN.035US
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; SEQ ID NO 5797
; LENGTH: 1018
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-09-815-242-5797

Query Match          91.7%; Score 110; DB 9; Length 1018;
Best Local Similarity 95.2%; Pred. No. 1.1e-07;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Q# 1 KPSYQFGHNSVDFEEDTPK 21
Db 837 KPSYQFGHNSVDFEEDTPK 857

RESULT 6
US-09-815-242-12838
; Sequence 12838, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Karl L.
; APPLICANT: Zyekind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; FILE REFERENCE: ELITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12838
; LENGTH: 1018
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-09-815-242-12838

Query Match          91.7%; Score 110; DB 9; Length 1018;
Best Local Similarity 95.2%; Pred. No. 1.1e-07;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Q# 1 KPSYQFGHNSVDFEEDTPK 21
Db 837 KPSYQFGHNSVDFEEDTPK 857

RESULT 7
US-10-470-048B-68
; Sequence 68, Application US/10470048B
; Publication No. US2005003744A1
; GENERAL INFORMATION:
; APPLICANT: MEINKE ET AL.
; TITLE OF INVENTION: A METHOD FOR IDENTIFICATION, ISOLATION AND PRODUCTION OF
; FILE REFERENCE: SOINN.035US
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;; CURRENT APPLICATION NUMBER: US/10/470,048B
;; CURRENT FILING DATE: 2003-07-25
;; NUMBER OF SEQ ID NOS: 603
;; SOFTWARE: PatentIn version 3.1
;; SEQ ID NO: 68
;; LENGTH: 1018
;; TYPE: PRT
;; ORGANISM: Staphylococcus aureus
US-10-470-048B-68

Query Match 91.7%; Score 110; DB 17; Length 1018;
Best Local Similarity 95.2%; Pred. No. 1,1e-07;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KPSYFGGHSVDFEEDTLPK 21
DB 837 KPSYFGGHSVDFEEDTLPK 857

RESULT 8
US-08-781-986A-5254
; Sequence 5254, Application US/08781986A
; Publication No. US20030054436A1
; GENERAL INFORMATION:
; APPLICANT: Charles Kunach
; TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
; NUMBER OF SEQUENCES: 5255
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/781,986A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Benson, Bob
; REGISTRATION NUMBER: 30,446
; REFERENCE/DOCKET NUMBER: PB248BP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 5254:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1027 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-781-986A-5254

Query Match 91.7%; Score 110; DB 8; Length 1027;
Best Local Similarity 95.2%; Pred. No. 1,1e-07;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KPSYFGGHSVDFEEDTLPK 21
DB 846 KPSYFGGHSVDFEEDTLPK 866

RESULT 9
US-10-329-624-5254

;; Sequence 5254, Application US/10329624
;; Publication No. US20040043037A1
;; GENERAL INFORMATION:
;; APPLICANT: Charles Kunach
;; Gil H. Choi
;; Patrick S. Dillon
;; Craig A. Rosen
;; Steven C. Barash
;; Michael R. Fannon
;; TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
;; NUMBER OF SEQUENCES: 5256
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Human Genome Sciences, Inc.
;; STREET: 9410 Key West Avenue
;; CITY: Rockville
;; STATE: Maryland
;; COUNTRY: USA
;; ZIP: 20850
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
;; COMPUTER: HP Vectra 486/33
;; OPERATING SYSTEM: MSDOS version 6.2
;; SOFTWARE: ASCII Text
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/10/329,624
;; FILING DATE: 27-Dec-2002
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 08/956,171
;; FILING DATE: October 20, 1997
;; APPLICATION NUMBER: 60/009,861
;; FILING DATE: January 5, 1996
;; APPLICATION NUMBER: 08/781,986
;; FILING DATE: January 3, 1997
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Mark J. Hyman
;; REGISTRATION NUMBER: 46,789
;; REFERENCE/DOCKET NUMBER: PB248P1D1
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (240) 314-1224
;; TELEFAX: (301) 309-8439
;; INFORMATION FOR SEQ ID NO: 5254:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 1027 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; SEQUENCE DESCRIPTION: SEQ ID NO: 5254:
US-10-329-624-5254

Query Match 91.7%; Score 110; DB 15; Length 1027;
Best Local Similarity 95.2%; Pred. No. 1,1e-07;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KPSYFGGHSVDFEEDTLPK 21
DB 846 KPSYFGGHSVDFEEDTLPK 866

RESULT 10
US-10-282-122A-43778
; Sequence 43778, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant

```
APPLICANT: Yamamoto, Robert
APPLICANT: Foreyth, R.
TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REFERENCE: ELITRA.034A
CURRENT FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/230,335
PRIOR FILING DATE: 2000-09-06
PRIOR APPLICATION NUMBER: 60/230,347
PRIOR FILING DATE: 2000-09-09
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/267,636
PRIOR FILING DATE: 2001-02-09
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 78614
SOFTWARE: PatentIn version 3.1
SEQ ID NO 43778
LENGTH: 961
TYPE: PRF
ORGANISM: Staphylococcus aureus
US-10-282-122A-43778

Query Match      89.2% Score 107; DB 15; Length 961;
Best Local Similarity 90.5% Pred. No. 2.8e-07;
Matches 19; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
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QY 1 KPSYOGGHSVDFEEDTPK 21
DB 784 KPNYOGGHSVDFEEDTLPK 804
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RESULT 11
US-09-815-242-5456
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Sequence 5456, Application US/09815242
Patent No. US20020061569A1
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```
GENERAL INFORMATION:
```

```
APPLICANT: Haselbeck, Robert
```

```
APPLICANT: Ohlsen, Karl L.
```

```
APPLICANT: Zyskind, Judith W.
```

```
APPLICANT: Wall, Daniel
```

```
APPLICANT: Trawick, John D.
```

```
APPLICANT: Carr, Grant J.
```

```
APPLICANT: Yamamoto, Robert T.
```

```
APPLICANT: Xu, H. Howard
```

```
TITLE OF INVENTION: Identification of Essential Genes in
```

```
FILE REFERENCE: ELITRA.011A
```

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CURRENT APPLICATION NUMBER: US/09/815,242
```

```
CURRENT FILING DATE: 2001-03-21
```

```
PRIOR APPLICATION NUMBER: 60/191,078
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PRIOR FILING DATE: 2000-03-21
```

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PRIOR APPLICATION NUMBER: 60/206,848
```

```
PRIOR FILING DATE: 2000-05-23
```

```
PRIOR APPLICATION NUMBER: 60/207,727
```

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PRIOR FILING DATE: 2000-05-26
```

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PRIOR APPLICATION NUMBER: 60/242,578
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PRIOR FILING DATE: 2000-10-23
```

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PRIOR APPLICATION NUMBER: 60/253,625
```

```
PRIOR FILING DATE: 2000-11-27
```

```
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 5456
LENGTH: 978
TYPE: PRF
ORGANISM: Staphylococcus aureus
US-09-815-242-5456

Query Match      89.2% Score 107; DB 9; Length 978;
Best Local Similarity 90.5% Pred. No. 2.9e-07;
Matches 19; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
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QY 1 KPSYOGGHSVDFEEDTPK 21
DB 815 KPNYOGGHSVDFEEDTLPK 835
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RESULT 12
US-09-815-242-12686
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Sequence 12686, Application US/09815242
Patent No. US20020061569A1
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```
GENERAL INFORMATION:
```

```
APPLICANT: Haselbeck, Robert
```

```
APPLICANT: Ohlsen, Karl L.
```

```
APPLICANT: Zyskind, Judith W.
```

```
APPLICANT: Wall, Daniel
```

```
APPLICANT: Trawick, John D.
```

```
APPLICANT: Carr, Grant J.
```

```
APPLICANT: Yamamoto, Robert T.
```

```
APPLICANT: Xu, H. Howard
```

```
TITLE OF INVENTION: Identification of Essential Genes in
```

```
FILE REFERENCE: ELITRA.011A
```

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CURRENT APPLICATION NUMBER: US/09/815,242
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CURRENT FILING DATE: 2001-03-21
```

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PRIOR APPLICATION NUMBER: 60/191,078
```

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PRIOR FILING DATE: 2000-03-21
```

```
PRIOR APPLICATION NUMBER: 60/206,848
```

```
PRIOR FILING DATE: 2000-05-23
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PRIOR APPLICATION NUMBER: 60/207,727
```

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PRIOR FILING DATE: 2000-05-26
```

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PRIOR APPLICATION NUMBER: 60/242,578
```

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PRIOR FILING DATE: 2000-10-23
```

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PRIOR APPLICATION NUMBER: 60/253,625
```

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PRIOR FILING DATE: 2000-11-27
```

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PRIOR APPLICATION NUMBER: 60/257,931
```

```
PRIOR FILING DATE: 2000-12-22
```

```
PRIOR APPLICATION NUMBER: 60/269,308
```

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PRIOR FILING DATE: 2001-02-16
```

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NUMBER OF SEQ ID NOS: 14110
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SOFTWARE: FastSeq for Windows Version 4.0
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SEQ ID NO 12686
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LENGTH: 1001
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TYPE: PRF
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```
ORGANISM: Staphylococcus aureus
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US-09-815-242-12686
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Query Match      89.2% Score 107; DB 9; Length 1001;
Best Local Similarity 90.5% Pred. No. 2.9e-07;
Matches 19; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
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QY 1 KPSYOGGHSVDFEEDTPK 21
DB 838 KPNYOGGHSVDFEEDTLPK 858
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RESULT 13
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US-10-282-122A-43827
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Sequence 43827, Application US/10282122A
```

Publication No. US20040029129A1
GENERAL INFORMATION:
APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Karl
APPLICANT: Zyskind, Judith
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John
APPLICANT: Carr, Grant
APPLICANT: Yamamoto, Robert
APPLICANT: Forsyth, R.
APPLICANT: Xu, H.
TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REFERENCE: ELITRA.034A
CURRENT APPLICATION NUMBER: US/10/282.122A
CURRENT FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/230,335
PRIOR FILING DATE: 2000-09-06
PRIOR APPLICATION NUMBER: 60/230,347
PRIOR FILING DATE: 2000-09-09
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/267,636
PRIOR FILING DATE: 2001-02-09
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 78614
SOFTWARE: PatentIn version 3.1
SEQ ID NO 43827
LENGTH: 1038
TYPE: PRT
ORGANISM: Staphylococcus aureus
US-10-282-122A-43827
Query Match
Best Local Similarity 89.2%; Score 107; DB 15; Length 1038;
Matches 19; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 KPSYQFGGHSVDPEDTLPK 21
DB 833 KPNYQFGGHSVDPEDTLPK 853
RESULT 14
US-10-731-238-14
Sequence 14, Application US/10731238
Publication No. US20050123552A1
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
Patli, Joseph M.
House-Pompeo, Karen L.
Speziale, Pietro
Joh, Danny
McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433

CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/731.238
FILING DATE: 10-Dec-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/010.317
FILING DATE: 21-Jan-1998
APPLICATION NUMBER: US 60/036.139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TMMK.189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 14:
US-10-731-238-14
Query Match
Best Local Similarity 87.5%; Score 105; DB 18; Length 21;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2 PSYQFGGHSVDPEDTLPK 21
DB 2 PSYQFGGHSVDPEDTLPK 21
RESULT 15
US-10-731-238-16
Sequence 16, Application US/10731238
Publication No. US20050123552A1
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
Patli, Joseph M.
House-Pompeo, Karen L.
Speziale, Pietro
Joh, Danny
McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/731.238
FILING DATE: 10-Dec-2003
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/09/010,317
 FILING DATE: 21-Jan-1998
 APPLICATION NUMBER: US 60/036,139
 FILING DATE: 21-JAN-1997
 ATTORNEY/AGENT INFORMATION:
 NAME: Hibler, David W.
 REGISTRATION NUMBER: 41,071
 REFERENCE/DOCKET NUMBER: TAMK:189
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 512-418-3000
 TELEFAX: 512-474-7577
 INFORMATION FOR SEQ ID NO: 16:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 21 amino acids
 TYPE: amino acid
 STRANDEDNESS: <Unknown>
 TOPOLOGY: linear
 SEQUENCE DESCRIPTION: SEQ ID NO: 16:
 US-10-731-238-16

Query Match 87.5%; Score 105; DB 18; Length 21;
 Best Local Similarity 90.5%; Pred. No. 1e-08;
 Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 KPSTQFGHNSVDFEEDTPPK 21
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 Db 1 KPSTQFGHNSVDFEEDTLPK 21

Search completed: October 22, 2005, 11:34:44
 Job time : 60.2367 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 22, 2005, 02:23:36 / Search time 10.5465 Seconds
(without alignments)
191.586 Million cell updates/sec

Title: US-10-731-238-31

Sequence: 1 KPSYQFGHNSVDFEEDTPPK 21

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	110	91.7	1018	2	A32192 fibronectin-binding
2	107	89.2	961	2	G90053 hypothetical prote
3	107	89.2	1038	2	H90053 hypothetical prote
4	103	85.8	940	2	S19702 fibronectin-binding
5	51	42.5	445	2	F90562 hypothetical prote
6	47.5	39.6	973	2	T21463 hypothetical prote
7	46	38.3	382	2	H69904 hypothetical prote
8	46	38.3	453	2	H70333 conserved hypotet
9	46	38.3	474	2	B84357 serine-tRNA synthe
10	45.5	37.9	234	2	T30473 late expression fa
11	45	37.5	216	2	A39926 hypothetical prote
12	45	37.5	229	2	AG0698 probable pathogeni
13	45	37.5	347	1	HPMS haptoglobin precu
14	45	37.5	462	1	A39356 3-oxoacyl-l-acyl-ca
15	45	37.5	469	2	T10061 conserved hypotet
16	45	37.5	808	2	F81180 myosin heavy chain
17	45	37.5	1322	2	A59288 amino acid transpo
18	44.5	37.1	594	2	T43246 transcription regu
19	44	36.7	188	2	E97318 dTDP-4-dehydrothm
20	44	36.7	302	2	E83000 squamosa promoter
21	44	36.7	323	2	T52297 conserved hypotet
22	44	36.7	361	2	B83151 hypothetical prote
23	44	36.7	392	2	T32555 vesicle-associated
24	44	36.7	433	2	T01405 chlophen / furan o
25	44	36.7	459	2	AE2390 hypothetical prote
26	44	36.7	1038	2	T15098 hypothetical prote
27	44	36.7	1224	2	F96795 hypothetical prote
28	43.5	36.2	105	2	T10350 hypothetical prote
29	43	35.8	197	2	C69779 NAD(P)H oxidoreduc

30	43	35.8	288	2	T37395 probable 33.6K pro
31	43	35.8	288	2	A42518 ABR protein - vacc
32	43	35.8	296	2	T29892 hypothetical prote
33	43	35.8	417	2	T34930 probable secreted
34	43	35.8	427	2	D95159 3-phosphoshikimate
35	43	35.8	431	2	D98025 hypothetical prote
36	43	35.8	468	2	T26081 glycoprotein B pre
37	43	35.8	928	1	VCBEMC hypothetical prote
38	43	35.8	1071	2	B85343 hypothetical prote
39	43	35.8	1097	2	T31504 trigger factor (pr
40	42.5	35.4	431	2	B84031 very hypothetical
41	42	35.0	184	2	T38315 hypothetical prote
42	42	35.0	222	2	S74066 MHC class I histoc
43	42	35.0	257	2	A36057 fructokinase - Dei
44	42	35.0	303	2	B75485 hypothetical prote
45	42	35.0	317	2	S57546

ALIGNMENTS

RESULT 1

A32192
fibronectin-binding protein - Staphylococcus aureus
C/Species: Staphylococcus aureus
C/Date: 31-Jul-1989 #sequence_revision 31-Jul-1989 #text_change 16-Feb-1997
R/Accession: A32192
R/Signaes, C./Raucel, G./Joensson, K./Lindgren, P.E./Anantharamiah, G.M./Hoecek, M.
Proc. Natl. Acad. Sci. U.S.A. 86, 699-703, 1989
A/Title: Nucleotide sequence of the gene for a fibronectin-binding protein from Staphyloc
A/Reference number: A32192; MUID:8909898; PMID:2521391
A/Accession: A32192
A/Status: Preliminary
A/Molecule type: DNA
A/Residues: 1-1018 <SIG>
A/Cross-references: GB:J04151
C/Keywords: fibronectin binding

Query Match 91.7% Score 110; DB 2; Length 1018;
Best Local Similarity 95.2% Pred. No. 3.8e-09;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KPSYQFGHNSVDFEEDTPPK 21
DB 837 KPSYQFGHNSVDFEEDTPPK 857

RESULT 2

G90053
hypothetical protein fnb [imported] - Staphylococcus aureus (strain N315)
C/Species: Staphylococcus aureus
C/Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C/Accession: G90053
R/Kuruda, M./Ohta, T./Uchiyama, I./Baba, T./Yuzawa, H./Kobayashi, I./Cui, L./Oguch
ma, A./Mizutani-Ui, Y./Kobayashi, N./Sawano, T./Inoue, R./Kaito, C./Sekimizu, K./
C./Shiba, T./Hattori, M./Ogasawara, N./Hayashi, H./Hiramatsu, K.
Lancet 357, 1225-1240, 2001
A/Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.
A/Reference number: A69758; MUID:21311952; PMID:11418146
A/Accession: G90053
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-961 <KUR>
A/Cross-references: UNIPROT:Q99RD3; GB:BA000018; PID:g13702452; PIDN:BA843593.1; GSPDB:G
A/Experimental source: strain N315
C/Genetics: fnb8
A/Genes: fnb8

Query Match 89.2% Score 107; DB 2; Length 961;
Best Local Similarity 90.5% Pred. No. 1.1e-08;
Matches 19; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 KPSYQFGHNSVDFEEDTPPK 21

Db 784 KPNYQFGHNSVDPEDPTLPK 804

RESULT 3

H90053

hypothetical protein fnb [imported] - Staphylococcus aureus (strain N315)

C/Species: Staphylococcus aureus

C/Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004

C/Accession: H90053

R/Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguc

ma, A.; Mitutani-Uji, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.;

C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramoto, K.

Lancet 357, 1225-1240, 2001

A/Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.

A/Reference number: A89758; MUID:21311952; PMID:11418146

A/Accession: H90053

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-1038 <KUR>

A/Cross-references: UNIPROT:Q99RD2; GB:BA000018; PID:g13702453; PIDN:BAB43594.1; GSPDB:C

A/Experimental source: strain N315

C/Genetics:

A/Gene: fnb

Query Match 89.2%; Score 107; DB 2; Length 1038;

Best Local Similarity 90.5%; Pred. No. 1.2e-08;

Matches 19; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 KPSYQFGHNSVDPEDPTLPK 21

Db 833 KPNYQFGHNSVDPEDPTLPK 853

RESULT 4

S19702

fibronectin-binding protein B - Staphylococcus aureus

C/Species: Staphylococcus aureus

C/Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004

C/Accession: S19702

R./Jensen, K.; Signaes, C.; Mueller, H.P.; Lindberg, M.

Eur. J. Biochem. 202, 1041-1048, 1991

A/Title: Two different genes encode fibronectin binding proteins in Staphylococcus aure

A/Reference number: S19702; MUID:92111475; PMID:1837266

A/Accession: S19702

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-940 <JOB>

A/Cross-references: UNIPROT:Q53682; EMBL:X62992; NID:g49040; PIDN:CAA44726.1; PID:g58156

C/Keywords: fibronectin binding

Query Match 85.8%; Score 103; DB 2; Length 940;

Best Local Similarity 85.7%; Pred. No. 4.5e-08;

Matches 18; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 1 KPSYQFGHNSVDPEDPTLPK 21

Db 773 KPNYQFGHNSVDPEDPTLPK 793

RESULT 5

P90562

hypothetical protein MYPU_4060 [imported] - Mycoplasma pulmonis (strain UAB CTIP)

C/Species: Mycoplasma pulmonis

C/Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 09-Jul-2004

C/Accession: P90562

R./Chambaud, I.; Heiliger, R.; Ferris, S.; Barbe, V.; Samson, D.; Gallison, F.; Moszer, I.;

Nucleic Acids Res. 29, 2145-2153, 2001

A/Title: The complete genome sequence of the murine respiratory pathogen Mycoplasma pulm

A/Reference number: A95512; MUID:21267165; PMID:11353084

A/Accession: P90562

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-445 <KUR>
A/Cross-references: UNIPROT:Q98Q0; GB:AL445566; PID:g14089820; PIDN:CAC13579.1; GSPDB:G
A/Experimental source: strain UAB CTIP
C/Species: MyPU_4060
C/Genetic8:
A/Gene: MYPU_4060
A/Genetic code: SGCC

Query Match 42.5%; Score 51; DB 2; Length 445;
Best Local Similarity 42.1%; Pred. No. 3.7;
Matches 8; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

OY 1 KPSYQFGHNSVDPEDPTLPK 19

Db 334 KPDQVAGHNTYHQEVVP 352

RESULT 6

T21463

hypothetical protein F28B1.2 - Caenorhabditis elegans

C/Species: Caenorhabditis elegans

C/Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004

C/Accession: T21463

R./Matthews, L.

submitted to the EMBL Data Library, November 1996

A/Reference number: Z19426

A/Accession: T21463

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: DNA

A/Residues: 1-973 <WIL>

A/Cross-references: UNIPROT:O45412; EMBL:Z81517; PIDN:CAB04209.1; GSPDB:GN00023; CESP:F2

A/Experimental source: clone F28B1

C/Genetics:

A/Gene: CESP:F28B1.2

A/Map position: 5

A/Introns: 70/3; 234/1; 267/3; 380/3; 600/3; 711/3; 926/3

Query Match 39.6%; Score 47.5; DB 2; Length 973;

Best Local Similarity 41.7%; Pred. No. 32;

Matches 10; Conservative 3; Mismatches 6; Indels 5; Gaps 1;

OY 2 PSYQF-----GHNNSVDPEDPTLPK 20

Db 242 PSWFMFCEDGHPVFSNNPP 265

RESULT 7

H69904

hypothetical protein yodV - Bacillus subtilis

C/Species: Bacillus subtilis

C/Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004

C/Accession: H69904

R./Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Bertec

C.; Bron, S.; Brouillet, S.; Brusch, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Cho

A.; Ehrlich, S.D.; Emmerison, P.T.; Entian, K.D.; Errington, J.; Fabeirc, C.; Ferrari, E.

Nature 390, 249-256, 1997

A/Authors: Foulger, D.; Fritze, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Gallizzi, A.; Gallert

lech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holappel, S.; Hosono, S.; Hullo, M.F.;

Koertter, P.; Koningsstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois,

Y., M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portecello,

Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadale, Y.; Sato, T.; Scanlon,

A/Authors: Schleich, S.; Schroeter, R.; Scottone, F.; Sekiguchi, J.; Sekowska, A.; Serot,

akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terestre, P.; Tognoni, A.; Tosato, V.; Uchiyama,

T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K.

A/Authors: Yoshikawa, H.F.; Zumbstein, E.; Yoshikawa, H.; Danchin, A.

A/Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.

A/Reference number: A69580; MUID:98044033; PMID:9384377

A/Accession: H69904

A/Status: preliminary; nucleic acid sequence not shown; translation not shown

A/Molecule type: DNA

A/Residues: 1-382 <KUN>

A/Cross-references: UNIPROT:P42094; GB:Z99114; GB:AL009126; NID:g2634230; PIDN:CAB13871.1

A/Experimental source: strain 168

C:Genetics:
A:Gene: yodV
C:Superfamily: Bacillus subtilis hypothetical protein yodV

Query Match 38.3%; Score 46; DB 2; Length 382;
Best Local Similarity 52.9%; Pred. No. 19;
Matches 9; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

Qy 3 SYOFGHNSVDFEETP 19
|||:|:|:|:|
Db 91 SYEFGKNNVLDKRYFP 107

RESULT 8
H70333
conserved hypothetical protein aq_378 - Aquifex aeolicus

C:Species: Aquifex aeolicus
C:Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 09-Jul-2004
C:Accession: H70333
R:Decker, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.; Ov

Nature 392, 353-358, 1998
A:Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.
A:Reference number: AV0300; MUID:98196666; PMID:9537320
A:Accession: H70333
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA

A:Residues: 1-453 <AOP>
A:Cross-references: UNIPROT:066700; GB:AE000687; NID:g2983050; PIDN:AA06670.1; PID:g298
A:Experimental source: strain VFS
C:Genetics:
A:Gene: aq_378

Query Match 38.3%; Score 46; DB 2; Length 453;
Best Local Similarity 53.8%; Pred. No. 23;
Matches 7; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 3 SYOFGHNSVDFE 15
|||:|:|:|:|
Db 114 SYFSGSYNLFEE 126

RESULT 9
B84357

serine-tRNA synthetase [imported] - Halobacterium sp. NRC-1
C:Species: Halobacterium sp. NRC-1
C:Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
C:Accession: B84357
R:Ng, W.V.; Kennedy, S.P.; Mahatras, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Laeky, S

; Leitbauer, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Jablo
Jung, K.H.; Alam, M.; Freitas, T.
Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000

A:Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ehardt, H.; Lowe, T.M.; Li
A:Title: Genome sequence of Halobacterium species NRC-1.
A:Reference number: A84160; MUID:20504483; PMID:11016950
A:Accession: B84357
A:Status: preliminary
A:Molecule type: DNA

A:Residues: 1-474 <STO>
A:Cross-references: UNIPROT:Q9HNU8; GB:AE004437; NID:g10581491; PIDN:AA02022.1; GSPDB:G
C:Genetics:
A:Gene: sers
C:Superfamily: serine-tRNA ligase

Query Match 38.3%; Score 46; DB 2; Length 474;
Best Local Similarity 40.0%; Pred. No. 25;
Matches 6; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

Qy 3 SYOFGHNSVDFEED 17
|||:|:|:|:|
Db 234 AYRIGENDADYDD 248

RESULT 10

T30473
late expression factor 1 - Lymantria dispar nuclear polyhedrosis virus

C:Species: Lymantria dispar nuclear polyhedrosis virus, LDMNPV
C:Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
C:Accession: T30473
R:Kurto, J.; Pearson, M.N.; Harwood, S.H.; Funk, C.J.; Evans, J.T.; Slavicek, J.M.; Rohm

Virology 251, 17-34, 1999
A:Title: Sequence and analysis of the genome of a baculovirus pathogenic for Lymantria di
A:Reference number: Z20836; MUID:99124785; PMID:9887315
A:Accession: T30473
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA

A:Residues: 1-234 <KUZ>
A:Cross-references: UNIPROT:Q9YWK4; EMBL:AF081810; NID:g3822234; PIDN:AA070309.1; PID:g31
C:Superfamily: viral DNA primase, left-1

Query Match 37.9%; Score 45.5; DB 2; Length 234;
Best Local Similarity 45.8%; Pred. No. 13;
Matches 11; Conservative 2; Mismatches 8; Indels 3; Gaps 1;

Qy 1 KPSYQFGHNSVDFEETPPK 21
|||:|:|:|:|
Db 67 KPLPENGREWVLDVDFEETPPR 90

RESULT 11
A39926
hypothetical protein 1 - chicken anemia virus

C:Species: chicken anemia virus, CAV
C:Date: 17-Jan-1992 #sequence_revision 17-Jan-1992 #text_change 09-Jul-2004
C:Accession: A39926
R:Notoborn, M.H.M.; de Boer, G.F.; van Roozelaar, D.J.; Karreman, C.; Kranenburg, O.; Vo

J. Virol. 65, 3131-3139, 1991
A:Title: Characterization of cloned chicken anemia virus DNA that contains all elements
A:Reference number: A39926; MUID:91237831; PMID:1851873
A:Accession: A39926
A:Status: preliminary
A:Molecule type: DNA

A:Residues: 1-216 <NOT>
A:Cross-references: UNIPROT:Q99151; GB:M55918; NID:g323250; PIDN:AA01822.1; PID:g323251
C:Comment: This virus is unclassified.

Query Match 37.5%; Score 45; DB 2; Length 216;
Best Local Similarity 56.2%; Pred. No. 15;
Matches 9; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 2 PSYQFGHNSVDFEED 17
|||:|:|:|:|
Db 172 PSEEDGTTSDPDED 187

RESULT 12
AG0698
probable pathogenicity island effector protein seeg [imported] - Salmonella enterica sub

C:Species: Salmonella enterica subsp. enterica serovar Typh
A:Note: this species has also been called Salmonella typh
C:Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
C:Accession: AG0698
R:Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher,

th, T.; Connor, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar,
S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A:Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.;
A:Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov
A:Reference number: AB0502; MUID:21534947; PMID:11677608
A:Accession: AG0698
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-229 <PAR>
A:Cross-references: GB:AL513382; PIDN:CA01960.1; PID:g16502802; GSPDB:GN00176
C:Genetics:
A:Gene: seeg

Query Match 37.5% Score 45; DB 2; Length 229;
 Best Local Similarity 42.1% Pred. No. 16;
 Matches 8; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

QY 2 PSYQFGHNSVDFEDTPK 20
 | : | | | : | : | |
 Db 6 PNAQVGGRPNNAPEBSP 24

RESULT 13
 HPMs
 HaptoGlobin precursor - mouse
 N:Contains: haptoGlobin alpha chain; haptoGlobin beta chain
 C:Species: Mus musculus (house mouse)
 C>Date: 23-Mar-1995 #sequence_revision 31-May-1996 #text_change 18-Jun-1999
 C/Accession: A48918
 R/Yang, F.; Linahan, L.A.; Friedrichs, W.E.; Lalley, P.A.; Sakaguchi, A.Y.; Bowman, B.H.
 Genome 18, 374-380, 1993
 A>Title: Characterization of the mouse haptoGlobin gene.
 A/Reference number: A48918; MUID:94117006; PMID:8288241
 A/Accession: A48918
 A/Molecule type: mRNA
 A/Residues: 1-347 <YAN>
 A/Cross-references: GB:567972; NID:9461137; PIDN:AA829697.1; PID:9461138
 A/Note: sequence extracted from NCBI backbone (NCBI:142156, NCBI:142157); sequence inc
 C/Comment: The mature haptoGlobin molecule is a dimer of heterodimers, the two chains of
 C/Genetics: HaptoGlobin is a plasma glycoprotein; haptoGlobin forms a complex with hemogl
 A/Genes: Hp
 A/Map position: 8
 C:Superfamily: haptoGlobin; complement factor H repeat homology; trypsin homology
 C/Keywords: acute phase; glycoprotein; hemoglobin binding; heterotetramer; iron transport
 F:1-18/Domain: signal sequence #status predicted <SIG>
 F:19-101/Product: haptoGlobin alpha chain #status predicted <ACH>
 F:103-86/Domain: complement factor H repeat homology <FH2>
 F:103-347/Product: haptoGlobin beta chain #status predicted <BCH>
 F:103-340/Domain: trypsin homology <TRY>
 F:133/Diulfide bonds: interchain #status predicted
 F:52-86,90-207,250-281,282-322/Diulfide bonds: #status predicted
 F:148,182,256,264/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 37.5% Score 45; DB 1; Length 347;
 Best Local Similarity 50.0% Pred. No. 25;
 Matches 7; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

QY 8 GHNSVDFEDTPK 21
 | : | | | | : | : | : |
 Db 22 GNDAMDFEDDCPK 35

RESULT 14
 A39356
 3-oxoacyl-[acyl-carrier-protein] synthase (EC 2.3.1.41) I beta chain precursor, chloropl
 N/Alternate names: beta-ketoacyl-[acyl carrier protein] synthase I
 C/Species: Hordeum vulgare (barley)
 C>Date: 06-Mar-1992 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
 C/Accession: A39356; A45129
 R/Siggaard-Andersen, M.; Kauppinen, S.; von Wettstein-Knowles, P.
 Proc. Natl. Acad. Sci. U.S.A. 89, 4114-4118, 1991
 A>Title: Primary structure of a cerulenin-binding beta-ketoacyl-[acyl carrier protein] s
 A/Reference number: A39356; MUID:91239517; PMID:2034657
 A/Accession: A39356
 A/Molecule type: mRNA
 A/Residues: 1-462 <SIG>
 A/Cross-references: UNIPROT:P23902; GB:M60410; NID:9167064; PIDN:AAA32968.1; PID:9167065
 A/Experimental source: cv. Bonus, leaf
 A/Note: parts of this sequence, including the amino end of the mature protein, were conf
 R/Kauppinen, S. 267, 23999-24006, 1992
 J. Biol. Chem. 267, 23999-24006, 1992
 A>Title: Structure and expression of the Kas12 gene encoding a beta-ketoacyl-acyl carrie
 A/Reference number: A45129; MUID:93054767; PMID:1429736
 A/Accession: A45129

A/Molecule type: DNA
 A/Residues: 1-395,397-414,'T',415-462 <KAU>
 A/Experimental source: cv. Bonus
 A/Note: sequence inconsistent with the nucleotide translation; translation agrees with ge
 A/Note: sequence extracted from NCBI backbone (NCBI:118934)
 C/Genetics:
 A/Genes: Kas12
 A/Map position: 2
 A/Introns: 144/3; 288/3; 346/3; 384/3; 418/3; 441/1
 C/Complex: homodimer or heterodimer with alpha chain
 C:Superfamily: 3-oxoacyl-[acyl-carrier-protein] synthase I; 3-oxoacyl-[acyl-carrier-prote
 C/Keywords: acyltransferase; chloroplast; fatty acid biosynthesis; heterodimer; homodime
 F:1-36/Domain: transfer peptide (chloroplast) #status predicted <TNP>
 F:36-462/Product: 3-oxoacyl-[acyl-carrier-protein] synthase I beta chain #status experime
 F:68-457/Domain: 3-oxoacyl-[acyl-carrier-protein] synthase I homology <OAS>
 F:213/Active site: Cys #status experimental

Query Match 37.5% Score 45; DB 1; Length 462;
 Best Local Similarity 80.0% Pred. No. 35;
 Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 SYQFGHNSV 12
 | : | | | | |
 Db 445 SFQFGHNSV 454

RESULT 15
 T10061
 3-oxoacyl-[acyl-carrier-protein] synthase (EC 2.3.1.41) precursor, chloroplast - castor l
 N/Alternate names: beta-ketoacyl-[acyl carrier protein] synthase
 C/Species: Ricinus communis (castor bean)
 C/Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004
 C/Accession: T10061
 R/Genez, A.L.
 submitted to the EMBL Data Library, April 1993
 A/Description: Cloning and molecular characterization of B-ketoacyl-ACP synthases from enr
 A/Reference number: Z16924
 A/Accession: T10061
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: mRNA
 A/Residues: 1-469 <GEN>
 A/Cross-references: UNIPROT:Q41135; EMBL:L13242; NID:9294667; PID:9294668
 C/Genetics:
 A/Genome: nuclear
 C/Function:
 A/Pathway: fatty acid biosynthesis
 C:Superfamily: 3-oxoacyl-[acyl-carrier-protein] synthase I; 3-oxoacyl-[acyl-carrier-prote
 C/Keywords: acyltransferase; chloroplast; fatty acid biosynthesis
 F:1-42/Domain: transfer peptide (chloroplast) #status predicted <TNP>
 F:43-469/Product: 3-oxoacyl-[acyl-carrier-protein] synthase #status predicted <OAS>
 F:77-464/Domain: 3-oxoacyl-[acyl-carrier-protein] synthase I homology <OAS>

Query Match 37.5% Score 45; DB 2; Length 469;
 Best Local Similarity 80.0% Pred. No. 35;
 Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 SYQFGHNSV 12
 | : | | | | |
 Db 452 SFQFGHNSV 461

Search completed: October 22, 2005, 04:13:59
 Job time : 11.5465 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 22, 2005, 02:23:35 ; Search time 51.4314 Seconds
(without alignments)
209.087 Million cell updates/sec

Title: US-10-731-238-31
Perfect score: 120
Sequence: 1 KPSYQFGHNSVDFEEDTPPK 21

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_03:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	110	91.7	1018 1	FNBA_STPAU P14738 staphylococ
2	107	89.2	961 2	Q99RD3 Q997d3 staphylococ
3	107	89.2	961 2	Q7A3J8 Q7a3j8 staphylococ
4	107	89.2	965 2	Q6GDU5 Q6gdu5 staphylococ
5	107	89.2	1015 2	Q8NUU7 Q8nuu7 staphylococ
6	107	89.2	1015 2	Q6G6H3 Q6g6h3 staphylococ
7	107	89.2	1038 2	Q99RD2 Q99rd2 staphylococ
8	107	89.2	1038 2	Q7A3J7 Q7a3j7 staphylococ
9	103	85.8	940 2	Q53682 Q53682 staphylococ
10	103	85.8	943 2	Q8NUU8 Q8nuu8 staphylococ
11	103	85.8	957 2	Q6G6H4 Q6g6h4 staphylococ
12	98	81.7	152 1	Q9AEP9 Q9aep9 staphylococ
13	54	45.0	598 1	P608B3 P608b3 mus musculu
14	54	45.0	600 1	LZRT_MOUSE LZrt_MOUSE
15	53.5	44.6	305 2	Q6DF66 Q6df66 xenopus tro
16	52	43.3	595 1	LZRT_HUMAN LZrt_HUMAN
17	52	43.3	952 1	CYLD_MOUSE CYld_MOUSE
18	52	43.3	953 2	Q66H62 Q66h62 rattus norv
19	52	43.3	956 1	CYLD_HUMAN CYld_HUMAN
20	52	43.3	1013 2	Q7PIB2 Q7piB2 anopheles g
21	52	43.3	1043 2	Q7G5L5 Q7g5l5 anopheles g
22	52	43.3	1679 2	Q7KRT6 Q7krt6 drosophila
23	51	42.5	445 2	Q98GQ0 Q98gq0 mycoplasma
24	50	41.7	245 2	Q08866 Q08866 carassius a
25	50	41.7	454 2	Q08866 Q08866 carassius a
26	49	40.8	224 2	Q99WQ0 Q99wq0 rattus norv
27	49	40.8	224 2	Q9DJ14 Q9dj14 mus musculu
28	49	40.8	328 2	Q8VNC2 Q8vnc2 mus musculu
29	49	40.8	341 2	Q9CUJ2 Q9cuJ2 mus musculu
30	49	40.8	1726 2	Q6G4Z9 Q6g4z9 bartonella
31	48	40.0	197 2	Q9FII2 Q9fii2 arabidopsis

ALIGNMENTS

RESULT 1	FNBA_STPAU	STANDARD;	PRT; 1018 AA.	
AC	P14738;			OBx16 clostridium
DT	01-APR-1990 (Rel. 14, Created)			OB1fd7 arabidopsis
DT	01-APR-1990 (Rel. 14, Last sequence update)			Q99y68 gossypium h
DT	25-OCT-2004 (Rel. 45, Last annotation update)			Q81sc8 gossypium h
DE	Fibronectin-binding protein precursor (FNBP).			Q6gn22 xenopus lae
GN	Name=fnba;			Q9fyu7 brassica na
OS	Staphylococcus aureus.			Q9ad03 streptomyce
OC	Bacteria; Firmicutes; Bacillales; Staphylococcus.			Q6k6b0 oryza sativ
OX	NCBI_Taxid=1280;			Q8axb7 brachydanio
RN	(1)			Q45412 ctenomabadi
RP	SEQUENCE FROM N.A.			Q7nw12 chromobacte
RC	STRAIN=NCITC 8325-4;			Q7nmk3 chromobacte
RX	MEDLINE=89098998; PubMed=2521391;			Q6fzm2 bartonella
RA	Signaes C., Raucel G., Joensson K., Lindberg M.;			Q6p319 xenopus tro
RA	Anantharamiah G.M., Hooeok M., Lindberg M.;			
RT	"Nucleotide sequence of the gene for a fibronectin-binding protein			
RT	from Staphylococcus aureus: use of this peptide sequence in the			
RT	synthesis of biologically active peptides."			
RL	Proc. Natl. Acad. Sci. U.S.A. 86:699-703(1989).			
CC	- FUNCTION: The ability of bacteria to bind fibronectin has been			
CC	proposed as a virulence factor enabling bacteria to colonize wound			
CC	tissues and blood clots. Binding of plasma fibronectin to the			
CC	bacterial surface might block adhesion receptors on S.aureus, thus			
CC	representing an important defense mechanism against tissue			
CC	invasion.			
CC	- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by			
CC	an amide bond (Potential).			
CC	-----			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration			
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -			
CC	the European Bioinformatics Institute. There are no restrictions on its			
CC	use by non-profit institutions as long as its content is in no way			
CC	modified and this statement is not removed. Usage by and for commercial			
CC	entities requires a license agreement (See http://www.tsb-sib.ch/announce/			
CC	or send an email to license@sib-sib.ch).			
CC	-----			
DR	EMBL: J04151; AAA6632.1; -			
DR	InterPro: IPR004237; Fn_bind.			
DR	InterPro: IPR005877; Gpos_YsIRK.			
DR	InterPro: IPR001899; Gram_pos_anchor.			
DR	Pfam: PF02986; Fn_bind; 1.			
DR	Pfam: PF00746; Gram_pos_anchor; 1.			
DR	TIGRPFAM: TIGR01167; LpxNG signal; 1.			
DR	TIGRPFAM: TIGR01168; YsIRK signal; 1.			
DR	PROSITE: PS50847; GRAM_POS_ANCHORING; 1.			
KW	Cell adhesion; Cell wall; Peptidoglycan-anchor; Repeat; Signal;			
KW	Virulence.			
FT	SIGNAL 1 36			
FT	CHAIN 37 985			
FT	PROPEP 986 1018			
				Fibronectin-binding protein.
				Removed by sortase (Potential).

```
FT REPEAT 545 574 B-1.
FT REPEAT 575 604 B-2.
FT DOMAIN 745 878 4 X approximate tandem repeats,
  fibronectin-binding domain.
FT REPEAT 745 782 D-1.
FT REPEAT 783 820 D-2.
FT REPEAT 821 859 D-3.
FT REPEAT 860 878 D-4 (incomplete).
FT DOMAIN 879 948 5 X tandem repeats, Pro-rich (WR).
FT REPEAT 879 892 WR 1.
FT REPEAT 893 906 WR 2.
FT REPEAT 907 920 WR 3.
FT REPEAT 921 934 WR 4.
FT REPEAT 935 948 WR 5.
FT SITE 982 986 LPXTG sorting signal (Potential).
FT MOD_RS 985 985 Pentaglycyl murein peptidoglycan amidated
  threonine (Potential).
SQ SEQUENCE 1018 AA; 111780 MW; 58175E0020B81P1F CRC64;

Query Match 91.7%; Score 110; DB 1; Length 1018;
Best Local Similarity 95.2%; Pred. No. 8.1e-08;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KPSYQFGHNSVDFEEDTPK 21
Db 837 KPSYQFGHNSVDFEEDTPK 857
```

```
RESULT 2
ID 099RD3 PRELIMINARY; PRT; 961 AA.
AC 099RD3:
DT 01-JUN-2001 (TRENBLrel. 17, Created)
DT 01-JUN-2001 (TRENBLrel. 17, Last sequence update)
DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)
DE Fibronectin-binding protein homolog.
GN Name=fnb3; OrderedLocuNames=SAV2502;
OS Staphylococcus aureus (strain Muso / ATCC 700699).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxId=158879;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MSU / ATCC 700699;
RX MEDLINE=21311952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2;
RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
  Cui L., Oguchi A., Aoki K.-I., Nagai Y., Iian J.-Q., Ito T.,
  Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,
  Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
  Sekimizu K., Hiraoka H., Kohara S., Goto S., Yabuzaki J.,
  Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
  Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
RA "Whole genome sequencing of methicillin-resistant Staphylococcus
  aureus."
RT Lancet 357:1225-1240(2001).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
  an amide bond (By similarity).
EMBL: AP003365; BAB58664.1; -.
CC PIR: G90053; G90053.
DR HSP; Q53653; I167.
DR GO; GO:0009986; C:cell surface; IEA.
DR GO; GO:0005618; C:cell wall; IEA.
DR GO; GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0007155; P:cell adhesion; IEA.
DR InterPro; IPR008966; Adhes_bact.
DR InterPro; IPR004237; Fn_bind.
DR InterPro; IPR005877; Gpos_Ysirk.
DR InterPro; IPR001899; Gram_pos_anchor.
DR Pfam; PF02986; Fn_bind; 1.
DR Pfam; PF00746; Gram_pos_anchor; 1.
DR Pfam; PF04650; Ysirk_signal; 1.
DR TIGRfams; TIGR01167; LPXTG_anchor; 1.
DR TIGRfams; TIGR01167; LPXTG_anchor; 1.
DR TIGRfams; TIGR01168; Ysirk_signal; 1.
DR TIGRfams; TIGR01168; Ysirk_signal; 1.
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DR PROSITE; PSS0847; GRAM_POS_ANCHORING; 1.
KW Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ SEQUENCE 961 AA; 106010 MW; 364940F884EA4101 CRC64;
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Query Match 89.2%; Score 107; DB 2; Length 961;
Best Local Similarity 90.5%; Pred. No. 2.2e-07;
Matches 19; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
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Qy 1 KPSYQFGHNSVDFEEDTPK 21
Db 784 KPSYQFGHNSVDFEEDTPK 804
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RESULT 3
ID 07A3J8 PRELIMINARY; PRT; 961 AA.
AC 07A3J8:
DT 05-JUL-2004 (TRENBLrel. 27, Created)
DT 05-JUL-2004 (TRENBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TRENBLrel. 27, Last annotation update)
DE Fnb3 protein.
GN Name=fnb3; OrderedLocuNames=SA2290;
OS Staphylococcus aureus (strain N315).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxId=158879;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=21311952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2;
RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
  Cui L., Oguchi A., Aoki K.-I., Nagai Y., Iian J.-Q., Ito T.,
  Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,
  Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
  Sekimizu K., Hiraoka H., Kohara S., Goto S., Yabuzaki J.,
  Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
  Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
RA "Whole genome sequencing of methicillin-resistant Staphylococcus
  aureus."
RT Lancet 357:1225-1240(2001).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
  an amide bond (By similarity).
EMBL: AP003137; BAB43593.1; -.
DR GO; GO:0009986; C:cell surface; IEA.
DR GO; GO:0005618; C:cell wall; IEA.
DR GO; GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0007155; P:cell adhesion; IEA.
DR InterPro; IPR008966; Adhes_bact.
DR InterPro; IPR004237; Fn_bind.
DR InterPro; IPR005877; Gpos_Ysirk.
DR InterPro; IPR001899; Gram_pos_anchor.
DR Pfam; PF02986; Fn_bind; 1.
DR Pfam; PF00746; Gram_pos_anchor; 1.
DR Pfam; PF04650; Ysirk_signal; 1.
DR TIGRfams; TIGR01167; LPXTG_anchor; 1.
DR TIGRfams; TIGR01168; Ysirk_signal; 1.
DR PROSITE; PSS0847; GRAM_POS_ANCHORING; 1.
KW Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ SEQUENCE 961 AA; 106010 MW; 364940F884EA4101 CRC64;
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Query Match 89.2%; Score 107; DB 2; Length 961;
Best Local Similarity 90.5%; Pred. No. 2.2e-07;
Matches 19; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KPSYQFGHNSVDFEEDTPK 21
Db 784 KPSYQFGHNSVDFEEDTPK 804

RESULT 4
ID 06GDUS PRELIMINARY; PRT; 965 AA.
AC 06GDUS:
DT 05-JUL-2004 (TRENBLrel. 27, Created)
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DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE Fibronectin-binding protein.
GN Name=fdbA; OrderedLocustNames=SAR2580;
OS Staphylococcus aureus (strain MRSA252).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=282458;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=15213324; DOI=10.1073/pnas.0402521101;
RA Holden M.T.G., Fell E.J., Lindsay J.A., Peacock S.J., Day N.P.J.,
RA Enright M.C., Foster T.J., Moore C.E., Hurst L., Atkin R., Barron A.,
RA Baeson N., Bentley S.D., Chillingworth C., Chillingworth T.,
RA Churcher C., Clark L., Corton C., Cronin A., Doggett J., Dowd L.,
RA Felwell T., Hance Z., Harris B., Hauser H., Holroyd S., Jagels K.,
RA James K.D., Leonard N., Line A., Mayes R., Moulé S., Mungall K.,
RA Ormond D., Quail M.A., Rabinowitch B., Rutherford K.M., Sanders M.,
RA Sharp S., Simmonds M., Stevens K., Whitehead S., Barrett B.G.,
RA Spratt B.G., Parhill J.;
RT "Complete genomes of two clinical Staphylococcus aureus strains:
RT evidence for the rapid evolution of virulence and drug resistance.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:9786-9791(2004).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC an amide bond (By similarity).
CC EMBL: BX571856; CAG41560.1; -.
DR GO: GO:0009986; C:cell surface; IEA.
DR GO: GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO: GO:0016020; C:membrane; IEA.
DR GO: GO:0007155; P:cell adhesion; IEA.
DR InterPro: IPR008966; Adhes_bact.
DR InterPro: IPR004237; Fn_bind.
DR InterPro: IPR005877; Gpos_YsIRK.
DR InterPro: IPR001899; Gram_pos_anchor.
DR Pfam: PF00746; Gram_pos_anchor; 1.
DR Pfam: PF04650; YsIRK_signal; 1.
DR TIGRFAMs: TIGR01167; LpxTG_anchor; 1.
DR TIGRFAMs: TIGR01168; YsIRK_signal; 1.
DR PROSITE: PS50847; GRAM_POS_ANCHORING; 1.
KW Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ SEQUENCE 965 AA; 10561 MW; 2982E132164D0551 CRC64;

Query Match 89.2%; Score 107; DB 2; Length 965;
Best Local Similarity 90.5%; Pred. No. 2.2e-07;
Matches 19; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 KPSYQFGHNSVDFEDTLPK 21
DB 802 KENYQFGHNSVDFEDTLPK 822

RESULT 5
Q8NUU7 PRELIMINARY; PRT; 1015 AA.
AC Q8NUU7;
DT 01-OCT-2002 (TREMBLrel. 22, Created)
DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Fmb protein.
GN Name=fmb; OrderedLocustNames=MM2421;
OS Staphylococcus aureus (strain MM2).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=196620;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MM2;
RX MEDLINE=22040717; PubMed=12044378; DOI=10.1016/S0140-6736(02)08713-5;
RA Baba T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Oguchi A.,
RA Nagai Y., Iwano K., Amano K., Naimi T., Kuroda H., Cui L.,
RA Yamamoto K., Hiramatsu K.;
RT "Genome and virulence determinants of high virulence community-
RT acquired MRSA.";
RL Lancet 359:1819-1827(2002).
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CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC an amide bond (By similarity).
CC EMBL: AP004830; BAB96286.1; -.
DR GO: GO:0009986; C:cell surface; IEA.
DR GO: GO:0005618; C:cell wall; IEA.
DR GO: GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO: GO:0016020; C:membrane; IEA.
DR GO: GO:0007155; P:cell adhesion; IEA.
DR InterPro: IPR008966; Adhes_bact.
DR InterPro: IPR004237; Fn_bind.
DR InterPro: IPR005877; Gpos_YsIRK.
DR InterPro: IPR001899; Gram_pos_anchor.
DR Pfam: PF00746; Gram_pos_anchor; 1.
DR Pfam: PF04650; YsIRK_signal; 1.
DR TIGRFAMs: TIGR01167; LpxTG_anchor; 1.
DR TIGRFAMs: TIGR01168; YsIRK_signal; 1.
DR PROSITE: PS50847; GRAM_POS_ANCHORING; 1.
KW Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ SEQUENCE 1015 AA; 11145 MW; D0F9281B864D44D2 CRC64;

Query Match 89.2%; Score 107; DB 2; Length 1015;
Best Local Similarity 90.5%; Pred. No. 2.3e-07;
Matches 19; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 KPSYQFGHNSVDFEDTLPK 21
DB 838 KENYQFGHNSVDFEDTLPK 858

RESULT 6
Q6G6H3 PRELIMINARY; PRT; 1015 AA.
AC Q6G6H3;
DT 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE Fibronectin-binding protein.
GN OrderedLocustNames=SAS2388;
OS Staphylococcus aureus (strain MSSA476).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=282459;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=15213324; DOI=10.1073/pnas.0402521101;
RA Holden M.T.G., Fell E.J., Lindsay J.A., Peacock S.J., Day N.P.J.,
RA Enright M.C., Foster T.J., Moore C.E., Hurst L., Atkin R., Barron A.,
RA Baeson N., Bentley S.D., Chillingworth C., Chillingworth T.,
RA Churcher C., Clark L., Corton C., Cronin A., Doggett J., Dowd L.,
RA Felwell T., Hance Z., Harris B., Hauser H., Holroyd S., Jagels K.,
RA James K.D., Leonard N., Line A., Mayes R., Moulé S., Mungall K.,
RA Ormond D., Quail M.A., Rabinowitch B., Rutherford K.M., Sanders M.,
RA Sharp S., Simmonds M., Stevens K., Whitehead S., Barrett B.G.,
RA Spratt B.G., Parhill J.;
RT "Complete genomes of two clinical Staphylococcus aureus strains:
RT evidence for the rapid evolution of virulence and drug resistance.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:9786-9791(2004).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC an amide bond (By similarity).
CC EMBL: BX571857; CAG44202.1; -.
DR GO: GO:0009986; C:cell surface; IEA.
DR GO: GO:0005618; C:cell wall; IEA.
DR GO: GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO: GO:0016020; C:membrane; IEA.
DR GO: GO:0007155; P:cell adhesion; IEA.
DR InterPro: IPR008966; Adhes_bact.
DR InterPro: IPR004237; Fn_bind.
DR InterPro: IPR005877; Gpos_YsIRK.
DR InterPro: IPR001899; Gram_pos_anchor.
DR Pfam: PF00746; Gram_pos_anchor; 1.
DR Pfam: PF04650; YsIRK_signal; 1.
DR TIGRFAMs: TIGR01167; LpxTG_anchor; 1.
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DR TIGRFAMs; TIGR01168; YSIRK signal; 1.
 DR PROSITE; PS50847; GRAM_POS_ANCHORING; 1.
 KW Cell wall; Complete proteome; Peptidoglycan-anchor.
 SQ SEQUENCE 1015 AA; 111145 MW; D0F9281B864D44D2 CRC64;

Query Match 89.2%; Score 107; DB 2; Length 1015;
 Best Local Similarity 90.5%; Pred. No. 2.3e-07;
 Matches 19; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Oy 1 KPSYQFGGHSVDFEEDTPK 21
 Db 838 KPNYQFGGHSVDFEEDTLPK 858

RESULT 7

O99RD2 PRELIMINARY; PRT; 1038 AA.
 AC O99RD2;
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Fibronectin-binding protein homolog.
 GN Name=fnb; OrderedLocuNames=SAV2503;
 OS Staphylococcus aureus (strain Mu50 / ATCC 700699).
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 NX NCBI_TaxID=158878;

[1]
 SEQUENCE FROM N.A.
 RC STRAIN=Mu50 / ATCC 700699;
 RX MEDLINE=21311952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2;
 RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
 RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Lian J.-Q., Ito T.,
 RA Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,
 RA Mitutani U. Y., Takahashi N.K., Sawano T., Inoue R.-I., Kato C.,
 RA Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
 RA Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
 RA Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
 RT "Whole genome sequencing of methicillin-resistant Staphylococcus
 aureus."
 RL Lancet 357:1225-1240(2001).
 CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
 an amide bond (By similarity).
 DR EMBL; AP003365; BAB58665.1; -

DR PIR; H90053; H90053.
 DR GO; GO:0009986; C:cell surface; IEA.
 DR GO; GO:0005618; C:cell wall; IEA.
 DR GO; GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0007155; P:cell adhesion; IEA.
 DR InterPro; IPR008965; Adhes_bact.
 DR InterPro; IPR004237; Fn_bind.
 DR InterPro; IPR005877; Gpos_YSIRK.
 DR InterPro; IPR001899; Gram_pos_anchor.
 DR Pfam; PF02986; Fn_bind; 1.
 DR Pfam; PF00746; Gram_pos_anchor; 1.
 DR Pfam; PF04650; YSIRK_signal; 1.
 DR TIGRFAMs; TIGR01167; LPTXG_anchor; 1.
 DR TIGRFAMs; TIGR01168; YSIRK_signal; 1.
 DR PROSITE; PS50847; GRAM_POS_ANCHORING; 1.
 KW Cell wall; Complete proteome; Peptidoglycan-anchor.
 SQ SEQUENCE 1038 AA; 113618 MW; 666BF6BF2BFBB12 CRC64;

Query Match 89.2%; Score 107; DB 2; Length 1038;
 Best Local Similarity 90.5%; Pred. No. 2.4e-07;
 Matches 19; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Oy 1 KPSYQFGGHSVDFEEDTPK 21
 Db 833 KPNYQFGGHSVDFEEDTLPK 853

RESULT 8

Q7A3J7

ID Q7A3J7 PRELIMINARY; PRT; 1038 AA.
 AC Q7A3J7;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Fnb protein.
 GN Name=fnb; OrderedLocuNames=SA2291;
 OS Staphylococcus aureus (strain N315).
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 NX NCBI_TaxID=158879;

[1]
 SEQUENCE FROM N.A.

RC MEDLINE=21311952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2;
 RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
 RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Lian J.-Q., Ito T.,
 RA Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,
 RA Mitutani U. Y., Takahashi N.K., Sawano T., Inoue R.-I., Kato C.,
 RA Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
 RA Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
 RA Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
 RT "Whole genome sequencing of methicillin-resistant Staphylococcus
 aureus."
 RL Lancet 357:1225-1240(2001).
 CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
 an amide bond (By similarity).
 DR EMBL; AP003365; BAB58665.1; -

DR GO; GO:0009986; C:cell surface; IEA.
 DR GO; GO:0005618; C:cell wall; IEA.
 DR GO; GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0007155; P:cell adhesion; IEA.
 DR InterPro; IPR008965; Adhes_bact.
 DR InterPro; IPR004237; Fn_bind.
 DR InterPro; IPR005877; Gpos_YSIRK.
 DR InterPro; IPR001899; Gram_pos_anchor.
 DR Pfam; PF02986; Fn_bind; 1.
 DR Pfam; PF00746; Gram_pos_anchor; 1.
 DR Pfam; PF04650; YSIRK_signal; 1.
 DR TIGRFAMs; TIGR01167; LPTXG_anchor; 1.
 DR TIGRFAMs; TIGR01168; YSIRK_signal; 1.
 DR PROSITE; PS50847; GRAM_POS_ANCHORING; 1.
 KW Cell wall; Complete proteome; Peptidoglycan-anchor.
 SQ SEQUENCE 1038 AA; 113618 MW; 666BF6BF2BFBB12 CRC64;

Query Match 89.2%; Score 107; DB 2; Length 1038;
 Best Local Similarity 90.5%; Pred. No. 2.4e-07;
 Matches 19; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Oy 1 KPSYQFGGHSVDFEEDTPK 21
 Db 833 KPNYQFGGHSVDFEEDTLPK 853

RESULT 9

ID Q53682 PRELIMINARY; PRT; 940 AA.
 AC Q53682;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Fibronectin binding protein B.
 GN Name=fnbB;
 OS Staphylococcus aureus.
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 NX NCBI_TaxID=1280;

[1]
 SEQUENCE FROM N.A.

RC STRAIN=8325-4;
 RX MEDLINE=92111475; PubMed=1837266;
 RA Johnson K., Sigmas C., Muller H.P., Lindberg M.;
 RT "Two different genes encode fibronectin binding proteins in
 Staphylococcus aureus. The complete nucleotide sequence and
 characterization of the second gene.";

BL Eur. J. Biochem. 202:1041-1048(1991).
 CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
 CC an amide bond (By similarity).
 DR EMBL: X62992; CAA44726.1; -.
 DR PIR: S19702; S19702.
 DR HSBP: Q53653; IN67.
 DR GO: GO:0009986; C:cell surface; IEA.
 DR GO: GO:0005618; C:cell wall; IEA.
 DR GO: GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
 DR GO: GO:0016020; C:membrane; IEA.
 DR GO: GO:0007155; P:cell adhesion; IEA.
 DR InterPro: IPR008966; Adhes_bact.
 DR InterPro: IPR004237; Fn_bind.
 DR InterPro: IPR005877; Gpos_YsIRK.
 DR InterPro: IPR001899; Gram_pos_anchor.
 DR Pfam: PF02986; Fn_bind; 2.
 DR Pfam: PF00746; Gram_pos_anchor; 1.
 DR Pfam: PF04650; YsIRK_signal; 1.
 DR TIGRFAMs: TIGR01167; LpxTG_anchor; 1.
 DR TIGRFAMs: TIGR01168; YsIRK_signal; 1.
 DR PROSITE: PS00847; GRAM_POS_ANCHORING; 1.
 DR Cell wall; Peptidoglycan-anchor.
 KM SEQUENCE 940 AA; 103555 MW; E35FBBCA907AE345 CRC64;
 SQ
 Query Match 85.8%; Score 103; DB 2; Length 940;
 Best Local Similarity 85.7%; Pred. No. 8.7e-07;
 Matches 18; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 QY 1 KPSYQFGCHNSVDFEEDTPK 21
 DB 773 KPNYQFGCHNSVDFEEDTLQ 793
 ID Q8NTU8 PRELIMINARY; PRT; 943 AA.
 AC Q8NTU8; 01-OCT-2002 (TREMBLrel. 22, Created)
 DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update)
 DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
 DE FndB protein.
 GN Name=fndB; OrderedLocustNames=WM2420;
 OS Staphylococcus aureus (strain WM2).
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 OX NCBI_Taxid=196620;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=WM2;
 RX MEDLINE=22040717; PubMed=12044378; DOI=10.1016/S0140-6736(02)08713-5;
 RA Baba T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Oguchi A.,
 RA Nagai Y., Iwano N., Asano K., Naito T., Kuroda H., Cui L.,
 RA Yamamoto K., Hiramoto K.;
 RT "Genome and virulence determinants of high virulence community-
 RT acquired MRSA.";
 RT Lancet 359:1819-1827(2002).
 RL -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
 CC an amide bond (By similarity).
 CC EMBL: AB004830; BAB96285.1; -.
 DR HSBP: Q53653; IN67.
 DR GO: GO:0009986; C:cell surface; IEA.
 DR GO: GO:0005618; C:cell wall; IEA.
 DR GO: GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
 DR GO: GO:0016020; C:membrane; IEA.
 DR GO: GO:0007155; P:cell adhesion; IEA.
 DR InterPro: IPR008966; Adhes_bact.
 DR InterPro: IPR004237; Fn_bind.
 DR InterPro: IPR005877; Gpos_YsIRK.
 DR InterPro: IPR001899; Gram_pos_anchor.
 DR Pfam: PF02986; Fn_bind; 1.
 DR Pfam: PF00746; Gram_pos_anchor; 1.
 DR Pfam: PF04650; YsIRK_signal; 1.
 DR TIGRFAMs: TIGR01167; LpxTG_anchor; 1.
 DR TIGRFAMs: TIGR01168; YsIRK_signal; 1.
 DR PROSITE: PS00847; GRAM_POS_ANCHORING; 1.
 DR Cell wall; Complete proteome; Peptidoglycan-anchor.
 KM SEQUENCE 957 AA; 105980 MW; 28F8BA7FFDF3EAF CRC64;
 SQ

DR PROSITE: PS00847; GRAM_POS_ANCHORING; 1.
 KM Cell wall; Complete proteome; Peptidoglycan-anchor.
 SQ SEQUENCE 943 AA; 104537 MW; DA8A5F31947E1B6A CRC64;
 SQ
 Query Match 85.8%; Score 103; DB 2; Length 943;
 Best Local Similarity 85.7%; Pred. No. 8.8e-07;
 Matches 18; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 QY 1 KPSYQFGCHNSVDFEEDTPK 21
 DB 780 KPNYQFGCHNSVDFEEDTLQ 800
 ID Q6G6H4 PRELIMINARY; PRT; 957 AA.
 AC Q6G6H4; 05-JUL-2004 (TREMBLrel. 27, Created)
 DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
 DE Fibrinectin-binding protein.
 GN Name=fndB; OrderedLocustNames=SAS2387;
 OS Staphylococcus aureus (strain MSSA476).
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 OX NCBI_Taxid=282459;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX PubMed=15213324; DOI=10.1073/pnas.0402521101;
 RA Holden M.T.G., Fell E.J., Lindsay J.A., Peacock S.J., Day N.P.J.,
 RA Enright M.C., Foster T.J., Moore C.E., Hurst L., Atkin R., Barron A.,
 RA Baeson N., Bentley S.D., Chillingworth C., Chillingworth T.,
 RA Churcher C., Clark L., Cotton C., Cronin A., Doggett J., Dowd L.,
 RA Feltwell T., Hance Z., Harris B., Hauser H., Holtroyd S., Jagels K.,
 RA James K.D., Kennard N., Line A., Mayes R., Moutie S., Mungall K.,
 RA Ormond D., Quail M.A., Rabinowitch E., Rutherford K.M., Sanders M.,
 RA Sharp S., Simmonds M., Stevens K., Whitehead S., Barrell B.G.,
 RA Spratt B.G., Parkhill J.;
 RT "Complete genomes of two clinical Staphylococcus aureus strains:
 RT evidence for the rapid evolution of virulence and drug resistance.";
 RT Proc. Natl. Acad. Sci. U.S.A. 101:9786-9791(2004).
 RL CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
 CC an amide bond (By similarity).
 CC EMBL: BX571857; CAG44201.1; -.
 DR GO: GO:0009986; C:cell surface; IEA.
 DR GO: GO:0005618; C:cell wall; IEA.
 DR GO: GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
 DR GO: GO:0016020; C:membrane; IEA.
 DR GO: GO:0007155; P:cell adhesion; IEA.
 DR InterPro: IPR008966; Adhes_bact.
 DR InterPro: IPR004237; Fn_bind.
 DR InterPro: IPR005877; Gpos_YsIRK.
 DR InterPro: IPR001899; Gram_pos_anchor.
 DR Pfam: PF02986; Fn_bind; 1.
 DR Pfam: PF00746; Gram_pos_anchor; 1.
 DR Pfam: PF04650; YsIRK_signal; 1.
 DR TIGRFAMs: TIGR01167; LpxTG_anchor; 1.
 DR TIGRFAMs: TIGR01168; YsIRK_signal; 1.
 DR PROSITE: PS00847; GRAM_POS_ANCHORING; 1.
 DR Cell wall; Complete proteome; Peptidoglycan-anchor.
 KM SEQUENCE 957 AA; 105980 MW; 28F8BA7FFDF3EAF CRC64;
 SQ
 Query Match 85.8%; Score 103; DB 2; Length 957;
 Best Local Similarity 85.7%; Pred. No. 8.9e-07;
 Matches 18; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 QY 1 KPSYQFGCHNSVDFEEDTPK 21
 DB 780 KPNYQFGCHNSVDFEEDTLQ 800
 ID Q9AEP9 PRELIMINARY; PRT; 152 AA.
 AC Q9AEP9

```

AC 09A99;
DT 01-JUN-2001 (TREMblrel. 17, Created)
DT 01-JUN-2001 (TREMblrel. 17, Last sequence update)
DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)
DE Fibronectin-binding protein (fragment).
GN Name=fnb;
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1280;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CMRSA-1;
RX MEDLINE=21246681; PubMed=11349044;
RX DOI=10.1128/IAI.69.6.3791-3799.2001;
RA Rice K., Huebner M., Var D., McGavin M.J.;
RT "Variance in fibronectin binding and fnb locus polymorphisms in
RT Staphylococcus aureus: identification of antigenic variation in a
RT fibronectin binding protein adhesin of the epidemic CMRSA-1 strain of
RT methicillin-resistant S. aureus."
RL Infect. Immun. 69:3791-3799(2001).
DR EMBL; AY029184; AAK31388.1; -.
FT NON_TER 1 152
FT TER 152
SQ SEQUENCE 152 AA; 17193 MW; CFA3913C2B11C025 CRC64;

Query March 81.7%; Score 98; DB 2; Length 152;
Best Local Similarity 81.0%; Pred. No. 6.8e-07;
Matches 17; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 KPSYQFGHNSVDFEEDTPPK 21
Db 130 KPSYQFGHNSVDFEEDTPPK 150

RESULT 13
LZT1 MOUSE STANDARD; PRT; 598 AA.
AC P60853;
DT 05-JUL-2004 (Rel. 44, Created)
DT 05-JUL-2004 (Rel. 44, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Leucine zipper putative tumor suppressor 1 (F37/Besophageal cancer-
DE related gene-coding leucine-zipper motif) (Fez1).
GN Name=Lzst1; Synonyms=Fez1;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=129/J;
RX MEDLINE=99199287; PubMed=10097140; DOI=10.1073/pnas.96.7.3928;
RA Ishii H., Bafra R., Nunata S.-I., Murakumo Y., Rattan S., Inoue H.,
RA Mori M., Fidanza V., Alder H., Croce C.M.;
RT "The Fez1 gene at chromosome 8p22 encodes a leucine-zipper protein,
RT and its expression is altered in multiple human tumors."
RL Proc. Natl. Acad. Sci. U.S.A. 96:3928-3933(1999).
CC -1- FUNCTION: Involved in the regulation of cell growth. May stabilize
CC the active CDC2-cyclin B1 complex and thereby contribute to the
CC regulation of the cell cycle and the prevention of uncontrolled
CC cell proliferation. May act as tumor suppressor (By similarity).
CC -1- SUBUNIT: Binds ERF1G and CDC2 (By similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic; associated with the plasma
CC membrane and with microtubules. Detected in dendritic spines,
CC especially in the postsynaptic density (By similarity).
CC -1- PTM: Phosphorylated on serine residues. Hyperphosphorylated by the
CC cAMP-dependent kinase PKA during cell-cycle progression (By
CC similarity).
CC -1- SIMILARITY: Belongs to the LZTS family.
CC -----
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CC -----
CC DR EMBL; AF288601; AAQ14349.1; -.
CC Anti-oncogene; Cell cycle; Coiled coil; Lipoprotein; Membrane;
KM Myristate; Phosphorylation.
FT INT MET 0 0
FT LIPID 1 1 By similarity.
FT DOMAIN 255 571 Coiled coil (potential).
SQ SEQUENCE 598 AA; 67176 MW; D45781BECF2A6C70 CRC64;

Query March 45.0%; Score 54; DB 1; Length 598;
Best Local Similarity 40.7%; Pred. No. 16;
Matches 11; Conservative 2; Mismatches 8; Indels 6; Gaps 1;

Qy 1 KPSY-----QFGHNSVDFEEDTPPK 21
Db 78 RPDYTLASGDMGQGTGVDPDATPK 104

RESULT 14
LZT1 RAT STANDARD; PRT; 600 AA.
AC Q8CFG9;
DT 05-JUL-2004 (Rel. 44, Created)
DT 05-JUL-2004 (Rel. 44, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Leucine zipper putative tumor suppressor 1 (PSD-Zip70).
GN Name=Lzst1;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.; N-MYRISTOYLATION, TISSUE SPECIFICITY, AND
RP SUBCELLULAR LOCATION.
RC STRAIN=Sprague-Dawley; TISSUE=Brain;
RX MEDLINE=22302083; PubMed=12415013;
RA Kono D., Ko J.-A., Uebi S., Hori K., Maruoka H., Inui M.,
RA Fujikado T., Tano Y., Suzuki T., Toyama K., Sobue K.;
RT "The postsynaptic density and dendritic raft localization of PSD-
RT Zip70, which contains an N-myristoylation sequence and leucine-zipper
RT motifs."
RL J. Cell Sci. 115:4695-4706(2002).
CC -1- FUNCTION: Involved in the regulation of cell growth. May stabilize
CC the active CDC2-cyclin B1 complex and thereby contribute to the
CC regulation of the cell cycle and the prevention of uncontrolled
CC cell proliferation. May act as tumor suppressor (By similarity).
CC -1- SUBUNIT: Binds ERF1G and CDC2 (By similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic; associated with the plasma
CC membrane and with microtubules (By similarity). Detected in
CC dendritic spines, especially in the postsynaptic density.
CC -1- TISSUE SPECIFICITY: Highly expressed in brain, in particular in
CC cortex, the CA2 region of the hippocampus, olfactory bulb,
CC striatum and pons. Not detectable in the other tissues tested.
CC -1- DEVELOPMENTAL STAGE: Highly expressed in cerebellum in 1 to 3 week
CC old rats. Expression levels before and after are much lower.
CC Expression in total brain increases slightly during development
CC and remains at a constant high level after birth.
CC -1- PTM: Phosphorylated on serine residues. Hyperphosphorylated by the
CC cAMP-dependent kinase PKA during cell-cycle progression (By
CC similarity).
CC -1- SIMILARITY: Belongs to the LZTS family.
CC -----
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CC  EMBL; AB075607; BAC16535.1; -
DR  InterPro: IPR009638; Fez1.
DR  Pfam; PF06818; Fez1; 2.
KM  Anti-oncogene; Cell cycle; Coiled coil; Lipoprotein; Membrane;
KW  Myristate; Phosphorylation.
FT  INIT MET 0
FT  LIPID 1
FT  DOMAIN 254 572 N-myristoyl glycine.
SQ  SEQUENCE 600 AA; 67434 MW; F14C02D8761529AD CRC64;

Query Match 45.0%; Score 54; DB 1; Length 600;
Best Local Similarity 40.7%; Pred. No. 16;
Matches 11; Conservative 2; Mismatches 8; Indels 6; Gaps 1;

QY 1 KPSY-----QFGHNSVDFEETPPK 21
DB 78 RFDYALSSGDMGQTGVDFDPATPPK 104

RESULT 15
Q6DF66 PRELIMINARY; PRT; 305 AA.
ID Q6DF66;
AC Q6DF66;
DT 25-OCT-2004 (TRENBLREL. 28, Created)
DT 25-OCT-2004 (TRENBLREL. 28, Last sequence update)
DT 25-OCT-2004 (TRENBLREL. 28, Last annotation update)
DE Atf5-prov protein.
GN Name=atf5-prov;
OS Xenopus tropicalis (Western clawed frog) (Silurana tropicalis).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipridae; Pipidae;
OC Xenopodinae; Xenopus.
NCBI_TaxID=6364;
OX NCBI_TaxID=6364;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Whole body;
RX PubMed=12477932; DOI=10.1073/pnas.242603999;
RA Klausner R.D., Collins F.S., Wagner L.H., Derge J.G.,
RA Strausberg R.L., Feingold E.A., Grouse L.H., Shennan C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Wax S.I., Wang J., Haich F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stables M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udell T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loggellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Ketterman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smalls D.E., Scherch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Whole body;
RA Klein S., Gerhard D.S.;
RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Belongs to the bZIP family.
EMBL; BC076876; AAH76876.1; -
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro: IPR008917; Btk transcr_DNA.
DR InterPro: IPR004827; TF_bZIP.
DR Pfam; PF00170; bZIP_1; 1.
DR SMART; SM00338; BRLZ; 1.
DR PROSITE; PS50217; BZIP; 1.

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DR  PROSITE; PS00036; BZIP_BASIC; 1.
KW  DNA-binding; Nuclear protein.
SQ  SEQUENCE 305 AA; 34690 MW; CC72E4C5E22ED3F0 CRC64;

Query Match 44.6%; Score 53.5; DB 2; Length 305;
Best Local Similarity 52.2%; Pred. No. 9.1;
Matches 12; Conservative 4; Mismatches 2; Indels 5; Gaps 2;

QY 2 PSYQFGHNSVDF---EEDTTP 20
DB 138 PDHQFGG-SEVERFQDYVEETTP 159

Search completed: October 22, 2005, 04:10:24
Job time : 52.4314 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 25, 2005, 18:43:07 ; Search time 59.0973 Seconds
(without alignments)
137.434 Million cell updates/sec

Title: US-10-731-238-32

Perfect score: 114
Sequence: 1 KPSYQFGHNSVDFEEDTLAK 21

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: Geneseq16Dec04:*
2: geneseqp1980s:*
3: geneseqp1990s:*
4: geneseqp2000s:*
5: geneseqp2001s:*
6: geneseqp2002s:*
7: geneseqp2003as:*
8: geneseqp2003bs:*
9: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	114	100.0	21	2	AAW65688 Fibrinect
2	109	95.6	21	2	AAW65665 Fibrinect
3	109	95.6	22	2	AAW65665 Fibrinect
4	109	95.6	37	1	AAW65665 Fibrinect
5	109	95.6	38	1	AAW65665 Fibrinect
6	109	95.6	134	2	AAW65665 Fibrinect
7	109	95.6	139	2	AAW65665 Fibrinect
8	109	95.6	1018	1	AAW65665 Fibrinect
9	109	95.6	1018	4	AAW65665 Fibrinect
10	109	95.6	1018	4	AAW65665 Fibrinect
11	109	95.6	1018	6	AAW65665 Fibrinect
12	109	95.6	1018	6	AAW65665 Fibrinect
13	109	95.6	1027	2	AAW65665 Fibrinect
14	106	93.0	961	6	AAW65665 Fibrinect
15	106	93.0	978	4	AAW65665 Fibrinect
16	106	93.0	1001	4	AAW65665 Fibrinect
17	106	93.0	1038	6	AAW65665 Fibrinect
18	105	92.1	21	2	AAW65665 Fibrinect
19	104	91.2	21	2	AAW65665 Fibrinect
20	104	91.2	21	2	AAW65665 Fibrinect
21	104	91.2	21	2	AAW65665 Fibrinect
22	103	90.4	21	2	AAW65665 Fibrinect
23	103	90.4	21	2	AAW65665 Fibrinect
24	103	90.4	21	2	AAW65665 Fibrinect
25	103	90.4	21	2	AAW65665 Fibrinect

26	103	90.4	21	2	AAW65674	AAW65674 Fibrinect
27	102	89.5	21	2	AAW65685	AAW65685 Fibrinect
28	102	89.5	21	2	AAW65687	AAW65687 Fibrinect
29	102	89.5	21	2	AAW65681	AAW65681 Fibrinect
30	102	89.5	77	2	AAW65681	AAW65681 Fibrinect
31	102	89.5	101	2	AAW65681	AAW65681 Fibrinect
32	102	89.5	113	2	AAW65681	AAW65681 Fibrinect
33	102	89.5	124	2	AAW65681	AAW65681 Fibrinect
34	102	89.5	128	2	AAW65681	AAW65681 Fibrinect
35	102	89.5	130	2	AAW65681	AAW65681 Fibrinect
36	102	89.5	130	2	AAW65681	AAW65681 Fibrinect
37	102	89.5	130	2	AAW65681	AAW65681 Fibrinect
38	102	89.5	130	2	AAW65681	AAW65681 Fibrinect
39	102	89.5	134	2	AAW65681	AAW65681 Fibrinect
40	102	89.5	162	2	AAW65681	AAW65681 Fibrinect
41	102	89.5	164	2	AAW65681	AAW65681 Fibrinect
42	102	89.5	174	2	AAW65681	AAW65681 Fibrinect
43	102	89.5	174	2	AAW65681	AAW65681 Fibrinect
44	102	89.5	181	2	AAW65681	AAW65681 Fibrinect
45	102	89.5	181	2	AAW65681	AAW65681 Fibrinect

ALIGNMENTS

RESULT 1
AAW65688
ID AAW65688 standard; peptide; 21 AA.
XX
AC AAW65688;
XX
DT 16-OCT-1998 (first entry)
XX
DE Fibrinectin binding protein-derived peptide #32.
XX
KW microbial surface components recognising adhesive matrix molecule;
XX MSCRAMM; fibrinectin; fibrinectin-binding protein; antibody; epitope;
XX antibiotic; bacterial infection; antibiotic-resistant strain.
XX
OS Synthetic.
OS Staphylococcus aureus.
OS
PN WO981389-A2.
XX
PD 23-JUL-1998.
XX
PF 21-JAN-1998; 98WO-US001222.
XX
PR 21-JAN-1997; 97US-0036139P.
XX
PA (TEXA) UNIV TEXAS A & M SYSTEM.
XX
PI Hoeek M, Patti JM, House-Pompeo KL, Speziale P, Joh D;
PI Mcgavin MJ;
XX
XX WPI; 1998-413816/35.
XX
XX Antibody that binds to fibrinectin-binding protein, preventing its
XX binding to fibrinectin - used to treat or prevent bacterial infection,
XX especially by Staphylococci and Streptococci.
XX
XX Example 8; Page 101; 201pp; English.
XX
XX The invention relates to antibodies that bind to a fibrinectin-binding
XX domain of a fibrinectin-binding protein, and inhibit binding of the
XX protein to fibrinectin. Also claimed are: (1) isolated peptides of a
XX fibrinectin-binding protein that do not bind to fibrinectin; (2) fusion
XX protein containing at least one peptide of a fibrinectin-binding protein
XX linked to a second amino acid sequence; (3) nucleic acid encoding the
XX isolated peptide of (1). Antibodies, the isolated peptides of (1) and the
XX nucleic acids are all useful for immunisation (active or passive) and (by
XX inhibiting binding of bacteria to fibrinectin) for preventing or treating
XX infection in humans or other animals, particularly by staphylococci or

CC streptococci, e.g. meningitis, otitis media, pneumonia, endocarditis,
 CC mastitis in cattle, abortion in horses and many others. Since the
 CC antibodies block binding of bacteria, they should be effective against
 CC antibiotic-resistant strains, and may replace antibiotic therapy or
 CC increase its effectiveness. Sequences AAW65670-90 represent a series of
 CC synthetic peptides based on the D3 repeat of *S. aureus* fibronectin
 CC binding protein A. They were synthesised to contain a proline residue at
 CC each position through the sequence (ie a proline scan)
 XX
 SQ Sequence 21 AA;
 Query Match 100.0%; Score 114; DB 2; Length 21;
 Best Local Similarity 100.0%; Pred. No. 6.8e-11;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 KPSYQFGHNSVDFEEDTLAK 21
 Db 1 KPSYQFGHNSVDFEEDTLAK 21
 RESULT 2
 ID AAW65665 standard; peptide; 21 AA.
 XX AAW65665;
 AC
 DT 16-OCF-1998 (first entry)
 DE Fibronectin binding protein-derived peptide #9.
 XX
 XX microbial surface components recognising adhesive matrix molecule;
 KW MSCRAMM; fibronectin; fibronectin-binding protein; antibody; epitope;
 KM antibiotic; bacterial infection; antibiotic-resistant strain.
 XX
 OS Synthetic.
 OS *Staphylococcus aureus*.
 XX
 PN MO9831389-A2.
 PD 23-JUL-1998.
 XX
 PF 21-JAN-1998; 98WO-US001222.
 XX
 PR 21-JAN-1997; 97US-0036139P.
 XX
 PA (TEXA) UNIV TEXAS A & M SYSTEM.
 PI
 PI Hoeek M, Patti JM, House-Pompeo KL, Speciale P, Joh D;
 PI McGavin MJ;
 XX WPI; 1998-413816/35.
 DR
 XX
 PT Antibody that binds to fibronectin-binding protein, preventing its
 PT binding to fibronectin - used to treat or prevent bacterial infection,
 PT especially by *Staphylococci* and *Streptococci*.
 PS
 PS Example 2; Page 92; 201pp; English.
 XX
 CC The invention relates to antibodies that bind to a fibronectin-binding
 CC domain of a fibronectin-binding protein, and inhibit binding of the
 CC protein to fibronectin. Also claimed are: (1) isolated peptides of a
 CC fibronectin-binding protein that do not bind to fibronectin; (2) fusion
 CC protein containing at least one peptide of a fibronectin-binding protein
 CC linked to a second amino acid sequence; (3) nucleic acid encoding the
 CC isolated peptide of (1). Antibodies, the isolated peptides of (1) and the
 CC nucleic acids are all useful for immunisation (active or passive) and (by
 CC inhibiting binding of bacteria to fibronectin) for preventing or treating
 CC infection in humans or other animals, particularly by *staphylococci* or
 CC streptococci, e.g. meningitis, otitis media, pneumonia, endocarditis,
 CC mastitis in cattle, abortion in horses and many others. Since the
 CC antibodies block binding of bacteria, they should be effective against
 CC antibiotic-resistant strains, and may replace antibiotic therapy or
 CC increase its effectiveness. Sequences AAW65659-68 represent synthetic

CC epitopes from the fibronectin binding domains DU and D1-D4 of the S.
 CC aureus fnbA gene
 XX
 SQ Sequence 21 AA;
 Query Match 95.6%; Score 109; DB 2; Length 21;
 Best Local Similarity 95.2%; Pred. No. 4.2e-10;
 Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 1 KPSYQFGHNSVDFEEDTLAK 21
 Db 1 KPSYQFGHNSVDFEEDTLAK 21
 RESULT 3
 ID AAR21340 standard; peptide; 22 AA.
 XX AAR21340;
 AC
 DT 25-MAR-2003 (revised)
 DT 15-JUN-1992 (first entry)
 XX
 DE Fibronectin binding protein.
 XX
 KW FnbP; wound infection reduction; vaccination; mastitis;
 KW *Staphylococcal* infections; D3.
 XX
 OS Synthetic.
 OS
 PN MO9202555-A.
 PD 20-FEB-1992.
 XX
 PF 10-AUG-1990; 90SE-00002617.
 XX
 PR 10-AUG-1990; 90SE-00002617.
 XX
 PA (ALFA) ALFA LAVAL AGRIC INT AB.
 PI
 PI Hook M, McGavin M, Raucel G;
 DR WPI; 1992-080035/10.
 XX
 XX
 PT New fibronectin binding peptide - combines with fusion peptide to form
 PT large antigen, used in immunisation, diagnosis and for treating wounds.
 PS
 PS Claim 1; Page 22; 33pp; English.
 XX
 CC The sequence comprises amino acids 17-33 of a tandem repeat, designated
 CC D3 of the fibronectin binding site of *Staphylococcus aureus* 8325-4 FnbP.
 CC The N-terminal DK may be replaced with H or K, and the C-terminal LKP may
 CC be replaced by either L, LP, or OH. The peptides were synthesised using
 CC standard methods and purified using reverse phase HPLC. The appropriate
 CC fractions were dialysed and lyophilised. Peptide sequencing was performed
 CC and the peptides digested and chemically modified by dihydroxypropylation
 CC of the amino side chain of lysine. The carboxylic side chains were
 CC converted to glycine methyl esters. The phenyl side chains of tyrosine
 CC residues were oxidised. Chemically modified peptide D3 was compared to
 CC unmodified D3. Lysine and tyrosine modifications only partially
 CC diminished its activity whereas modification of aspartic/glutamic
 CC residues resulted in complete loss of activity. The peptide can be used
 CC for the prevention or reduction of the risk of wound infection. The
 CC peptide can be used to create a large antigen for vaccinating ruminants
 CC against mastitis caused by *Staphylococcal* infections. It can also be used
 CC to diagnose *Staphylococcal* infections using ELISA or DNA probes. (Updated
 CC on 25-MAR-2003 to correct PA field.)
 XX
 SQ Sequence 22 AA;
 Query Match 95.6%; Score 109; DB 2; Length 22;
 Best Local Similarity 95.2%; Pred. No. 4.2e-10;
 Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 KPSYQFGHNSVDFEEDTLAK 21
 DB 2 KPSYQFGHNSVDFEEDTLPK 22

RESULT 4
 AAB91958
 ID AAB91958 standard; peptide; 37 AA.

XX AAB91958;
 XX 22-JUN-2001 (first entry)

XX Fibronectin fragment and fibrin related peptide SEQ ID NO:1134.

XX Protection; endogenous therapeutic peptide; peptidase; conjugation;
 KW blood component; modification; succinimidyl; maleimido group; amino;
 KM hydroxyl; thiol; hormone; growth factor; neurotransmitter.

XX Homo sapiens.
 OS Synthetic.

XX WO200069900-A2.

XX 23-NOV-2000.

XX 17-MAY-2000; 2000WO-US013576.

XX 17-MAY-1999; 99US-0134406P.

XX 10-SEP-1999; 99US-0153406P.

XX 15-OCT-1999; 99US-0159783P.

XX (CONJ-) CONJUCHEM INC.

XX Bridon DP, Ezrin AM, Milner PG, Holmes DL, Thibaudau K;

XX WPI: 2001-112059/12.

PT Modifying and attaching therapeutic peptides to albumin prevents
 PT peptidase degradation, useful for increasing length of in vivo activity.

XX Disclosure; Page 566; 733pp; English.

CC The present invention describes a modified therapeutic peptide (I)
 CC comprising a therapeutically active amino acid region (III) and a
 CC reactive group (II) (e.g. succinimidyl and maleimido groups) attached to
 CC a less therapeutically active amino acid region (IV), which covalently
 CC bonds with amino/hydroxyl/thiol groups on blood components to form a
 CC peptidase stabilised therapeutic peptide composed of 3-50 amino acids.
 CC (I) are useful for modifying therapeutic peptides e.g. hormones, growth
 CC factors and neurotransmitters, to protect them from peptidase activity in
 CC vivo for the treatment of various disorders. Endogenous therapeutic
 CC peptides are not suitable as drug candidates as they require frequent
 CC administration due to rapid degradation by peptidases in the body.
 CC Modifying and attaching therapeutic peptides to albumin prevents or
 CC reduces the action of peptidases to increase length of activity (half
 CC life) and specificity as bonding to large molecules decreases
 CC intracellular uptake and interference with physiological processes.
 CC AAB90829 to AAB92441 represent peptides which can be used in the
 CC exemplification of the present invention

XX Sequence 37 AA;

Query Match 95.6%; Score 109; DB 4; Length 37;
 Best Local Similarity 95.2%; Pred. No. 7.8e-10;
 Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 KPSYQFGHNSVDFEEDTLAK 21
 DB 16 KPSYQFGHNSVDFEEDTLPK 36

RESULT 5
 AAB80662
 ID AAB80662 standard; protein; 38 AA.

XX AAB80662;

XX 25-MAR-2003 (revised)

XX 07-OCT-1990 (first entry)

XX Protein with fibronectin binding ability.

XX Hybrid DNA molecule; fibronectin binding; mastitis; ruminants;
 KW wound infection.

XX Staphylococcus aureus.

XX EP294349-A.

XX 07-DEC-1988.

XX 30-MAY-1988; 88EP-00850188.

XX 01-JUN-1987; 87SE-00002272.

XX (ALFA) ALFA LAVAL AGRIC INT AB.

XX Lindberg MK, Signas LC, Wadstrom TM, Froman G;

XX WPI: 1988-347978/49.

XX N-PSDB; AAN81099.

PT Hybrid DNA encoding Staphylococcus aureus fibronectin binding protein -
 PT useful for immunisation and topical application to prevent staphylococcal
 PT infections.

XX Claim 11; Page 12; 23pp; English.

CC The peptide has fibronectin binding ability. It is useful for immunising
 CC ruminants against staphylococcal mastitis, pre. when used at 0.5-5
 CC micrograms/kg, using 3 doses given at 1-3 week intervals; for topical
 CC application to prevent wound infection, using an isotonic saline soln. of
 CC concn. 25-250 micrograms/ml; and, when immobilised on a carrier, for
 CC diagnosing staphylococcal infections. (Updated on 25-MAR-2003 to correct
 CC PF field.) (Updated on 25-MAR-2003 to correct PA field.)

XX Sequence 38 AA;

Query Match 95.6%; Score 109; DB 1; Length 38;
 Best Local Similarity 95.2%; Pred. No. 8.1e-10;
 Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 KPSYQFGHNSVDFEEDTLAK 21
 DB 17 KPSYQFGHNSVDFEEDTLPK 37

RESULT 6
 AAY29087
 ID AAY29087 standard; protein; 134 AA.

XX AAY29087;

XX 28-SEP-1999 (first entry)

XX S. aureus fibronectin binding protein A (FnBA) binding domain.

XX Bovine herpes virus-2; BHV-2; cytokine; immune response; immunogen; IL;

XX tumour necrosis factor; CSF; interferon; IFN; TNF;

XX mastitis; breast cancer; stress-induced disease; binding domain; FnBA;

XX Staphylococcus aureus.

```
XX  XX  WO9916892-A1.
XX  XX  08-APR-1999.
XX  XX  29-SEP-1998; 98WO-GB002927.
XX  XX  29-SEP-1997; 97GB-00020633.
XX  XX  (UYBR-) UNIV BRISTOL.
XX  XX  Bradley AJ, Duffas WPH;
XX  XX  WPI; 1999-255101/21.
XX  XX  DR N-PSDB; AAX91504.
XX  XX  New bovine herpes virus-2 vectors.
XX  XX  Example 2; Fig 8A-B; 130pp; English.
XX  XX  The invention provides bovine herpes virus-2 (BHV-2) based vectors that
XX  XX  comprise at least one cytokine-encoding DNA sequence. The expression of
XX  XX  cytokines in mammals can up-regulate immune responses to the immunogens.
XX  XX  The cytokine is selected from interleukins (IL), colony stimulating
XX  XX  factors (CSF), interferons (IFN) and tumour necrosis factors (TNF). The
XX  XX  BHV-2 based vector or recombinant virus can be used as vaccines. They can
XX  XX  be used for preventing or treating a mucosal disease in a subject, e.g.
XX  XX  ruminants, cattle, sheep, goats, dogs, cats, horses, or man, particularly
XX  XX  mastitis in cows or breast cancers in humans. They can also be used for
XX  XX  preventing or treating a stress-induced disease. The present sequence
XX  XX  represents the binding domain of a previously published S. aureus
XX  XX  fibronectin binding protein A (FnBA) sequence. The FnB binding domain
XX  XX  gene sequence FnBAB, cloned for use in this invention has 97.8 percent
XX  XX  identity when compared to the previously published FnBA and FnBB gene
XX  XX  sequences
XX  XX  Sequence 134 AA;
XX  XX  SQ
XX  XX  Query Match 95.6%; Score 109; DB 2; Length 134;
XX  XX  Best Local Similarity 95.2%; Pred. No. 3.2e-09;
XX  XX  Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX  XX  QY 1 KPSYQFGGHSVDFEEDTLAK 21
XX  XX  Db 93 KPSYQFGGHSVDFEEDTLPK 113
XX  XX  RESULT 7
XX  XX  AAW31556
XX  XX  ID AAW31556 standard; protein; 139 AA.
XX  XX  AC AAW31556;
XX  XX  XX 27-AUG-2003 (revised)
XX  XX  DT 25-MAR-2003 (revised)
XX  XX  DT 21-MAY-1998 (first entry)
XX  XX  DE Fibronectin-binding MSCRAMM derivative POD.
XX  XX  KW Fibronectin; POD; collagen binding protein; sepsis; infection;
XX  XX  KW microbial surface component regonising adhesive matrix molecule; MSCRAMM;
XX  XX  KW adhesin; vaccine; immunisation; diagnosis; therapy; mastitis.
XX  XX  OS Staphylococcus aureus.
XX  XX  XX  Key Location/Qualifiers
XX  XX  FT Peptide 1..12
XX  XX  FT /note= "vector pOE30-derived peptide"
XX  XX  MO9743314-A2.
XX  XX  FN 20-NOV-1997.
XX  XX  PD
XX  XX  XX
```

```
PF 14-MAY-1997; 97WO-US008210.
XX  XX  XX 16-MAY-1996; 96US-0017678P.
XX  XX  XX (TEXA ) UNIV TEXAS A & M SYSTEM.
XX  XX  PA (UABR-) UAB RES FOUND.
XX  XX  PI Hoeoek M, Patil JM, House-Pompeo K, Sthanam N, Symersky J;
XX  XX  DR WPI; 1998-008801/01.
XX  XX  XX  Antibody that interacts with collagen binding domain of Staphylococcal
XX  XX  PT cna gene product - useful to prevent bacterial sepsis in animal infected
XX  XX  PT with Staphylococcus aureus.
XX  XX  PS Disclosure; Page 91; 143pp; English.
XX  XX  XX  This protein comprises Staphylococcus aureus fibronectin-binding
XX  XX  CC microbial surface component regonising adhesive matrix molecule (MSCRAMM)
XX  XX  CC derivative POD, plus a vector-derived N-terminal peptide. The invention
XX  XX  CC relates to claimed nucleic acid sequences (see AAT93436-38) encoding S.
XX  XX  CC aureus collagen binding protein (CBP) epitopes M17, M31 and M55 (see
XX  XX  CC AAW31552-54) that confer protection against S. aureus infection. CBP
XX  XX  CC protein and antigenic epitopes are contemplated for use in the treatment
XX  XX  CC of pathological infections, especially to prevent bacterial adhesion to
XX  XX  CC collagen. The epitopes are also contemplated for use in the preparation
XX  XX  CC of vaccines and as carrier proteins in vaccine formulations, as well as
XX  XX  CC in the formulation of compositions for the prevention of S. aureus
XX  XX  CC infection. pCF33 and POD (see AAW31556) were used to raise anti-MSCRAMM
XX  XX  CC polyclonal antibodies used in passive immunisation against bovine
XX  XX  CC mastitis. (Updated on 25-MAR-2003 to correct PI field.) (Updated on 27-
XX  XX  CC AUG-2003 to correct OS field.)
XX  XX  SQ Sequence 139 AA;
XX  XX  Query Match 95.6%; Score 109; DB 2; Length 139;
XX  XX  Best Local Similarity 95.2%; Pred. No. 3.2e-09;
XX  XX  Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX  XX  QY 1 KPSYQFGGHSVDFEEDTLAK 21
XX  XX  Db 107 KPSYQFGGHSVDFEEDTLPK 127
XX  XX  RESULT 8
XX  XX  AAP82115
XX  XX  ID AAP82115 standard; protein; 1018 AA.
XX  XX  AC AAP82115;
XX  XX  XX 25-MAR-2003 (revised)
XX  XX  DT 05-JAN-1990 (first entry)
XX  XX  DE Fibronectin binding protein.
XX  XX  KW Fibronectin binding protein; S. aureus; immunisation; mastitis; ruminants;
XX  XX  KW wound infection; diagnosis.
XX  XX  OS Staphylococcus aureus.
XX  XX  XX  EP294349-A.
XX  XX  PD 07-DEC-1988.
XX  XX  PF 30-MAY-1988; 88EP-00850188.
XX  XX  PR 01-JUN-1987; 87SE-00002272.
XX  XX  PA (ALFA ) ALFA LAVAL AGRIC INT AB.
XX  XX  PI Lindberg MK, Signas LC, Wadstrom TM, Froman G;
XX  XX  DR WPI; 1988-347978/49.
XX  XX  XX
```

DR P-PSDB; AAP82115.
 XX Hybrid DNA encoding Staphylococcus aureus fibronectin binding protein -
 PT useful for immunisation and topical application to prevent staphylococcal
 PT infections.
 XX Disclousure; Fig. 8A:1-8A:2; 23pp; English.
 XX The S aureus fibronectin binding protein may be included in a hybrid
 CC protein. The protein may be used to immunise ruminants against
 CC staphylococcal mastitis; pref. when given at 0.5-5 microg/kg, using 3
 CC doses at 1-3 week intervals; and for topical applicn. to prevent wound
 CC infection; pref. using isoelectric saline soln. of concn. 25-250 microg/mg.
 CC The DNA encoding the binding protein and the hybrid protein may be
 CC immobilised on a carrier and used to diagnose staphylococcal infections.
 CC (updated on 25-MAR-2003 to correct PA field.)
 XX
 SQ Sequence 1018 AA;
 Query Match 95.6%; Score 109; DB 1; Length 1018;
 Best Local Similarity 95.2%; Pred. No. 2.8e-08;
 Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Oy 1 KPSYQFGGHSVDFEEDTLAK 21
 DB 837 KPSYQFGGHSVDFEEDTLPK 857
 RESULT 9
 AAU37245
 ID AAU37245 standard; protein; 1018 AA.
 AC AAU37245;
 DT 14-FEB-2002 (first entry)
 DE Staphylococcus aureus cellular proliferation protein #1415.
 XX Antisense; prokaryotic cellular proliferation protein; antibiotic;
 KW antibacterial; drug design.
 OS Staphylococcus aureus.
 XX WO200170955-A2.
 PN 27-SEP-2001.
 PD 27-SEP-2001.
 PF 21-MAR-2001; 2001WO-US009180.
 XX 21-MAR-2000; 2000US-0191078P.
 PR 23-MAY-2000; 2000US-0206848P.
 PR 26-MAY-2000; 2000US-0207727P.
 PR 23-OCT-2000; 2000US-0242578P.
 PR 27-NOV-2000; 2000US-0253625P.
 PR 22-DEC-2000; 2000US-0257931P.
 PR 16-FEB-2001; 2001US-0269308P.
 XX
 PA (ELIT-) ELITRA PHARM INC.
 XX Haselbeck R, Ohlsen KL, Zyskind JW, Wall D, Trawick JD, Carr GJ;
 PI Yamamoto RT, Xu HH;
 DR WPI; 2001-611495/70.
 DR N-PSDB; AAS55104.
 PT New polynucleotides for the identification and development of
 PT antibiotics, comprise sequences of antisense nucleic acids.
 XX New polynucleotides for the identification and development of
 PS antibiotics, comprise sequences of antisense nucleic acids.
 XX Example 3; SEQ ID NO 12838; 511pp; English.
 CC The invention relates to antisense inhibitors of genes essential to
 CC prokaryotic cellular proliferation, their use in identifying the genes,
 CC their use in the discovery of novel antibiotics, the essential genes

CC themselves and the encoded proteins. The prokaryotes used are Escherichia
 CC coli, Staphylococcus aureus, Salmonella typhi, Klebsiella pneumoniae,
 CC Pseudomonas aeruginosa and Enterococcus faecalis. The invention is also
 CC useful for the identification of potential new targets for antibiotic
 CC development. The antisense nucleic acids can also be used to identify
 CC proteins used in proliferation, to express these proteins, and to obtain
 CC antibodies capable of binding to the expressed proteins. The proteins can
 CC be used to screen compounds in rational drug discovery programmes. The
 CC antisense nucleic acid sequence is also useful to screen for homologous
 CC nucleic acids which are required for cell proliferation in a wide variety
 CC of organisms. The present sequence represents an essential prokaryotic
 CC cellular proliferation protein. Note: The sequence data for this patent
 CC did not form part of the printed specification, but was obtained in
 CC electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 1018 AA;
 Query Match 95.6%; Score 109; DB 4; Length 1018;
 Best Local Similarity 95.2%; Pred. No. 2.8e-08;
 Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Oy 1 KPSYQFGGHSVDFEEDTLAK 21
 DB 837 KPSYQFGGHSVDFEEDTLPK 857
 RESULT 10
 AAU34301
 ID AAU34301 standard; protein; 1018 AA.
 AC AAU34301;
 DT 14-FEB-2002 (first entry)
 DE Staphylococcus aureus cellular proliferation protein #577.
 XX Antisense; prokaryotic cellular proliferation protein; antibiotic;
 KW antibacterial; drug design.
 OS Staphylococcus aureus.
 XX WO200170955-A2.
 PN 27-SEP-2001.
 PD 27-SEP-2001.
 PF 21-MAR-2001; 2001WO-US009180.
 XX 21-MAR-2000; 2000US-0191078P.
 PR 23-MAY-2000; 2000US-0206848P.
 PR 26-MAY-2000; 2000US-0207727P.
 PR 23-OCT-2000; 2000US-0242578P.
 PR 27-NOV-2000; 2000US-0253625P.
 PR 22-DEC-2000; 2000US-0257931P.
 PR 16-FEB-2001; 2001US-0269308P.
 XX
 PA (ELIT-) ELITRA PHARM INC.
 XX Haselbeck R, Ohlsen KL, Zyskind JW, Wall D, Trawick JD, Carr GJ;
 PI Yamamoto RT, Xu HH;
 DR WPI; 2001-611495/70.
 DR N-PSDB; AAS52160.
 PT New polynucleotides for the identification and development of
 PT antibiotics, comprise sequences of antisense nucleic acids.
 XX New polynucleotides for the identification and development of
 PS antibiotics, comprise sequences of antisense nucleic acids.
 XX Example 3; SEQ ID NO 5797; 511pp; English.
 CC The invention relates to antisense inhibitors of genes essential to
 CC prokaryotic cellular proliferation, their use in identifying the genes,
 CC their use in the discovery of novel antibiotics, the essential genes
 CC themselves and the encoded proteins. The prokaryotes used are Escherichia

CC coli, *Staphylococcus aureus*, *Salmonella typhi*, *Klebsiella pneumoniae*,
CC *Pseudomonas aeruginosa* and *Enterococcus faecalis*. The invention is also
CC useful for the identification of potential new targets for antibiotic
CC development. The antisense nucleic acids can also be used to identify
CC proteins used in proliferation, to express these proteins, and to obtain
CC antibodies capable of binding to the expressed proteins. The proteins can
CC be used to screen compounds in rational drug discovery programmes. The
CC antisense nucleic acid sequence is also useful to screen for homologous
CC nucleic acids which are required for cell proliferation in a wide variety
CC of organisms. The present sequence represents an essential prokaryotic
CC cellular proliferation protein. Note: The sequence data for this patent
CC did not form part of the printed specification, but was obtained in
CC electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 1018 AA;

QY Query Match 95.6%; Score 109; DB 4; Length 1018;
Best Local Similarity 95.2%; Pred. No. 2.8e-08;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 1 KPSYQFGGHSVDFEEDTLAK 21
837 KPSYQFGGHSVDFEEDTLPK 857

RESULT 11
ABJ18922
ID ABJ18922 standard; protein; 1018 AA.
XX
AC ABJ18922;
XX
DT 06-MAR-2003 (first entry)
XX
DE Pathogen specific antigen related staphylococcal protein SEQ ID No 68.
XX
XX Antibacterial; virucide; fungicide; protozoacide; cytostatic; anti-HIV;
KW hyperimmune; serum-reactive; antigen; pathogen; tumour; allergen;
KW auto-immunity; vaccine; staphylococcal infection; antibody; cancer;
KW autoimmune disease; HIV; hepatitis.
XX
OS Staphylococcus sp.
XX
PN WO200259148-A2.
XX
PD 01-AUG-2002.
XX
PF 21-JAN-2002; 2002WO-EP000546.
XX
PR 26-JAN-2001; 2001AT-00000130.
XX
PA (CIST-) CISTEM BIOTECHNOLOGIES GMBH.
XX
PI Meinke A, Nagy E, Von Ahnen U, Klade C, Henice T, Zauner W,
PI Miah DB, Vytvytska O, Eitz H, Dryla A, Weichardt T, Hafner M;
PI Tempelmeier B;
XX
XX WPI; 2003-075410/07.
XX
XX Identifying, isolating and producing hyperimmune serum-reactive antigens
XX from a pathogen, for preparing vaccine or medicament for treating or
XX preventing e.g. staphylococcal infections, comprises providing antibody
XX preparation.
XX
XX Example 7; Page 157; 252pp; English.
XX
XX The invention relates to a novel method for identifying, isolating and
XX producing hyperimmune serum-reactive antigens from a pathogen, tumour,
XX allergen, a tissue or host prone to auto-immunity, where the antigens are
XX used in a vaccine, comprises providing antibody preparation from a plasma
XX pool of a type of animal, or individual sera with antibodies against the
XX specific pathogen, tumour, allergen, tissue or host prone to auto-
XX immunity. The hyperimmune serum-reactive antigens comprising any of the

CC 62 sequences of 53-2261 amino acids fully defined in the specification,
CC or their hyperimmune fragments are useful for the manufacture of a
CC pharmaceutical preparation, particularly a vaccine against staphylococcal
CC infections or colonisation against *S. aureus* or *S. epidermidis*. The
CC preparation of antibodies is useful for the manufacture of a medicament
CC for treating or preventing staphylococcal infections or colonisation
CC against *S. aureus* or *S. epidermidis*. The antibody preparations may also
CC be used for diagnostic and imaging purposes. Other conditions that can be
CC treated include cancer, autoimmune diseases or infections caused by viral
CC (e.g. HIV, hepatitis A, B or C), fungal or protozoan pathogens. This
CC sequence represents a staphylococcal protein relating to the method for
CC identifying and producing pathogen specific antigens of the invention

XX SQ Sequence 1018 AA;

QY Query Match 95.6%; Score 109; DB 6; Length 1018;
Best Local Similarity 95.2%; Pred. No. 2.8e-08;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 1 KPSYQFGGHSVDFEEDTLAK 21
837 KPSYQFGGHSVDFEEDTLPK 857

RESULT 12
ABM72537
ID ABM72537 standard; protein; 1018 AA.
XX
AC ABM72537;
XX
DT 20-NOV-2003 (first entry)
XX
DE Staphylococcus aureus protein #1777.
XX
KW Antibacterial; vaccine; gene therapy; infection; sepsis; diagnosis;
KW enzymatic assay; antibiotic target.
XX
OS Staphylococcus aureus.
XX
PN WO200294868-A2.
XX
PD 28-NOV-2002.
XX
PF 27-MAR-2002; 2002WO-IB002637.
XX
PR 27-MAR-2001; 2001GB-00007661.
XX
PA (CHIR-) CHIRON SPA.
XX
PI Maigman V, Mora M, Scarselli M;
XX
XX WPI; 2003-120786/11.
XX
XX N-PSDB; ACF74097.
XX
XX New Staphylococcus aureus protein, useful as a vaccine for treating or
XX preventing Staphylococcal infection, specifically an infection caused by
XX *S. aureus*, e.g. sepsis.
XX
XX Claim 1; SEQ ID NO 3554; 49pp; English.
XX
XX The invention relates to novel genes and encoded proteins from
XX *Staphylococcus aureus*. A composition comprising the *S. aureus* protein, a
XX nucleic acid encoding the protein, or an antibody to the protein, is
XX useful as a pharmaceutical, particularly as a vaccine for treating or
XX preventing infection due to *Staphylococcus bacteria*, specifically an
XX infection caused by *S. aureus*. The composition is particularly useful for
XX treating or preventing sepsis in a patient. The composition can also be
XX used for diagnostics. The protein is also used in an assay for enzymatic
XX studies and as a target for antibiotics. This sequence represents one of
XX the novel *S. aureus* proteins of the invention

XX SQ Sequence 1018 AA;

Query Match 95.6%; Score 109; DB 6; Length 1018;
Best Local Similarity 95.2%; Pred. No. 2.8e-08;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KPSYQFGHNSVDFEEDTLAK 21
DB 837 KPSYQFGHNSVDFEEDTLAK 857

RESULT 13

AAM89806
ID AAM89806 standard; protein; 1027 AA.

AC AAM89806;

DT 16-MAR-1999 (first entry)

DE Staphylococcus aureus protein SEQ ID #5254.

XX Computer readable medium; vaccine; S. aureus infection; immunodetection;

KW cellulitis; eyelid infection; food poisoning; osteomyelitis; therapy;

KM skin infection; surgical wound infection; scalded skin syndrome;

KM toxic shock syndrome.

OS Staphylococcus aureus.

PN EP786519-A2.

PD 30-JUL-1997.

PF 07-JAN-1997; 97EP-00100117.

PR 05-JAN-1996; 96US-0009861P.

PA (HUMA-) HUMAN GENOME SCI INC.

PI Kunach CA, Choi GH, Barash SC, Dillon PJ, Fannon MR, Rosen CA;

PT WPI; 1997-374922/35.

PR Polynucleotide(s) and proteins derived from Staphylococcus aureus -

PT stored on computer readable medium and used in the production of anti-

PR S. aureus vaccines.

PS Claim 23; Page 3263-3267; 3271pp; English.

XX This sequence represents a Staphylococcus aureus protein sequence of the
CC invention. The DNA sequences encoding the S. aureus proteins are recorded
CC on a computer readable medium, preferably selected from a floppy or hard
CC disk, random access memory (RAM), read-only memory (ROM) or CD-ROM.
CC Homology searches using the S. aureus DNA sequences allows putative
CC functions to be assigned so that protein-encoding or regulatory regions
CC of commercial, therapeutic or industrial importance can be obtained.
CC Specifically, sequences which are likely to encode antigens have been
CC identified and these polypeptides can be used in a vaccine composition
CC against S. aureus infection. The polypeptides can also be used in a kit
CC for the immunodetection of S. aureus in a sample. S. aureus is implicated
CC in numerous human diseases, including cellulitis, eyelid infections, food
CC poisoning, osteomyelitis, skin and surgical wound infections, scalded
CC skin syndrome, toxic shock syndrome, etc. Organisms transformed with the
CC DNA sequences can be used for recombinant production of the polypeptides.
CC The new DNA sequences (and their fragments) are useful as primers or
CC probes for isolating homologues of any of the 5191 S. aureus DNA sequences
CC contained on the computer readable medium

XX Sequence 1027 AA;

QY Query Match 95.6%; Score 109; DB 2; Length 1027;

Best Local Similarity 95.2%; Pred. No. 2.9e-08;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KPSYQFGHNSVDFEEDTLAK 21

DB 846 KPSYQFGHNSVDFEEDTLAK 866

RESULT 14

ABU15854
ID ABU15854 standard; protein; 961 AA.

AC ABU15854;

DT 19-JUN-2003 (first entry)

DE Protein encoded by Prokaryotic essential gene #1381.

KM Antisense; prokaryotic essential gene; cell proliferation; drug design.

OS Staphylococcus aureus.

PN WO20027183-A2.

PD 03-OCT-2002.

PF 21-MAR-2002; 2002WO-US0009107.

PR 21-MAR-2001; 2001US-00815242.

PR 06-SEP-2001; 2001US-00948993.

PR 25-OCT-2001; 2001US-0342923P.

PR 08-FEB-2002; 2002US-00072851.

PR 06-MAR-2002; 2002US-0362699P.

PA (ELIT-) ELITRA PHARM INC.

PI Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zykkind JW;

PT Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;

DR WPI; 2003-029926/02.

DR N-PSDB; ACA19724.

PR New antisense nucleic acid, useful for identifying proteins or screening

PT for homologous nucleic acids required for cellular proliferation to

PR isolate candidate molecules for rational drug discovery programs.

PS Claim 25; SEQ ID NO 43778; 1766pp; English.

XX The invention relates to an isolated nucleic acid comprising any one of
CC the 623 antisense sequences given in the specification where expression
CC of the nucleic acid inhibits proliferation of a cell. Also included are:
CC (1) a vector comprising a promoter operably linked to the nucleic acid
CC encoding a polypeptide whose expression is inhibited by the antisense
CC nucleic acid; (2) a host cell containing the vector; (3) an isolated
CC polypeptide or its fragment whose expression is inhibited by the
CC antisense nucleic acid; (4) an antibody capable of specifically binding
CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular
CC proliferation or the activity of a gene in an operon required for
CC proliferation; (7) identifying a compound that influences the activity of
CC the gene product or that has an activity against a biological pathway
CC required for proliferation, or that inhibits cellular proliferation; (8)
CC identifying a gene required for cellular proliferation or the biological
CC pathway in which a proliferation-regulated gene or its gene product lies
CC or a gene on which the test compound that inhibits proliferation of an
CC organism acts; (9) manufacturing an antibiotic; (10) profiling a
CC compound's activity; (11) a culture comprising strains in which the gene
CC product is overexpressed or underexpressed; (12) determining the extent
CC to which each of the strains is present in a culture or collection of
CC strains; or (13) identifying the target of a compound that inhibits the
CC proliferation of an organism. The antisense nucleic acids are useful for
CC identifying proteins or screening for homologous nucleic acids required
CC for cellular proliferation to isolate candidate molecules for rational
CC drug discovery programs, or for screening homologous nucleic acids
CC required for proliferation in cells other than S. aureus, S. typhimurium,
CC K. pneumoniae or P. aeruginosa. The present sequence is encoded by one of
CC the target prokaryotic essential genes. Note: The sequence data for this
CC patent did not form part of the printed specification, but was obtained
CC in electronic format directly from WIPO at

CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 961 AA;
Query Match 93.0%; Score 106; DB 6; Length 961;
Best Local Similarity 90.5%; Pred. No. 8e-08;
Matches 19; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 KPSYQFGHNSVDFEEDTLAK 21
DB 784 KPNYQFGHNSVDFEEDTLPK 804
RESULT 15
AAUJ3960
ID AAUJ3960 standard; protein; 978 AA.
XX
XX AAUJ3960;
XX
XX 14-FEB-2002 (first entry)
XX
XX Staphylococcus aureus cellular proliferation protein #236.
XX
XX Antisense; prokaryotic cellular proliferation protein; antibiotic;
XX
XX antibacterial; drug design.
XX
XX Staphylococcus aureus.
XX
XX WO200170955-A2.
XX
XX 27-SEP-2001.
XX
XX 21-MAR-2001; 2001WO-US009180.
XX
XX 21-MAR-2000; 2000US-0191078P.
XX
XX 23-MAY-2000; 2000US-0206848P.
XX
XX 26-MAY-2000; 2000US-0207727P.
XX
XX 23-OCT-2000; 2000US-0242578P.
XX
XX 27-NOV-2000; 2000US-0253625P.
XX
XX 22-DEC-2000; 2000US-0257931P.
XX
XX 16-FEB-2001; 2001US-0269308P.
XX
XX
XX (ELIT-) ELITRA PHARM INC.
XX
XX Haseelbeck R, Ohlsen KI, Zyskind JW, Wall D, Trawick JD, Carr GJ;
XX
XX Yamamoto RT, Xu HH;
XX
XX WPI; 2001-611495/70.
XX
XX N-PSDB; AAS51819.
XX
XX New polynucleotides for the identification and development of
XX
XX antibiotics, comprise sequences of antisense nucleic acids.
XX
XX
XX Example 3; SEQ ID NO 5456; 511bp; English.
XX
XX
XX The invention relates to antisense inhibitors of genes essential to
XX
XX prokaryotic cellular proliferation, their use in identifying the genes,
XX
XX their use in the discovery of novel antibiotics, the essential genes
XX
XX themselves and the encoded proteins. The prokaryotes used are Escherichia
XX
XX coli, Staphylococcus aureus, Salmonella typhi, Klebsiella pneumoniae,
XX
XX Pseudomonas aeruginosa and Enterococcus faecalis. The invention is also
XX
XX useful for the identification of potential new targets for antibiotic
XX
XX development. The antisense nucleic acids can also be used to identify
XX
XX proteins used in proliferation, to express these proteins, and to obtain
XX
XX antibodies capable of binding to the expressed proteins. The proteins can
XX
XX be used to screen compounds in rational drug discovery programmes. The
XX
XX antisense nucleic acid sequence is also useful to screen for homologous
XX
XX nucleic acids which are required for cell proliferation in a wide variety
XX
XX of organisms. The present sequence represents an essential prokaryotic
XX
XX cellular proliferation protein. Note: The sequence data for this patent
XX
XX did not form part of the printed specification, but was obtained in
XX
XX electronic format directly from WIPO at
XX
XX ftp.wipo.int/pub/published_pct_sequences

XX
SQ Sequence 978 AA;
Query Match 93.0%; Score 106; DB 4; Length 978;
Best Local Similarity 90.5%; Pred. No. 8.2e-08;
Matches 19; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 KPSYQFGHNSVDFEEDTLAK 21
DB 815 KPNYQFGHNSVDFEEDTLPK 835
Search completed: October 25, 2005, 19:38:31
Job time : 59.1473 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using SW model

Run on: October 22, 2005, 02:23:36 ; Search time 15.9358 seconds
(without alignments)
98.371 Million cell updates/sec

Title: US-10-731-238-32
Perfect score: 114
Sequence: 1 KPSYQFGHNSVDFEEDTLAK 21

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA: *
1: /cgn2_6/prodata/1/1aa/5A_COMB.pep: *
2: /cgn2_6/prodata/1/1aa/5B_COMB.pep: *
3: /cgn2_6/prodata/1/1aa/5A_COMB.pep: *
4: /cgn2_6/prodata/1/1aa/5B_COMB.pep: *
5: /cgn2_6/prodata/1/1aa/6B_COMB.pep: *
6: /cgn2_6/prodata/1/1aa/backfill1.pep: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	114	100.0	21	4	US-09-010-317-32 Sequence 32, Appl
2	109	95.6	21	4	US-09-010-317-9 Sequence 9, Appl
3	109	95.6	37	1	US-08-234-622A-4 Sequence 4, Appl
4	109	95.6	38	1	US-08-294-189-8 Sequence 8, Appl
5	109	95.6	38	1	US-08-729-767-5 Sequence 5, Appl
6	109	95.6	114	1	US-08-259-000-3 Sequence 3, Appl
7	109	95.6	139	3	US-08-856-253-8 Sequence 8, Appl
8	109	95.6	178	2	US-08-459-135A-12 Sequence 12, Appl
9	109	95.6	178	2	US-08-495-559-12 Sequence 12, Appl
10	109	95.6	1027	4	US-08-956-171E-5254 Sequence 5254, Ap
11	109	95.6	1027	4	US-08-781-986A-5254 Sequence 5254, Ap
12	105	92.1	21	4	US-09-010-317-33 Sequence 33, Appl
13	104	91.2	21	4	US-09-010-317-14 Sequence 14, Appl
14	104	91.2	21	4	US-09-010-317-16 Sequence 16, Appl
15	104	91.2	21	4	US-09-010-317-23 Sequence 23, Appl
16	103	90.4	21	4	US-09-010-317-18 Sequence 18, Appl
17	103	90.4	21	4	US-09-010-317-24 Sequence 24, Appl
18	103	90.4	21	4	US-09-010-317-27 Sequence 27, Appl
19	103	90.4	21	4	US-09-010-317-28 Sequence 28, Appl
20	103	90.4	21	4	US-09-010-317-30 Sequence 30, Appl
21	102	89.5	21	4	US-09-010-317-25 Sequence 25, Appl
22	102	89.5	21	4	US-09-010-317-29 Sequence 29, Appl
23	102	89.5	21	4	US-09-010-317-31 Sequence 31, Appl
24	102	89.5	130	2	US-08-459-135A-7 Sequence 7, Appl
25	102	89.5	130	2	US-08-459-135A-8 Sequence 8, Appl
26	102	89.5	130	3	US-08-495-559-7 Sequence 7, Appl
27	102	89.5	130	3	US-08-495-559-8 Sequence 8, Appl

28	102	89.5	174	2	US-08-459-135A-10 Sequence 10, Appl
29	102	89.5	174	2	US-08-459-135A-13 Sequence 13, Appl
30	102	89.5	174	3	US-08-495-559-10 Sequence 10, Appl
31	102	89.5	174	3	US-08-495-559-13 Sequence 13, Appl
32	102	89.5	176	2	US-08-495-559-6 Sequence 6, Appl
33	102	89.5	181	2	US-08-459-135A-6 Sequence 6, Appl
34	102	89.5	559	4	US-08-956-171E-5251 Sequence 5251, Ap
35	102	89.5	559	4	US-08-781-986A-5251 Sequence 5251, Ap
36	101	88.6	21	4	US-09-010-317-10 Sequence 10, Appl
37	101	88.6	21	4	US-09-010-317-15 Sequence 15, Appl
38	101	88.6	21	4	US-09-010-317-20 Sequence 20, Appl
39	101	88.6	21	4	US-09-010-317-22 Sequence 22, Appl
40	101	88.6	22	4	US-09-010-317-13 Sequence 13, Appl
41	99	86.8	21	4	US-09-010-317-17 Sequence 17, Appl
42	99	86.8	21	4	US-09-010-317-19 Sequence 19, Appl
43	99	86.8	21	4	US-09-010-317-21 Sequence 21, Appl
44	99	86.8	21	4	US-09-010-317-26 Sequence 26, Appl
45	96	84.2	19	1	US-08-234-622A-1 Sequence 1, Appl

ALIGNMENTS

RESULT 1
US-09-010-317-32
Sequence 32, Application US/09010317
Patent No. 6685943
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
APPLICANT: Patti, Joseph M.
APPLICANT: House-Pompeo, Karen L.
APPLICANT: Speziale, Pietro
APPLICANT: Ubi, Danny
APPLICANT: McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
TITLE OF INVENTION: AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAMK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 32:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-09-010-317-32
Query Match 100.0%; Score 114; DB 4; Length 21;
Best Local Similarity 100.0%; Pred. No. 4.1e-12;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 KPSYQFGHNSVDFEEDTLAK 21
Db 1 KPSYQFGHNSVDFEEDTLAK 21

RESULT 2

US-09-010-317-9
Sequence 9, Application US/09010317
Patent No. 6685943
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
APPLICANT: Patti, Joseph M.
APPLICANT: House-Pompeo, Karen L.
APPLICANT: Speziale, Pietro
APPLICANT: Joh, Danny
APPLICANT: McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
TITLE OF INVENTION: AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/010.317
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/036.139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hieber, David W.
REGISTRATION NUMBER: 41.071
REFERENCE/DOCKET NUMBER: TAMK.189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-09-010-317-9

Query Match 95.6%; Score 109; DB 4; Length 21;
Best Local Similarity 95.2%; Pred. No. 2.8e-11;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 KPSYQFGHNSVDFEEDTLAK 21
Db 1 KPSYQFGHNSVDFEEDTLAK 21

RESULT 3

US-08-234-622A-4
Sequence 4, Application US/08234622A
Patent No. 5440014
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
APPLICANT: MCGAVIN, Martin
APPLICANT: RAUCCI, Giuseppe
TITLE OF INVENTION: A FIBRONECTIN BINDING PEPTIDE

NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Burne, Doane, Swecker & Mathis
STREET: P.O. Box 1404
CITY: Alexandria
STATE: Virginia
COUNTRY: United States
ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/234.622A
FILING DATE: 28-APR-1994
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: SE 9002617-0
FILING DATE: 10-AUG-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/SE91/00534
FILING DATE: 09-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: Meuth, Donna M
REGISTRATION NUMBER: 36.607
REFERENCE/DOCKET NUMBER: 012885-044
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-6620
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 37 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-234-622A-4

Query Match 95.6%; Score 109; DB 1; Length 37;
Best Local Similarity 95.2%; Pred. No. 5.3e-11;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 KPSYQFGHNSVDFEEDTLAK 21
Db 16 KPSYQFGHNSVDFEEDTLAK 36

RESULT 4

US-08-294-189-8
Sequence 8, Application US/08294189
Patent No. 5707822
GENERAL INFORMATION:
APPLICANT: Fischetti, Vincent A.
APPLICANT: Rakonjac, Jasna
APPLICANT: Robbins, John
TITLE OF INVENTION: GENE SERUM OPACITY FACTOR
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack Avenue
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/294.189
FILING DATE: 22-AUG-1994

CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-118
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 487-5800
TELEFAX: 201 343-1684
TELEX: 133521
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
ORGANISM: Streptococcus pyogenes
STRAIN: D7J34
INDIVIDUAL ISOLATE: 22
IMMEDIATE SOURCE:
CLONE: SAUSA
US-08-294-189-8

Query Match 95.6%; Score 109; DB 1; Length 38;
Best Local Similarity 95.2%; Pred. No. 5.4e-11;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KPSYQFGHNSVDFEEDTLAK 21
Db 10 KPSYQFGHNSVDFEEDTLPK 30

RESULT 5
US-08-729-767-5
Sequence 5, Application US/08729767
Patent No. 5770702
GENERAL INFORMATION:
APPLICANT: HOOK, Magnus
APPLICANT: LINDBERG, Martin Kjell
APPLICANT: SIGNAS, Lars Christer
APPLICANT: WADSTROM, Torkel Mikael
APPLICANT: FROMAN, Gunnar
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN AS WELL AS
TITLE OF INVENTION: ITS PREPARATION
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Burns, Doane, Swecker & Mathis, L.L.P.
STREET: P.O. Box 1404
CITY: Alexandria
STATE: Virginia
COUNTRY: United States
ZIP: 22113-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/729,767
FILING DATE: 07-OCT-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/259,000
FILING DATE: 13-JUN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/007,817
FILING DATE: 22-JAN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/201,028
FILING DATE: 01-JUN-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: SE 8702272-9

FILING DATE: 01-JUN-1987
ATTORNEY/AGENT INFORMATION:
NAME: McGowan, Malcolm K.
REGISTRATION NUMBER: 39,300
REFERENCE/DOCKET NUMBER: 012889-036
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-729-767-5

Query Match 95.6%; Score 109; DB 1; Length 38;
Best Local Similarity 95.2%; Pred. No. 5.4e-11;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KPSYQFGHNSVDFEEDTLAK 21
Db 17 KPSYQFGHNSVDFEEDTLPK 37

RESULT 6
US-08-259-000-3
Sequence 3, Application US/08259000
Patent No. 5571514
GENERAL INFORMATION:
APPLICANT: HOOK, Magnus
APPLICANT: LINDBERG, Martin Kjell
APPLICANT: SIGNAS, Lars Christer
APPLICANT: WADSTROM, Torkel Mikael
APPLICANT: FROMAN, Gunnar
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN AS WELL AS
TITLE OF INVENTION: ITS PREPARATION
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Burns, Doane, Swecker & Mathis
STREET: P.O. Box 1404
CITY: Alexandria
STATE: Virginia
COUNTRY: United States
ZIP: 22113-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/259,000
FILING DATE: 13-JUN-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: SE 8702272-9
FILING DATE: 01-JUN-1987
ATTORNEY/AGENT INFORMATION:
NAME: Meuth, Donna M
REGISTRATION NUMBER: 36,607
REFERENCE/DOCKET NUMBER: 012885-062
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 114 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-259-000-3

Query Match 95.6%; Score 109; DB 1; Length 114;
Best Local Similarity 95.2%; Pred. No. 1.9e-10;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 KPSYQFGHNSVDFEEDTLAK 21
DB 93 KPSYQFGHNSVDFEEDTLPK 113

RESULT 7
US-08-856-253-8
; Sequence 8, Application US/08856253
; Patent No. 6286214
; GENERAL INFORMATION:
; APPLICANT: Hook, Magnus
; APPLICANT: Patti, Joseph M.
; APPLICANT: House-Pompeo, Karen
; APPLICANT: Stannam, Narayana
; APPLICANT: Symerky, Jindrich
; TITLE OF INVENTION: COLLAGEN BINDING PROTEIN COMPOSITIONS
; TITLE OF INVENTION: AND METHODS OF USE
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: U.S.
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/856,253
; FILING DATE: Concurrently Herewith
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/017,678
; FILING DATE: 16-MAY-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Kitchell, Barbara S.
; REGISTRATION NUMBER: 33,928
; REFERENCE/DOCKET NUMBER: TAWK:193
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (512) 418-3000
; TELEFAX: (512) 474-7577
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 139 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
US-08-856-253-8

Query Match 95.6%; Score 109; DB 3; Length 139;
Best Local Similarity 95.2%; Pred. No. 2.4e-10;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 KPSYQFGHNSVDFEEDTLAK 21
DB 107 KPSYQFGHNSVDFEEDTLPK 127

RESULT 8
US-08-459-135A-12
; Sequence 12, Application US/08459135A
; Patent No. 5955078
; GENERAL INFORMATION:
; APPLICANT: BURHAM, Martin Karl Russel
; APPLICANT: CHOPRA, Ian

APPLICANT: CRITCHLEY, Ian Alfred
APPLICANT: KNOWLES, David Justin Charles
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN: MONOCLONAL ANTIBODY AND THEIR US
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
STATE: PA
COUNTRY: U.S.A.
ZIP: 19406-0939
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: Fastseq, Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/459,135A
; FILING DATE: 02-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB/94/00215
; FILING DATE: 04-Feb-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Gimml, Edward R.
; REGISTRATION NUMBER: 38,891
; REFERENCE/DOCKET NUMBER: P30591C2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-270-4478
; TELEFAX: 610-270-5090
; TELEX:
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 178 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Protein
US-08-459-135A-12

Query Match 95.6%; Score 109; DB 2; Length 178;
Best Local Similarity 95.2%; Pred. No. 3.2e-10;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 KPSYQFGHNSVDFEEDTLAK 21
DB 93 KPSYQFGHNSVDFEEDTLPK 113

RESULT 9
US-08-495-559-12
; Sequence 12, Application US/08495559A
; Patent No. 6054572
; GENERAL INFORMATION:
; APPLICANT: BURHAM, Martin Karl Russel
; APPLICANT: CHOPRA, Ian
; APPLICANT: CRITCHLEY, Ian Alfred
; APPLICANT: KNOWLES, David Justin Charles
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN: MONOCLONAL
; TITLE OF INVENTION: ANTIBODY AND THEIR USE IN PREVENTING BACTERIAL ADHESION
; FILE REFERENCE: P30591
; CURRENT APPLICATION NUMBER: US/08/495,559A
; CURRENT FILING DATE: 1995-08-03
; EARLIER APPLICATION NUMBER: GB 9302289.5
; EARLIER FILING DATE: 1993-02-05
; EARLIER APPLICATION NUMBER: GB 9321592.9
; EARLIER FILING DATE: 1993-10-20
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 12
; LENGTH: 178
; TYPE: PRT

ORGANISM: Staphylococcus aureus
US-08-495-559-12

Query Match 95.6%; Score 109; DB 3; Length 178;
Best Local Similarity 95.2%; Pred. No. 3.2e-10;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KPSYFGGHSVDFEEDTLAK 21
Db 93 KPSYFGGHSVDFEEDTLPK 113

RESULT 10

US-08-956-171E-5254
Sequence 5254, Application US/08956171E
Patent No. 6593114

GENERAL INFORMATION:

APPLICANT: Charles Kunsch

Gill H. Choi

Patrick S. Dillon

Craig A. Rosen

Steven C. Barash

Michael R. Fannon

TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences

NUMBER OF SEQUENCES: 5256

CORRESPONDENCE ADDRESS:

ADDRESSEE: Human Genome Sciences, Inc.

STREET: 9410 Key West Avenue

CITY: Rockville

STATE: Maryland

COUNTRY: USA

ZIP: 20850

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.50 inch, 1.4mb storage

COMPUTER: HP Vectra 486/33

OPERATING SYSTEM: MSDOS version 6.2

SOFTWARE: ASCII Text

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/956,171E

FILING DATE: 20-Oct-1997

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 60/009,861

FILING DATE: January 5, 1996

APPLICATION NUMBER: 08/781,986

FILING DATE: January 3, 1997

ATTORNEY/AGENT INFORMATION:

NAME: Mark J. Hyman

REGISTRATION NUMBER: 46,789

REFERENCE/DOCKET NUMBER: PB248P1

TELECOMMUNICATION INFORMATION:

TELEPHONE: (240) 314-1224

TELEFAX: (301) 309-8439

INFORMATION FOR SEQ ID NO: 5254:

SEQUENCE CHARACTERISTICS:

LENGTH: 1027 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 5254:

US-08-956-171E-5254

Query Match 95.6%; Score 109; DB 4; Length 1027;
Best Local Similarity 95.2%; Pred. No. 2.3e-09;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KPSYFGGHSVDFEEDTLAK 21
Db 846 KPSYFGGHSVDFEEDTLPK 866

RESULT 11

US-08-781-986A-5254
Sequence 5254, Application US/08781986A
Patent No. 6737248

GENERAL INFORMATION:

APPLICANT: Charles Kunsch

TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences

NUMBER OF SEQUENCES: 5255

CORRESPONDENCE ADDRESS:

ADDRESSEE: Human Genome Sciences, Inc.

STREET: 9410 Key West Avenue

CITY: Rockville

STATE: Maryland

COUNTRY: USA

ZIP: 20850

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.50 inch, 1.4mb storage

COMPUTER: HP Vectra 486/33

OPERATING SYSTEM: MSDOS version 6.2

SOFTWARE: ASCII Text

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/781,986A

FILING DATE:

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Benson, Bob

REGISTRATION NUMBER: 30,446

REFERENCE/DOCKET NUMBER: PB248BP

TELECOMMUNICATION INFORMATION:

TELEPHONE: (301) 309-8504

TELEFAX: (301) 309-8512

INFORMATION FOR SEQ ID NO: 5254:

SEQUENCE CHARACTERISTICS:

LENGTH: 1027 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-781-986A-5254

QY 1 KPSYFGGHSVDFEEDTLAK 21
Db 846 KPSYFGGHSVDFEEDTLPK 866

RESULT 12

US-09-010-317-33
Sequence 33, Application US/09010317
Patent No. 6685943

GENERAL INFORMATION:

APPLICANT: Hook, Magnus

APPLICANT: Patil, Joseph M.

APPLICANT: House-Pompeo, Karen L.

APPLICANT: Speziale, Pietro

APPLICANT: Jon, Danny

APPLICANT: McGavin, Martin J.

TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS

NUMBER OF SEQUENCES: 105

CORRESPONDENCE ADDRESS:

ADDRESSEE: Arnold, White & Durkee

STREET: P.O. Box 4433

CITY: Houston

STATE: TX

COUNTRY: USA

ZIP: 77210-4433

COMPUTER READABLE FORM:

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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/010.317
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/036.139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-09-010-317-33

Query Match      92.1%; Score 105; DB 4; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.3e-10;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KPSYFGGHSVDPEEDTL 19
Db      1 KPSYFGGHSVDPEEDTL 19

RESULT 13
US-09-010-317-14
Sequence 14, Application US/09010317
Patent No. 6685943
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
APPLICANT: Patli, Joseph M.
APPLICANT: House-Pompeo, Karen L.
APPLICANT: Speziale, Pietro
APPLICANT: Joh, Danny
APPLICANT: Mcgavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/010.317
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/036.139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-09-010-317-16

Query Match      91.2%; Score 104; DB 4; Length 21;
Best Local Similarity 90.5%; Pred. No. 1.8e-10;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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```

TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-09-010-317-14

Query Match      91.2%; Score 104; DB 4; Length 21;
Best Local Similarity 95.0%; Pred. No. 1.8e-10;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      2 PSYFGGHSVDPEEDTLAK 21
Db      2 PSYFGGHSVDPEEDTLPK 21

RESULT 14
US-09-010-317-16
Sequence 16, Application US/09010317
Patent No. 6685943
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
APPLICANT: Patli, Joseph M.
APPLICANT: House-Pompeo, Karen L.
APPLICANT: Speziale, Pietro
APPLICANT: Joh, Danny
APPLICANT: Mcgavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/010.317
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/036.139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-09-010-317-16

Query Match      91.2%; Score 104; DB 4; Length 21;
Best Local Similarity 90.5%; Pred. No. 1.8e-10;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      1 KPSYFGGHSVDPEEDTLAK 21
Db      1 KPSYFGGHSVDPEEDTLAK 21
```

Db 1 KPPYOGGHNSVDFEEDTLPK 21

RESULT 15

US-09-010-317-23
 ; Sequence 23, Application US/09010317
 ; Patent No. 6685943
 ; GENERAL INFORMATION:
 ; APPLICANT: Hook, Magnus
 ; APPLICANT: Patti, Joseph M.
 ; APPLICANT: House, Pompeo, Karen L.
 ; APPLICANT: Speziale, Pietro
 ; APPLICANT: Joh, Danny
 ; APPLICANT: McGavin, Martin J.
 ; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
 ; TITLE OF INVENTION: AND METHODS OF USE
 ; NUMBER OF SEQUENCES: 105
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Arnold, White & Durkee
 ; STREET: P.O. Box 4433
 ; CITY: Houston
 ; STATE: TX
 ; COUNTRY: USA
 ; ZIP: 77210-4433
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patentin Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/010,317
 ; FILING DATE:
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 60/036,139
 ; FILING DATE: 21-JAN-1997
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Hibler, David W.
 ; REGISTRATION NUMBER: 41,071
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 512-418-3000
 ; TELEFAX: 512-474-7577
 ; INFORMATION FOR SEQ ID NO: 23:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 21 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS:
 ; TOPOLOGY: linear
 ; US-09-010-317-23

Query Match 91.2%; Score 104; DB 4; Length 21;
 Best Local Similarity 90.5%; Pred. No. 1.8e-10;
 Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 KPSYOGGHNSVDFEEDTLAK 21
 |||||
 Db 1 KPSYOGGHNSVDFEEDTLPK 21

Search completed: October 22, 2005, 03:51:15
 Job time : 16.9358 secs

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GenCore version 5.1.6
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OM protein - protein search, using SW model

Run on: October 22, 2005, 10:49:15 ; Search time 59.2367 Seconds
(without alignments)
148.005 Million cell updates/sec

Title: US-10-731-238-32

Perfect score: 114
Sequence: 1 KPSYQFGHNSVDEEDTLAK 21

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1862951 seqs, 417491010 residues

Total number of hits satisfying chosen parameters: 1862951

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

Published Applications AA:*

- 1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
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- 9: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep.*
- 10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep.*
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- 14: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
- 15: /cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/2/pubpaa/US10E_PUBCOMB.pep.*
- 17: /cgn2_6/ptodata/2/pubpaa/US10F_PUBCOMB.pep.*
- 18: /cgn2_6/ptodata/2/pubpaa/US10G_PUBCOMB.pep.*
- 19: /cgn2_6/ptodata/2/pubpaa/US11A_PUBCOMB.pep.*
- 20: /cgn2_6/ptodata/2/pubpaa/US11B_PUBCOMB.pep.*
- 21: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
- 22: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	114	100.0	21	18	US-10-731-238-32
2	109	95.6	21	18	US-10-731-238-32
3	109	95.6	37	20	US-11-066-697-1134
4	109	95.6	139	9	US-09-813-820-8
5	109	95.6	1018	9	US-09-815-242-5797
6	109	95.6	1018	9	US-09-815-242-12838
7	109	95.6	1018	17	US-10-470-048B-68
8	109	95.6	1027	15	US-08-781-986A-5254
9	109	95.6	1027	15	US-10-329-624-5254
10	106	93.0	961	15	US-10-282-122A-43778
11	106	93.0	978	9	US-09-815-242-5456

Result No.	Score	Query Match	Length DB	ID	Description
12	106	93.0	1001	9	US-09-815-242-12686
13	106	93.0	1038	15	US-10-282-122A-43827
14	105	92.1	21	18	US-10-731-238-33
15	104	91.2	21	18	US-10-731-238-14
16	104	91.2	21	18	US-10-731-238-16
17	104	91.2	21	18	US-10-731-238-23
18	103	90.4	21	18	US-10-731-238-18
19	103	90.4	21	18	US-10-731-238-24
20	103	90.4	21	18	US-10-731-238-27
21	103	90.4	21	18	US-10-731-238-28
22	103	90.4	21	18	US-10-731-238-30
23	102	89.5	21	18	US-10-731-238-25
24	102	89.5	21	18	US-10-731-238-29
25	102	89.5	21	18	US-10-731-238-31
26	102	89.5	388	8	US-08-901-062-1
27	102	89.5	559	15	US-08-781-986A-5251
28	102	89.5	559	15	US-10-329-624-5251
29	102	89.5	940	17	US-10-470-048A-424
30	102	89.5	948	17	US-10-470-048B-69
31	101	88.6	21	18	US-10-731-238-10
32	101	88.6	21	18	US-10-731-238-15
33	101	88.6	21	18	US-10-731-238-20
34	101	88.6	21	18	US-10-731-238-22
35	101	88.6	21	18	US-10-731-238-13
36	99	86.8	21	18	US-10-731-238-17
37	99	86.8	21	18	US-10-731-238-19
38	99	86.8	21	18	US-10-731-238-21
39	99	86.8	21	18	US-10-731-238-26
40	81	71.1	21	18	US-10-731-238-34
41	78	68.4	14	18	US-10-731-238-61
42	59	51.8	10	18	US-10-731-238-96
43	58	50.9	10	18	US-10-731-238-97
44	57	50.0	10	18	US-10-731-238-98
45	56	49.1	10	18	US-10-731-238-99

ALIGNMENTS

RESULT 1
US-10-731-238-32
Sequence 32, Application US/10731238
Publication No. US20050123552A1
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
Pattl, Joseph M.
House-Pompeo, Karen L.
Speziale, Pietro
Uth, Danny
McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESSES:
ADDRESSER: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/731,238
FILING DATE: 10-Dec-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE: 21-Jan-1998
APPLICATION NUMBER: US 60/036,139

FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAMK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 32:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 32:
US-10-731-238-32

Query Match 100.0%; Score 114; DB 18; Length 21;
Best Local Similarity 100.0%; Pred. No. 7e-11;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KPSYFGHNSVDFEEDTLAK 21
1 KPSYFGHNSVDFEEDTLAK 21

Db 1 KPSYFGHNSVDFEEDTLAK 21

RESULT 2
US-10-731-238-9
Sequence 9, Application US/10731238
Publication No. US20050123552A1
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
Pacti, Joseph M.
House-Pompeo, Karen L.
Speziale, Pietro
Joh, Danny
McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P. O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/731,238
FILING DATE: 10-Dec-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE: 21-Jan-1998
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAMK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>

TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 9:
US-10-731-238-9

Query Match 95.6%; Score 109; DB 18; Length 21;
Best Local Similarity 95.2%; Pred. No. 4.3e-10;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KPSYFGHNSVDFEEDTLAK 21
1 KPSYFGHNSVDFEEDTLAK 21

Db 1 KPSYFGHNSVDFEEDTLAK 21

RESULT 3
US-11-066-697-1134
Sequence 1134, Application US/11066697
Publication No. US20050187159A1
GENERAL INFORMATION:
APPLICANT: Bridon, Dominique P.
APPLICANT: Ezrin, Alan M.
APPLICANT: Milner, Peter G.
APPLICANT: Holmes, Darren L.
APPLICANT: Thibaudau, Karen
TITLE OF INVENTION: PROTECTION OF ENDOGENOUS THERAPEUTIC PEPTIDES FROM
TITLE OF INVENTION: PEPTIDASE ACTIVITY THROUGH CONJUGATION TO BLOOD
TITLE OF INVENTION: COMPONENTS
FILE REFERENCE: 500662002301
CURRENT APPLICATION NUMBER: US/11/066,697
CURRENT FILING DATE: 2005-02-25
PRIOR APPLICATION NUMBER: 09/657,276
PRIOR FILING DATE: 2000-09-07
PRIOR APPLICATION NUMBER: 60/153,406
PRIOR FILING DATE: 1999-09-10
PRIOR APPLICATION NUMBER: 60/159,783
PRIOR FILING DATE: 1999-10-15
NUMBER OF SEQ ID NOS: 1617
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 1134
LENGTH: 37
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
OTHER INFORMATION: Peptide
US-11-066-697-1134

Query Match 95.6%; Score 109; DB 20; Length 37;
Best Local Similarity 95.2%; Pred. No. 8e-10;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KPSYFGHNSVDFEEDTLAK 21
1 KPSYFGHNSVDFEEDTLAK 21

Db 16 KPSYFGHNSVDFEEDTLAK 36

RESULT 4
US-09-813-820-8
Sequence 8, Application US/09813820
Patent No. US20020102262A1
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
Pacti, Joseph M.
House-Pompeo, Karen
Stanam, Marayana
Symersky, Jindrich
TITLE OF INVENTION: COLLAGEN BINDING PROTEIN COMPOSITIONS
AND METHODS OF USE
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P. O. Box 4433
CITY: Houston
STATE: Texas

```

; SEQ ID NO 5797
; LENGTH: 1018
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-09-815-242-5797

Query Match
Best Local Similarity 95.6%; Score 109; DB 9; Length 1018;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KPSYQFGHNSVDFEEDTLAK 21
|||
Db 837 KPSYQFGHNSVDFEEDTLPK 857

RESULT 6
US-09-815-242-12838
; Sequence 12838, Application US/09815242
; Patent No. US20020061569A1
GENERAL INFORMATION:
APPLICANT: Haezelbeck, Robert
APPLICANT: Ohlssen, Karl L.
APPLICANT: Zyskind, Judith W.
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John D.
APPLICANT: Carr, Grant J.
APPLICANT: Yamamoto, Robert T.
TITLE OF INVENTION: Identification of Essential Genes in
FILE REFERENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,948
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 12838
LENGTH: 1018
TYPE: PRT
ORGANISM: Staphylococcus aureus
US-09-815-242-12838

Query Match
Best Local Similarity 95.6%; Score 109; DB 9; Length 1018;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KPSYQFGHNSVDFEEDTLAK 21
|||
Db 837 KPSYQFGHNSVDFEEDTLPK 857

RESULT 7
US-10-470-048B-68
; Sequence 68, Application US/10470048B
; Publication No. US2005003744A1
GENERAL INFORMATION:
APPLICANT: MEINKE ET AL.
TITLE OF INVENTION: A METHOD FOR IDENTIFICATION, ISOLATION AND PRODUCTION OF
FILE REFERENCE: SONN.0305US

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;; CURRENT APPLICATION NUMBER: US/10/470,0488
;; CURRENT FILING DATE: 2003-07-25
;; NUMBER OF SEQ ID NOS: 603
;; SOFTWARE: PatentIn version 3.1
;; SEQ ID NO 68
;; LENGTH: 1018
;; TYPE: PR1
;; ORGANISM: Staphylococcus aureus
US-10-470-0488-68

Query Match 95.6%; Score 109; DB 17; Length 1018;
Best Local Similarity 95.2%; Pred. No. 2.8e-08;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 KPSYQFGHNSVDFEEDTLAK 21
|||
Db 837 KPSYQFGHNSVDFEEDTLPK 857

RESULT 8
US-08-781-986A-5254
; Sequence 5254, Application US/08/81986A
; Publication No. US2003005436A1
; GENERAL INFORMATION:
; APPLICANT: Charles Kunach
; TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
; NUMBER OF SEQUENCES: 5255
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/781,986A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Benson, Bob
; REGISTRATION NUMBER: 30,446
; REFERENCE/DOCKET NUMBER: PB248PP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 5254:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1027 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-781-986A-5254

Query Match 95.6%; Score 109; DB 8; Length 1027;
Best Local Similarity 95.2%; Pred. No. 2.9e-08;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 KPSYQFGHNSVDFEEDTLAK 21
|||
Db 846 KPSYQFGHNSVDFEEDTLPK 866

RESULT 9
US-10-329-624-5254

;; Sequence 5254, Application US/10329624
;; Publication No. US20040043037A1
;; GENERAL INFORMATION:
;; APPLICANT: Charles Kunach
;; Gil H. Choi
;; Patrick S. Dillon
;; Craig A. Rosen
;; Steven C. Barash
;; Michael R. Fannon
;; TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
;; NUMBER OF SEQUENCES: 5256
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Human Genome Sciences, Inc.
;; STREET: 9410 Key West Avenue
;; CITY: Rockville
;; STATE: Maryland
;; COUNTRY: USA
;; ZIP: 20850
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
;; COMPUTER: HP Vectra 486/33
;; OPERATING SYSTEM: MSDOS version 6.2
;; SOFTWARE: ASCII Text
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/10/329,624
;; FILING DATE: 27-Dec-2002
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 08/956,171
;; FILING DATE: October 20, 1997
;; APPLICATION NUMBER: 60/009,861
;; FILING DATE: January 5, 1996
;; APPLICATION NUMBER: 08/781,986
;; FILING DATE: January 3, 1997
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Mark J. Hyman
;; REGISTRATION NUMBER: 46,789
;; REFERENCE/DOCKET NUMBER: PB248P1D1
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (240) 314-1224
;; TELEFAX: (301) 309-8439
;; INFORMATION FOR SEQ ID NO: 5254:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 1027 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; SEQUENCE DESCRIPTION: SEQ ID NO: 5254:
US-10-329-624-5254

Query Match 95.6%; Score 109; DB 15; Length 1027;
Best Local Similarity 95.2%; Pred. No. 2.9e-08;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 KPSYQFGHNSVDFEEDTLAK 21
|||
Db 846 KPSYQFGHNSVDFEEDTLPK 866

RESULT 10
US-10-282-122A-43778
; Sequence 43778, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyckind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant

```
APPLICANT: Yamamoto, Robert
APPLICANT: Forsyth, R.
APPLICANT: Xu, H.
TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REFERENCE: ELITRA.034A
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/230,335
PRIOR FILING DATE: 2000-09-06
PRIOR APPLICATION NUMBER: 60/230,347
PRIOR FILING DATE: 2000-09-09
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/267,636
PRIOR FILING DATE: 2001-02-09
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 78614
SOFTWARE: PatentIn version 3.1
SEQ ID NO 43778
LENGTH: 961
TYPE: PRF
ORGANISM: Staphylococcus aureus
US-10-282-122A-43778
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Query Match          93.0%; Score 106; DB 15; Length 961;
Best Local Similarity 90.5%; Pred. No. 8e-08;
Matches 19; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
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QY 1 KPSYOGGHSVDFEEDTLAK 21
DB 784 KPNYOGGHSVDFEEDTLPK 804
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```
RESULT 11
US-09-815-242-5456
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Sequence 5456, Application US/09815242
Patent No. US20020061569A1
GENERAL INFORMATION:
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Karl L.
APPLICANT: Zyskind, Judith W.
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John D.
APPLICANT: Carr, Grant J.
APPLICANT: Yamamoto, Robert T.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in
FILE REFERENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
```

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PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 5456
LENGTH: 978
TYPE: PRF
ORGANISM: Staphylococcus aureus
US-09-815-242-5456
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Query Match          93.0%; Score 106; DB 9; Length 978;
Best Local Similarity 90.5%; Pred. No. 8.1e-08;
Matches 19; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
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QY 1 KPSYOGGHSVDFEEDTLAK 21
DB 815 KPNYOGGHSVDFEEDTLPK 835
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RESULT 12
US-09-815-242-12686
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Sequence 12686, Application US/09815242
Patent No. US20020061569A1
GENERAL INFORMATION:
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Karl L.
APPLICANT: Zyskind, Judith W.
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John D.
APPLICANT: Carr, Grant J.
APPLICANT: Yamamoto, Robert T.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in
FILE REFERENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 12686
LENGTH: 1001
TYPE: PRF
ORGANISM: Staphylococcus aureus
US-09-815-242-12686
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Query Match          93.0%; Score 106; DB 9; Length 1001;
Best Local Similarity 90.5%; Pred. No. 8.4e-08;
Matches 19; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
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QY 1 KPSYOGGHSVDFEEDTLAK 21
DB 838 KPNYOGGHSVDFEEDTLPK 858
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RESULT 13
US-10-282-122A-43827
Sequence 43827, Application US/10282122A
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Publication No. US200400291229A1
GENERAL INFORMATION:
APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Karl
APPLICANT: Zykend, Judith
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John
APPLICANT: Carr, Grant
APPLICANT: Yamamoto, Robert
APPLICANT: Forsyth, R.
APPLICANT: Xu, H.
TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REFERENCE: EILTRA.034A
CURRENT APPLICATION NUMBER: US/10/282.122A
CURRENT FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/230,335
PRIOR FILING DATE: 2000-09-06
PRIOR APPLICATION NUMBER: 60/230,347
PRIOR FILING DATE: 2000-09-09
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/267,636
PRIOR FILING DATE: 2001-02-09
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
Remaining Prior Application data removed - See file wrapper or PALM.
NUMBER OF SEQ ID NOS: 78614
SOFTWARE: PatentIn version 3.1
SEQ ID NO 43827
LENGTH: 1038
TYPE: PRT
ORGANISM: Staphylococcus aureus
US-10-282-122A-43827
Query Match 93.0%; Score 106; DB 15; Length 1038;
Best Local Similarity 90.5%; Pred. No. 8.7e-08;
Matches 19; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 KPSTQFGHNSVDFEEDTLAK 21
Db 833 KPNTQFGHNSVDFEEDTLPK 853
RESULT 14
US-10-731-238-33
Sequence 33, Application US/10731238
Publication No. US20050123552A1
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
Patel, Joseph M.
House-Pompeo, Karen L.
Speziale, Pietro
Joh, Danny
McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433

CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/731.238
FILING DATE: 10-Dec-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/010.317
FILING DATE: 21-Jan-1998
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TMMK.189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 33:
US-10-731-238-33
Query Match 92.1%; Score 105; DB 18; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.9e-09;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 KPSTQFGHNSVDFEEDTL 19
Db 1 KPSTQFGHNSVDFEEDTL 19
RESULT 15
US-10-731-238-14
Sequence 14, Application US/10731238
Publication No. US20050123552A1
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
Patel, Joseph M.
House-Pompeo, Karen L.
Speziale, Pietro
Joh, Danny
McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/731.238
FILING DATE: 10-Dec-2003
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE: 21-Jan-1998
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAMK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 14:
US-10-731-238-14

Query Match 91.2%; Score 104; DB 18; Length 21;
Best Local Similarity 95.0%; Pred. No. 2,7e-09;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 2 PSYQFGHNSVDFEEDTLAK 21
|||
Db 2 PSYQFGHNSVDFEEDTLPK 21

Search completed: October 22, 2005, 11:34:44
Job time : 59.2367 secs

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GenCore version 5.1.6
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OW protein - protein search, using sw model

Run on: October 22, 2005, 02:23:36 ; Search time 10.5465 Seconds
(without alignments)
191.586 Million cell updates/sec

Title: US-10-731-238-32

Perfect score: 114

Sequence: 1 KPSYQFGHNSVDFEEDTLAK 21

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

PIR_79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	109	95.6	1018	2	A32192 fibronectin-binding
2	106	93.0	961	2	G90053 hypothetical prote
3	106	93.0	1038	2	H90053 hypothetical prote
4	102	89.5	940	2	S19702 fibronectin-bindin
5	49	43.0	474	2	B84357 serine-tRNA synthet
6	47.5	41.7	453	2	H70333 conserved hypotet
7	47	41.2	445	2	F90562 hypothetical prote
8	46	40.4	118	2	A81186 negative regulato
9	46	40.4	118	2	A11543 negative regulato
10	46	40.4	257	2	A36057 MHC class I histoc
11	46	40.4	705	2	C84406 hypothetical prote
12	45.5	39.9	345	2	AB1448 gp18 (Bacteriophag
13	45	39.5	216	2	A39926 hypothetical prote
14	45	39.5	462	1	A39356 3-oxoacyl--lacyl-ca
15	45	39.5	469	2	A39356 3-oxoacyl--lacyl-ca
16	45	39.5	739	2	T10061 subtilisin homolo
17	45	39.5	765	2	C42632 cell adhesion mole
18	45	39.5	812	2	B42632 cell adhesion mole
19	45	39.5	932	2	A42632 myosin heavy chain
20	45	39.5	1322	2	A59288 transcription regu
21	44	38.6	322	2	D95078 regulatory functio
22	44	38.6	348	2	A97946 probable glycine C
23	44	38.6	398	2	F75017 probable glycine C
24	44	38.6	398	2	E71454 3-phosphoshikimate
25	44	38.6	427	2	D95159 3-phosphoshikimate
26	44	38.6	431	2	D98025 vesicle-associated
27	44	38.6	433	2	T01405 HPB17-7 protein -
28	44	38.6	551	2	S57447 hypothetical prote
29	44	38.6	690	2	T33321

30	43.5	38.2	366	2	G71067 hypothetical prote
31	43	37.7	81	4	S12496 hypothetical prote
32	43	37.7	288	2	T37395 probable 33 kD pro
33	43	37.7	288	2	A42518 ABR protein - vacc
34	43	37.7	417	2	T34930 probable secreted
35	43	37.7	578	2	S52913 nuclear receptor R
36	43	37.7	755	2	S58718 probable nuclear p
37	43	37.7	928	1	VGRCWC glycoprotein B pre
38	42.5	37.3	251	2	B64048 hypothetical prote
39	42.5	37.3	431	2	E84031 trigger factor (pr
40	42.5	37.3	585	2	S06958 sphingomyelin phos
41	42.5	37.3	627	1	S27393 sphingomyelin phos
42	42.5	37.3	629	1	A39825 sphingomyelin phos
43	42	36.8	222	2	B75406 hypothetical prote
44	42	36.8	303	2	B75485 fructokinase - Dei
45	42	36.8	331	2	T51419 CARBONIC ANHYDRASE

ALIGNMENTS

RESULT 1

A32192
fibronectin-binding protein - Staphylococcus aureus
C:Species: Staphylococcus aureus
C:Date: 31-Jul-1989 #sequence_revision 31-Jul-1989 #text_change 16-Feb-1997
C:Accession: A32192
R:Signaas, C.; Raucel, G.; Joensson, K.; Lindgren, P.E.; Anantharamiah, G.M.; Hoecek, M.
Proc. Natl. Acad. Sci. U.S.A. 86, 699-703, 1989
A:Title: Nucleotide sequence of the gene for a fibronectin-binding protein from Staphyloc
A:Reference number: A32192; MUID:89098998; PMID:2521391
A:Accession: A32192
A:Status: Preliminary
A:Molecule type: DNA
A:Residues: 1-1018 <SIG>
A:Cross-references: GB:J04151
C:Keywords: fibronectin binding

Query Match 95.6%; Score 109; DB 2; Length 1018;
Best Local Similarity 95.2%; Pred. No. 2.4e-09;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KPSYQFGHNSVDFEEDTLAK 21

DB 837 KPSYQFGHNSVDFEEDTLAK 857

RESULT 2

G90053
hypothetical protein fnb [imported] - Staphylococcus aureus (strain N315)
C:Species: Staphylococcus aureus
C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004

R:Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; O
ma, A.; Mizutani-U, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.
C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Haysahi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
A:Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.

A:Reference number: A89758; MUID:21311952; PMID:11418146
A:Accession: G90053
A:Status: Preliminary

A:Molecule type: DNA
A:Residues: 1-961 <KUN>

A:Cross-references: UNIPROT:Q99RD3; GB:BA000018; PID:g13702452; PIDN:BA843593.1; GS
A:Experimental source: strain N315
C:Genetics:

A:Gene: fnb

Query Match 93.0%; Score 106; DB 2; Length 961;
Best Local Similarity 90.5%; Pred. No. 7e-09;
Matches 19; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 KPSYQFGHNSVDFEEDTLAK 21

Db 784 KPNYQFGHNSVDFEEDTLRK 804

RESULT 3

H90053

hypothetical protein fnb [imported] - Staphylococcus aureus (strain N315)

C:Species: Staphylococcus aureus

C>Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004

C:Accession: H90053

C:Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Ogura, A.; Mizutani, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.; C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiratsuka, K.

Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000

A:Title: Genome sequence of Halobacterium species NRC-1.

A:Reference number: A84160; MUID:20504483; PMID:11016950

A:Accession: H90053

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-1038 <KUR>

A:Cross-references: UNIPROT:Q99RD2; GB:BA000018; PID:g13702453; PIDN:BA03594.1; GSPDB:C

A:Experimental source: strain N315

C:Genetics:

A:Gene: fnb

Query Match 93.0%; Score 106; DB 2; Length 1038;

Best Local Similarity 90.5%; Pred. No. 7.6e-09;

Matches 19; Conservative 1; Indels 0; Gaps 0;

QY 1 KPSYQFGHNSVDFEEDTLAK 21

Db 833 KPNYQFGHNSVDFEEDTLRK 853

RESULT 4

S19702

fibronectin-binding protein B - Staphylococcus aureus

C:Species: Staphylococcus aureus

C>Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004

C:Accession: S19702

R:Johnson, K.; Signaev, C.; Mueller, H.P.; Lindberg, M.

Eur. J. Biochem. 202, 1041-1048, 1991

A:Title: Two different genes encode fibronectin binding proteins in Staphylococcus aureus

A:Reference number: S19702; MUID:92111475; PMID:1837266

A:Accession: S19702

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-940 <JOE>

A:Cross-references: UNIPROT:Q53682; EMBL:X62992; NID:g49040; PIDN:CAA44726.1; PID:g58156

C:Keywords: fibronectin binding

Query Match 89.5%; Score 102; DB 2; Length 940;

Best Local Similarity 94.7%; Pred. No. 3.1e-08;

Matches 18; Conservative 1; Indels 0; Gaps 0;

QY 1 KPSYQFGHNSVDFEEDTL 19

Db 773 KPNYQFGHNSVDFEEDTL 791

RESULT 5

B84357

serine-RNA synthetase [imported] - Halobacterium sp. NRC-1

C:Species: Halobacterium sp. NRC-1

C>Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004

C:Accession: B84357

R:Ng, W.V.; Kennedy, S.P.; Mahatree, G.G.; Bergquist, B.; Pan, M.; Shukla, H.D.; Lasky, S.; Leithner, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Uchida, J.; Jung, K.H.; Alam, M.; Freitas, T.

Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000

A:Title: Genome sequence of Halobacterium species NRC-1.

A:Reference number: A84160; MUID:20504483; PMID:11016950

A:Accession: B84357

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-445 <KUR>

A:Cross-references: UNIPROT:Q99RD2; GB:BA000018; PID:g13702453; PIDN:BA03594.1; GSPDB:C

A:Experimental source: strain N315

C:Genetics:

A:Gene: fnb

Query Match 93.0%; Score 106; DB 2; Length 1038;

Best Local Similarity 90.5%; Pred. No. 7.6e-09;

Matches 19; Conservative 1; Indels 0; Gaps 0;

QY 1 KPSYQFGHNSVDFEEDTLAK 21

Db 833 KPNYQFGHNSVDFEEDTLRK 853

RESULT 6

H70333

conserved hypothetical protein aq_378 - Aquifex aeolicus

C:Species: Aquifex aeolicus

C>Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 09-Jul-2004

C:Accession: H70333

R:Decker, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.; Over,

Nature 392, 353-358, 1998

A:Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.

A:Reference number: A70300; MUID:98196666; PMID:9537320

A:Accession: H70333

A:Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-453 <AQF>

A:Cross-references: UNIPROT:Q66700; GB:AE000687; NID:g2983050; PIDN:AAC06670.1; PID:g2983

A:Experimental source: strain VFS

C:Genetics:

A:Gene: aq_378

Query Match 41.7%; Score 47.5; DB 2; Length 453;

Best Local Similarity 47.6%; Pred. No. 9.8e-04;

Matches 10; Conservative 4; Indels 3; Gaps 1;

QY 3 SYQFGHNSVDFEEDTLA 20

Db 114 SYRFGSYNTLTFEGQADFFA 134

RESULT 7

F90562

hypothetical protein MYPU 4060 [imported] - Mycoplasma pulmonis (strain UAB CTIP)

C:Species: Mycoplasma pulmonis

C>Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 09-Jul-2004

C:Accession: F90562

R:Chambud, I.; Heilig, R.; Ferris, S.; Barbe, V.; Samson, D.; Galisson, F.; Mosser, I.; Nucleic Acids Res. 29, 2145-2153, 2001

A:Title: The complete genome sequence of the murine respiratory pathogen Mycoplasma pulm

A:Reference number: A9512; MUID:21267165; PMID:11353084

A:Accession: F90562

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-445 <KUR>

A:Cross-references: UNIPROT:Q99RD2; GB:BA000018; PID:g13702453; PIDN:BA03594.1; GSPDB:C

A:Experimental source: strain N315

C:Genetics:

A:Gene: fnb

Query Match 41.2%; Score 47; DB 2; Length 445;

Best Local Similarity 43.8%; Pred. No. 12;

Matches 7; Conservative 4; Indels 0; Gaps 0;

QY 1 KPSYQFGHNSVDFEED 16

Db 114 SYRFGSYNTLTFEGQADFFA 134

Db 334 KPDRVAGHNTYHOE 349

RESULT 8

AB1186 negative regulation of sigma-B activity homolog rbsbs [imported] - *Listeria monocytogenes*

C/Species: *Listeria monocytogenes*

C/Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004

C/Accession: AB1186

R/Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloeker, R.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Duesurget, O.; Entian, K.D.; Fshih, H.; Jones, L.M.; Karsc, U.

Science 294, 849-852, 2001

A/Authors: Kref, J.; Kuhn, M.; Kunst, F.; Kurapk, G.; Madueno, E.; Maitournam, A.; Maok, C.; Schluter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, A.; Title: Comparative genomics of *Listeria* species.

A/Reference number: AB1077; MUID:21537279; PMID:11679669

A/Accession: AB1186

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-118 <GLA>

A/Cross-references: UNIPROT:Q92DC5; GB:NC_003210; PIDN:CA98968.1; PID:G16410293; GSPDB: A/Experimental source: strain EGD-e

C/Genetics:

A/Genes: rbsbs

Query Match 40.4%; Score 46; DB 2; Length 118;

Best Local Similarity 61.5%; Pred. No. 3.9;

Matches 8; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 9 HNSVDFEEDTLAK 21

DB 23 HTAVFQEDLAK 35

RESULT 9

AB1543 negative regulation of sigma-B activity homolog rbsbs [imported] - *Listeria innocua* (strain C/Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004

C/Species: *Listeria innocua*

C/Accession: AB1543

R/Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloeker, R.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Duesurget, O.; Entian, K.D.; Fshih, H.; Jones, L.M.; Karsc, U.

Science 294, 849-852, 2001

A/Authors: Kref, J.; Kuhn, M.; Kunst, F.; Kurapk, G.; Madueno, E.; Maitournam, A.; Maok, C.; Schluter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, A.; Title: Comparative genomics of *Listeria* species.

A/Reference number: AB1077; MUID:21537279; PMID:11679669

A/Accession: AB1543

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-118 <GLA>

A/Cross-references: UNIPROT:Q92DC5; GB:AL592022; PIDN:CA98968.1; PID:G16413339; GSPDB: A/Experimental source: strain C11p1262

C/Genetics:

A/Genes: rbsbs

Query Match 40.4%; Score 46; DB 2; Length 118;

Best Local Similarity 61.5%; Pred. No. 3.9;

Matches 8; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 9 HNSVDFEEDTLAK 21

DB 23 HTAVFQEDLAK 35

RESULT 10

AB16057 MHC class I histocompatibility antigen alpha chain 1 (clone-lambda1AI-1) - common carp

C/Species: *Cyprinus carpio* (common carp)

C/Date: 18-Jan-1991 #sequence_revision 18-Jan-1991 #text_change 09-Jul-2004

C/Accession: AB16057

R/Hashimoto, K.; Nakanishi, T.; Kurosawa, Y.
Proc. Natl. Acad. Sci. U.S.A. 87, 6863-6867, 1990

A/Title: Isolation of carp genes encoding major histocompatibility complex antigens.

A/Reference number: AB16057; MUID:90370884; PMID:2395879

A/Accession: AB16057

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-257 <HMS>

A/Cross-references: UNIPROT:Q95589; GB:M37106

Query Match 40.4%; Score 46; DB 2; Length 257;

Best Local Similarity 56.2%; Pred. No. 9.2;

Matches 9; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 4 YQFGHNSVDFEEDTL 19

DB 108 YQFGGDCVAFNSDTL 123

RESULT 11

C84406 hypothetical protein Vng2566h [imported] - *Halobacterium* sp. NRC-1

C/Species: *Halobacterium* sp. NRC-1

C/Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004

C/Accession: C84406

R/Ing, W.V.; Kennedy, S.P.; Mahairas, G.G.; Bergquist, B.; Pan, M.; Shukla, H.D.; Lasky, S.; Leitbauer, B.; Keller, K.; Cruz, R.; Danson, M.D.; Hough, D.W.; Maddocks, D.G.; Jablok, Jung, K.H.; Alam, M.; Freitas, T.

Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000

A/Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ebhardt, H.; Lowe, T.M.; Li, A.; Title: Genome sequence of *Halobacterium* species NRC-1.

A/Reference number: AB160; MUID:20504483; PMID:11016950

A/Accession: C84406

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-705 <STO>

A/Cross-references: UNIPROT:Q9HMF6; GB:AE004437; NID:G10581952; PIDN:AG20615.1; GSPDB: A/Genetics:

A/Genes: VNG2566h

Query Match 40.4%; Score 46; DB 2; Length 705;

Best Local Similarity 45.0%; Pred. No. 28;

Matches 9; Conservative 1; Mismatches 10; Indels 0; Gaps 0;

QY 2 PSYQGHNSVDFEEDTLAK 21

DB 235 PSYTAGGHQIATFPRDTLGR 254

RESULT 12

AB1448 gp18 (Bacteriophage A118) homolog lin0121 [imported] - *Listeria innocua* (strain C11p1262

C/Species: *Listeria innocua*

C/Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004

C/Accession: AB1448

R/Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloeker, R.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Duesurget, O.; Entian, K.D.; Fshih, H.; Jones, L.M.; Karsc, U.

Science 294, 849-852, 2001

A/Authors: Kref, J.; Kuhn, M.; Kunst, F.; Kurapk, G.; Madueno, E.; Maitournam, A.; Maok, C.; Schluter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, A.; Title: Comparative genomics of *Listeria* species.

A/Reference number: AB1077; MUID:21537279; PMID:11679669

A/Accession: AB1448

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-345 <GLA>

A/Cross-references: UNIPROT:Q92R14; GB:AL592022; PIDN:CA98968.1; PID:G16412540; GSPDB: A/Experimental source: strain C11p1262

C/Genetics:

A/Genes: lin0121

Query Match 39.9%; Score 45.5; DB 2; Length 345;

Best Local Similarity 36.7%; Pred. No. 15;
Matches 11; Conservative 3; Mismatches 5; Indels 11; Gaps 1;

QY 2 PSYQFGCH-----NSVDFEEDTLA 20
||:|||||
178 PSDDYGEHTENEIRYNGHTNEVDPEDDITLS 207

RESULT 13

A39926
hypothetical protein 1 - chicken anemia virus
C:Species: chicken anemia virus, CAV
C:Date: 17-Jan-1992 #sequence_revision 17-Jan-1992 #text_change 09-Jul-2004
C:Accession: A39926
R:Notedorn, M.H.W.; de Boer, G.F.; van Roozelaar, D.J.; Karreman, C.; Kranenburg, O.; Vc
J. Virol. 65, 3131-3139, 1991
A>Title: Characterization of cloned chicken anemia virus DNA that contains all elements
A:Reference number: A39926; MUID:91237831; PMID:1851873
A:Accession: A39926
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-216 <NOT>
A:Cross-references: UNIPROT:Q99151; GB:M55918; NID:G323250; PID:AAA91822.1; PID:G323251
C:Comment: This virus is unclassified.

Query Match 39.5%; Score 45; DB 2; Length 216;
Best Local Similarity 56.2%; Pred. No. 11;
Matches 9; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 2 PSYQFGCHNSVDFEED 17
||:|||||
Db 172 PSDDGTTSDPDED 187

RESULT 14

A39356
3-oxoacyl-[acyl-carrier-protein] synthase (EC 2.3.1.41) I beta chain precursor, chloroplast
N:Alternate names: beta-ketoacyl-[acyl carrier protein] synthase I
C:Species: Hordeum vulgare (barley)
C:Date: 06-Mar-1992 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
C:Accession: A39356; A45129
R:Sigsgaard-Andersen, M.; Kauppinen, S.; von Wettstein-Knowl, P.
Proc. Natl. Acad. Sci. U.S.A. 88, 4114-4118, 1991
A>Title: Primary structure of a cerulenin-binding beta-ketoacyl-[acyl carrier protein] S
A:Reference number: A39356; MUID:91239517; PMID:2034657
A:Accession: A39356
A:Molecule type: mRNA
A:Residues: 1-462 <SIG>
A:Cross-references: UNIPROT:P23902; GB:M60410; NID:G167064; PID:AAA32968.1; PID:G167065
A:Experimental source: cv. Bonus, leaf
A>Note: parts of this sequence, including the amino end of the mature protein, were conf
R;Kauppinen, S.
J. Biol. Chem. 267, 23999-24006, 1992
A>Title: Structure and expression of the Kas12 gene encoding a beta-ketoacyl-acyl carrie
A:Reference number: A45129; MUID:99054767; PMID:1429736
A:Accession: A45129
A:Molecule type: DNA
A:Residues: 1-395,397-414, 'T', 415-462 <KAU>
A:Experimental source: cv. Bonus
A>Note: sequence inconsistent with the nucleotide translation; translation agrees with S
C:Genetics:
A:Gene: Kas12
A:Map position: 2
A:Intons: 144/3; 288/3; 346/3; 384/3; 418/3; 441/1
C:Complex: homodimer or heterodimer with alpha chain
C:Superfamily: 3-oxoacyl-[acyl-carrier-protein] synthase I; 3-oxoacyl-[acyl-carrier-prot
C:Keywords: acyltransferase; chloroplast; fatty acid biosynthesis; heterodimer; homodime
F:1-36/Domain: transit peptide (chloroplast) #status predicted <TMP>
F:36-462/Product: 3-oxoacyl-[acyl-carrier-protein] synthase I beta chain #status experin
F:68-457/Domain: 3-oxoacyl-[acyl-carrier-protein] synthase I homology <OAS>
F:213/Active site: Cys #status experimental

Query Match 39.5%; Score 45; DB 1; Length 462;
Best Local Similarity 80.0%; Pred. No. 26;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 SYQFGCHNSV 12
||:|||||
Db 445 SFGFGCHNSV 454

RESULT 15

T10061
3-oxoacyl-[acyl-carrier-protein] synthase (EC 2.3.1.41) precursor, chloroplast - castor l
N:Alternate names: beta-ketoacyl-[acyl carrier protein] synthase
C:Species: Ricinus communis (castor bean)
C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004
C:Accession: T10061
R:Genev, A.L.
Submitted to the EMBL Data Library, April 1993
A:Description: Cloning and molecular characterization of B-ketoacyl-ACP synthases from enc
A:Reference number: Z16924
A:Accession: T10061
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-469 <GEN>
A:Cross-references: UNIPROT:Q41135; EMBL:L13242; NID:G294667; PID:G294668
C:Genome:
A:Genome: nuclear
C:Function: fatty acid biosynthesis
C:Superfamily: 3-oxoacyl-[acyl-carrier-protein] synthase I; 3-oxoacyl-[acyl-carrier-prote
C:Keywords: acyltransferase; chloroplast; fatty acid biosynthesis
F:1-42/Domain: transit peptide (chloroplast) #status predicted <TMP>
F:43-469/Product: 3-oxoacyl-[acyl-carrier-protein] synthase #status predicted <OAS>
F:77-464/Domain: 3-oxoacyl-[acyl-carrier-protein] synthase I homology <OAS>

Query Match 39.5%; Score 45; DB 2; Length 469;
Best Local Similarity 80.0%; Pred. No. 26;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 SYQFGCHNSV 12
||:|||||
Db 452 SFGFGCHNSV 461

Search completed: October 22, 2005, 04:13:59
Job time : 10.5465 secs


```
FT REPEAT 545 574 B-1.
FT REPEAT 575 604 B-2.
FT DOMAIN 745 878 4 X approximate tandem repeats,
  fibronectin-binding domain.
FT REPEAT 745 782 D-1.
FT REPEAT 783 820 D-2.
FT REPEAT 821 859 D-3.
FT REPEAT 860 878 D-4 (incomplete).
FT DOMAIN 879 948 5 X tandem repeats, Pro-rich (WR).
FT REPEAT 879 892 WR 1.
FT REPEAT 893 906 WR 2.
FT REPEAT 907 920 WR 3.
FT REPEAT 921 934 WR 4.
FT REPEAT 935 948 WR 5.
FT SITE 982 986 LPXTG sorting signal (Potential).
FT MOD_RES 985 985 Pentaglycyl murein peptidoglycan amidated
  threonine (Potential).
SQ SEQUENCE 1018 AA; 111780 MW; 58175E0020B81F1F CRC64;

Query Match 95.6%; Score 109; DB 1; Length 1018;
Best Local Similarity 95.2%; Pred. No. 2.8e-08;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 KPSYQFGHNSVDFEEDTLAK 21
DB 837 KPSYQFGHNSVDFEEDTLPK 857

RESULT 2
ID 099RD3 PRELIMINARY; PRT; 961 AA.
AC 099RD3;
CD 01-JUN-2001 (TRENMBLrel. 17, Created)
DT 01-JUN-2001 (TRENMBLrel. 17, Last sequence update)
DT 01-JUN-2003 (TRENMBLrel. 24, Last annotation update)
DE Filtronec tin-binding protein homolog.
GN Name=fnbB; OrderedlocusNames=SAV2502;
OS Staphylococcus aureus (strain Mu50 / ATCC 700699).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=158878;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=21311952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2;
RX Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
  RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Lian J.-Q., Ito T.,
  RA Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hoshoyama A.,
  RA Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
  RA Sekimizu K., Hiraoka H., Kuhara S., Goto S., Yabuzaki J.,
  RA Kanehisa M., Yamaehita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
  RA Hatori M., Ogasawara N., Hayashi H., Hiratake K.,
  RT "Whole genome sequencing of methicillin-resistant Staphylococcus
  aureus."
RL Lancet 357:1225-1240(2001).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
  an amide bond (By similarity).
EMBL, AP003365; BAB58664.1; -.
DR HSP; G90053; G90053.
DR HSP; G53653; I167.
DR GO; GO:0009986; C:cell surface; IEA.
DR GO; GO:0005618; C:cell wall; IEA.
DR GO; GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:007155; P:cell adhesion; IEA.
DR InterPro; IPR008966; Adhes_bact.
DR InterPro; IPR004237; Fn_bind.
DR InterPro; IPR005877; Gpos_YsIRK.
DR InterPro; IPR001899; Gram_pos_anchor.
DR Pfam; PF02986; Fn_bind; 1.
DR Pfam; PF00746; Gram_pos_anchor; 1.
DR Pfam; PF04650; YsIRK_signal; 1.
DR TIGRFAMs; TIGR01167; LPXTG_anchor; 1.
DR TIGRFAMs; TIGR01167; YsIRK_signal; 1.
DR TIGRFAMs; TIGR01167; LPXTG_anchor; 1.
DR TIGRFAMs; TIGR01168; YsIRK_signal; 1.
DR TIGRFAMs; TIGR01168; YsIRK_signal; 1.
```

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DR PROSITE; PS50847; GRAM_POS_ANCHORING; 1.
KW Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ SEQUENCE 961 AA; 106010 MW; 364940F884EA4101 CRC64;

Query Match 93.0%; Score 106; DB 2; Length 961;
Best Local Similarity 90.5%; Pred. No. 7.9e-08;
Matches 19; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 KPSYQFGHNSVDFEEDTLAK 21
DB 784 KPSYQFGHNSVDFEEDTLPK 804

RESULT 3
ID 07A3J8 PRELIMINARY; PRT; 961 AA.
AC 07A3J8;
DT 05-JUL-2004 (TRENMBLrel. 27, Created)
DT 05-JUL-2004 (TRENMBLrel. 27, Last sequence update)
DE FnbB protein.
GN Name=fnbB; OrderedlocusNames=SA2290;
OS Staphylococcus aureus (strain N315).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=158879;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=21311952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2;
RX Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
  RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Lian J.-Q., Ito T.,
  RA Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hoshoyama A.,
  RA Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
  RA Sekimizu K., Hiraoka H., Kuhara S., Goto S., Yabuzaki J.,
  RA Kanehisa M., Yamaehita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
  RA Hatori M., Ogasawara N., Hayashi H., Hiratake K.,
  RT "Whole genome sequencing of methicillin-resistant Staphylococcus
  aureus."
RL Lancet 357:1225-1240(2001).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
  an amide bond (By similarity).
EMBL, AP003317; BAB43593.1; -.
DR GO; GO:0009986; C:cell surface; IEA.
DR GO; GO:0005618; C:cell wall; IEA.
DR GO; GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:007155; P:cell adhesion; IEA.
DR InterPro; IPR008966; Adhes_bact.
DR InterPro; IPR004237; Fn_bind.
DR InterPro; IPR005877; Gpos_YsIRK.
DR InterPro; IPR001899; Gram_pos_anchor.
DR Pfam; PF02986; Fn_bind; 1.
DR Pfam; PF00746; Gram_pos_anchor; 1.
DR Pfam; PF04650; YsIRK_signal; 1.
DR TIGRFAMs; TIGR01167; LPXTG_anchor; 1.
DR TIGRFAMs; TIGR01167; YsIRK_signal; 1.
DR PROSITE; PS50847; GRAM_POS_ANCHORING; 1.
KW Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ SEQUENCE 961 AA; 106010 MW; 364940F884EA4101 CRC64;

Query Match 93.0%; Score 106; DB 2; Length 961;
Best Local Similarity 90.5%; Pred. No. 7.9e-08;
Matches 19; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 KPSYQFGHNSVDFEEDTLAK 21
DB 784 KPSYQFGHNSVDFEEDTLPK 804

RESULT 4
ID 06GDUS PRELIMINARY; PRT; 965 AA.
AC 06GDUS;
DT 05-JUL-2004 (TRENMBLrel. 27, Created)
```

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DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE Fibronectin-binding protein.
GN Name=fnbA; OrderedLocNames=SAR2580;
OS Staphylococcus aureus (strain MRSA252).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=282458;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=15213324; DOI=10.1073/pnas.0402521101;
RA Holden M.T.G., Fell E.J., Lindsey J.A., Peacock S.J., Day N.P.J.,
RA Enright M.C., Foster T.J., Moore C.E., Hurst L., Atkin R., Barron A.,
RA Baason N., Bentley S.D., Chillingworth C., Chillingworth T.,
RA Churcher C., Clark L., Corton C., Cronin A., Doggett J., Dowd L.,
RA Felwell T., Hance Z., Harris B., Hauser H., Holroyd S., Jagels K.,
RA James K.D., Leonard N., Line A., Mayes R., Moulé S., Mungall K.,
RA Ormond D., Quail M.A., Rabinowitch E., Rutherford K.M., Sanders M.,
RA Sharp S., Simmonds M., Stevens K., Whitehead S., Barrett B.G.,
RA Spratt B.G., Parkhill J.;
RT "Complete genomes of two clinical Staphylococcus aureus strains:
RT evidence for the rapid evolution of virulence and drug resistance."
RL Proc. Natl. Acad. Sci. U.S.A. 101:9786-9791(2004).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC an amide bond (By similarity).
CC EMBL: BX571856; CAG41560.1; -
CC DR GO:0009986; C:cell surface; IEA.
CC DR GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
CC DR GO:0016020; C:membrane; IEA.
CC DR GO:0007155; P:cell adhesion; IEA.
CC DR InterPro: IPR008966; Adhes_bact.
CC DR InterPro: IPR004237; Fn_bind.
CC DR InterPro: IPR005877; Gpos_YsIRK.
CC DR InterPro: IPR001899; Gram_pos_anchor.
CC DR Pfam: PF00746; Gram_pos_anchor; 1.
CC DR Pfam: PF04650; YsIRK_signal; 1.
CC DR TIGRFAMs: TIGR01167; LpxTG_anchor; 1.
CC DR TIGRFAMs: TIGR01168; YsIRK_signal; 1.
CC DR PROSITE: PS50847; GRAM_POS_ANCHORING; 1.
CC DR Cell wall; Complete proteome; Peptidoglycan-anchor.
CC KW SEQUENCE 965 AA; 10561 MW; 2982E132164D0551 CRC64;
SQ
Query Match 93.0%; Score 106; DB 2; Length 965;
Best Local Similarity 90.5%; Pred. No. 8e-08;
Matches 19; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 KPSYQFGHNSVDFEDTLAK 21
DB 802 KENYQFGHNSVDFEDTLPK 822
RESULT 5
Q8NUU7 PRELIMINARY; PRT; 1015 AA.
ID Q8NUU7;
AC Q8NUU7;
DT 01-OCT-2002 (TREMBLrel. 22, Created)
DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Fmb protein.
GN Name=fmb; OrderedLocNames=MW2421;
OS Staphylococcus aureus (strain MW2).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=196620;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22040717; PubMed=12044378; DOI=10.1016/S0140-6736(02)08713-5;
RA Baba T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Oguchi A.,
RA Nagai Y., Iwama N., Amano K., Naimi T., Kuroda H., Cui L.,
RA Yamamoto K., Hiramatsu K.;
RT "Genome and virulence determinants of high virulence community-
RT acquired MRSA."
RL Lancet 359:1819-1827(2002).

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CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC an amide bond (By similarity).
CC EMBL: AP004830; BAB96286.1; -
CC DR GO:0009986; C:cell surface; IEA.
CC DR GO:0005618; C:cell wall; IEA.
CC DR GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
CC DR GO:0016020; C:membrane; IEA.
CC DR GO:0007155; P:cell adhesion; IEA.
CC DR InterPro: IPR008966; Adhes_bact.
CC DR InterPro: IPR004237; Fn_bind.
CC DR InterPro: IPR005877; Gpos_YsIRK.
CC DR InterPro: IPR001899; Gram_pos_anchor.
CC DR Pfam: PF02986; Fn_bind; 1.
CC DR Pfam: PF00746; Gram_pos_anchor; 1.
CC DR TIGRFAMs: TIGR01167; LpxTG_anchor; 1.
CC DR TIGRFAMs: TIGR01168; YsIRK_signal; 1.
CC DR PROSITE: PS50847; GRAM_POS_ANCHORING; 1.
CC DR Cell wall; Complete proteome; Peptidoglycan-anchor.
CC KW SEQUENCE 1015 AA; 11145 MW; D0F9281BB64D44D2 CRC64;
SQ
Query Match 93.0%; Score 106; DB 2; Length 1015;
Best Local Similarity 90.5%; Pred. No. 8.4e-08;
Matches 19; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 KPSYQFGHNSVDFEDTLAK 21
DB 838 KENYQFGHNSVDFEDTLPK 858
RESULT 6
Q6G6H3 PRELIMINARY; PRT; 1015 AA.
ID Q6G6H3;
AC Q6G6H3;
DT 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE Fibronectin-binding protein.
GN OrderedLocNames=SAS2388;
OS Staphylococcus aureus (strain MSSA476).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=282459;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=15213324; DOI=10.1073/pnas.0402521101;
RA Holden M.T.G., Fell E.J., Lindsey J.A., Peacock S.J., Day N.P.J.,
RA Enright M.C., Foster T.J., Moore C.E., Hurst L., Atkin R., Barron A.,
RA Baason N., Bentley S.D., Chillingworth C., Chillingworth T.,
RA Churcher C., Clark L., Corton C., Cronin A., Doggett J., Dowd L.,
RA Felwell T., Hance Z., Harris B., Hauser H., Holroyd S., Jagels K.,
RA James K.D., Leonard N., Line A., Mayes R., Moulé S., Mungall K.,
RA Ormond D., Quail M.A., Rabinowitch E., Rutherford K.M., Sanders M.,
RA Sharp S., Simmonds M., Stevens K., Whitehead S., Barrett B.G.,
RA Spratt B.G., Parkhill J.;
RT "Complete genomes of two clinical Staphylococcus aureus strains:
RT evidence for the rapid evolution of virulence and drug resistance."
RL Proc. Natl. Acad. Sci. U.S.A. 101:9786-9791(2004).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC an amide bond (By similarity).
CC EMBL: BX571857; CAG44202.1; -
CC DR GO:0009986; C:cell surface; IEA.
CC DR GO:0005618; C:cell wall; IEA.
CC DR GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
CC DR GO:0016020; C:membrane; IEA.
CC DR GO:0007155; P:cell adhesion; IEA.
CC DR InterPro: IPR008966; Adhes_bact.
CC DR InterPro: IPR004237; Fn_bind.
CC DR InterPro: IPR005877; Gpos_YsIRK.
CC DR InterPro: IPR001899; Gram_pos_anchor.
CC DR Pfam: PF02986; Fn_bind; 1.
CC DR Pfam: PF00746; Gram_pos_anchor; 1.
CC DR TIGRFAMs: TIGR01167; LpxTG_anchor; 1.

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DR TIGRFAMS; TIGR01168; YSIRK_signal; 1.
DR PROSITE; PS50847; GRAM_POS_ANCHORING; 1.
KW Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ SEQUENCE 1015 AA; 111145 MW; D0F9281BB64D44D2 CRC64;
Query Match 93.0%; Score 106; DB 2; Length 1015;
Best Local Similarity 90.5%; Pred. No. 8.4e-08;
Matches 19; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
OY 1 KPSYQFGGHSVDFEEDTLAK 21
DB 838 KPNYQFGGHSVDFEEDTLPK 858
RESULT 7
OY99RD2 PRELIMINARY; PRT; 1038 AA.
ID OY99RD2;
AC OY99RD2;
DT 01-JUN-2001 (TReMBLrel. 17, Created)
DT 01-MAR-2004 (TReMBLrel. 26, Last sequence update)
DE Fibronectin-binding protein homolog.
GN Name=fnb; OrderedLocustNames=SAV2503;
OS Staphylococcus aureus (strain Mu50 / ATCC 700699).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
CX NCBI_TaxID=158879;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=21311952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2;
RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
Cui L., Oguchi A., Aoki K.-I., Nagai Y., Iino T.,
Kanamori M., Matsunaru H., Maruyama A., Murakami H., Hoshiyama A.,
Sekimizu K., Hiraoka H., Kuhara S., Goto S., Inoue R.-I., Kaito C.,
Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
RT "Whole genome sequencing of methicillin-resistant Staphylococcus
aureus.";
RT Lancet 357:1225-1240(2001).
RL -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC an amide bond (By similarity).
CC EMBL; AP003137; BAB5865.1; -.
DR PIR; H90053;
DR GO; GO:0009986; C:cell surface; IEA.
DR GO; GO:0005618; C:cell wall; IEA.
DR GO; GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0007155; P:cell adhesion; IEA.
DR InterPro; IPR008966; Adhes_bact.
DR InterPro; IPR004237; Fn_bind.
DR InterPro; IPR005877; Gpos_YSIRK.
DR InterPro; IPR001899; Gram_pos_anchor.
DR Pfam; PF02986; Fn_bind; 1.
DR Pfam; PF00746; Gram_pos_anchor; 1.
DR Pfam; PF04650; YSIRK_signal; 1.
DR TIGRFAMS; TIGR01167; LPXTG_anchor; 1.
DR TIGRFAMS; TIGR01168; YSIRK_signal; 1.
DR PROSITE; PS50847; GRAM_POS_ANCHORING; 1.
KW Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ SEQUENCE 1038 AA; 113618 MW; 666BF6BF2BFBEB12 CRC64;

ID O7A3J7 PRELIMINARY; PRT; 1038 AA.
AC O7A3J7;
DT 05-JUN-2004 (TReMBLrel. 27, Created)
DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TReMBLrel. 27, Last annotation update)
DE Fnb protein.
GN Name=fnb; OrderedLocustNames=SA2291;
OS Staphylococcus aureus (strain N315).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
CX NCBI_TaxID=158879;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=21311952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2;
RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
Cui L., Oguchi A., Aoki K.-I., Nagai Y., Iino T.,
Kanamori M., Matsunaru H., Maruyama A., Murakami H., Hoshiyama A.,
Sekimizu K., Hiraoka H., Kuhara S., Goto S., Inoue R.-I., Kaito C.,
Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
RT "Whole genome sequencing of methicillin-resistant Staphylococcus
aureus.";
RT Lancet 357:1225-1240(2001).
RL -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC an amide bond (By similarity).
CC EMBL; AP003137; BAB43594.1; -.
DR GO; GO:0009986; C:cell surface; IEA.
DR GO; GO:0005618; C:cell wall; IEA.
DR GO; GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0007155; P:cell adhesion; IEA.
DR InterPro; IPR008966; Adhes_bact.
DR InterPro; IPR004237; Fn_bind.
DR InterPro; IPR005877; Gpos_YSIRK.
DR InterPro; IPR001899; Gram_pos_anchor.
DR Pfam; PF02986; Fn_bind; 1.
DR Pfam; PF00746; Gram_pos_anchor; 1.
DR Pfam; PF04650; YSIRK_signal; 1.
DR TIGRFAMS; TIGR01167; LPXTG_anchor; 1.
DR TIGRFAMS; TIGR01168; YSIRK_signal; 1.
DR PROSITE; PS50847; GRAM_POS_ANCHORING; 1.
KW Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ SEQUENCE 1038 AA; 113618 MW; 666BF6BF2BFBEB12 CRC64;
Query Match 93.0%; Score 106; DB 2; Length 1038;
Best Local Similarity 90.5%; Pred. No. 8.6e-08;
Matches 19; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
OY 1 KPSYQFGGHSVDFEEDTLAK 21
DB 833 KPNYQFGGHSVDFEEDTLPK 853
RESULT 9
OY93682 PRELIMINARY; PRT; 940 AA.
ID OY93682;
AC OY93682;
DT 01-NOV-1996 (TReMBLrel. 01, Created)
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)
DE Fibronectin binding protein B.
GN Name=fnbB;
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
CX NCBI_TaxID=1280;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=8325-4;
RX MEDLINE=92111475; PubMed=1837266;
RA Jonsson K., Sigmas C., Muller H.P., Lindberg M.;
RT "Two different genes encode fibronectin binding proteins in
Staphylococcus aureus. The complete nucleotide sequence and
characterization of the second gene.";

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RL Eur. J. Biochem. 202:1041-1048(1991).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
EMBL: X62992; CAA44726.1; -.
DR PIR: S19702; S19702.
DR HSSP: Q53653; 1N67.
DR GO: GO:0009986; C:cell surface; IEA.
DR GO: GO:0005618; C:cell wall; IEA.
DR GO: GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO: GO:0016020; C:membrane; IEA.
DR GO: GO:0007155; P:cell adhesion; IEA.
DR InterPro: IPR008966; Adhes_bact.
DR InterPro: IPR004237; Fn_bind.
DR InterPro: IPR005877; Gpos_YsIRK.
DR Pfam: PF02986; Fn_bind; 2.
DR Pfam: PF00746; Gram_pos_anchor; 1.
DR TIGRfams: TIGR01167; LpXTG_anchor; 1.
DR TIGRfams: TIGR01168; YsIRK_signal; 1.
DR PROSITE: PS50847; GRAM_POS_ANCHORING; 1.
KW Cell wall; Peptidoglycan-anchor.
SQ SEQUENCE 940 AA; 10355 MW; E35FBBCA907AE345 CRC64;

Query Match 89.5%; Score 102; DB 2; Length 940;
Best Local Similarity 94.7%; Pred. No. 3.4e-07;
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KPSYQFGHNSVDFEEDTL 19
DB 773 KPNYQFGHNSVDFEEDTL 791
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Q8NTU8 PRELIMINARY; PRT; 943 AA.
ID Q8NTU8
AC Q8NTU8; 01-OCT-2002 (TREMBLrel. 22, Created)
DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update)
DE 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE FndB protein.
GN Name=fndB; OrderedlocusNames=WM2420;
OS Staphylococcus aureus (strain WM2).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_Taxid=196620;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=WM2;
RX MEDLINE=22040717; PubMed=12044378; DOI=10.1016/S0140-6736(02)08713-5;
RA Baba T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Oguchi A.,
RA Nagai Y., Iwana N., Asano K., Naito T., Kuroda H., Cui L.,
RA Yamamoto K., Hiramoto K.;
RT "Genome and virulence determinants of high virulence community-
RT acquired MRSA."
RT Lancet 359:1819-1827(2002).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
an amide bond (By similarity).
EMBL: AP004830; BAB96285.1; -.
DR HSSP: Q53653; 1N67.
DR GO: GO:0009986; C:cell surface; IEA.
DR GO: GO:0005618; C:cell wall; IEA.
DR GO: GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO: GO:0016020; C:membrane; IEA.
DR GO: GO:0007155; P:cell adhesion; IEA.
DR InterPro: IPR008966; Adhes_bact.
DR InterPro: IPR004237; Fn_bind.
DR InterPro: IPR005877; Gpos_YsIRK.
DR InterPro: IPR001899; Gram_pos_anchor.
DR Pfam: PF02986; Fn_bind; 1.
DR Pfam: PF00746; Gram_pos_anchor; 1.
DR TIGRfams: TIGR01167; LpXTG_anchor; 1.
DR TIGRfams: TIGR01168; YsIRK_signal; 1.
DR TIGRfams: TIGR01168; YsIRK_signal; 1.

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DR PROSITE: PS50847; GRAM_POS_ANCHORING; 1.
KW Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ SEQUENCE 943 AA; 104537 MW; DA8A5F31947E1B8A CRC64;

Query Match 89.5%; Score 102; DB 2; Length 943;
Best Local Similarity 94.7%; Pred. No. 3.4e-07;
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KPSYQFGHNSVDFEEDTL 19
DB 780 KPNYQFGHNSVDFEEDTL 798
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Q6G6H4 PRELIMINARY; PRT; 957 AA.
ID Q6G6H4
AC Q6G6H4; 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DE 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE Fibronectin-binding protein.
GN Name=fndB; OrderedlocusNames=SAS2387;
OS Staphylococcus aureus (strain MSSA476).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_Taxid=282459;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=15213324; DOI=10.1073/pnas.0402521101;
RA Holden M.T.G., Fell E.J., Lindsay J.A., Peacock S.J., Day N.P.J.,
RA Enright M.C., Foster T.J., Moore C.E., Hurst L., Atkin R., Barron A.,
RA Bason N., Bentley S.D., Chillingworth C., Chillingworth T.,
RA Churcher C., Clark L., Corson C., Cronin A., Doggett J., Dowd L.,
RA Feltwell T., Hance Z., Harris B., Hauser H., Holtroyd S., Jagels K.,
RA James K.D., Kennard N., Line A., Mayes R., Moule S., Murgall K.,
RA Ormond D., Quail M.A., Rabinovitch E., Rutherford K.M., Sanders M.,
RA Sharp S., Simmonds M., Stevens K., Whitehead S., Barrett B.G.,
RA Spratt B.G., Parhill J.;
RT "Complete genomes of two clinical Staphylococcus aureus strains:
RT evidence for the rapid evolution of virulence and drug resistance."
RT Proc. Natl. Acad. Sci. U.S.A. 101:9786-9791(2004).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
an amide bond (By similarity).
EMBL: BX571857; CAG44201.1; -.
DR GO: GO:0009986; C:cell surface; IEA.
DR GO: GO:0005618; C:cell wall; IEA.
DR GO: GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO: GO:0016020; C:membrane; IEA.
DR GO: GO:0007155; P:cell adhesion; IEA.
DR InterPro: IPR008966; Adhes_bact.
DR InterPro: IPR004237; Fn_bind.
DR InterPro: IPR005877; Gpos_YsIRK.
DR InterPro: IPR001899; Gram_pos_anchor.
DR Pfam: PF02986; Fn_bind; 1.
DR Pfam: PF00746; Gram_pos_anchor; 1.
DR Pfam: PF04650; YsIRK_signal; 1.
DR TIGRfams: TIGR01167; LpXTG_anchor; 1.
DR TIGRfams: TIGR01168; YsIRK_signal; 1.
DR PROSITE: PS50847; GRAM_POS_ANCHORING; 1.
KW Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ SEQUENCE 957 AA; 105980 MW; 28F8BA7FDFD3EAF CRC64;

Query Match 89.5%; Score 102; DB 2; Length 957;
Best Local Similarity 94.7%; Pred. No. 3.4e-07;
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KPSYQFGHNSVDFEEDTL 19
DB 780 KPNYQFGHNSVDFEEDTL 798
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Q9AEP9 PRELIMINARY; PRT; 152 AA.
ID Q9AEP9

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AC 09AEP9;
DT 01-JUN-2001 (Tremblrel. 17, Created)
DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE Fibronectin-binding protein (fragment).
GN Name=fnb;
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1280;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CMRSA-1;
RX MEDLINE=21246681; PubMed=11349044;
RX DOI=10.1128/IAI.69.6.3791-3799.2001;
RA Rice K., Huesca M., Var D., McGavin M.J.;
RT "Variance in fibronectin binding and fnb locus polymorphisms in
RT Staphylococcus aureus: identification of antigenic variation in a
RT fibronectin binding protein adhesin of the epidemic CMRSA-1 strain of
RT methicillin-resistant S. aureus.";
RL Infect. Immun. 69:3791-3799 (2001).
DR EMBL; AY029184; AAKJ1588.1; -.
FT NON_TER
FT 152
SQ SEQUENCE 152 AA; 17193 MW; CFA3913C2B11C025 CRC64;

Query March 85.1%; Score 97; DB 2; Length 152;
Best Local Similarity 81.0%; Pred. No. 3e-07;
Matches 17; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

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QY 1 KPSYQFGHNSVDFEEDTLAK 21
DB 130 KPSYQFGHNGIDVFEDTLPK 150

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RESULT 13
Q08866
ID 008866 PRELIMINARY; PRT; 245 AA.
AC 008866; 031374;
DT 01-NOV-1996 (Tremblrel. 01, Created)
DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)
DE Carassius auratus langsdorffii MHC (fragment).
OS Carassius auratus (Goldfish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Carassius.
OX NCBI_TaxID=7957;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Blood;
RX MEDLINE=93315835; PubMed=8326125;
RX Okamura K., Nakamishi T., Kurosawa Y., Hashimoto K.;
RT "Expansion of genes that encode MHC class I molecules in cyprinid
RT fishes.";
RL J. Immunol. 151:188-200 (1993).
DR EMBL; L10418; AAA72345.1; -.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF07654; C1-sect.1.
DR SMART; SM00407; IGL1.1.
DR PROSITE; PS50835; IG_LIKE; 1.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
FT NON_TER
FT 1
SQ SEQUENCE 245 AA; 28128 MW; C3E33032BA998A43 CRC64;

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Query March 43.9%; Score 50; DB 2; Length 245;
Best Local Similarity 60.0%; Pred. No. 15;
Matches 9; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

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QY 4 YQFGHNSVDFEEDTL 18
DB 102 YQFGHNSVDFEEDTL 116

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RESULT 14
SYS_HALNT
ID SYS_HALNT STANDARD; PRT; 460 AA.
AC 09HNU8;
DT 16-OCT-2001 (Rel. 40, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Seryl-tRNA synthetase (EC 6.1.1.11) (Serine--tRNA ligase) (Sers).
GN Name=sers; OrderedLocNames=VNC072G;
OS Archaea; Euryarchaeota; Halobacteriales;
OC Halobacteriaceae; Halobacterium.
OX NCBI_TaxID=64091;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20504483; PubMed=11016950; DOI=10.1073/pnas.190337797;
RX Ng W.V., Kennedy S.P., Mahairas G.G., Bergquist B., Pan M.,
RX Shukla H.D., Laeky S.R., Baliga N.S., Thorsson V., Shroga J.,
RX Swartzell S., Weir D., Hall J., Dahl T.A., Weili R., Goo Y.A.,
RX Leithauer B., Keller K., Cruz R., Danson M.J., Hough D.W.,
RX Maddocks D.G., Jablonerki P.E., Krebs M.P., Angvine C.M., Dale H.,
RX Isenbarger T.A., Peck R.F., Pohlschroder M., Spudich J.L., Jung K.-H.,
RX Alam M., Freitas T., Hou S., Daniels C.J., Dennis P.P., Omer A.D.,
RX Eberhardt H., Lowe T.M., Liang P., Riley M., Hood L., DasSarma S.;
RT "Genome sequence of Halobacterium species NRC-1."
RL Proc. Natl. Acad. Sci. U.S.A. 97:12176-12181 (2000).
CC -1- CATALYTIC ACTIVITY: ATP + L-serine + tRNA(Ser) = AMP + diphosphate
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- SIMILARITY: Belongs to the class-II aminoacyl-tRNA synthetase
CC family.

```

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CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
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CC or send an email to license@ebi.ac.uk).
CC -----

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DR EMBL; AE005098; AAG20222.1; ALT_INIT.
DR PIR; B84357; B84357.
DR HSSP; P34945; 1SER.
DR HAMAP; MF_00176; -.
DR InterPro; IPR002314; tRNA-synt_2b.
DR InterPro; IPR002317; tRNA-synt_ser.
DR InterPro; IPR010978; tRNA-binding_arm.
DR InterPro; IPR006195; tRNA_ligase_II.
DR Pfam; PF02403; Seryl tRNA N; 1.
DR Pfam; PF00587; tRNA-synt_2b; 1.
DR PRINTS; PR00981; TRNASYNTHSER.
DR TRIFAMs; TIGR00414; sers; 1.
DR PROSITE; PS50862; AA tRNA_LIGASE_II; 1.
KW Aminoacyl-tRNA synthetase; ATP-binding; Complete proteome; Ligase;
KW Protein biosynthesis.
SQ SEQUENCE 460 AA; 51986 MW; E26DAAB46908A1D CRC64;

```

```

Query March 43.0%; Score 49; DB 1; Length 460;
Best Local Similarity 41.2%; Pred. No. 41;
Matches 7; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

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```

QY 3 SYQFGHNSVDFEEDTL 19
DB 220 AYRIGENDADYDDDL 236

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RESULT 15
Q6G429
ID Q6G429 PRELIMINARY; PRT; 1726 AA.
AC Q6G429;
DT 05-JUL-2004 (Tremblrel. 27, Created)

```

DT 05-JUL-2004 (TrEMBLrel. 27, last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, last annotation update)
 DE Surface protein/Bartonella adhesion.
 GN Name=Badai; OrderedlocusNames=BH01490;
 OS Bartonella henselae (Rochalimaea henselae).
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
 CC Bartonellaceae; Bartonella.
 OX NCBI_TaxID=38323;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 49882 / Houston 1;
 RX PubMed=15210978; DOI=10.1073/pnas.0305659101;
 RA Almaraz U.C.M., Frank A.C., Karlberg E.O., Legault B.-A., Ardell D.H.,
 RA Canaback B., Eriksson A.-S., Naeslund A.K., Handley S.A., Huvel M.,
 RA La Scola B., Holmberg M., Andersson S.G.E.;
 RT "The louse-borne human pathogen Bartonella quintana is a genomic
 derivative of the zoonotic agent Bartonella henselae.";
 RL Proc. Natl. Acad. Sci. U.S.A. 101:9716-9721 (2004).
 DR EMBL; BX897699; CAF26961.1; -.
 DR GO; GO:0019867; C:outer membrane; IEA.
 DR GO; GO:0009405; P:pathogenesis; IEA.
 DR InterPro; IPR008640; Hep_Hag.
 DR InterPro; IPR008635; Htm.
 DR Pfam; PF05658; Hep_Hag; 5.
 DR Pfam; PF05662; Htm; 12.
 KW Complete proteome.
 SQ SEQUENCE 1726 AA; 182288 MW; 4F253F255456098E CRC64;

QY 3 SYQFGHNSVDPEED 17
 ||||| | : | |
 DB 51 SYQFGSHGSIYFAGD 65

Query Match 43.0%; Score 49; DB 2; Length 1726;
 Best Local Similarity 60.0%; Pred.No. 1.7e+02;
 Matches 9; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Search completed: October 22, 2005, 04:10:25
 Job time : 52.4314 secs

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CC streptococci, e.g. meningitis, otitis media, pneumonia, endocarditis,
 CC mastitis in cattle, abortion in horses and many others. Since the
 CC antibodies block binding of bacteria, they should be effective against
 CC antibiotic-resistant strains, and may replace antibiotic therapy or
 CC increase its effectiveness. Sequences AAW65670-90 represent a series of
 CC synthetic peptides based on the D3 repeat of *S. aureus* fibronectin
 CC binding protein A. They were synthesised to contain a proline residue at
 CC each position through the sequence (ie a proline scan)

XX
 SQ Sequence 21 AA;
 Query Match 100.0%; Score 119; DB 2; Length 21;
 Best Local Similarity 100.0%; Pred. No. 3,1e-11;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 KPSYQFGGHSVDPEDTLP 21
 DB 1 KPSYQFGGHSVDPEDTLP 21

RESULT 2
 AAW65665
 ID AAW65665 standard; peptide; 21 AA.
 AC AAW65665;
 XX
 DT 16-OCT-1998 (first entry)
 DE Fibronectin binding protein-derived peptide #9.
 XX
 KM microbial surface components recognising adhesive matrix molecule;
 KM MSCRAMM; fibronectin; fibronectin-binding protein; antibody; epitope;
 KM antibiotic; bacterial infection; antibiotic-resistant strain.
 XX
 OS Synthetic.
 OS Staphylococcus aureus.
 XX
 PN W09831389-A2.
 PD 23-JUL-1998.
 XX
 PF 21-JAN-1998; 98WO-US001222.
 XX
 PR 21-JAN-1997; 97US-0036139P.
 XX
 PA (TEXA) UNIV TEXAS A & M SYSTEM.
 XX
 PI Hoseok M, Patti JM, House-Pompeo KL, Speziale P, Joh D;
 PI Mcgavin MJ;
 XX
 DR WPI; 1998-413816/35.
 XX
 PT Antibody that binds to fibronectin-binding protein, preventing its
 PT binding to fibronectin - used to treat or prevent bacterial infection,
 PT especially by Staphylococci and Streptococci.
 XX
 PS Example 2; Page 92; 201pp; English.

CC The invention relates to antibodies that bind to a fibronectin-binding
 CC domain of a fibronectin-binding protein, and inhibit binding of the
 CC protein to fibronectin. Also claimed are: (1) isolated peptides of a
 CC fibronectin-binding protein that do not bind to fibronectin; (2) fusion
 CC protein containing at least one peptide of a fibronectin-binding protein
 CC linked to a second amino acid sequence; (3) nucleic acid encoding the
 CC isolated peptide of (1). Antibodies, the isolated peptides of (1) and the
 CC nucleic acids are all useful for immunisation (active or passive) and (by
 CC inhibiting binding of bacteria to fibronectin) for preventing or treating
 CC infection in humans or other animals, particularly by staphylococci or
 CC streptococci, e.g. meningitis, otitis media, pneumonia, endocarditis,
 CC mastitis in cattle, abortion in horses and many others. Since the
 CC antibodies block binding of bacteria, they should be effective against
 CC antibiotic-resistant strains, and may replace antibiotic therapy or
 CC increase its effectiveness. Sequences AAW65659-68 represent synthetic

CC epitopes from the fibronectin binding domains DU and D1-D4 of the S.
 CC aureus fbnA gene
 XX
 SQ Sequence 21 AA;
 Query Match 94.1%; Score 112; DB 2; Length 21;
 Best Local Similarity 100.0%; Pred. No. 3,8e-10;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 KPSYQFGGHSVDPEDTLP 20
 DB 1 KPSYQFGGHSVDPEDTLP 20

RESULT 3
 AAR21340
 ID AAR21340 standard; peptide; 22 AA.
 AC AAR21340;
 XX
 DT 25-MAR-2003 (revised)
 DT 15-JUN-1992 (first entry)
 DE Fibronectin binding protein.
 XX
 KM FBNP; wound infection reduction; vaccination; mastitis;
 KM Staphylococcal infections; D3.
 XX
 OS Synthetic.
 OS WO9202555-A.
 PN 20-FEB-1992.
 PD 10-AUG-1990; 90SE-00002617.
 XX
 PF 10-AUG-1990; 90SE-00002617.
 XX
 PR 10-AUG-1990; 90SE-00002617.
 XX
 PA (ALFA) ALFA LAVAL AGRIC INT AB.
 XX
 PI Hook M, Mcgavin M, Raucsi G;
 PI WPI; 1992-080035/10.
 DR
 XX
 PT New fibronectin binding peptide - combines with fusion peptide to form
 PT large antigen, used in immunisation, diagnosis and for treating wounds.
 XX
 PS Claim 1; Page 22; 33pp; English.

CC The sequence comprises amino acids 17-33 of a tandem repeat, designated
 CC D3 of the fibronectin binding site of Staphylococcus aureus 8325-4 FBNP.
 CC The N-terminal DK may be replaced with H or K, and the C-terminal LKP may
 CC be replaced by either L, LP, or OH. The peptides were synthesised using
 CC standard methods and purified using reverse phase HPLC. The appropriate
 CC fractions were dialysed and lyophilised. Peptide sequencing was performed
 CC and the peptides digested and chemically modified by dihydropyridylation
 CC of the amino side chain of lysine. The carboxylic side chains were
 CC converted to glycine methyl esters. The phenyl side chains of tyrosine
 CC residues were oxidised. Chemically modified peptide D3 was compared to
 CC unmodified D3. Lysine and tyrosine modifications only partially
 CC diminished its activity whereas modification of aspartic/glutamic
 CC residues resulted in complete loss of activity. The peptide can be used
 CC for the prevention or reduction of the risk of wound infection. The
 CC peptide can be used to create a large antigen for vaccinating ruminants
 CC against mastitis caused by Staphylococcal infections. It can also be used
 CC to diagnose Staphylococcal infections using ELISA or DNA probes. (Updated
 CC on 25-MAR-2003 to correct PA field.)

XX
 SQ Sequence 22 AA;
 Query Match 94.1%; Score 112; DB 2; Length 22;
 Best Local Similarity 100.0%; Pred. No. 4e-10;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KPSYQFGGNSVDFEEDTLP 20
 Db 2 KPSYQFGGNSVDFEEDTLP 21

RESULT 4
 ID AAB91958 standard; peptide; 37 AA.

AC AAB91958;

DT 22-JUN-2001 (first entry)

XX Fibronection fragment and fibrin related peptide SEQ ID NO:1134.

XX Protection; endogenous therapeutic peptide; peptidase; conjugation;
 KW blood component; modification; succinimide; maleimide group; amino;
 KW hydroxyl; thiol; hormone; growth factor; neurotransmitter.

XX Homo sapiens.
 OS Synthetic.

FN WO200069900-A2.

PD 23-NOV-2000.

PF 17-MAY-2000; 2000WO-US013576.

PR 17-MAY-1999; 99US-0134406P.

PR 10-SEP-1999; 99US-0153406P.

PR 15-OCT-1999; 99US-0159783P.

PA (CONJ-) CONJUCHEM INC.

PI Bridon DP, Errin AM, Milner PG, Holmes DL, Thibaudeau K;

DR WPI; 2001-112059/12.

PT Modifying and attaching therapeutic peptides to albumin prevents
 PT peptidase degradation, useful for increasing length of in vivo activity.

PS Disclosure; Page 566; 733pp; English.

XX The present invention describes a modified therapeutic peptide (I)
 CC comprising a therapeutically active amino acid region (III) and a
 CC reactive group (II) (e.g. succinimide) and maleimide groups) attached to
 CC a less therapeutically active amino acid region (IV), which covalently
 CC bonds with amino/hydroxyl/thiol groups on blood components to form a
 CC peptide stabilised therapeutic peptide composed of 3-50 amino acids.
 CC (I) are useful for modifying therapeutic peptides e.g. hormones, growth
 CC factors and neurotransmitters, to protect them from peptidase activity in
 CC vivo for the treatment of various disorders. Endogenous therapeutic
 CC peptides are not suitable as drug candidates as they require frequent
 CC administration due to rapid degradation by peptidases in the body.
 CC Modifying and attaching therapeutic peptides to albumin prevents or
 CC reduces the action of peptidases to increase length of activity (half
 CC life) and specifically as bonding to large molecules decreases
 CC intracellular uptake and interference with physiological processes.
 CC AAB90829 to AAB92441 represent peptides which can be used in the
 CC exemplification of the present invention

XX Sequence 37 AA;

Query Match 94.1%; Score 112; DB 4; Length 37;

Best Local Similarity 100.0%; Pred. No. 7.1e-10; Mismatches 0; Gaps 0;

Qy 1 KPSYQFGGNSVDFEEDTLP 20
 Db 16 KPSYQFGGNSVDFEEDTLP 35

RESULT 5
 ID AAB80662 standard; protein; 38 AA.

AC AAB80662;

DT 25-MAR-2003 (revised)

DT 07-OCT-1990 (first entry)

DE Protein with fibronectin binding ability.

XX Hybrid DNA molecule; fibronectin binding; mastitis; ruminants;
 KW wound infection.

XX Staphylococcus aureus.

OS EP294349-A.

PN 07-DEC-1988.

PF 30-MAY-1988; 88EP-00850188.

PR 01-JUN-1987; 87SE-00002272.

PA (ALFA) ALFA LAVAL AGRIC INT AB.

PI Lindberg MK, Signae LC, Wadstrom TM, Froman G;

DR WPI; 1988-347978/49.

DR N-PSDB; AAN81099.

PT Hybrid DNA encoding Staphylococcus aureus fibronectin binding protein -
 PT useful for immunisation and topical application to prevent staphylococcal
 PT infections.

PS Claim 11; Page 12; 23pp; English.

XX The peptide has fibronectin binding ability. It is useful for immunising
 CC ruminants against staphylococcal mastitis, pref. when used at 0.5-5
 CC micrograms/kg, using 3 doses given at 1-3 week intervals; for topical
 CC application to prevent wound infection, using an isotonic saline soln. of
 CC concn. 25-250 micrograms/ml; and, when immobilised on a carrier, for
 CC diagnosing staphylococcal infections. (Updated on 25-MAR-2003 to correct
 CC PF field.) (Updated on 25-MAR-2003 to correct PA field.)

XX Sequence 38 AA;

Query Match 94.1%; Score 112; DB 1; Length 38;

Best Local Similarity 100.0%; Pred. No. 7.3e-10; Mismatches 0; Gaps 0;

Qy 1 KPSYQFGGNSVDFEEDTLP 20
 Db 17 KPSYQFGGNSVDFEEDTLP 36

RESULT 6
 ID AAY29087 standard; protein; 134 AA.

AC AAY29087;

DT 28-SEP-1999 (first entry)

DE S. aureus fibronectin binding protein A (FnBA) binding domain.

XX Bovine herpes virus-2; BHV-2; cytokine; immune response; immunogen; IL;
 KW interleukin; colony stimulating factor; CSF; interferon; IFN; TNF;
 KW tumour necrosis factor; recombinant virus; vaccine; mucosal disease;
 KW mastitis; breast cancer; stress-induced disease; binding domain; FnBA;
 KW fibronectin binding protein.

OS Staphylococcus aureus.


```

XX  WO9916892-A1.
XX
XX  08-APR-1999.
XX
XX  29-SEP-1998; 98WO-G8002927.
XX
XX  29-SEP-1997; 97GB-00020633.
XX
XX  (UYBR-) UNIV BRISTOL.
XX
XX  Bradley AJ, Duffae WPH;
XX
XX  WPI; 1999-255101/21.
XX
XX  N-PSDB; AAX91504.
XX
XX  New bovine herpes virus-2 vectors.
XX
XX  Example 2; Fig 8A-B; 130pp; English.
XX
XX  The invention provides bovine herpes virus-2 (BHV-2) based vectors that
XX  comprise at least one cytokine-encoding DNA sequence. The expression of
XX  cytokines in mammals can up-regulate immune responses to the immunogens.
XX  The cytokine is selected from interleukins (IL), colony stimulating
XX  factors (CSF), interferons (IFN) and tumour necrosis factors (TNF). The
XX  BHV-2 based vector or recombinant virus can be used as vaccines. They can
XX  be used for preventing or treating a mucosal disease in a subject, e.g.
XX  ruminants, cattle, sheep, goats, dogs, cats, horses, or man, particularly
XX  mastitis in cows or breast cancers in humans. The present sequence
XX  preventing or treating a stress-induced disease. The present sequence
XX  represents the binding domain of a previously published S. aureus
XX  fibronectin binding protein A (FnBA) sequence. The FnB binding domain
XX  gene sequence FNBA1. Cloned for use in this invention has 97.8 percent
XX  identity when compared to the previously published FnBA and FnB8 gene
XX  sequences
XX
XX  Sequence 134 AA;
XX
XX  Query Match 94.1%; Score 112; DB 2; Length 134;
XX  Best Local Similarity 100.0%; Pred. No. 2.9e-09;
XX  Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX  1 KPSYQFGHNSVDPEDTLP 20
XX  |||||||||||||||||||
XX  Db 93 KPSYQFGHNSVDPEDTLP 112
XX
XX  RESULT 7
XX  AAW31556
XX  ID AAW31556 standard; protein; 139 AA.
XX
XX  AAW31556;
XX
XX  27-AUG-2003 (revised)
XX  25-MAR-2003 (revised)
XX  21-MAY-1998 (first entry)
XX
XX  Fibronectin-binding MSCRAMM derivative POD.
XX
XX  Fibronectin; POD; collagen binding protein; sepsis; infection;
XX  microbial surface component regioning adhesive matrix molecule; MSCRAMM;
XX  adhesin; vaccine; immunisation; diagnosis; therapy; mastitis.
XX
XX  Staphylococcus aureus.
XX
XX  OS
XX  Key Location/Qualifiers
XX  FH 1. .12
XX  FT Peptide /note= "vector pQE30-derived peptide"
XX
XX  W09743314-A2.
XX
XX  20-NOV-1997.
XX

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PF  14-MAY-1997; 97WO-US008210.
XX
XX  16-MAY-1996; 96US-0017678P.
XX
XX  (TEXA ) UNIV TEXAS A & M SYSTEM.
XX
XX  (UABR-) UAB RES FOUND.
XX
XX  Heoek M, Patti JM, House-Pompeo K, Sthanam N, Symersky J;
XX
XX  WPI; 1998-008801/01.
XX
XX  Antibody that interacts with collagen binding domain of Staphylococcal
XX  cna gene product - useful to prevent bacterial sepsis in animal infected
XX  with Staphylococcus aureus.
XX
XX  Disclosure; Page 91; 143pp; English.
XX
XX  This protein comprises Staphylococcus aureus fibronectin-binding
XX  microbial surface component regioning adhesive matrix molecule (MSCRAMM)
XX  derivative POD, plus a vector-derived N-terminal peptide. The invention
XX  relates to claimed nucleic acid sequences (see AAT93436-38) encoding S.
XX  aureus collagen binding protein (CBP) epitopes M17, M31 and M55 (see
XX  AAW31552-54) that confer protection against S. aureus infection. CBP
XX  protein and antigenic epitopes are contemplated for use in the treatment
XX  of pathological infections, especially to prevent bacterial adhesion to
XX  collagen. The epitopes are also contemplated for use in the preparation
XX  of vaccines and as carrier proteins in vaccine formulations, as well as
XX  in the formulation of compositions for the prevention of S. aureus
XX  infection. pCF33 and POD (see AAW31556) were used to raise anti-MSCRAMM
XX  polyclonal antibodies used in passive immunisation against bovine
XX  mastitis. (Updated on 25-MAR-2003 to correct PI field.) (Updated on 27-
XX  AUG-2003 to correct OS field.)
XX
XX  Sequence 139 AA;
XX
XX  Query Match 94.1%; Score 112; DB 2; Length 139;
XX  Best Local Similarity 100.0%; Pred. No. 2.9e-09;
XX  Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX  1 KPSYQFGHNSVDPEDTLP 20
XX  |||||||||||||||||||
XX  Db 107 KPSYQFGHNSVDPEDTLP 126
XX
XX  RESULT 8
XX  AAP82115
XX  ID AAP82115 standard; protein; 1018 AA.
XX
XX  AAP82115;
XX
XX  25-MAR-2003 (revised)
XX  05-JAN-1990 (first entry)
XX
XX  Fibronectin binding protein.
XX
XX  Fibronectin binding protein.
XX
XX  Fibronectin binding protein; S. aureus; immunisation; mastitis; ruminants;
XX  wound infection; diagnosis.
XX
XX  Staphylococcus aureus.
XX
XX  OS
XX  EP294349-A.
XX
XX  PD 07-DEC-1988.
XX
XX  30-MAY-1988; 88EP-00850188.
XX
XX  01-JUN-1987; 87SE-00002272.
XX
XX  (ALFA ) ALFA LAVAL AGRIC INT AB.
XX
XX  Lindberg MK, Signas LC, Wadstrom TM, Froman G;
XX
XX  WPI; 1988-347978/49.
XX

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```

XX P-PSDB; AAP82115.
PT Hybrid DNA encoding Staphylococcus aureus fibronectin binding protein -
PT useful for immunisation and topical application to prevent staphylococcal
PT infections.
XX
PS Disclosure; Fig. 8A:1-8A:2; 23pp; English.
XX
XX The S.aureus fibronectin binding protein may be included in a hybrid
CC protein. The protein may be used to immunise ruminants against
CC staphylococcal mastitis, pref. when given at 0.5-5 microg/kg, using 3
CC does at 1-3 week intervals; and for topical applicn. to prevent wound
CC infection, pref. using isotonic saline soln. of concn..25-250 microg/mg.
CC The DNA encoding the binding protein and the hybrid protein may be
CC immobilised on a carrier and used to diagnose staphylococcal infections.
CC (Updated on 25-MAR-2003 to correct PA field.)
CC
SQ Sequence 1018 AA;

Query Match          94.1%; Score 112; DB 1; Length 1018;
Best Local Similarity 100.0%; Pred. No. 2.Se-08;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0

Oy      1 KPSYQFGHNSVDPEDTLTP 20
        |||||
Db       837 KPSYQFGHNSVDPEDTLTP 856

RESULT 9
ID AUJ37245 standard; protein; 1018 AA.
AC AUJ37245;
XX
DT 14-FEB-2002 (first entry)
XX
DE Staphylococcus aureus cellular proliferation protein #1415.
XX
KW Antisense; prokaryotic cellular proliferation protein; antibiotic;
XX antibacterial; drug design.
XX
OS Staphylococcus aureus.
XX
PN WO200170955-A2.
XX
PD 27-SEP-2001.
XX
PF 21-MAR-2001; 2001WO-US009180.
XX
XX
PR 21-MAR-2000; 2000US-0191078P.
PR 23-MAY-2000; 2000US-0206848P.
PR 26-MAY-2000; 2000US-0207727P.
PR 23-OCT-2000; 2000US-0242578P.
PR 27-NOV-2000; 2000US-0253625P.
PR 22-DEC-2000; 2000US-0257931P.
PR 16-FEB-2001; 2001US-0269308P.
XX
XX
PA (ELIT-) ELITRA PHARM INC.
XX
PI Haselbeck R, Ohlgen KL, Zyskind JW, Wall D, Trawick JD, Carr GJ;
PI Yamamoto RT, Xu HH;
XX
XX WPI; 2001-611495/70.
DR N-PSDB; AAS55104.
XX
XX New polynucleotides for the identification and development of
PT antibiotics, comprise sequences of antisense nucleic acids.
XX
XX Example 3; SEQ ID NO 12838; 51pp; English.
CC The invention relates to antisense inhibitors of genes essential to
CC prokaryotic cellular proliferation, their use in identifying the genes,
CC their use in the discovery of novel antibiotics, the essential genes

```

```
CC themselves and the encoded proteins. The prokaryotes used are Escherichia
CC coli, Staphylococcus aureus, Salmonella typhi, Klebsiella pneumoniae,
CC Pseudomonas aeruginosa and Enterococcus faecalis. The invention is also
CC useful for the identification of potential new targets for antibiotic
CC development. The antisense nucleic acids can also be used to identify
CC proteins used in proliferation, to express these proteins, and to obtain
CC antibodies capable of binding to the expressed proteins. The proteins can
CC be used to screen compounds in rational drug discovery programmes. The
CC antisense nucleic acid sequence is also useful to screen for homologous
CC nucleic acids which are required for cell proliferation in a wide variety
CC of organisms. The present sequence represents an essential prokaryotic
CC cellular proliferation protein. Note: The sequence data for this patent
CC did not form part of the printed specification, but was obtained in
CC electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 1018 AA;
Query Match          94.1%; Score 112; DB 4; Length 1018;
Best Local Similarity 100.0%; Pred. No. 2.5e-08;
Matches    20; Conservative    0; Mismatches    0; Indels    0; Gaps    0;
OY      1 KPSYQFGHNSVDFEEDTLP 20
Db       |||||
         837 KPSYQFGHNSVDFEEDTLP 856
RESULT 10
ID AUAU34301
AA AUAU34301 standard; protein; 1018 AA.
XX
AC AUAU34301;
DT 14-FEB-2002 (first entry)
XX
DE Staphylococcus aureus cellular proliferation protein #577.
XX
KW Antisense; prokaryotic cellular proliferation protein; antibiotic;
XX antibacterial; drug design.
XX
OS Staphylococcus aureus.
XX
PN WO200170955-A2.
PD 27-SEP-2001.
PF 21-MAR-2001; 2001WO-US009180.
XX
PR 21-MAR-2000; 2000US-0191078P.
PR 23-MAY-2000; 2000US-0206848P.
PR 26-MAY-2000; 2000US-0207727P.
PR 23-OCT-2000; 2000US-0242578P.
PR 27-NOV-2000; 2000US-0253625P.
PR 22-DEC-2000; 2000US-0257931P.
PR 16-FEB-2001; 2001US-0269308P.
XX
PA (ELIT-) ELITRA PHARM INC.
PI Haselbeck R, Ohlsen KU, Zyskind JW, Wall D, Trawick JD, Carr GJ;
PI Yamamoto RT, Xu HH;
XX WPI; 2001-611495/70.
DR N-PsDB; AAS52160.
XX
PT New polynucleotides for the identification and development of
PT antibiotics, comprise sequences of antisense nucleic acids.
XX
PS Example 3; SEQ ID NO 5797; 511pp; English.
CC The invention relates to antisense inhibitors of genes essential to
CC prokaryotic cellular proliferation, their use in identifying the genes,
CC their use in the discovery of novel antibiotics, the essential genes
CC themselves and the encoded proteins. The prokaryotes used are Escherichia
```

CC coli, *Staphylococcus aureus*, *Salmonella typhi*, *Klebsiella pneumoniae*,
CC *Pseudomonas aeruginosa* and *Enterococcus faecalis*. The invention is also
CC useful for the identification of potential new targets for antibiotic
CC development. The antisense nucleic acids can also be used to identify
CC proteins used in proliferation, to express these proteins, and to obtain
CC antibodies capable of binding to the expressed proteins. The proteins can
CC be used to screen compounds in rational drug discovery programmes. The
CC antisense nucleic acid sequence is also useful to screen for homologous
CC nucleic acids which are required for cell proliferation in a wide variety
CC of organisms. The present sequence represents an essential prokaryotic
CC cellular proliferation protein. Note: The sequence data for this patent
CC did not form part of the printed specification, but was obtained in
CC electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences

XX Sequence 1018 AA;
SQ

Query Match 94.1%; Score 112; DB 4; Length 1018;
Best Local Similarity 100.0%; Pred. No. 2.5e-08;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 KPSYQFGGHSVDPEDTLP 20
|||
DB 837 KPSYQFGGHSVDPEDTLP 856

RESULT 11
ABU18922
ID ABU18922 standard; protein; 1018 AA.
XX
AC ABU18922;
XX
DT 06-MAR-2003 (first entry)
XX
DE Pathogen specific antigen related staphylococcal protein SEQ ID No 68.
XX
XX Antibacterial; virucide; fungicide; protozoacide; cytostatic; anti-HIV;
KM hyperimmune; serum-reactive; antigen; pathogen; tumour; allergen;
KM auto-immunity; vaccine; staphylococcal infection; antibody; cancer;
KM autoimmune disease; HIV; hepatitis.
XX
OS Staphylococcus sp.
XX
PN WO200259148-A2.
XX
PD 01-AUG-2002.
XX
PF 21-JAN-2002; 2002WO-EP000546.
XX
PR 26-JAN-2001; 2001AT-00000130.
XX
PA (CIST-) CISTEM BIOTECHNOLOGIES GMBH.
XX
PI Meinke A, Nagy E, Von Ahnen U, Klade C, Henice T, Zauner W;
PI Minh DB, Vycvytska O, Ecz H, Dryla A, Weichart T, Hafner M;
PI Tempelmeier B;
XX
XX WPI; 2003-075410/07.
XX
XX Identifying, isolating and producing hyperimmune serum-reactive antigens
PT from a pathogen, for preparing vaccine or medicament for treating or
PT preventing e.g. staphylococcal infections, comprises providing antibody
PT preparation.
XX
XX Example 7, Page 157; 252pp; English.
XX
PS The invention relates to a novel method for identifying, isolating and
CC producing hyperimmune serum-reactive antigens from a pathogen, tumour,
CC allergen, a tissue or host prone to auto-immunity, where the antigens are
CC used in a vaccine, comprises providing antibody preparation from a plasma
CC pool of a type of animal, or individual sera with antibodies against the
CC specific pathogen, tumour, allergen, tissue or host prone to auto-
CC immunity. The hyperimmune serum-reactive antigens comprising any of the

CC 62 sequences of 53-2261 amino acids fully defined in the specification,
CC or their hyperimmune fragments are useful for the manufacture of a
CC pharmaceutical preparation, particularly a vaccine against staphylococcal
CC infections or colonisation against *S. aureus* or *S. epidermidis*. The
CC preparation of antibodies is useful for the manufacture of a medicament
CC for treating or preventing staphylococcal infections or colonisation
CC against *S. aureus* or *S. epidermidis*. The antibody preparations may also
CC be used for diagnostic and imaging purposes. Other conditions that can be
CC treated include cancer, autoimmune diseases or infections caused by viral
CC (e.g. HIV, hepatitis A, B or C), fungal or protozoan pathogens. This
CC sequence represents a staphylococcal protein relating to the method for
CC identifying and producing pathogen specific antigens of the invention
XX

SQ Sequence 1018 AA;
SQ

Query Match 94.1%; Score 112; DB 6; Length 1018;
Best Local Similarity 100.0%; Pred. No. 2.5e-08;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 KPSYQFGGHSVDPEDTLP 20
|||
DB 837 KPSYQFGGHSVDPEDTLP 856

RESULT 12
ABM72537
ID ABM72537 standard; protein; 1018 AA.
XX
AC ABM72537;
XX
DT 20-NOV-2003 (first entry)
XX
DE Staphylococcus aureus protein #1777.
XX
XX Antibacterial; vaccine; gene therapy; infection; sepsis; diagnosis;
KM enzymatic assay; antibiotic target.
XX
OS Staphylococcus aureus.
XX
PN WO200294868-A2.
XX
PD 28-NOV-2002.
XX
PF 27-MAR-2002; 2002WO-IB002637.
XX
PR 27-MAR-2001; 2001GB-00007661.
XX
PA (CHIR-) CHIRON SPA.
XX
PI Maigman V, Mora M, Scarselli M;
XX
XX WPI; 2003-120786/11.
XX
XX N-PSDB; ACF74097.
XX
XX New Staphylococcus aureus protein, useful as a vaccine for treating or
PT preventing Staphylococcal infection, specifically an infection caused by
PT *S. aureus*, e.g. sepsis.
XX
XX Claim 1; SEQ ID NO 3554; 49pp; English.
XX
XX The invention relates to novel genes and encoded proteins from
CC Staphylococcus aureus. A composition comprising the *S. aureus* protein, a
CC nucleic acid encoding the protein, or an antibody to the protein, is
CC useful as a pharmaceutical, particularly as a vaccine for treating or
CC preventing infection due to Staphylococcus bacteria, specifically an
CC infection caused by *S. aureus*. The composition is particularly useful for
CC treating or preventing sepsis in a patient. The composition can also be
CC used for diagnostics. The protein is also used in an assay for enzymatic
CC studies and as a target for antibiotics. This sequence represents one of
CC the novel *S. aureus* proteins of the invention
XX
SQ Sequence 1018 AA;

Query Match 94.1%; Score 112; DB 6; Length 1018;
 Best Local Similarity 100.0%; Pred. No. 2.5e-08;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KPSYFGGHSVDFEDTLP 20
 |||
 DB 837 KPSYFGGHSVDFEDTLP 856

RESULT 13

AAW89806 standard; protein; 1027 AA.

AC AAW89806;

DT 16-MAR-1999 (first entry)

DE Staphylococcus aureus protein SEQ ID #5254.

KM Computer readable medium; vaccine; S. aureus infection; immunodetection;

KM cellulitis; eyelid infection; food poisoning; osteomyelitis; therapy;

KM skin infection; surgical wound infection; scalded skin syndrome;

OS Staphylococcus aureus.

PN EP76519-A2.

PD 30-JUL-1997.

PF 07-JAN-1997; 97EP-00100117.

PR 05-JAN-1996; 96US-0009861P.

XX (HUMA-) HUMAN GENOME SCI INC.

PI Kunesh CA, Choi GH, Barash SC, Dillon PJ, Fannon MR, Rosen CA;

DR WPI; 1997-374922/35.

PT polynucleotide(s) and proteins derived from Staphylococcus aureus -
 stored on computer readable medium and used in the production of anti-
 S. aureus vaccines.

PS Claim 23; Page 3263-3267; 3271pp; English.

CC This sequence represents a Staphylococcus aureus protein sequence of the
 invention. The DNA sequences encoding the S. aureus proteins are recorded
 on a computer readable medium, preferably selected from a floppy or hard
 disk, random access memory (RAM), read-only memory (ROM) or CD-ROM.

CC Homology searches using the S. aureus DNA sequences allows putative
 functions to be assigned so that protein-encoding or regulatory regions

CC of commercial, therapeutic or industrial importance can be obtained.
 Specifically, sequences which are likely to encode antigens have been

CC identified and these polypeptides can be used in a vaccine composition
 against S. aureus infection. The polypeptides can also be used in a kit

CC for the immunodetection of S. aureus in a sample. S. aureus is implicated
 in numerous human diseases, including cellulitis, eyelid infections, food

CC poisoning, osteomyelitis, skin and surgical wound infections, scalded
 skin syndrome, toxic shock syndrome, etc. Organisms transformed with the

CC DNA sequences can be used for recombinant production of the polypeptides.
 The new DNA sequences (and their fragments) are useful as primers or

CC probes for isolating homologues of any of the 5191 S. aureus DNA sequences
 confined on the computer readable medium

XX Sequence 1027 AA;

Query Match 94.1%; Score 112; DB 2; Length 1027;
 Best Local Similarity 100.0%; Pred. No. 2.5e-08;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KPSYFGGHSVDFEDTLP 20
 |||

DB 846 KPSYFGGHSVDFEDTLP 865

RESULT 14

AAW8749 standard; protein; 77 AA.

AC AAW8749;

DT 24-SEP-1996 (first entry)

DE S. aureus fibronectin binding protein D2D3 polypeptide.

KM Fibronectin binding protein; D2D3; prevention; adhesion; bacteria;

KM gram positive; extra-cellular matrix protein; in-dwelling device;

OS Staphylococcus aureus.

PN WO9604380-A1.

PD 15-FEB-1996.

PF 28-JUL-1995; 95WO-EP003039.

PR 05-AUG-1994; 94GB-00015901.

XX (SMIK) SMITHKLINE BEECHAM PLC.

PI Critchley IA, Dodd I, Barnett P, Mossakowska DEI;

DR WPI; 1996-129396/13.

XX N-PSDB; AAT12582.

PT Staphylococcus aureus fibronectin binding protein D2D3 polypeptide -
 useful for combating infection at wound sites, surgical implants, etc.
 and as antiadherent agent in oral hygiene.

PS Claim 5; Page 26; 38pp; English.

CC The present sequence is the S. aureus fibronectin binding protein
 CC polypeptide D2D3, which can be used to prevent adhesion of (e.g. gram
 CC positive) bacteria, to extra-cellular matrix proteins on in-dwelling
 CC devices, e.g. catheters or in wounds. D2D3 can also be used to prevent

CC oral pathogens from binding to extra-cellular matrix proteins, in the
 CC oral cavity. D2D3 was found to be effective at inhibiting S. aureus 8325-

CC 4, and 120 adhesion to fibronectin coated PMMA coverslips, at a min.
 CC adhesion inhibitor concn. of 10 microg/ml. D2D3 was derived from the D2

CC and D3 regions of the S. aureus J2385 (NCIMB 40532) fibronectin binding
 CC protein

SQ Sequence 77 AA;

Query Match 91.6%; Score 109; DB 2; Length 77;
 Best Local Similarity 95.0%; Pred. No. 4.5e-09;
 Matches 19; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KPSYFGGHSVDFEDTLP 20
 |||
 DB 55 KPSYFGGHSVDFEDTLP 74

RESULT 15

AAW90939 standard; peptide; 101 AA.

AC AAW90939;

DT 23-SEP-1996 (first entry)

DE D3D4 polypeptide #3.

KM Fibronectin binding protein; Fbp; S. aureus J2385; monoclonal antibody;

KW infection; surgical implant; antiadherent agent; hygiene; adhesion;
 KW extracellular matrix protein; oral pathogen; oral cavity.

OS Staphylococcus aureus.

Key	Location/Qualifiers
FT Region	1..35 /note= "D3 region fragment"
FT Region	36..50 /note= "D4 region"
FT Region	51..101 /note= "WRI region fragment"

XX W09604381-A1.

XX 15-FEB-1996.

XX 28-JUL-1995; 95WO-EP003040.

XX 05-AUG-1994; 94GB-00015900.

XX (SMIK) SMITHKLINE BEECHAM PLC.

XX Critchley IA, Dodd I, Barnett P, Mcbay DL;

XX WPI; 1996-12397/13.

XX Polypeptide(s) derived from Staphylococcus aureus fibronectin binding
 PT protein - inhibit binding of bacteria to extracellular matrix proteins,
 PT for combating infection at the site of wounds and surgical implants, and
 PT in oral hygiene.

XX Claim 6; Page 24; 35pp; English.

XX AAR90937-R90942 represent D3D4 polypeptides. These sequences correspond
 CC to fragments of the Staphylococcus aureus fibronectin binding protein
 CC (Fbp). This sequence corresponds to residues 81-181 of S.aureus J2385
 CC Fbp, and also contains a portion of the wall region 1 (WRI). These
 CC sequences, and monoclonal antibodies against them can be used to combat
 CC infection at the site of wounds, surgical implants and other in-dwelling
 CC devices (such as catheters), and as antiadherent agents in oral hygiene.
 CC They can also be used in the manufacture of a medicament for the
 CC prevention of adhesion of bacteria to extracellular matrix proteins
 CC present on in-dwelling devices or in wounds, or of oral pathogens to
 CC similar proteins on surfaces in the oral cavity

XX Sequence 101 AA;

Query Match 91.6%; Score 109; DB 2; Length 101;
 Best Local Similarity 95.0%; Pred. No. 6.1e-09;
 Matches 19; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KPSYQFGGHSVDFEEDTLP 20
 ||:|||||||
 Db 13 KPNVQFGGHSVDFEEDTLP 32

Search completed: October 25, 2005, 19:38:32
 Job time : 60.1473 secs

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OM protein - protein search, using SW model

Run on: October 22, 2005, 02:23:36 ; Search time 15.9358 Seconds
(without alignments)
98.371 Million cell updates/sec

Title: US-10-731-238-33

Perfect score: 119
Sequence: 1 KPSYQFGHNSVDFEEDTLPP 21

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

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5: /cgn2_6/ptodata/1/1aa/6C_COMB.pep:*
6: /cgn2_6/ptodata/1/1aa/6D_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	119	100.0	21	4	US-09-010-317-33
2	112	94.1	21	4	US-09-010-317-9
3	112	94.1	37	1	US-08-234-622A-4
4	112	94.1	38	1	US-08-294-189-8
5	112	94.1	38	1	US-08-729-767-5
6	112	94.1	114	1	US-08-259-000-3
7	112	94.1	139	3	US-08-856-253-8
8	112	94.1	178	2	US-08-459-135A-12
9	112	94.1	178	3	US-08-495-559-12
10	112	94.1	1027	4	US-08-956-171E-5254
11	112	94.1	1027	4	US-08-781-986A-5254
12	109	91.6	130	2	US-08-459-135A-7
13	109	91.6	130	2	US-08-459-135A-8
14	109	91.6	130	2	US-08-495-559-7
15	109	91.6	130	2	US-08-495-559-8
16	109	91.6	174	3	US-08-459-135A-10
17	109	91.6	174	3	US-08-459-135A-13
18	109	91.6	174	3	US-08-459-559-10
19	109	91.6	174	3	US-08-495-559-13
20	109	91.6	176	3	US-08-495-559-6
21	109	91.6	181	2	US-08-459-135A-6
22	109	91.6	559	4	US-08-956-171E-5251
23	109	91.6	559	4	US-08-781-986A-5251
24	107	89.9	21	4	US-09-010-317-14
25	107	89.9	21	4	US-09-010-317-16
26	107	89.9	21	4	US-09-010-317-23
27	106	89.1	21	4	US-09-010-317-18

28	106	89.1	21	4	US-09-010-317-24	Sequence 24, Appl
29	106	89.1	21	4	US-09-010-317-27	Sequence 27, Appl
30	106	89.1	21	4	US-09-010-317-28	Sequence 28, Appl
31	106	89.1	21	4	US-09-010-317-30	Sequence 30, Appl
32	105	88.2	21	4	US-09-010-317-25	Sequence 25, Appl
33	105	88.2	21	4	US-09-010-317-29	Sequence 29, Appl
34	105	88.2	21	4	US-09-010-317-31	Sequence 31, Appl
35	105	88.2	21	4	US-09-010-317-32	Sequence 32, Appl
36	104	87.4	21	4	US-09-010-317-15	Sequence 15, Appl
37	104	87.4	21	4	US-09-010-317-20	Sequence 20, Appl
38	104	87.4	21	4	US-09-010-317-22	Sequence 22, Appl
39	104	87.4	22	4	US-09-010-317-13	Sequence 13, Appl
40	104	87.4	22	4	US-09-010-317-17	Sequence 17, Appl
41	102	85.7	21	4	US-09-010-317-19	Sequence 19, Appl
42	102	85.7	21	4	US-09-010-317-21	Sequence 21, Appl
43	102	85.7	21	4	US-09-010-317-26	Sequence 26, Appl
44	102	85.7	21	4	US-08-234-622A-1	Sequence 1, Appl
45	96	80.7	19	1	US-08-234-622A-1	Sequence 1, Appl

ALIGNMENTS

RESULT 1
US-09-010-317-33
Sequence 33, Application US/09010317
Patent No. 6685943
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
APPLICANT: Patti, Joseph M.
APPLICANT: House-Pompeo, Karen L.
APPLICANT: Speziale, Pietro
APPLICANT: Joh, Danny
APPLICANT: McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
TITLE OF INVENTION: AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P. O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/010.317
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hihler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TANK:189
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-09-010-317-33
Query Match 100.0% Score 119; DB 4; Length 21;
Best Local Similarity 100.0% Pred. No. 2.4e-12;

Matches 21: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 KPSYFGGHSVDFEEDTLP 21
Db 1 KPSYFGGHSVDFEEDTLP 21

RESULT 2

US-09-010-317-9
; Sequence 9, Application US/09010317
; Patent No. 6685943
; GENERAL INFORMATION:
; APPLICANT: Hook, Magnus
; APPLICANT: Patti, Joseph M.
; APPLICANT: House-Pompeo, Karen L.
; APPLICANT: Speziale, Pietro
; APPLICANT: McGavin, Martin J.
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
; TITLE OF INVENTION: AND METHODS OF USE
; NUMBER OF SEQUENCES: 105
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: TX
; COUNTRY: USA
; ZIP: 77210-4433
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/010.317
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/036,139
; FILING DATE: 21-JAN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Hibler, David W.
; REGISTRATION NUMBER: 41,071
; REFERENCE/DOCKET NUMBER: TAMK-189
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 512-418-3000
; TELEFAX: 512-474-7577
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; US-09-010-317-9

Query Match 94.1%; Score 112; DB 4; Length 21;
Best Local Similarity 100.0%; Pred. No. 3.2e-11;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 KPSYFGGHSVDFEEDTLP 20
Db 1 KPSYFGGHSVDFEEDTLP 20

RESULT 3

US-08-234-622A-4
; Sequence 4, Application US/08234622A
; Patent No. 5440014
; GENERAL INFORMATION:
; APPLICANT: HOOK, Magnus
; APPLICANT: MCGAVIN, Martin
; APPLICANT: RAUCCI, Giuseppe
; TITLE OF INVENTION: A FIBRONECTIN BINDING PEPTIDE

NUMBER OF SEQUENCES: 4

CORRESPONDENCE ADDRESS:

ADDRESSEE: Burns, Doane, Swecker & Mathis

STREET: P.O. Box 1404

CITY: Alexandria

STATE: Virginia

COUNTRY: United States

ZIP: 22313-1404

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/234,622A

FILING DATE: 28-APR-1994

CLASSIFICATION: 530

PRIOR APPLICATION DATA:

APPLICATION NUMBER: SE 9002617-0

FILING DATE: 10-AUG-1990

PRIOR APPLICATION DATA:

APPLICATION NUMBER: WO PCT/SE91/00534

FILING DATE: 09-AUG-1991

ATTORNEY/AGENT INFORMATION:

NAME: Meuth, Donna M

REGISTRATION NUMBER: 36,607

REFERENCE/DOCKET NUMBER: 012885-044

TELECOMMUNICATION INFORMATION:

TELEPHONE: (703) 836-6620

TELEFAX: (703) 836-6620

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 37 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-234-622A-4

Query Match 94.1%; Score 112; DB 1; Length 37;

Best Local Similarity 100.0%; Pred. No. 6e-11;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 KPSYFGGHSVDFEEDTLP 20
Db 16 KPSYFGGHSVDFEEDTLP 35

RESULT 4

US-08-294-189-8
; Sequence 8, Application US/08294189
; Patent No. 5707822
; GENERAL INFORMATION:
; APPLICANT: Fischetti, Vincent A.
; APPLICANT: Rakonjac, Jasna
; APPLICANT: Robbins, John
; TITLE OF INVENTION: GENE SERUM OPACITY FACTOR
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klauber & Jackson
; STREET: 411 Hackensack Avenue
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/294,189
; FILING DATE: 22-AUG-1994

```

CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-118
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 487-5800
TELEFAX: 201 343-1684
TELEX: 133521
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
ORGANISM: Streptococcus pyogenes
STRAIN: D734
INDIVIDUAL ISOLATE: 22
IMMEDIATE SOURCE:
CLONE: GAUJA
US-08-294-189-8

Query Match          94.1%; Score 112; DB 1; Length 38;
Best Local Similarity 100.0%; Pred. No. 6,2e-11;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy      1 KPSYQFGGHSVDPEEDTLP 20
Db      10 KPSYQFGGHSVDPEEDTLP 29

RESULT 5
US-08-729-767-5
Sequence 5, Application US/08729767
Patent No. 5770702
GENERAL INFORMATION:
APPLICANT: HOOK, Magnus
APPLICANT: LINDBERG, Martin Kjell
APPLICANT: SIGNAS, Lars Christer
APPLICANT: WADSTROM, Torkel Mikael
APPLICANT: FROMAN, Gunnar
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN AS WELL AS
TITLE OF INVENTION: ITS PREPARATION
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSER: Burns, Doane, Swecker & Mathis, L.L.P.
STREET: P. O. Box 1404
CITY: Alexandria
STATE: Virginia
COUNTRY: United States
ZIP: 22113-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/729,767
FILING DATE: 07-OCT-1996
CLASSIFICATION: 435
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-6620
TELEX: 133521
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
ORGANISM: Streptococcus pyogenes
STRAIN: D734
INDIVIDUAL ISOLATE: 22
IMMEDIATE SOURCE:
CLONE: GAUJA
US-08-294-189-8

```

```

FILING DATE: 01-JUN-1987
ATTORNEY/AGENT INFORMATION:
NAME: McGowan, Malcolm K.
REGISTRATION NUMBER: 39,300
REFERENCE/DOCKET NUMBER: 012889-036
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-6620
TELEX: 133521
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-729-767-5

Query Match          94.1%; Score 112; DB 1; Length 38;
Best Local Similarity 100.0%; Pred. No. 6,2e-11;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy      1 KPSYQFGGHSVDPEEDTLP 20
Db      17 KPSYQFGGHSVDPEEDTLP 36

RESULT 6
US-08-259-000-3
Sequence 3, Application US/08259000
Patent No. 5571514
GENERAL INFORMATION:
APPLICANT: HOOK, Magnus
APPLICANT: LINDBERG, Martin Kjell
APPLICANT: SIGNAS, Lars Christer
APPLICANT: WADSTROM, Torkel Mikael
APPLICANT: FROMAN, Gunnar
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN AS WELL AS
TITLE OF INVENTION: ITS PREPARATION
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSER: Burns, Doane, Swecker & Mathis
STREET: P. O. Box 1404
CITY: Alexandria
STATE: Virginia
COUNTRY: United States
ZIP: 22113-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/259,000
FILING DATE: 13-JUN-1994
CLASSIFICATION: 435
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-6620
TELEX: 133521
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 114 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-259-000-3

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Query Match 94.1%; Score 112; DB 1; Length 114;
Best Local Similarity 100.0%; Pred. NO. 2.2e-10;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 KPSYFGGHSVDPEEDTLP 20
Db 93 KPSYFGGHSVDPEEDTLP 112

RESULT 7

US-08-856-253-8
; Sequence 8, Application US/08856253
; Patent No. 6288214
; GENERAL INFORMATION:
; APPLICANT: Hook, Magnus
; APPLICANT: Patti, Joseph M.
; APPLICANT: House-Pompeo, Karen
; APPLICANT: Schanham, Narayana
; APPLICANT: Symersky, Jindrich
; TITLE OF INVENTION: COLLAGEN BINDING PROTEIN COMPOSITIONS
; TITLE OF INVENTION: AND METHODS OF USE
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: U.S.
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/856,253
; FILING DATE: Concurrently Herewith
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/017,678
; FILING DATE: 16-MAY-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Kitchell, Barbara S.
; REGISTRATION NUMBER: 33,928
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (512) 418-3000
; TELEFAX: (512) 474-7577
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 139 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
US-08-856-253-8

Query Match 94.1%; Score 112; DB 3; Length 139;
Best Local Similarity 100.0%; Pred. NO. 2.7e-10;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 KPSYFGGHSVDPEEDTLP 20
Db 107 KPSYFGGHSVDPEEDTLP 126

RESULT 8

US-08-459-135A-12
; Sequence 12, Application US/08459135A
; Patent No. 5955078
; GENERAL INFORMATION:
; APPLICANT: BURHAM, Martin Karl Russel
; APPLICANT: CHOPRA, Ian

APPLICANT: CRITCHLEY, Ian Alfred
; APPLICANT: KNOWLES, David Justin Charles
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN: MONOCLONAL ANTIBODY AND THEIR US
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corporation
; STREET: 709 Swedeland Road
; CITY: King of Prussia
; STATE: PA
; COUNTRY: U.S.A.
; ZIP: 19406-0939

COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: Fastseq, Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/459,135A
; FILING DATE: 02-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB/94/00215
; FILING DATE: 04-Feb-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Gimmil, Edward R.
; REGISTRATION NUMBER: 38,891
; REFERENCE/DOCKET NUMBER: P30591C2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-270-4478
; TELEFAX: 610-270-5090
; TELEX:
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 178 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Protein
US-08-459-135A-12

Query Match 94.1%; Score 112; DB 2; Length 178;
Best Local Similarity 100.0%; Pred. NO. 3.6e-10;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 KPSYFGGHSVDPEEDTLP 20
Db 93 KPSYFGGHSVDPEEDTLP 112

RESULT 9

US-08-495-559-12
; Sequence 12, Application US/08495559A
; Patent No. 6054572
; GENERAL INFORMATION:
; APPLICANT: BURHAM, Martin Karl Russel
; APPLICANT: CHOPRA, Ian
; APPLICANT: CRITCHLEY, Ian Alfred
; APPLICANT: KNOWLES, David Justin Charles
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN: MONOCLONAL
; TITLE OF INVENTION: ANTIBODY AND THEIR USE IN PREVENTING BACTERIAL ADHESION
; FILE REFERENCE: P30591
; CURRENT APPLICATION NUMBER: US/08/495,559A
; EARLIER FILING DATE: 1995-08-03
; EARLIER APPLICATION NUMBER: GB 9302289.5
; EARLIER FILING DATE: 1993-02-05
; EARLIER APPLICATION NUMBER: GB 9321592.9
; EARLIER FILING DATE: 1993-10-20
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 12
; LENGTH: 178
; TYPE: PRT

ORGANISM: Staphylococcus aureus
US-08-495-559-12

Query Match 94.1%; Score 112; DB 3; Length 178;
Best Local Similarity 100.0%; Pred. No. 3.6e-10;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KPSYOGGHSVDFEETLP 20
DB 93 KPSYOGGHSVDFEETLP 112

RESULT 10
US-08-956-171E-5254

Sequence 5254, Application US/08956171E
Patent No. 6593114

GENERAL INFORMATION:

APPLICANT: Charles Kunach

Gail H. Choi

Patrick S. Dillon

Craig A. Rosen

Steven C. Barash

Michael R. Fannon

TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences

NUMBER OF SEQUENCES: 5256

CORRESPONDENCE ADDRESS:

ADDRESSEE: Human Genome Sciences, Inc.

STREET: 9410 Key West Avenue

CITY: Rockville

STATE: Maryland

COUNTRY: USA

ZIP: 20850

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.50 inch, 1.4mb storage

COMPUTER: HP Vectra 486/33

OPERATING SYSTEM: MSDOS version 6.2

SOFTWARE: ASCII Text

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/956,171E

FILING DATE: 20-Oct-1997

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 60/009,861

FILING DATE: January 5, 1996

APPLICATION NUMBER: 08/781,986

FILING DATE: January 3, 1997

ATTORNEY/AGENT INFORMATION:

NAME: Mark J. Hyman

REGISTRATION NUMBER: 46,789

REFERENCE/DOCKET NUMBER: PB248P1

TELEPHONE: (240) 314-1224

TELEFAX: (301) 309-8439

INFORMATION FOR SEQ ID NO: 5254:

SEQUENCE CHARACTERISTICS:

LENGTH: 1027 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 5254:

Query Match 94.1%; Score 112; DB 4; Length 1027;
Best Local Similarity 100.0%; Pred. No. 2.7e-09;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KPSYOGGHSVDFEETLP 20
DB 846 KPSYOGGHSVDFEETLP 865

RESULT 11

US-08-781-986A-5254
Sequence 5254, Application US/08781986A

Patent No. 6737248

GENERAL INFORMATION:

APPLICANT: Charles Kunach

TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences

NUMBER OF SEQUENCES: 5255

CORRESPONDENCE ADDRESS:

ADDRESSEE: Human Genome Sciences, Inc.

STREET: 9410 Key West Avenue

CITY: Rockville

STATE: Maryland

COUNTRY: USA

ZIP: 20850

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.50 inch, 1.4mb storage

COMPUTER: HP Vectra 486/33

OPERATING SYSTEM: MSDOS version 6.2

SOFTWARE: ASCII Text

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/781,986A

FILING DATE:

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER:

ATTORNEY/AGENT INFORMATION:

NAME: Benson, Bob

REGISTRATION NUMBER: 30,446

REFERENCE/DOCKET NUMBER: PB248PP

TELEPHONE: (301) 309-8504

TELEFAX: (301) 309-8512

INFORMATION FOR SEQ ID NO: 5254:

SEQUENCE CHARACTERISTICS:

LENGTH: 1027 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-781-986A-5254

Query Match 94.1%; Score 112; DB 4; Length 1027;
Best Local Similarity 100.0%; Pred. No. 2.7e-09;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KPSYOGGHSVDFEETLP 20
DB 846 KPSYOGGHSVDFEETLP 865

RESULT 12
US-08-459-135A-7

Sequence 7, Application US/08459135A

Patent No. 5955078

GENERAL INFORMATION:

APPLICANT: BURNHAM, Martin Karl Russel

APPLICANT: CHOPRA, Ian

APPLICANT: CRITCHLEY, Ian Alfred

APPLICANT: KNOWLES, David Justin Charles

TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN: MONOCLONAL ANTIBODY AND THEIR US

NUMBER OF SEQUENCES: 15

CORRESPONDENCE ADDRESS:

ADDRESSEE: SmithKline Beecham Corporation

STREET: 709 Swedeland Road

CITY: King of Prussia

STATE: PA

COUNTRY: U.S.A.

ZIP: 19406-0939

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

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SOFTWARE: Fastseq, Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/459,135A
FILING DATE: 02-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB/94/00215
FILING DATE: 04-Feb-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Gimm, Edward R
REGISTRATION NUMBER: 38,891
REFERENCE/DOCKET NUMBER: P30591C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-4478
TELEFAX: 610-270-5090
TELEX:
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 130 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-459-135A-7

Query Match          91.6%; Score 109; DB 2; Length 130;
Best Local Similarity 95.0%; Pred. No. 7,6e-10;
Matches 19; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 KPSYQFGGHSVDFEEDTLF 20
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DB      93 KPNYQFGGHSVDFEEDTLF 112

RESULT 13
US-08-459-135A-8
Sequence 8, Application US/08459135A
Patent No. 5955078
GENERAL INFORMATION:
APPLICANT: BURHAM, Martin Karl Russel
APPLICANT: CHOPRA, Ian
APPLICANT: CRITCHLEY, Ian Alfred
APPLICANT: KNOWLES, David Justin Charles
TITLE OF INVENTION: FIBROBLAST BINDING PROTEIN: MONOCLONAL ANTIBODY AND THEIR USE
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Smithkline Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
STATE: PA
COUNTRY: U.S.A.
ZIP: 19406-0939
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: Fastseq, Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/459,135A
FILING DATE: 02-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB/94/00215
FILING DATE: 04-Feb-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Gimm, Edward R
REGISTRATION NUMBER: 38,891
REFERENCE/DOCKET NUMBER: P30591C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-4478
TELEFAX: 610-270-5090
TELEX:

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; INFORMATION FOR SEQ ID NO: 8 :
; SEQUENCE CHARACTERISTICS:
;     LENGTH: 130 amino acids
;     TYPE: amino acid
;     TOPOLOGY: linear
;     MOLECULE TYPE: protein
;     US-08-459-135A-8

Query Match      91.6%; Score 109; DB 2; Length 130;
Best Local Similarity 95.0%; Pred. No. 7,6e-10;
Matches 19; Conservative 1; Mismatches 0; Indels 0; Gaps 0

OY      1 KPSTQFGGHSVDPEDTLP 20
      ||:|||||
Db      93 KPNTQFGGHSVDPEDTLP 112

RESULT 14
US-08-495-559-7
; Sequence 7, Application US/08495559A
; Patent No. 6054572
; GENERAL INFORMATION:
; APPLICANT: BURNAM, Martin Karl Russel
; APPLICANT: CHOPRA, Ian
; APPLICANT: CRITCHLEY, Ian Alfred
; APPLICANT: KNOWLES, David Justin Charles
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN: MONOCLONAL
; FILE REFERENCE: P30591
; CURRENT APPLICATION NUMBER: US/08/495,559A
; EARLIER FILING DATE: 1995-08-03
; EARLIER APPLICATION NUMBER: GB 9302289.5
; EARLIER FILING DATE: 1993-02-05
; EARLIER APPLICATION NUMBER: GB 9321592.9
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FASTSEQ for Windows Version 3.0
; SEQ ID NO 7
; LENGTH: 130
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
; US-08-495-559-7

Query Match      91.6%; Score 109; DB 3; Length 130;
Best Local Similarity 95.0%; Pred. No. 7,6e-10;
Matches 19; Conservative 1; Mismatches 0; Indels 0; Gaps 0

OY      1 KPSTQFGGHSVDPEDTLP 20
      ||:|||||
Db      93 KPNTQFGGHSVDPEDTLP 112

RESULT 15
US-08-495-559-8
; Sequence 8, Application US/08495559A
; Patent No. 6054572
; GENERAL INFORMATION:
; APPLICANT: BURNAM, Martin Karl Russel
; APPLICANT: CHOPRA, Ian
; APPLICANT: CRITCHLEY, Ian Alfred
; APPLICANT: KNOWLES, David Justin Charles
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN: MONOCLONAL
; FILE REFERENCE: P30591
; CURRENT APPLICATION NUMBER: US/08/495,559A
; EARLIER FILING DATE: 1995-08-03
; EARLIER APPLICATION NUMBER: GB 9302289.5
; EARLIER FILING DATE: 1993-02-05
; EARLIER APPLICATION NUMBER: GB 9321592.9
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FASTSEQ for Windows Version 3.0
; SEQ ID NO 8

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LENGTH: 130
TYPE: PRT
ORGANISM: Staphylococcus aureus
US-08-495-559-8

Query Match 91.6%; Score 109; DB 3; Length 130;
Best Local Similarity 95.0%; Pred. No. 7.6e-10;
Matches 19; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KPSYQFGGHSVDFEEDTLP 20
|:|||||||||||||
Db 93 KPNYQFGGHSVDFEEDTLP 112

Search completed: October 22, 2005, 03:51:15
Job time : 15.9358 secs

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GenCore version 5.1.6
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OM protein - protein search, using BW model

Run on: October 22, 2005, 10:49:15 ; Search time 59.2367 Seconds
(without alignments)
148.005 Million cell updates/sec

Title: US-10-731-238-33

Perfect score: 119

Sequence: 1 KPSYQFGHNSVDFEEDTLPP 21

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1862951 seqs, 417491010 residues

Total number of hits satisfying chosen parameters: 1862951

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA.*
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3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
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8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
9: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep.*
10: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep.*
11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep.*
12: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
13: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
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19: /cgn2_6/ptodata/2/pubpaa/US11A_PUBCOMB.pep.*
20: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep.*
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22: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	119	100.0	21	18	US-10-731-238-33	Sequence 33, Appl
2	112	94.1	21	20	US-10-731-238-9	Sequence 9, Appl
3	112	94.1	37	20	US-11-066-697-1134	Sequence 1134, Ap
4	112	94.1	139	9	US-09-813-820-8	Sequence 8, Appl
5	112	94.1	1018	9	US-09-815-242-5797	Sequence 5797, Ap
6	112	94.1	1018	9	US-09-815-242-12838	Sequence 12838, A
7	112	94.1	1018	17	US-10-470-048B-68	Sequence 68, Appl
8	112	94.1	1027	8	US-08-781-986A-5254	Sequence 5254, Ap
9	112	94.1	1027	15	US-10-329-624-5254	Sequence 5254, Ap
10	109	91.6	388	8	US-08-901-062-1	Sequence 1, Appl
11	109	91.6	559	8	US-08-781-986A-5251	Sequence 5251, Ap

12	109	91.6	559	15	US-10-329-624-5251	Sequence 5251, Ap
13	109	91.6	940	17	US-10-470-048B-424	Sequence 424, Appl
14	109	91.6	948	17	US-10-470-048B-69	Sequence 69, Appl
15	109	91.6	961	15	US-10-282-122A-43778	Sequence 43778, A
16	109	91.6	978	9	US-09-815-242-5456	Sequence 5456, A
17	109	91.6	1001	9	US-09-815-242-12686	Sequence 12686, A
18	109	91.6	1038	15	US-10-282-122A-43827	Sequence 43827, A
19	107	89.9	21	18	US-10-731-238-16	Sequence 16, Appl
20	107	89.9	21	18	US-10-731-238-16	Sequence 16, Appl
21	107	89.9	21	18	US-10-731-238-23	Sequence 23, Appl
22	106	89.1	21	18	US-10-731-238-18	Sequence 18, Appl
23	106	89.1	21	18	US-10-731-238-27	Sequence 27, Appl
24	106	89.1	21	18	US-10-731-238-27	Sequence 27, Appl
25	106	89.1	21	18	US-10-731-238-28	Sequence 28, Appl
26	106	89.1	21	18	US-10-731-238-30	Sequence 30, Appl
27	105	88.2	21	18	US-10-731-238-25	Sequence 25, Appl
28	105	88.2	21	18	US-10-731-238-31	Sequence 31, Appl
29	105	88.2	21	18	US-10-731-238-31	Sequence 31, Appl
30	105	88.2	21	18	US-10-731-238-32	Sequence 32, Appl
31	104	87.4	21	18	US-10-731-238-10	Sequence 10, Appl
32	104	87.4	21	18	US-10-731-238-15	Sequence 15, Appl
33	104	87.4	21	18	US-10-731-238-20	Sequence 20, Appl
34	104	87.4	21	18	US-10-731-238-22	Sequence 22, Appl
35	104	87.4	21	18	US-10-731-238-13	Sequence 13, Appl
36	102	85.7	21	18	US-10-731-238-17	Sequence 17, Appl
37	102	85.7	21	18	US-10-731-238-19	Sequence 19, Appl
38	102	85.7	21	18	US-10-731-238-21	Sequence 21, Appl
39	102	85.7	21	18	US-10-731-238-26	Sequence 26, Appl
40	84	70.6	21	18	US-10-731-238-34	Sequence 34, Appl
41	78	65.5	14	18	US-10-731-238-61	Sequence 61, Appl
42	59	48.6	10	18	US-10-731-238-96	Sequence 96, Appl
43	58	48.7	10	18	US-10-731-238-97	Sequence 97, Appl
44	57	47.9	10	18	US-10-731-238-98	Sequence 98, Appl
45	56	47.1	10	18	US-10-731-238-99	Sequence 99, Appl

ALIGNMENTS

RESULT 1
US-10-731-238-33
Sequence 33, Application US/10731238
Publication No. US20050123552A1
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
Patli, Joseph M.
House-Pompeo, Karen L.
Speziale, Pietro
Joh, Danny
McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSER: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/731,238
FILING DATE: 10-Dec-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE: 21-Jan-1998
APPLICATION NUMBER: US 60/036,139

```

1 FILING DATE: 21-JAN-1997
2 ATTORNEY/AGENT INFORMATION:
3 NAME: Hihler, David W.
4 REGISTRATION NUMBER: 41,071
5 REFERENCE/DOCKET NUMBER: TAWK:189
6 TELECOMMUNICATION INFORMATION:
7 TELEPHONE: 512-418-3000
8 TELEFAX: 512-474-7577
9 INFORMATION FOR SEQ ID NO: 33:
10 SEQUENCE CHARACTERISTICS:
11 LENGTH: 21 amino acids
12 TYPE: amino acid
13 STRANDEDNESS: <Unknown>
14 TOPOLOGY: linear
15 SEQUENCE DESCRIPTION: SEQ ID NO: 33:
16
17 US-10-731-238-33
18
19 Query Match 100.0%; Score 119; DB 18; Length 21;
20 Best Local Similarity 100.0%; Pred. No. 4,1e-11;
21 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
22
23 QY 1 KPSYFGGHSVDFEEDTLPP 21
24 1 KPSYFGGHSVDFEEDTLPP 21
25 Db 1 KPSYFGGHSVDFEEDTLPP 21
26
27 RESULT 2
28 US-10-731-238-9
29 Sequence 9, Application US/10731238
30 Publication No. US20050123552A1
31 GENERAL INFORMATION:
32 APPLICANT: Hook, Magnus
33 Patil, Joseph M.
34 House-Pompeo, Karen L.
35 Speziale, Pietro
36 Joh, Danny
37 McGavin, Martin J.
38 TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
39 AND METHODS OF USE
40 NUMBER OF SEQUENCES: 105
41 CORRESPONDENCE ADDRESSES:
42 ADDRESSEE: Arnold, White & Durkee
43 STREET: P. O. Box 4433
44 CITY: Houston
45 STATE: TX
46 COUNTRY: USA
47 ZIP: 77210-4433
48 COMPUTER READABLE FORM:
49 MEDIUM TYPE: Floppy disk
50 COMPUTER: IBM PC compatible
51 OPERATING SYSTEM: PC-DOS/MS-DOS
52 SOFTWARE: Patentin Release #1.0, Version #1.30
53 CURRENT APPLICATION DATA:
54 APPLICATION NUMBER: US/10/731,238
55 FILING DATE: 10-Dec-2003
56 CLASSIFICATION: <Unknown>
57 PRIOR APPLICATION DATA:
58 APPLICATION NUMBER: US/09/010,317
59 FILING DATE: 21-Jan-1998
60 APPLICATION NUMBER: US 60/036,139
61 FILING DATE: 21-Jan-1997
62 ATTORNEY/AGENT INFORMATION:
63 NAME: Hihler, David W.
64 REGISTRATION NUMBER: 41,071
65 REFERENCE/DOCKET NUMBER: TAWK:189
66 TELECOMMUNICATION INFORMATION:
67 TELEPHONE: 512-418-3000
68 TELEFAX: 512-474-7577
69 INFORMATION FOR SEQ ID NO: 9:
70 SEQUENCE CHARACTERISTICS:
71 LENGTH: 21 amino acids
72 TYPE: amino acid
73 STRANDEDNESS: <Unknown>

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;          TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 9:
US-10-731-238-9

Query Match      94.1%; Score 112; DB 18; Length 21;
Best Local Similarity 100.0%; Freq. No. 4.9e-10;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy      1 KPSYQFGHNSVDFEEDTLP 20
        |||
Db      1 KPSYQFGHNSVDFEEDTLP 20

RESULT 3
US-11-066-697-1134
; Sequence 1134, Application US/11066697
; Publication No. US20050187159A1
GENERAL INFORMATION:
APPLICANT: Bridon, Dominique P.
APPLICANT: Ezrin, Alan M.
APPLICANT: Malner, Peter G.
APPLICANT: Holmes, Darren L.
APPLICANT: Thibaudau, Karen
TITLE OF INVENTION: PROTECTION OF ENDOGENOUS THERAPEUTIC PEPTIDES FROM
PPTIDASE ACTIVITY THROUGH CONJUGATION TO BLOOD
TITLE OF INVENTION: COMPONENTS
FILE REFERENCE: 500862002301
CURRENT APPLICATION NUMBER: US/11/066,697
CURRENT FILING DATE: 2005-02-25
PRIOR APPLICATION NUMBER: 09/657,276
PRIOR FILING DATE: 2000-09-07
PRIOR APPLICATION NUMBER: 60/153,406
PRIOR FILING DATE: 1999-09-10
PRIOR APPLICATION NUMBER: 60/159,783
PRIOR FILING DATE: 1999-10-15
NUMBER OF SEQ ID NOS: 1617
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1134
LENGTH: 37
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
OTHER INFORMATION: Peptide
US-11-066-697-1134

Query Match      94.1%; Score 112; DB 20; Length 37;
Best Local Similarity 100.0%; Freq. No. 9e-10;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy      1 KPSYQFGHNSVDFEEDTLP 20
        |||
Db      16 KPSYQFGHNSVDFEEDTLP 35

RESULT 4
US-09-813-820-8
; Sequence 8, Application US/09813820
; Patent No. US20020102262A1
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
APPLICANT: Patil, Joseph M.
APPLICANT: House-Pompeo, Karen
APPLICANT: Sthanam, Narayana
APPLICANT: Symsky, Jindrich
TITLE OF INVENTION: COLLAGEN BINDING PROTEIN COMPOSITIONS
AND METHODS OF USE
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: Texas

```

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; COUNTRY: U.S.
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/813,820
; FILING DATE: 22-Mar-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/856,253
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Kitchell, Barbara S.
; REGISTRATION NUMBER: 33,928
; REFERENCE/DOCKET NUMBER: TANK:193
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (512) 418-3000
; TELEFAX: (512) 474-7577
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 139 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-09-813-820-8

Query Match      94.1%; Score 112; DB 9; Length 139;
Best Local Similarity 100.0%; Pred. No. 3.7e-09;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Q# 1 KPSYQFGHNSVDFEEDTLP 20
DB 107 KPSYQFGHNSVDFEEDTLP 126

RESULT 5
US-09-815-242-5797
; Sequence 5797, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Karl L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; FILE OF INVENTION: Prokaryotes
; FILE REFERENCE: ELITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version 4.0
; FILE REFERENCE: SONN:035US
; SOFTWARE: FastSeq for Windows Version 4.0
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; SEQ ID NO 5797
; LENGTH: 1018
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-09-815-242-5797

Query Match      94.1%; Score 112; DB 9; Length 1018;
Best Local Similarity 100.0%; Pred. No. 3.2e-08;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Q# 1 KPSYQFGHNSVDFEEDTLP 20
DB 837 KPSYQFGHNSVDFEEDTLP 856

RESULT 6
US-09-815-242-12838
; Sequence 12838, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Karl L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; FILE OF INVENTION: Prokaryotes
; FILE REFERENCE: ELITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12838
; LENGTH: 1018
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-09-815-242-12838

Query Match      94.1%; Score 112; DB 9; Length 1018;
Best Local Similarity 100.0%; Pred. No. 3.2e-08;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Q# 1 KPSYQFGHNSVDFEEDTLP 20
DB 837 KPSYQFGHNSVDFEEDTLP 856

RESULT 7
US-10-470-048B-68
; Sequence 68, Application US/10470048B
; Publication No. US2005003744A1
; GENERAL INFORMATION:
; APPLICANT: MEINKE ET AL.
; TITLE OF INVENTION: A METHOD FOR IDENTIFICATION, ISOLATION AND PRODUCTION OF
; FILE OF INVENTION: ANTIGENS TO A SPECIFIC PATHOGEN
; FILE REFERENCE: SONN:035US
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;; CURRENT APPLICATION NUMBER: US/10/470,048B
;; CURRENT FILING DATE: 2003-07-25
;; NUMBER OF SEQ ID NOS: 603
;; SOFTWARE: PatentIn version 3.1
;; SEQ ID NO: 68
;; LENGTH: 1018
;; TYPE: PRF
;; ORGANISM: Staphylococcus aureus
US-10-470-048B-68

Query Match 94.1%; Score 112; DB 17; Length 1018;
Best Local Similarity 100.0%; Pred. No. 3.2e-08;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KPSYQFGHNSVDFEEDTLP 20
|||
Db 837 KPSYQFGHNSVDFEEDTLP 856

RESULT 8
US-08-781-986A-5254
; Sequence 5254, Application US/08781986A
; Publication No. US20030054436A1
; GENERAL INFORMATION:
; APPLICANT: Charles Kunsch
; TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
; NUMBER OF SEQUENCES: 525
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/781,986A
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Benson, Bob
REGISTRATION NUMBER: 30,446
REFERENCE/DOCKET NUMBER: PB248PP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 5254:
SEQUENCE CHARACTERISTICS:
LENGTH: 1027 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-781-986A-5254

Query Match 94.1%; Score 112; DB 8; Length 1027;
Best Local Similarity 100.0%; Pred. No. 3.2e-08;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KPSYQFGHNSVDFEEDTLP 20
|||
Db 846 KPSYQFGHNSVDFEEDTLP 865

RESULT 9
US-10-329-624-5254

; Sequence 5254, Application US/10329624
; Publication No. US20040043037A1
; GENERAL INFORMATION:
; APPLICANT: Charles Kunsch
; Gil H. Choi
; Patrick S. Dillon
; Craig A. Rosen
; Steven C. Barash
; Michael R. Fannon
; TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
; NUMBER OF SEQUENCES: 5256
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/329,624
FILING DATE: 27-Dec-2002
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/956,171
FILING DATE: October 20, 1997
APPLICATION NUMBER: 60/009,861
FILING DATE: January 5, 1996
APPLICATION NUMBER: 08/781,986
FILING DATE: January 3, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Mark J. Hyman
REGISTRATION NUMBER: 46,789
REFERENCE/DOCKET NUMBER: PB248P1D1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (240) 314-1224
TELEFAX: (301) 309-8439
INFORMATION FOR SEQ ID NO: 5254:
SEQUENCE CHARACTERISTICS:
LENGTH: 1027 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 5254:
US-10-329-624-5254

Query Match 94.1%; Score 112; DB 15; Length 1027;
Best Local Similarity 100.0%; Pred. No. 3.2e-08;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KPSYQFGHNSVDFEEDTLP 20
|||
Db 846 KPSYQFGHNSVDFEEDTLP 865

RESULT 10
US-08-901-062-1
; Sequence 1, Application US/08901062
; Publication No. US20020025324A1
; GENERAL INFORMATION:
; APPLICANT: SEALS, JONATHAN R.
; TITLE OF INVENTION: RECOMBINANT BIVALENT BACTERIAL VACCINE
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HALE AND DORR LLP
; STREET: 60 State Street
; CITY: Boston
; STATE: MA

COUNTRY: United States Of America
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/901,062
FILING DATE: 25-JUL-1997
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Baker, Hollie L.
REGISTRATION NUMBER: 31,321
REFERENCE/DOCKET NUMBER: 106941.153
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 526-6000
TELEFAX: (617) 526-5000
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 388 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-901-062-1

Query Match 91.6%; Score 109; DB 8; Length 388;
Best Local Similarity 95.0%; Pred. No. 3.2e-08;
Matches 19; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KPSYOGGHSVDFEETLP 20
DB 356 KPNYOGGHSVDFEETLP 375

RESULT 11
US-08-781-986A-5251
Sequence 5251, Application US/08781986A
Publication No. US20030054436A1
GENERAL INFORMATION:
APPLICANT: Charles Kunesh
TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
NUMBER OF SEQUENCES: 5255
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COUNTRY: USA
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4MB storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/781,986A
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Benson, Bob
REGISTRATION NUMBER: 30,446
REFERENCE/DOCKET NUMBER: PB248PP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 5251:

SEQUENCE CHARACTERISTICS:
LENGTH: 559 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-781-986A-5251

Query Match 91.6%; Score 109; DB 8; Length 559;
Best Local Similarity 95.0%; Pred. No. 4.8e-08;
Matches 19; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KPSYOGGHSVDFEETLP 20
DB 392 KPNYOGGHSVDFEETLP 411

RESULT 12
US-10-329-624-5251
Sequence 5251, Application US/10329624
Publication No. US20040043037A1
GENERAL INFORMATION:
APPLICANT: Charles Kunesh
GIL H. Choi
Patrick S. Dillon
Craig A. Rosen
Steven C. Barash
Michael R. Fannon

TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
NUMBER OF SEQUENCES: 5256
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COUNTRY: USA
ZIP: 20850

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4MB storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/329,624
FILING DATE: 27-Dec-2002

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/956,171
FILING DATE: October 20, 1997
APPLICATION NUMBER: 60/009,861
FILING DATE: January 5, 1996
APPLICATION NUMBER: 08/781,986
FILING DATE: January 3, 1997

ATTORNEY/AGENT INFORMATION:
NAME: Mark J. Hyman
REGISTRATION NUMBER: 46,789
REFERENCE/DOCKET NUMBER: PB248PDI

TELECOMMUNICATION INFORMATION:
TELEPHONE: (240) 314-1224
TELEFAX: (301) 309-8439
INFORMATION FOR SEQ ID NO: 5251:
SEQUENCE CHARACTERISTICS:
LENGTH: 559 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 5251:

US-10-329-624-5251

Query Match 91.6%; Score 109; DB 15; Length 559;
Best Local Similarity 95.0%; Pred. No. 4.8e-08;
Matches 19; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 KPSYFGGHSVDPEDTLP 20
 ||:||||||||||||||
 Db 392 KPNYFGGHSVDPEDTLP 411

RESULT 13

US-10-470-048B-424
 ; Sequence 424, Application US/10470048B
 ; Publication No. US2005003744A1
 ; GENERAL INFORMATION:
 ; APPLICANT: MEINKE ET AL.
 ; TITLE OF INVENTION: A METHOD FOR IDENTIFICATION, ISOLATION AND PRODUCTION OF
 ; TITLE OF INVENTION: ANTIGENS TO A SPECIFIC PATHOGEN
 ; FILE REFERENCE: SONN.035US
 ; CURRENT APPLICATION NUMBER: US/10/470.048B
 ; CURRENT FILING DATE: 2003-07-25
 ; NUMBER OF SEQ ID NOS: 603
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 424
 ; LENGTH: 940
 ; TYPE: PRT
 ; ORGANISM: Staphylococcus aureus
 ; US-10-470-048B-424

Query Match 91.6%; Score 109; DB 17; Length 940;
 Best Local Similarity 95.0%; Pred. No. 8.4e-08;
 Matches 19; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 KPSYFGGHSVDPEDTLP 20
 ||:||||||||||||||
 Db 773 KPNYFGGHSVDPEDTLP 792

RESULT 14

US-10-470-048B-69
 ; Sequence 69, Application US/10470048B
 ; Publication No. US2005003744A1
 ; GENERAL INFORMATION:
 ; APPLICANT: MEINKE ET AL.
 ; TITLE OF INVENTION: A METHOD FOR IDENTIFICATION, ISOLATION AND PRODUCTION OF
 ; TITLE OF INVENTION: ANTIGENS TO A SPECIFIC PATHOGEN
 ; FILE REFERENCE: SONN.035US
 ; CURRENT APPLICATION NUMBER: US/10/470.048B
 ; CURRENT FILING DATE: 2003-07-25
 ; NUMBER OF SEQ ID NOS: 603
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 69
 ; LENGTH: 948
 ; TYPE: PRT
 ; ORGANISM: Staphylococcus aureus
 ; US-10-470-048B-69

Query Match 91.6%; Score 109; DB 17; Length 948;
 Best Local Similarity 95.0%; Pred. No. 8.5e-08;
 Matches 19; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 KPSYFGGHSVDPEDTLP 20
 ||:||||||||||||||
 Db 781 KPNYFGGHSVDPEDTLP 800

RESULT 15

US-10-282-122A-43778
 ; Sequence 43778, Application US/10282122A
 ; Publication No. US20040029129A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Wang, Liangsu
 ; APPLICANT: Zamudio, Carlos
 ; APPLICANT: Malone, Cheryl
 ; APPLICANT: Habelbeck, Robert
 ; APPLICANT: Ohlsen, Kari
 ; APPLICANT: Zvekind, Judith
 ; APPLICANT: Wall, Daniel

; APPLICANT: Trawick, John
 ; APPLICANT: Carr, Grant
 ; APPLICANT: Yamamoto, Robert
 ; APPLICANT: Forsyth, R.
 ; APPLICANT: Xu, H.

; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
 ; FILE REFERENCE: ELITRA.034A
 ; CURRENT APPLICATION NUMBER: US/10/282.122A
 ; CURRENT FILING DATE: 2003-02-20
 ; PRIOR APPLICATION NUMBER: 60/191,078
 ; PRIOR FILING DATE: 2000-03-21
 ; PRIOR APPLICATION NUMBER: 60/206,848
 ; PRIOR FILING DATE: 2000-05-23
 ; PRIOR APPLICATION NUMBER: 60/207,727
 ; PRIOR FILING DATE: 2000-05-26
 ; PRIOR APPLICATION NUMBER: 60/230,335
 ; PRIOR FILING DATE: 2000-09-06
 ; PRIOR APPLICATION NUMBER: 60/230,347
 ; PRIOR FILING DATE: 2000-09-09
 ; PRIOR APPLICATION NUMBER: 60/242,578
 ; PRIOR FILING DATE: 2000-10-23
 ; PRIOR APPLICATION NUMBER: 60/253,625
 ; PRIOR FILING DATE: 2000-11-27
 ; PRIOR APPLICATION NUMBER: 60/257,931
 ; PRIOR FILING DATE: 2000-12-22
 ; PRIOR APPLICATION NUMBER: 60/267,636
 ; PRIOR FILING DATE: 2001-02-09
 ; PRIOR APPLICATION NUMBER: 60/269,308
 ; PRIOR FILING DATE: 2001-02-16
 ; Remaining Prior Application data removed - See File Wrapper or PALM.
 ; NUMBER OF SEQ ID NOS: 78614
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 43778
 ; LENGTH: 961
 ; TYPE: PRT
 ; ORGANISM: Staphylococcus aureus
 ; US-10-282-122A-43778

Query Match 91.6%; Score 109; DB 15; Length 961;
 Best Local Similarity 95.0%; Pred. No. 8.6e-08;
 Matches 19; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 KPSYFGGHSVDPEDTLP 20
 ||:||||||||||||||
 Db 784 KPNYFGGHSVDPEDTLP 803

Search completed: October 22, 2005, 11:34:45
 Job time : 60.2367 secs

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OM protein - protein search, using sw model

Run on: October 22, 2005, 02:23:36 ; Search time 10.5465 Seconds
(without alignments)
191.586 Million cell updates/sec

Title: US-10-731-238-33

Perfect score: 119
Sequence: 1 KPSYQFGGNSVDFEEDTLPP 21

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 segs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	112	94.1	1018	2	A32192 fibronectin-binding
2	109	91.6	940	2	S19702 fibronectin-binding
3	109	91.6	961	2	G90053 hypothetical prote
4	109	91.6	1038	2	H90053 hypothetical prote
5	54	45.4	387	2	I18449 extracellular prote
6	52.5	44.1	1038	2	T15098 hypothetical prote
7	49	41.2	474	2	B84357 serine-tryptophan synthase
8	49	41.2	493	2	JC5621 epidermal growth f
9	49	41.2	551	2	S57447 HPBRII-7 protein -
10	47	39.5	445	2	P90562 hypothetical prote
11	47	39.5	468	2	T26081 hypothetical prote
12	46.5	39.1	859	2	T35785 probable beta-gluc
13	46	38.7	257	2	A36057 MHC class I histoc
14	46	38.7	453	2	H70333 conserved hypotet
15	46	38.7	525	2	AD2022 hypothetical prote
16	45	37.8	216	2	A39926 3-oxoacyl-l-acyl-ca
17	45	37.8	462	1	A39356 3-oxoacyl-l-acyl-ca
18	45	37.8	469	2	T10061 starch debranching
19	45	37.8	962	2	T01688 myosin heavy chain
20	45	37.8	1322	2	A59288 gp18 (Bacteriophag
21	44.5	37.4	345	2	AB1448 immunophilin FKBP5
22	44.5	37.4	459	2	A46372 fibronectin-binding
23	44.5	37.4	1091	2	S33850 laminin alpha-1 ch
24	44.5	37.4	3712	2	S18253 50K protein - rat
25	44	37.0	32	2	S59800 hypothetical prote
26	44	37.0	275	2	D96826 fructokinase - Del
27	44	37.0	303	2	B75485 permease protein o
28	44	37.0	313	2	AE2057 3-phosphoinositide
29	44	37.0	427	2	D95159

30	44	37.0	431	2	D98025 3-phosphoinositide
31	44	37.0	433	2	T01405 vesicle-associated
32	44	37.0	690	2	T13321 hypothetical prote
33	44	37.0	705	2	C84406 hypothetical prote
34	44	37.0	808	2	F81180 conserved hypotet
35	43.5	36.6	458	2	JN0873 immunophilin p59 -
36	43.5	36.6	1097	2	T15104 hypothetical prote
37	43	36.1	188	2	T31504 transcription regu
38	43	36.1	288	2	T17395 probable 33.6K pro
39	43	36.1	288	2	A42518 ABR protein - vac
40	43	36.1	296	2	T02573 CDR protein - vac
41	43	36.1	417	2	T14930 probable secreted
42	43	36.1	823	2	S14055 nucleoskeletal-lik
43	43	36.1	928	1	VCBEMC glycoprotein B pre
44	43	36.1	1289	2	AB2217 hypothetical prote
45	43	36.1	1926	2	JC4842 DNA-binding nuclea

ALIGNMENTS

RESULT 1

A32192
fibronectin-binding protein - Staphylococcus aureus
C:Species: Staphylococcus aureus
C:Date: 31-Jul-1989 #sequence_revision 31-Jul-1989 #text_change 16-Feb-1997
C:Accession: A32192
R:Signaes, C.; Raucel, G.; Joensson, K.; Lindgren, P.E.; Anantharamiah, G.M.; Hoecek, M.
Proc. Natl. Acad. Sci. U.S.A. 86, 699-703, 1989
A:Title: Nucleotide sequence of the gene for a fibronectin-binding protein from Staphyloc
A:Reference number: A32192; MUID:89098998; PMID:2521391
A:Accession: A32192
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1018 <SIG>
A:Cross-references: GB:J04151
C:Keywords: fibronectin binding

Query Match 94.1%; Score 112; DB 2; Length 1018;
Best Local Similarity 100.0%; Pred. No. 2.3e-09;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KPSYQFGGNSVDFEEDTLPP 20

Db 837 KPSYQFGGNSVDFEEDTLPP 856

RESULT 2

S19702
fibronectin-binding protein B - Staphylococcus aureus
C:Species: Staphylococcus aureus
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
C:Accession: S19702
R:Joensson, K.; Signaes, C.; Mueller, H.P.; Lindberg, M.
Eur. J. Biochem. 202, 1041-1048, 1991
A:Title: Two different genes encode fibronectin binding proteins in Staphylococcus aureu
A:Reference number: S19702; MUID:92111475; PMID:1837266
A:Accession: S19702
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-940 <JOB>
A:Cross-references: UNIPROT:Q53682; EMBL:X62992; NID:q49040; PIDD:CAA44726.1; PTD:958156;
C:Keywords: fibronectin binding

Query Match 91.6%; Score 109; DB 2; Length 940;
Best Local Similarity 95.0%; Pred. No. 6.3e-09;
Matches 19; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KPSYQFGGNSVDFEEDTLPP 20

Db 773 KPSYQFGGNSVDFEEDTLPP 792

```

RESULT 3
G90053
hypothetical protein fnb [imported] - Staphylococcus aureus (strain N315)
C/Species: Staphylococcus aureus
C/Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C/Accession: G90053
R/Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguc
ma, A.; Mitutani-Uji, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.;
C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramoto, K.
Lancet 357, 1225-1240, 2001
A/Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.
A/Reference number: A89758; MUID:21311952; PMID:11418146
A/Accession: G90053
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-961 <KIR>
A/Cross-references: UNIPROT:Q99RD3; GB:BA000018; PID:g13702452; PIDN:BAB43593.1; GSPDB:C
A/Experimental source: strain N315
C/Genetics:
A/Gene: fnbB

Query Match          91.6%; Score 109; DB 2; Length 961;
Best Local Similarity 95.0%; Pred. No. 6.4e-09;
Matches 19; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY      1 KPSYQFGHNSVDFEEDTLP 20
DB      784 KPNYQFGHNSVDFEEDTLP 803

RESULT 4
H90053
hypothetical protein fnb [imported] - Staphylococcus aureus (strain N315)
C/Species: Staphylococcus aureus
C/Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C/Accession: H90053
R/Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguc
ma, A.; Mitutani-Uji, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.;
C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramoto, K.
Lancet 357, 1225-1240, 2001
A/Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.
A/Reference number: A89758; MUID:21311952; PMID:11418146
A/Accession: H90053
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-1038 <KIR>
A/Cross-references: UNIPROT:Q99RD2; GB:BA000018; PID:g13702453; PIDN:BAB43594.1; GSPDB:C
A/Experimental source: strain N315
C/Genetics:
A/Gene: fnbB

Query Match          91.6%; Score 109; DB 2; Length 1038;
Best Local Similarity 95.0%; Pred. No. 7e-09;
Matches 19; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY      1 KPSYQFGHNSVDFEEDTLP 20
DB      833 KPNYQFGHNSVDFEEDTLP 852

RESULT 5
I38449
extracellular protein - human
C/Species: Homo sapiens (man)
C/Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 21-Jul-2000
C/Accession: I38449
R/Lecka-Czerwik, B.; Lumpkin, C.K.
Mol. Cell. Biol. 15, 120-128, 1995
A/Title: An overexpressed gene transcript in senescent and quiescent human fibroblasts e
A/Reference number: I38449; MUID:95097983; PMID:7799918
A/Accession: I38449
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA

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A/Residues: 1-387 <RES>
A/Cross-references: EMBL:U03877; NID:g458227; PIDN:AAA65590.1; PID:g458228
C/Genetics:
A/Gene: Sl-5

Query Match          45.4%; Score 54; DB 2; Length 387;
Best Local Similarity 50.0%; Pred. No. 1.2;
Matches 10; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

OY      2 PSYQFGHNSVDFEEDTLP 21
DB      97 PGYQKRGECQVDIDECTIP 116

RESULT 6
T15098
hypothetical protein T22B11.5 - Caenorhabditis elegans
C/Species: Caenorhabditis elegans
C/Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C/Accession: T15098
R/Rohlfing, T.; Wohldmann, P.
submitted to the EMBL Data Library, December 1997
A/Description: The sequence of C. elegans cosmid T22B11.
A/Reference number: Z18292
A/Accession: T15098
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-1038 <ROH>
A/Cross-references: UNIPROT:O61199; EMBL:AF039040; NID:g2736374; PID:g2736379; PIDN:AA89<
A/Experimental source: strain Bristol N2; clone T22B11
C/Genetics:
A/Gene: CESP:T22B11.5
A/Map position: 4
A/Intons: 45/3; 128/2; 225/3; 659/3; 707/3; 820/3; 969/3
C/Superfamily: oxoglutarate dehydrogenase (lipoamide); thiamin pyrophosphate-binding dome
F:420-465/Domain: thiamin pyrophosphate-binding domain homology <TPB>

Query Match          44.1%; Score 52.5; DB 2; Length 1038;
Best Local Similarity 39.3%; Pred. No. 6.1;
Matches 11; Conservative 3; Mismatches 5; Indels 9; Gaps 1;

OY      3 SYQFGHNSVDFE-----EDTLP 21
DB      156 SYQTRGHNIADLPDGLINSADLDDTIP 183

RESULT 7
B84357
serine-tRNA synthetase [imported] - Halobacterium sp. NRC-1
C/Species: Halobacterium sp. NRC-1
C/Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
C/Accession: B84357
R/Ng, W.V.; Kennedy, S.P.; Mahliras, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Lasky, S.
; Letchusner, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Jablot
Jung, K.H.; Alam, M.; Freilasz, T.
Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000
A/Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ehardt, H.; Lowe, T.M.; Lit
A/Title: Genome sequence of Halobacterium species NRC-1.
A/Reference number: A84160; MUID:20504483; PMID:11016550
A/Accession: B84357
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-474 <STO>
A/Cross-references: UNIPROT:Q9HNB6; GB:AE004437; NID:g10561491; PIDN:AMG2022.1; GSPDB:G<
C/Genetics:
A/Gene: serS
C/Superfamily: serine-tRNA ligase

Query Match          41.2%; Score 49; DB 2; Length 474;
Best Local Similarity 41.2%; Pred. No. 9.1;
Matches 7; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

OY      3 SYQFGHNSVDFEEDTLP 19

```

Db 234 AYRIGENDADYDDDL 250

RESULT 8

JC5621
epidermal growth factor-like protein, T16 precursor - rat
C/Species: Rattus norvegicus (Norway rat)
C/Date: 09-Oct-1997 #sequence_revision 07-Nov-1997 #text_change 09-Jul-2004
C/Accession: JC5621
R/Ozaki, T.; Kondo, K.; Nakamura, Y.; Ichimiya, S.; Nakagawara, A.; Sakiyama, S.
Biochem. Biophys. Res. Commun. 237, 245-250, 1997
A/Title: Interaction of DA41, a DAN-binding protein, with the epidermal growth factor-1
A/Reference number: JC5621; MUID:97415782; PMID:9268694
A/Accession: JC5621
A/Molecule type: mRNA
A/Residues: 1-93 <OZ>
A/Cross-references: UNIPROT:Q35568; DBJ:P89730; NID:G2429082; PIDN:BA22265.1; PID:dl02
C/Comment: This protein plays a role in the regulation of cell growth by interacting wit
C/Keywords: glycoprotein
F/1-17/Domain: signal sequence #status predicted <SIG>
F/28-70, 158-199, 200-237, 238-277, 318-359/Region: epidermal growth factor-like ref
F/249/Binding site: carbohydrate (asn) (covalent) #status predicted

Query Match 41.2%; Score 49; DB 2; Length 493;
Best Local Similarity 45.0%; Pred. No. 9.5;
Matches 9; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

Qy 2 PSYOGCHNSVDFEETLP 21
Db 203 FGQKRGSCVDIDECVVP 222

RESULT 9

S57447
HPBRII-7 protein - human
N/Alternate names: HPBRII-4 protein
C/Species: Homo sapiens (man)
C/Date: 10-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 16-Aug-2004
C/Accession: S57447; S57489
R./Fleischauer, K.L.
Submitted to the EMBL Data Library, June 1992
A/Reference number: S57447
A/Accession: S57447
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-551 <FLB>
A/Cross-references: UNIPROT:Q16630; EMBL:X67336; NID:G871300; PIDN:CAA47751.1; PID:G8713
A/Accession: S57489
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-551 <FL2>
A/Cross-references: EMBL:X67337; NID:G871298; PIDN:CAA47752.1; PID:G871299
C/Genetics: 231/3
A/Introns: 231/3
C/Superfamily: ribonucleoprotein repeat homology
F/82-151/Domain: ribonucleoprotein repeat homology <RBM4>

Query Match 41.2%; Score 49; DB 2; Length 551;
Best Local Similarity 35.3%; Pred. No. 11;
Matches 6; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

Qy 5 ORGCHNSVDFEETLP 21
Db 23 EYGHQDIDLYDVIVP 39

RESULT 10

P90562
hypothetical protein MYPU_4060 [imported] - Mycoplasma pulmonis (strain UAB CTIP)
C/Species: Mycoplasma pulmonis
C/Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 09-Jul-2004
C/Accession: P90562

R./Chamblaud, I.; Heilig, R.; Ferris, S.; Barde, V.; Samson, D.; Gallison, F.; Moszer, I.;
Nucleic Acids Res. 29, 2145-2153, 2001
A/Title: The complete genome sequence of the murine respiratory pathogen Mycoplasma pulmk
A/Reference number: A9512; MUID:21267165; PMID:11553084
A/Accession: P90562
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-445 <KUR>
A/Cross-references: UNIPROT:Q98Q60; GB:AL445566; PID:G14089820; PIDN:CAC13579.1; GSPDB:GB
A/Experimental source: strain UAB CTIP
C/Genetics:
A/Genetic code: SGC3

Query Match 39.5%; Score 47; DB 2; Length 445;
Best Local Similarity 43.8%; Pred. No. 18;
Matches 7; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

Qy 1 KPSYOGCHNSVDPEE 16
Db 334 KPQVAGSHNYHQE 349

RESULT 11

T26081
hypothetical protein W02A2.7 - Caenorhabditis elegans
C/Species: Caenorhabditis elegans
C/Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C/Accession: T26081
R./Alncough, R.
Submitted to the EMBL Data Library, November 1996
A/Reference number: Z20148
A/Accession: T26081
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-468 <WIL>
A/Cross-references: UNIPROT:Q9XUB2; EMBL:Z82286; PIDN:CAB05310.1; GSPDB:GN00022; CESP:W0;
A/Experimental source: clone W02A2
C/Genetics:
A/Gene: CESP:W02A2.7
A/Map position: 4
A/Introns: 38/3; 212/2; 353/3; 403/2

Query Match 39.5%; Score 47; DB 2; Length 468;
Best Local Similarity 36.8%; Pred. No. 19;
Matches 7; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

Qy 2 PSYOGCHNSVDFEETLP 20
Db 351 PPYQMSHDDPDYDVIVP 369

RESULT 12

T35785
probable beta-glucosidase - Streptomyces coelicolor
C/Species: Streptomyces coelicolor
C/Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 09-Jul-2004
C/Accession: T35785
R./Seeger, K.J.; Harris, D.; Parkhill, J.; Barrrell, B.G.; Rajandream, M.A.
Submitted to the EMBL Data Library, July 1998
A/Reference number: Z21570
A/Accession: T35785
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-859 <SEB>
A/Cross-references: UNIPROT:O87852; EMBL:AL031013; PIDN:CAA19790.1; GSPDB:GN00070; SGOEDI
A/Experimental source: strain A3 (2)
C/Genetics:
A/Gene: SGOEDB:SC8A6.18
C/Superfamily: beta-glucosidase

Query Match 39.1%; Score 46.5; DB 2; Length 859;
Best Local Similarity 43.5%; Pred. No. 44;


```
FT REPEAT 545 574 B-1.
FT REPEAT 575 604 B-2.
FT DOMAIN 745 878 4 X approximate tandem repeats,
FT REPEAT 745 782 D-1.
FT REPEAT 783 820 D-2.
FT REPEAT 821 859 D-3.
FT REPEAT 860 878 D-4 (incomplete).
FT DOMAIN 879 948 5 X tandem repeats, Pro-rich (WR).
FT REPEAT 879 892 WR 1.
FT REPEAT 893 906 WR 2.
FT REPEAT 907 920 WR 3.
FT REPEAT 921 934 WR 4.
FT REPEAT 935 948 WR 5.
FT SITE 982 986 LPXTG sorting signal (Potential).
FT MOD_RES 985 985 Pentaglycyl murein peptidoglycan amidated
SQ SEQUENCE 1018 AA; 111780 MW; 58175B0020E81P1F CRC64;

Query Match 94.1%; Score 112; DB 1; Length 1018;
Best Local Similarity 100.0%; Pred. No. 3.1e-08;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KPSYQFGHNSVDFEEDTLP 20
Db 837 KPSYQFGHNSVDFEEDTLP 856

RESULT 2
ID Q53682 PRELIMINARY; PRT; 940 AA.
AC Q53682;
DT 01-NOV-1996 (TREMblrel. 01, Last sequence update)
DT 01-NOV-1996 (TREMblrel. 01, Last sequence update)
DT 01-MAR-2004 (TREMblrel. 26, Last annotation update)
DE Fibronectin binding protein B.
GN Name=fnbB;
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxId=1280;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=8325-4;
RX MEDLINE=9211475; PubMed=1837266;
RA "Johnson K., Signas C., Muller H.P., Lindberg M.;
RT "Two different genes encode fibronectin binding proteins in
RT Staphylococcus aureus. The complete nucleotide sequence and
RT characterization of the second gene."
RL Eur. J. Biochem. 202:1041-1048(1991).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC an amide bond (By similarity).
DR EMBL; X62992; CAA44726.1; -.
DR FTR; S19702; S19702.
DR HSP; Q53653; IN67.
DR GO; GO:0009986; C:cell surface; IEA.
DR GO; GO:0005618; C:cell wall; IEA.
DR GO; GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:007155; P:cell adhesion; IEA.
DR InterPro; IPR008966; Adhes_bact.
DR InterPro; IPR004237; Fn_bind.
DR InterPro; IPR005877; Gpos_YsIRK.
DR InterPro; IPR01899; Gram_pos_anchor.
DR Pfam; PF02986; Fn_bind_2.
DR Pfam; PF00746; Gram_pos_anchor_1.
DR Pfam; PF04650; YsIRK_signal_1.
DR TIGRfams; TIGR01167; LPXTG_anchor_1.
DR TIGRfams; TIGR01168; YsIRK_signal_1.
DR PROSITE; PS50847; GRAM_POS_ANCHORING; 1.
KW Cell wall; peptidoglycan-anchor.
SQ SEQUENCE 940 AA; 103555 MW; E35FBBCA907AE345 CRC64;

Query Match 91.6%; Score 109; DB 2; Length 940;
```

```
Best Local Similarity 95.0%; Pred. No. 8.2e-08;
Matches 19; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KPSYQFGHNSVDFEEDTLP 20
Db 773 KPSYQFGHNSVDFEEDTLP 792

RESULT 3
ID Q8NU8 PRELIMINARY; PRT; 943 AA.
AC Q8NU8;
DT 01-OCT-2002 (TREMblrel. 22, Created)
DT 01-OCT-2002 (TREMblrel. 22, Last sequence update)
DT 01-OCT-2003 (TREMblrel. 25, Last annotation update)
DE FnB protein.
GN Name=fnbB; OrderedLocNames=MW2420;
OS Staphylococcus aureus (strain MW2).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxId=196620;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MW2;
RX MEDLINE=22040717; PubMed=12044378; DOI=10.1016/S0140-6736(02)08713-5;
RA Baba T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Oguchi A.,
RA Nagai Y., Iwama N., Asano K., Naito T., Kuroda H., Cui L.,
RA Yamamoto K., Hiramatsu K.;
RT "Genome and virulence determinants of high virulence community-
RT acquired MRSA."
RL Lancet 359:1819-1827(2002).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC an amide bond (By similarity).
DR EMBL; AP004830; BAB96285.1; -.
DR HSP; Q53653; IN67.
DR GO; GO:0009986; C:cell surface; IEA.
DR GO; GO:0005618; C:cell wall; IEA.
DR GO; GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:007155; P:cell adhesion; IEA.
DR InterPro; IPR008966; Adhes_bact.
DR InterPro; IPR004237; Fn_bind.
DR InterPro; IPR005877; Gpos_YsIRK.
DR InterPro; IPR01899; Gram_pos_anchor.
DR Pfam; PF02986; Fn_bind_1.
DR Pfam; PF00746; Gram_pos_anchor_1.
DR TIGRfams; TIGR01167; LPXTG_anchor_1.
DR TIGRfams; TIGR01168; YsIRK_signal_1.
DR PROSITE; PS50847; GRAM_POS_ANCHORING; 1.
KW Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ SEQUENCE 943 AA; 104537 MW; DAB5F31947E1B6A CRC64;

Query Match 91.6%; Score 109; DB 2; Length 943;
Best Local Similarity 95.0%; Pred. No. 8.3e-08;
Matches 19; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KPSYQFGHNSVDFEEDTLP 20
Db 780 KPSYQFGHNSVDFEEDTLP 799

RESULT 4
ID Q6G6H4 PRELIMINARY; PRT; 957 AA.
AC Q6G6H4;
DT 05-JUL-2004 (TREMblrel. 27, Created)
DT 05-JUL-2004 (TREMblrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMblrel. 27, Last annotation update)
DE Fibronectin-binding protein.
GN Name=fnbB; OrderedLocNames=SA62387;
OS Staphylococcus aureus (strain MSA476).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxId=282459;
```

```
[1]
RN SEQUENCE FROM N.A.
RX PubMed=15213324; DOI=10.1073/pnas.0402521101;
RA Holden M.T.G., Fell E.J., Lindsey J.A., Peacock S.J., Day N.P.J.,
RA Enright M.C., Foster T.J., Moore C.E., Hurst L., Atkin R., Barton A.,
RA Baeson N., Bentley S.D., Chillingworth C., Chillingworth T.,
RA Churcher C., Clark L., Cotton C., Cronin A., Doggett J., Dowd L.,
RA Felwell T., Hance Z., Harris B., Hauser H., Holroyd S., Jagsle K.,
RA James K.D., Leonard N., Line A., Mayes R., Moule S., Mungall K.,
RA Ommond D., Quail M.A., Rabinowitch E., Rutherford K.M., Sanders M.,
RA Sharp S., Simmonds M., Stevens K., Whitehead S., Barrall B.G.,
RA Spratt B.G., Parkhill J.;
RT "Complete genomes of two clinical Staphylococcus aureus strains:
RT evidence for the rapid evolution of virulence and drug resistance.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:9786-9791(2004).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC an amide bond (By similarity).
CC EMBL: BX571857; CAG4201.1; -.
DR GO: GO:0009986; C:cell surface; IEA.
DR GO: GO:0005618; C:cell wall; IEA.
DR GO: GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO: GO:0016020; C:membrane; IEA.
DR GO: GO:0007155; P:cell adhesion; IEA.
DR InterPro: IPR008966; Adhes_bact.
DR InterPro: IPR004237; Fn_bind.
DR InterPro: IPR005877; Gpos_YsIRK.
DR InterPro: IPR01899; Gram_pos_anchor.
DR Pfam: PF02986; Fn_bind; 1.
DR Pfam: PF00746; Gram_pos_anchor; 1.
DR Pfam: PF04650; YsIRK_signal; 1.
DR TIGRFAMs: TIGR01167; LpXTG_anchor; 1.
DR TIGRFAMs: TIGR01168; YsIRK_signal; 1.
DR PROSITE: PS50847; GRAM_POS_ANCHORING; 1.
KW Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ SEQUENCE 957 AA; 105960 MW; 2878BA7FDFD3EAF CRC64;

Query Match 91.6%; Score 109; DB 2; Length 957;
Best Local Similarity 95.0%; Pred. No. 8.4e-08;
Matches 19; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KPSYQFGHNSVDFEDTLP 20
Db 780 KENYQFGHNSVDFEDTLP 799

RESULT 5
Q99RD3 PRELIMINARY; PRT; 961 AA.
AC Q99RD3;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Fibronectin-binding protein homolog.
GN Name=fnbB; OrderedLocustNames=SAV2502;
OS Staphylococcus aureus (strain Mu50 / ATCC 700699).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxId=158878;
RN [1]
RN SEQUENCE FROM N.A.
RP STRAIN=Mu50 / ATCC 700699;
RX MEDLINE=21311952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2;
RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Iian J.-Q., Ito T.,
RA Kanamori M., Matsunami H., Maruyama A., Murakami H., Hosoyama A.,
RA Mizutani U.I., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
RA Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
RA Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
RA Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
RT "Whole genome sequencing of methicillin-resistant Staphylococcus
RT aureus ";
RL Lancet 357:1225-1240(2001).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC an amide bond (By similarity).
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DR EMBL: AP003365; BAB58664.1; -.
DR PIR: G90053; G90053.
DR HSSP: Q53653; IN67.
DR GO: GO:0009986; C:cell surface; IEA.
DR GO: GO:0005618; C:cell wall; IEA.
DR GO: GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO: GO:0016020; C:membrane; IEA.
DR GO: GO:0007155; P:cell adhesion; IEA.
DR InterPro: IPR008966; Adhes_bact.
DR InterPro: IPR004237; Fn_bind.
DR InterPro: IPR005877; Gpos_YsIRK.
DR InterPro: IPR01899; Gram_pos_anchor.
DR Pfam: PF02986; Fn_bind; 1.
DR Pfam: PF00746; Gram_pos_anchor; 1.
DR Pfam: PF04650; YsIRK_signal; 1.
DR TIGRFAMs: TIGR01167; LpXTG_anchor; 1.
DR TIGRFAMs: TIGR01168; YsIRK_signal; 1.
DR PROSITE: PS50847; GRAM_POS_ANCHORING; 1.
KW Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ SEQUENCE 961 AA; 106010 MW; 364940F884EA4101 CRC64;

Query Match 91.6%; Score 109; DB 2; Length 961;
Best Local Similarity 95.0%; Pred. No. 8.4e-08;
Matches 19; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KPSYQFGHNSVDFEDTLP 20
Db 784 KENYQFGHNSVDFEDTLP 803

RESULT 6
Q7A3J8 PRELIMINARY; PRT; 961 AA.
ID Q7A3J8;
AC Q7A3J8;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE FnBb protein.
GN Name=fnbB; OrderedLocustNames=SA2290;
OS Staphylococcus aureus (strain N315).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxId=158879;
RN [1]
RN SEQUENCE FROM N.A.
RP MEDLINE=21311952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2;
RX Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Iian J.-Q., Ito T.,
RA Kanamori M., Matsunami H., Maruyama A., Murakami H., Hosoyama A.,
RA Mizutani U.I., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
RA Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
RA Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
RA Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
RT "Whole genome sequencing of methicillin-resistant Staphylococcus
RT aureus ";
RL Lancet 357:1225-1240(2001).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC an amide bond (By similarity).
CC EMBL: AP003137; BAB43593.1; -.
DR GO: GO:0009986; C:cell surface; IEA.
DR GO: GO:0005618; C:cell wall; IEA.
DR GO: GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO: GO:0016020; C:membrane; IEA.
DR GO: GO:0007155; P:cell adhesion; IEA.
DR InterPro: IPR008966; Adhes_bact.
DR InterPro: IPR004237; Fn_bind.
DR InterPro: IPR005877; Gpos_YsIRK.
DR InterPro: IPR01899; Gram_pos_anchor.
DR Pfam: PF02986; Fn_bind; 1.
DR Pfam: PF00746; Gram_pos_anchor; 1.
DR Pfam: PF04650; YsIRK_signal; 1.
DR TIGRFAMs: TIGR01167; LpXTG_anchor; 1.
DR TIGRFAMs: TIGR01168; YsIRK_signal; 1.
DR PROSITE: PS50847; GRAM_POS_ANCHORING; 1.
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KW Cell wall, Complete proteome; Peptidoglycan-anchor.
SQ SEQUENCE 961 AA: 106010 MW: 364940FB84EA4101 CRC64;

Query Match          91.6%; Score 109; DB 2; Length 961;
Best Local Similarity 95.0%; Pred. No. 8.4e-08;
Matches 19; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KPSYQFGHNSVDPEDTLP 20
   ||:|||||
Db 784 KPNYQFGHNSVDPEDTLP 803

RESULT 7
O6GDUS PRELIMINARY; PRT; 965 AA.
AC O6GDUS;
DT 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DE 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE Fibronectin-binding protein.
CN Name=fnbA, OrderedLocusNames=SKR2580;
OC Staphylococcus aureus (strain MRSA252).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=282458;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=15213324; DOI=10.1073/pnas.0402521101;
RA Holden M.T.G., Feil E.J., Lindsay J.A., Peacock S.J., Day N.P.J.,
RA Enright M.C., Foster T.J., Moore C.E., Hurst L., Atkin R., Barron A.,
RA Baason N., Bentley S.D., Chillingworth C., Chillingworth T.,
RA Churcher C., Clark L., Cotton C., Cronin A., Doggett J., Dowd L.,
RA Feltwell T., Hance Z., Harris B., Hauser H., Holtroyd S., Jørgels K.,
RA James K.D., Lennard N., Line A., Mayes R., Moule S., Mungall K.,
RA Ommond D., Quail M.A., Rabinowitch E., Rutherford K.M., Sanders M.,
RA Sharp S., Simmonds M., Stevens K., Whitehead S., Barrall B.G.,
RA Spratt B.G., Parkhill J.;
RT "Complete genomes of two clinical Staphylococcus aureus strains:
RT evidence for the rapid evolution of virulence and drug resistance.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:9786-9791(2004)
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC an amide bond (By similarity).
CC EMBL: BX571856; CAC41560.1; -
DR GO: GO:0009986; C:cell surface; IEA.
DR GO: GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO: GO:0016020; C:membrane; IEA.
DR GO: GO:007155; P:cell adhesion; IEA.
DR InterPro: IPR008966; Adhes_bact.
DR InterPro: IPR004237; Fn_bind.
DR InterPro: IPR005877; Gpos_Ysirk.
DR InterPro: IPR001899; Gram_pos_anchor.
DR Pfam: PF02986; Fn_bind.1.
DR Pfam: PF00746; Gram_pos_anchor.1.
DR Pfam: PF04650; Ysirk_signal.1.
DR TIGRFAMs: TIGR01167; LPXTG_anchor.1.
DR TIGRFAMs: TIGR01168; Ysirk_signal.1.
DR PROSITE: PS0847; GRAM_POS_ANCHORING.1.
KW Cell wall, Complete proteome; Peptidoglycan-anchor.
SQ SEQUENCE 965 AA: 105691 MW: 298281321640551 CRC64;

Query Match          91.6%; Score 109; DB 2; Length 965;
Best Local Similarity 95.0%; Pred. No. 8.5e-08;
Matches 19; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KPSYQFGHNSVDPEDTLP 20
   ||:|||||
Db 802 KPNYQFGHNSVDPEDTLP 821

RESULT 8
O8NUU7 PRELIMINARY; PRT; 1015 AA.
AC O8NUU7;
RT 01-OCT-2002 (TREMBLrel. 22, Created)
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DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Fnb protein.
CN Name=fnb, OrderedLocusNames=MM2421;
OC Staphylococcus aureus (strain MM2).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=196620;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22040717; PubMed=12044378; DOI=10.1016/S0140-6736(02)08713-5;
RA Baba T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Oguchi A.,
RA Nagai Y., Iwano N., Asano K., Naito T., Kuroda H., Cui L.,
RA Yamamoto K., Hiramatsu K.;
RT "Genome and virulence determinants of high virulence community-
RT acquired MRSA.";
RL Lancet 359:1819-1827(2002).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC an amide bond (By similarity).
CC EMBL: AP004830; BAB96286.1; -
DR GO: GO:0009986; C:cell surface; IEA.
DR GO: GO:0005618; C:cell wall; IEA.
DR GO: GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO: GO:0016020; C:membrane; IEA.
DR GO: GO:007155; P:cell adhesion; IEA.
DR InterPro: IPR008966; Adhes_bact.
DR InterPro: IPR004237; Fn_bind.
DR InterPro: IPR005877; Gpos_Ysirk.
DR InterPro: IPR001899; Gram_pos_anchor.
DR Pfam: PF02986; Fn_bind.1.
DR Pfam: PF00746; Gram_pos_anchor.1.
DR Pfam: PF04650; Ysirk_signal.1.
DR TIGRFAMs: TIGR01167; LPXTG_anchor.1.
DR TIGRFAMs: TIGR01168; Ysirk_signal.1.
DR PROSITE: PS0847; GRAM_POS_ANCHORING.1.
KW Cell wall, Complete proteome; Peptidoglycan-anchor.
SQ SEQUENCE 1015 AA: 111145 MW: D0F9281BB64D44D2 CRC64;

Query Match          91.6%; Score 109; DB 2; Length 1015;
Best Local Similarity 95.0%; Pred. No. 9e-08;
Matches 19; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KPSYQFGHNSVDPEDTLP 20
   ||:|||||
Db 838 KPNYQFGHNSVDPEDTLP 857

RESULT 9
O6G6H3 PRELIMINARY; PRT; 1015 AA.
AC O6G6H3;
ID O6G6H3;
DT 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DE Fibronectin-binding protein.
CN OrderedLocusNames=SMS2388;
OC Staphylococcus aureus (strain MSSA476).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=282459;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=15213324; DOI=10.1073/pnas.0402521101;
RA Holden M.T.G., Feil E.J., Lindsay J.A., Peacock S.J., Day N.P.J.,
RA Enright M.C., Foster T.J., Moore C.E., Hurst L., Atkin R., Barron A.,
RA Baason N., Bentley S.D., Chillingworth C., Chillingworth T.,
RA Churcher C., Clark L., Cotton C., Cronin A., Doggett J., Dowd L.,
RA Feltwell T., Hance Z., Harris B., Hauser H., Holtroyd S., Jørgels K.,
RA James K.D., Lennard N., Line A., Mayes R., Moule S., Mungall K.,
RA Ommond D., Quail M.A., Rabinowitch E., Rutherford K.M., Sanders M.,
RA Sharp S., Simmonds M., Stevens K., Whitehead S., Barrall B.G.,
RA Spratt B.G., Parkhill J.;
RT "Complete genomes of two clinical Staphylococcus aureus strains:
RT evidence for the rapid evolution of virulence and drug resistance.";
```

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RL Proc. Natl. Acad. Sci. U.S.A. 101:9786-9791(2004).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
   an amide bond (By similarity).
DR EMBL: BX571857; CAG44202.1; -.
DR GO: GO:0009986; C:cell surface; IEA.
DR GO: GO:0005618; C:cell wall; IEA.
DR GO: GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO: GO:0016020; C:membrane; IEA.
DR GO: GO:0007155; P:cell adhesion; IEA.
DR InterPro: IPR008966; Adhes_bact.
DR InterPro: IPR004237; Fn_bind.
DR InterPro: IPR005877; Gpos_YsIRK.
DR InterPro: IPR001899; Gram_pos_anchor.
DR Pfam: PF02986; Fn_bind; 1.
DR Pfam: PF00746; Gram_pos_anchor; 1.
DR TIGRFAMs: TIGR01167; LPXTG_anchor; 1.
DR TIGRFAMs: TIGR01168; YsIRK_signal; 1.
DR PROSITE: PS50847; GRAM_POS_ANCHORING; 1.
KW Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ SEQUENCE 1015 AA; 111145 MW; D0F9281BB64D4D2 CRC64;

Query Match          91.6%; Score 109; DB 2; Length 1015;
Best Local Similarity 95.0%; Pred. No. 9e-08;
Matches 19; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 KPSYQFGHNSVDFEDTLP 20
DB 838 KPNYQFGHNSVDFEDTLP 857

RESULT 10
O99RD2 PRELIMINARY; PRT; 1038 AA.
AC O99RD2;
DT 01-JUN-2001 (TRENBLREL. 17, Created)
DT 01-JUN-2001 (TRENBLREL. 17, Last sequence update)
DT 01-MAR-2004 (TRENBLREL. 26, Last annotation update)
DE Fibronectin-binding protein homolog.
DE Name=fnb; Ordered locusNames=SAV2503;
OS Staphylococcus aureus (strain MU50 / ATCC 700699).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=158878;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MU50 / ATCC 700699;
RX MEDLINE=21311952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2;
RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Lian J.-Q., Ito T.,
RA Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyma A.,
RA Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
RA Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
RA Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
RA Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
RT "Whole genome sequencing of methicillin-resistant Staphylococcus
   aureus.";
RL Lancet 357:1225-1240(2001).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
   an amide bond (By similarity).
DR EMBL: AP003137; BAB58665.1; -.
DR PIR: H90053; H90053.
DR GO: GO:0009986; C:cell surface; IEA.
DR GO: GO:0005618; C:cell wall; IEA.
DR GO: GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO: GO:0016020; C:membrane; IEA.
DR GO: GO:0007155; P:cell adhesion; IEA.
DR InterPro: IPR008966; Adhes_bact.
DR InterPro: IPR004237; Fn_bind.
DR InterPro: IPR005877; Gpos_YsIRK.
DR InterPro: IPR001899; Gram_pos_anchor.
DR Pfam: PF02986; Fn_bind; 1.
DR Pfam: PF00746; Gram_pos_anchor; 1.
DR TIGRFAMs: TIGR01167; LPXTG_anchor; 1.
DR TIGRFAMs: TIGR01168; YsIRK_signal; 1.
DR PROSITE: PS50847; GRAM_POS_ANCHORING; 1.
KW Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ SEQUENCE 1038 AA; 113618 MW; 666BF6BF2BFEB12 CRC64;

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DR TIGRFAMs: TIGR01167; LPXTG_anchor; 1.
DR TIGRFAMs: TIGR01168; YsIRK_signal; 1.
DR PROSITE: PS50847; GRAM_POS_ANCHORING; 1.
KW Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ SEQUENCE 1038 AA; 113618 MW; 666BF6BF2BFEB12 CRC64;

Query Match          91.6%; Score 109; DB 2; Length 1038;
Best Local Similarity 95.0%; Pred. No. 9.2e-08;
Matches 19; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 KPSYQFGHNSVDFEDTLP 20
DB 833 KPNYQFGHNSVDFEDTLP 852

RESULT 11
O7A3J7 PRELIMINARY; PRT; 1038 AA.
AC O7A3J7;
DT 05-JUL-2004 (TRENBLREL. 27, Created)
DT 05-JUL-2004 (TRENBLREL. 27, Last sequence update)
DT 05-JUL-2004 (TRENBLREL. 27, Last annotation update)
DE Fnb protein.
DE Name=fnb; Ordered locusNames=SA2291;
OS Staphylococcus aureus (strain N315).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=158879;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21311952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2;
RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Lian J.-Q., Ito T.,
RA Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyma A.,
RA Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
RA Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
RA Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
RA Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
RT "Whole genome sequencing of methicillin-resistant Staphylococcus
   aureus.";
RL Lancet 357:1225-1240(2001).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
   an amide bond (By similarity).
DR EMBL: AP003137; BAB43594.1; -.
DR GO: GO:0009986; C:cell surface; IEA.
DR GO: GO:0005618; C:cell wall; IEA.
DR GO: GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO: GO:0016020; C:membrane; IEA.
DR GO: GO:0007155; P:cell adhesion; IEA.
DR InterPro: IPR008966; Adhes_bact.
DR InterPro: IPR004237; Fn_bind.
DR InterPro: IPR005877; Gpos_YsIRK.
DR InterPro: IPR001899; Gram_pos_anchor.
DR Pfam: PF02986; Fn_bind; 1.
DR Pfam: PF00746; Gram_pos_anchor; 1.
DR TIGRFAMs: TIGR01167; LPXTG_anchor; 1.
DR TIGRFAMs: TIGR01168; YsIRK_signal; 1.
DR PROSITE: PS50847; GRAM_POS_ANCHORING; 1.
KW Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ SEQUENCE 1038 AA; 113618 MW; 666BF6BF2BFEB12 CRC64;

Query Match          91.6%; Score 109; DB 2; Length 1038;
Best Local Similarity 95.0%; Pred. No. 9.2e-08;
Matches 19; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 KPSYQFGHNSVDFEDTLP 20
DB 833 KPNYQFGHNSVDFEDTLP 852

RESULT 12
O9AEP9 PRELIMINARY; PRT; 152 AA.

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AC 09AEP9;
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Fibronectin-binding protein (fragment).
GN Name=fnb;
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1280;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CMRSA-1;
RX MEDLINE=21246681; PubMed=11349044;
RX DOI=10.1128/IAI.69.6.3791-3799.2001;
RX Rice K., Huebner M., Var D., McGavin M.J.;
RT "Variation in fibronectin binding and fnb locus polymorphisms in
RT Staphylococcus aureus: identification of antigenic variation in a
RT fibronectin binding protein adhesin of the epidemic CMRSA-1 strain of
RT methicillin-resistant S. aureus."
RT Infect. Immun. 69:3791-3799(2001).
DR EMBL, AY029184; AAK31588.1; -.
FT NON_TER 1
FT NON_TER 152
SQ SEQUENCE 152 AA; 17193 MW; CFA3913C2B11C025 CRC64;

Query Match 84.0%; Score 100; DB 2; Length 152;
Best Local Similarity 85.0%; Pred. No. 2.7e-07;
Matches 17; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 KPSYQFGHNSVDEPDTLP 20
Db 130 KPSYQFGHNSVDEPDTLP 149

RESULT 13
FBL3 HUMAN STANDARD; PRT; 493 AA.
AC Q12805;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE EGF-containing fibulin-like extracellular matrix protein 1 precursor
DE (Fibulin-3) (FIBL-3) (Fibrillin-like protein) (Extracellular protein
DE SI-5).
CN Name=EFEMP1; Synonyms=FBLN3, FBLN;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. AND POSSIBLE ALTERNATIVE SPLICING.
RC TISSUE=Skin;
RX MEDLINE=95097983; PubMed=7799918;
RX Lecka-Czernik B., Lumpkin C.K. Jr., Goldstein S.;
RT "An overexpressed gene transcript in senescent and quiescent human
RT fibroblasts encoding a novel protein in the epidermal growth factor-
RT like repeat family stimulates DNA synthesis."
RT Mol. Cell. Biol. 15:120-128(1995).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=97001163; PubMed=8812496; DOI=10.1006/geno.1996.0402;
RX Ikegawa S., Toda T., Okui K., Nakamura Y.;
RT "Structure and chromosomal assignment of the human SI-5 gene (FBLN)
RT that is highly homologous to fibrillin."
RX Genomics 35:590-592(1996).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=20068041; PubMed=10601734; DOI=10.1016/S0945-053X(99)00038-4;
RX Giltay R., Timpl R., Kostka G.;
RT "Sequence, recombinant expression and tissue localization of two novel
RT extracellular matrix proteins, fibulin-3 and fibulin-4."
RX Matrix Biol. 18:469-480(1999).
RN [4]

```

```

RP SEQUENCE FROM N.A. (ISOFORM 1).
RC TISSUE=Lung;
RX MEDLINE=22386257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RX Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RX Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RX Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RX Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh P.,
RX Diatchenko L., Marusik K., Farmer A.A., Rubin G.M., Hong L.,
RX Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RX Brownstein M.J., Uedin T.B., Teshiguchi S., Carninci P., Prange C.,
RX Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RX Boesak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RX Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Huylk S.W.,
RX Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RX Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RX Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RX Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RX Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RX Butlerfield Y.S.N., Krzywinski M.I., Skalska U., Smallue D.E.,
RX Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [5]
RP VARIANT DHRD TRP-345, AND VARIANT PHE-220.
RX MEDLINE=99295941; PubMed=10369267; DOI=10.1038/9722;
RX Stone E.M., Lotery A.J., Munier F.L., Heon E., Piguet B., Guymer R.H.,
RX Vandenburgh K., Cousin P., Nishimura D., Swiderki R.E., Silvestri G.,
RX Mackey D.A., Hagerman G.S., Bird A.C., Sheffield V.C.,
RX Schorderet D.F.;
RT "A single EFEMP1 mutation associated with both marattia Leventinese
RT and Doyle honeycomb retinal dystrophy."
RT Nat. Genet. 22:199-202(1999).
RN [6]
RP VARIANT DHRD TRP-345.
RX MEDLINE=21278111; PubMed=11384588; DOI=10.1016/S0002-9394(00)00926-0;
RX Matsunoto M., Traboulsi E.I.;
RT "Dominant radial drusen and Arg345Trp EFEMP1 mutation."
RX Am. J. Ophthalmol. 131:810-812(2001).
RN [7]
RP SUBCELLULAR LOCATION: Secreted.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC Comment=Experimental confirmation may be lacking for some
CC isoforms;
CC Name=1;
CC IsoId=Q12805-1; Sequence=Displayed;
CC Name=2;
CC IsoId=Q12805-2; Sequence=VSP_001392;
CC Name=3;
CC IsoId=Q12805-3; Sequence=VSP_001393;
CC Name=4;
CC IsoId=Q12805-4; Sequence=VSP_001394;
CC -1- DISEASE: Defects in EFEMP1 are a cause of Doyle honeycomb retinal
CC dystrophy (DHRD) [MIM:126600]; also known as marattia Leventinese
CC (MLVT) OR ML. DHRD is an autosomal dominant disease characterized
CC by yellow-white deposits known as drusen that accumulate beneath
CC the retinal pigment epithelium.
CC -1- SIMILARITY: Belongs to the fibulin family.
CC -1- SIMILARITY: Contains 6 EGF-like domains.
CC -1- DATABASE: NAME=Mutations of the EFEMP1 gene;
CC NOTE=Retina International's Scientific Newsletter;
CC WWW="http://www.retina-international.com/sci-news/efempmut.htm".
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.ebi.ac.uk/announcements
CC or send an email to license@ebi.ac.uk).
CC -----
CC DR EMBL, U03877; AAA65590.1; -.
CC EMBL, BC014410; AAH14410.1; -.

```


RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy U., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skalska U., Smallus D.E., Scherch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RT Proc. Natl. Acad. Sci. U.S.A. 99:16999-16903(2002).
 [2]
 RN
 RP SEQUENCE FROM N.A.
 RC STRAIN=FVB/N; TISSUE=colon;
 RA Strausberg R.;
 RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC031184; AAH31184.1; -.
 DR HSSP; P35555; IEMN.
 DR MGD; MGI:133998; Etempl.
 DR GO; GO:0005615; C:extracellular space; TAS.
 DR InterPro; IPR000152; Asx_hydroxyl_S.
 DR InterPro; IPR00742; EGF_2.
 DR InterPro; IPR001881; EGF_Ca.
 DR InterPro; IPR006209; EGF_like.
 DR InterPro; IPR009030; Grow_fac_recept.
 DR Pfam; PF07645; EGF_CA; 5.
 DR SMART; SM00179; EGF_CA; 4.
 DR PROSITE; PS00010; ASX_HYDROXYL; 4.
 DR PROSITE; PS01186; EGF_2; 4.
 DR PROSITE; PS50026; EGF_3; 4.
 DR PROSITE; PS01187; EGF_CA; 5.
 KM EGF-like domain; Matrix protein.
 SQ SEQUENCE 387 AA; 43334 MW; EE88DC9D1422C1C7 CRC64;

Query Match 44.5%; Score 53; DB 2; Length 387;
 Best Local Similarity 50.0%; Pred. No. 13;
 Matches 10; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

QY 2 PSYQFGHNSVDFEDTLPP 21
 DB 97 PGYQKRGECVDIDECTVPP 116

Search completed: October 22, 2005, 04:10:26
 Job time : 52.4314 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 25, 2005, 18:43:07 ; Search time 59.0973 Seconds
(without alignments)
137.434 Million cell updates/sec

Title: US-10-731-238-34
Perfect score: 118
Sequence: 1 PASYOFPNNSVDFEEDTLPK 21

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:*

- 1: geneeqp1980s:*
- 2: geneeqp1990s:*
- 3: geneeqp2000s:*
- 4: geneeqp2001s:*
- 5: geneeqp2002s:*
- 6: geneeqp2003as:*
- 7: geneeqp2003bs:*
- 8: geneeqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	118	100.0	21	2	AAW65690
2	98	83.1	21	2	AAW65666
3	98	83.1	21	2	AAW65676
4	98	83.1	22	2	AAW65659
5	95	80.5	21	2	AAW65670
6	93	78.8	21	2	AAW65671
7	89	75.4	21	2	AAW65665
8	89	75.4	22	2	AAW65665
9	89	75.4	37	4	AAW65662
10	89	75.4	38	1	AAW65662
11	89	75.4	134	2	AAW65662
12	89	75.4	139	2	AAW65662
13	89	75.4	1018	1	AAW65662
14	89	75.4	1018	1	AAW65662
15	89	75.4	1018	1	AAW65662
16	89	75.4	1018	6	AAW65662
17	89	75.4	1018	6	AAW65662
18	89	75.4	1027	6	AAW65662
19	86	72.9	961	6	AAW65662
20	86	72.9	978	4	AAW65662
21	86	72.9	1001	4	AAW65662
22	86	72.9	1038	6	AAW65662
23	85	72.0	21	2	AAW65672
24	84	71.2	21	2	AAW65679
25	84	71.2	21	2	AAW65679

26	83	70.3	21	2	AAW65680
27	83	70.3	21	2	AAW65683
28	83	70.3	21	2	AAW65684
29	83	70.3	21	2	AAW65686
30	83	70.3	21	2	AAW65674
31	82	69.5	21	2	AAW65685
32	82	69.5	21	2	AAW65687
33	82	69.5	21	2	AAW65681
34	82	69.5	77	2	AAW65681
35	82	69.5	101	2	AAW65681
36	82	69.5	113	2	AAW65681
37	82	69.5	124	2	AAW65681
38	82	69.5	128	2	AAW65681
39	82	69.5	130	2	AAW65680
40	82	69.5	130	2	AAW65680
41	82	69.5	130	2	AAW65680
42	82	69.5	130	2	AAW65680
43	82	69.5	134	2	AAW65680
44	82	69.5	162	2	AAW65680
45	82	69.5	164	2	AAW65680

ALIGNMENTS

RESULT 1
AAW65690
ID AAW65690 standard; peptide: 21 AA.
AC AAW65690;
DT 16-OCT-1998 (first entry)
XX
DE Fibronectin binding protein-derived peptide #34.
XX
KW microbial surface components recognising adhesive matrix molecule;
KW MSCRAMM; fibronectin; fibronectin-binding protein; antibody; epitope;
KW antibiotic; bacterial infection; antibiotic-resistant strain.
XX
OS Synthetic.
OS Staphylococcus aureus.
XX
PN WO9831389-A2.
XX
PD 23-JUL-1998.
XX
PF 21-JAN-1998; 98WO-US001222.
XX
PR 21-JAN-1997; 97US-0036139P.
XX
PA (TEXA) UNIV TEXAS A & M SYSTEM.
XX
PI Hoeek M, Patti JM, House-Pompeo KL, Speziale P, Joh D;
PI McGavin MJ;
XX
DR WPI, 1998-413816/35.
XX
PT Antibody that binds to fibronectin-binding protein, preventing its
PT binding to fibronectin - used to treat or prevent bacterial infection,
PT especially by Staphylococci and Streptococci.
XX
PS Example 8, Page 101, 201pp; English.
XX
CC The invention relates to antibodies that bind to a fibronectin-binding
CC domain of a fibronectin-binding protein, and inhibit binding of the
CC protein to a fibronectin. Also claimed are: (1) isolated peptides of a
CC fibronectin-binding protein that do not bind to fibronectin; (2) fusion
CC protein containing at least one peptide of a fibronectin-binding protein
CC linked to a second amino acid sequence; (3) nucleic acid encoding the
CC isolated peptide of (1). Antibodies, the isolated peptides of (1) and the
CC nucleic acids are all useful for immunisation (active or passive) and (b)
CC inhibiting binding of bacteria to fibronectin for preventing or treating
CC infection in humans or other animals, particularly by staphylococci or

CC streptococci, e.g. meningitis, otitis media, pneumonia, endocarditis,
 CC mastitis in cattle, abortion in horses and many others. Since the
 CC antibodies block binding of bacteria, they should be effective against
 CC antibiotic-resistant strains, and may replace antibiotic therapy or
 CC increase its effectiveness. Sequences AAW65670-90 represent a series of
 CC synthetic peptides based on the D3 repeat of *S. aureus* fibronectin
 CC binding protein A. They were synthesised to contain a proline residue at
 CC each position through the sequence (ie a proline scan)

XX SQ Sequence 21 AA;
 Query Match 100.0%; Score 118; DB 2; Length 21;
 Best Local Similarity 100.0%; Pred. No. 1.5e-10;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 PASYPFPHNSVDFEEDTLPK 21
 |||||
 1 PASYPFPHNSVDFEEDTLPK 21

Db

RESULT 2
 AAW65666
 ID AAW65666 standard; peptide; 21 AA.
 XX AAW65666;
 AC
 XX 16-OCT-1998 (first entry)
 DT
 XX Fibronectin binding protein-derived peptide #10.
 DE
 XX microbial surface components recognising adhesive matrix molecule;
 KM MSCRAMM; fibronectin; fibronectin-binding protein; antibody; epitope;
 KW antibiotic; bacterial infection; antibiotic-resistant strain.
 XX Synthetic.
 OS Staphylococcus aureus.
 XX WO9813389-A2.
 XX 23-JUL-1998.
 PD
 XX 21-JAN-1998; 98WO-US001222.
 PF
 XX 21-JAN-1997; 97US-0036139P.
 PR
 XX (TEXA) UNIV TEXAS A & M SYSTEM.
 PA
 XX Hoeoek M, Patti JM, House-Pompeo KL, Speciale P, Joh D;
 PI Mcgavin MJ;
 PT WPI; 1998-413816/35.
 XX

XX Antibody that binds to fibronectin-binding protein, preventing its
 PT binding to fibronectin - used to treat or prevent bacterial infection,
 PT especially by Staphylococci and Streptococci.

PS Example 2; Page 92; 201pp; English.

XX The invention relates to antibodies that bind to a fibronectin-binding
 CC domain of a fibronectin-binding protein, and inhibit binding of the
 CC protein to fibronectin. Also claimed are: (1) isolated peptides of a
 CC fibronectin-binding protein that do not bind to fibronectin; (2) fusion
 CC protein containing at least one peptide of a fibronectin-binding protein
 CC linked to a second amino acid sequence; (3) nucleic acid encoding the
 CC isolated peptide of (1). Antibodies, the isolated peptides of (1) and the
 CC nucleic acids are all useful for immunisation (active or passive) and (by
 CC inhibiting binding of bacteria to fibronectin) for preventing or treating
 CC infection in humans or other animals, particularly by staphylococci or
 CC streptococci, e.g. meningitis, otitis media, pneumonia, endocarditis,
 CC mastitis in cattle, abortion in horses and many others. Since the
 CC antibodies block binding of bacteria, they should be effective against
 CC antibiotic-resistant strains, and may replace antibiotic therapy or
 CC increase its effectiveness. Sequences AAW65659-68 represent synthetic
 CC

CC epitopes from the fibronectin binding domains DU and DI-D4 of the *S.*
 CC aureus fmbA gene

XX SQ Sequence 21 AA;
 Query Match 83.1%; Score 98; DB 2; Length 21;
 Best Local Similarity 94.7%; Pred. No. 1.5e-07;
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 3 SYQFPCHNSVDFEEDTLPK 21
 |||||
 3 SYQFPCHNSVDFEEDTLPK 21

Db

RESULT 3
 AAW65676
 ID AAW65676 standard; peptide; 21 AA.
 XX AAW65676;
 AC
 XX 16-OCT-1998 (first entry)
 DT
 XX Fibronectin binding protein-derived peptide #20.
 DE
 XX microbial surface components recognising adhesive matrix molecule;
 KM MSCRAMM; fibronectin; fibronectin-binding protein; antibody; epitope;
 KW antibiotic; bacterial infection; antibiotic-resistant strain.
 XX Synthetic.
 OS Staphylococcus aureus.
 XX WO9813389-A2.
 XX 23-JUL-1998.
 PD
 XX 21-JAN-1998; 98WO-US001222.
 PF
 XX 21-JAN-1997; 97US-0036139P.
 PR
 XX (TEXA) UNIV TEXAS A & M SYSTEM.
 PA
 XX Hoeoek M, Patti JM, House-Pompeo KL, Speciale P, Joh D;
 PI Mcgavin MJ;
 PT WPI; 1998-413816/35.
 XX

XX Antibody that binds to fibronectin-binding protein, preventing its
 PT binding to fibronectin - used to treat or prevent bacterial infection,
 PT especially by Staphylococci and Streptococci.

PS Example 8; Page 100; 201pp; English.

XX The invention relates to antibodies that bind to a fibronectin-binding
 CC domain of a fibronectin-binding protein, and inhibit binding of the
 CC protein to fibronectin. Also claimed are: (1) isolated peptides of a
 CC fibronectin-binding protein that do not bind to fibronectin; (2) fusion
 CC protein containing at least one peptide of a fibronectin-binding protein
 CC linked to a second amino acid sequence; (3) nucleic acid encoding the
 CC isolated peptide of (1). Antibodies, the isolated peptides of (1) and the
 CC nucleic acids are all useful for immunisation (active or passive) and (by
 CC inhibiting binding of bacteria to fibronectin) for preventing or treating
 CC infection in humans or other animals, particularly by staphylococci or
 CC streptococci, e.g. meningitis, otitis media, pneumonia, endocarditis,
 CC mastitis in cattle, abortion in horses and many others. Since the
 CC antibodies block binding of bacteria, they should be effective against
 CC antibiotic-resistant strains, and may replace antibiotic therapy or
 CC increase its effectiveness. Sequences AAW65670-90 represent a series of
 CC synthetic peptides based on the D3 repeat of *S. aureus* fibronectin
 CC binding protein A. They were synthesised to contain a proline residue at
 CC each position through the sequence (ie a proline scan)

XX Sequence 21 AA;
 SQ

Query Match 83.1%; Score 98; DB 2; Length 21;
 Best Local Similarity 94.7%; Pred. No. 1.5e-07;
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 SYOFPPHNSVDFEEDTLPK 21
 DB 3 SYOFPPHNSVDFEEDTLPK 21

RESULT 4

AAW65669
 ID AAW65669 standard; peptide; 22 AA.

AAW65669;

16-OCT-1998 (first entry)

Peptide #13.

microbial surface components recognising adhesive matrix molecule;
 MSCRAMM; fibronectin; fibronectin-binding protein; antibody; epitope;
 antibiotic; bacterial infection; antibiotic-resistant strain.

Synthetic.

WO9831389-A2.

23-JUL-1998.

21-JAN-1998; 98WO-US001222.

21-JAN-1997; 97US-0036139P.

(TEXA) UNIV TEXAS A & M SYSTEM.

Hoecek M, Patti JM, House-Pompeo KL, Speziale P, Joh D;

McGavin MJ;

WPI; 1998-413816/35.

Antibody that binds to fibronectin-binding protein, preventing its
 binding to fibronectin - used to treat or prevent bacterial infection,
 especially by Staphylococci and Streptococci.

Example 3; Page 93; 201pp; English.

The invention relates to antibodies that bind to a fibronectin-binding
 domain of a fibronectin-binding protein, and inhibit binding of the
 protein to fibronectin. Also claimed are: (1) isolated peptides of a
 fibronectin-binding protein that do not bind to fibronectin; (2) fusion
 protein containing at least one peptide of a fibronectin-binding protein
 linked to a second amino acid sequence; (3) nucleic acid encoding the
 isolated peptide of (1). Antibodies, the isolated peptides of (1) and the
 nucleic acids are all useful for immunisation (active or passive) and (b)
 inhibiting binding of bacteria to fibronectin) for preventing or treating
 infection in humans or other animals, particularly by staphylococci or
 streptococci, e.g. meningitis, otitis media, pneumonia, endocarditis,
 mastitis in cattle, abortion in horses and many others. Since the
 antibodies block binding of bacteria, they should be effective against
 antibiotic-resistant strains, and may replace antibiotic therapy or
 increase its effectiveness. The present sequence is shown in the
 specification

Sequence 22 AA:

Query Match 83.1%; Score 98; DB 2; Length 22;
 Best Local Similarity 94.7%; Pred. No. 1.5e-07;
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 SYOFPPHNSVDFEEDTLPK 21
 DB 3 SYOFPPHNSVDFEEDTLPK 21

RESULT 5
 AAW65670
 ID AAW65670 standard; peptide; 21 AA.

AAW65670;

16-OCT-1998 (first entry)

Fibronectin binding protein-derived peptide #14.

microbial surface components recognising adhesive matrix molecule;
 MSCRAMM; fibronectin; fibronectin-binding protein; antibody; epitope;
 antibiotic; bacterial infection; antibiotic-resistant strain.

Synthetic.

Staphylococcus aureus.

WO9831389-A2.

23-JUL-1998.

21-JAN-1998; 98WO-US001222.

21-JAN-1997; 97US-0036139P.

(TEXA) UNIV TEXAS A & M SYSTEM.

Hoecek M, Patti JM, House-Pompeo KL, Speziale P, Joh D;

McGavin MJ;

WPI; 1998-413816/35.

Antibody that binds to fibronectin-binding protein, preventing its
 binding to fibronectin - used to treat or prevent bacterial infection,
 especially by Staphylococci and Streptococci.

Example 8; Page 100; 201pp; English.

The invention relates to antibodies that bind to a fibronectin-binding
 domain of a fibronectin-binding protein, and inhibit binding of the
 protein to fibronectin. Also claimed are: (1) isolated peptides of a
 fibronectin-binding protein that do not bind to fibronectin; (2) fusion
 protein containing at least one peptide of a fibronectin-binding protein
 linked to a second amino acid sequence; (3) nucleic acid encoding the
 isolated peptide of (1). Antibodies, the isolated peptides of (1) and the
 nucleic acids are all useful for immunisation (active or passive) and (b)
 inhibiting binding of bacteria to fibronectin) for preventing or treating
 infection in humans or other animals, particularly by staphylococci or
 streptococci, e.g. meningitis, otitis media, pneumonia, endocarditis,
 mastitis in cattle, abortion in horses and many others. Since the
 antibodies block binding of bacteria, they should be effective against
 antibiotic-resistant strains, and may replace antibiotic therapy or
 increase its effectiveness. Sequences AAW65670-90 represent a series of
 synthetic peptides based on the D3 repeat of S. aureus fibronectin
 binding protein A. They were synthesised to contain a proline residue at
 each position through the sequence (ie a proline scan)

Sequence 21 AA:

Query Match 80.5%; Score 95; DB 2; Length 21;
 Best Local Similarity 85.7%; Pred. No. 4.1e-07;
 Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 PASYOFPFHNSVDFEEDTLPK 21
 DB 1 PASYOFPFHNSVDFEEDTLPK 21

RESULT 6
 AAW65671
 ID AAW65671 standard; peptide; 21 AA.

```

AC AAM65671;
XX
XX 16-OCT-1998 (first entry)
XX
XX Fibronectin binding protein-derived peptide #15.
DE
XX
XX microbial surface components recognising adhesive matrix molecule;
KM MGRMM; fibronectin; fibronectin-binding protein; antibody; epitope;
KW antibiotic; bacterial infection; antibiotic-resistant strain.
XX
XX Synthetic.
OS Staphylococcus aureus.
XX
XX MO9831389-A2.
XX
XX 23-JUL-1998.
XX
XX 21-JAN-1998; 98WO-US001222.
XX
XX 21-JAN-1997; 97US-0036139P.
XX
XX (TEXA ) UNIV TEXAS A & M SYSTEM.
XX
XX Hoeoek M, Patcl JM, House-Pompeo KL, Speciale P, Joh D;
PI McGavin MJ;
XX
XX WPI; 1998-413816/35.
XX
XX Antibody that binds to fibronectin-binding protein, preventing its
PT binding to fibronectin - used to treat or prevent bacterial infection,
PT especially by Staphylococci and Streptococci.
XX
XX Example 8; Page 100; 201pp; English.
XX
XX The invention relates to antibodies that bind to a fibronectin-binding
CC domain of a fibronectin-binding protein, and inhibit binding of the
CC protein to fibronectin. Also claimed are: (1) isolated peptides of a
CC fibronectin-binding protein that do not bind to fibronectin; (2) fusion
CC protein containing at least one peptide of a fibronectin-binding protein
CC linked to a second amino acid sequence; (3) nucleic acid encoding the
CC isolated peptide of (1). Antibodies, the isolated peptides of (1) and the
CC nucleic acids are all useful for immunisation (active or passive) and (by
CC inhibiting binding of bacteria to fibronectin) for preventing or treating
CC infection in humans or other animals, particularly by staphylococci or
CC streptococci, e.g. meningitis, otitis media, pneumonia, endocarditis,
CC mastitis in cattle, abortion in horses and many others. Since the
CC antibodies block binding of bacteria, they should be effective against
CC antibiotic-resistant strains, and may replace antibiotic therapy or
CC increase its effectiveness. Sequences AAM65670-90 represent a series of
CC synthetic peptides based on the D3 repeat of S. aureus fibronectin
CC binding protein A. They were synthesised to contain a proline residue at
CC each position throughout the sequence (ie a proline scan)
XX
XX Sequence 21 AA;
SQ
Query Match 78.8%; Score 93; DB 2; Length 21;
Best Local Similarity 90.0%; Pred. No. 8.2e-07;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY 2 ASYQFPNHSVDFEDTLPK 21
DB 2 ASYQFGHNSVDFEDTLPK 21

```

```

XX
XX microbial surface components recognising adhesive matrix molecule;
KM MGRMM; fibronectin; fibronectin-binding protein; antibody; epitope;
KW antibiotic; bacterial infection; antibiotic-resistant strain.
XX
XX Synthetic.
OS Staphylococcus aureus.
XX
XX MO9831389-A2.
XX
XX 23-JUL-1998.
XX
XX 21-JAN-1998; 98WO-US001222.
XX
XX 21-JAN-1997; 97US-0036139P.
XX
XX (TEXA ) UNIV TEXAS A & M SYSTEM.
XX
XX Hoeoek M, Patcl JM, House-Pompeo KL, Speciale P, Joh D;
PI McGavin MJ;
XX
XX WPI; 1998-413816/35.
XX
XX Antibody that binds to fibronectin-binding protein, preventing its
PT binding to fibronectin - used to treat or prevent bacterial infection,
PT especially by Staphylococci and Streptococci.
XX
XX Example 2; Page 92; 201pp; English.
XX
XX The invention relates to antibodies that bind to a fibronectin-binding
CC domain of a fibronectin-binding protein, and inhibit binding of the
CC protein to fibronectin. Also claimed are: (1) isolated peptides of a
CC fibronectin-binding protein that do not bind to fibronectin; (2) fusion
CC protein containing at least one peptide of a fibronectin-binding protein
CC linked to a second amino acid sequence; (3) nucleic acid encoding the
CC isolated peptide of (1). Antibodies, the isolated peptides of (1) and the
CC nucleic acids are all useful for immunisation (active or passive) and (by
CC inhibiting binding of bacteria to fibronectin) for preventing or treating
CC infection in humans or other animals, particularly by staphylococci or
CC streptococci, e.g. meningitis, otitis media, pneumonia, endocarditis,
CC mastitis in cattle, abortion in horses and many others. Since the
CC antibodies block binding of bacteria, they should be effective against
CC antibiotic-resistant strains, and may replace antibiotic therapy or
CC increase its effectiveness. Sequences AAM65659-68 represent synthetic
CC epitopes from the fibronectin binding domains DU and D1-D4 of the S.
CC aureus fnbA gene
XX
XX Sequence 21 AA;
SQ
Query Match 75.4%; Score 89; DB 2; Length 21;
Best Local Similarity 89.5%; Pred. No. 3.3e-06;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY 3 SYQFPNHSVDFEDTLPK 21
DB 3 SYQFGHNSVDFEDTLPK 21

```

```

RESULT 7
AAM65665
ID AAM65665 standard; peptide; 21 AA.
XX
XX AAM65665;
AC
XX 16-OCT-1998 (first entry)
DT
XX
XX Fibronectin binding protein-derived peptide #9.
DE

```

```

RESULT 8
AAR21340
ID AAR21340 standard; peptide; 22 AA.
XX
XX AAR21340;
AC
XX 25-MAR-2003 (revised)
DT 15-JUN-1992 (first entry)
XX
XX Fibronectin binding protein.
DE
XX FMBP; wound infection reduction; vaccination; mastitis;
KM Staphylococcal infections; D3.
KW
XX Synthetic.
OS

```

XX MO9202555-A.
 XX 20-FEB-1992.
 XX 10-AUG-1990; 90SE-00002617.
 XX 10-AUG-1990; 90SE-00002617.
 XX (ALFA) ALFA LAVAL AGRIC INT AB.
 XX Hook M, McGavin M, Raucci G;
 XX WPI; 1992-080035/10.
 XX
 XX New fibronectin binding peptide - combines with fusion peptide to form
 XX large antigen, used in immunisation, diagnosis and for treating wounds.
 XX
 XX Claim 1; Page 22; 33pp; English.
 XX
 XX The sequence comprises amino acids 17-33 of a tandem repeat, designated
 XX D3 of the fibronectin binding site of *Staphylococcus aureus* 8325-4 FMBP.
 XX The N-terminal DK may be replaced with H or K, and the C-terminal LKP may
 XX be replaced by either L, LP, or OH. The peptides were synthesised using
 XX standard methods and purified using reverse phase HPLC. The appropriate
 XX fractions were dialysed and lyophilised. Peptide sequencing was performed
 XX of the amino side chain of lysine. The carboxylic side chains were
 XX converted to glycine methyl esters. The phenyl side chains of tyrosine
 XX residues were oxidised. Chemically modified peptide D3 was compared to
 XX unmodified D3. Lysine and tyrosine modifications only partially
 XX diminished its activity whereas modification of aspartic/glutamic
 XX residues resulted in complete loss of activity. The peptide can be used
 XX for the prevention or reduction of the risk of wound infection. The
 XX peptide can be used to create a large antigen for vaccinating ruminants
 XX against mastitis caused by *Staphylococcal* infections. It can also be used
 XX to diagnose *Staphylococcal* infections using ELISA or DNA probes. (Updated
 XX on 25-MAR-2003 to correct PA field.)
 XX
 XX Sequence 22 AA:
 XX
 XX Query Match 75.4%; Score 89; DB 2; Length 22;
 XX Best Local Similarity 89.5%; Pred. No. 3.4e-06;
 XX Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 XX
 XX 3 SYQPPPHNSVDFEEDTLPK 21
 XX ||||| ||||| ||||| |||||
 XX 4 SYQFGHNSVDFEEDTLPK 22
 XX
 XX RESULT 9
 XX AAB91958
 XX ID AAB91958 standard; peptide; 37 AA.
 XX
 XX AAB91958;
 XX
 XX 22-JUN-2001 (first entry)
 XX
 XX Fibronectin fragment and fibrin related peptide SEQ ID NO:1134.
 XX
 XX Protection; endogenous therapeutic peptide; peptidase; conjugation;
 XX blood component; modification; succinimidy1; maleimido group; amino;
 XX hydroxy1; thiol; hormone; growth factor; neurotransmitter.
 XX
 XX Homo sapiens.
 XX Synthetic.
 XX
 XX MO200069900-A2.
 XX
 XX 23-NOV-2000.
 XX
 XX 17-MAY-2000; 2000MO-US013576.
 XX

PR 17-MAY-1999; 99US-0134406P.
 PR 10-SEP-1998; 99US-0153406P.
 PR 15-OCT-1999; 99US-0159783P.
 XX
 XX (CONJ-) CONJUCHEM INC.
 XX
 XX Bridon DP, Ezrin AM, Milner PG, Holmes DL, Thibaudau K;
 XX WPI; 2001-112059/12.
 XX
 XX Modifying and attaching therapeutic peptides to albumin prevents
 XX peptidase degradation, useful for increasing length of in vivo activity.
 XX
 XX Disclosure; Page 566; 733pp; English.
 XX
 XX The present invention describes a modified therapeutic peptide (I)
 XX comprising a therapeutically active amino acid region (II) and a
 XX reactive group (II) (e.g. succinimidy1 and maleimido groups) attached to
 XX a less therapeutically active amino acid region (IV), which covalently
 XX bonds with amino/hydroxy1/thiol groups on blood components to form a
 XX peptide stable therapeutic peptide composed of 3-50 amino acids.
 XX (I) are useful for modifying therapeutic peptides e.g. hormones, growth
 XX factors and neurotransmitters, to protect them from peptidase activity in
 XX vivo for the treatment of various disorders. Endogenous therapeutic
 XX peptides are not suitable as drug candidates as they require frequent
 XX administration due to rapid degradation by peptidases in the body.
 XX Modifying and attaching therapeutic peptides to albumin prevents or
 XX reduces the action of peptidases to increase length of activity (half
 XX life) and specificity as bonding to large molecules decreases
 XX intracellular uptake and interference with physiological processes.
 XX AAB90829 to AAB92441 represent peptides which can be used in the
 XX exemplification of the present invention
 XX
 XX Sequence 37 AA:
 XX
 XX Query Match 75.4%; Score 89; DB 4; Length 37;
 XX Best Local Similarity 89.5%; Pred. No. 6.1e-06;
 XX Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 XX
 XX 3 SYQPPPHNSVDFEEDTLPK 21
 XX ||||| ||||| ||||| |||||
 XX 18 SYQFGHNSVDFEEDTLPK 36
 XX
 XX RESULT 10
 XX AAP80662
 XX ID AAP80662 standard; protein; 38 AA.
 XX
 XX AAP80662;
 XX
 XX 25-MAR-2003 (revised)
 XX DT 07-OCT-1990 (first entry)
 XX
 XX Protein with fibronectin binding ability.
 XX
 XX Hybrid DNA molecule; fibronectin binding; mastitis; ruminants;
 XX wound infection.
 XX
 XX *Staphylococcus aureus*.
 XX
 XX EP294349-A.
 XX
 XX 07-DEC-1988.
 XX
 XX 30-MAY-1988; 88EP-00850188.
 XX
 XX 01-JUN-1987; 87SE-00002272.
 XX
 XX (ALFA) ALFA LAVAL AGRIC INT AB.
 XX
 XX Lindberg MK, Sigmas LC, Wadstrom TM, Froman G;
 XX WPI; 1988-347978/49.
 XX

DR N-PSDB; AAN01099.
XX Hybrid DNA encoding Staphylococcus aureus fibronectin binding protein -
PT useful for immunisation and topical application to prevent staphylococcal
PT infections.
XX
PS Claim 11; Page 12; 23pp; English.
XX
CC The peptide has fibronectin binding ability. It is useful for immunising
CC ruminants against staphylococcal mastitis, pref. when used at 0.5-5
CC micrograms/kg, using 3 doses given at 1-3 week intervals; for topical
CC application to prevent wound infection, using an isotonic saline soln. of
CC concn. 25-250 micrograms/ml; and, when immobilised on a carrier, for
CC diagnosing staphylococcal infections. (updated on 25-MAR-2003 to correct
CC PF field.) (updated on 25-MAR-2003 to correct PA field.)
XX
SQ Sequence 38 AA;

Query Match 75.4%; Score 89; DB 1; Length 38;
Best Local Similarity 89.5%; Pred. No. 6.3e-06;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 3 SYGFPPHNSVDFEDTLPK 21
Db ||||| ||||| ||||| |||||
19 SYGFSGHNSVDFEDTLPK 37

RESULT 11
AAV29087
ID AAV29087 standard; protein; 134 AA.
XX
AC AAV29087;
XX
DT 28-SEP-1999 (first entry)
XX
XX S. aureus fibronectin binding protein A (FnBA) binding domain.
XX
KM Bovine herpes virus-2; BHV-2; cytokine; immune response; immunogen; IL;
KM interleukin; colony stimulating factor; CSF; interferon; IFN; TNF;
KM tumour necrosis factor; recombinant virus; vaccine; mucosal disease;
KM mastitis; breast cancer; stress-induced disease; binding domain; FnBA;
KM fibronectin binding protein.
XX
OS Staphylococcus aureus.
XX
XX MO9916892-A1.
XX
XX 08-APR-1999.
XX
XX 29-SEP-1998; 98WO-GB002927.
XX
XX 29-SEP-1997; 97GB-00020633.
XX
XX (UYBR-) UNIV BRISTOL.
XX
XX Bradley AJ, Duffas WPH;
XX WPI; 1999-255101/21.
XX
XX N-PSDB; AAX91504.
XX
XX New bovine herpes virus-2 vectors.
XX
XX Example 2; Fig 8A-B; 130pp; English.
XX
CC The invention provides bovine herpes virus-2 (BHV-2) based vectors that
CC comprise at least one cytokine-encoding DNA sequence. The expression of
CC cytokines in mammals can up-regulate immune responses to the immunogens.
CC The cytokine is selected from interleukins (IL), colony stimulating
CC factors (CSF), interferons (IFN) and tumour necrosis factors (TNF). The
CC BHV-2 based vector or recombinant virus can be used as vaccines. They can
CC be used for preventing or treating a mucosal disease in a subject, e.g.
CC ruminants, cattle, sheep, goats, dogs, cats, horses, or man, particularly
CC mastitis in cows or breast cancers in humans. They can also be used for

CC preventing or treating a stress-induced disease. The present sequence
CC represents the binding domain of a previously published S. aureus
CC fibronectin binding protein A (FnBA) sequence. The FnB binding domain
CC gene sequence FNBAH, cloned for use in this invention has 97.8 percent
CC identity when compared to the previously published FnBA and Fnbb gene
CC sequences
XX
SQ Sequence 134 AA;

Query Match 75.4%; Score 89; DB 2; Length 134;
Best Local Similarity 89.5%; Pred. No. 2.3e-05;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 3 SYGFPPHNSVDFEDTLPK 21
Db ||||| ||||| ||||| |||||
95 SYGFSGHNSVDFEDTLPK 113

RESULT 12
AAW31556
ID AAW31556 standard; protein; 139 AA.
XX
AC AAW31556;
XX
XX 27-AUG-2003 (revised)
DT 25-MAR-2003 (revised)
DT 21-MAY-1998 (first entry)
XX
XX Fibronectin-binding MSCRAMM derivative pOD.
XX
XX Fibronectin; pOD; collagen binding protein; sepsis; infection;
KM microbial surface component recognising adhesive matrix molecule; MSCRAMM;
KM adhesin; vaccine; immunisation; diagnosis; therapy; mastitis.
XX
OS Staphylococcus aureus.
XX
XX Key Location/Qualifiers
FT Peptide 1..12
FT /note= "vector pOE30-derived peptide"
XX
XX MO9743314-A2.
XX
XX 20-NOV-1997.
XX
XX 14-MAY-1997; 97WO-US008210.
XX
XX 16-MAY-1996; 96US-0017678P.
XX
XX (TEXA) UNIV TEXAS A & M SYSTEM.
XX (UABR-) UAB RES FOUND.
XX
XX Hoeoek M, Patti JM, House-Pompeo K, Sthanam N, Symersky J;
XX WPI; 1998-008801/01.
XX
XX Antibody that interacts with collagen binding domain of Staphylococcal
PT cna gene product - useful to prevent bacterial sepsis in animal infected
PT with Staphylococcus aureus.
XX
XX Disclosure; Page 91; 143pp; English.
XX
XX This protein comprises Staphylococcus aureus fibronectin-binding
CC microbial surface component recognising adhesive matrix molecule (MSCRAMM)
CC derivative pOD, plus a vector-derived N-terminal peptide. The invention
CC relates to claimed nucleic acid sequences (see AAV193436-38) encoding S.
CC aureus collagen binding protein (CBP) epitopes M17, M31 and M55 (see
CC AAW31552-54) that confer protection against S. aureus infection. CBP
CC protein and antigenic epitopes are contemplated for use in the treatment
CC of pathological infections, especially to prevent bacterial adhesion to
CC collagen. The epitopes are also contemplated for use in the preparation
CC of vaccines and as carrier proteins in vaccine formulations, as well as
CC in the formulation of compositions for the prevention of S. aureus
CC infection. pCF33 and pOD (see AAW31556) were used to raise anti-MSCRAMM

CC polyclonal antibodies used in passive immunisation against bovine
 CC mastitis. (Updated on 25-MAR-2003 to correct PI field.) (Updated on 27-
 CC AUG-2003 to correct OS field.)

XX
 XX
 SQ Sequence 139 AA;

Query Match 75.4%; Score 89; DB 2; Length 139;
 Best Local Similarity 89.5%; Pred. No. 2.6e-05;
 Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 SYQPPHNSVDFEEDTLPK 21
 DB 109 SYQFGHNSVDFEEDTLPK 127

RESULT 13
 AAP82115
 ID AAP82115 standard; protein; 1018 AA.

XX AAP82115;
 AC 25-MAR-2003 (revised)
 XX 05-JAN-1990 (first entry)
 DT
 DT Fibronection binding protein.
 XX Fibronection binding protein.
 XX Fibronection binding protein; S. aureus; immunisation; mastitis; ruminants;
 KW wound infection; diagnosis.
 XX Staphylococcus aureus.
 XX EP294349-A.
 XX 07-DEC-1988.
 PD
 PF 30-MAY-1988; 88EP-00850188.
 XX 01-JUN-1987; 87SE-00002272.
 PR
 XX (ALFA) ALFA LAVAL AGRIC INT AB.
 PA
 XX Lindberg MK, Signas LC, Wadstrom TM, Froman G;
 PI WPI; 1988-347978/49.
 XX P-PSDB; AAP82115.
 DR
 XX Hybrid DNA encoding Staphylococcus aureus fibronection binding protein -
 PT useful for immunisation and topical application to prevent staphylococcal
 PT infections.
 XX
 XX Disclosure; Fig. 8A:1-8A:2; 23pp; English.

XX The S. aureus fibronection binding protein may be included in a hybrid
 CC protein. The protein may be used to immunise ruminants against
 CC staphylococcal mastitis, pref. when given at 0.5-5 microg/kg, using 3
 CC doses at 1-3 week intervals; and for topical applicn. to prevent wound
 CC infection, pref. using isotonic saline soln. of concn. 25-250 microg/mg.
 CC The DNA encoding the binding protein and the hybrid protein may be
 CC immobilised on a carrier and used to diagnose staphylococcal infections.
 CC (Updated on 25-MAR-2003 to correct PA field.)
 CC
 CC

SQ Sequence 1018 AA;

Query Match 75.4%; Score 89; DB 1; Length 1018;
 Best Local Similarity 89.5%; Pred. No. 0.00024;
 Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 SYQPPHNSVDFEEDTLPK 21
 DB 839 SYQFGHNSVDFEEDTLPK 857

RESULT 14

AAU37245
 ID AAU37245 standard; protein; 1018 AA.

XX AAU37245;
 AC 14-FEB-2002 (first entry)
 XX
 DT
 DT Staphylococcus aureus cellular proliferation protein #1415.
 DE
 XX Antisense; prokaryotic cellular proliferation protein; antibiotic;
 XX antibacterial; drug design.
 KW
 XX Staphylococcus aureus.
 OS
 XX WO200170955-A2.
 PN
 XX 27-SEP-2001.
 PD
 XX 21-MAR-2001; 2001WO-US009180.
 PF
 XX 21-MAR-2000; 2000US-0191078P.
 PR 23-MAY-2000; 2000US-0206848P.
 PR 26-MAY-2000; 2000US-0207727P.
 PR 23-OCT-2000; 2000US-0242578P.
 PR 27-NOV-2000; 2000US-0253625P.
 PR 22-DEC-2000; 2000US-0257931P.
 PR 16-FEB-2001; 2001US-0269308P.

XX (ELIT-) ELITRA PHARM INC.
 PA
 XX Haselbeck R, Ohlsen KL, Zyskind JW, Wall D, Trawick JD, Carr GJ;
 PI Yamamoto RT, Xu HH;
 PI WPI; 2001-61495/70.
 DR N-PSDB; AAS5104.
 DR
 XX New polynucleotides for the identification and development of
 PT antibiotics, comprise sequences of antisense nucleic acids.
 PT
 XX Example 3; SEQ ID NO 12838; 511pp; English.

XX The invention relates to antisense inhibitors of genes essential to
 CC prokaryotic cellular proliferation, their use in identifying the genes,
 CC their use in the discovery of novel antibiotics, the essential genes
 CC themselves and the encoded proteins. The prokaryotes used are Escherichia
 CC coli, Staphylococcus aureus, Salmonella typhi, Klebsiella pneumoniae,
 CC Pseudomonas aeruginosa and Enterococcus faecalis. The invention is also
 CC useful for the identification of potential new targets for antibiotic
 CC development. The antisense nucleic acids can also be used to identify
 CC proteins used in proliferation, to express these proteins, and to obtain
 CC antibodies capable of binding to the expressed proteins. The proteins can
 CC be used to screen compounds in rational drug discovery programmes. The
 CC antisense nucleic acid sequence is also useful to screen for homologous
 CC nucleic acids which are required for cell proliferation in a wide variety
 CC of organisms. The present sequence represents an essential prokaryotic
 CC cellular proliferation protein. Note: The sequence data for this patent
 CC did not form part of the printed specification, but was obtained in
 CC electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 CC
 CC

SQ Sequence 1018 AA;

Query Match 75.4%; Score 89; DB 4; Length 1018;
 Best Local Similarity 89.5%; Pred. No. 0.00024;
 Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 SYQPPHNSVDFEEDTLPK 21
 DB 839 SYQFGHNSVDFEEDTLPK 857

RESULT 15
 AAU34301

```

ID  AAU34301 standard; protein; 1018 AA.
XX
AC  AAU34301;
XX
DT  14-FEB-2002 (first entry)
XX
DE  Staphylococcus aureus cellular proliferation protein #577.
XX
KW  Antisense; prokaryotic cellular proliferation protein; antibiotic;
XX  antibacterial; drug design.
XX
OS  Staphylococcus aureus.
XX
PN  WO200170955-A2.
XX
PD  27-SEP-2001.
XX
PF  21-MAR-2001; 2001WO-US009180.
XX
PR  21-MAR-2000; 2000US-0191078P.
PR  23-MAY-2000; 2000US-0206848P.
PR  26-MAY-2000; 2000US-0207727P.
PR  23-OCT-2000; 2000US-0242578P.
PR  27-NOV-2000; 2000US-0253625P.
PR  22-DEC-2000; 2000US-0257931P.
PR  16-FEB-2001; 2001US-0269308P.
XX
PA  (ELIT-) ELITRA PHARM INC.
XX
PI  Haeelbeck R, Ohlsen KU, Zyskind JW, Wall D, Trawick JD, Carr GJ;
PI  Yamamoto RT, Xu HH;
XX
DR  WPI; 2001-611495/70.
DR  N-PSDB; AAS52160.
XX
PT  New polynucleotides for the identification and development of
XX  antibiotics, comprise sequences of antisense nucleic acids.
XX
PS  Example 3; SEQ ID NO 5797; 511pp; English.
XX
CC  The invention relates to antisense inhibitors of genes essential to
CC  prokaryotic cellular proliferation, their use in identifying the genes,
CC  their use in the discovery of novel antibiotics, the essential genes
CC  themselves and the encoded proteins. The prokaryotes used are Escherichia
CC  coli, Staphylococcus aureus, Salmonella typhi, Klebsiella pneumoniae,
CC  Pseudomonas aeruginosa and Enterococcus faecalis. The invention is also
CC  useful for the identification of potential new targets for antibiotic
CC  development. The antisense nucleic acids can also be used to identify
CC  proteins used in proliferation, to express these proteins, and to obtain
CC  antibodies capable of binding to the expressed proteins. The proteins can
CC  be used to screen compounds in rational drug discovery programmes. The
CC  antisense nucleic acid sequence is also useful to screen for homologous
CC  nucleic acids which are required for cell proliferation in a wide variety
CC  of organisms. The present sequence represents an essential prokaryotic
CC  cellular proliferation protein. Note: The sequence data for this patent
CC  did not form part of the printed specification, but was obtained in
CC  electronic format directly from WIPO at
CC  ftp.wipo.int/pub/published_pct_sequences
XX
SQ  Sequence 1018 AA;

```

```

Query Match      75.4%; Score 89; DB 4; Length 1018;
Best Local Similarity 89.5%; Pred. No. 0.00024;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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OY  3 SYQFPNNSVDFEEDLPK 21
    ||| |||||
DB  839 SYQFGHNSVDFEEDLPK 857

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Search completed: October 25, 2005, 19:38:32
 Job time : 59.1473 secs

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OM protein - protein search, using sw model

Run on: October 22, 2005, 02:23:36 ; Search time 15.9358 seconds
(without alignments)
98.371 Million cell updates/sec

Title: US-10-731-238-34

Perfect score: 118
Sequence: 1 PASYQPPHNSVDFEEDTLPK 21

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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1: Issued Patents_AA:*
2: /cgn2_6/prodata/1/iaa/5A_COMB.pep:*
3: /cgn2_6/prodata/1/iaa/5B_COMB.pep:*
4: /cgn2_6/prodata/1/iaa/5C_COMB.pep:*
5: /cgn2_6/prodata/1/iaa/5D_COMB.pep:*
6: /cgn2_6/prodata/1/iaa/5E_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	118	100.0	21	4	US-09-010-317-34
2	98	83.1	21	4	US-09-010-317-10
3	98	83.1	21	4	US-09-010-317-20
4	98	83.1	22	4	US-09-010-317-13
5	95	80.5	21	4	US-09-010-317-14
6	93	78.8	21	4	US-09-010-317-15
7	89	75.4	21	4	US-09-010-317-9
8	89	75.4	37	1	US-08-234-622A-4
9	89	75.4	38	1	US-08-294-189-8
10	89	75.4	38	1	US-08-729-767-5
11	89	75.4	114	1	US-08-259-000-3
12	89	75.4	139	3	US-08-856-253-8
13	89	75.4	178	2	US-08-459-135A-12
14	89	75.4	178	3	US-08-495-559-12
15	89	75.4	1027	4	US-08-956-1718-5254
16	89	75.4	1027	4	US-08-781-986A-5254
17	85	72.0	21	4	US-09-010-317-16
18	84	71.2	21	4	US-09-010-317-23
19	84	71.2	21	4	US-09-010-317-13
20	83	70.3	21	4	US-09-010-317-18
21	83	70.3	21	4	US-09-010-317-24
22	83	70.3	21	4	US-09-010-317-27
23	83	70.3	21	4	US-09-010-317-28
24	83	70.3	21	4	US-09-010-317-30
25	82	69.5	21	4	US-09-010-317-25
26	82	69.5	21	4	US-09-010-317-29
27	82	69.5	21	4	US-09-010-317-31

28	82	69.5	130	2	US-08-459-135A-7	Sequence 7, Appl
29	82	69.5	130	2	US-08-459-135A-8	Sequence 8, Appl
30	82	69.5	130	3	US-08-495-559-7	Sequence 7, Appl
31	82	69.5	130	3	US-08-495-559-8	Sequence 8, Appl
32	82	69.5	174	2	US-08-459-135A-10	Sequence 10, Appl
33	82	69.5	174	2	US-08-459-135A-13	Sequence 13, Appl
34	82	69.5	174	3	US-08-495-559-10	Sequence 10, Appl
35	82	69.5	174	3	US-08-495-559-13	Sequence 13, Appl
36	82	69.5	176	3	US-08-495-559-6	Sequence 6, Appl
37	82	69.5	181	2	US-08-459-135A-6	Sequence 6, Appl
38	82	69.5	559	4	US-08-956-171E-5251	Sequence 5251, Ap
39	82	69.5	559	4	US-08-781-986A-5251	Sequence 5251, Ap
40	81	68.6	21	4	US-09-010-317-22	Sequence 22, Appl
41	81	68.6	21	4	US-09-010-317-32	Sequence 32, Appl
42	79	66.9	21	4	US-09-010-317-17	Sequence 17, Appl
43	79	66.9	21	4	US-09-010-317-19	Sequence 19, Appl
44	79	66.9	21	4	US-09-010-317-21	Sequence 21, Appl
45	79	66.9	21	4	US-09-010-317-26	Sequence 26, Appl

ALIGNMENTS

RESULT 1
US-09-010-317-34
Sequence 34, Application US/09010317
Patent No. 6685943
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
APPLICANT: Patti, Joseph M.
APPLICANT: House-Pompeo, Karen L.
APPLICANT: Speziale, Pietro
APPLICANT: John, Danny
APPLICANT: McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
TITLE OF INVENTION: AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSES: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE:
CLASSIFICATION:
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TANKK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 34:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: amino acid
STRANDEDNESS: linear
TOPOLOGY: linear
US-09-010-317-34
Query Match 100.0%
Best Local Similarity 100.0%
Score 118; DB 4; Length 21;
Pred. No. 4,6e-12;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 PASYPFHNSVDPEEDTLPK 21
Db 1 PASYPFHNSVDPEEDTLPK 21

RESULT 2

US-09-010-317-10
; Sequence 10, Application US/09010317
; Patent No. 6685943
; GENERAL INFORMATION:
; APPLICANT: Hook, Magnus
; APPLICANT: Patti, Joseph M.
; APPLICANT: House-Pompeo, Karen L.
; APPLICANT: Speziale, Pietro
; APPLICANT: Joh, Danny
; APPLICANT: McGavin, Martin J.
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
; NUMBER OF SEQUENCES: 105
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: TX
; COUNTRY: USA
; ZIP: 77210-4433
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/010.317
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/036,139
; FILING DATE: 21-JAN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Hibler, David W.
; REGISTRATION NUMBER: 41,071
; REFERENCE/DOCKET NUMBER: TAMK:189
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 512-418-3000
; TELEFAX: 512-474-7577
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; US-09-010-317-10

Query Match 83.1%; Score 98; DB 4; Length 21;
Best Local Similarity 94.7%; Pred. No. 6.5e-09;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 3 SYQFPFHNSVDPEEDTLPK 21
Db 3 SYQFPFHNSVDPEEDTLPK 21

RESULT 3

US-09-010-317-20
; Sequence 20, Application US/09010317
; Patent No. 6685943
; GENERAL INFORMATION:
; APPLICANT: Hook, Magnus
; APPLICANT: Patti, Joseph M.
; APPLICANT: House-Pompeo, Karen L.
; APPLICANT: Speziale, Pietro

APPLICANT: Joh, Danny
APPLICANT: McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/010.317
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAMK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-09-010-317-20

Query Match 83.1%; Score 98; DB 4; Length 21;
Best Local Similarity 94.7%; Pred. No. 6.5e-09;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 3 SYQFPFHNSVDPEEDTLPK 21
Db 3 SYQFPFHNSVDPEEDTLPK 21

RESULT 4

US-09-010-317-13
; Sequence 13, Application US/09010317
; Patent No. 6685943
; GENERAL INFORMATION:
; APPLICANT: Hook, Magnus
; APPLICANT: Patti, Joseph M.
; APPLICANT: House-Pompeo, Karen L.
; APPLICANT: Speziale, Pietro
; APPLICANT: Joh, Danny
; APPLICANT: McGavin, Martin J.
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
; NUMBER OF SEQUENCES: 105
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: TX
; COUNTRY: USA
; ZIP: 77210-4433
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TANK:189
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 22 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-09-010-317-13

Query Match 83.1%; Score 98; DB 4; Length 22;
Best Local Similarity 94.7%; Pred. No. 6.9e-09;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 SYQFPFPHNSVDFEEDTLPK 21
Db 3 SYQFGHNSVDFEEDTLPK 21

RESULT 5
US-09-010-317-14
Sequence 14, Application US/09010317
Patent No. 6685943
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
APPLICANT: Patti, Joseph M.
APPLICANT: House-Pompeo, Karen L.
APPLICANT: Speziale, Pietro
APPLICANT: John, Danny
APPLICANT: McGavin, Martin J.
TITLE OF INVENTION: FIBROECTIN BINDING PROTEIN COMPOSITIONS
TITLE OF INVENTION: AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CURRENT APPLICATION DATA:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TANK:189
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 14:

SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-09-010-317-14

Query Match 80.5%; Score 95; DB 4; Length 21;
Best Local Similarity 85.7%; Pred. No. 1.9e-08;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 PASYQFPFPHNSVDFEEDTLPK 21
Db 1 PPSYQFGHNSVDFEEDTLPK 21

RESULT 6
US-09-010-317-15
Sequence 15, Application US/09010317
Patent No. 6685943
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
APPLICANT: Patti, Joseph M.
APPLICANT: House-Pompeo, Karen L.
APPLICANT: Speziale, Pietro
APPLICANT: John, Danny
APPLICANT: McGavin, Martin J.
TITLE OF INVENTION: FIBROECTIN BINDING PROTEIN COMPOSITIONS
TITLE OF INVENTION: AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CURRENT APPLICATION DATA:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TANK:189
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-09-010-317-15

Query Match 78.8%; Score 93; DB 4; Length 21;
Best Local Similarity 90.0%; Pred. No. 4e-08;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 ASYQFPFPHNSVDFEEDTLPK 21
Db 2 ASYQFGHNSVDFEEDTLPK 21

```
RESULT 7
US-09-010-317--9
; Sequence 9, Application US/09010317
; Patent No. 6685943
; GENERAL INFORMATION:
; APPLICANT: Hook, Magnus
; APPLICANT: Patti, Joseph M.
; APPLICANT: House-Pompeo, Karen L.
; APPLICANT: Speziale, Pietro
; APPLICANT: John, Danny
; APPLICANT: McGavin, Martin J.
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
; TITLE OF INVENTION: AND METHODS OF USE
; NUMBER OF SEQUENCES: 105
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: TX
; COUNTRY: USA
; ZIP: 77210-4433
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/010.317
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/036.139
; FILING DATE: 21-JAN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Hibler, David W.
; REGISTRATION NUMBER: 41,071
; REFERENCE/DOCKET NUMBER: TAMK:189
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 512-418-3000
; TELEFAX: 512-474-7577
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
;
US-09-010-317-9
Query March 75.4%; Score 89; DB 4; Length 21;
Best Local Similarity 89.5%; Pred. No. 1.7e-07;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 SYGFPPHNSVDFEEDTLPK 21
Db 3 SYGFCHNSVDFEEDTLPK 21

RESULT 8
US-08-234-622A-4
; Sequence 4, Application US/08234622A
; Patent No. 5440014
; GENERAL INFORMATION:
; APPLICANT: Hook, Magnus
; APPLICANT: MCGAVIN, Martin
; APPLICANT: RAUCCI, Giuseppe
; TITLE OF INVENTION: A FIBRONECTIN BINDING PEPTIDE
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Burns, Doane, Swecker & Mathis
; STREET: P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
```

```
ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/234,622A
; FILING DATE: 28-APR-1994
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: SE 9002617-0
; FILING DATE: 10-AUG-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/SE91/00534
; FILING DATE: 09-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Meuth, Donna M
; REGISTRATION NUMBER: 36,607
; REFERENCE/DOCKET NUMBER: 012885-044
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-2021
; TELEFAX: (703) 836-6620
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 37 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
;
US-08-234-622A-4
Query March 75.4%; Score 89; DB 1; Length 37;
Best Local Similarity 89.5%; Pred. No. 3.3e-07;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 SYGFPPHNSVDFEEDTLPK 21
Db 18 SYGFCHNSVDFEEDTLPK 36

RESULT 9
US-08-294-189-8
; Sequence 8, Application US/08294189
; Patent No. 5707822
; GENERAL INFORMATION:
; APPLICANT: Fischetti, Vincent A.
; APPLICANT: Rakonjac, Jasna
; APPLICANT: Robbins, John
; TITLE OF INVENTION: GENE SERUM OPACITY FACTOR
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Klauber & Jackson
; STREET: 411 Hackensack Avenue
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/294,189
; FILING DATE: 22-AUG-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Bag., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 600-1-118
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201 487-5800
```

TELEFAX: 201 343-1684
TELEX: 133521
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
ORGANISM: Streptococcus pyogenes
STRAIN: D734
INDIVIDUAL ISOLATE: 22
IMMEDIATE SOURCE:
CLONE: BAU3a
US-08-294-189-8

Query Match 75.4%; Score 89; DB 1; Length 38;
Best Local Similarity 89.5%; Pred. No. 3.4e-07;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 3 SYQPPHNSVDFEETLPK 21
Db 12 SYQFGHNSVDFEETLPK 30

RESULT 10
US-08-729-767-5
Sequence 5, Application US/08729767
Patent No. 5770702
GENERAL INFORMATION:
APPLICANT: HOOK, Magnus
APPLICANT: LINDBERG, Martin Kjell
APPLICANT: SIGNAS, Lars Christer
APPLICANT: WADSTROM, Torkel Mikael
APPLICANT: FROMAN, Gunnar
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN AS WELL AS
TITLE OF INVENTION: ITS PREPARATION
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Burns, Doane, Swecker & Mathis, L.L.P.
STREET: P.O. Box 1404
CITY: Alexandria
STATE: Virginia
COUNTRY: United States
ZIP: 22113-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/729,767
FILING DATE: 07-OCT-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/259,000
FILING DATE: 13-JUN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/007,817
FILING DATE: 22-JAN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/201,028
FILING DATE: 01-JUN-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: SE 8702272-9
FILING DATE: 01-JUN-1987
ATTORNEY/AGENT INFORMATION:
NAME: McGowan, Malcolm K.
REGISTRATION NUMBER: 39,300
REFERENCE/DOCKET NUMBER: 012889-036
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620

TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-729-767-5

Query Match 75.4%; Score 89; DB 1; Length 38;
Best Local Similarity 89.5%; Pred. No. 3.4e-07;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 3 SYQPPHNSVDFEETLPK 21
Db 19 SYQFGHNSVDFEETLPK 37

RESULT 11
US-08-259-000-3
Sequence 3, Application US/08259000
Patent No. 5571514
GENERAL INFORMATION:
APPLICANT: HOOK, Magnus
APPLICANT: LINDBERG, Martin Kjell
APPLICANT: SIGNAS, Lars Christer
APPLICANT: WADSTROM, Torkel Mikael
APPLICANT: FROMAN, Gunnar
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN AS WELL AS
TITLE OF INVENTION: ITS PREPARATION
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Burns, Doane, Swecker & Mathis
STREET: P.O. Box 1404
CITY: Alexandria
STATE: Virginia
COUNTRY: United States
ZIP: 22113-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/259,000
FILING DATE: 13-JUN-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: SE 8702272-9
FILING DATE: 01-JUN-1987
ATTORNEY/AGENT INFORMATION:
NAME: Meuth, Donna M
REGISTRATION NUMBER: 36,607
REFERENCE/DOCKET NUMBER: 012885-062
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 114 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-259-000-3

Query Match 75.4%; Score 89; DB 1; Length 114;
Best Local Similarity 89.5%; Pred. No. 1.2e-06;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 3 SYQPPHNSVDFEETLPK 21

Db 95 SYORGHNSVDFEDTLPK 113

```
RESULT 12
US-08-856-253-8
; Sequence 8, Application US/08856253
; Patent No. 6288214
; GENERAL INFORMATION:
; APPLICANT: Hook, Magnus
; APPLICANT: Patti, Joseph M.
; APPLICANT: House-Pompeo, Karen
; APPLICANT: Schanam, Narayana
; APPLICANT: Symersky, Jindrich
; TITLE OF INVENTION: COLLAGEN BINDING PROTEIN COMPOSITIONS
; TITLE OF INVENTION: AND METHODS OF USE
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: U.S.
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/856,253
; FILING DATE: Concurrently Herewith
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/017,678
; FILING DATE: 16-MAY-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Kitchell, Barbara S.
; REGISTRATION NUMBER: 33,928
; REFERENCE/DOCKET NUMBER: TAMK:193
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (512) 418-3000
; TELEFAX: (512) 474-7577
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 139 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; US-08-856-253-8

Query Match 75.4%; Score 89; DB 3; Length 139;
Best Local Similarity 89.5%; Pred. No. 1.5e-06;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Cy 3 SYORPHNSVDFEDTLPK 21
|||||
Db 109 SYORGHNSVDFEDTLPK 127

RESULT 13
US-08-459-135A-12
; Sequence 12, Application US/08459135A
; Patent No. 5955078
; GENERAL INFORMATION:
; APPLICANT: BURHAM, Martin Karl Russel
; APPLICANT: CHOPRA, Ian
; APPLICANT: CRITCHLEY, Ian Alfred
; APPLICANT: KNOWLES, David Justin Charles
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN: MONOCLONAL ANTIBODY AND THEIR US
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corporation
; STREET: 709 Swedeland Road
```

```
CITY: King of Prussia
STATE: PA
COUNTRY: U.S.A.
ZIP: 19406-0939
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: DOS
; SOFTWARE: Fastseq, Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/459,135A
; FILING DATE: 02-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB/94/00215
; FILING DATE: 04-Feb-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Gimmil, Edward R
; REGISTRATION NUMBER: 38,891
; REFERENCE/DOCKET NUMBER: P30591C2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-270-4478
; TELEFAX: 610-270-5090
; TELEX:
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 178 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Protein
; US-08-459-135A-12

Query Match 75.4%; Score 89; DB 2; Length 178;
Best Local Similarity 89.5%; Pred. No. 2e-06;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Cy 3 SYORPHNSVDFEDTLPK 21
|||||
Db 95 SYORGHNSVDFEDTLPK 113

RESULT 14
US-08-495-559-12
; Sequence 12, Application US/08495559A
; Patent No. 6054572
; GENERAL INFORMATION:
; APPLICANT: BURHAM, Martin Karl Russel
; APPLICANT: CHOPRA, Ian
; APPLICANT: CRITCHLEY, Ian Alfred
; APPLICANT: KNOWLES, David Justin Charles
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN: MONOCLONAL
; TITLE OF INVENTION: ANTIBODY AND THEIR USE IN PREVENTING BACTERIAL ADHESION
; FILE REFERENCE: P30591
; CURRENT APPLICATION NUMBER: US/08/495,559A
; CURRENT FILING DATE: 1995-08-03
; EARLIER APPLICATION NUMBER: GB 9302289.5
; EARLIER FILING DATE: 1993-02-05
; EARLIER APPLICATION NUMBER: GB 9321592.9
; EARLIER FILING DATE: 1993-10-20
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: Fastseq for Windows Version 3.0
; SEQ ID NO 12
; LENGTH: 178
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
; US-08-495-559-12

Query Match 75.4%; Score 89; DB 3; Length 178;
Best Local Similarity 89.5%; Pred. No. 2e-06;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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QY 3 SYQPPHNSVDFEEDTLPK 21
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Db 95 SYQFGHNSVDFEEDTLPK 113

RESULT 15
US-08-956-171E-5254

; Sequence 5254, Application US/08956171E
; Patent No. 6593114

GENERAL INFORMATION:

APPLICANT: Charles Kunach

Gil H. Choi

Patrick S. Dillon

Craig A. Rosen

Steven C. Barash

Michael R. Fannon

TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences

NUMBER OF SEQUENCES: 5256

CORRESPONDENCE ADDRESS:

ADDRESSEE: Human Genome Sciences, Inc.

STREET: 9410 Key West Avenue

CITY: Rockville

STATE: Maryland

COUNTRY: USA

ZIP: 20850

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage

COMPUTER: HP Vectra 486/33

OPERATING SYSTEM: MSDOS version 6.2

SOFTWARE: ASCII Text

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/956,171E

FILING DATE: 20-Oct-1997

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 60/009,861

FILING DATE: January 5, 1996

APPLICATION NUMBER: 08/781,986

FILING DATE: January 3, 1997

ATTORNEY/AGENT INFORMATION:

NAME: Mark J. Hyman

REGISTRATION NUMBER: 46,789

REFERENCE/DOCKET NUMBER: PB248P1

TELECOMMUNICATION INFORMATION:

TELEPHONE: (240) 314-1224

TELEFAX: (301) 309-8439

INFORMATION FOR SEQ ID NO: 5254:

SEQUENCE CHARACTERISTICS:

LENGTH: 1027 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 5254:

US-08-956-171E-5254

Query Match 75.4%; Score 89; DB 4; Length 1027;
Best Local Similarity 89.5%; Pred. No. 1.4e-05;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 SYQPPHNSVDFEEDTLPK 21
||| |||||
Db 848 SYQFGHNSVDFEEDTLPK 866

Search completed: October 22, 2005, 03:51:15
Job time : 15.9358 sec

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 22, 2005, 10:49:15 ; Search time 59.2367 Seconds
(without alignments)
148.005 Million cell updates/sec

Title: US-10-731-238-34

Perfect score: 118
Sequence: 1 PASYPFPHNSVDEPDLTPK 21

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1862951 seqs, 417491010 residues

Total number of hits satisfying chosen parameters: 1862951

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

Published Applications_A1:*

- 1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
- 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
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- 20: /cgn2_6/ptodata/2/pubpaa/US11B_PUBCOMB.pep:*
- 21: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*
- 22: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	118	100.0	21	18 US-10-731-238-34	Sequence 34, Appl
2	98	83.1	21	18 US-10-731-238-10	Sequence 10, Appl
3	98	83.1	21	18 US-10-731-238-20	Sequence 20, Appl
4	98	83.1	21	18 US-10-731-238-13	Sequence 13, Appl
5	95	80.5	21	18 US-10-731-238-14	Sequence 14, Appl
6	93	78.8	21	18 US-10-731-238-15	Sequence 15, Appl
7	89	75.4	21	18 US-10-731-238-9	Sequence 9, Appl
8	89	75.4	37	20 US-11-066-697-1134	Sequence 1134, Ap
9	89	75.4	139	9 US-09-813-920-8	Sequence 8, Appl
10	89	75.4	1018	9 US-09-815-242-5797	Sequence 5797, Ap
11	89	75.4	1018	9 US-09-815-242-12838	Sequence 12838, A

12	89	75.4	1018	17 US-10-470-048B-68	Sequence 68, Appl
13	89	75.4	1027	8 US-08-781-986A-5254	Sequence 5254, Ap
14	89	75.4	1027	15 US-10-329-624-5254	Sequence 5254, Ap
15	86	72.9	961	15 US-10-282-122A-4378	Sequence 4378, A
16	86	72.9	978	9 US-09-815-242-5456	Sequence 5456, A
17	86	72.9	1001	9 US-09-815-242-12686	Sequence 12686, A
18	86	72.9	1038	15 US-10-282-122A-43827	Sequence 43827, A
19	85	72.0	21	18 US-10-731-238-16	Sequence 16, Appl
20	84	71.2	21	18 US-10-731-238-23	Sequence 23, Appl
21	84	71.2	21	18 US-10-731-238-33	Sequence 33, Appl
22	83	70.3	21	18 US-10-731-238-18	Sequence 18, Appl
23	83	70.3	21	18 US-10-731-238-24	Sequence 24, Appl
24	83	70.3	21	18 US-10-731-238-27	Sequence 27, Appl
25	83	70.3	21	18 US-10-731-238-28	Sequence 28, Appl
26	83	70.3	21	18 US-10-731-238-30	Sequence 30, Appl
27	82	69.5	21	18 US-10-731-238-25	Sequence 25, Appl
28	82	69.5	21	18 US-10-731-238-29	Sequence 29, Appl
29	82	69.5	21	18 US-10-731-238-31	Sequence 31, Appl
30	82	69.5	388	8 US-08-901-062-1	Sequence 1, Appl
31	82	69.5	559	8 US-08-781-986A-5251	Sequence 5251, Ap
32	82	69.5	559	15 US-10-329-624-5251	Sequence 5251, Ap
33	82	69.5	940	17 US-10-470-048B-424	Sequence 424, App
34	82	69.5	948	17 US-10-470-048B-69	Sequence 69, Appl
35	81	68.6	21	18 US-10-731-238-32	Sequence 32, Appl
36	81	68.6	21	18 US-10-731-238-32	Sequence 32, Appl
37	79	66.9	21	18 US-10-731-238-17	Sequence 17, Appl
38	79	66.9	21	18 US-10-731-238-19	Sequence 19, Appl
39	79	66.9	21	18 US-10-731-238-21	Sequence 21, Appl
40	79	66.9	21	18 US-10-731-238-26	Sequence 26, Appl
41	62	52.5	14	18 US-10-731-238-61	Sequence 61, Appl
42	53	44.9	10	18 US-10-731-238-101	Sequence 101, Appl
43	53	44.9	11	18 US-10-731-238-86	Sequence 86, Appl
44	53	44.9	129	16 US-10-425-115-33992	Sequence 33992, Sequence 822, App
45	53	44.9	183	9 US-09-764-853-622	

ALIGNMENTS

RESULT 1
US-10-731-238-34
Sequence 34, Application US/10731238
Publication No. US20050123552A1
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
Patti, Joseph M.
House-Pompeo, Karen L.
Speziale, Pietro
McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSER: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/731, 238
FILING DATE: 10-Dec-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE: 21-Jan-1998
APPLICATION NUMBER: US 60/036,139

FLING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TANK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 34:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 34:
US-10-731-238-34

Query Match 100.0%; Score 118; DB 18; Length 21;
Best Local Similarity 100.0%; Pred. No. 4.6e-10;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PASYQPPHNSVDFEEDTLPK 21
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1 PASYQPPHNSVDFEEDTLPK 21

Db 1 PASYQPPHNSVDFEEDTLPK 21

RESULT 2
US-10-731-238-10
Sequence 10, Application US/10731238
Publication No. US20050123552A1
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
Patti, Joseph M.
House-Pompeo, Karen L.
Speziale, Pietro
Joh, Danny
McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/731,238
FILING DATE: 10-Dec-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE: 21-Jan-1998
APPLICATION NUMBER: US 60/036,139
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TANK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>

TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 10:
US-10-731-238-10

Query Match 83.1%; Score 98; DB 18; Length 21;
Best Local Similarity 94.7%; Pred. No. 3.6e-07;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 SYQFPPHNSVDFEEDTLPK 21
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3 SYQFPPHNSVDFEEDTLPK 21

Db 3 SYQFPPHNSVDFEEDTLPK 21

RESULT 3
US-10-731-238-20
Sequence 20, Application US/10731238
Publication No. US20050123552A1
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
Patti, Joseph M.
House-Pompeo, Karen L.
Speziale, Pietro
Joh, Danny
McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/731,238
FILING DATE: 10-Dec-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE: 21-Jan-1998
APPLICATION NUMBER: US 60/036,139
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TANK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 20:
US-10-731-238-20

Query Match 83.1%; Score 98; DB 18; Length 21;
Best Local Similarity 94.7%; Pred. No. 3.6e-07;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 SYQFPPHNSVDFEEDTLPK 21
|||
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Db 3 SYQFPPHNSVDFEEDTLPK 21

RESULT 4
US-10-731-238-13
Sequence 13, Application US/10731238
Publication No. US20050123552A1
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
Patti, Joseph M.
House-Pompeo, Karen L.
Speziale, Pietro
Joh, Danny
McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/731,238
FILING DATE: 10-Dec-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE: 21-Jan-1998
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAMK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 22 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 13:
US-10-731-238-13
Query Match 83.1%; Score 98; DB 18; Length 22;
Best Local Similarity 94.7%; Pred. No. 3.8e-07;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 3 SYQPPPHNSVDFEEDTLPK 21
Db 3 STQFGHNSVDFEEDTLPK 21
RESULT 5
US-10-731-238-14
Sequence 14, Application US/10731238
Publication No. US20050123552A1
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
Patti, Joseph M.
House-Pompeo, Karen L.
Speziale, Pietro
Joh, Danny
McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
AND METHODS OF USE

NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/731,238
FILING DATE: 10-Dec-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE: 21-Jan-1998
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAMK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 14:
US-10-731-238-14

Query Match 80.5%; Score 95; DB 18; Length 21;
Best Local Similarity 85.7%; Pred. No. 9.9e-07;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 PASQPPPHNSVDFEEDTLPK 21
Db 1 PPSYQFGHNSVDFEEDTLPK 21

RESULT 6
US-10-731-238-15
Sequence 15, Application US/10731238
Publication No. US20050123552A1
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
Patti, Joseph M.
House-Pompeo, Karen L.
Speziale, Pietro
Joh, Danny
McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30

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CURRENT APPLICATION DATA:
  APPLICATION NUMBER: US/10/731,238
  FILING DATE: 10-Dec-2003
  CLASSIFICATION: <Unknown>
  PRIOR APPLICATION DATA:
    APPLICATION NUMBER: US/09/010,317
    FILING DATE: 21-Jan-1998
    APPLICATION NUMBER: US 60/036,139
    FILING DATE: 21-Jan-1997
  ATTORNEY/AGENT INFORMATION:
    NAME: Hibler, David W.
    REGISTRATION NUMBER: 41, 071
    REFERENCE/DOCKET NUMBER: TANK:189
  TELECOMMUNICATION INFORMATION:
    TELEPHONE: 512-418-3000
    TELEFAX: 512-474-7577
  INFORMATION FOR SEQ ID NO: 15:
    SEQUENCE CHARACTERISTICS:
      LENGTH: 21 amino acids
      TYPE: amino acid
      STRANDEDNESS: <Unknown>
      TOPOLOGY: linear
    SEQUENCE DESCRIPTION: SEQ ID NO: 15:
US-10-731-238-15

Query Match      78.8%; Score 93; DB 18; Length 21;
Best Local Similarity 90.0%; Pred. No. 1.9e-06;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      2 ASYQPPPNASVDFEEDTLPK 21
      ||||| ||||| ||||| |||||
Db      2 ASYQFGHNSVDFEEDTLPK 21

RESULT 7
US-10-731-238-9
  Sequence 9, Application US/10731238
  Publication No. US20050123552A1
  GENERAL INFORMATION:
    APPLICANT: Hook, Magnus
    Patil, Joseph M.
    House-Pompeo, Karen L.
    Speciale, Pietro
    Joh, Danny
    McGavin, Martin J.
  TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
    AND METHODS OF USE
  NUMBER OF SEQUENCES: 105
  CORRESPONDENCE ADDRESS:
    ADDRESSEE: Arnold, White & Durkee
    STREET: P.O. Box 4433
    CITY: Houston
    STATE: TX
    COUNTRY: USA
    ZIP: 77210-4433
  COMPUTER READABLE FORM:
    MEDIUM TYPE: Floppy disk
    COMPUTER: IBM PC compatible
    OPERATING SYSTEM: PC-DOS/MS-DOS
    SOFTWARE: PatentIn Release #1.0, Version #1.30
  CURRENT APPLICATION DATA:
    APPLICATION NUMBER: US/10/731,238
    FILING DATE: 10-Dec-2003
    CLASSIFICATION: <Unknown>
  PRIOR APPLICATION DATA:
    APPLICATION NUMBER: US/09/010,317
    FILING DATE: 21-Jan-1998
    APPLICATION NUMBER: US 60/036,139
    FILING DATE: 21-Jan-1997
  ATTORNEY/AGENT INFORMATION:
    NAME: Hibler, David W.
    REGISTRATION NUMBER: 41, 071
    REFERENCE/DOCKET NUMBER: TANK:189
  TELECOMMUNICATION INFORMATION:
    TELEPHONE: 512-418-3000
    TELEFAX: 512-474-7577
  INFORMATION FOR SEQ ID NO: 15:
    SEQUENCE CHARACTERISTICS:
      LENGTH: 21 amino acids
      TYPE: amino acid
      STRANDEDNESS: <Unknown>
      TOPOLOGY: linear
    SEQUENCE DESCRIPTION: SEQ ID NO: 15:
US-10-731-238-15

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TITLE OF INVENTION: COLLAGEN BINDING PROTEIN COMPOSITIONS
AND METHODS OF USE
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: Texas
COUNTRY: U.S.
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/813,820
FILING DATE: 22-Mar-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/856,253
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Kitchell, Barbara S.
REGISTRATION NUMBER: 33,928
REFERENCE/DOCKET NUMBER: TANK:193
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
TELEFAX: (512) 474-7577
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 139 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-09-813-820-8
Query Match 75.4%; Score 89; DB 9; Length 139;
Best Local Similarity 89.5%; Pred. No. 5.5e-05;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 3 SYQPPHNSVDFEEDTLPK 21
Db 109 SYQFGHNSVDFEEDTLPK 127
RESULT 10
US-09-815-242-5797
Sequence 5797, Application US/09815242
Patent No. US20020061569A1
GENERAL INFORMATION:
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Karl L.
APPLICANT: Zyskind, Judith W.
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John D.
APPLICANT: Carr, Grant J.
APPLICANT: Yamamoto, Robert T.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in
FILE REFERENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: US/09/815,242
FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23

PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 5797
LENGTH: 1018
TYPE: PRT
ORGANISM: Staphylococcus aureus
US-09-815-242-5797
Query Match 75.4%; Score 89; DB 9; Length 1018;
Best Local Similarity 89.5%; Pred. No. 0.00046;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 3 SYQPPHNSVDFEEDTLPK 21
Db 839 SYQFGHNSVDFEEDTLPK 857
RESULT 11
US-09-815-242-12838
Sequence 12838, Application US/09815242
Patent No. US20020061569A1
GENERAL INFORMATION:
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Karl L.
APPLICANT: Zyskind, Judith W.
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John D.
APPLICANT: Carr, Grant J.
APPLICANT: Yamamoto, Robert T.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in
FILE REFERENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: US/09/815,242
FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 12838
LENGTH: 1018
TYPE: PRT
ORGANISM: Staphylococcus aureus
US-09-815-242-12838
Query Match 75.4%; Score 89; DB 9; Length 1018;
Best Local Similarity 89.5%; Pred. No. 0.00046;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 3 SYQPPHNSVDFEEDTLPK 21
Db 839 SYQFGHNSVDFEEDTLPK 857
RESULT 12

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US-10-470-048B-68
; Sequence 68, Application US/10470048B
; Publication No. US20050037444A1
; GENERAL INFORMATION:
; APPLICANT: MEINKE ET AL.
; TITLE OF INVENTION: A METHOD FOR IDENTIFICATION, ISOLATION AND PRODUCTION OF
; FILE REFERENCE: SONN-03505
; CURRENT APPLICATION NUMBER: US/10/470,048B
; NUMBER OF SEQ ID NOS: 603
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 68
; LENGTH: 1018
; TYPE: PRF
; ORGANISM: Staphylococcus aureus
US-10-470-048B-68

Query Match          75.4%; Score 89; DB 17; Length 1018;
Best Local Similarity 89.5%; Pred. No. 0.00046;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      3 SYGPPHNSVDFEEDTLPK 21
Db      839 SYGFGHNSVDFEEDTLPK 857

RESULT 13
US-08-781-986A-5254
; Sequence 5254, Application US/08781986A
; Publication No. US20030054436A1
; GENERAL INFORMATION:
; APPLICANT: Charles Kunsch
; TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
; NUMBER OF SEQUENCES: 5255
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/781,986A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Benson, Bob
; REGISTRATION NUMBER: 30,446
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 5254:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1027 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-781-986A-5254

Query Match          75.4%; Score 89; DB 8; Length 1027;
Best Local Similarity 89.5%; Pred. No. 0.00046;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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QY      3 SYGPPHNSVDFEEDTLPK 21
Db      848 SYGFGHNSVDFEEDTLPK 866

RESULT 14
US-10-329-624-5254
; Sequence 5254, Application US/10329624
; Publication No. US20040043037A1
; GENERAL INFORMATION:
; APPLICANT: Charles Kunsch
; Gil H. Choi
; Patrick S. Dillon
; Craig A. Rosen
; Steven C. Barash
; Michael R. Farnon
; TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
; NUMBER OF SEQUENCES: 5256
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/329,624
; FILING DATE: 27-Dec-2002
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/956,171
; FILING DATE: October 20, 1997
; APPLICATION NUMBER: 60/009,861
; FILING DATE: January 5, 1996
; APPLICATION NUMBER: 08/781,986
; FILING DATE: January 3, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Mark J. Hyman
; REGISTRATION NUMBER: 46,789
; REFERENCE/DOCKET NUMBER: PB248P1D1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (240) 314-1224
; TELEFAX: (301) 309-8439
; INFORMATION FOR SEQ ID NO: 5254:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1027 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 5254:
US-10-329-624-5254

Query Match          75.4%; Score 89; DB 15; Length 1027;
Best Local Similarity 89.5%; Pred. No. 0.00046;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      3 SYGPPHNSVDFEEDTLPK 21
Db      848 SYGFGHNSVDFEEDTLPK 866

RESULT 15
US-10-282-122A-43778
; Sequence 43778, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
```

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; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Karl
; APPLICANT: Zyckind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 43778
; LENGTH: 961
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-10-282-122A-43778

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Query Match 72.9%; Score 86; DB 15; Length 961;
 Best Local Similarity 84.2%; Pred. No. 0.0012;
 Matches 16; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

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OY      3 SYQPPHNSVDFEEDTLPR 21
      :||| ||||| |||||
DB      786 NYQFGHNSVDFEEDTLPR 804

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Search completed: October 22, 2005, 11:34:45
 Job time : 59.2367 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 22, 2005, 02:23:36 / Search time 10.5465 Seconds
(without alignments)
191.586 Million cell updates/sec

Title: US-10-731-238-34
Perfect score: 118
Sequence: 1 PASYPFHNSVDFEEDTLPK 21

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	89	75.4	1018 2	A32192 fibronectin-binding
2	86	72.9	961 2	G90053 hypothetical prote
3	86	72.9	1038 2	H90053 fibronectin-bindin
4	82	69.5	940 2	S19702 transcripition fact
5	48.5	41.1	2578 2	A56922 early E3 6.4K prot
6	48	40.7	61 1	ERAD64 hypothetical prote
7	48	40.7	176 2	D83207 hypothetical prote
8	48	40.7	186 2	E89980 hypothetical prote
9	47.5	40.3	1041 2	P00442 polyproteins - barl
10	47	39.8	1584 2	F96573 protein F12M16.25
11	45	38.1	250 2	G56539 glucose-1-phosphat
12	45	38.1	475 2	JX0344 legumain (EC 3.4.2
13	45	38.1	476 2	E83796 two-component sens
14	45	38.1	493 2	T12044 probable legumain
15	45	38.1	551 2	T30806 metabotropic gluta
16	45	38.1	703 2	T19420 hypothetical prote
17	45	38.1	908 2	T48899 disease resistance
18	45	38.1	1265 2	T07397 kinesin heavy chai
19	44.5	37.7	128 2	T24266 hypothetical prote
20	44	37.3	128 2	C84052 hypothetical prote
21	44	37.3	134 2	T34185 hypothetical prote
22	44	37.3	173 2	F70481 probable iron-upca
23	44	37.3	334 2	F81435 epithelial sodium
24	43.5	36.9	640 2	I51915 hypothetical prote
25	43.5	36.9	769 2	D96634 hypothetical prote
26	43	36.4	93 2	AG2290 hypothetical prote
27	43	36.4	253 2	S76336 hypothetical prote
28	43	36.4	270 2	G75334 hypothetical prote
29	43	36.4	288 2	T18721 hypothetical prote

30	43	36.4	385	2	AE2651	hypothetical prote
31	43	36.4	385	2	D97433	polyamine transpor
32	43	36.4	477	2	A24115	transcription init
33	43	36.4	652	2	T39409	hypothetical prote
34	43	36.4	871	2	A46742	metabotropic gluta
35	43	36.4	1041	2	A81960	probable DNA helic
36	43	36.4	1544	2	T29482	hypothetical prote
37	43	36.4	2500	1	MMHUR2	HIV-1PR2 enhancer-b
38	42.5	36.0	416	1	A42332	carboxypeptidase B
39	42.5	36.0	636	2	D84823	hypothetical prote
40	42.5	36.0	651	2	S53415	hypothetical prote
41	42.5	36.0	683	2	T51821	1-phosphatidylinos
42	42.5	36.0	859	2	G86242	hypothetical prote
43	42.5	36.0	1092	2	T20117	hypothetical prote
44	42	35.6	121	2	S47148	hypothetical prote
45	42	35.6	199	2	D75563	hypothetical prote

ALIGNMENTS

RESULT 1

A32192

C:Species: Staphylococcus aureus

C:Date: 31-Jul-1989 #sequence_revision 31-Jul-1989 #text_change 16-Feb-1997

C:Accession: A32192

R:Signaes, C.; Raucet, G.; Joensson, K.; Lindgren, P.E.; Anantharamiah, G.M.; Hoesek, M.

Proc. Natl. Acad. Sci. U.S.A. 86, 699-703, 1989

A:Title: Nucleotide sequence of the gene for a fibronectin-binding protein from Staphyloc

A:Reference number: A32192; MUID:89098998; PMID:2521391

A:Accession: A32192

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-1018 <SIG>

A:Cross-references: GB:J04151

C:Keywords: fibronectin binding

Query Match 75.4% Score 89; DB 2; Length 1018;
Best Local Similarity 89.5%; Pred. No. 1.1e-05;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 SYQFPFHNSVDFEEDTLPK 21

DB 839 SYQFGHNSVDFEEDTLPK 857

RESULT 2

G90053 hypothetical protein fnb (imported) - Staphylococcus aureus (strain N315)

C:Species: Staphylococcus aureus

C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004

C:Accession: G90053

R:Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguc

ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Swano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.;

C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hirataetsu, K.

Lancet 357, 1225-1240, 2001

A:Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.

A:Reference number: AB9758; MUID:21311952; PMID:11418146

A:Accession: G90053

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-961 <KUR>

A:Cross-references: UNIPROT:Q99RD3; GB:BA000018; PID:g13702452; PIDN:BA843593.1; GSPDB:G

A:Experimental source: strain N315

C:Genetics:

A:Gene: fnbB

Query Match 72.9% Score 86; DB 2; Length 961;
Best Local Similarity 84.2%; Pred. No. 3.2e-05;
Matches 16; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 SYQFPFHNSVDFEEDTLPK 21

Db 786 NYQFGHNSVDFEEDTLPK 804

RESULT 3

H90053

hypothetical protein fnb [imported] - Staphylococcus aureus (strain N315)

C/Species: Staphylococcus aureus

C/Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004

C/Accession: H90053

R/Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguc

ma, A.; Mitsuhashi, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.;

C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.

Lancet 357, 1225-1240, 2001

A/Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.

A/Reference number: A89758; MUID:21311952; PMID:11418146

A/Accession: H90053

A/Status: Preliminary

A/Molecule type: DNA

A/Residues: 1-1038 <KUR>

A/Cross-references: UNIPROT:Q99RD2; GB:BA000018; PID:g13702453; PIDN:BA043594.1; GSPDB:C

A/Experimental source: strain N315

C/Genetics:

A/Gene: fnb

Query Match 72.9%; Score 86; DB 2; Length 1038;

Best Local Similarity 84.2%; Pred. No. 3.5e-05;

Matches 16; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 3 SYQFPFPHNSVDFEEDTLPK 21

Db 835 NYQFGHNSVDFEEDTLPK 853

RESULT 4

S19702

fibronectin-binding protein B - Staphylococcus aureus

C/Species: Staphylococcus aureus

C/Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004

C/Accession: S19702

R./Jensen, K.; Signaes, C.; Mueller, H.P.; Lindberg, M.

Eur. J. Biochem. 202, 1041-1048, 1991

A/Title: Two different genes encode fibronectin binding proteins in Staphylococcus aure

A/Reference number: S19702; MUID:92111475; PMID:1837265

A/Accession: S19702

A/Status: Preliminary

A/Molecule type: DNA

A/Residues: 1-940 <JOE>

A/Cross-references: UNIPROT:Q53682; EMBL:X62992; NID:g49040; PIDN:CAA44726.1; PID:g58156

C/Keywords: fibronectin binding

Query Match 69.5%; Score 82; DB 2; Length 940;

Best Local Similarity 78.9%; Pred. No. 0.00013;

Matches 15; Conservative 2; Indels 0; Gaps 0;

OY 3 SYQFPFPHNSVDFEEDTLPK 21

Db 775 NYQFGHNSVDFEEDTLPK 793

RESULT 5

A56922

transcription factor ehn - fruit fly (Drosophila melanogaster)

C/Species: Drosophila melanogaster

C/Date: 11-Aug-1995 #sequence_revision 11-Aug-1995 #text_change 09-Jul-2004

C/Accession: A56922

R./Arora, K.; Dai, H.; Kazuko, S.G.; Jamal, J.; O'Connor, M.B.; Letsou, A.; Warrior, R.

Cell 81, 781-790, 1995

A/Title: The Drosophila echnurri gene acts in the Dpp/TGFbeta signaling pathway and enc

A/Reference number: A56922; MUID:95292345; PMID:7774017

A/Accession: A56922

A/Status: Preliminary

A/Molecule type: mRNA

A/Keywords: nucleic acid sequence not shown; not compared with conceptual tra

A/Residues: 1-2578 <ARO>

A/Cross-references: UNIPROT:Q24107

C/Genetics:

A/Gene: FlyBase:ehn

A/Cross-references: FlyBase:FBgn0003396

Query Match 41.1%; Score 48.5; DB 2; Length 2578;

Best Local Similarity 52.4%; Pred. No. 81;

Matches 11; Conservative 2; Mismatches 7; Indels 1; Gaps 1;

OY 1 PASYQFPFPHNSVDFEEDTLPK 20

Db 1404 PQHGFPPPHNSVDFEEDTLPK 1424

RESULT 6

E8AD64

early E3 6.4K protein - human adenovirus 35

C/Species: Mastadenovirus h35 (human adenovirus 35)

A/Note: host Homo sapiens (man)

C/Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 09-Jul-2004

C/Accession: B31162

R./Flomenberg, P.R.; Chen, M.; Horwitz, M.S.

J. Virol. 62, 4431-4437, 1988

A/Title: Sequence and genetic organization of adenovirus type 35 early region 3.

A/Reference number: A93039; MUID:89012230; PMID:3172347

A/Accession: B31162

A/Molecule type: DNA

A/Residues: 1-61 <FLD>

A/Cross-references: UNIPROT:P17591; GB:M23195; NID:g516584; PIDN:AAA42436.1; PID:g516586

C/Superfamily: adenovirus early E3 6.4K protein

C/Keywords: early protein

Query Match 40.7%; Score 48; DB 1; Length 61;

Best Local Similarity 42.1%; Pred. No. 1.2;

Matches 8; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

OY 1 PASYQFPFPHNSVDFEEDTL 19

Db 15 PQHGFPPPHNSVDFEEDTL 33

RESULT 7

D83207

hypothetical protein PA3510 [imported] - Pseudomonas aeruginosa (strain PA01)

C/Species: Pseudomonas aeruginosa

C/Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004

C/Accession: D83207

R./Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mitsuhashi, S.D.; Warren, P.; Hickey, M.J.; Br

adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim,

; Lory, S.; Olson, M.V.

Nature 406, 959-964, 2000

A/Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patho

A/Reference number: A82950; MUID:20437337; PMID:10984043

A/Accession: D83207

A/Status: Preliminary

A/Molecule type: DNA

A/Residues: 1-176 <STO>

A/Cross-references: UNIPROT:Q9HY99; GB:AE004771; GB:AE004091; NID:g9949650; PIDN:AA06893

A/Experimental source: strain PA01

C/Genetics:

A/Gene: PA3510

Query Match 40.7%; Score 48; DB 2; Length 176;

Best Local Similarity 50.0%; Pred. No. 4.2;

Matches 8; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

OY 1 PASYQFPFPHNSVDFEED 16

Db 86 PQHGFPPPHNSVDFEED 101

RESULT 8

E89980
 hypothetical protein SA1734 [imported] - Staphylococcus aureus (strain N315)
 C:Species: Staphylococcus aureus
 C>Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
 C:Accession: E89980
 C:Authors: Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguc, M.; A.; Mitsuhashi, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.; C.; Shiba, T.; Hatori, M.; Ogasawara, N.; Hayashi, H.; Hiramoto, K.
 Lancet 357, 1225-1240, 2001
 A>Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.
 A:Reference number: A89758; MUID:21311952; PMID:11418146
 A:Accession: E89980
 A:Status: Preliminary
 A:Molecule type: DNA
 A:Residues: 1-186 <KIR>
 A:Cross-references: UNIPROT:Q998W9; GB:BA000018; PID:g13701711; PIDN:BA043004.1; GSPDB:C
 A:Experimental source: strain N315
 C:Genetics:
 A:Gene: SA1734
 C:Superfamily: hypothetical protein b1011

Query Match 40.7%; Score 48; DB 2; Length 186;
 Best Local Similarity 69.2%; Pred. No. 4.5;
 Matches 9; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 PASVQPPHNSVD 13
 DB 64 PESKLPFHNIYD 76

RESULT 9

P00442
 polyprotein - barley mild mosaic virus (strain Na1) (fragment)
 N:Contains: capsid protein; N1a protein; N1b protein
 C:Species: barley mild mosaic virus
 C>Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 09-Jul-2004
 C:Accession: P00442; P00443
 R:Kashiwazaki, S.; Nomura, K.; Kuroda, H.; Ito, K.; Hibino, H.
 J. Gen. Virol. 73, 2173-2181, 1992
 A>Title: Sequence analysis of the 3'-terminal halves of RNA 1 of two strains of barley mild mosaic virus.
 A:Reference number: P00440; MUID:93019037; PMID:1402809
 A:Accession: P00442
 A:Molecule type: mRNA
 A:Residues: 1-1041 <KAS>
 A:Cross-references: UNIPROT:Q02442; DDBJ:D10947; NID:G221057; PIDN:BA01741.1; PID:dl002
 A:Experimental source: strain Na1
 A:Accession: P00443
 A:Molecule type: protein
 A:Residues: 791-800 <KA2>
 C:Keywords: polyprotein
 F:1-255/Product: N1a protein #status predicted <N1a>
 F:256-790/Product: N1b protein #status predicted <N1b>
 F:791-1041/Product: capsid protein #status predicted <CAP>

Query Match 40.3%; Score 47.5; DB 2; Length 1041;
 Best Local Similarity 66.7%; Pred. No. 40;
 Matches 12; Conservative 0; Mismatches 5; Indels 1; Gaps 1;

QY 4 YQPPHNSVDFEEDLPK 21
 DB 361 YDRPFAV-FCEDTLTK 377

RESULT 10

P96573
 protein P12M16.25 [imported] - Arabidopsis thaliana
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C>Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
 C:Accession: P96573
 R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, J.; Chiu, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; aneem, N.F.; Hughes, B.; Huizart, L.
 Nature 408, 816-820, 2000

A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.; C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Lucero, J.S.; Malt, R.; Marziani, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
 A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, I. ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
 A>Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
 A:Reference number: A86141; MUID:21016719; PMID:11130712
 A:Accession: P96573
 A:Status: Preliminary
 A:Molecule type: DNA
 A:Residues: 1-1584 <STO>
 A:Cross-references: UNIPROT:Q9MAG6; GB:AE005173; NID:G7769860; PIDN:AAE9538.1; GSPDB:GNC
 C:Genetics:
 A:Gene: P12M16.25
 A:Map position: 1

Query Match 39.8%; Score 47; DB 2; Length 1584;
 Best Local Similarity 38.5%; Pred. No. 79;
 Matches 10; Conservative 3; Mismatches 7; Indels 6; Gaps 1;

QY 1 PASVQPPHNS-----VDFEEDLPK 20
 DB 1074 PDYRFPFHIAHWLIGCRMEDEPVP 1099

RESULT 11

C56639
 glucose-1-phosphate adenylyltransferase (EC 2.7.7.27) - Bacillus caldolyticus (fragment)
 N:Alternate names: ADP-glucose pyrophosphorylase
 C:Species: Bacillus caldolyticus
 C>Date: 11-Aug-1995 #sequence_revision 11-Aug-1995 #text_change 09-Jul-2004
 C:Accession: C56639; S23857
 R:Kiel, J.A.; Boels, J.M.; Belman, G.; Venema, G.
 DNA Seq. 3, 221-232, 1992
 A>Title: The glgB gene from the thermophilic Bacillus caldolyticus encodes a thermostable
 A:Reference number: A56639; MUID:93208370; PMID:1296817
 A:Accession: C56639
 A:Molecule type: DNA
 A:Residues: 1-250 <KIE>
 A:Cross-references: UNIPROT:P30522; EMBL:214057; NID:G39423; PIDN:CAA78441.1; PID:G39425
 A>Note: sequence extracted from NCBI backbone (NCBIP:128235)
 C:Genetics:
 A:Gene: glgC
 C:Function: catalyzes the formation of ADPglucose and pyrophosphate from alpha-D-glucose
 A:Description: glycogen/starch biosynthesis (ADPglucose-utlizing)
 A:Pathway: glycogen/starch biosynthesis
 C:Superfamily: glucose-1-phosphate adenylyltransferase
 C:Keywords: glycogen/starch biosynthesis; nucleotidylyltransferase

Query Match 38.1%; Score 45; DB 2; Length 250;
 Best Local Similarity 50.0%; Pred. No. 19;
 Matches 7; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 8 PHNSVDFEEDLPK 21
 DB 212 PHSHPFGKDVLPK 225

RESULT 12

JX0344
 legumain (EC 3.4.22.34) precursor - jack bean
 N:Alternate names: asparaginyl endopeptidase
 C:Species: Canavalia ensiformis (jack bean)
 C>Date: 22-Apr-1995 #sequence_revision 26-May-1995 #text_change 09-Jul-2004
 C:Accession: JX0344
 R:Takeda, O.; Miura, Y.; Mitsu, M.; Matsushita, H.; Kato, I.; Abe, Y.; Yokosawa, H.; Ishi, J.; Biochem. 116, 541-546, 1994
 A>Title: Isolation and analysis of cDNA encoding a precursor of Canavalia ensiformis aspe
 A:Reference number: JX0344; MUID:95155263; PMID:7852272
 A:Accession: JX0344
 A:Molecule type: mRNA
 A:Residues: 1-475 <YAK>
 A:Cross-references: UNIPROT:P49046; DDBJ:D31787; NID:G499293; PIDN:BA06596.1; PID:G49929;

A:Experimental source: seed
 C:Comment: This enzyme is involved in posttranslational processing of concanavalin A precursor
 C:Superfamily: Legumain
 C:Keywords: cysteine proteinase; glycoprotein; hydrolase
 F:1-15/Domain: signal sequence #status predicted <SIG>
 F:16-35/Domain: propeptide #status predicted <PRO>
 F:36-475/Product: legumain #status experimental <MAT>
 F:300/Binding site: carbohydrate (asn) (covalent) #status predicted

Query Match 38.1%; Score 45; DB 2; Length 475;
 Best Local Similarity 70.0%; Pred. No. 40;
 Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 PASQPFPPHN 10
 ||: |||||
 Db 314 PATVFPFPHN 323

RESULT 13
 E83796 two-component sensor histidine kinase BH1173 [imported] - Bacillus halodurans (strain C-
 C:Species: Bacillus halodurans
 C:Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004
 C:Accession: E83796
 R:Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, F.; Hira
 Nucleic Acids Res. 28, 4317-4331, 2000
 A>Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and
 A:Reference number: A83650; MUID:20515582; PMID:11058132
 A:Accession: E83796
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-476 <570>
 A:Cross-references: UNIPROT:Q9KDN6; GB:AP001511; GB:BA000004; NID:g10173727; PIDN:BA0046
 A:Experimental source: strain C-125
 C:Genetics:
 A:Gene: BH1173
 C:Superfamily: envZ protein; sensor histidine kinase homology

Query Match 38.1%; Score 45; DB 2; Length 476;
 Best Local Similarity 61.5%; Pred. No. 40;
 Matches 8; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 4 YQFPNNSVDPFE 16
 ||| |||||
 Db 59 YANPPRNDVDFRE 71

RESULT 14
 T12044 probable legumain (EC 3.4.22.34) precursor - kidney bean
 N:Alternate names: asparaginyl endopeptidase; bean endopeptidase; phaseolin; vicilin per
 C:Species: Phaseolus vulgaris (kidney bean)
 C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004
 C:Accession: T12044
 R:Senyuk, V.; Becker, C.; Muenz, K.
 submitted to the EMBL Data Library, October 1997
 A:Description: Isolation of cDNA clone encoding legumain-like proteinase (LUP2) from a c
 A:Reference number: Z17390
 A:Accession: T12044
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-493 <SEN>
 A:Cross-references: UNIPROT:O24326; EMBL:Z99957
 A:Experimental source: cultivar Moldavian; cotyledon; clone p21b
 C:Superfamily: legumain
 C:Keywords: cysteine proteinase; hydrolase
 F:1-53/Domain: propeptide #status predicted <PRO>
 F:54-493/Product: probable legumain #status predicted <MAT>

Query Match 38.1%; Score 45; DB 2; Length 493;
 Best Local Similarity 70.0%; Pred. No. 41;
 Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 PASQPFPPHN 10
 ||: |||||
 Db 332 PATVFPFPHN 341

RESULT 15
 T30806 metabotropic glutamate receptor 7 - Fugu rubripes (fragment)
 C:Species: Fugu rubripes
 C:Date: 02-Sep-2000 #sequence_revision 02-Sep-2000 #text_change 09-Jul-2004
 C:Accession: T30806
 R:Cottage, A.J.; Clark, M.; Hawker, K.; Umrانيا, Y.; Wheller, D.; Bishop, M.; Elgar, G.
 FEBS Lett. 443, 370-374, 1999
 A>Title: Three receptor genes for plasminogen related growth factors in the genome of the
 A:Reference number: Z20880; MUID:99148833; PMID:10025966
 A:Accession: T30806
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-551 <COT>
 A:Cross-references: UNIPROT:Q9PMQ0; EMBL:AJ010317; NID:e1355235; PID:e1355236; PIDN:CAA05
 C:Genetics:
 A:Gene: GRN7
 A>Note: Intron positions not resolved (incomplete sequence)
 C:Superfamily: metabotropic glutamate receptor 4

Query Match 38.1%; Score 45; DB 2; Length 551;
 Best Local Similarity 50.0%; Pred. No. 47;
 Matches 7; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 7 PPHNSVDPEETLP 20
 ||| :|||
 Db 380 PPHIIDYEQKP 393

Search completed: October 22, 2005, 04:14:08
 Job time : 18.5465 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 22, 2005, 02:23:35 ; Search time 51.4314 Seconds
(without alignments)
209.087 Million cell updates/sec

Title: US-10-731-238-34
Perfect score: 118
Sequence: 1 PASYQPPHNSVDFEEDTLPK 21

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_03:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	89	75.4	1018 1	FNBA STAU
2	86	72.9	961 2	Q99RD3
3	86	72.9	961 2	Q7A3J8
4	86	72.9	965 2	Q6GDU5
5	86	72.9	1015 2	Q8NUT7
6	86	72.9	1015 2	Q6G6H3
7	86	72.9	1038 2	Q7A3J7
8	86	72.9	1038 2	Q99RD2
9	82	69.5	940 2	Q53682
10	82	69.5	943 2	Q8NUT8
11	82	69.5	957 2	Q6G6H4
12	77	65.3	152 2	Q9AEP9
13	54	45.8	379 2	Q8PZS1
14	53	44.9	385 2	Q8BWM6
15	53	44.9	1310 1	G125_MOUSE
16	53	44.9	1321 1	G125_HUMAN
17	52	44.1	214 2	Q6ML40
18	51	43.2	260 2	Q6CJ03
19	50	42.4	327 1	HUNB_MANSE
20	50	42.4	489 2	Q6X6J1
21	50	42.4	507 2	Q6XW21
22	50	42.4	507 2	Q6XW23
23	50	42.4	911 2	Q6XW44
24	50	42.4	911 2	Q6XWBI
25	49.5	41.9	371 2	Q931H6
26	49	41.5	209 2	Q9NRY9
27	49	41.5	209 2	Q9NVX1
28	49	41.5	272 2	Q8MUK5
29	49	41.5	457 2	P96964
30	49	41.5	671 2	Q7TPU5
31	49	41.5	671 2	Q9CXF4

32	49	41.5	674 2	Q9HA83	Q9HA83 homo sapien
33	49	41.5	691 2	Q8TC07	Q8TC07 homo sapien
34	48.5	41.1	2527 2	Q24107	Q24107 drosophila
35	48.5	41.1	2532 2	Q9V5T5	Q9V5T5 drosophila
36	48.5	41.1	2577 2	Q7KR14	Q7KR14 drosophila
37	48	40.7	61 1	E306_ADE35	P17591 human adeno
38	48	40.7	156 2	Q6TAA3	Q6TAA3 symbiont ba
39	48	40.7	176 2	Q9HY99	Q9HY99 pseudomonas
40	48	40.7	186 2	Q9SW89	Q9SW89 staphylococ
41	48	40.7	186 2	Q7A0G7	Q7A0G7 staphylococ
42	48	40.7	186 2	Q7A4P6	Q7A4P6 staphylococ
43	48	40.7	186 2	Q6G814	Q6G814 staphylococ
44	48	40.7	186 2	Q6GPD8	Q6GPD8 staphylococ
45	48	40.7	265 2	Q70EB9	Q70EB9 methanospira

ALIGNMENTS

```

RESULT 1
FNBA STAU          STANDARD;          PRT; 1018 AA.
ID FNBA STAU
AC P14738;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Fibronectin-binding protein precursor (FNBP).
GN Name=fnba;
OC Staphylococcus aureus.
OS Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1280;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NCTC 8325-4;
RX MEDLINE=89098998; PubMed=2521391;
RA Signaes C., Rancui G., Joensen K., Lindgren P.-E.,
  Anantharamiah G.M., Hoeoek M., Lindberg M.;
  "Nucleotide sequence of the gene for a fibronectin-binding protein
  from Staphylococcus aureus: use of this peptide sequence in the
  synthesis of biologically active peptides.";
  Proc. Natl. Acad. Sci. U.S.A. 86:699-703(1989).
RL
CC -I- FUNCTION: The ability of bacteria to bind fibronectin has been
  proposed as a virulence factor enabling bacteria to colonize wound
  tissues and blood clots. Binding of plasma fibronectin to the
  bacterial surface might block adhesion receptors on S.aureus, thus
  representing an important defense mechanism against tissue
  invasion.
CC -I- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
  an amide bond (Potential).
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
  between the Swiss Institute of Bioinformatics and the EMBL outstation-
  the European Bioinformatics Institute. There are no restrictions on its
  use by non-profit institutions as long as its content is in no way
  modified and this statement is not removed. Usage by and for commercial
  entities requires a license agreement (See http://www.isb-sib.ch/announce/
  or send an email to license@isb-sib.ch).
CC
CC EMBL: J04151; AAA26632.1; -.
  InterPro: IPR004237; Fn_bind.
  InterPro: IPR005877; Gpos_YsIRK.
  InterPro: IPR001899; Gram_pos_anchor.
  Pfam: PF02986; Fn_bind. 1.
  Pfam: PF00746; Gram_pos_anchor; 1.
  Pfam: PF04650; YsIRK_signal; 1.
  TIGRfam: TIGR01167; LPXTG_anchor; 1.
  TIGRfam: TIGR01168; YsIRK_signal; 1.
  DR PROSITE: PS00847; GRAM_POS_ANCHORING; 1.
  DR Cell adhesion; Cell wall; Peptidoglycan-anchor; Repeat; Signal;
  virulence.
  FT SIGNAL 1 36
  FT CHAIN 37 985 Fibronectin-binding protein.
  FT PROPEP 986 1018 Removed by sortase (Potential).

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FT REPEAT 545 574 B-1.
FT REPEAT 575 604 B-2.
FT DOMAIN 745 878 4 X approximate tandem repeats,
  fibronectin-binding domain.
FT REPEAT 745 782 D-1.
FT REPEAT 783 820 D-2.
FT REPEAT 821 859 D-3.
FT REPEAT 860 878 D-4 (incomplete).
FT DOMAIN 879 948 5 X tandem repeats, Pro-rich (WR).
FT REPEAT 879 892 WR 1.
FT REPEAT 893 906 WR 2.
FT REPEAT 907 920 WR 3.
FT REPEAT 921 934 WR 4.
FT REPEAT 935 948 WR 5.
FT SITE 982 986 LPXTG sorting signal (Potential).
FT MOD_RES 985 985 Pentaglycyl murein peptidoglycan amidated
  chreonine (Potential).
SQ SEQUENCE 1018 AA; 111780 MW; 58175E0020E81F1F CRC64;

Query Match 75.4%; Score 89; DB 1; Length 1018;
Best Local Similarity 89.5%; Pred. No. 5.9e-05;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Cy 3 SYOFPPHNSVDFEEDTLPK 21
Db 839 SYOFGHNNSVDFEEDTLPK 857

RESULT 2
O99RD3 PRELIMINARY; PRT; 961 AA.
AC O99RD3;
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE Fibronectin-binding protein homolog.
GN Name=fnb3; OrderedLocustNames=SAV2502;
OS Staphylococcus aureus (strain Mu50 / ATCC 700699).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=158879;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Mu50 / ATCC 700699;
RX MEDLINE=21311952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2;
RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
  Cui L., Oguchi A., Aoki K.-I., Nagai Y., Iian J.-Q., Ito T.,
  Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hoshoyama A.,
  Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
  Sekimizu K., Hiraoka H., Kuhara S., Goto S., Yabuzaki J.,
  Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
  Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
RA "Whole genome sequencing of methicillin-resistant Staphylococcus
  aureus."
RL Lancet 357:1225-1240(2001).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
  an amide bond (by similarity).
CC EMBL; AP003365; BAB58664.1; -.
DR HSHP; Q53653; 1N67.
DR GO; GO:0009986; C:cell surface; IEA.
DR GO; GO:0005618; C:cell wall; IEA.
DR GO; GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0007155; P:cell adhesion; IEA.
DR InterPro; IPR008966; Adhes_bact.
DR InterPro; IPR004237; Fn_bind.
DR InterPro; IPR005877; Gpos_YsIRK.
DR InterPro; IPR001899; Gram_pos_anchor.
DR Pfam; PF02986; Fn_bind; 1.
DR Pfam; PF00746; Gram_pos_anchor; 1.
DR Pfam; PF04650; YsIRK_signal; 1.
DR TIGRFAMS; TIGR01167; LPXTG_anchor; 1.
DR TIGRFAMS; TIGR01168; YsIRK_signal; 1.
DR TIGRFAMS; TIGR01167; LPXTG_anchor; 1.
DR TIGRFAMS; TIGR01168; YsIRK_signal; 1.
```

```
DR PROSITE; PS50847; GRAM_POS_ANCHORING; 1.
KW Cell wall, Complete proteome; Peptidoglycan-anchor.
SQ SEQUENCE 961 AA; 106010 MW; 364940F884DA4101 CRC64;

Query Match 72.9%; Score 86; DB 2; Length 961;
Best Local Similarity 84.2%; Pred. No. 0.00016;
Matches 16; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Cy 3 SYOFPPHNSVDFEEDTLPK 21
Db 786 NYOFGHNNSVDFEEDTLPK 804

RESULT 3
O7A3J8 PRELIMINARY; PRT; 961 AA.
AC O7A3J8;
DT 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE PNB protein.
GN Name=fnb3; OrderedLocustNames=SA2290;
OS Staphylococcus aureus (strain N315).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=158879;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21311952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2;
RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
  Cui L., Oguchi A., Aoki K.-I., Nagai Y., Iian J.-Q., Ito T.,
  Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hoshoyama A.,
  Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
  Sekimizu K., Hiraoka H., Kuhara S., Goto S., Yabuzaki J.,
  Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
  Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
RA "Whole genome sequencing of methicillin-resistant Staphylococcus
  aureus."
RL Lancet 357:1225-1240(2001).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
  an amide bond (by similarity).
CC EMBL; AP003137; BAB43593.1; -.
DR GO; GO:0009986; C:cell surface; IEA.
DR GO; GO:0005618; C:cell wall; IEA.
DR GO; GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0007155; P:cell adhesion; IEA.
DR InterPro; IPR008966; Adhes_bact.
DR InterPro; IPR004237; Fn_bind.
DR InterPro; IPR005877; Gpos_YsIRK.
DR InterPro; IPR001899; Gram_pos_anchor.
DR Pfam; PF02986; Fn_bind; 1.
DR Pfam; PF00746; Gram_pos_anchor; 1.
DR Pfam; PF04650; YsIRK_signal; 1.
DR TIGRFAMS; TIGR01167; LPXTG_anchor; 1.
DR TIGRFAMS; TIGR01168; YsIRK_signal; 1.
DR PROSITE; PS50847; GRAM_POS_ANCHORING; 1.
KW Cell wall, Complete proteome; Peptidoglycan-anchor.
SQ SEQUENCE 961 AA; 106010 MW; 364940F884DA4101 CRC64;

Query Match 72.9%; Score 86; DB 2; Length 961;
Best Local Similarity 84.2%; Pred. No. 0.00016;
Matches 16; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Cy 3 SYOFPPHNSVDFEEDTLPK 21
Db 786 NYOFGHNNSVDFEEDTLPK 804

RESULT 4
O6GDUS PRELIMINARY; PRT; 965 AA.
AC O6GDUS;
DT 05-JUL-2004 (TREMBLrel. 27, Created)
```

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DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE Fibronectin-binding protein.
GN Name=fnbA; OrderedLocNames=SAR2580;
OS Staphylococcus aureus (strain MRSA252).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=282458;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed1513324; DOI=10.1073/pnas.0402521101;
RA Holden M.T.G., Fell E.J., Lindsay J.A., Peacock S.J., Day N.P.J.,
RA Enright M.C., Foster T.J., Moore C.E., Hurst L., Atkin R., Barron A.,
RA Baeson N., Bentley S.D., Chillingworth C., Chillingworth T.,
RA Churcher C., Clark L., Corton C., Cronin A., Doggett J., Dowd L.,
RA Felwell T., Hance Z., Harris B., Hauser H., Holroyd S., Jagels K.,
RA James K.D., Leonard N., Line A., Mayes R., Moulé S., Mungall K.,
RA Ormond D., Quail M.A., Rabinowitch E., Rutherford K.M., Sanders M.,
RA Sharp S., Simmonds M., Stevens K., Whitehead S., Barrett B.G.,
RA Spratt B.G., Parkhill J.;
RT "Complete genomes of two clinical Staphylococcus aureus strains:
RT evidence for the rapid evolution of virulence and drug resistance.";
RU Proc. Natl. Acad. Sci. U.S.A. 101:9786-9791(2004).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC an amide bond (By similarity).
CC EMBL: BX571856; CAG41560.1; -.
DR GO: GO:0009986; C:cell surface; IEA.
DR GO: GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO: GO:0016020; C:membrane; IEA.
DR GO: GO:0007155; P:cell adhesion; IEA.
DR InterPro: IPR008966; Adhes_Bact.
DR InterPro: IPR004237; Fn_bind.
DR InterPro: IPR005877; Gpos_YsIRK.
DR InterPro: IPR001899; Gram_pos_anchor.
DR Pfam: PF00746; Gram_pos_anchor; 1.
DR Pfam: PF04650; YsIRK_signal; 1.
DR TIGRFAMs: TIGR01167; LpXTG_anchor; 1.
DR TIGRFAMs: TIGR01168; YsIRK_signal; 1.
DR TIGRFAMs: TIGR01167; LpXTG_anchor; 1.
DR PROSITE: PS50847; GRAM_POS_ANCHORING; 1.
KW Cell wall, Complete proteome; Peptidoglycan-anchor.
SQ SEQUENCE 965 AA; 105691 MW; 29828132164D0551 CRC64;

Query Match 72.9%; Score 86; DB 2; Length 965;
Best Local Similarity 84.2%; Pred. No. 0.00017;
Matches 16; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 SYOPEPHNSVDFEDTLPK 21
DB 804 NYOFGHNSVDFEDTLPK 822

RESULT 5
Q8NUU7 PRELIMINARY; PRT; 1015 AA.
ID Q8NUU7;
AC Q8NUU7;
DT 01-OCT-2002 (TREMBlrel. 22, Created)
DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Fmb protein.
GN Name=fmb; OrderedLocNames=MM2421;
OS Staphylococcus aureus (strain MM2).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=196620;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=MM2;
RX MEDLINE=22040717; PubMed=12044378; DOI=10.1016/S0140-6736(02)08713-5;
RA Baba T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Oguchi A.,
RA Nagai Y., Iwama N., Amano K., Naimi T., Kuroda H., Cui L.,
RA Yamamoto K., Hiramatsu K.;
RT "Genome and virulence determinants of high virulence community-
RT acquired MRSA.";
RU Lancet 359:1819-1827(2002).
```

```
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC an amide bond (By similarity).
CC EMBL: AP004830; BAB96286.1; -.
DR GO: GO:0009986; C:cell surface; IEA.
DR GO: GO:0005618; C:cell wall; IEA.
DR GO: GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO: GO:0016020; C:membrane; IEA.
DR GO: GO:0007155; P:cell adhesion; IEA.
DR InterPro: IPR008966; Adhes_Bact.
DR InterPro: IPR004237; Fn_bind.
DR InterPro: IPR005877; Gpos_YsIRK.
DR InterPro: IPR001899; Gram_pos_anchor.
DR Pfam: PF02986; Fn_bind; 1.
DR Pfam: PF00746; Gram_pos_anchor; 1.
DR Pfam: PF04650; YsIRK_signal; 1.
DR TIGRFAMs: TIGR01167; LpXTG_anchor; 1.
DR TIGRFAMs: TIGR01168; YsIRK_signal; 1.
DR PROSITE: PS50847; GRAM_POS_ANCHORING; 1.
KW Cell wall, Complete proteome; Peptidoglycan-anchor.
SQ SEQUENCE 1015 AA; 111145 MW; D0F9281B864D44D2 CRC64;

Query Match 72.9%; Score 86; DB 2; Length 1015;
Best Local Similarity 84.2%; Pred. No. 0.00017;
Matches 16; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 SYOPEPHNSVDFEDTLPK 21
DB 840 NYOFGHNSVDFEDTLPK 858

RESULT 6
Q6G6H3 PRELIMINARY; PRT; 1015 AA.
ID Q6G6H3;
AC Q6G6H3;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE Fibronectin-binding protein.
GN OrderedLocNames=SAS2388;
OS Staphylococcus aureus (strain MSSA476).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=282459;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=15213324; DOI=10.1073/pnas.0402521101;
RA Holden M.T.G., Fell E.J., Lindsay J.A., Peacock S.J., Day N.P.J.,
RA Enright M.C., Foster T.J., Moore C.E., Hurst L., Atkin R., Barron A.,
RA Baeson N., Bentley S.D., Chillingworth C., Chillingworth T.,
RA Churcher C., Clark L., Corton C., Cronin A., Doggett J., Dowd L.,
RA Felwell T., Hance Z., Harris B., Hauser H., Holroyd S., Jagels K.,
RA James K.D., Leonard N., Line A., Mayes R., Moulé S., Mungall K.,
RA Ormond D., Quail M.A., Rabinowitch E., Rutherford K.M., Sanders M.,
RA Sharp S., Simmonds M., Stevens K., Whitehead S., Barrett B.G.,
RA Spratt B.G., Parkhill J.;
RT "Complete genomes of two clinical Staphylococcus aureus strains:
RT evidence for the rapid evolution of virulence and drug resistance.";
RU Proc. Natl. Acad. Sci. U.S.A. 101:9786-9791(2004).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC an amide bond (By similarity).
CC EMBL: BX571857; CAG44202.1; -.
DR GO: GO:0009986; C:cell surface; IEA.
DR GO: GO:0005618; C:cell wall; IEA.
DR GO: GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO: GO:0016020; C:membrane; IEA.
DR GO: GO:0007155; P:cell adhesion; IEA.
DR InterPro: IPR008966; Adhes_Bact.
DR InterPro: IPR004237; Fn_bind.
DR InterPro: IPR005877; Gpos_YsIRK.
DR InterPro: IPR001899; Gram_pos_anchor.
DR Pfam: PF00746; Gram_pos_anchor; 1.
DR Pfam: PF04650; YsIRK_signal; 1.
DR TIGRFAMs: TIGR01167; LpXTG_anchor; 1.
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DR TIGRFAMS; TIGR01168; YSIRK signal; 1.
DR PROSITE; PS50847; GRAM_POS_ANCHORING; 1.
KM Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ SEQUENCE 1015 AA; 111145 MW; D0F9281BB64D44D2 CRC64;

Query Match 72.9%; Score 86; DB 2; Length 1015;
Best Local Similarity 84.2%; Pred. No. 0.00017;
Matches 16; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 SYQFPPHNSVDFEEDTLPK 21
Db 840 NYQFGCHNSVDFEEDTLPK 858

RESULT 7
QY 099RD2 PRELIMINARY; PRT; 1038 AA.
AC 099RD2;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE Fibronectin-binding protein homolog.
GN Name=fnb; OrderedLocuNames=SAV2503;
OS Staphylococcus aureus (strain Mu50 / ATCC 700699).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
CX NCBI_TaxID=158879;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Mu50 / ATCC 700699;
RX MEDLINE=21311952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2;
RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Iian J.-O., Ito T.,
RA Kanamori M., Matsunaru H., Maruyama A., Murakami H., Hoshiyama A.,
RA Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
RA Sekimizu K., Hiraoka H., Kuhara S., Goto S., Yabuzaki J.,
RA Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
RA Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
RT "Whole genome sequencing of methicillin-resistant Staphylococcus
RT aureus."
RL Lancet 357:1225-1240(2001).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC an amide bond (By similarity).
DR EMBL; AP003137; BAB3594.1; -.
DR PIR; H90053; H90053.
DR GO; GO:0009986; C:cell surface; IEA.
DR GO; GO:0005618; C:cell wall; IEA.
DR GO; GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0007155; P:cell adhesion; IEA.
DR InterPro; IPR008966; Adhes_bact.
DR InterPro; IPR004237; Fn_bind.
DR InterPro; IPR005877; Gpos_YSIRK.
DR InterPro; IPR001899; Gram_pos_anchor.
DR Pfam; PF02986; Fn_bind. 1.
DR Pfam; PF00746; Gram_pos_anchor; 1.
DR Pfam; PF04650; YSIRK_signal; 1.
DR TIGRFAMS; TIGR01167; LPXTG_anchor; 1.
DR TIGRFAMS; TIGR01168; YSIRK_signal; 1.
DR PROSITE; PS50847; GRAM_POS_ANCHORING; 1.
KM Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ SEQUENCE 1038 AA; 113618 MW; 666BF6BF2BFBB12 CRC64;

Query Match 72.9%; Score 86; DB 2; Length 1038;
Best Local Similarity 84.2%; Pred. No. 0.00018;
Matches 16; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 SYQFPPHNSVDFEEDTLPK 21
Db 835 NYQFGCHNSVDFEEDTLPK 853

RESULT 8
QY 07A3J7 PRELIMINARY; PRT; 1038 AA.
AC 07A3J7;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE Fnb protein.
GN Name=fnb; OrderedLocuNames=SA2291;
OS Staphylococcus aureus (strain N315).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
CX NCBI_TaxID=158879;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=8325-4;
RX MEDLINE=92111475; PubMed=1837266;
RA Jonsson K., Sigmas C., Muller H.-P., Lindberg M.;
RT "Two different genes encode fibronectin binding proteins in
RT Staphylococcus aureus. The complete nucleotide sequence and
RT characterization of the second gene."/;
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ID 07A3J7 PRELIMINARY; PRT; 1038 AA.
AC 07A3J7;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE Fnb protein.
GN Name=fnb; OrderedLocuNames=SA2291;
OS Staphylococcus aureus (strain N315).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
CX NCBI_TaxID=158879;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=8325-4;
RX MEDLINE=92111475; PubMed=1837266;
RA Jonsson K., Sigmas C., Muller H.-P., Lindberg M.;
RT "Two different genes encode fibronectin binding proteins in
RT Staphylococcus aureus. The complete nucleotide sequence and
RT characterization of the second gene."/;
```

```

RL Eur. J. Biochem. 202:1041-1048(1991).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC an amide bond (By similarity).
DR EMBL; X62992; CAA4726.1; -.
DR PIR; S19702; S19702.
DR HSSP; Q53653; IN67.
DR GO; GO:0009986; C:cell surface; IEA.
DR GO; GO:0005618; C:cell wall; IEA.
DR GO; GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0007155; P:cell adhesion; IEA.
DR InterPro; IPR008966; Adhes_bact.
DR InterPro; IPR004237; Fn_bind.
DR InterPro; IPR005877; Gpos_YsIRK.
DR Pfam; PF02986; Fn_bind_2.
AC Q6G6H4; PRELIMINARY; PRT; 943 AA.
DR PFam; PF00746; Gram_pos_anchor; 1.
DR PFam; PF04650; YsIRK_signal; 1.
DR TIGRFAMs; TIGR01167; LPXTG_anchor; 1.
DR TIGRFAMs; TIGR01168; YsIRK_signal; 1.
DR PROSITE; PS50847; GRAM_POS_ANCHORING; 1.
KM Cell wall; Peptidoglycan-anchor.
SQ SEQUENCE 940 AA; 10355 MW; E35FBBCA907AE345 CRC64;

Query Match 69.5%; Score 82; DB 2; Length 940;
Best Local Similarity 78.9%; Pred. No. 0.00068;
Matches 15; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 3 SYOPEPHNSVDFEEDTLPK 21
DB 775 NYQFGHNSVDFEEDTLPO 793

RESULT 10
Q8NUB8 PRELIMINARY; PRT; 943 AA.
AC Q8NUB8;
DR 01-OCT-2002 (TREMBlrel. 22, Created)
DR 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
DR 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE FmbB protein.
GN Name=fmbB; OrderedLocustNames=MM2420;
OS Staphylococcus aureus (strain MM2).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=196620;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MM2;
RX MEDLINE=22040717; PubMed=12044378; DOI=10.1016/S0140-6736(02)08713-5;
RA Baba T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Oguchi A.,
RA Nagai Y., Iwana N., Asano K., Naimi T., Kuroda H., Cui L.,
RA Yamamoto K., Hiratake K.;
"Genome and virulence determinants of high virulence community-
RT acquired MRSA."
RL Lancet 359:1819-1827(2002).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC an amide bond (By similarity).
DR EMBL; AF004830; BAB96285.1; -.
DR HSSP; Q53653; IN67.
DR GO; GO:0009986; C:cell surface; IEA.
DR GO; GO:0005618; C:cell wall; IEA.
DR GO; GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0007155; P:cell adhesion; IEA.
DR InterPro; IPR008966; Adhes_bact.
DR InterPro; IPR004237; Fn_bind.
DR InterPro; IPR005877; Gpos_YsIRK.
DR InterPro; IPR001899; Gram_pos_anchor.
DR Pfam; PF02986; Fn_bind_1.
DR Pfam; PF00746; Gram_pos_anchor; 1.
DR Pfam; PF04650; YsIRK_signal; 1.
DR TIGRFAMs; TIGR01167; LPXTG_anchor; 1.
DR TIGRFAMs; TIGR01168; YsIRK_signal; 1.

```

```

DR PROSITE; PS50847; GRAM_POS_ANCHORING; 1.
KM Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ SEQUENCE 943 AA; 104537 MW; DA8A5F31947E1B8A CRC64;

Query Match 69.5%; Score 82; DB 2; Length 943;
Best Local Similarity 78.9%; Pred. No. 0.00069;
Matches 15; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 3 SYOPEPHNSVDFEEDTLPK 21
DB 782 NYQFGHNSVDFEEDTLPO 800

RESULT 11
Q6G6H4 PRELIMINARY; PRT; 957 AA.
AC Q6G6H4;
DR 05-JUL-2004 (TREMBlrel. 27, Created)
DR 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DR 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE Fibronectin-binding protein.
GN Name=fmbB; OrderedLocustNames=SA52387;
OS Staphylococcus aureus (strain MSSA476).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=282459;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=15213324; DOI=10.1073/pnas.0402521101;
RA Holden M.T.G., Fell E.J., Lindsey J.A., Peacock S.J., Day N.P.J.,
RA Enright M.C., Foster T.J., Moore C.E., Hurst L., Atkin R., Barton A.,
RA Bason N., Bentley S.D., Chillingworth C., Chillingworth T.,
RA Churcher C., Clark L., Cotton C., Cronin A., Doggett J., Dowd L.,
RA Felwell T., Hance Z., Harris B., Hauser H., Holtroyd S., Jagels K.,
RA James K.D., Lennard N., Line A., Mayes R., Moutie S., Mungall K.,
RA Ormond D., Quail M.A., Rabinowitch E., Rutherford K.M., Sanders M.,
RA Sharp S.G., Simmonds M., Stevens K., Whitehead S., Barrell B.G.,
RA Spratt B.G., Parkhill J.;
"Complete genomes of two clinical Staphylococcus aureus strains:
RT evidence for the rapid evolution of virulence and drug resistance."
RL Proc. Natl. Acad. Sci. U.S.A. 101:9786-9791(2004).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC an amide bond (By similarity).
DR EMBL; BX571857; CAG44201.1; -.
DR GO; GO:0009986; C:cell surface; IEA.
DR GO; GO:0005618; C:cell wall; IEA.
DR GO; GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0007155; P:cell adhesion; IEA.
DR InterPro; IPR008966; Adhes_bact.
DR InterPro; IPR004237; Fn_bind.
DR InterPro; IPR005877; Gpos_YsIRK.
DR InterPro; IPR001899; Gram_pos_anchor.
DR Pfam; PF02986; Fn_bind_1.
DR Pfam; PF00746; Gram_pos_anchor; 1.
DR Pfam; PF04650; YsIRK_signal; 1.
DR TIGRFAMs; TIGR01167; LPXTG_anchor; 1.
DR TIGRFAMs; TIGR01168; YsIRK_signal; 1.
DR PROSITE; PS50847; GRAM_POS_ANCHORING; 1.
KM Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ SEQUENCE 957 AA; 105980 MW; 28F8BA7FFDFD3EAF CRC64;

Query Match 69.5%; Score 82; DB 2; Length 957;
Best Local Similarity 78.9%; Pred. No. 0.0007;
Matches 15; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 3 SYOPEPHNSVDFEEDTLPK 21
DB 782 NYQFGHNSVDFEEDTLPO 800

RESULT 12
Q9AEP9 PRELIMINARY; PRT; 152 AA.
ID Q9AEP9

```


AC	Q9AEP9; 2001 (TReMBLrel. 17, Created)
DT	01-JUN-2001 (TReMBLrel. 17, Last sequence update)
DT	01-JUN-2001 (TReMBLrel. 17, Last annotation update)
DE	01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DR	Fibronectin-binding protein (Fragment).
GN	Name=fnb;
OS	Staphylococcus aureus.
OC	Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX	NCB1_TaxID=1280;
RN	(1)
RP	SEQUENCE FROM N.A.
RC	STRAIN=CMRSA-1;
RX	MEDLINE=21246681; PubMed=11349044;
RX	DOI=10.1128/JAI.69.6.3791-3799.2001;
RA	Rice K., Huerea M., Vaz D., McGavin M.J.;
RT	"Variation in fibronectin binding and fnb locus polymorphisms in
RT	Staphylococcus aureus: identification of antigenic variation in a
RT	fibrinectin binding protein adhesin of the epidemic CMRSA-1 strain of
RL	methicillin-resistant S. aureus.";
RL	Infect. Immun. 69:3791-3799(2001).
FT	EMBL; AY029184; AAK31588.1; ..
FT	NON_TER 1
FT	NON_TER 1
SQ	SEQUENCE 152 AA; 17193 MW; CFA3913C2B11C025 CRC64;
Query Match	65.3%; Score 77; DB 2; Length 152;
Best Local Similarity	73.7%; Pred. No. 0.00051;
Matches 14; Conservative 1; Mismatches 4; Indels 0; Gaps 0;	
OY	3 SYGPPHNSVDFEEDTLPK 21
Db	132 SYGFGHGNDIFVEDTLPK 150
RESULT 13	
OBPZSI	
ID	OBPZSI PRELIMINARY; PRT; 379 AA.
AC	OBPZSI;
DT	01-OCT-2002 (TReMBLrel. 22, Created)
DT	01-OCT-2002 (TReMBLrel. 22, Last sequence update)
DT	01-MAR-2004 (TReMBLrel. 26, Last annotation update)
DE	Transposase.
GN	OrderedLocNames=MW0421;
OS	Methanosarcina mazei (Methanosarcina frisia).
OC	Archaea; Euryarchaeota; Methanomicrobia; Methanosarcinales;
OC	Methanosarcinaceae; Methanosarcinia.
OX	NCBI_TaxID=22209;
RN	(1)
RP	SEQUENCE FROM N.A.
RC	STRAIN=Goe1 / ATCC BAA-199 / DSM 3647 / OCM 88;
RC	MEDLINE=22120827; PubMed=12125824;
RA	Depemeler U., Johann A., Harsesh T., Merkl R., Schmitz R.A.,
RA	Martinez-Arias R., Henne A., Wietzer A., Baumer S., Jacobi C.,
RA	Brieglebmann H., Lienard T., Christmann A., Boennecke M., Steckel S.,
RA	Bhatnagar Y.A., Lykidis A., Overbeek R., Kleink H.-P., Gunsalus R.P.,
RA	Fritz H.-O., Gottschalk G.;
RT	"The genome of Methanosarcina mazei: evidence for lateral gene
RT	transfer between Bacteria and Archaea.";
RU	J. Mol. Microbiol. Biotechnol. 4:453-461(2002).
DR	EMBL; AE013267; AM30117.1; ..
DR	InterPro; IPR001959; Transposase_2.
DR	InterPro; IPR010095; Tspase1_feng_C.
DR	Pfam; PF01385; Transposase_2; 1.
DR	Pfam; PF07282; Transposase_35; 1.
KW	TIGRFAMs; TIGR01766; tspase1_feng_C; 1.
SQ	Complete proteome.
SQ	SEQUENCE 379 AA; 43321 MW; 28EDCS85AB04BDC5 CRC64;
Query Match	45.8%; Score 54; DB 2; Length 379;
Best Local Similarity	57.1%; Pred. No. 6.3;
Matches 12; Conservative 3; Mismatches 4; Indels 2; Gaps 1;	
OY	3 SYGPPHNSVDFEEDTL--LPK 21

Db 117 SFPVPGHYSVDPEKNTIKLKP 137

RESULT 14

ID	OBEMM6	PRELIMINARY;	PRT:	385 AA.
AC	OBEMM6;			
D7	01-MAR-2003 (TREMBLrel_23, Created)			
D7	01-MAR-2003 (TREMBLrel_23, Last sequence update)			
D7	01-MAR-2004 (TREMBLrel_26, Last annotation update)			
DE	Mus musculus 18 days pregnant adult female placenta and extra embryonic tissue cDNA, RIKEN full-length enriched library, clone:J3830613O22 product:weakly similar to TUMOR ENDOTHELIAL MARKER 5.			
DE	Name=Gpr125;			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX	NCBI_TaxID=10090;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=C57BL/6J; TISSUE=Placenta and extra embryonic tissue;			
RX	MEDLINE=99299253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;			
RA	Carninci P., Hayashizaki Y.;			
RT	"High-efficiency full-length cDNA cloning.";			
RL	Meth. Enzymol. 303:19-44(1999).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=C57BL/6J; TISSUE=Placenta and extra embryonic tissue;			
RX	MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;			
RA	RIKEN FANTOM Consortium;			
RT	"Functional annotation of a full-length mouse cDNA collection.";			
RL	Nature 409:685-690(2001).			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=C57BL/6J; TISSUE=Placenta and extra embryonic tissue;			
RA	The FANTOM Consortium,			
RT	"Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs.";			
RL	Nature 420:563-573(2002).			
RN	[4]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=C57BL/6J; TISSUE=Placenta and extra embryonic tissue;			
RX	MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;			
RA	Carninci P., Shibata K., Hayatsu N., Sugahara Y., Shibata K., Itoh M., Kono H., Okazaki Y., Muramatsu M., Hayashizaki Y.;			
RT	"Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes.";			
RL	Genome Res. 10:1617-1630(2000).			
RN	[5]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=C57BL/6J; TISSUE=Placenta and extra embryonic tissue;			
XX	MEDLINE=20530913; PubMed=11076661; DOI=10.1101/gr.152600;			
RA	Shibata K., Itoh M., Aizawa K., Nagaoaka S., Saeki N., Carninci P., Kono H., Akiyama J., Nishi K., Kitajima T., Tashiro H., Itoh M., Sumi N., Ishii Y., Nakamura S., Hazama M., Nishino T., Harada A., Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kasaihiagi K., Fujimake S., Inoue K., Togawa Y., Izawa M., Ohara E., Matsubiki M., Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J., Okazaki Y., Muramatsu M., Inoue Y., Kita A., Hayashizaki Y.;			
RT	"RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multichannel sequencer.";			
RL	Genome Res. 10:1757-1771(2000).			
RN	[6]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=C57BL/6J; TISSUE=Placenta and extra embryonic tissue;			
RA	Adechi U., Aizawa K., Akhita S., Akimura T., Arai A., Aono H., Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M., Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Horii F., Imachi K., Ishii Y., Itoh M., Izawa M., Kaubawa T., Kato H., Kawai J., Kohji Y., Kono H., Kouda M., Koya S., Kurihara C.,			

CC -1- SIMILARITY: Belongs to the G-protein coupled receptor 2 family.

CC		IN-TM7 subfamily.	
CC	-1-	SIMILARITY: Contains 1 GPS domain.	
CC	-1-	SIMILARITY: Contains 1 immunoglobulin-like domain.	
CC	-1-	SIMILARITY: Contains 4 leucine-rich (LRR) repeats.	
CC		-----	
CC		This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outcateration - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or_send_an_email_to_license@isb-sib.ch).	
CC		-----	
DR	EMBL; BC019649;	AABH9649.1; "	
DR	EMBL; BC052391;	AAH52391.1; ALT_INIT.	
DR	EMBL; BC058251;	AAH58251.1; "	
DR	MGI; MGI:1917943;	3830613022Rik.	
DR	InterPro; IPR000832;	GPCR_secretin.	
DR	InterPro; IPR001879;	hormn_receptor.	
DR	InterPro; IPR003599;	IG_1.	
DR	InterPro; IPR007110;	IG-like.	
DR	InterPro; IPR001611;	LRR.	
DR	InterPro; IPR000483;	LRR_Cterm.	
DR	InterPro; IPR003591;	LRR_Typ.	
DR	InterPro; IPR000203;	PXD_cys_rich.	
DR	Pfam; PF00002;	7tm_2; 1.	
DR	Pfam; PF01825;	GPS; 1.	
DR	Pfam; PF00047;	IG; 1.	
DR	Pfam; PF00560;	LRR; 4.	
DR	Pfam; PF01463;	LRRCT; 1.	
DR	SMART; SMO0303;	GPS; 1.	
DR	SMART; SMO0409;	IG; 1.	
DR	SMART; SMO0369;	LRR_TYP; 3.	
DR	SMART; SMO0082;	LRRCT; 1.	
DR	PROSITE; PS00649;	G_PROTEIN_RECPE_F2_1; FALSE_NEG.	
DR	PROSITE; PS00650;	G_PROTEIN_RECPE_F2_2; FALSE_NEG.	
DR	PROSITE; PS50227;	G_PROTEIN_RECPE_F2_3; 1.	
DR	PROSITE; PS50261;	G_PROTEIN_RECPE_F2_4; 1.	
DR	PROSITE; PS50221;	GPS; 1.	
KW	DR	PROSITE; PS50835;	IG_LIKE; 1.
KW	DR	G-protein coupled receptor; Receptor; Signal; Transmembrane.	
KW	LEUCINE-RICH REPEAT; REPEAT; SIGNAL; TRANSMEMBRANE.		
FT	CHAIN	1 27	Potential.
FT	DOMAIN	28 1310	Probable G protein-coupled receptor 125.
FT	TRANSMEM	28 747	Extracellular (Potential).
FT	DOMAIN	748 768	1 (Potential).
FT	TRANSMEM	769 785	Cytoplasmic (Potential).
FT	TRANSMEM	786 806	2 (Potential).
FT	DOMAIN	807 815	Extracellular (Potential).
FT	TRANSMEM	816 836	3 (Potential).
FT	DOMAIN	837 865	Cytoplasmic (Potential).
FT	TRANSMEM	866 886	4 (Potential).
FT	DOMAIN	887 908	Extracellular (Potential).
FT	TRANSMEM	909 929	5 (Potential).
FT	DOMAIN	930 985	Cytoplasmic (Potential).
FT	TRANSMEM	986 1006	6 (Potential).
FT	DOMAIN	1007 1013	Extracellular (Potential).
FT	TRANSMEM	1014 1034	7 (Potential).
FT	DOMAIN	1035 1310	Cytoplasmic (Potential).
FT	REPEAT	68 92	LRR 1.
FT	REPEAT	93 116	LRR 2.
FT	REPEAT	117 140	LRR 3.
FT	REPEAT	142 164	LRR 4.
FT	DOMAIN	687 738	GPS.
FT	DOMAIN	231 329	IG-like.
FT	DOMAIN	44 48	Poly-Ala.
FT	DOMAIN	1109 1112	Poly-Ala.
FT	CARBOHYD	70 70	N-linked (GlcNAc . .) (potential).
FT	CARBOHYD	87 87	N-linked (GlcNAc . .) (potential).
FT	CARBOHYD	148 148	N-linked (GlcNAc . .) (potential).
FT	CARBOHYD	195 195	N-linked (GlcNAc . .) (potential).
FT	CARBOHYD	290 290	N-linked (GlcNAc . .) (potential).
FT	CARBOHYD	321 321	N-linked (GlcNAc . .) (potential).

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OM protein - protein search, using sw model

Run on: October 25, 2005, 18:43:07 ; Search time 106.338 Seconds
(without alignments)
137.434 Million cell updates/sec

Title: US-10-731-238-35
Perfect score: 206
Sequence: 1 ONSGNQSPEDTEEDPKRYEQGNIVDIDFDSVPQIHG 38

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_1dDec04:*

- 1: geneseqp1980s:*
- 2: geneseqp1990s:*
- 3: geneseqp2000s:*
- 4: geneseqp2001s:*
- 5: geneseqp2002s:*
- 6: geneseqp2003as:*
- 7: geneseqp2003bs:*
- 8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	206	100.0	38	2	AAW65691 Fibronec
2	195	94.7	38	2	AAW65661 Fibronec
3	195	94.7	130	2	AAW58806 Fibronec
4	195	94.7	130	2	AAW58807 Fibronec
5	195	94.7	130	2	AAW91202 Fibronec
6	195	94.7	130	2	AAW91201 Fibronec
7	195	94.7	134	2	AAW29089 Cloned fi
8	195	94.7	134	2	AAW29088 S. aureus
9	195	94.7	134	2	AAW29087 S. aureus
10	195	94.7	139	2	AAW31556 Fibronec
11	195	94.7	174	2	AAW58808 Fibronec
12	195	94.7	174	2	AAW91203 Fibronec
13	195	94.7	181	2	AAW58805 Fibronec
14	195	94.7	181	2	AAW91200 Fibronec
15	195	94.7	559	2	AAW69803 Staphyloc
16	195	94.7	767	4	AAW34403 Staphyloc
17	195	94.7	767	4	AAW37547 Staphyloc
18	195	94.7	940	2	AAW07070 Fibronec
19	195	94.7	940	6	ABU19111 Pathogen
20	195	94.7	948	6	ABU18923 Staphyloc
21	195	94.7	948	6	ABU18923 Pathogen
22	195	94.7	948	6	ABU18923 Staphyloc
23	195	94.7	961	6	ABU15854 Protein e
24	195	94.7	1018	1	AAW62115 Fibronec
25	195	94.7	1018	4	AAU37245 Staphyloc

26	195	94.7	1018	4	AAU34301 Staphyloc
27	195	94.7	1018	6	ABU18922 Pathogen
28	195	94.7	1018	6	ABU18922 Staphyloc
29	195	94.7	1027	2	AAW89806 Staphyloc
30	195	94.7	1038	6	ABU15903 Protein e
31	189	91.7	38	2	AAW65692 Fibronec
32	189	91.7	38	2	AAW65695 Fibronec
33	189	91.7	38	2	AAW65696 Fibronec
34	189	91.7	38	2	AAW65697 Fibronec
35	189	91.7	38	2	AAW65693 Fibronec
36	188	91.3	38	2	AAW65694 Fibronec
37	188	91.3	38	2	AAW65698 Fibronec
38	187	90.8	38	2	AAW65701 Fibronec
39	187	90.8	38	2	AAW65662 Fibronec
40	187	90.8	38	2	AAW65699 Fibronec
41	187	90.8	978	4	AAU33960 Staphyloc
42	187	90.8	1001	4	AAU37093 Staphyloc
43	186	90.3	38	1	AAW80660 Protein w
44	186	90.3	38	1	AAW82116 Fibronec
45	184.5	89.6	39	2	AAW65712 Fibronec

ALIGNMENTS

RESULT 1
AAW65691 ID AAW65691 standard; peptide; 38 AA.
XX
AC AAW65691;
XX
DT 16-OCT-1998 (first entry)
XX
DE Fibronectin binding protein-derived peptide #35.
XX
KW microbial surface components recognising adhesive matrix molecule;
KW MSCRAMM; fibrinectin; fibrinectin-binding protein; antibody; epitope;
KW antitoxic; bacterial infection; antibiotic-resistant strain.
XX
OS Synthetic.
OS Staphylococcus aureus.
XX
PN WO9831389-A2.
XX
PD 23-JUL-1998.
XX
PF 21-JAN-1998; 98WO-US001222.
XX
PR 21-JAN-1997; 97US-0036139P.
XX
PA (TEXAS) UNIV TEXAS A & M SYSTEM.
XX
PI Hoeek M, Patti JM, House-Pompeo KL, Speziale P, Joh D;
PI McGavin MJ;
XX
DR WPI; 1998-413816/35.
XX
PT Antibody that binds to fibrinectin-binding protein, preventing its
PT binding to fibrinectin - used to treat or prevent bacterial infection,
PT especially by Staphylococci and Streptococci.
XX
PS Example 8; Page 101; 201pp; English.
XX
CC The invention relates to antibodies that bind to a fibrinectin-binding
CC domain of a fibrinectin-binding protein, and inhibit binding of the
CC protein to a fibrinectin. Also claimed are: (1) isolated peptides of a
CC fibrinectin-binding protein that do not bind to fibrinectin; (2) fusion
CC protein containing at least one peptide of a fibrinectin-binding protein
CC linked to a second amino acid sequence; (3) nucleic acid encoding the
CC isolated peptide of (1). Antibodies, the isolated peptides of (1) and the
CC nucleic acids are all useful for immunisation (active or passive) and (by
CC inhibiting binding of bacteria to fibrinectin) for preventing or treating
CC infection in humans or other animals, particularly by staphylococci or

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CC streptococci, e.g. meningitis, otitis media, pneumonia, endocarditis,
CC mastitis in cattle, abortion in horses and many others. Since the
CC antibodies block binding of bacteria, they should be effective against
CC antibiotic-resistant strains, and may replace antibiotic therapy or
CC increase its effectiveness. Sequences AAW65691-700 represent a series of
CC synthetic peptides based on the D1 region of S. aureus fibronectin
CC binding protein A. They were synthesised to contain mutations
XX
SQ Sequence 38 AA;
Query Match 100.0%; Score 206; DB 2; Length 38;
Best Local Similarity 100.0%; Pred. No. 3,4e-20;
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 QNSGNOSPEEDTEBDKPKYEGGNIYDIDFDSVPQIHG 38
DB 1 QNSGNOSPEEDTEBDKPKYEGGNIYDIDFDSVPQIHG 38
RESULT 2
AAW65661
ID AAW65661 standard; peptide; 38 AA.
AC AAW65661;
XX
XX 16-OCT-1998 (first entry)
DE Fibronectin binding protein-derived peptide #5.
XX
XX microbial surface components recognising adhesive matrix molecule;
XX MSCRAMM; fibronectin; fibronectin-binding protein; antibody; epitope;
XX antibiotic; bacterial infection; antibiotic-resistant strain.
XX
XX Synthetic.
XX Staphylococcus aureus.
XX
XX WO9831389-A2.
XX
XX 23-JUL-1998.
XX
XX 21-JAN-1998; 98WO-US001222.
XX
XX 21-JAN-1997; 97US-0036139P.
XX
XX (TEXA ) UNIV TEXAS A & M SYSTEM.
XX
XX Hoeoek M, Patel JM, House-Pompeo KL, Speziale P, Joh D,
XX McGavin MJ;
XX
XX WPI; 1998-413816/35.
XX
XX
XX Antibody that binds to fibronectin-binding protein, preventing its
XX binding to fibronectin - used to treat or prevent bacterial infection,
XX especially by Staphylococci and Streptococci.
XX
XX Example 2; Page 92; 201pp; English.
XX
XX The invention relates to antibodies that bind to a fibronectin-binding
XX domain of a fibronectin-binding protein, and inhibit binding of the
XX protein to fibronectin. Also claimed are: (1) isolated peptides of a
XX fibronectin-binding protein that do not bind to fibronectin; (2) fusion
XX protein containing at least one peptide of a fibronectin-binding protein
XX linked to a second amino acid sequence; (3) nucleic acid encoding the
XX isolated peptide of (1). Antibodies, the isolated peptides of (1) and the
XX nucleic acids are all useful for immunisation (active or passive) and (by
XX inhibiting binding of bacteria to fibronectin) for preventing or treating
XX infection in humans or other animals, particularly by staphylococci or
XX streptococci, e.g. meningitis, otitis media, pneumonia, endocarditis,
XX mastitis in cattle, abortion in horses and many others. Since the
XX antibodies block binding of bacteria, they should be effective against
XX antibiotic-resistant strains, and may replace antibiotic therapy or
XX increase its effectiveness. Sequences AAW65659-68 represent synthetic
XX epitopes from the fibronectin binding domains DU and D1-D4 of the S.

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CC aureus fnaA gene
XX
SQ Sequence 38 AA;
Query Match 94.7%; Score 195; DB 2; Length 38;
Best Local Similarity 97.4%; Pred. No. 1e-18;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 QNSGNOSPEEDTEBDKPKYEGGNIYDIDFDSVPQIHG 38
DB 1 QNSGNOSPEEDTEBDKPKYEGGNIYDIDFDSVPQIHG 38
RESULT 3
AAR58806
ID AAR58806 standard; protein; 130 AA.
AC AAR58806;
XX
XX 25-MAR-2003 (revised)
XX 30-MAR-1995 (first entry)
XX
XX Fibronectin binding domain D1-D4 (709-838 (P838T)).
XX
XX Fibronectin binding protein; Fbp; fibronectin binding domain;
XX monoclonal antibody; Mab; adhesion; Gram-positive bacterium; bacteremia;
XX Escherichia coli.
XX
XX Staphylococcus aureus.
XX
XX WO9418327-A1.
XX
XX 18-AUG-1994.
XX
XX 04-FEB-1994; 94WO-GB000215.
XX
XX 05-FEB-1993; 93GB-00002289.
XX
XX 20-OCT-1993; 93GB-00021592.
XX
XX (SMIK ) SMITHKLINE BEECHAM PLC.
XX
XX Burnham MKR, Chopra I, Critchley IA, Knowles DJC,
XX
XX WPI; 1994-279748/34.
XX
XX
XX Fibronectin binding protein and monoclonal antibodies specific for Fbp -
XX useful to prevent adherence of Gram-positive bacteria to indwelling
XX devices or wounds.
XX
XX Disclosure; Page 30; 40pp; English.
XX
XX Polypeptides corresponding to residues G709-T886 plus PRIVPPT, G709-
XX P838 (P838T) and G709-P838 (AAR58805-07, respectively) of S. aureus J2385
XX (NCIMB 40532) Fbp type A fibronectin binding domain D1-D4 region
XX (AAR58808) were expressed in E. coli BL21 (DE4) and used to raise MAb
XX specific for Fbp. (Updated on 25-MAR-2003 to correct PN field.)
XX
XX
XX Sequence 130 AA;
Query Match 94.7%; Score 195; DB 2; Length 130;
Best Local Similarity 97.4%; Pred. No. 4.5e-18;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 QNSGNOSPEEDTEBDKPKYEGGNIYDIDFDSVPQIHG 38
DB 2 QNSGNOSPEEDTEBDKPKYEGGNIYDIDFDSVPQIHG 39
RESULT 4
AAR58807
ID AAR58807 standard; protein; 130 AA.
AC AAR58807;

```

```

XX 25-MAR-2003 (revised)
DT 30-MAR-1995 (first entry)
XX
DE Fibronectin binding domain D1-D4(709-838).
XX
KM Fibronectin binding protein; Fbp; fibronectin binding domain;
KM monoclonal antibody; MAb; adhesion; Gram-positive bacterium; bacteremia;
KM Escherichia coli.
XX
OS Staphylococcus aureus.
XX
PN WO9418327-A1.
PD 18-AUG-1994.
XX
PF 04-FEB-1994; 94WO-GB000215.
XX
PR 05-FEB-1993; 93GB-00002289.
PR 20-OCT-1993; 93GB-00021592.
XX
PA (SMIK ) SMITHKLINE BEECHAM PLC.
XX
PI Burnham MKR, Chopra I, Critchley IA, Knowles DUC;
XX
DR WPI; 1994-279748/34.
XX
PT Fibronectin binding protein and monoclonal antibodies specific for Fbp -
PT useful to prevent adherence of Gram-positive bacteria to indwelling
PT devices or wounds.
XX
PS Disclosure; Page 30; 40pp; English.
XX
CC Polypeptides corresponding to residues G709-T886 plus PPIVPT, G709-
CC P838(P838T) and G709-P838 (AAR58805-07, respectively) of S. aureus J2385
CC (NCIMB 40532) Fbp type A fibronectin binding domain D1-D4 region
CC (AAR58808) were expressed in E. coli BL21(DE4) and used to raise Mabs
CC specific for Fbp. (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ Sequence 130 AA;

Query Match 94.7%; Score 195; DB 2; Length 130;
Best Local Similarity 97.4%; Pred. No. 4.5e-18;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QNSGNQSPEDTBDKPKYEGGNIVDIDFDSVPQIHG 38
DB 2 QNSGNQSPEDTBDKPKYEGGNIVDIDFDSVPQIHG 39

RESULT 5
AAR91202
ID AAR91202 standard; peptide; 130 AA.
XX
AC AAR91202;
XX
DT 13-NOV-1996 (first entry)
XX
DE D1-D4 fibronectin binding domains.
XX
KM Fibronectin; oral hygiene; gingivitis; gum disease; adhesion;
KM periodontitis; oral pathogen; caries; calculus; candidiasis; oral surgery;
KM tissue regeneration; irrigation; toothpaste; dentifrice; mouthwash;
KM lozenge.
XX
OS Staphylococcus aureus.
XX
PN WO9604003-A1.
XX
PD 15-FEB-1996.
XX
PF 18-JUL-1995; 95WO-EP002825.
XX
PT
XX

```

```

PR 05-AUG-1994; 94GB-00015902.
XX
PA (SMIK ) SMITHKLINE BEECHAM PLC.
XX
PI Barnett P, Critchley IA, Dodd I;
XX
DR WPI; 1996-129122/13.
XX
PT Prevention of adherence of oral pathogens in the oral cavity, partic.
PT tooth surfaces - by application of a fibronectin binding protein or
PT polypeptide or a monoclonal antibody or fragment against it.
XX
PS Claim 5; Page 32; 41pp; English.
XX
CC Adherence of oral pathogens, particularly to tooth surfaces, can be
CC prevented by application of a fibronectin binding protein or polypeptide.
CC The fibronectin binding protein or polypeptide is useful in the
CC manufacture of oral hygiene compositions, eg. toothpaste, liquid
CC dentifrice, mouthwash or lozenge. They are useful to prevent the plaque-
CC related development of carious lesions, gingivitis, calculus or
CC periodontal disease and to combat oral cavity infections, eg.
CC candidiasis. They may also be useful in oral surgery e.g. in guided
CC tissue regeneration procedures to prevent subsequent bacterial infection,
CC and for irrigation of periodontal pockets. This sequence corresponds to
CC amino acids 709-838 of the D1-D4 fibronectin binding domain of
CC Staphylococcus aureus
XX
SQ Sequence 130 AA;

Query Match 94.7%; Score 195; DB 2; Length 130;
Best Local Similarity 97.4%; Pred. No. 4.5e-18;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QNSGNQSPEDTBDKPKYEGGNIVDIDFDSVPQIHG 38
DB 2 QNSGNQSPEDTBDKPKYEGGNIVDIDFDSVPQIHG 39

RESULT 6
AAR91201
ID AAR91201 standard; peptide; 130 AA.
XX
AC AAR91201;
XX
DT 13-NOV-1996 (first entry)
XX
DE D1-D4 fibronectin binding domains.
XX
KM Fibronectin; oral hygiene; gingivitis; gum disease; adhesion;
KM periodontitis; oral pathogen; caries; calculus; candidiasis; oral surgery;
KM tissue regeneration; irrigation; toothpaste; dentifrice; mouthwash;
KM lozenge.
XX
OS Staphylococcus aureus.
XX
PN WO9604003-A1.
XX
PD 15-FEB-1996.
XX
PF 18-JUL-1995; 95WO-EP002825.
XX
PR 05-AUG-1994; 94GB-00015902.
XX
PA (SMIK ) SMITHKLINE BEECHAM PLC.
XX
PI Barnett P, Critchley IA, Dodd I;
XX
DR WPI; 1996-129122/13.
XX
PT Prevention of adherence of oral pathogens in the oral cavity, partic.
PT tooth surfaces - by application of a fibronectin binding protein or
PT polypeptide or a monoclonal antibody or fragment against it.
XX

```

PS Claim 5; Page 31-32; 41pp; English.

XX Adherence of oral pathogens, particularly to tooth surfaces, can be

CC prevented by application of a fibronectin binding protein or polypeptide.

CC The fibronectin binding protein or polypeptide is useful in the

CC manufacture of oral hygiene compositions, eg. toothpaste, liquid

CC dentifrice, mouthwash or lozenge. They are useful to prevent the plaque-

CC related development of carious lesions, gingivitis, calculus or

CC periodontal disease and to combat oral cavity infections, e.g.

CC candidiasis. They may also be useful in oral surgery e.g. in guided

CC tissue regeneration procedures to prevent subsequent bacterial infection,

CC and for irrigation of periodontal pockets. This sequence corresponds to

CC amino acids 709-838 of the D1-D4 fibronectin binding domain of

CC Staphylococcus aureus with a P838T substitution

XX

SQ Sequence 130 AA;

Query Match 94.7%; Score 195; DB 2; Length 130;

Best Local Similarity 97.4%; Pred. No. 4.5e-18;

Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QNSGNQSPBEDTEDEKPKYEGQGNIVDIDFDSVPQIHG 38

2 QNSGNQSPBEDTEDEKPKYEGQGNIVDIDFDSVPQIHG 39

Db

RESULT 7

AAV29089

ID AAV29089 standard; protein; 134 AA.

XX

AC AAV29089;

XX

DT 28-SEP-1999 (first entry)

XX

DE Cloned fibronectin binding protein binding domain (FnBAB) sequence.

XX

KW Bovine herpes virus-2; BHV-2; cytokine; immune response; immunogen; IL;

KW Interleukin; colony stimulating factor; CSF; interferon; IFN; TNF;

KW tumour necrosis factor; recombinant virus; vaccine; mucosal disease;

KW mastitis; breast cancer; stress-induced disease; binding domain; FnBAB;

KW fibronectin binding protein.

XX

OS Staphylococcus aureus.

XX

PN WO9916892-A1.

PD 08-APR-1999.

XX

PF 29-SEP-1998; 98WO-GB002927.

XX

PR 29-SEP-1997; 97GB-00020633.

XX

PA (UYBR-) UNIV BRISTOL.

XX

PI Bradley AJ, Duffas WPJ;

XX WPI; 1999-255101/21.

DR N-PSDB; AAX91506.

XX

PT New bovine herpes virus-2 vectors.

XX

PS Example 2; Fig 8A-B; 130pp; English.

XX

CC The invention provides bovine herpes virus-2 (BHV-2) based vectors that

CC comprise at least one cytokine-encoding DNA sequence. The expression of

CC cytokines in mammals can up-regulate immune responses to the immunogens.

CC The cytokine is selected from interleukins (IL), colony stimulating

CC factors (CSF), interferons (IFN) and tumour necrosis factors (TNF). The

CC BHV-2 based vector or recombinant virus can be used as vaccine. They can

CC be used for preventing or treating a mucosal disease in a subject, e.g.

CC ruminants, cattle, sheep, goats, dogs, cats, horses, or man, particularly

CC mastitis in cows or breast cancers in humans. They can also be used for

CC preventing or treating a stress-induced disease. The present sequence

CC represents a S. aureus fibronectin binding protein binding domain

CC sequence FnBAB, the gene cloned for use in this invention. The gene has

CC 97.8 percent identity when compared to the previously published sequences

CC FnBA and FnBB

XX

SQ Sequence 134 AA;

Query Match 94.7%; Score 195; DB 2; Length 134;

Best Local Similarity 97.4%; Pred. No. 4.7e-18;

Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QNSGNQSPBEDTEDEKPKYEGQGNIVDIDFDSVPQIHG 38

2 QNSGNQSPBEDTEDEKPKYEGQGNIVDIDFDSVPQIHG 39

Db

RESULT 8

AAV29088

ID AAV29088 standard; protein; 134 AA.

XX

AC AAV29088;

XX

DT 28-SEP-1999 (first entry)

XX

DE S. aureus fibronectin binding protein B (FnBB) binding domain.

XX

KW Bovine herpes virus-2; BHV-2; cytokine; immune response; immunogen; IL;

KW Interleukin; colony stimulating factor; CSF; interferon; IFN; TNF;

KW tumour necrosis factor; recombinant virus; vaccine; mucosal disease;

KW mastitis; breast cancer; stress-induced disease; binding domain; FnBB;

KW fibronectin binding protein.

XX

OS Staphylococcus aureus.

XX

PN WO9916892-A1.

PD 08-APR-1999.

XX

PF 29-SEP-1998; 98WO-GB002927.

XX

PR 29-SEP-1997; 97GB-00020633.

XX

PA (UYBR-) UNIV BRISTOL.

XX

PI Bradley AJ, Duffas WPJ;

XX WPI; 1999-255101/21.

DR N-PSDB; AAX91505.

XX

PT New bovine herpes virus-2 vectors.

XX

PS Example 2; Fig 8A-B; 130pp; English.

XX

CC The invention provides bovine herpes virus-2 (BHV-2) based vectors that

CC comprise at least one cytokine-encoding DNA sequence. The expression of

CC cytokines in mammals can up-regulate immune responses to the immunogens.

CC The cytokine is selected from interleukins (IL), colony stimulating

CC factors (CSF), interferons (IFN) and tumour necrosis factors (TNF). The

CC BHV-2 based vector or recombinant virus can be used as vaccine. They can

CC be used for preventing or treating a mucosal disease in a subject, e.g.

CC ruminants, cattle, sheep, goats, dogs, cats, horses, or man, particularly

CC mastitis in cows or breast cancers in humans. They can also be used for

CC preventing or treating a stress-induced disease. The present sequence

CC represents the binding domain of a previously published S. aureus

CC fibronectin binding protein B (FnBB) sequence. The Fnb binding domain

CC gene sequence FnBAB, cloned for use in this invention has 97.8 percent

CC identity when compared to the previously published FnBA and FnBB gene

CC sequences

XX

SQ Sequence 134 AA;

Query Match 94.7%; Score 195; DB 2; Length 134;

Best Local Similarity 97.4%; Pred. No. 4.7e-18;

Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QNSGNQSPEDTEEDKPKYEGGNIYDIDFDSVPQIHG 38
 DB 2 QNSGNQSPEDTEEDKPKYEGGNIYDIDFDSVPQIHG 39

RESULT 9

AAV29087 standard; protein; 134 AA.

AC AAV29087;

DT 28-SEP-1999 (first entry)

DE S. aureus fibronectin binding protein A (FnBA) binding domain.

XX Bovine herpes virus-2; BHV-2; cytokine; immune response; immunogen; IL;
 XX Interleukin; colony stimulating factor; CSF; interferon; IFN; TNF;
 XX Tumour necrosis factor; recombinant virus; vaccine; mucosal disease;
 XX Mastitis; breast cancer; stress-induced disease; binding domain; FnBA;
 XX fibronectin binding protein.

OS Staphylococcus aureus.

PN WO9916892-A1.

XX 08-APR-1999.

XX 29-SEP-1998; 98WO-GB002927.

XX 29-SEP-1997; 97GB-00020633.

XX (UYBR-) UNIV BRISTOL.

XX Bradley AJ, Duffas WP;

XX WPI; 1999-255101/21.

XX N-PSDB; AAX91504.

XX New bovine herpes virus-2 vectors.

XX Example 2; Fig 8A-B; 130pp; English.

CC The invention provides bovine herpes virus-2 (BHV-2) based vectors that
 CC comprise at least one cytokine-encoding DNA sequence. The expression of
 CC cytokines in mammals can up-regulate immune responses to the immunogens.
 CC The cytokine is selected from interleukins (IL), colony stimulating
 CC factors (CSF), interferons (IFN) and tumour necrosis factors (TNF). The
 CC BHV-2 based vector or recombinant virus can be used as vaccines. They can
 CC be used for preventing or treating a mucosal disease in a subject, e.g.
 CC ruminants, cattle, sheep, goats, dogs, cats, horses, or man, particularly
 CC mastitis in cows or breast cancers in humans. They can also be used for
 CC preventing or treating a stress-induced disease. The present sequence
 CC represents the binding domain of a previously published S. aureus
 CC fibronectin binding protein A (FnBA) sequence. The FnB binding domain
 CC gene sequence FnBAB, cloned for use in this invention has 97.8 percent
 CC identity when compared to the previously published FnBA and FnBB gene
 CC sequences

XX Sequence 134 AA;

QY Query Match 94.7%; Score 195; DB 2; Length 134;
 DB Best Local Similarity 97.4%; Pred. No. 4,7e-18;
 Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QNSGNQSPEDTEEDKPKYEGGNIYDIDFDSVPQIHG 38
 DB 2 QNSGNQSPEDTEEDKPKYEGGNIYDIDFDSVPQIHG 39

RESULT 10
 AAW31556

ID AAW31556 standard; protein; 139 AA.

XX AAW31556;

XX 27-AUG-2003 (revised)

XX 25-MAR-2003 (revised)

XX 21-MAY-1998 (first entry)

XX Fibronectin-binding MSCRAMM derivative POD.

XX Fibronectin; POD; collagen binding protein; sepsis; infection;
 XX microbial surface component recognising adhesive matrix molecule; MSCRAMM;
 XX adhesin; vaccine; immunisation; diagnosis; therapy; mastitis.

XX Staphylococcus aureus.

XX Key Location/Qualifiers

XX Peptide 1..12 /note= "vector pQE30-derived peptide"

XX WO9743314-A2.

XX 20-NOV-1997.

XX 14-MAY-1997; 97WO-US008210.

XX 16-MAY-1996; 96US-0017678P.

XX (TEXA) UNIV TEXAS A & M SYSTEM.

XX (UABR) UAB RES FOUND.

XX Hoeck M, Patti JM, House-Pompeo K, Schanham N, Symersky J;

XX WPI; 1998-008801/01.

XX Antibody that interacts with collagen binding domain of Staphylococcal
 XX cna gene product - useful to prevent bacterial sepsis in animal infected
 XX with Staphylococcus aureus.

XX Disclosure; Page 91; 143pp; English.

XX This protein comprises Staphylococcus aureus fibronectin-binding
 CC microbial surface component recognising adhesive matrix molecule (MSCRAMM)
 CC derivative POD, plus a vector-derived N-terminal peptide. The invention
 CC relates to claimed nucleic acid sequences (see AAT93436-38) encoding S.
 CC aureus collagen binding protein (CBP) epitopes M17, M31 and M55 (see
 CC AAW31552-54) that confer protection against S. aureus infection. CBP
 CC protein and antigenic epitopes are contemplated for use in the treatment
 CC of pathological infections, especially to prevent bacterial adhesion to
 CC collagen. The epitopes are also contemplated for use in the preparation
 CC of vaccines and as carrier proteins in vaccine formulations, as well as
 CC in the formulation of compositions for the prevention of S. aureus
 CC infection. pCF33 and POD (see AAW31556) were used to raise anti-MSCRAMM
 CC polyclonal antibodies used in passive immunisation against bovine
 CC mastitis. (Updated on 25-MAR-2003 to correct PI field.) (Updated on 27-
 CC AUG-2003 to correct OS field.)

XX Sequence 139 AA;

QY Query Match 94.7%; Score 195; DB 2; Length 139;
 DB Best Local Similarity 97.4%; Pred. No. 4.9e-18;
 Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QNSGNQSPEDTEEDKPKYEGGNIYDIDFDSVPQIHG 38
 DB 16 QNSGNQSPEDTEEDKPKYEGGNIYDIDFDSVPQIHG 53

RESULT 11
 AAR58808
 ID AAR58808 standard; protein; 174 AA.
 XX AAR58808;

PT Fibronectin binding protein and monoclonal antibodies specific for Fbp -
 PT useful to prevent adherence of Gram-positive bacteria to indwelling
 PT devices or wounds.
 XX
 PS Disclosure; Page 29-30; 40pp; English.
 CC Polypeptides corresponding to residues G709-T886 plus PPIVPT, G709-
 CC P838(P838T) and G709-P838 (AAR58805-07, respectively) of S. aureus J2395
 CC (NCIMB 40532) Fbp type A fibronectin binding domain D1-D4 region
 CC (AAR58808) were expressed in E. coli BL21 (DE4) and used to raise Mabs
 CC specific for Fbp. (Updated on 25-MAR-2003 to correct PN field.)
 CC
 XX
 SQ Sequence 181 AA;
 Query Match 94.7%; Score 195; DB 2; Length 181;
 Best Local Similarity 97.4%; Pred. No. 6.7e-18;
 Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 ONSGNQSPEDTEBDKPKYEQGNIYDIDPDSVPQIHG 38
 DB 2 ONSGNQSPEDTEBDKPKYEQGNIYDIDPDSVPQIHG 39
 RESULT 14
 AAR91200
 ID AAR91200 standard; peptide; 181 AA.
 XX
 AC AAR91200;
 DT 13-NOV-1996 (first entry)
 DE D1-D4 fibronectin binding domains.
 XX
 KM Fibronectin; oral hygiene; gingivitis; gum disease; adhesion;
 KM periodontitis; oral pathogens; caries; calculus; candidiasis; oral surgery;
 KM tissue regeneration; irrigation; toothpaste; dentifrice; mouthwash;
 KM lozenge.
 XX
 OS Staphylococcus aureus.
 XX
 PN WO9604003-A1.
 PD 15-FEB-1996.
 XX
 PF 18-JUL-1995; 95WO-EP002825.
 XX
 PR 05-AUG-1994; 94GB-00015902.
 XX
 PA (SMIK) SMITHKLINE BEECHAM PLC.
 XX
 PI Barnett P, Critchley IA, Dodd I;
 XX WPI; 1996-129122/13.
 DR N-PSDB; AAT18307.
 XX
 PT Prevention of adherence of oral pathogens in the oral cavity, partic.
 PT tooth surfaces - by application of a fibronectin binding protein or
 PT polypeptide or a monoclonal antibody or fragment against it.
 XX
 PS Claim 5; Page 31; 41pp; English.
 CC Adherence of oral pathogens, particularly to tooth surfaces, can be
 CC prevented by application of a fibronectin binding protein or polypeptide.
 CC The fibronectin binding protein or polypeptide is useful in the
 CC manufacture of oral hygiene compositions, eg. toothpaste, liquid
 CC dentifrice, mouthwash or lozenge. They are useful to prevent the plaque-
 CC related development of carious lesions, gingivitis, calculus or
 CC periodontal disease and to combat oral cavity infections, e.g.
 CC candidiasis. They may also be useful in oral surgery e.g. in guided
 CC tissue regeneration procedures to prevent subsequent bacterial infection,
 CC and for irrigation of periodontal pockets. This sequence corresponds to
 CC amino acids 709-886 of the D1-D4 fibronectin binding domain of
 CC Staphylococcus aureus

XX
 SQ Sequence 181 AA;
 Query Match 94.7%; Score 195; DB 2; Length 181;
 Best Local Similarity 97.4%; Pred. No. 6.7e-18;
 Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 ONSGNQSPEDTEBDKPKYEQGNIYDIDPDSVPQIHG 38
 DB 2 ONSGNQSPEDTEBDKPKYEQGNIYDIDPDSVPQIHG 39
 RESULT 15
 AAM89803
 ID AAM89803 standard; protein; 559 AA.
 XX
 AC AAM89803;
 DT 16-MAR-1999 (first entry)
 DE Staphylococcus aureus protein SEQ ID #5251.
 XX
 KM Computer readable medium; vaccine; S.aureus infection; immunodetection;
 KM cellulitis; eyelid infection; food poisoning; osteomyelitis; therapy;
 KM skin infection; surgical wound infection; scalded skin syndrome;
 KM toxic shock syndrome.
 XX
 OS Staphylococcus aureus.
 XX
 PN EP786519-A2.
 PD 30-JUL-1997.
 XX
 PF 07-JAN-1997; 97EP-00100117.
 XX
 PR 05-JAN-1996; 96US-0009861P.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 XX
 PI Kunsch CA, Choi GH, Barash SC, Dillon PJ, Fannon MR, Rosen CA;
 XX WPI; 1997-374922/35.
 DR
 XX
 PT Polynucleotide(s) and proteins derived from Staphylococcus aureus -
 PT stored on computer readable medium and used in the production of anti-
 PT S.aureus vaccines.
 XX
 PS Claim 23; Page 3259-3261; 3271pp; English.
 CC This sequence represents a Staphylococcus aureus protein sequence of the
 CC invention. The DNA sequences encoding the S.aureus proteins are recorded
 CC on a computer readable medium, preferably selected from a floppy or hard
 CC disk, random access memory (RAM), read-only memory (ROM) or CD-ROM.
 CC Homology searches using the S.aureus DNA sequences allows putative
 CC functions to be assigned so that protein-encoding or regulatory regions
 CC of commercial, therapeutic or industrial importance can be obtained.
 CC Specifically, sequences which are likely to encode antigens have been
 CC identified and these polypeptides can be used in a vaccine composition
 CC against S.aureus infection. The polypeptides can also be used in a kit
 CC for the immunodetection of S.aureus in a sample. S.aureus is implicated
 CC in numerous human diseases, including cellulitis, eyelid infections, food
 CC poisoning, osteomyelitis, skin and surgical wound infections, scalded
 CC skin syndrome, toxic shock syndrome, etc. Organisms transformed with the
 CC DNA sequences can be used for recombinant production of the polypeptides.
 CC The new DNA sequences (and their fragments) are useful as primers or
 CC probes for isolating homologues of any of the 5191 S.aureus DNA sequences
 CC contained on the computer readable medium
 XX
 SQ Sequence 559 AA;
 Query Match 94.7%; Score 195; DB 2; Length 559;
 Best Local Similarity 97.4%; Pred. No. 2.6e-17;
 Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Wed Oct 26 15:02:15 2005

us-10-731-238-35.rag

Page 8

QY 1 QNSGNQSPEDDTEDBKPKYEQQGNIVIDIDFDSVPQIHG 38
 |||||
Dd 301 QNSGNQSFEEDTDEBKPKEQGGINIVIDIDFSVPIQHIG 338

Search completed: October 25, 2005, 19:38:32
Job time : 106.988 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 22, 2005, 02:23:36 ; Search time 28.8363 Seconds
(without alignments)
98.371 Million cell updates/sec

Title: US-10-731-238-35
Perfect score: 206
Sequence: 1 QNSGNQSPEDTEEDKPKYEQGNIVDIDFDSVPQIHG 38

Scoring table: BLAST62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 7464964 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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1: /cgn2_6/ptodata/1/1aa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/1aa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/1aa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/1aa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/1aa/6C_COMB.pep:*
6: /cgn2_6/ptodata/1/1aa/Backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	206	100.0	38	4	US-09-010-317-35 Sequence 35, Appl
2	195	94.7	38	1	US-08-234-622A-2 Sequence 2, Appl
3	195	94.7	38	4	US-09-010-317-5 Sequence 5, Appl
4	195	94.7	114	1	US-08-259-000-3 Sequence 3, Appl
5	195	94.7	130	2	US-08-459-135A-7 Sequence 7, Appl
6	195	94.7	130	2	US-08-459-135A-8 Sequence 8, Appl
7	195	94.7	130	3	US-08-495-559-7 Sequence 7, Appl
8	195	94.7	130	3	US-08-495-559-8 Sequence 8, Appl
9	195	94.7	139	3	US-08-856-253-8 Sequence 8, Appl
10	195	94.7	174	2	US-08-459-135A-10 Sequence 10, Appl
11	195	94.7	174	2	US-08-459-135A-13 Sequence 10, Appl
12	195	94.7	174	3	US-08-495-559-10 Sequence 10, Appl
13	195	94.7	174	3	US-08-495-559-13 Sequence 13, Appl
14	195	94.7	176	3	US-08-495-559-6 Sequence 6, Appl
15	195	94.7	178	2	US-08-459-135A-12 Sequence 12, Appl
16	195	94.7	178	2	US-08-495-559-12 Sequence 12, Appl
17	195	94.7	181	4	US-08-459-135A-6 Sequence 6, Appl
18	195	94.7	559	4	US-08-956-171E-5251 Sequence 5251, Ap
19	195	94.7	559	4	US-08-956-171E-5251 Sequence 5251, Ap
20	195	94.7	1027	4	US-08-956-171E-5254 Sequence 5254, Ap
21	195	94.7	1027	4	US-08-956-171E-5254 Sequence 5254, Ap
22	189	91.7	38	1	US-08-729-767-3 Sequence 3, Appl
23	189	91.7	38	4	US-09-010-317-36 Sequence 36, Appl
24	189	91.7	38	4	US-09-010-317-37 Sequence 37, Appl
25	189	91.7	38	4	US-09-010-317-39 Sequence 39, Appl
26	189	91.7	38	4	US-09-010-317-40 Sequence 40, Appl
27	189	91.7	38	4	US-09-010-317-41 Sequence 41, Appl

28	188	91.3	38	4	US-09-010-317-38 Sequence 38, Appl
29	188	91.3	38	4	US-09-010-317-42 Sequence 42, Appl
30	187	90.8	38	4	US-09-010-317-6 Sequence 6, Appl
31	187	90.8	38	4	US-09-010-317-43 Sequence 43, Appl
32	187	90.8	38	4	US-09-010-317-45 Sequence 45, Appl
33	184.5	89.6	39	4	US-09-010-317-56 Sequence 56, Appl
34	176.5	85.7	39	4	US-09-010-317-57 Sequence 57, Appl
35	176	85.4	38	1	US-08-234-622A-3 Sequence 3, Appl
36	176	85.4	38	4	US-09-010-317-7 Sequence 7, Appl
37	170	82.5	38	1	US-08-729-767-4 Sequence 4, Appl
38	170	82.5	38	4	US-09-010-317-46 Sequence 46, Appl
39	170	82.5	38	4	US-09-010-317-47 Sequence 47, Appl
40	169	82.0	38	4	US-09-010-317-48 Sequence 48, Appl
41	168	81.6	38	4	US-09-010-317-8 Sequence 8, Appl
42	168	81.6	38	4	US-09-010-317-49 Sequence 49, Appl
43	167	81.1	38	4	US-09-010-317-44 Sequence 44, Appl
44	153	74.3	36	4	US-09-010-317-58 Sequence 58, Appl
45	148	71.8	38	4	US-09-010-317-50 Sequence 50, Appl

ALIGNMENTS

RESULT 1
US-09-010-317-35
; Sequence 35, Application US/09010317
; Patent No. 6685943
; GENERAL INFORMATION:
; APPLICANT: Hook, Magnus
; APPLICANT: Patl, Joseph M.
; APPLICANT: House-Pompeo, Karen L.
; APPLICANT: Speziale, Pietro
; APPLICANT: McGavin, Martin J.
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
; TITLE OF INVENTION: AND METHODS OF USE
; NUMBER OF SEQUENCES: 105
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: TX
; COUNTRY: USA
; ZIP: 77210-4433
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/010,317
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/036,139
; FILING DATE: 21-JAN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Hblber, David W.
; REGISTRATION NUMBER: 41,071
; REFERENCE/DOCKET INFORMATION:
; TELEPHONE: 512-418-3000
; TELEFAX: 512-474-7577
; INFORMATION FOR SEQ ID NO: 35:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 38 amino acids
; TYPE: amino acid
; STRANDEDNESS: linear
; TOPOLOGY: linear
US-09-010-317-35
Query Match 100.0%; Score 206; DB 4; Length 38;
Best Local Similarity 100.0%; Pred. No. 6e-21;

Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QNSGNQSPEDTDEKPKYEGGNIIVDIDFDSVPQIHG 38
Db 1 QNSGNQSPEDTDEKPKYEGGNIIVDIDFDSVPQIHG 38

RESULT 2
US-08-234-622A-2

Sequence 2, Application US/08234622A
Patent No. 5440014
GENERAL INFORMATION:
APPLICANT: HOOK, Magnus
APPLICANT: MCGAVIN, Martin
APPLICANT: RAUCCI, Giuseppe
TITLE OF INVENTION: A FIBRONECTIN BINDING PEPTIDE
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Burns, Doane, Swecker & Mathis
STREET: P.O. Box 1404
CITY: Alexandria
STATE: Virginia
COUNTRY: United States
ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/234,622A
FILING DATE: 28-APR-1994
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: SE 9002617-0
FILING DATE: 10-AUG-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/SE91/00534
FILING DATE: 09-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: Meuth, Donna M
REGISTRATION NUMBER: 36,607
REFERENCE/DOCKET NUMBER: 012885-044
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-234-622A-2

Query Match 94.7%; Score 195; DB 1; Length 38;
Best Local Similarity 97.4%; Pred. No. 1.8e-19;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QNSGNQSPEDTDEKPKYEGGNIIVDIDFDSVPQIHG 38
Db 1 QNSGNQSPEDTDEKPKYEGGNIIVDIDFDSVPQIHG 38

RESULT 3
US-09-010-317-5

Sequence 5, Application US/09010317
Patent No. 6685943
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
APPLICANT: Patil, Joseph M.
APPLICANT: House-Pompeo, Karen L.
APPLICANT: Spziale, Pietro

APPLICANT: Jon, Danny
APPLICANT: McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
TITLE OF INVENTION: AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAMK.189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-09-010-317-5

Query Match 94.7%; Score 195; DB 4; Length 38;
Best Local Similarity 97.4%; Pred. No. 1.8e-19;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QNSGNQSPEDTDEKPKYEGGNIIVDIDFDSVPQIHG 38
Db 1 QNSGNQSPEDTDEKPKYEGGNIIVDIDFDSVPQIHG 38

RESULT 4
US-08-259-000-3

Sequence 3, Application US/08259000
Patent No. 5571514
GENERAL INFORMATION:
APPLICANT: HOOK, Magnus
APPLICANT: LINDBERG, Martin Kjell
APPLICANT: SIGNAS, Lars Christer
APPLICANT: WADSTROM, Torkel Mikael
APPLICANT: FROWAN, Gunnar
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN AS WELL AS
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Burns, Doane, Swecker & Mathis
STREET: P.O. Box 1404
CITY: Alexandria
STATE: Virginia
COUNTRY: United States
ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/259,000
FILING DATE: 13-JUN-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: SE 8702272-9
FILING DATE: 01-JUN-1987
ATTORNEY/AGENT INFORMATION:
NAME: Meuth, Donna M
REGISTRATION NUMBER: 36,607
REFERENCE/DOCKET NUMBER: 012885-062
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-2021
TELEFAX: (703) 836-6620
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 114 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-259-000-3

Query Match 94.7%; Score 195; DB 1; Length 114;
Best Local Similarity 97.4%; Pred. No. 6,8e-19;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 QNSGNQSPEDTEEDKPKYEGGNIIVDIDPSVPOIHG 38
Db 2 QNSGNQSPEDTEEDKPKYEGGNIIVDIDPSVPOIHG 39

RESULT 5
US-08-459-135A-7
Sequence 7, Application US/08459135A
Patent No. 5955078
GENERAL INFORMATION:
APPLICANT: BURNHAM, Martin Karl Russel
APPLICANT: CHOPRA, Ian
APPLICANT: CRITCHLEY, Ian Alfred
APPLICANT: KNOWLES, David Justin Charles
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN: MONOCLONAL ANTIBODY AND THEIR US
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESS: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
STATE: PA
COUNTRY: U.S.A.
ZIP: 19406-0939
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: Fastseq, Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/459,135A
FILING DATE: 02-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB/94/00215
FILING DATE: 04-Feb-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Gimm, Edward R
REGISTRATION NUMBER: 38,891
REFERENCE/DOCKET NUMBER: P30591C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-4478
TELEFAX: 610-270-5090
TELEX:
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:

LENGTH: 130 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-459-135A-7

Query Match 94.7%; Score 195; DB 2; Length 130;
Best Local Similarity 97.4%; Pred. No. 8e-19;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 QNSGNQSPEDTEEDKPKYEGGNIIVDIDPSVPOIHG 38
Db 2 QNSGNQSPEDTEEDKPKYEGGNIIVDIDPSVPOIHG 39

RESULT 6
US-08-459-135A-8
Sequence 8, Application US/08459135A
Patent No. 5955078
GENERAL INFORMATION:
APPLICANT: BURNHAM, Martin Karl Russel
APPLICANT: CHOPRA, Ian
APPLICANT: CRITCHLEY, Ian Alfred
APPLICANT: KNOWLES, David Justin Charles
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN: MONOCLONAL ANTIBODY AND THEIR US
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESS: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
STATE: PA
COUNTRY: U.S.A.
ZIP: 19406-0939
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: Fastseq, Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/459,135A
FILING DATE: 02-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB/94/00215
FILING DATE: 04-Feb-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Gimm, Edward R
REGISTRATION NUMBER: 38,891
REFERENCE/DOCKET NUMBER: P30591C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-4478
TELEFAX: 610-270-5090
TELEX:
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 130 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-459-135A-8

Query Match 94.7%; Score 195; DB 2; Length 130;
Best Local Similarity 97.4%; Pred. No. 8e-19;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 QNSGNQSPEDTEEDKPKYEGGNIIVDIDPSVPOIHG 38
Db 2 QNSGNQSPEDTEEDKPKYEGGNIIVDIDPSVPOIHG 39

RESULT 7
US-08-495-559-7

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; Sequence 7, Application US/08495559A
; Patent No. 6054572
; GENERAL INFORMATION:
; APPLICANT: BURHAM, Martin Karl Russel
; APPLICANT: CHOPRA, Ian
; APPLICANT: CRITCHLEY, Ian Alfred
; APPLICANT: KNOWLES, David Justin Charles
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN: MONOCLONAL
; TITLE OF INVENTION: ANTIBODY AND THEIR USE IN PREVENTING BACTERIAL ADHESION
; FILE REFERENCE: P30591
; CURRENT APPLICATION NUMBER: US/08/495,559A
; CURRENT FILING DATE: 1995-08-03
; EARLIER APPLICATION NUMBER: GB 9302289.5
; EARLIER FILING DATE: 1993-02-05
; EARLIER APPLICATION NUMBER: GB 9321592.9
; EARLIER FILING DATE: 1993-10-20
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 7
; LENGTH: 130
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-08-495-559-7

Query Match      94.7%; Score 195; DB 3; Length 130;
Best Local Similarity 97.4%; Pred. No. 8e-19;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1  QNSGNQSPBEDTEBDKPKYEQGNIVDIDPDSVPQIHG 38
Db      2  QNSGNQSFEEBTEBDKPKYEQGNIVDIDPDSVPQIHG 39

; Sequence 8
US-08-495-559-8
; Sequence 8, Application US/08495559A
; Patent No. 6054572
; GENERAL INFORMATION:
; APPLICANT: BURHAM, Martin Karl Russel
; APPLICANT: CHOPRA, Ian
; APPLICANT: CRITCHLEY, Ian Alfred
; APPLICANT: KNOWLES, David Justin Charles
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN: MONOCLONAL
; TITLE OF INVENTION: ANTIBODY AND THEIR USE IN PREVENTING BACTERIAL ADHESION
; FILE REFERENCE: P30591
; CURRENT APPLICATION NUMBER: US/08/495,559A
; CURRENT FILING DATE: 1995-08-03
; EARLIER APPLICATION NUMBER: GB 9302289.5
; EARLIER FILING DATE: 1993-02-05
; EARLIER APPLICATION NUMBER: GB 9321592.9
; EARLIER FILING DATE: 1993-10-20
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 8
; LENGTH: 130
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-08-495-559-8

Query Match      94.7%; Score 195; DB 3; Length 130;
Best Local Similarity 97.4%; Pred. No. 8e-19;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1  QNSGNQSPBEDTEBDKPKYEQGNIVDIDPDSVPQIHG 38
Db      2  QNSGNQSFEEBTEBDKPKYEQGNIVDIDPDSVPQIHG 39

; Sequence 9
US-08-856-253-8
; Sequence 8, Application US/08856253
; Patent No. 6288214
; GENERAL INFORMATION:
; APPLICANT: BURHAM, Martin Karl Russel
; APPLICANT: CHOPRA, Ian
; APPLICANT: CRITCHLEY, Ian Alfred
; APPLICANT: KNOWLES, David Justin Charles
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN: MONOCLONAL
; TITLE OF INVENTION: ANTIBODY AND THEIR USE IN PREVENTING BACTERIAL ADHESION
; FILE REFERENCE: P30591
; CURRENT APPLICATION NUMBER: US/08/856,253
; CURRENT FILING DATE: 1995-08-03
; EARLIER APPLICATION NUMBER: GB 9302289.5
; EARLIER FILING DATE: 1993-02-05
; EARLIER APPLICATION NUMBER: GB 9321592.9
; EARLIER FILING DATE: 1993-10-20
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 9
; LENGTH: 130
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-08-856-253-8

Query Match      94.7%; Score 195; DB 3; Length 130;
Best Local Similarity 97.4%; Pred. No. 8e-19;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1  QNSGNQSPBEDTEBDKPKYEQGNIVDIDPDSVPQIHG 38
Db      2  QNSGNQSFEEBTEBDKPKYEQGNIVDIDPDSVPQIHG 39
```

```

; APPLICANT: Hook, Magnus
; APPLICANT: Patti, Joseph M.
; APPLICANT: House-Pompeo, Karen
; APPLICANT: Stenham, Narayana
; APPLICANT: Symeisky, Jindrich
; TITLE OF INVENTION: COLLAGEN BINDING PROTEIN COMPOSITIONS
; TITLE OF INVENTION: AND METHODS OF USE
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: U.S.
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/856,253
; FILING DATE: Concurrently Herewith
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/017,678
; FILING DATE: 16-MAY-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Kitchell, Barbara S.
; REGISTRATION NUMBER: 33,928
; REFERENCE/DOCKET NUMBER: TAMK:193
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (512) 418-3000
; TELEFAX: (512) 474-7577
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 139 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
US-08-856-253-8

Query Match      94.7%; Score 195; DB 3; Length 139;
Best Local Similarity 97.4%; Pred. No. 8.7e-19;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1  QNSGNQSPBEDTEBDKPKYEQGNIVDIDPDSVPQIHG 38
Db      16 QNSGNQSFEEBTEBDKPKYEQGNIVDIDPDSVPQIHG 53

; Sequence 10
US-08-459-135A-10
; Sequence 10, Application US/08459135A
; Patent No. 5955078
; GENERAL INFORMATION:
; APPLICANT: BURHAM, Martin Karl Russel
; APPLICANT: CHOPRA, Ian
; APPLICANT: CRITCHLEY, Ian Alfred
; APPLICANT: KNOWLES, David Justin Charles
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN: MONOCLONAL
; TITLE OF INVENTION: ANTIBODY AND THEIR USE IN PREVENTING BACTERIAL ADHESION
; FILE REFERENCE: P30591
; CURRENT APPLICATION NUMBER: US/08/459,135A
; CURRENT FILING DATE: 1995-08-03
; EARLIER APPLICATION NUMBER: GB 9302289.5
; EARLIER FILING DATE: 1993-02-05
; EARLIER APPLICATION NUMBER: GB 9321592.9
; EARLIER FILING DATE: 1993-10-20
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 10
; LENGTH: 139
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-08-459-135A-10

Query Match      94.7%; Score 195; DB 3; Length 139;
Best Local Similarity 97.4%; Pred. No. 8.7e-19;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1  QNSGNQSPBEDTEBDKPKYEQGNIVDIDPDSVPQIHG 38
Db      16 QNSGNQSFEEBTEBDKPKYEQGNIVDIDPDSVPQIHG 53

; Sequence 11
US-08-856-253-8
; Sequence 8, Application US/08856253
; Patent No. 6288214
; GENERAL INFORMATION:
; APPLICANT: BURHAM, Martin Karl Russel
; APPLICANT: CHOPRA, Ian
; APPLICANT: CRITCHLEY, Ian Alfred
; APPLICANT: KNOWLES, David Justin Charles
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN: MONOCLONAL
; TITLE OF INVENTION: ANTIBODY AND THEIR USE IN PREVENTING BACTERIAL ADHESION
; FILE REFERENCE: P30591
; CURRENT APPLICATION NUMBER: US/08/856,253
; CURRENT FILING DATE: 1995-08-03
; EARLIER APPLICATION NUMBER: GB 9302289.5
; EARLIER FILING DATE: 1993-02-05
; EARLIER APPLICATION NUMBER: GB 9321592.9
; EARLIER FILING DATE: 1993-10-20
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 11
; LENGTH: 130
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-08-856-253-8

Query Match      94.7%; Score 195; DB 3; Length 130;
Best Local Similarity 97.4%; Pred. No. 8e-19;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1  QNSGNQSPBEDTEBDKPKYEQGNIVDIDPDSVPQIHG 38
Db      2  QNSGNQSFEEBTEBDKPKYEQGNIVDIDPDSVPQIHG 39
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; SOFTWARE: Fastseq, Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/459.135A
; FILING DATE: 02-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB/94/00215
; FILING DATE: 04-Feb-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Glimm, Edward R
; REGISTRATION NUMBER: 38,891
; REFERENCE/DOCKET NUMBER: P30591C2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-270-4478
; TELEFAX: 610-270-5090
; TELEX:
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 174 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: Protein
; US-08-459-135A-10

Query Match      94.7%; Score 195; DB 2; Length 174;
Best Local Similarity 97.4%; Pred. No. 1.1e-18;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QNSGNQSPEDTDEBDKPKYEGGNIIVDIDFDSVPQIHG 38
DB 2 QNSGNQSPEDTDEBDKPKYEGGNIIVDIDFDSVPQIHG 39

RESULT 11
US-08-459-135A-13
; Sequence 13, Application US/08459135A
; Patent No. 5955078
; GENERAL INFORMATION:
; APPLICANT: BURHAM, Martin Karl Russel
; APPLICANT: CHOPRA, Ian
; APPLICANT: CRITCHLEY, Ian Alfred
; APPLICANT: KNOWLES, David Justin Charles
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN: MONOCLONAL ANTIBODY AND THEIR US
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corporation
; STREET: 709 Swedeland Road
; CITY: King of Prussia
; STATE: PA
; COUNTRY: U.S.A.
; ZIP: 19406-0939
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: Fastseq, Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/459.135A
; FILING DATE: 02-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB/94/00215
; FILING DATE: 04-Feb-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Glimm, Edward R
; REGISTRATION NUMBER: 38,891
; REFERENCE/DOCKET NUMBER: P30591C2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-270-4478
; TELEFAX: 610-270-5090
; TELEX:

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; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 174 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-459-135A-13

Query Match      94.7%; Score 195; DB 2; Length 174;
Best Local Similarity 97.4%; Pred. No. 1.1e-18;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QNSGNQSPEDTDEBDKPKYEGGNIIVDIDFDSVPQIHG 38
DB 2 QNSGNQSPEDTDEBDKPKYEGGNIIVDIDFDSVPQIHG 39

RESULT 12
US-08-495-559-10
; Sequence 10, Application US/08495559A
; Patent No. 6054572
; GENERAL INFORMATION:
; APPLICANT: BURHAM, Martin Karl Russel
; APPLICANT: CHOPRA, Ian
; APPLICANT: CRITCHLEY, Ian Alfred
; APPLICANT: KNOWLES, David Justin Charles
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN: MONOCLONAL
; TITLE OF INVENTION: ANTIBODY AND THEIR USE IN PREVENTING BACTERIAL ADHESION
; FILE REFERENCE: P30591
; CURRENT APPLICATION NUMBER: US/08/495.559A
; CURRENT FILING DATE: 1995-08-03
; EARLIER APPLICATION NUMBER: GB 9302289.5
; EARLIER FILING DATE: 1993-02-05
; EARLIER APPLICATION NUMBER: GB 9321592.9
; EARLIER FILING DATE: 1993-10-20
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 10
; LENGTH: 174
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
; US-08-495-559-10

Query Match      94.7%; Score 195; DB 3; Length 174;
Best Local Similarity 97.4%; Pred. No. 1.1e-18;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QNSGNQSPEDTDEBDKPKYEGGNIIVDIDFDSVPQIHG 38
DB 2 QNSGNQSPEDTDEBDKPKYEGGNIIVDIDFDSVPQIHG 39

RESULT 13
US-08-495-559-13
; Sequence 13, Application US/08495559A
; Patent No. 6054572
; GENERAL INFORMATION:
; APPLICANT: BURHAM, Martin Karl Russel
; APPLICANT: CHOPRA, Ian
; APPLICANT: CRITCHLEY, Ian Alfred
; APPLICANT: KNOWLES, David Justin Charles
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN: MONOCLONAL
; TITLE OF INVENTION: ANTIBODY AND THEIR USE IN PREVENTING BACTERIAL ADHESION
; FILE REFERENCE: P30591
; CURRENT APPLICATION NUMBER: US/08/495.559A
; CURRENT FILING DATE: 1995-08-03
; EARLIER APPLICATION NUMBER: GB 9302289.5
; EARLIER FILING DATE: 1993-02-05
; EARLIER APPLICATION NUMBER: GB 9321592.9
; EARLIER FILING DATE: 1993-10-20
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 3.0

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; SEQ ID NO 13
; LENGTH: 174
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-08-495-559-13

Query Match          94.7%; Score 195; DB 3; Length 174;
Best Local Similarity 97.4%; Pred. No. 1,2e-18;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QNSGNQSPEDTDEBKPKYEQGNIVDIDFDSVPQING 38
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Db 2 QNSGNQSPEDTDEBKPKYEQGNIVDIDFDSVPQING 39

RESULT 14
US-08-495-559-6
; Sequence 6, Application US/08495559A
; Patent No. 6054572
; GENERAL INFORMATION:
; APPLICANT: BURHAM, Martin Karl Russel
; APPLICANT: CHOPRA, Ian
; APPLICANT: CRITCHLEY, Ian Alfred
; APPLICANT: KNOWLES, David Justin Charles
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN: MONOCLONAL
; TITLE OF INVENTION: ANTIBODY AND THEIR USE IN PREVENTING BACTERIAL ADHESION
; FILE REFERENCE: P30591
; CURRENT APPLICATION NUMBER: US/08/495,559A
; CURRENT FILING DATE: 1995-08-03
; EARLIER APPLICATION NUMBER: GB 9302289.5
; EARLIER FILING DATE: 1993-02-05
; EARLIER APPLICATION NUMBER: GB 9321592.9
; EARLIER FILING DATE: 1993-10-20
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 176
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-08-495-559-6

Query Match          94.7%; Score 195; DB 3; Length 176;
Best Local Similarity 97.4%; Pred. No. 1,2e-18;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QNSGNQSPEDTDEBKPKYEQGNIVDIDFDSVPQING 38
    |||||
Db 2 QNSGNQSPEDTDEBKPKYEQGNIVDIDFDSVPQING 39

RESULT 15
US-08-459-135A-12
; Sequence 12, Application US/08459135A
; Patent No. 5955078
; GENERAL INFORMATION:
; APPLICANT: BURHAM, Martin Karl Russel
; APPLICANT: CHOPRA, Ian
; APPLICANT: CRITCHLEY, Ian Alfred
; APPLICANT: KNOWLES, David Justin Charles
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN: MONOCLONAL ANTIBODY AND THEIR US
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: SmithKline Beecham Corporation
; STREET: 709 Swedeland Road
; CITY: King of Prussia
; STATE: PA
; COUNTRY: U.S.A.
; ZIP: 19406-0939
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: Fastseq, Version 2.0
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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/459,135A
; FILING DATE: 02-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA: PCT/GB/94/00215
; APPLICATION NUMBER: 435
; FILING DATE: 04-Feb-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Glimi, Edward R
; REGISTRATION NUMBER: 38,891
; REFERENCE/DOCKET NUMBER: P30591C2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-270-4478
; TELEFAX: 610-270-5090
; TELEX:
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 178 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Protein
US-08-459-135A-12

Query Match          94.7%; Score 195; DB 2; Length 178;
Best Local Similarity 97.4%; Pred. No. 1,2e-18;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QNSGNQSPEDTDEBKPKYEQGNIVDIDFDSVPQING 38
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Db 2 QNSGNQSPEDTDEBKPKYEQGNIVDIDFDSVPQING 39
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Search completed: October 22, 2005, 03:51:16
Job time : 29.8363 secs

GenCore version 5.1.6
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OM protein - protein search, using 8w model

Run on: October 22, 2005, 10:49:15 ; Search time 107.19 Seconds
(without alignments)
148.005 Million cell updates/sec

Title: US-10-731-238-35

Perfect score: 206
Sequence: 1 QNSGNQSPEDTEDEPKRYEGGNIVDIDFSDVPQIHG 38

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1862951 seqs, 417491010 residues

Total number of hits satisfying chosen parameters: 1862951

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

Published Applications AA.*
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19: /cgn2_6/ptodata/2/pubpaa/US11A_PUBCOMB.pep.*
20: /cgn2_6/ptodata/2/pubpaa/US11A_NEW_PUB.pep.*
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22: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	195	94.7	38	9	US-10-731-238-5
3	195	94.7	139	8	US-09-813-820-8
4	195	94.7	388	8	US-08-501-062-1
5	195	94.7	559	15	US-10-329-624-5251
6	195	94.7	559	15	US-10-329-624-5251
7	195	94.7	767	9	US-09-815-242-5899
8	195	94.7	767	9	US-09-815-242-13140
9	195	94.7	940	17	US-10-470-048B-424
10	195	94.7	948	17	US-10-470-048B-69
11	195	94.7	961	15	US-10-282-122A-43778

12	195	94.7	1018	9	US-09-815-242-5797	Sequence 5797, Ap
13	195	94.7	1018	9	US-09-815-242-12838	Sequence 12838, A
14	195	94.7	1018	17	US-10-470-048B-68	Sequence 68, Appl
15	195	94.7	1027	8	US-08-781-986A-5254	Sequence 5254, Ap
16	195	94.7	1027	15	US-10-329-624-5254	Sequence 5254, Ap
17	195	94.7	1038	15	US-10-282-122A-43827	Sequence 43827, A
18	189	91.7	38	18	US-10-731-238-36	Sequence 36, Appl
19	189	91.7	38	18	US-10-731-238-37	Sequence 37, Appl
20	189	91.7	38	18	US-10-731-238-39	Sequence 39, Appl
21	189	91.7	38	18	US-10-731-238-40	Sequence 40, Appl
22	189	91.7	38	18	US-10-731-238-41	Sequence 41, Appl
23	188	91.3	38	18	US-10-731-238-38	Sequence 38, Appl
24	188	91.3	38	18	US-10-731-238-42	Sequence 42, Appl
25	187	90.8	38	18	US-10-731-238-6	Sequence 6, Appl
26	187	90.8	38	18	US-10-731-238-43	Sequence 43, Appl
27	187	90.8	38	18	US-10-731-238-45	Sequence 45, Appl
28	187	90.8	978	9	US-09-815-242-5456	Sequence 5456, Ap
29	187	90.8	1001	9	US-09-815-242-12686	Sequence 12686, A
30	184.5	89.6	39	18	US-10-731-238-57	Sequence 57, Appl
31	176.5	85.7	38	18	US-10-731-238-7	Sequence 7, Appl
32	176	85.4	38	18	US-10-731-238-46	Sequence 46, Appl
33	170	82.5	38	18	US-10-731-238-47	Sequence 47, Appl
34	170	82.5	38	18	US-10-731-238-48	Sequence 48, Appl
35	169	82.0	38	18	US-10-731-238-48	Sequence 48, Appl
36	168	81.6	38	18	US-10-731-238-8	Sequence 8, Appl
37	168	81.6	38	18	US-10-731-238-49	Sequence 49, Appl
38	167	81.1	38	18	US-10-731-238-44	Sequence 44, Appl
39	153	74.3	36	18	US-10-731-238-58	Sequence 58, Appl
40	148	71.8	38	18	US-10-731-238-50	Sequence 50, Appl
41	145	70.4	36	18	US-10-731-238-59	Sequence 59, Appl
42	137	66.5	30	14	US-10-287-821-1	Sequence 1, Appl
43	137	66.5	31	14	US-10-287-821-2	Sequence 2, Appl
44	80.5	39.1	37	20	US-11-066-697-1134	Sequence 1134, Ap
45	74	35.9	14	18	US-10-731-238-60	Sequence 60, Appl

ALIGNMENTS

RESULT 1
US-10-731-238-35
; Sequence 35, Application US/10731238
; Publication No. US20050123552A1
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
Patli, Joseph M.
House-Pompeo, Karen L.
Speziale, Pietro
Job, Danny
McGavin, Martin J.
TITLE OF INVENTION: FIBROBLAST BINDING PROTEIN COMPOSITIONS
AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESSES:
ADDRESSER: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/731,238
FILING DATE: 10-Dec-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE: 21-Jan-1998
APPLICATION NUMBER: US 60/036,139

FILED DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE//DOCKET NUMBER: TAMK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 35:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
US-10-731-238-35
SEQUENCE DESCRIPTION: SEQ ID NO: 35:
Query Match 100.0%; Score 206; DB 18; Length 38;
Best Local Similarity 100.0%; Pred. No. 6.8e-19;
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 QNSGNQSPEDTDEKPKYEQGNIVDIDFDSVPQIHG 38
Db 1 QNSGNQSPEDTDEKPKYEQGNIVDIDFDSVPQIHG 38
RESULT 2
US-10-731-238-5
Sequence 5, Application US/10731238
Publication No. US20050123552A1
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
Patti, Joseph M.
House-Pompeo, Karen L.
Speziale, Pietro
Joh, Danny
McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P. O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10731,238
FILING DATE: 10-Dec-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE: 21-Jan-1998
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE//DOCKET NUMBER: TAMK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>

TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-10-731-238-5
Query Match 94.7%; Score 195; DB 18; Length 38;
Best Local Similarity 97.4%; Pred. No. 1.7e-17;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 QNSGNQSPEDTDEKPKYEQGNIVDIDFDSVPQIHG 38
Db 1 QNSGNQSPEDTDEKPKYEQGNIVDIDFDSVPQIHG 38
RESULT 3
US-09-813-820-8
Sequence 8, Application US/09813820
Patent No. US20020102262A1
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
Patti, Joseph M.
House-Pompeo, Karen
Stenham, Narayana
Symersky, Jindrich
TITLE OF INVENTION: COLLAGEN BINDING PROTEIN COMPOSITIONS
AND METHODS OF USE
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P. O. Box 4433
CITY: Houston
STATE: Texas
COUNTRY: U.S.
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/813,820
FILING DATE: 22-Mar-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/856,253
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Kitchell, Bairdara S.
REGISTRATION NUMBER: 33,928
REFERENCE//DOCKET NUMBER: TAMK:193
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
TELEFAX: (512) 474-7577
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 139 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
US-09-813-820-8
SEQUENCE DESCRIPTION: SEQ ID NO: 8:
Query Match 94.7%; Score 195; DB 9; Length 139;
Best Local Similarity 97.4%; Pred. No. 7.7e-17;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 QNSGNQSPEDTDEKPKYEQGNIVDIDFDSVPQIHG 38
Db 16 QNSGNQSPEDTDEKPKYEQGNIVDIDFDSVPQIHG 53
RESULT 4
US-08-901-062-1
Sequence 1, Application US/08901062

Publication No. US2002002324A1
GENERAL INFORMATION:
APPLICANT: SEALS, JONATHAN R.
TITLE OF INVENTION: RECOMBINANT BIVALENT BACTERIAL VACCINE
TITLE OF INVENTION: FOR THE PREVENTION OF MASTITIS
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: HALE AND DORR LLP
STREET: 60 State Street
CITY: Boston
STATE: MA
COUNTRY: United States Of America
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/901,062
FILING DATE: 25-JUL-1997
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Baker, Hollie L.
REGISTRATION NUMBER: 31,321
REFERENCE/DOCKET NUMBER: 106941.153
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 526-6000
TELEFAX: (617) 526-5000
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 388 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-901-062-1

Query Match 94.7%; Score 195; DB 8; Length 388;
Best Local Similarity 97.4%; Pred. No. 2.5e-16;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ONSGNSPEEDTEBDKPKYEOGNIYDIDFDSVPQIHG 38
Db 265 ONSGNSPEEDTEBDKPKYEOGNIYDIDFDSVPQIHG 302

RESULT 5
US-08-781-986A-5251
Sequence 5251, Application US/08781986A
Publication No. US20030054436A1
GENERAL INFORMATION:
APPLICANT: Charles Kunsch
TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
NUMBER OF SEQUENCES: 5255
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COUNTRY: USA
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/781,986A
FILING DATE:
CLASSIFICATION: 435

PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Benson, Bob
REGISTRATION NUMBER: 30,446
REFERENCE/DOCKET NUMBER: PB248PP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 5251:
SEQUENCE CHARACTERISTICS:
LENGTH: 559 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-781-986A-5251

Query Match 94.7%; Score 195; DB 8; Length 559;
Best Local Similarity 97.4%; Pred. No. 3.9e-16;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ONSGNSPEEDTEBDKPKYEOGNIYDIDFDSVPQIHG 38
Db 301 ONSGNSPEEDTEBDKPKYEOGNIYDIDFDSVPQIHG 338

RESULT 6
US-10-329-624-5251
Sequence 5251, Application US/10329624
Publication No. US20040043037A1
GENERAL INFORMATION:
APPLICANT: Charles Kunsch
Gill H. Choi
Patrick S. Dillon
Craig A. Rosen
Steven C. Barash
Michael R. Fannon
TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
NUMBER OF SEQUENCES: 5256
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COUNTRY: USA
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/329,624
FILING DATE: 27-Dec-2002
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/956,171
FILING DATE: October 20, 1997
APPLICATION NUMBER: 60/009,861
FILING DATE: January 5, 1996
APPLICATION NUMBER: 08/781,986
FILING DATE: January 3, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Mark J. Hyman
REGISTRATION NUMBER: 46,789
REFERENCE/DOCKET NUMBER: PB248P1D1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (240) 314-1224
TELEFAX: (301) 309-8439
INFORMATION FOR SEQ ID NO: 5251:
SEQUENCE CHARACTERISTICS:
LENGTH: 559 amino acids

```

;
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 5251:
US-10-329-624-5251

Query Match      94.7%; Score 195; DB 15; Length 559;
Best Local Similarity 97.4%; Pred. No. 3,9e-16;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy      1  QNSGNQSPEDTDEBKPKYEGGNIIVDIDFDSVPQIHG 38
Db      301 QNSGNQSPEDTDEBKPKYEGGNIIVDIDFDSVPQIHG 338

RESULT 7
US-09-815-242-5899
; Sequence 5899, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Karl L.
; APPLICANT: Zykkind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; FILE REFERENCE: ELITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5899
; LENGTH: 767
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-09-815-242-5899

Query Match      94.7%; Score 195; DB 9; Length 767;
Best Local Similarity 97.4%; Pred. No. 5,6e-16;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy      1  QNSGNQSPEDTDEBKPKYEGGNIIVDIDFDSVPQIHG 38
Db      682 QNSGNQSPEDTDEBKPKYEGGNIIVDIDFDSVPQIHG 719

RESULT 8
US-09-815-242-13140
; Sequence 13140, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Karl L.
; APPLICANT: Zykkind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; FILE REFERENCE: ELITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13140
; LENGTH: 767
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-09-815-242-13140

Query Match      94.7%; Score 195; DB 9; Length 767;
Best Local Similarity 97.4%; Pred. No. 5,6e-16;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy      1  QNSGNQSPEDTDEBKPKYEGGNIIVDIDFDSVPQIHG 38
Db      682 QNSGNQSPEDTDEBKPKYEGGNIIVDIDFDSVPQIHG 719

RESULT 9
US-10-470-048B-424
; Sequence 424, Application US/10470048B
; Publication No. US20050037444A1
; GENERAL INFORMATION:
; APPLICANT: MEINKE ET AL.
; TITLE OF INVENTION: A METHOD FOR IDENTIFICATION, ISOLATION AND PRODUCTION OF
; FILE REFERENCE: SONN:035US
; CURRENT APPLICATION NUMBER: US/10/470,048B
; CURRENT FILING DATE: 2003-07-25
; NUMBER OF SEQ ID NOS: 603
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 424
; LENGTH: 940
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-10-470-048B-424

Query Match      94.7%; Score 195; DB 17; Length 940;
Best Local Similarity 97.4%; Pred. No. 7e-16;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy      1  QNSGNQSPEDTDEBKPKYEGGNIIVDIDFDSVPQIHG 38
Db      682 QNSGNQSPEDTDEBKPKYEGGNIIVDIDFDSVPQIHG 719

RESULT 10
US-10-470-048B-69
; Sequence 69, Application US/10470048B
; Publication No. US20050037444A1
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```

; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; FILE REFERENCE: ELITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13140
; LENGTH: 767
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-09-815-242-13140

Query Match      94.7%; Score 195; DB 9; Length 767;
Best Local Similarity 97.4%; Pred. No. 5,6e-16;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy      1  QNSGNQSPEDTDEBKPKYEGGNIIVDIDFDSVPQIHG 38
Db      682 QNSGNQSPEDTDEBKPKYEGGNIIVDIDFDSVPQIHG 719

RESULT 9
US-10-470-048B-424
; Sequence 424, Application US/10470048B
; Publication No. US20050037444A1
; GENERAL INFORMATION:
; APPLICANT: MEINKE ET AL.
; TITLE OF INVENTION: A METHOD FOR IDENTIFICATION, ISOLATION AND PRODUCTION OF
; FILE REFERENCE: SONN:035US
; CURRENT APPLICATION NUMBER: US/10/470,048B
; CURRENT FILING DATE: 2003-07-25
; NUMBER OF SEQ ID NOS: 603
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 424
; LENGTH: 940
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-10-470-048B-424

Query Match      94.7%; Score 195; DB 17; Length 940;
Best Local Similarity 97.4%; Pred. No. 7e-16;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy      1  QNSGNQSPEDTDEBKPKYEGGNIIVDIDFDSVPQIHG 38
Db      682 QNSGNQSPEDTDEBKPKYEGGNIIVDIDFDSVPQIHG 719

RESULT 10
US-10-470-048B-69
; Sequence 69, Application US/10470048B
; Publication No. US20050037444A1
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; GENERAL INFORMATION:
; APPLICANT: MEINKE ET AL.
; TITLE OF INVENTION: A METHOD FOR IDENTIFICATION, ISOLATION AND PRODUCTION OF
; TITLE OF INVENTION: ANTIGENS TO A SPECIFIC PATHOGEN
; FILE REFERENCE: SOON-035US
; CURRENT APPLICATION NUMBER: US/10/470,048B
; NUMBER OF SEQ ID NOS: 603
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 69
; LENGTH: 948
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
; US-10-470-048B-69

Query Match      94.7% Score 195; DB 17; Length 948;
Best Local Similarity 97.4%; Pred. No. 7,1e-16;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1  ONSGNQSPEDTEEDKPKYEGGNIIVDIDFDSVPQIHG 38
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Db      690  ONSGNQSPEDTEEDKPKYEGGNIIVDIDFDSVPQIHG 727

RESULT 11
US-10-282-122A-43778
; Sequence 43778, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zykkind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Foreyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 43778
; LENGTH: 961
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
; US-10-282-122A-43778
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Query Match      94.7% Score 195; DB 15; Length 961;
Best Local Similarity 97.4%; Pred. No. 7,2e-16;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1  ONSGNQSPEDTEEDKPKYEGGNIIVDIDFDSVPQIHG 38
        |||||  |||||  |||||  |||||  |||||  |||||
Db      693  ONSGNQSPEDTEEDKPKYEGGNIIVDIDFDSVPQIHG 730

RESULT 12
US-09-815-242-5797
; Sequence 5797, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari L.
; APPLICANT: Zykkind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; TITLE OF INVENTION: Prokaryotes
; FILE REFERENCE: ELITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5797
; LENGTH: 1018
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
; US-09-815-242-5797

Query Match      94.7% Score 195; DB 9; Length 1018;
Best Local Similarity 97.4%; Pred. No. 7,7e-16;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1  ONSGNQSPEDTEEDKPKYEGGNIIVDIDFDSVPQIHG 38
        |||||  |||||  |||||  |||||  |||||  |||||
Db      746  ONSGNQSPEDTEEDKPKYEGGNIIVDIDFDSVPQIHG 783

RESULT 13
US-09-815-242-12838
; Sequence 12838, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari L.
; APPLICANT: Zykkind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
```

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; TITLE OF INVENTION: Prokaryotes
; FILE REFERENCE: EUTRA.011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 12838
; LENGTH: 1018
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-09-815-242-12838

Query Match      94.7%; Score 195; DB 9; Length 1018;
Best Local Similarity 97.4%; Pred. No. 7.7e-16;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1  QNSGNQSPEDTEEDKPKYEQGNIVDIDFDSVPOIHG 38
Db      746  QNSGNQSPEDTEEDKPKYEQGNIVDIDFDSVPOIHG 783

RESULT 14
US-10-470-048B-68
; Sequence 68, Application US/10470048B
; Publication No. US20050037444A1
; GENERAL INFORMATION:
; APPLICANT: MEINKE ET AL.
; TITLE OF INVENTION: A METHOD FOR IDENTIFICATION, ISOLATION AND PRODUCTION OF
; FILE REFERENCE: SONN:035US
; CURRENT FILING DATE: 2003-07-25
; CURRENT APPLICATION NUMBER: US/10/470,048B
; NUMBER OF SEQ ID NOS: 603
; SOFTWARE: Patentin version 3.1
; SEQ ID NO: 68
; LENGTH: 1018
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-10-470-048B-68

Query Match      94.7%; Score 195; DB 17; Length 1018;
Best Local Similarity 97.4%; Pred. No. 7.7e-16;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1  QNSGNQSPEDTEEDKPKYEQGNIVDIDFDSVPOIHG 38
Db      746  QNSGNQSPEDTEEDKPKYEQGNIVDIDFDSVPOIHG 783

RESULT 15
US-08-781-986A-5254
; Sequence 5254, Application US/08781986A
; Publication No. US20030054436A1
; GENERAL INFORMATION:
; APPLICANT: Charles Kunach
; TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
; NUMBER OF SEQUENCES: 5255
; CORRESPONDENCE ADDRESS:
; ADDRESSSEE: Human Genome Sciences, Inc.
```

```

; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/781,986A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Benson, Bob
; REGISTRATION NUMBER: 30,446
; REFERENCE/DOCKET NUMBER: PB248PP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 5254:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1027 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-781-986A-5254

Query Match      94.7%; Score 195; DB 8; Length 1027;
Best Local Similarity 97.4%; Pred. No. 7.8e-16;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1  QNSGNQSPEDTEEDKPKYEQGNIVDIDFDSVPOIHG 38
Db      755  QNSGNQSPEDTEEDKPKYEQGNIVDIDFDSVPOIHG 792
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Search completed: October 22, 2005, 11:34:46
Job time : 108.19 secs

GenCore version 5.1.6
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OW protein - protein search, using BW model

Run on: October 22, 2005, 02:23:36 ; Search time 19.0841 Seconds
(without alignments)
191.586 Million cell updates/sec

Title: US-10-731-238-35
Perfect score: 206
Sequence: 1 QNSGNQSPEDTEBDKPKRYEQGNGNIVDIDFDSVPQIHG 38

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	195	94.7	940	2	S19702 fibronectin-binding
2	195	94.7	961	2	S19702 fibronectin-binding
3	195	94.7	1018	2	A32192 fibronectin-binding
4	195	94.7	1038	2	H90053 fibronectin-binding
5	63	30.6	273	2	T46108 fibronectin-binding
6	60	29.1	1817	2	T34249 fibronectin-binding
7	57.5	27.9	784	2	T45971 fibronectin-binding
8	57	27.7	329	2	S07577 fibronectin-binding
9	57	27.7	335	2	S07576 fibronectin-binding
10	57	27.7	465	2	S69038 fibronectin-binding
11	57	27.7	484	2	A24942 fibronectin-binding
12	57	27.7	882	1	IJHUCB fibronectin-binding
13	57	27.7	1022	2	I53078 fibronectin-binding
14	57	27.7	1613	2	S39059 fibronectin-binding
15	57	27.7	1647	2	S45252 fibronectin-binding
16	56	27.2	345	2	T33906 fibronectin-binding
17	55.5	26.9	558	2	C71609 fibronectin-binding
18	55.5	26.9	817	2	T03852 fibronectin-binding
19	55.5	26.9	1020	2	T29108 fibronectin-binding
20	55.5	26.9	1273	1	TDPR1T fibronectin-binding
21	55.5	26.9	1291	1	A28334 fibronectin-binding
22	55.5	26.9	1426	2	T30817 fibronectin-binding
23	55	26.7	335	2	S07578 fibronectin-binding
24	55	26.7	491	1	IJB0CP fibronectin-binding
25	55	26.7	822	1	IJHSCP fibronectin-binding
26	55	26.7	829	1	IJHSCP fibronectin-binding
27	54.5	26.5	2128	2	I52577 fibronectin-binding
28	54	26.2	833	2	E90577 fibronectin-binding
29	54	26.2	871	2	S47518 fibronectin-binding

30	54	26.2	884	1	IJMSCE B-cadherin precurs
31	54	26.2	884	2	S34438 B-cadherin precurs
32	54	26.2	1091	2	S33850 B-cadherin precurs
33	54	26.2	1231	2	T24415 B-cadherin precurs
34	54	26.2	1369	2	S58160 B-cadherin precurs
35	54	26.2	1952	2	T48814 B-cadherin precurs
36	53.5	26.0	133	2	S62573 B-cadherin precurs
37	53.5	26.0	406	2	H84590 B-cadherin precurs
38	53.5	26.0	603	2	S34130 B-cadherin precurs
39	53	25.7	265	2	S57978 B-cadherin precurs
40	53	25.7	310	2	T13528 B-cadherin precurs
41	53	25.7	346	2	S49653 B-cadherin precurs
42	53	25.7	568	2	G83558 B-cadherin precurs
43	52.5	25.5	349	2	A88197 B-cadherin precurs
44	52.5	25.5	354	2	T37211 B-cadherin precurs
45	52	25.2	131	2	S70792 B-cadherin precurs

ALIGNMENTS

RESULT 1
S19702
fibronectin-binding protein B - Staphylococcus aureus
C:Species: Staphylococcus aureus
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
C:Accession: S19702
R:Johansson, K.; Signaes, C.; Mueller, H.P.; Lindberg, M.
Eur. J. Biochem. 202, 1041-1048, 1991
A:Title: Two different genes encode fibronectin binding proteins in Staphylococcus aureus
A:Reference number: S19702; MUID:92111475; PMID:1837266
A:Accession: S19702
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-940 <JOB>
A:Cross-references: UNIPROT:Q53682; EMBL:X62992; NID:G49040; PIDN:CAA44726.1; PID:G58156;
C:Keywords: fibronectin binding

Query Match 94.7% ; Score 195; DB 2; Length 940;
Best Local Similarity 97.4% ; Pred. No. 4.3e-16;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QNSGNQSPEDTEBDKPKRYEQGNGNIVDIDFDSVPQIHG 38
DB 682 QNSGNQSPEDTEBDKPKRYEQGNGNIVDIDFDSVPQIHG 719

RESULT 2

G90053
hypothetical protein fnb [imported] - Staphylococcus aureus (strain N315)
C:Species: Staphylococcus aureus
C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
R:Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguchi, A.; Mizutani-U, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.; C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiratake, K.
Lancet 357, 1225-1240, 2001
A:Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.
A:Reference number: A89758; MUID:21311952; PMID:11418146
A:Accession: G90053
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-961 <KUR>
A:Cross-references: UNIPROT:Q99RD3; GB:BA000018; PID:g13702452; PIDN:BA843593.1; GSPDB:G
C:Experimental source: strain N315
C:Genetics:
A:Gene: fnbB

Query Match 94.7% ; Score 195; DB 2; Length 961;
Best Local Similarity 97.4% ; Pred. No. 4.4e-16;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QNSGNQSPEDTEBDKPKRYEQGNGNIVDIDFDSVPQIHG 38

Db 693 QNSGNQSFEDTEBDKPKRYEGGNNIVDIDFDSVPQIHG 730

RESULT 3

A32192

fibronectin-binding protein - Staphylococcus aureus

C:Species: Staphylococcus aureus
C:Date: 31-Jul-1989 #sequence_revision 31-Jul-1989 #text_change 16-Feb-1997
C:Accession: A32192
R:Signees, C.; Raucsi, G.; Joensson, K.; Lindgren, P.E.; Anantharamiah, G.M.; Heeock, M
Proc. Natl. Acad. Sci. U.S.A. 86, 699-703, 1989
A:Title: Nucleotide sequence of the gene for a fibronectin-binding protein from Staphylo
A:Reference number: A32192; MUID:89089898; PMID:2521391
A:Accession: A32192
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1018 <SIG>
A:Cross-references: GB:J04151
C:Keywords: fibronectin binding

Query Match 94.7%; Score 195; DB 2; Length 1018;
Best Local Similarity 97.4%; Pred. No. 4.7e-16;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QNSGNQSFEDTEBDKPKRYEGGNNIVDIDFDSVPQIHG 38

Db 746 QNSGNQSFEDTEBDKPKRYEGGNNIVDIDFDSVPQIHG 783

RESULT 4

H90053

hypothetical protein fnb [imported] - Staphylococcus aureus (strain N315)

C:Species: Staphylococcus aureus
C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C:Accession: H90053
R:Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Ogun
ma, A.; Mitsuhashi, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Katoh, C.; Sekimizu, K.;
C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
A:Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.
A:Reference number: A89758; MUID:21311952; PMID:11418146
A:Accession: H90053
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1038 <KUR>
A:Cross-references: UNIPROT:Q99RD2; GB:BA000018; PID:913702453; PIDN:BAB43594.1; GSPDB:C
A:Experimental source: strain N315
C:Genetics:

Query Match 94.7%; Score 195; DB 2; Length 1038;
Best Local Similarity 97.4%; Pred. No. 4.8e-16;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QNSGNQSFEDTEBDKPKRYEGGNNIVDIDFDSVPQIHG 38

Db 742 QNSGNQSFEDTEBDKPKRYEGGNNIVDIDFDSVPQIHG 779

RESULT 5

T46108

hypothetical protein T27B3.10 - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 09-Jul-2004
C:Accession: T46108
R:Nakatsuma, G.; Fartmann, B.; Dauner, D.; Steier, W.; Holland, R.; Weichselgartner, M.;
Submitted to the Protein Sequence Database, January 2000
A:Reference number: 223022
A:Accession: T46108
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-273 <NYA>

A:Cross-references: UNIPROT:Q9W2N8; EMBL:AL137079
A:Experimental source: cultivar Columbia; BAC clone T27B3
C:Genetics:
A:Map position: 3
A:Introns: 47/2; 143/1
A:Note: T27B3.10

Query Match 30.6%; Score 63; DB 2; Length 273;
Best Local Similarity 33.3%; Pred. No. 2.4;
Matches 12; Conservative 7; Mismatches 17; Indels 0; Gaps 0;

QY 3 SGNSPEEDTEBDKPKRYEGGNNIVDIDFDSVPQIHG 38

Db 173 SGNSPEADDDDDDDDDANEDHDPVGDNDPDQVHG 208

RESULT 6

T34249

hypothetical protein F31D5.5 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans
C:Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
C:Accession: T34249
R:Wilcox, L.
Submitted to the EMBL Data Library, June 1995
A:Description: The sequence of C. elegans cosmid F31D5.
A:Reference number: 221494
A:Accession: T34249
A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA
A:Residues: 1-1817 <WIL>
A:Cross-references: UNIPROT:Q19931; EMBL:U28941; PIDN:ACG71101.1; GSPDB:GN00020; CESP:F31
A:Experimental source: strain Bristol N2; clone F31D5
C:Genetics:
A:Gene: CESP:F31D5.5
A:Map position: 2
A:Introns: 22/2; 107/2; 199/2; 291/2; 384/2; 476/2; 566/2; 648/2; 728/2; 904/2; 1047/2; 1

Query Match 29.1%; Score 60; DB 2; Length 1817;
Best Local Similarity 47.8%; Pred. No. 48;
Matches 11; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

QY 1 QNSGNQSFEDTEBDKPKRYEGG 23

Db 1357 RNYGSSEEDDEBDPAMEAG 1379

RESULT 7

T45971

hypothetical protein F9D24.20 - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 09-Jul-2004
C:Accession: T45971
R:DiAngelo, M.; Vezzi, A.; Modesto, D.; Pigazzi, M.; Valle, G.; Mewes, H.W.; Lemcke, K.;
Submitted to the Protein Sequence Database, January 2000
A:Reference number: 223011
A:Accession: T45971
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-784 <DNM>
A:Cross-references: UNIPROT:Q9W2K5; EMBL:AL137081
A:Experimental source: cultivar Columbia; BAC clone F9D24
C:Genetics:
A:Map position: 3
A:Note: F9D24.20
C:Superfamily: Arabidopsis thaliana hypothetical protein F9D24.20

Query Match 27.9%; Score 57.5; DB 2; Length 784;
Best Local Similarity 30.0%; Pred. No. 38;
Matches 18; Conservative 7; Mismatches 10; Indels 25; Gaps 3;

QY 4 GNQSP-----EDTEBDKPKRYEGG-----GNIV-----DIDFDSVPQIHG 38

Db 450 GEDEPIEDVEEETEDTERKGGGFPFPNGDSLQGVGGNNLMDGASPLGVNSGLQIHG 509

RESULT 8

legumin storage protein LeB6 - fava bean (fragment)
 A:Residues: 1-329 <HE>
 C:Species: Vicia faba (fava bean)
 C>Date: 21-Nov-1993 #sequence_revision 26-Jul-1996 #text_change 09-Jul-2004
 C:Accession: S07577
 R:Heim, U.; Schubert, R.; Baumelein, H.; Wobus, U.
 Plant Mol. Biol. 13, 653-663, 1989
 A>Title: The legumin gene family: structure and evolutionary implications of Vicia faba
 A:Reference number: S07576; MUID:91370849; PMID:2491681
 A:Accession: S07577
 A:Status: translation not shown
 A:Molecule type: DNA
 A:Residues: 1-329 <HE>
 A:Cross-references: UNIPROT:P16079; EMBL:X14240; NID:g22020; PIDN:CAA32456.1; PID:g29584
 C:Genetics:
 A:Gene: LeB6
 A:Introns: 34/3; 204/3
 C:Superfamily: glycinin
 C:Keywords: seed; storage protein

Query Match 27.7%; Score 57; DB 2; Length 329;
 Best Local Similarity 52.4%; Pred. No. 16;
 Matches 11; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

QY 4 GNSPEEDTEDEPKYEOGNN 24
 DB 128 GQEEEBEERKORSEOGNN 148

RESULT 9

legumin storage protein LeB2 - fava bean (fragment)
 A:Residues: 1-335 <HE>
 C:Species: Vicia faba (fava bean)
 C>Date: 21-Nov-1993 #sequence_revision 26-May-1995 #text_change 09-Jul-2004
 C:Accession: S07576
 R:Heim, U.; Schubert, R.; Baumelein, H.; Wobus, U.
 Plant Mol. Biol. 13, 653-663, 1989
 A>Title: The legumin gene family: structure and evolutionary implications of Vicia faba
 A:Reference number: S07576; MUID:91370849; PMID:2491681
 A:Accession: S07576
 A:Status: translation not shown
 A:Molecule type: DNA
 A:Residues: 1-335 <HE>
 A:Cross-references: UNIPROT:P16078; EMBL:X14237; NID:g22013; PIDN:CAA32454.1; PID:g29584
 C:Genetics:
 A:Gene: LeB2
 A:Introns: 34/3; 210/3
 C:Superfamily: glycinin
 C:Keywords: seed; storage protein

Query Match 27.7%; Score 57; DB 2; Length 335;
 Best Local Similarity 52.4%; Pred. No. 17;
 Matches 11; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

QY 4 GNSPEEDTEDEPKYEOGNN 24
 DB 134 GQEEEBEERKORSEOGNN 154

RESULT 10

hypothetical protein YPR152c - yeast (Saccharomyces cerevisiae)
 A:Residues: 1-544 <HE>
 C:Species: Saccharomyces cerevisiae
 C>Date: 22-Aug-1996 #sequence_revision 06-Sep-1996 #text_change 09-Jul-2004
 C:Accession: S69038
 R:Pulion, L.
 Submitted to the EMBL Data Library, November 1995
 A:Description: The sequence of S. cerevisiae cosmid 9659.
 A:Reference number: S69022
 A:Accession: S69038

A:Molecule type: DNA

A:Residues: 1-465 <FUL>
 A:Cross-references: UNIPROT:Q06525; EMBL:U04029; NID:g1066476; PID:g1066497; GSPDB:GN0001
 C:Genetics:
 A:Gene: MIPS:YPR152c
 A:Cross-references: SGD:S0006356
 A:Map position: 16R
 C:Superfamily: formin binding protein, WW repeat homology
 F.1-36/Domain: WW repeat homology #status atypical <WW>

Query Match 27.7%; Score 57; DB 2; Length 465;
 Best Local Similarity 38.1%; Pred. No. 24;
 Matches 16; Conservative 6; Mismatches 12; Indels 8; Gaps 2;

QY 2 NSGNSPEEDTEDEPKYEOGNN----IVD---IDPVSQ 35
 DB 174 SSGEEDDEDEBENEQIVNODISIDLRIDTDIDE 215

RESULT 11

legumin B4 precursor - fava bean
 A:Residues: 1-484 <BAE>
 C:Species: Vicia faba (fava bean)
 C>Date: 30-Jun-1988 #sequence_revision 30-Jun-1988 #text_change 13-Nov-1998
 C:Accession: A24942
 R:Baumelein, H.; Wobus, U.; Pustell, J.; Kafatos, F.C.
 Nucleic Acids Res. 14, 2707-2720, 1986
 A>Title: The legumin gene family: structure of a B type gene of Vicia faba and a possible
 A:Reference number: A24942; MUID:86176760; PMID:3960730
 A:Accession: A24942
 A:Molecule type: DNA
 A:Residues: 1-484 <BAE>
 A>Note: the authors translated the codon GTT for residue 188 as Gly and CAC for residue 1
 C:Superfamily: glycinin
 F.1-20/Domain: signal sequence #status predicted <SIG>
 F.21-483/Product: legumin B4 #status predicted <WAT>

Query Match 27.7%; Score 57; DB 2; Length 484;
 Best Local Similarity 52.4%; Pred. No. 25;
 Matches 11; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

QY 4 GNSPEEDTEDEPKYEOGNN 24
 DB 283 GQEEEBEERKORSEOGNN 303

RESULT 12

cadherin 1 precursor [validated] - human
 N:Alternate names: ARC-1; cell CAM 120/80; E-cadherin; epithelial cadherin; L-CAM; uvomor
 C:Species: Homo sapiens (man)
 C>Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 09-Jul-2004
 C:Accession: S37654; S31430; S05475; S31460; S06716; A5171; J02230; I52294; I52704; S251
 R:Bussemakers, M.J.G.; van Bokhoven, A.; Mees, S.G.M.; Kemler, R.; Schalken, J.A.
 Mol. Biol. Rep. 17, 123-128, 1993
 A>Title: Molecular cloning and characterization of the human E-cadherin cDNA.
 A:Reference number: S37654; MUID:93211394; PMID:8459805
 A:Accession: S37654
 A:Molecule type: mRNA
 A:Residues: 1-882 <BUS>
 A:Cross-references: UNIPROT:P12810; EMBL:Z13009; NID:g31072; PIDN:CAA78353.1; PID:g31073
 R:Keller, W.; Warda, A.; Oda, T.; Hirohashi, S.; Kemler, R.; Birchmeier, W.
 submitted to the EMBL Data Library, December 1992
 A:Description: Sequence of human E-cadherin cDNA.
 A:Reference number: S31430
 A:Accession: S31430
 A:Molecule type: mRNA
 A:Residues: 1-542; F. 544-882 <KE>
 A:Cross-references: EMBL:Z18923; NID:g31074; PIDN:CAA79356.1; PID:g31075
 R:Mansouri, A.; Spurr, N.; Goodfellow, P.N.; Kemler, R.
 Differentiation 38, 67-71, 1998
 A>Title: Characterization and chromosomal localization of the gene encoding the human ce
 A:Reference number: S05475; MUID:89031725; PMID:3263290

A:Accession: S05475
A:Molecule type: mRNA
A:Residues: 157-311 <MAN>
A:Cross-references: EMBL:X12790
A>Note: nucleotide sequence is not complete
R:Fixen, U.H.
submitted to the EMBL Data Library, March 1990
A:Reference number: S31460
A:Accession: S31460
A:Molecule type: mRNA
A:Residues: 265-392 <R1>
A:Cross-references: EMBL:X52279; NID:g28821; PIDN:CA35522.1; PID:g28822
R:Wheeler, M.J.; Buck, C.A.; Becholt, K.B.; Damsky, C.H.
J. Cell. Biochem. 34, 187-202, 1987
A:Title: Soluble 80-kd fragment of cell-CAM 120/80 disrupts cell-cell adhesion.
A:Reference number: S06716; MUID:87280410; PMID:3611200
A:Accession: S06716
A:Molecule type: protein
A:Residues: 'XQ',157-162,'V',164-179 <MHE>
R:Bex, G.; Stees, K.; van Hengel, J.; Molemans, F.; Bussemakers, M.J.G.; van Bokhoven,
Genomics 26, 281-289, 1995
A:Title: Cloning and characterization of the human invasion suppressor gene E-cadherin
A:Reference number: A57171; MUID:95324920; PMID:7601454
A:Accession: A57171
A:Status: nucleic acid sequence not shown; not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 1-30,32-882 <BER>
A:Cross-references: GB:L34784
R:Rimm, D.L.; Morrow, J.S.
Biochem. Biophys. Res. Commun. 200, 1754-1761, 1994
A:Title: Molecular cloning of human E-cadherin suggests a novel subdivision of the cadherin
A:Reference number: J02230; MUID:94242050; PMID:8185635
A:Accession: J02230
A:Molecule type: mRNA
A:Residues: 1-9,'G',11-15,'NSPLGSORSPPCTREIHYHGAPAPKPR',52-67,'I',69,'LTPIP',76-94
A:Cross-references: GB:U0659; NID:g340184; PIDN:AA61259.1; PID:g340185
A>Note: the majority of differences between this and other reports represent apparent first
A:Note: the authors translated the codon CCG for residue 668 as Arg
R:Bussemakers, M.J.G.; Grol, L.A.; van Bokhoven, A.; Schalken, J.A.
Biochem. Biophys. Res. Commun. 203, 1284-1290, 1994
A:Title: Transcriptional regulation of the human E-cadherin gene in human prostate cancer
A:Reference number: I52294; MUID:94380041; PMID:8093045
A:Accession: I52294
A:Status: translation not shown; translated from GB/EMBL/DBD
A:Molecule type: DNA
A:Residues: 1-16 <RES>
A:Cross-references: GB:L24545; NID:g509604; PIDN:AA21764.1; PID:g509605
R:Becker, K.F.; Atkinson, M.J.; Reich, U.; Becker, I.; Nekarda, H.; Stewert, J.R.; Hofler
Cancer Res. 54, 3845-3852, 1994
A:Title: E-cadherin gene mutations provide clues to diffuse type gastric carcinomas.
A:Reference number: I52704; MUID:94306394; PMID:8033105
A:Accession: I52704
A:Status: translated from GB/EMBL/DBD
A:Molecule type: DNA
A:Residues: 337-476 <R2>
A:Cross-references: GB:S72497; NID:g632756; PIDN:AA14108.1; PID:g4261808
C:Comment: Cadherins mediate calcium-dependent intercellular adhesion and are thought to
C:Genetics:
A:Gene: GDB:CDH1; UVO
A:Cross-references: GDB:120484; OMIM:192090
A:Map position: 16q22.1-16q22.1
A:Introns: 379/3; 440/3
A:Superfamily: cadherin; cadherin repeat homology
C:Keywords: calcium binding; cell adhesion; duplication; glycoprotein; transmembrane prot
F:1-27/Domain: signal sequence #status predicted <SIG>
F:28-154/Domain: propeptide #status predicted <PRO>
F:155-882/Product: E-cadherin #status experimental <MAN>
F:155-697/Domain: extracellular #status predicted <EXT>
F:157-266/Domain: cadherin repeat homology <CR1>
F:233-237/Domain: cadherin binding #status predicted
F:265-375/Domain: cadherin repeat homology <CR2>
F:378-486/Domain: cadherin repeat homology <CR3>
F:487-595/Domain: cadherin repeat homology <CR4>

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F:596-700/Domain: cadherin repeat homology <CRS>
F:698-731/Domain: transmembrane #status predicted <TM>
F:733-882/Domain: intracellular #status predicted <INT>
F:840-853/Region: serine-rich
F:376,558,570,622,637,849/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match      27.7%: Score 57; DB 1; Length 882;
Best Local Similarity 45.2%; Pred. No. 50;
Matches 14; Conservative 6; Mismatches 9; Indels 2; Gaps 2;

QY      8 PEEDTEEDPKK-EGGNIIVDIDPDSVPQIH 37
DB      744 PEDTRDNYVYDEEGGEGEDQDFD-LSQLH 773

RESULT 13
153078
homeotic gene regulator - mouse (fragment)
C:Species: Mus sp. (mouse)
C:Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 09-Jul-2004
A:Accession: I53078
R.Randazzo, F.M.; Khavari, P.; Crabtree, G.; Tamkun, J.; Rossant, J.
Dev. Biol. 161, 229-242, 1994
A>Title: brg1: a putative murine homologue of the Drosophila brahma gene, a homeotic gene
A:Reference number: I53078; MUID:94123856; PMID:7904567
A:Accession: I53078
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-1022 <RES>
A:Cross-references: UNIPROT:Q63928; GB:S68108; NID:9545017; PIDN:AAC60670.1; PID:9545018
C:Genetics:
A:Gene: brg1
C:Superfamily: human SNF2alpha protein; bromodomain homology
F:860-915/Domain: bromodomain homology <BRO>

Query Match      27.7%: Score 57; DB 2; Length 1022;
Best Local Similarity 29.5%; Pred. No. 59;
Matches 13; Conservative 10; Mismatches 13; Indels 8; Gaps 1;

QY      1 QNSGNQSPEDTEEDPK-----YEOGNIIVDIDPDSVPQI 36
DB      66 EESGSEEEEEEEOQPQAPPTLPVEEKXKIPDPSDDVSEV 109

RESULT 14
539059
protein BRG1 - human
C:Species: Homo sapiens (man)
C:Date: 25-Feb-1994 #sequence_revision 17-Nov-1995 #text_change 09-Jul-2004
A:Accession: S39059
R.Khavari, P.A.; Peterson, C.L.; Tamkun, J.W.; Mendel, D.B.; Crabtree, G.R.
Nature 366, 170-174, 1993
A>Title: BRG1 contains a conserved domain of the SWI/SNF2 family necessary for normal mi
A:Reference number: S39059; MUID:94050144; PMID:8232556
A:Accession: S39059
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-1613 <KHA>
A:Cross-references: UNIPROT:Q9HBD3
C:Superfamily: human SNF2alpha protein; bromodomain homology
F:1451-1506/Domain: bromodomain homology <BRO>

Query Match      27.7%: Score 57; DB 2; Length 1613;
Best Local Similarity 29.5%; Pred. No. 98;
Matches 13; Conservative 10; Mismatches 13; Indels 8; Gaps 1;

QY      1 QNSGNQSPEDTEEDPK-----YEOGNIIVDIDPDSVPQI 36
DB      657 EESGSEEEEEEEOQPQAPPTLPVEEKXKIPDPSDDVSEV 700

RESULT 15
545252

```

SNF2beta protein - human

C;Species: Homo sapiens (man)

C; Accession: S45252

R; Chiba, H.; Muramatsu, M.; Nomoto, A.; Kato, H.

Nucleic Acids Res. 22, 1815-1820, 1994

A; Title: Two human homologues of *Saccharomyces cerevisiae* SWI2/SNF2 and *Drosophila* brahma

A;Reference number: S45251; MUID:94268902; PMID:8208605

A;Accession: S45252

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-1647 <CHI>

A: Cross-references: UNIPROT:P51532; GB:D26156; NID:g505087; PIDN:BAA05143.1; PID:g505088

C/Superfamily: human SNF2alpha protein; bromodomain homology

F;1485-1540/Domain: bromodomain homology <BRO>

Query Match	Score	DB	Length
27.7%	57	2	1647

Best Local Similarity	29.5%	Pred. No. 1e+02;
-----------------------	-------	------------------

Matches 13; Conservative 10; Mismatches 13; Indels 8; Gaps 1;

QY 1 QNSGNQSPEDTEEDKPK-----YEQGGNIVDIDFDSVPQI 36

658 EESGSEEEEEEEQPOAQPTLPVEKKKIPDPDSDDVSEV 701

Search completed: October 22, 2005, 04:14:10

Job time : 21.0841 secs

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OM protein - protein search, using sw model

Run on: October 22, 2005, 02:23:35 ; Search time 93.0664 Seconds
(without alignments)
209.087 Million cell updates/sec

Title: US-10-731-238-35
Perfect score: 206
Sequence: 1 QNSGNQSPEDTEBDKPKYEQGNGNIVDIDFDSVPQIHG 38

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : UniProt_03:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	195	94.7	940 2 Q53682	Q53682 staphylococ
2	195	94.7	943 2 Q8NNU8	Q8NNU8 staphylococ
3	195	94.7	957 2 Q6G6H4	Q6G6H4 staphylococ
4	195	94.7	961 2 Q99RD3	Q99RD3 staphylococ
5	195	94.7	961 2 Q7A3J8	Q7A3J8 staphylococ
6	195	94.7	1018 1 FNBA-STPAU	F14738 staphylococ
7	195	94.7	1038 2 Q99RD2	Q99RD2 staphylococ
8	195	94.7	1038 2 Q7A3J7	Q7A3J7 staphylococ
9	194	94.2	965 2 Q6GDU5	Q6GDU5 staphylococ
10	187	90.8	1015 2 Q8NNU7	Q8NNU7 staphylococ
11	187	90.8	1015 2 Q6G6H3	Q6G6H3 staphylococ
12	184	89.3	152 2 Q9AEP9	Q9AEP9 staphylococ
13	184	89.3	152 2 Q6CBW0	Q6CBW0 yarrowia 11
14	184	89.3	152 2 Q6CBW0	Q6CBW0 yarrowia 11
15	184	89.3	152 2 Q6CBW0	Q6CBW0 yarrowia 11
16	184	89.3	152 2 Q6CBW0	Q6CBW0 yarrowia 11
17	184	89.3	152 2 Q6CBW0	Q6CBW0 yarrowia 11
18	184	89.3	152 2 Q6CBW0	Q6CBW0 yarrowia 11
19	184	89.3	152 2 Q6CBW0	Q6CBW0 yarrowia 11
20	184	89.3	152 2 Q6CBW0	Q6CBW0 yarrowia 11
21	184	89.3	152 2 Q6CBW0	Q6CBW0 yarrowia 11
22	184	89.3	152 2 Q6CBW0	Q6CBW0 yarrowia 11
23	184	89.3	152 2 Q6CBW0	Q6CBW0 yarrowia 11
24	184	89.3	152 2 Q6CBW0	Q6CBW0 yarrowia 11
25	184	89.3	152 2 Q6CBW0	Q6CBW0 yarrowia 11
26	184	89.3	152 2 Q6CBW0	Q6CBW0 yarrowia 11
27	184	89.3	152 2 Q6CBW0	Q6CBW0 yarrowia 11
28	184	89.3	152 2 Q6CBW0	Q6CBW0 yarrowia 11
29	184	89.3	152 2 Q6CBW0	Q6CBW0 yarrowia 11
30	184	89.3	152 2 Q6CBW0	Q6CBW0 yarrowia 11
31	184	89.3	152 2 Q6CBW0	Q6CBW0 yarrowia 11

32	58.5	28.4	641 2 Q6CF59	Q6CF59 yarrowia 11
33	58.5	28.4	1791 2 Q8IHX4	Q8IHX4 plasmodium
34	58	28.2	297 2 Q7PNE6	Q7PNE6 mus musculu
35	58	28.2	604 2 Q8IAM8	Q8IAM8 mus musculu
36	58	28.2	674 2 Q9FIP1	Q9FIP1 arabidopsis
37	58	28.2	918 2 Q8OUES	Q8OUES mus musculu
38	58	28.2	988 1 FAL2 MOUSE	Q70318 mus musculu
39	58	28.2	988 2 Q8OU53	Q8OU53 mus musculu
40	58	28.2	1257 2 Q7PT33	Q7PT33 anopheles 9
41	58	28.2	1350 2 Q6LFP5	Q6LFP5 plasmodium
42	57.5	27.9	580 2 Q47942	Q47942 streptococ
43	57.5	27.9	784 2 Q9M2K5	Q9M2K5 arabidopsis
44	57.5	27.9	966 1 PRD2 MOUSE	Q35245 mus musculu
45	57.5	27.9	966 2 Q7TS17	Q7TS17 mus musculu

ALIGNMENTS

RESULT 1

ID	Q53682	PRELIMINARY;	PRT;	940 AA.
AC	Q53682;			
DT	01-NOV-1996 (TREMBLrel. 01, Created)			
DT	01-NOV-1996 (TREMBLrel. 01, Last sequence update)			
DE	01-MAR-2004 (TREMBLrel. 26, Last annotation update)			
DE	Fibronectin binding protein B.			
GN	Name=fnbB;			
OS	Staphylococcus aureus.			
OC	Bacteria; Firmicutes; Bacillales; Staphylococcus.			
OX	NCBI_Taxid=1280;			
RN	(1)			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=8325-4;			
RX	MEDLINE=92111475; PubMed=1837266;			
RA	Johnson K., Sigmas C., Muller H.P., Lindberg M.;			
RT	"Two different genes encode fibronectin binding proteins in staphylococcus aureus. The complete nucleotide sequence and characterization of the second gene."			
RT	Eur. J. Biochem. 202:1041-1048 (1991).			
RL	-1 SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by an amide bond (By similarity).			
CC				
DR	EMBL: X62992; CAA44726.1; -.			
DR	PIR: S19702; S19702.			
DR	HSSP: Q53653; IN67.			
DR	GO: GO:000986; C:cell surface; IEA.			
DR	GO: GO:0005618; C:cell wall; IEA.			
DR	GO: GO:0009275; C:cell wall (senu Gram-positive Bacteria); IEA.			
DR	GO: GO:0016020; C:membrane; IEA.			
DR	GO: GO:0007155; P:cell adhesion; IEA.			
DR	InterPro: IPR008966; Adhes. Bact.			
DR	InterPro: IPR004237; Fn. bind.			
DR	InterPro: IPR005877; Gpos. YSIRK.			
DR	InterPro: IPR001899; Gram_pos_anchor.			
DR	PFam: PF02986; Fn_bind; 2.			
DR	PFam: PF00746; Gram_pos_anchor; 1.			
DR	PFam: PF04650; YSIRK_signal; 1.			
DR	TIGRFAMs: TIGR01167; LpYTG_anchor; 1.			
DR	TIGRFAMs: TIGR01168; YSIRK_signal; 1.			
DR	PROSITE: PS50847; GRAM_POS_ANCHORING; 1.			
KW	Cell wall; Peptidoglycan-anchor.			
SQ	SEQUENCE 940 AA; 10355 MW; E35FBBCA907AE345 CRC64;			
Query Match	94.7%;	Score 195;	DB 2;	Length 940;
Best local Similarity	97.4%;	Pred. No. 26-14;		
Matches	37;	Conservative	0;	Mismatches 1;
			Indels	0;
			Gaps	0;
QY	1 QNSGNQSPEDTEBDKPKYEQGNGNIVDIDFDSVPQIHG 38			
DB	682 QNSGNQSPEDTEBDKPKYEQGNGNIVDIDFDSVPQIHG 719			
RESULT 2				

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08NTU8
ID 08NTU8      PRELIMINARY;      PRT;      943 AA.
AC 08NTU8;
DT 01-OCT-2002 (TReMBLrel. 22, Created)
DT 01-OCT-2002 (TReMBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE FnbB protein.
GN Name=fnbB; OrderedLocuNames=MM2420;
OS Staphylococcus aureus (strain MM2);
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=196620;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MM2;
RX MEDLINE=22040717; PubMed=12044378; DOI=10.1016/S0140-6736(02)08713-5;
RA Baba T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Oguchi A.,
RA Nagai Y., Iwama N., Asano K., Naimi T., Kuroda H., Cui L.,
RA Yamamoto K., Hiramatsu K.;
RT "Genome and virulence determinants of high virulence community-
RT acquired MRSA.";
RL Lancet 359:1819-1827(2002).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC an amide bond (By similarity).
DR HSP; Q53653; IN67.
DR GO; GO:0009986; C:cell wall; IEA.
DR GO; GO:0005618; C:cell wall; IEA.
DR GO; GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0007155; P:cell adhesion; IEA.
DR InterPro; IPR008966; Adhes_bact.
DR InterPro; IPR004237; Fb_bind.
DR InterPro; IPR005877; Gpos_YsIRK.
DR InterPro; IPR001899; Gram_pos_anchor.
DR Pfam; PF02986; Fb_bind; 1.
DR Pfam; PF00746; Gram_pos_anchor; 1.
DR TIGRFAMs; TIGR01167; LPXTG_signal; 1.
DR TIGRFAMs; TIGR01168; YsIRK_signal; 1.
DR PROSITE; PS50847; GRAM_POS_ANCHORING; 1.
DR Cell wall; Complete proteome; Peptidoglycan-anchor.
KW SEQUENCE 943 AA; 104537 MW; DA8A5F31947E1B6A CRC64;
SQ
Query Match 94.7%; Score 195; DB 2; Length 943;
Best Local Similarity 97.4%; Pred. No. 2e-14;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 QNSGNQSPEDTBEEDKPKYEGQGNIVDIDFDSVPQIHG 38
DB 689 QNSGNQSPEDTBEEDKPKYEGQGNIVDIDFDSVPQIHG 726
RESULT 3
Q6G6H4 PRELIMINARY; PRT; 957 AA.
AC 06G6H4;
DT 05-JUN-2004 (TReMBLrel. 27, Created)
DT 05-JUN-2004 (TReMBLrel. 27, Last sequence update)
DT 05-JUN-2004 (TReMBLrel. 27, Last annotation update)
DE Fibronectin-binding protein.
GN Name=fnbB; OrderedLocuNames=SA52387;
OS Staphylococcus aureus (strain MSSA476).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=282459;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=15213124; DOI=10.1073/pnas.0402521101;
RA Holden M.T.G., Fell B.J., Lindsay J.A., Peacock S.J., Day N.P.J.,
RA Enright M.C., Foster T.J., Moore C.E., Hurst L., Atkin R., Barron A.,
RA Baon N., Bentley S.D., Chillingworth C., Chillingworth T.,
RA Churcher C., Clark L., Cotton C., Cronin A., Doggett J., Dowd L.,
RA Feltham T., Hance Z., Harris B., Hauser H., Holtroyd S., Jagsels K.,
RA James K.D., Lennard N., Lane A., Mayes R., Moutle S., Mungall K.,

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RA Ormond D., Quail M.A., Rabbintowtsch E., Rutherford K.M., Sanders M.,
RA Sharp S., Simmonds M., Stevens K., Whitehead S., Barrell B.G.,
RA Spratt B.G., Parkhill J.;
RT "Complete genomes of two clinical Staphylococcus aureus strains:
RT evidence for the rapid evolution of virulence and drug resistance.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:9786-9791(2004).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC an amide bond (By similarity).
DR EMBL; BX571857; CAG44201.1; -.
DR GO; GO:0009986; C:cell surface; IEA.
DR GO; GO:0005618; C:cell wall; IEA.
DR GO; GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0007155; P:cell adhesion; IEA.
DR InterPro; IPR008966; Adhes_bact.
DR InterPro; IPR004237; Fb_bind.
DR InterPro; IPR005877; Gpos_YsIRK.
DR InterPro; IPR001899; Gram_pos_anchor.
DR Pfam; PF02986; Fb_bind; 1.
DR Pfam; PF00746; Gram_pos_anchor; 1.
DR TIGRFAMs; TIGR01167; LPXTG_signal; 1.
DR TIGRFAMs; TIGR01168; YsIRK_signal; 1.
DR PROSITE; PS50847; GRAM_POS_ANCHORING; 1.
KW Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ SEQUENCE 957 AA; 105980 MW; 28F8BA7FFPDJBAF CRC64;
QY 1 QNSGNQSPEDTBEEDKPKYEGQGNIVDIDFDSVPQIHG 38
DB 689 QNSGNQSPEDTBEEDKPKYEGQGNIVDIDFDSVPQIHG 726
RESULT 4
Q99RD3 PRELIMINARY; PRT; 961 AA.
AC Q99RD3;
DT 01-JUN-2001 (TReMBLrel. 17, Created)
DT 01-JUN-2001 (TReMBLrel. 17, Last sequence update)
DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)
DE Fibronectin-binding protein homolog.
GN Name=fnbB; OrderedLocuNames=SAV2502;
OS Staphylococcus aureus (strain Mu50 / ATCC 700699).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=158878;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=Mu50 / ATCC 700699;
RX MEDLINE=21311952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2;
RA Kuroda M., Onota T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Lian J.-Q., Ito T.,
RA Kanamori M., Matsumaru H., Maruyama A., Miyakami H., Hoshoyama C.,
RA Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
RA Sekimizu K., Hiramatsu H., Kohara S., Goto S., Yabuuchi J.,
RA Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
RA Hattoni M., Ogasawara N., Hayaishi H., Hiramatsu K.;
RT "Whole genome sequencing of methicillin-resistant Staphylococcus
RT aureus.";
RL Lancet 357:1225-1240(2001).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC an amide bond (By similarity).
DR EMBL; AP003365; BAB58664.1; -.
DR PIR; G90053; G90053.
DR HSP; Q53653; IN67.
DR GO; GO:0009986; C:cell surface; IEA.
DR GO; GO:0005618; C:cell wall; IEA.
DR GO; GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0007155; P:cell adhesion; IEA.
DR InterPro; IPR008966; Adhes_bact.

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DR InterPro; IPR004237; Fn_bind.
 DR InterPro; IPR005877; Gpos_YsIRK.
 DR InterPro; IPR001899; Gram_pos_anchor.
 DR Pfam; PF02986; Fn_bind; 1.
 DR Pfam; PF00746; Gram_pos_anchor; 1.
 DR Pfam; PF04650; YsIRK_signal; 1.
 DR TIGRFAMs; TIGR01167; LpxTG_anchor; 1.
 DR TIGRFAMs; TIGR01168; YsIRK_signal; 1.
 DR PROSITE; PS00847; GRAM_POS_ANCHORING; 1.
 DR Cell wall; Complete proteome; Peptidoglycan-anchor.
 KW SEQUENCE 961 AA; 106010 MW; 364940F884EA4101 CRC64;

Query Match 94.7%; Score 195; DB 2; Length 961;
 Best Local Similarity 97.4%; Pred. No. 2,1e-14;
 Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 QNSGNQSFEDTEEDKPKYEGGNIVDIDFDSVPQIHG 38
 DB 693 QNSGNQSFEDTEEDKPKYEGGNIVDIDFDSVPQIHG 730

RESULT 5
 ID 07A3J8 PRELIMINARY; PRT; 961 AA.
 AC 07A3J8;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE FndB protein.
 GN Name=fndB; OrderedLocustNames=SA2290;
 OS Staphylococcus aureus (strain N315).
 CC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 CX NCBI_TaxID=158879;

RL [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=2311952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2;
 RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
 RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Iino J.-O., Ito T.,
 RA Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,
 RA Mizumoto-U Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
 RA Sekimizu K., Hirakawa H., Kohara S., Goto S., Yaburaki J.,
 RA Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
 RA Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.,
 RT "Whole genome sequencing of methicillin-resistant Staphylococcus
 aureus."
 CC Lancel 357.1225-1240(2001).
 CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
 CC an amide bond (By similarity).
 CC EMBL; AP003137; BAB43593.1; -
 DR GO; GO:0009986; C:cell surface; IEA.
 DR GO; GO:0005618; C:cell wall; IEA.
 DR GO; GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:007155; P:cell adhesion; IEA.
 DR InterPro; IPR008966; Adhes_bact.
 DR InterPro; IPR004237; Fn_bind.
 DR InterPro; IPR005877; Gpos_YsIRK.
 DR InterPro; IPR001899; Gram_pos_anchor.
 DR Pfam; PF02986; Fn_bind; 1.
 DR Pfam; PF00746; Gram_pos_anchor; 1.
 DR Pfam; PF04650; YsIRK_signal; 1.
 DR TIGRFAMs; TIGR01167; LpxTG_anchor; 1.
 DR TIGRFAMs; TIGR01168; YsIRK_signal; 1.
 DR PROSITE; PS00847; GRAM_POS_ANCHORING; 1.
 KW Cell wall; Complete proteome; Peptidoglycan-anchor.
 SQ SEQUENCE 961 AA; 106010 MW; 364940F884EA4101 CRC64;

Query Match 94.7%; Score 195; DB 2; Length 961;
 Best Local Similarity 97.4%; Pred. No. 2,1e-14;
 Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 OY 1 QNSGNQSFEDTEEDKPKYEGGNIVDIDFDSVPQIHG 38
 DB 693 QNSGNQSFEDTEEDKPKYEGGNIVDIDFDSVPQIHG 730

DB 693 QNSGNQSFEDTEEDKPKYEGGNIVDIDFDSVPQIHG 730

RESULT 6
 ID FNBA_STA0U STANDARD; PRT; 1018 AA.
 AC P14738;
 DT 01-APR-1990 (Rel. 14, Created)
 DT 01-APR-1990 (Rel. 14, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Fibronectin-binding protein precursor (FBNP).
 GN Name=fbnA;
 OS Staphylococcus aureus.
 CC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 CX NCBI_TaxID=1280;
 CX [1]

RP SEQUENCE FROM N.A.
 RC STRAIN=NCIC 8325-4;
 RX MEDLINE=89098998; PubMed=2521391;
 RA Signaes C., Raucsi G., Joensson K., Lindgren P.-E.,
 RA Anantharamaiah G.M., Hoeoek M., Lindberg M.,
 RT "Nucleotide sequence of the gene for a fibronectin-binding protein
 from Staphylococcus aureus: use of this peptide sequence in the
 synthesis of biologically active peptides."
 RT Proc. Natl. Acad. Sci. U.S.A. 86:699-703(1989).
 RL -1- FUNCTION: The ability of bacteria to bind fibronectin has been
 CC proposed as a virulence factor enabling bacteria to colonize wound
 CC tissues and blood clots. Binding of plasma fibronectin to the
 CC bacterial surface might block adhesion receptors on S.aureus, thus
 CC representing an important defense mechanism against tissue
 CC invasion.
 CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
 CC an amide bond (Potential).
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).

CC EMBL; J04151; AAA26632.1; -
 DR InterPro; IPR004237; Fn_bind.
 DR InterPro; IPR005877; Gpos_YsIRK.
 DR InterPro; IPR001899; Gram_pos_anchor.
 DR Pfam; PF02986; Fn_bind; 1.
 DR Pfam; PF00746; Gram_pos_anchor; 1.
 DR Pfam; PF04650; YsIRK_signal; 1.
 DR TIGRFAMs; TIGR01167; LpxTG_anchor; 1.
 DR TIGRFAMs; TIGR01168; YsIRK_signal; 1.
 DR PROSITE; PS00847; GRAM_POS_ANCHORING; 1.
 KW Cell adhesion; Cell wall; Peptidoglycan-anchor; Repeat; Signal;
 KM Virulence.
 FT SIGNAL 1 36
 FT CHAIN 37 985
 FT PROPE 986 1018
 FT REPEAT 545 574
 FT REPEAT 575 604
 FT DOMAIN 745 878
 FT REPEAT 745 782
 FT REPEAT 783 820
 FT REPEAT 821 859
 FT REPEAT 860 878
 FT REPEAT 879 948
 FT DOMAIN 879 882
 FT REPEAT 893 906
 FT REPEAT 907 920
 FT REPEAT 921 934
 FT REPEAT 935 948
 FT SITE 982 986
 FT MOD_RES 985 985
 B-1. Fibronectin-binding protein.
 B-2. Removed by sortase (Potential).
 B-1. D-1.
 D-2. D-3.
 D-4 (incomplete).
 5 X tandem repeats, Pro-rich (WR).
 4 X approximate tandem repeats,
 fibronectin-binding domain.
 D-1.
 D-2.
 D-3.
 D-4 (incomplete).
 5 X tandem repeats, Pro-rich (WR).
 WR 1.
 WR 2.
 WR 3.
 WR 4.
 WR 5.
 LpxTG sorting signal (Potential).
 Pentaglycyl murein peptidoglycan amidated


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FT      threonine (Potential).
SQ      SEQUENCE      1018 AA; 111780 MW; 58175E020B81F1F CRC64;

Query Match
Best Local Similarity 94.7%; Score 195; DB 1; Length 1018;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 QNSGNQSPEDTDEKPKYEGGNIYVDPDPSVPOIHG 38
Db      746 QNSGNQSPEDTDEKPKYEGGNIYVDPDPSVPOIHG 783

RESULT 7
ID      Q99RD2      PRELIMINARY;      PRT; 1038 AA.
AC      Q99RD2;
DT      01-JUN-2001 (TrEMBLrel. 17, Created)
DT      01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT      01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE      Fibronectin-binding protein homolog.
GN      Name=fnb; OrderedLocuNames=SAV2503;
OC      Staphylococcus aureus (strain MU50 / ATCC 700699).
OC      Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX      NCBI_TaxID=158878;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      MEDLINE=21311952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2;
RX      Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
RA      Cui L., Oguchi A., Aoki K.-I., Nagai Y., Iian J.-O., Ito T.,
RA      Kanamori M., Matsunaru H., Maruyama A., Murakami H., Hoshoyama A.,
RA      Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
RA      Sekimizu K., Hiraoka H., Kuhara S., Goto S., Yabuzaki J.,
RA      Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
RA      Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
RT      "Whole genome sequencing of methicillin-resistant Staphylococcus
RT      aureus.";
RL      Lancel 357:1225-1240(2001).
CC      -1 SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC      an amide bond (by similarity).
DR      EMBL; AP003365; BAB58665.1; -.
DR      PIR; H90053; H90053.
DR      GO; GO:0009986; C:cell surface; IEA.
DR      GO; GO:0005618; C:cell wall; IEA.
DR      GO; GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR      GO; GO:0016020; C:membrane; IEA.
DR      GO; GO:0007155; P:cell adhesion; IEA.
DR      InterPro; IPR008966; Adhes_bact.
DR      InterPro; IPR004237; Fn_bind.
DR      InterPro; IPR005877; Gpos_YsIRK.
DR      InterPro; IPR001899; Gram_pos_anchor.
DR      Pfam; PF02986; Fn_bind; 1.
DR      Pfam; PF00746; Gram_pos_anchor; 1.
DR      Pfam; PF04650; YsIRK_signal; 1.
DR      TIGRFAMs; TIGR01167; LPXTG_anchor; 1.
DR      TIGRFAMs; TIGR01168; YsIRK_signal; 1.
DR      PROSITE; PSS0847; GRAM_POS_ANCHORING; 1.
KW      Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ      SEQUENCE      1038 AA; 113618 MW; 666BF6BF2BFB812 CRC64;

Query Match
Best Local Similarity 94.7%; Score 195; DB 2; Length 1038;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 QNSGNQSPEDTDEKPKYEGGNIYVDPDPSVPOIHG 38
Db      742 QNSGNQSPEDTDEKPKYEGGNIYVDPDPSVPOIHG 779

RESULT 8
ID      Q7A3J7      PRELIMINARY;      PRT; 1038 AA.
AC      Q7A3J7;

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DT      05-JUL-2004 (TrEMBLrel. 27, Created)
DT      05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT      05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE      Fnb protein.
GN      Name=fnb; OrderedLocuNames=SA2291;
OC      Staphylococcus aureus (strain N315).
OC      Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX      NCBI_TaxID=158879;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      MEDLINE=21311952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2;
RX      Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
RA      Cui L., Oguchi A., Aoki K.-I., Nagai Y., Iian J.-O., Ito T.,
RA      Kanamori M., Matsunaru H., Maruyama A., Murakami H., Hoshoyama A.,
RA      Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
RA      Sekimizu K., Hiraoka H., Kuhara S., Goto S., Yabuzaki J.,
RA      Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
RA      Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
RT      "Whole genome sequencing of methicillin-resistant Staphylococcus
RT      aureus.";
RL      Lancel 357:1225-1240(2001).
CC      -1 SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC      an amide bond (by similarity).
DR      EMBL; AP003337; BAB43594.1; -.
DR      GO; GO:0009986; C:cell surface; IEA.
DR      GO; GO:0005618; C:cell wall; IEA.
DR      GO; GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR      GO; GO:0016020; C:membrane; IEA.
DR      GO; GO:0007155; P:cell adhesion; IEA.
DR      InterPro; IPR008966; Adhes_bact.
DR      InterPro; IPR004237; Fn_bind.
DR      InterPro; IPR005877; Gpos_YsIRK.
DR      InterPro; IPR001899; Gram_pos_anchor.
DR      Pfam; PF02986; Fn_bind; 1.
DR      Pfam; PF00746; Gram_pos_anchor; 1.
DR      Pfam; PF04650; YsIRK_signal; 1.
DR      TIGRFAMs; TIGR01167; LPXTG_anchor; 1.
DR      TIGRFAMs; TIGR01168; YsIRK_signal; 1.
DR      PROSITE; PSS0847; GRAM_POS_ANCHORING; 1.
KW      Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ      SEQUENCE      1038 AA; 113618 MW; 666BF6BF2BFB812 CRC64;

Query Match
Best Local Similarity 94.7%; Score 195; DB 2; Length 1038;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 QNSGNQSPEDTDEKPKYEGGNIYVDPDPSVPOIHG 38
Db      742 QNSGNQSPEDTDEKPKYEGGNIYVDPDPSVPOIHG 779

RESULT 9
ID      Q6GDUS      PRELIMINARY;      PRT; 965 AA.
AC      Q6GDUS;
DT      05-JUL-2004 (TrEMBLrel. 27, Created)
DT      05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT      05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE      Fibronectin-binding protein.
GN      Name=fnbA; OrderedLocuNames=SA2580;
OC      Staphylococcus aureus (strain MRSA252).
OC      Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX      NCBI_TaxID=282458;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      PubMed=15213324; DOI=10.1073/pnas.0402521101;
RX      Hoiden M.T.G., Fell E.J., Lindsay J.A., Peacock S.J., Day N.P.J.,
RA      Enright M.C., Foster T.J., Moore C.E., Hurst L., Atkin R., Barron A.,
RA      Bason N., Bentley S.D., Chillingworth C., Chillingworth T.,
RA      Churcher C., Clark L., Cotton C., Cronin A., Doggett J., Dowd L.,
RA      Feltham T., Hance Z., Harris B., Hauser H., Holtroyd S., Jegerla K.,
RA      James K.D., Lennard N., Line A., Mayes R., Moule S., Mungall K.,
RA      Ormond D., Quail M.A., Rabinowitsch E., Rutherford K.M., Sanders M.,

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RA Sharp S., Simmonds M., Stevens K., Whitehead S., Barrell B.G.,
 RA Spratt B.G., Parkhill J.,
 RT "Complete genomes of two clinical *Staphylococcus aureus* strains:
 RT evidence for the rapid evolution of virulence and drug resistance.",
 RL Proc. Natl. Acad. Sci. U.S.A. 101:9786-9791(2004)
 CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
 an amide bond (By similarity).
 DR EMBL: BX571856; CAC41560.1; -;
 DR GO: GO:0009986; C:cell surface; IEA.
 DR GO: GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
 DR GO: GO:0016020; C:membrane; IEA.
 DR GO: GO:0007155; P:cell adhesion; IEA.
 DR InterPro: IPR008966; Adhes_bact.
 DR InterPro: IPR004237; Fn_bind.
 DR InterPro: IPR005877; Gram_pos_Ysirk.
 DR InterPro: IPR001899; Gram_pos_anchor.
 DR Pfam: PF02986; Fn_bind; 1.
 DR Pfam: PF00746; Gram_pos_anchor; 1.
 DR Pfam: PF04650; Ysirk_signal; 1.
 DR TIGRPFAMs: TIGR01167; LpxTG_anchor; 1.
 DR TIGRPFAMs: TIGR01168; Ysirk_signal; 1.
 DR PROSITE: PS50847; GRAM_POS_ANCHORING; 1.
 DR Cell wall; Complete proteome; Peptidoglycan-anchor.
 KW Cell wall; 105691 MW; 2982E132164D0551 CRC64;
 SQ SEQUENCE 965 AA; 105691 MW; 2982E132164D0551 CRC64;
 Query Match 94.2%; Score 194; DB 2; Length 965;
 Best Local Similarity 94.7%; Pred. No. 2; 7e-14;
 Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 Oy 1 QNSGNQSPEDTEEDKPKYEGCGNIVDIDFDSVPQIG 38
 Db 749 QNSGNQSPEDTEEDKPKYEGCGNIVDIDFDSVPQIG 786
 RESULT 10
 Q8NUU7 PRELIMINARY; PRT; 1015 AA.
 ID Q8NUU7;
 AC Q8NUU7;
 DT 01-OCT-2002 (TREMBlrel. 22, Created)
 DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
 DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
 DE Fnb protein.
 GN Name=fnb; OrderedlocusNames=MM2421;
 OS *Staphylococcus aureus* (strain MM2).
 OC Bacteria; Firmicutes; Bacillales; *Staphylococcus*.
 OX NCBI_TaxId=196620;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC STRAIN=MM2;
 RX MEDLINE=22040717; PubMed=12044378; DOI=10.1016/S0140-6736(02)08713-5;
 RA Baba T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Oguchi A.,
 RA Nagai Y., Iwano N., Asano K., Naito T., Kuroda H., Cui L.,
 RA Yamamoto K., Hiratake K.,
 RT "Genome and virulence determinants of high virulence community-
 RT acquired MRSA.",
 RL Lancet 359:1819-1827(2002).
 CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
 an amide bond (By similarity).
 DR EMBL: AP004830; BAB96286.1; -;
 DR GO: GO:0009986; C:cell surface; IEA.
 DR GO: GO:0005618; C:cell wall; IEA.
 DR GO: GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
 DR GO: GO:0016020; C:membrane; IEA.
 DR GO: GO:0007155; P:cell adhesion; IEA.
 DR InterPro: IPR008966; Adhes_bact.
 DR InterPro: IPR004237; Fn_bind.
 DR InterPro: IPR005877; Gpos_Ysirk.
 DR InterPro: IPR001899; Gram_pos_anchor.
 DR Pfam: PF02986; Fn_bind; 1.
 DR Pfam: PF00746; Gram_pos_anchor; 1.
 DR Pfam: PF04650; Ysirk_signal; 1.
 DR TIGRPFAMs: TIGR01167; LpxTG_anchor; 1.
 DR TIGRPFAMs: TIGR01168; Ysirk_signal; 1.
 DR PROSITE: PS50847; GRAM_POS_ANCHORING; 1.
 KW Cell wall; Complete proteome; Peptidoglycan-anchor.
 SQ SEQUENCE 1015 AA; 111145 MW; D0F9281BB64D44D2 CRC64;

DR PROSITE: PS50847; GRAM_POS_ANCHORING; 1.
 KW Cell wall; Complete proteome; Peptidoglycan-anchor.
 SQ SEQUENCE 1015 AA; 111145 MW; D0F9281BB64D44D2 CRC64;
 Query Match 90.8%; Score 187; DB 2; Length 1015;
 Best Local Similarity 94.7%; Pred. No. 2e-13;
 Matches 36; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 Oy 1 QNSGNQSPEDTEEDKPKYEGCGNIVDIDFDSVPQIG 38
 Db 747 QNSGNQSPEDTEEDKPKYEGCGNIVDIDFDSVPQIG 784
 RESULT 11
 Q6G6H3 PRELIMINARY; PRT; 1015 AA.
 ID Q6G6H3;
 AC Q6G6H3;
 DT 05-JUL-2004 (TREMBlrel. 27, Created)
 DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
 DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
 DE Fibronectin-binding protein.
 GN OrderedlocusNames=SAS2388;
 OS *Staphylococcus aureus* (strain MSSA476).
 OC Bacteria; Firmicutes; Bacillales; *Staphylococcus*.
 OX NCBI_TaxId=282459;
 RN (1)
 RP SEQUENCE FROM N.A.
 RX PubMed=15213324; DOI=10.1073/pnas.0402521101;
 RA Holden M.T.G., Fell E.J., Lindsay J.A., Peacock S.J., Day N.P.J.,
 RA Knight M.C., Foster T.J., Moore C.E., Hurst L., Atkin R., Barton A.,
 RA Baeson N., Bentley S.D., Chillingworth T., Chillingworth T.,
 RA Churcher C., Clark L., Cotton C., Cronin A., Doggett J., Dowd L.,
 RA Fellwell T., Hance Z., Harris B., Hauser H., Holtroyd S., Jagsels K.,
 RA James K.D., Leonard N., Lane A., Mayes R., Moutie S., Mungall K.,
 RA Ormond D., Quail M.A., Rabinowitsch E., Rutherford K.M., Sanders M.,
 RA Sharp S., Simmonds M., Stevens K., Whitehead S., Barrell B.G.,
 RA Spratt B.G., Parkhill J.,
 RT "Complete genomes of two clinical *Staphylococcus aureus* strains:
 RT evidence for the rapid evolution of virulence and drug resistance.",
 RL Proc. Natl. Acad. Sci. U.S.A. 101:9786-9791(2004).
 CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
 an amide bond (By similarity).
 DR EMBL: BX571857; CAC44202.1; -;
 DR GO: GO:0009986; C:cell surface; IEA.
 DR GO: GO:0005618; C:cell wall; IEA.
 DR GO: GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
 DR GO: GO:0016020; C:membrane; IEA.
 DR GO: GO:0007155; P:cell adhesion; IEA.
 DR InterPro: IPR008966; Adhes_bact.
 DR InterPro: IPR004237; Fn_bind.
 DR InterPro: IPR005877; Gpos_Ysirk.
 DR InterPro: IPR001899; Gram_pos_anchor.
 DR Pfam: PF02986; Fn_bind; 1.
 DR Pfam: PF00746; Gram_pos_anchor; 1.
 DR Pfam: PF04650; Ysirk_signal; 1.
 DR TIGRPFAMs: TIGR01167; LpxTG_anchor; 1.
 DR TIGRPFAMs: TIGR01168; Ysirk_signal; 1.
 DR PROSITE: PS50847; GRAM_POS_ANCHORING; 1.
 KW Cell wall; Complete proteome; Peptidoglycan-anchor.
 SQ SEQUENCE 1015 AA; 111145 MW; D0F9281BB64D44D2 CRC64;
 Query Match 90.8%; Score 187; DB 2; Length 1015;
 Best Local Similarity 94.7%; Pred. No. 2e-13;
 Matches 36; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 Oy 1 QNSGNQSPEDTEEDKPKYEGCGNIVDIDFDSVPQIG 38
 Db 747 QNSGNQSPEDTEEDKPKYEGCGNIVDIDFDSVPQIG 784
 RESULT 12
 Q9AEP9 PRELIMINARY; PRT; 152 AA.
 ID Q9AEP9

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AC O9ABP9:
DT 01-JUN-2001 (TReMBLrel. 17, Created)
DT 01-JUN-2001 (TReMBLrel. 17, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE Fibronectin-binding protein (Fragment).
GN Name=fnb;
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1280;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CMRSA-1;
RX MEDLINE=21246681; PubMed=11349044;
RX DOI=10.1128/JAI.69.6.3791-3799.2001;
RA Rice K., Huebner M., Vaz D., McGavin M.J.;
RT "Variance in fibronectin binding and fnb locus polymorphisms in
RT Staphylococcus aureus: identification of antigenic variation in a
RT fibronectin binding protein adhesion of the epidemic CMRSA-1 strain of
RT methicillin-resistant S. aureus";
RL Infect. Immun. 69:3791-3799 (2001).
DR EMBL; AY029184; AAK31568.1; -.
FT NON TER 1 152 152
SQ SEQUENCE 152 AA; 17193 MW; CFA3913C2B11C025 CRC64;

Query Match 89.3%; Score 184; DB 2; Length 152;
Best Local Similarity 92.1%; Pred. No. 5.1e-14;
Matches 35; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 QNSGNSPEEDTEBDKPKYEGGNIIVDIDFDSVPOIHG 38
Db 1 QNTGNSFEEDTEBDKPKYEGGNIIVDIDFDSVPOIQG 38

RESULT 13
Q6CBM0 PRELIMINARY; PRT; 889 AA.
AC O6CBM0;
DT 25-OCT-2004 (TReMBLrel. 28, Created)
DT 25-OCT-2004 (TReMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TReMBLrel. 28, Last annotation update)
DE Similar to ep|P53935 Saccharomyces cerevisiae YNL091w.
GN ORFNames=YALI0C150709;
OS Yarrowia lipolytica CL1899.
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Dipodascaceae; Yarrowia.
OX NCBI_TaxID=284591;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CLIB99;
RG Genolevures;
RA Dujon B., Sherman D., Fischer G., Durrens P., Casaregola S.,
RA Lafontaine I., de Montigny J., Marck C., Neuvéglise C., Talla E.,
RA Goffard N., Frangeul L., Aigle M., Anthouard V., Babour A., Barbe V.,
RA Barnay S., Blanchin S., Beckerich J.M., Beyne E., Bleykasten C.,
RA Boistrume A., Boyer J., Cartolico L., Confalonieri F., de Daruvar A.,
RA Despons L., Fabre E., Fairhead C., Ferry-Dumazet H., Gropi A.,
RA Hantaye F., Hennequin C., Jauniaux N., Joyet P., Kachouri R.,
RA Karrest A., Koszul R., Lemaitre M., Lesur I., Ma L., Muller H.,
RA Nicaud J.M., Nikoleki M., Oztas S., Ozler-Kalogeropoulos O.,
RA Pellenz S., Porter S., Richard G.F., Straub M.L., Suleau A.,
RA Suenne D., Tekala F., Mesolowski-Louvel M., Westhof E., Wirth B.,
RA Zenon-Meyer M., Zivanovic I., Bolotin-Pukhara M., Thierry A.,
RA Bouchier C., Caudron B., Scarpelli C., Gallardin C., Weissenbach J.,
RA Wincker P., Souciet J.L.;
RT "Genome evolution in yeasts.";
RL Nature 430:35-44 (2004).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=CLIB99;
RG Genoscope;
RA Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; CR382129; CAG82165.1; -.

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SQ SEQUENCE 889 AA; 100256 MW; CC1B4588BAC17363 CRC64;

Query Match 32.5%; Score 67; DB 2; Length 889;
Best Local Similarity 45.7%; Pred. No. 30;
Matches 16; Conservative 7; Mismatches 10; Indels 2; Gaps 2;

Qy 1 QNSGNSPEE-DTEBDKP-KYEGGNIIVDIDFDSV 33
Db 230 QNIGKEIDEGDTEBDKPKYEGGNIIVDIDFDSV 264

RESULT 14
Q9M2N8 PRELIMINARY; PRT; 273 AA.
AC Q9M2N8;
DT 01-OCT-2000 (TReMBLrel. 15, Created)
DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE Hypothetical protein T27B3.10.
GN Name=T27B3.10;
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Wakatsuma G., Partmann B., Dauner D., Sterr W., Holland R.,
RA Weichenbergartner M., Mewes H.W., Lemcke K., Mayer K.F.X., Quetler F.,
RA Salanoubat M.;
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA EU Arabidopsis sequencing project;
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL137079; CAB68115.1; -.
DR PIR; T46108; T46108.
DR GO; GO:0003676; F:nucleic acid binding; IEA.
DR InterPro; IPR001878; Znf_C2HC.
DR SMART; SM00343; Znf_C2HC; 1.
KW Hypothetical protein.
SQ SEQUENCE 273 AA; 31429 MW; B06E21826068BEBB CRC64;

Query Match 30.6%; Score 63; DB 2; Length 273;
Best Local Similarity 33.3%; Pred. No. 23;
Matches 12; Conservative 7; Mismatches 17; Indels 0; Gaps 0;

Qy 3 SGNQSPHEEDTEBDKPKYEGGNIIVDIDFDSVPOIHG 38
Db 173 SGNQSPHEADDDDDDDNANEDHPDVGDPDQVHG 208

RESULT 15
Q6FVK3 PRELIMINARY; PRT; 260 AA.
AC Q6FVK3;
DT 05-JUL-2004 (TReMBLrel. 27, Created)
DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TReMBLrel. 27, Last annotation update)
DE Similar to tr|Q03768 Saccharomyces cerevisiae YDR155w.
GN ORFNames=CAG10E012219;
OS Candida glabrata CBS138.
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; mitosporic Saccharomycetales; Candida.
OX NCBI_TaxID=284593;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CBS138;
RG Genolevures;
RA Dujon B., Sherman D., Fischer G., Durrens P., Casaregola S.,
RA Lafontaine I., de Montigny J., Marck C., Neuvéglise C., Talla E.,
RA Goffard N., Frangeul L., Aigle M., Anthouard V., Babour A., Barbe V.,
RA Barnay S., Blanchin S., Beckerich J.M., Beyne E., Bleykasten C.,

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CC streptococci, e.g. meningitis, otitis media, pneumonia, endocarditis,
 CC mastitis in cattle, abortion in horses and many others. Since the
 CC antibodies block binding of bacteria, they should be effective against
 CC antibiotic-resistant strains, and may replace antibiotic therapy or
 CC increase its effectiveness. Sequences AAW65691-700 represent a series of
 CC synthetic peptides based on the D1 region of *S. aureus* fibronectin
 CC binding protein A. They were synthesised to contain mutations
 XX

SO Sequence 38 AA;
 Query Match 100.0%; Score 207, DB 2; Length 38;
 Best Local Similarity 100.0%; Pred. No. 6.6e-21;
 Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QNSGNOSFPEDTEBDKPKYEGGNIYDIDPDSVPQIHG 38
 DB 1 QNSGNOSFPEDTEBDKPKYEGGNIYDIDPDSVPQIHG 38

RESULT 2
 ID AAW65661 standard; peptide; 38 AA.
 AC AAW65661;
 XX
 DT 16-OCT-1998 (first entry)
 XX
 DE Fibronectin binding protein-derived peptide #5.
 XX
 KM microbial surface components recognising adhesive matrix molecule;
 KM MSCRAMM; fibronectin; fibronectin-binding protein; antibody; epitope;
 KM antibiotic; bacterial infection; antibiotic-resistant strain.
 XX
 OS Synthetic.
 OS *Staphylococcus aureus*.
 XX
 XX MO9831389-A2.
 XX
 PD 23-JUL-1998.
 XX
 PF 21-JAN-1998; 98WO-US001222.
 XX
 XX 21-JAN-1997; 97US-0036139P.
 XX
 XX (TEXA) UNIV TEXAS A & M SYSTEM.
 PA
 PI Hoeoek M, Patti JM, House-Pompeo KL, Speziale P, Joh D;
 PI McGavin MJ;
 XX
 DR WPI; 1998-413816/35.
 XX

PT Antibody that binds to fibronectin-binding protein, preventing its
 PT binding to fibronectin - used to treat or prevent bacterial infection,
 PT especially by *Staphylococci* and *Streptococci*.
 PT
 PS Example 2; Page 92; 201pp; English.
 XX

CC The invention relates to antibodies that bind to a fibronectin-binding
 CC domain of a fibronectin-binding protein, and inhibit binding of the
 CC protein to fibronectin. Also claimed are: (1) isolated peptides of a
 CC fibronectin-binding protein that do not bind to fibronectin; (2) fusion
 CC protein containing at least one peptide of a fibronectin-binding protein
 CC linked to a second amino acid sequence; (3) nucleic acid encoding the
 CC isolated peptide of (1). Antibodies, the isolated peptides of (1) and the
 CC nucleic acids are all useful for immunisation (active or passive) and (by
 CC inhibiting binding of bacteria to fibronectin) for preventing or treating
 CC infection in humans or other animals, particularly by *staphylococci* or
 CC streptococci, e.g. meningitis, otitis media, pneumonia, endocarditis,
 CC mastitis in cattle, abortion in horses and many others. Since the
 CC antibodies block binding of bacteria, they should be effective against
 CC antibiotic-resistant strains, and may replace antibiotic therapy or
 CC increase its effectiveness. Sequences AAW65659-68 represent synthetic
 CC epitopes from the fibronectin binding domains DU and D1-D4 of the *S.*

CC *aureus* fnaA gene
 XX
 SO Sequence 38 AA;
 Query Match 96.1%; Score 199, DB 2; Length 38;
 Best Local Similarity 97.4%; Pred. No. 8.3e-20;
 Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QNSGNOSFPEDTEBDKPKYEGGNIYDIDPDSVPQIHG 38
 DB 1 QNSGNOSFPEDTEBDKPKYEGGNIYDIDPDSVPQIHG 38

RESULT 3
 ID AAR58806 standard; protein; 130 AA.
 AC AAR58806;
 XX
 DT 25-MAR-2003 (revised)
 DT 30-MAR-1995 (first entry)
 XX
 DE Fibronectin binding domain D1-D4(709-838 (P838T)).
 XX
 KM Fibronectin binding protein; Fbp; fibronectin binding domain;
 KM monoclonal antibody; Mab; adhesion; Gram-positive bacterium; bacteremia;
 KM *Escherichia coli*.
 XX
 OS *Staphylococcus aureus*.
 XX
 PN WO9418327-A1.
 PD 18-AUG-1994.
 XX
 PF 04-FEB-1994; 94WO-GS000215.
 XX
 PR 05-FEB-1993; 93GB-00002289.
 PR 20-OCT-1993; 93GB-00021592.
 XX
 PA (SMIK) SMITHKLINE BEECHAM PLC.
 XX
 PI Burnham MKR, Chopra I, Critchley IA, Knowles DJC;
 XX
 DR WPI; 1994-279748/34.
 XX

PT Fibronectin binding protein and monoclonal antibodies specific for Fbp -
 PT useful to prevent adherence of Gram-positive bacteria to indwelling
 PT devices or wounds.
 PT
 PS Disclosure; Page 30; 40pp; English.
 XX

CC Polypeptides corresponding to residues G709-P886 plus PRIVPT, G709-
 CC P838(P838T) and G709-P838 (AAR58805-07, respectively) of *S. aureus* U2385
 CC (NCIMB 40532) Fbp type A fibronectin binding domain D1-D4 region
 CC (AAR58808) were expressed in *E. coli* BL21(DE4) and used to raise Mabs
 CC specific for Fbp. (Updated on 25-MAR-2003 to correct PN field.)
 XX

SO Sequence 130 AA;
 Query Match 96.1%; Score 199, DB 2; Length 130;
 Best Local Similarity 97.4%; Pred. No. 3.7e-19;
 Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QNSGNOSFPEDTEBDKPKYEGGNIYDIDPDSVPQIHG 38
 DB 2 QNSGNOSFPEDTEBDKPKYEGGNIYDIDPDSVPQIHG 39

RESULT 4
 ID AAR58807 standard; protein; 130 AA.
 AC AAR58807;

XX 25-MAR-2003 (revised)
 DT 30-MAR-1995 (first entry)
 XX
 DE Fibronectin binding domain D1-D4(709-838).
 XX
 KW Fibronectin binding protein; Fbp; fibronectin binding domain;
 KW monoclonal antibody; MAb; adhesion; Gram-positive bacterium; bacteremia;
 KW Escherichia coli.
 XX
 OS Staphylococcus aureus.
 XX
 PN W09418327-A1.
 XX
 PD 18-AUG-1994.
 XX
 PF 04-FEB-1994; 94WO-GB000215.
 XX
 PR 05-FEB-1993; 93GB-00002289.
 XX
 PR 20-OCT-1993; 93GB-00021592.
 XX
 PA (SMIK) SMITHKLINE BEECHAM PLC.
 XX
 PI Burnham MKR, Chopra I, Critchley IA, Knowles DUC;
 XX
 DR WPI, 1994-279748/34.
 XX
 PT Fibronectin binding protein and monoclonal antibodies specific for Fbp -
 PT useful to prevent adherence of Gram-positive bacteria to indwelling
 PT devices or wounds.
 PS
 PS Disclosure; Page 30; 40pp; English.
 XX
 CC Polypeptides corresponding to residues 6709-7886 plus PPIVPT, 6709-
 CC P83(P838T) and 6709-P838 (AAR58805-07, respectively) of S. aureus J2385
 CC (NCIMB 40532) Fbp type A fibronectin binding domain D1-D4 region
 CC (AAR58808) were expressed in E. coli BL21(DE4) and used to raise MAb
 CC specific for Fbp. (Updated on 25-MAR-2003 to correct PW field.)
 CC
 SQ Sequence 130 AA;
 XX

Query Match 96.1%; Score 199; DB 2; Length 130;
 Best Local Similarity 97.4%; Pred. No. 3.7e-19;
 Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QNSGNQSFEDTDEDPKRYEQGNIVDIDFDSVPOIHG 38
 |||||
 DB 2 QNSGNQSFEDTDEDPKRYEQGNIVDIDFDSVPOIHG 39

RESULT 5
 AAR91202
 ID AAR91202 standard; peptide; 130 AA.
 XX
 AC AAR91202;
 XX
 DT 13-NOV-1996 (first entry)
 XX
 DE D1-D4 fibronectin binding domains.
 XX
 KW Fibronectin; oral hygiene; gingivitis; gum disease; adhesion;
 KW periodontitis; oral pathogen; caries; calculus; candidiasis; oral surgery;
 KW tissue regeneration; irrigation; toothpaste; dentifrice; mouthwash;
 KW lozenge.
 XX
 OS Staphylococcus aureus.
 XX
 PN W09604003-A1.
 XX
 PD 15-FEB-1996.
 XX
 PF 18-JUL-1995; 95WO-EP002825.
 XX

PR 05-AUG-1994; 94GB-00015902.
 XX
 PA (SMIK) SMITHKLINE BEECHAM PLC.
 XX
 PI Barnett P, Critchley IA, Dodd I;
 XX
 DR WPI, 1996-129122/13.
 XX
 PT Prevention of adherence of oral pathogens in the oral cavity. Partic.
 PT tooth surfaces - by application of a fibronectin binding protein or
 PT polypeptide or a monoclonal antibody or fragment against it.
 XX
 PS Claim 5; Page 32; 41pp; English.
 XX
 CC Adherence of oral pathogens, particularly to tooth surfaces, can be
 CC prevented by application of a fibronectin binding protein or polypeptide.
 CC The fibronectin binding protein or polypeptide is useful in the
 CC manufacture of oral hygiene compositions, eg. toothpaste, liquid
 CC dentifrice, mouthwash or lozenge. They are useful to prevent the plaque-
 CC related development of carious lesions, gingivitis, calculus or
 CC periodontal disease and to combat oral cavity infections, eg.
 CC candidiasis. They may also be useful in oral surgery e.g. in guided
 CC tissue regeneration procedures to prevent subsequent bacterial infection,
 CC and for irrigation of periodontal pockets. This sequence corresponds to
 CC amino acids 709-838 of the D1-D4 fibronectin binding domain of
 CC Staphylococcus aureus
 XX
 SQ Sequence 130 AA;
 XX

Query Match 96.1%; Score 199; DB 2; Length 130;
 Best Local Similarity 97.4%; Pred. No. 3.7e-19;
 Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QNSGNQSFEDTDEDPKRYEQGNIVDIDFDSVPOIHG 38
 |||||
 DB 2 QNSGNQSFEDTDEDPKRYEQGNIVDIDFDSVPOIHG 39

RESULT 6
 AAR91201
 ID AAR91201 standard; peptide; 130 AA.
 XX
 AC AAR91201;
 XX
 DT 13-NOV-1996 (first entry)
 XX
 DE D1-D4 fibronectin binding domains.
 XX
 KW Fibronectin; oral hygiene; gingivitis; gum disease; adhesion;
 KW periodontitis; oral pathogen; caries; calculus; candidiasis; oral surgery;
 KW tissue regeneration; irrigation; toothpaste; dentifrice; mouthwash;
 KW lozenge.
 XX
 OS Staphylococcus aureus.
 XX
 PN W09604003-A1.
 XX
 PD 15-FEB-1996.
 XX
 PF 18-JUL-1995; 95WO-EP002825.
 XX
 PR 05-AUG-1994; 94GB-00015902.
 XX
 PA (SMIK) SMITHKLINE BEECHAM PLC.
 XX
 PI Barnett P, Critchley IA, Dodd I;
 XX
 DR WPI, 1996-129122/13.
 XX
 PT Prevention of adherence of oral pathogens in the oral cavity, partic.
 PT tooth surfaces - by application of a fibronectin binding protein or
 PT polypeptide or a monoclonal antibody or fragment against it.
 XX

PS Claim 5; Page 31-32; 41pp; English.

XX Adherence of oral pathogens, particularly to tooth surfaces, can be

CC prevented by application of a fibronectin binding protein or polypeptide.

CC The fibronectin binding protein or polypeptide is useful in the

CC manufacture of oral hygiene compositions, eg. toothpaste, liquid

CC dentifrice, mouthwash or lozenge. They are useful to prevent the plaque-

CC related development of carious lesions, gingivitis, calculus or

CC periodontal disease and to combat oral cavity infections, e.g.

CC candidiasis. They may also be useful in oral surgery e.g. in guided

CC tissue regeneration procedures to prevent subsequent bacterial infection,

CC and for irrigation of periodontal pockets. This sequence corresponds to

CC amino acids 709-838 of the D1-D4 fibronectin binding domain of

CC Staphylococcus aureus with a P838T substitution

XX

SQ Sequence 130 AA;

Query Match 96.1%; Score 199; DB 2; Length 130;

Best Local Similarity 97.4%; Pred. No. 3.7e-19;

Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QNSGNQSFPEDEKPKYEQGNIVDIDPDSVPQIHG 38

2 QNSGNQSFPEDEKPKYEQGNIVDIDPDSVPQIHG 39

Db

RESULT 7

AAV29089

ID AAV29089 standard; protein; 134 AA.

XX

AC AAV29089;

XX

DT 28-SEP-1999 (first entry)

DE Cloned fibronectin binding protein binding domain (FnBAB) sequence.

XX

XX Bovine herpes virus-2; BHV-2; cytokine; immune response; immunogen; IL;

KM Interleukin; colony stimulating factor; CSF; interferon; IFN; TNF;

KM tumour necrosis factor; recombinant virus; vaccine; mucosal disease;

KM mastitis; breast cancer; stress-induced disease; binding domain; FnBAB;

KM fibronectin binding protein.

XX

XX Staphylococcus aureus.

OS

PA W09916892-A1.

PN

XX

PD 08-APR-1999.

XX

PF 29-SEP-1998; 98WO-GB002927.

XX

PR 29-SEP-1997; 97GB-00020633.

XX

XX (UYBR-) UNIV BRISTOL.

PA

PI Bradley AJ, Duffas WPJ,

XX WPI; 1999-255101/21.

DR N-PSDB; AAX91505.

XX

XX New bovine herpes virus-2 vectors.

PT

PS Example 2; Fig 8A-B; 130pp; English.

XX

XX The invention provides bovine herpes virus-2 (BHV-2) based vectors that

CC comprise at least one cytokine-encoding DNA sequence. The expression of

CC cytokines in mammals can up-regulate immune responses to the immunogens.

CC The cytokine is selected from interleukins (IL), colony stimulating

CC factors (CSF), interferons (IFN) and tumour necrosis factors (TNF). The

CC BHV-2 based vector or recombinant virus can be used as vaccine. They can

CC be used for preventing or treating a mucosal disease in a subject, e.g.

CC ruminants, cattle, sheep, goats, dogs, cats, horses, or man, particularly

CC mastitis in cows or breast cancers in humans. They can also be used for

CC preventing or treating a stress-induced disease. The present sequence

CC represents a S. aureus fibronectin binding protein binding domain

CC sequence FnBAB, the gene cloned for use in this invention. The gene has

CC 97.8 percent identity when compared to the previously published sequences

CC FnBA and FnBB

XX

SQ Sequence 134 AA;

Query Match 96.1%; Score 199; DB 2; Length 134;

Best Local Similarity 97.4%; Pred. No. 3.8e-19;

Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QNSGNQSFPEDEKPKYEQGNIVDIDPDSVPQIHG 38

2 QNSGNQSFPEDEKPKYEQGNIVDIDPDSVPQIHG 39

Db

RESULT 8

AAV29088

ID AAV29088 standard; protein; 134 AA.

XX

AC AAV29088;

XX

DT 28-SEP-1999 (first entry)

DE S. aureus fibronectin binding protein B (FnBB) binding domain.

XX

XX Bovine herpes virus-2; BHV-2; cytokine; immune response; immunogen; IL;

KM Interleukin; colony stimulating factor; CSF; interferon; IFN; TNF;

KM tumour necrosis factor; recombinant virus; vaccine; mucosal disease;

KM mastitis; breast cancer; stress-induced disease; binding domain; FnBB;

KM fibronectin binding protein.

XX

XX Staphylococcus aureus.

OS

PA W09916892-A1.

PN

XX

PD 08-APR-1999.

XX

PF 29-SEP-1998; 98WO-GB002927.

XX

PR 29-SEP-1997; 97GB-00020633.

XX

XX (UYBR-) UNIV BRISTOL.

PA

PI Bradley AJ, Duffas WPJ;

XX WPI; 1999-255101/21.

DR N-PSDB; AAX91505.

XX

XX New bovine herpes virus-2 vectors.

PT

PS Example 2; Fig 8A-B; 130pp; English.

XX

XX The invention provides bovine herpes virus-2 (BHV-2) based vectors that

CC comprise at least one cytokine-encoding DNA sequence. The expression of

CC cytokines in mammals can up-regulate immune responses to the immunogens.

CC The cytokine is selected from interleukins (IL), colony stimulating

CC factors (CSF), interferons (IFN) and tumour necrosis factors (TNF). The

CC BHV-2 based vector or recombinant virus can be used as vaccine. They can

CC be used for preventing or treating a mucosal disease in a subject, e.g.

CC ruminants, cattle, sheep, goats, dogs, cats, horses, or man, particularly

CC mastitis in cows or breast cancers in humans. They can also be used for

CC preventing or treating a stress-induced disease. The present sequence

CC represents the binding domain of a previously published S. aureus

CC fibronectin binding protein B (FnBB) sequence. The FnB binding domain

CC gene sequence FnBAB, cloned for use in this invention has 97.8 percent

CC identity when compared to the previously published FnBA and FnBB gene

CC sequences

XX

SQ Sequence 134 AA;

Query Match 96.1%; Score 199; DB 2; Length 134;

Best Local Similarity 97.4%; Pred. No. 3.8e-19;

Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ONSGNQSPEDTEBDKPKYEGGNIIVDIDFDSVPQIHG 38
 DB 2 ONSGNQSPEDTEBDKPKYEGGNIIVDIDFDSVPQIHG 39

RESULT 9
 ID AAY29087 standard; protein; 134 AA.

XX AAY29087;

XX 28-SEP-1999 (first entry)

DE S. aureus fibronectin binding protein A (FnBA) binding domain.

XX Bovine herpes virus-2; BHV-2; cytokine; immune response; immunogen; IL;
 KW interleukin; colony stimulating factor; CSF; interferon; IFN; TNF;
 KW tumour necrosis factor; recombinant virus; vaccine; mucosal disease;
 KW mastitis; breast cancer; stress-induced disease; binding domain; FnBA;
 KW fibronectin binding protein.

XX Staphylococcus aureus.

OS WO916892-A1.

PN 08-APR-1999.

PD 29-SEP-1998; 98WO-GB002927.

XX 29-SEP-1997; 97GB-00020633.

XX (UYBR-) UNITV BRISTOL.

XX Bradley AJ, Duffas WPJ;

XX WPI; 1999-255101/21.

DR N-PSDB; AAX91504.

XX New bovine herpes virus-2 vectors.

XX Example 2; Fig 8A-B; 130pp; English.

XX The invention provides bovine herpes virus-2 (BHV-2) based vectors that
 CC comprise at least one cytokine-encoding DNA sequence. The expression of
 CC cytokines in mammals can up-regulate immune responses to the immunogens.
 CC The cytokine is selected from interleukins (IL), colony stimulating
 CC factors (CSF), interferons (IFN) and tumour necrosis factors (TNF). The
 CC BHV-2 based vector or recombinant virus can be used as vaccines. They can
 CC be used for preventing or treating a mucosal disease in a subject, e.g.
 CC ruminants, cattle, sheep, goats, dogs, cats, horses, or man, particularly
 CC mastitis in cows or breast cancers in humans. They can also be used for
 CC preventing or treating a stress-induced disease. The present sequence
 CC represents the binding domain of a previously published S. aureus
 CC fibronectin binding protein A (FnBA) sequence. The FnB binding domain
 CC gene sequence FNMBB, cloned for use in this invention has 97.8 percent
 CC identity when compared to the previously published FnBA and FnBB gene
 CC sequences

XX Sequence 134 AA;

Query Match 96.1%; Score 199; DB 2; Length 134;
 Best Local Similarity 97.4%; Pred. No. 3.8e-19;
 Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ONSGNQSPEDTEBDKPKYEGGNIIVDIDFDSVPQIHG 38
 DB 2 ONSGNQSPEDTEBDKPKYEGGNIIVDIDFDSVPQIHG 39

RESULT 10
 AAW31556

ID AAW31556 standard; protein; 139 AA.

XX AAW31556;

XX 27-AUG-2003 (revised)

DT 25-MAR-2003 (revised)

DT 21-MAY-1998 (first entry)

DE Fibronectin-binding MSCRAMM derivative pOD.

XX Fibronectin; pOD; collagen binding protein; sepsis; infection;
 KW microbial surface component recognising adhesive matrix molecule; MSCRAMM;
 KW adhesin; vaccine; immunisation; diagnosis; therapy; mastitis.

XX Staphylococcus aureus.

XX Key Location/Qualifiers

FT Peptide 1..12 /note= "vector pQE30-derived peptide"

XX WO9743314-A2.

XX 20-NOV-1997.

XX 14-MAY-1997; 97WO-US008210.

XX 16-MAY-1996; 96US-0017678P.

XX (TEXA-) UNITV TEXAS A & M SYSTEM.

XX (UABR-) UAB RES FOUND.

XX Hoecek M, Patti JM, House-Pompeo K, Schanam N, Symersky J;

XX WPI; 1998-008801/01.

XX Antibody that interacts with collagen binding domain of Staphylococcal

XX cna gene product - useful to prevent bacterial sepsis in animal infected

XX with Staphylococcus aureus.

XX Disclosure; Page 91; 143pp; English.

XX This protein comprises Staphylococcus aureus fibronectin-binding
 CC microbial surface component recognising adhesive matrix molecule (MSCRAMM)
 CC derivative pOD, plus a vector-derived N-terminal peptide. The invention
 CC relates to claimed nucleic acid sequences (see AAT93436-38) encoding S.
 CC aureus collagen binding protein (CBP) epitopes M17, M31 and M55 (see
 CC AAW1552-54) that confer protection against S. aureus infection. CBP
 CC protein and antigenic epitopes are contemplated for use in the treatment
 CC of pathological infections, especially to prevent bacterial adhesion to
 CC collagen. The epitopes are also contemplated for use in the preparation
 CC of vaccines and as carrier proteins in vaccine formulations, as well as
 CC in the formulation of compositions for the prevention of S. aureus
 CC infection. pCR33 and pOD (see AAW1556) were used to raise anti-MSCRAMM
 CC polyclonal antibodies used in passive immunisation against bovine
 CC mastitis. (Updated on 25-MAR-2003 to correct PI field.) (Updated on 27-
 CC AUG-2003 to correct OS field.)

XX Sequence 139 AA;

Query Match 96.1%; Score 199; DB 2; Length 139;
 Best Local Similarity 97.4%; Pred. No. 4e-19;
 Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ONSGNQSPEDTEBDKPKYEGGNIIVDIDFDSVPQIHG 38
 DB 16 ONSGNQSPEDTEBDKPKYEGGNIIVDIDFDSVPQIHG 53

RESULT 11
 ID AAR58808 standard; protein; 174 AA.

XX AAR58808;

[illegible]

XX	05-AUG-1994;	94GB-00015902.
PR		
XX	(SMIK) SMITHKLINE BEECHAM PLC.	
PA		
XX		
PI	Barnett P, Critchley IA, Dodd I;	
XX		
DR	WPI, 1996-129122/13.	
XX	N-PSDB; AAT18308.	
PT		
XX	Prevention of adherence of oral pathogens in the oral cavity, partic.	
XX	tooth surfaces - by application of a fibronectin binding protein or	
PT	polypeptide or a monoclonal antibody or fragment against it.	
XX		
PS	Claim 5; Page 32; 41pp; English.	
XX		
CC	Adherence of oral pathogens, particularly to tooth surfaces, can be	
CC	prevented by application of a fibronectin binding protein or polypeptide.	
CC	The fibronectin binding protein or polypeptide is useful in the	
CC	manufacture of oral hygiene compositions, eg. toothpaste, liquid	
CC	dentifrice, mouthwash or lozenge. They are useful to prevent the plaque-	
CC	related development of carious lesions, gingivitis, calculus or	
CC	periodontal disease and to combat oral cavity infections, e.g.	
CC	andidiasis. They may also be useful in oral surgery e.g. in guided	
CC	tissue regeneration procedures to prevent subsequent bacterial infection,	
CC	and for irritation of periodontal pockets. This sequence corresponds to	
CC	amino acids 709-838 of the D1-D4 fibronectin binding domain of	
CC	Staphylococcus aureus with a P838T substitution. (Updated on 16-OCT-2003	
XX	to standardise OS field)	
XX		
SQ	Sequence 174 AA:	
	Query Match	96.1%; Score 199; DB 2; Length 174;
	Best Local Similarity	97.4%; Pred. No. 5.3e-19;
	Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0.	
Oy	1 QNSGNOSFPEDEEDKPKYEGGNIIVDIDPDSVQIHG 38	
Db	2 QNSGNOSFPEDEEDKPKYEGGNIIVDIDPDSVQIHG 39	
RESULT 13		
AA558805		
ID	AA558805 standard; protein; 181 AA.	
XX		
AC	AA558805;	
XX		
DT	25-MAR-2003 (revised)	
DT	30-MAR-1995 (first entry)	
DE		
XX	Fibronectin binding domain D1-D4(709-886) .	
XX		
KW	Fibronectin binding protein; Fbp; fibronectin binding domain;	
KW	monoclonal antibody; Mab; adhesion; Gram-positive bacterium; bacteremia;	
KW	Escherichia coli.	
XX		
OS	Staphylococcus aureus.	
XX		
PN	MO9418327-A1.	
XX		
PD	18-AUG-1994.	
XX		
PF	04-FEB-1994; 94WO-GB000215.	
XX		
PR	05-FEB-1993; 93GB-00002289.	
PR	20-OCT-1993; 93GB-00021592.	
XX		
PA	(SMIK) SMITHKLINE BEECHAM PLC.	
XX		
PI	Burnham MKR, Chopra I, Critchley IA, Knowles DJC;	
XX		
DR	WPI; 1994-279748/34.	
XX		

PT Fibronectin binding protein and monoclonal antibodies specific for Fbp -
 PT useful to prevent adherence of Gram-positive bacteria to indwelling
 PT devices or wounds.
 PS Disclosure; Page 29-30; 40pp; English.
 XX
 CC Polypeptides corresponding to residues G709-T886 plus PPIVPT, G709-
 CC P838(P838T) and G709-P838 (AAR58805-07, respectively) of *S. aureus* J2385
 CC (NCIMB 40532) Fbp type A fibronectin binding domain D1-D4 region
 CC (AAR58808) were expressed in *E. coli* BL21(DE4) and used to raise Mabs
 CC specific for Fbp. (updated on 25-MAR-2003 to correct PN field.)
 CC
 SQ Sequence 181 AA;
 Query Match 96.1%; Score 199; DB 2; Length 181;
 Best Local Similarity 97.4%; Pred. No. 5.5e-19;
 Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 QNSGNQSPFEDTBDKPKYEGGNIVDIDPSVPIHG 38
 DB 2 QNSGNQSPFEDTBDKPKYEGGNIVDIDPSVPIHG 39
 RESULT 14
 AAR91200
 ID AAR91200 standard; peptide; 181 AA.
 XX
 AC AAR91200;
 XX
 DT 13-NOV-1996 (first entry)
 XX
 DE D1-D4 fibronectin binding domains.
 XX
 KM Fibronectin; oral hygiene; gingivitis; gum disease; adhesion;
 KM periodontitis; oral pathogen; caries; calculus; candidiasis; oral surgery;
 KM tissue regeneration; irrigation; toothpaste; dentifrice; mouthwash;
 KM lozenge.
 XX
 OS Staphylococcus aureus.
 XX
 PN W09604003-A1.
 XX
 PD 15-FEB-1996.
 XX
 PF 18-JUL-1995; 95WO-EP002825.
 XX
 PR 05-AUG-1994; 94GB-00015902.
 XX
 PA (SMITK) SMITHKLINE BEECHAM PLC.
 XX
 PI Barnett P, Critchley IA, Dodd I;
 XX
 DR WPI; 1996-129122/13.
 DR N-PSDB; AAT18307.
 XX
 PT Prevention of adherence of oral pathogens in the oral cavity, partic.
 PT tooth surfaces - by application of a fibronectin binding protein or
 PT polypeptide or a monoclonal antibody or fragment against it.
 XX
 PS Claim 5; Page 31; 41pp; English.
 XX
 CC Adherence of oral pathogens, particularly to tooth surfaces, can be
 CC prevented by application of a fibronectin binding protein or polypeptide.
 CC The fibronectin binding protein or polypeptide is useful in the
 CC manufacture of oral hygiene compositions, eg. toothpaste, liquid
 CC dentifrice, mouthwash or lozenge. They are useful to prevent the plaque-
 CC related development of carious lesions, gingivitis, calculus or
 CC periodontal disease and to combat oral cavity infections, e.g.
 CC candidiasis. They may also be useful in oral surgery e.g. in guided
 CC tissue regeneration procedures to prevent subsequent bacterial infection,
 CC and for irrigation of periodontal pockets. This sequence corresponds to
 CC amino acids 709-886 of the D1-D4 fibronectin binding domain of
 CC Staphylococcus aureus

XX
 SQ Sequence 181 AA;
 Query Match 96.1%; Score 199; DB 2; Length 181;
 Best Local Similarity 97.4%; Pred. No. 5.5e-19;
 Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 QNSGNQSPFEDTBDKPKYEGGNIVDIDPSVPIHG 38
 DB 2 QNSGNQSPFEDTBDKPKYEGGNIVDIDPSVPIHG 39
 RESULT 15
 AAR89803
 ID AAR89803 standard; protein; 559 AA.
 XX
 AC AAR89803;
 XX
 DT 16-MAR-1999 (first entry)
 XX
 DE Staphylococcus aureus protein SEQ ID #5251.
 XX
 KM Computer readable medium; vaccine; *S. aureus* infection; immunodetection;
 KM cellulitis; eyelid infection; food poisoning; osteomyelitis; therapy;
 KM skin infection; surgical wound infection; scalded skin syndrome;
 KM toxic shock syndrome.
 XX
 OS Staphylococcus aureus.
 XX
 PN EP786519-A2.
 XX
 PD 30-JUL-1997.
 XX
 PF 07-JAN-1997; 97EP-00100117.
 XX
 PR 05-JAN-1996; 96US-0009861P.
 XX
 PA (HUMA-) HUMA GENOME SCI INC.
 XX
 PI Kunach CA, Choi GH, Barash SC, Dillon PJ, Fannon MR, Rosen CA;
 XX
 DR WPI; 1997-374922/35.
 XX
 PT Polynucleotide(s) and proteins derived from Staphylococcus aureus -
 PT stored on computer readable medium and used in the production of anti-
 PT *S. aureus* vaccines.
 XX
 PS Claim 23; Page 3259-3261; 3271pp; English.
 XX
 CC This sequence represents a Staphylococcus aureus protein sequence of the
 CC invention. The DNA sequences encoding the *S. aureus* proteins are recorded
 CC on a computer readable medium, preferably selected from a floppy or hard
 CC disk, random access memory (RAM), read-only memory (ROM) or CD-ROM.
 CC Homology searches using the *S. aureus* DNA sequences allows putative
 CC functions to be assigned so that protein-encoding or regulatory regions
 CC of commercial, therapeutic or industrial importance can be obtained.
 CC Specifically, sequences which are likely to encode antigens have been
 CC identified and these polypeptides can be used in a vaccine composition
 CC against *S. aureus* infection. The polypeptides can also be used in a kit
 CC for the immunodetection of *S. aureus* in a sample. *S. aureus* is implicated
 CC in numerous human diseases, including cellulitis, eyelid infections, food
 CC poisoning, osteomyelitis, skin and surgical wound infections, scalded
 CC skin syndrome, toxic shock syndrome, etc. Organisms transformed with the
 CC DNA sequences can be used for recombinant production of the polypeptides.
 CC The new DNA sequences (and their fragments) are useful as primers or
 CC probes for isolating homologues of any of the 5191 *S. aureus* DNA sequences
 CC contained on the computer readable medium
 XX
 SQ Sequence 559 AA;
 Query Match 96.1%; Score 199; DB 2; Length 559;
 Best Local Similarity 97.4%; Pred. No. 2.2e-18;
 Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QNSGNOSFPEDTERDKPKYEQGNIVDIDPDSPQIHG 38
Db 301 QNSGNOSFPEDTERDKPKYEQGNIVDIDPDSPQIHG 338

Search completed: October 25, 2005, 19:38:33
Job time : 107.988 secs

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OM protein - protein search, using sw model

Run on: October 22, 2005, 02:23:36 ; Search time 28.8363 Seconds
(without alignments)
96.371 Million cell updates/sec

Title: US-10-731-238-36

Perfect score: 207
Sequence: 1 ONSGNQSPEDTEEDPKRYEQGNIVIDIDFDSVPQIHG 38

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: /cgn2_6/ptodata/1/1aa/5A.COMB.pep:*
2: /cgn2_6/ptodata/1/1aa/5B.COMB.pep:*
3: /cgn2_6/ptodata/1/1aa/6A.COMB.pep:*
4: /cgn2_6/ptodata/1/1aa/6B.COMB.pep:*
5: /cgn2_6/ptodata/1/1aa/6C.COMB.pep:*
6: /cgn2_6/ptodata/1/1aa/Backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	207	100.0	38	4	US-09-010-317-36
2	199	96.1	38	1	US-08-234-622A-2
3	199	96.1	38	4	US-09-010-317-5
4	199	96.1	114	1	US-08-259-000-3
5	199	96.1	130	2	US-08-459-135A-7
6	199	96.1	130	2	US-08-459-135A-8
7	199	96.1	130	3	US-08-495-559-7
8	199	96.1	130	3	US-08-495-559-8
9	199	96.1	139	3	US-08-856-253-8
10	199	96.1	174	2	US-08-459-135A-10
11	199	96.1	174	2	US-08-459-135A-13
12	199	96.1	174	3	US-08-495-559-10
13	199	96.1	174	3	US-08-495-559-13
14	199	96.1	176	3	US-08-495-559-6
15	199	96.1	178	2	US-08-459-135A-12
16	199	96.1	178	2	US-08-495-559-12
17	199	96.1	181	2	US-08-459-135A-6
18	199	96.1	559	4	US-08-956-171E-5251
19	199	96.1	559	4	US-08-781-986A-5251
20	199	96.1	1027	4	US-08-956-171E-5254
21	199	96.1	1027	4	US-08-781-986A-5254
22	193	93.2	38	1	US-08-729-767-3
23	193	93.2	38	4	US-09-010-317-37
24	193	93.2	38	4	US-09-010-317-39
25	193	93.2	38	4	US-09-010-317-40
26	193	93.2	38	4	US-09-010-317-41
27	192	92.8	38	4	US-09-010-317-38

28	192	92.8	38	4	US-09-010-317-42	Sequence 42, Appl
29	191	92.3	38	4	US-09-010-317-6	Sequence 6, Appl
30	191	92.3	38	4	US-09-010-317-43	Sequence 43, Appl
31	189	91.3	38	4	US-09-010-317-35	Sequence 35, Appl
32	188.5	91.1	39	4	US-09-010-317-56	Sequence 56, Appl
33	188	90.8	38	4	US-09-010-317-46	Sequence 46, Appl
34	185	89.4	38	4	US-09-010-317-44	Sequence 44, Appl
35	180.5	87.2	39	4	US-09-010-317-57	Sequence 57, Appl
36	180	87.0	38	1	US-08-234-622A-3	Sequence 3, Appl
37	180	87.0	38	4	US-09-010-317-7	Sequence 7, Appl
38	174	84.1	38	1	US-08-729-767-4	Sequence 4, Appl
39	174	84.1	38	4	US-09-010-317-47	Sequence 47, Appl
40	173	83.6	38	4	US-09-010-317-48	Sequence 48, Appl
41	172	83.1	38	4	US-09-010-317-8	Sequence 8, Appl
42	172	83.1	38	4	US-09-010-317-49	Sequence 49, Appl
43	170	82.1	38	4	US-09-010-317-45	Sequence 45, Appl
44	166	80.2	38	4	US-09-010-317-50	Sequence 50, Appl
45	157	75.8	36	4	US-09-010-317-58	Sequence 58, Appl

ALIGNMENTS

RESULT 1
US-09-010-317-36
; Sequence 36, Application US/09010317
; Patent No. 6685943
; GENERAL INFORMATION:
; APPLICANT: Hook, Magnus
; APPLICANT: Patti, Joseph M.
; APPLICANT: House-Pompeo, Karen L.
; APPLICANT: Speziale, Pietro
; APPLICANT: Joh, Danny
; APPLICANT: McGavin, Martin J.
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
; TITLE OF INVENTION: AND METHODS OF USE
; NUMBER OF SEQUENCES: 105
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: TX
; COUNTRY: USA
; ZIP: 77210-4433
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/010,317
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/036,139
; FILING DATE: 21-JAN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Hbler, David W.
; REGISTRATION NUMBER: 41,071
; REFERENCE/DOCKET NUMBER: TANK:189
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 512-418-3000
; TELEFAX: 512-474-7577
; INFORMATION FOR SEQ ID NO: 36:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 38 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; US-09-010-317-36
Query Match 100.0%; Score 207; DB 4; Length 38;
Best Local Similarity 100.0%; Pred. No. 1.8e-21;

Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QNSGNQSFPEDETDKPKYEQGNIIVDIDFDSVPQIHG 38
Db 1 QNSGNQSFPEDETDKPKYEQGNIIVDIDFDSVPQIHG 38

RESULT 2

US-08-234-622A-2
; Sequence 2, Application US/08234622A
; Patent No. 5440014
; GENERAL INFORMATION:
; APPLICANT: HOOK, Magnus
; APPLICANT: MCGAVIN, Martin
; APPLICANT: RAUCCI, Giuseppe
; TITLE OF INVENTION: A FIBRONECTIN BINDING PEPTIDE
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Doane, Swecker & Mathis
; STREET: P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/234,622A
; FILING DATE: 28-APR-1994
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: SE 9002617-0
; FILING DATE: 10-AUG-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/SE91/00534
; FILING DATE: 09-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Meuth, Donna M
; REGISTRATION NUMBER: 36,607
; REFERENCE/DOCKET NUMBER: 012885-044
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 38 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-234-622A-2

Query Match 96.1%; Score 199; DB 1; Length 38;
Best Local Similarity 97.4%; Pred. No. 2.2e-20;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QNSGNQSFPEDETDKPKYEQGNIIVDIDFDSVPQIHG 38
Db 1 QNSGNQSFPEDETDKPKYEQGNIIVDIDFDSVPQIHG 38

RESULT 3

US-09-010-317-5
; Sequence 5, Application US/09010317
; Patent No. 6685943
; GENERAL INFORMATION:
; APPLICANT: Hook, Magnus
; APPLICANT: Patli, Joseph M.
; APPLICANT: House-Pompeo, Karen L.
; APPLICANT: Speziale, Pietro

APPLICANT: Jon, Danny
APPLICANT: McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
TITLE OF INVENTION: AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX

COUNTRY: USA
ZIP: 77210-4433
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/010,317
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/036,139
; FILING DATE: 21-JAN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Hibler, David W.
; REGISTRATION NUMBER: 41,071
; REFERENCE/DOCKET NUMBER: TAMK:189
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 512-418-3000
; TELEFAX: 512-474-7577
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 38 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; US-09-010-317-5

Query Match 96.1%; Score 199; DB 4; Length 38;
Best Local Similarity 97.4%; Pred. No. 2.2e-20;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QNSGNQSFPEDETDKPKYEQGNIIVDIDFDSVPQIHG 38
Db 1 QNSGNQSFPEDETDKPKYEQGNIIVDIDFDSVPQIHG 38

RESULT 4

US-08-259-000-3
; Sequence 3, Application US/08259000
; Patent No. 5571514
; GENERAL INFORMATION:
; APPLICANT: HOOK, Magnus
; APPLICANT: LINDBERG, Martin Kjell
; APPLICANT: SIGNAS, Lars Christer
; APPLICANT: WADSTROM, Torkel Mikael
; APPLICANT: FROMAN, Gunnar
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN AS WELL AS
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Doane, Swecker & Mathis
; STREET: P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/259,000
FILING DATE: 13-JUN-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: SE 8702272-9
FILING DATE: 01-JUN-1987
ATTORNEY/AGENT INFORMATION:
NAME: Meuth, Donna M
REGISTRATION NUMBER: 36,607
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-2021
TELEFAX: (703) 836-6620
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 114 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-259-000-3

Query Match 96.1%; Score 199; DB 1; Length 114;
Best Local Similarity 97.4%; Pred. No. 8.4e-20;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 QNSGNQSFEDTDEKPKYEGGNIIVDIDFDSVPQIHG 38
Db 2 QNSGNQSFEDTDEKPKYEGGNIIVDIDFDSVPQIHG 39

RESULT 5
US-08-459-135A-7
Sequence 7, Application US/08459135A
Patent No. 5955078
GENERAL INFORMATION:
APPLICANT: BURNHAM, Martin Karl Russel
APPLICANT: CHOPRA, Ian
APPLICANT: CRITCHLEY, Ian Alfred
APPLICANT: KNOWLES, David Justin Charles
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN: MONOCLONAL ANTIBODY AND THEIR US
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
STATE: PA
COUNTRY: U.S.A.
ZIP: 19406-0939
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: Fastseq, Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/459,135A
FILING DATE: 02-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB/94/00215
FILING DATE: 04-Feb-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Gimm, Edward R
REGISTRATION NUMBER: 38,891
REFERENCE/DOCKET NUMBER: P30591C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-4478
TELEFAX: 610-270-5090
TELEX:
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:

LENGTH: 130 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-459-135A-7

Query Match 96.1%; Score 199; DB 2; Length 130;
Best Local Similarity 97.4%; Pred. No. 9.8e-20;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 QNSGNQSFEDTDEKPKYEGGNIIVDIDFDSVPQIHG 38
Db 2 QNSGNQSFEDTDEKPKYEGGNIIVDIDFDSVPQIHG 39

RESULT 6
US-08-459-135A-8
Sequence 8, Application US/08459135A
Patent No. 5955078
GENERAL INFORMATION:
APPLICANT: BURNHAM, Martin Karl Russel
APPLICANT: CHOPRA, Ian
APPLICANT: CRITCHLEY, Ian Alfred
APPLICANT: KNOWLES, David Justin Charles
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN: MONOCLONAL ANTIBODY AND THEIR US
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
STATE: PA
COUNTRY: U.S.A.
ZIP: 19406-0939
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: Fastseq, Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/459,135A
FILING DATE: 02-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB/94/00215
FILING DATE: 04-Feb-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Gimm, Edward R
REGISTRATION NUMBER: 38,891
REFERENCE/DOCKET NUMBER: P30591C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-4478
TELEFAX: 610-270-5090
TELEX:
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 130 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-459-135A-8

Query Match 96.1%; Score 199; DB 2; Length 130;
Best Local Similarity 97.4%; Pred. No. 9.8e-20;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 QNSGNQSFEDTDEKPKYEGGNIIVDIDFDSVPQIHG 38
Db 2 QNSGNQSFEDTDEKPKYEGGNIIVDIDFDSVPQIHG 39

RESULT 7
US-08-495-559-7


```
; Sequence 7, Application US/08495559A
; Patent No. 6054572
; GENERAL INFORMATION:
; APPLICANT: BURHAM, Martin Karl Russel
; APPLICANT: CHOPRA, Ian
; APPLICANT: CRITCHLEY, Ian Alfred
; APPLICANT: KNOWLES, David Justin Charles
; TITLE OF INVENTION: FIBROBLAST BINDING PROTEIN: MONOCLONAL
; TITLE OF INVENTION: ANTIBODY AND THEIR USE IN PREVENTING BACTERIAL ADHESION
; FILE REFERENCE: P30591
; CURRENT APPLICATION NUMBER: US/08/495,559A
; CURRENT FILING DATE: 1995-08-03
; EARLIER APPLICATION NUMBER: GB 9302289.5
; EARLIER FILING DATE: 1993-02-05
; EARLIER APPLICATION NUMBER: GB 9321592.9
; EARLIER FILING DATE: 1993-10-20
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FASTSEQ for Windows Version 3.0
; SEQ ID NO 7
; LENGTH: 130
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-08-495-559-7

Query Match          96.1%; Score 199; DB 3; Length 130;
Best Local Similarity 97.4%; Pred. No. 9.8e-20;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QNSGNQSFPEDETEDEKPKYEGGNIVIDIDPDSVPQIHG 38
DB 2 QNSGNQSFPEDETEDEKPKYEGGNIVIDIDPDSVPQIHG 39

RESULT 8
US-08-495-559-8
; Sequence 8, Application US/08495559A
; Patent No. 6054572
; GENERAL INFORMATION:
; APPLICANT: BURHAM, Martin Karl Russel
; APPLICANT: CHOPRA, Ian
; APPLICANT: CRITCHLEY, Ian Alfred
; APPLICANT: KNOWLES, David Justin Charles
; TITLE OF INVENTION: FIBROBLAST BINDING PROTEIN: MONOCLONAL
; TITLE OF INVENTION: ANTIBODY AND THEIR USE IN PREVENTING BACTERIAL ADHESION
; FILE REFERENCE: P30591
; CURRENT APPLICATION NUMBER: US/08/495,559A
; CURRENT FILING DATE: 1995-08-03
; EARLIER APPLICATION NUMBER: GB 9302289.5
; EARLIER FILING DATE: 1993-02-05
; EARLIER APPLICATION NUMBER: GB 9321592.9
; EARLIER FILING DATE: 1993-10-20
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FASTSEQ for Windows Version 3.0
; SEQ ID NO 8
; LENGTH: 130
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-08-495-559-8

Query Match          96.1%; Score 199; DB 3; Length 130;
Best Local Similarity 97.4%; Pred. No. 9.8e-20;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
; APPLICANT: Hook, Magnus
; APPLICANT: Partl, Joseph M.
; APPLICANT: House-Pompeo, Karen
; APPLICANT: Stnam, Narayana
; APPLICANT: Symersky, Jindrich
; TITLE OF INVENTION: COLLAGEN BINDING PROTEIN COMPOSITIONS
; TITLE OF INVENTION: AND METHODS OF USE
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: U.S.
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/856,253
; FILING DATE: Concurrently Herewith
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/017,678
; FILING DATE: 16-MAY-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Kitchell, Barbara S.
; REGISTRATION NUMBER: 33,928
; REFERENCE/DOCKET NUMBER: TAMK:193
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (512) 418-3000
; TELEFAX: (512) 474-7577
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 139 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
US-08-856-253-8

Query Match          96.1%; Score 199; DB 3; Length 139;
Best Local Similarity 97.4%; Pred. No. 1.1e-19;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QNSGNQSFPEDETEDEKPKYEGGNIVIDIDPDSVPQIHG 38
DB 16 QNSGNQSFPEDETEDEKPKYEGGNIVIDIDPDSVPQIHG 53

RESULT 10
US-08-459-135A-10
; Sequence 10, Application US/08459135A
; Patent No. 5955078
; GENERAL INFORMATION:
; APPLICANT: BURHAM, Martin Karl Russel
; APPLICANT: CHOPRA, Ian
; APPLICANT: CRITCHLEY, Ian Alfred
; APPLICANT: KNOWLES, David Justin Charles
; TITLE OF INVENTION: FIBROBLAST BINDING PROTEIN: MONOCLONAL ANTIBODY AND THEIR USE
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corporation
; STREET: 709 Swedeland Road
; CITY: King of Prussia
; STATE: PA
; COUNTRY: U.S.A.
; ZIP: 19406-0939
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
```

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SOFTWARE: Fastseq, Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/459,135A
FILING DATE: 02-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB/94/00215
FILING DATE: 04-Feb-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Gimm, Edward R
REGISTRATION NUMBER: 38,891
REFERENCE/DOCKET NUMBER: P30591C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-4478
TELEFAX: 610-270-5090
TELEX:
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 174 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: Protein
US-08-459-135A-10

Query Match      96.1%; Score 199; DB 2; Length 174;
Best Local Similarity 97.4%; Pred. No. 1.4e-19;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy      1  ONSGNQSPEDTEEDKPKYEGGNIVIDIDFSVPQIHG 38
Db      2  ONSGNQSPEDTEEDKPKYEGGNIVIDIDFSVPQIHG 39

RESULT 11
US-08-459-135A-13
Sequence 13, Application US/08459135A
Patent No. 5955078
GENERAL INFORMATION:
APPLICANT: BURHAM, Martin Karl Russel
APPLICANT: CHOPRA, Ian
APPLICANT: CRITCHLEY, Ian Alfred
APPLICANT: KNOWLES, David Justin Charles
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN: MONOCLONAL ANTIBODY AND THEIR US
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
STATE: PA
COUNTRY: U.S.A.
ZIP: 19406-0939
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: Fastseq, Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/459,135A
FILING DATE: 02-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB/94/00215
FILING DATE: 04-Feb-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Gimm, Edward R
REGISTRATION NUMBER: 38,891
REFERENCE/DOCKET NUMBER: P30591C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-4478
TELEFAX: 610-270-5090
TELEX:
```

```
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 174 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-459-135A-13

Query Match      96.1%; Score 199; DB 2; Length 174;
Best Local Similarity 97.4%; Pred. No. 1.4e-19;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy      1  ONSGNQSPEDTEEDKPKYEGGNIVIDIDFSVPQIHG 38
Db      2  ONSGNQSPEDTEEDKPKYEGGNIVIDIDFSVPQIHG 39

RESULT 12
US-08-495-559-10
Sequence 10, Application US/08495559A
Patent No. 6054572
GENERAL INFORMATION:
APPLICANT: BURHAM, Martin Karl Russel
APPLICANT: CHOPRA, Ian
APPLICANT: CRITCHLEY, Ian Alfred
APPLICANT: KNOWLES, David Justin Charles
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN: MONOCLONAL
FILE REFERENCE: P30591
CURRENT APPLICATION NUMBER: US/08/495,559A
CURRENT FILING DATE: 1995-08-03
EARLIER APPLICATION NUMBER: GB 9302289.5
EARLIER FILING DATE: 1993-02-05
EARLIER APPLICATION NUMBER: GB 9321592.9
EARLIER FILING DATE: 1993-10-20
NUMBER OF SEQ ID NOS: 13
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 10
LENGTH: 174
TYPE: PRT
ORGANISM: Staphylococcus aureus
US-08-495-559-10

Query Match      96.1%; Score 199; DB 3; Length 174;
Best Local Similarity 97.4%; Pred. No. 1.4e-19;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy      1  ONSGNQSPEDTEEDKPKYEGGNIVIDIDFSVPQIHG 38
Db      2  ONSGNQSPEDTEEDKPKYEGGNIVIDIDFSVPQIHG 39

RESULT 13
US-08-495-559-13
Sequence 13, Application US/08495559A
Patent No. 6054572
GENERAL INFORMATION:
APPLICANT: BURHAM, Martin Karl Russel
APPLICANT: CHOPRA, Ian
APPLICANT: CRITCHLEY, Ian Alfred
APPLICANT: KNOWLES, David Justin Charles
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN: MONOCLONAL
FILE REFERENCE: P30591
CURRENT APPLICATION NUMBER: US/08/495,559A
CURRENT FILING DATE: 1995-08-03
EARLIER APPLICATION NUMBER: GB 9302289.5
EARLIER FILING DATE: 1993-02-05
EARLIER APPLICATION NUMBER: GB 9321592.9
EARLIER FILING DATE: 1993-10-20
NUMBER OF SEQ ID NOS: 13
SOFTWARE: FastSeq for Windows Version 3.0
```

```

; SEQ ID NO 13
; LENGTH: 174
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-08-495-559-13

Query March          96.1%; Score 199; DB 3; Length 174;
Best Local Similarity 97.4%; Pred. No. 1.4e-19;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 QNSGNQSPFEDTEEDKPKYEQGNIVIDIDFDSVPQIHG 38
Db      2 QNSGNQSPFEDTEEDKPKYEQGNIVIDIDFDSVPQIHG 39

RESULT 14
US-08-495-559-6
; Sequence 6, Application US/08495559A
; Patent No. 6054572
; GENERAL INFORMATION:
; APPLICANT: BURHAM, Martin Karl Russel
; APPLICANT: CHOPRA, Ian
; APPLICANT: CRITCHLEY, Ian Alfred
; APPLICANT: KNOWLES, David Justin Charles
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN: MONOCLONAL
; TITLE OF INVENTION: ANTIBODY AND THEIR USE IN PREVENTING BACTERIAL ADHESION
; FILE REFERENCE: P30591
; CURRENT APPLICATION NUMBER: US/08/495,559A
; CURRENT FILING DATE: 1995-08-03
; EARLIER APPLICATION NUMBER: GB 9302289.5
; EARLIER FILING DATE: 1993-02-05
; EARLIER APPLICATION NUMBER: GB 9321592.9
; EARLIER FILING DATE: 1993-10-20
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 176
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-08-495-559-6

Query March          96.1%; Score 199; DB 3; Length 176;
Best Local Similarity 97.4%; Pred. No. 1.4e-19;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 QNSGNQSPFEDTEEDKPKYEQGNIVIDIDFDSVPQIHG 38
Db      2 QNSGNQSPFEDTEEDKPKYEQGNIVIDIDFDSVPQIHG 39

RESULT 15
US-08-459-135A-12
; Sequence 12, Application US/08459135A
; Patent No. 5955078
; GENERAL INFORMATION:
; APPLICANT: BURHAM, Martin Karl Russel
; APPLICANT: CHOPRA, Ian
; APPLICANT: CRITCHLEY, Ian Alfred
; APPLICANT: KNOWLES, David Justin Charles
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN: MONOCLONAL ANTIBODY AND THEIR US
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corporation
; STREET: 709 Swedeland Road
; CITY: King of Prussia
; STATE: PA
; COUNTRY: U.S.A.
; ZIP: 19406-0939
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: DOS
; SOFTWARE: Fastseq, Version 2.0
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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/459,135A
; FILING DATE: 02-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA: PCT/GB/94/00215
; APPLICATION NUMBER: PCT/GB/94/00215
; FILING DATE: 04-Feb-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Gimmì, Edward R
; REGISTRATION NUMBER: 38,891
; REFERENCE/DOCKET NUMBER: P30591C2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-270-4478
; TELEFAX: 610-270-5090
; TELEX:
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 178 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Protein
US-08-459-135A-12

Query March          96.1%; Score 199; DB 2; Length 178;
Best Local Similarity 97.4%; Pred. No. 1.4e-19;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 QNSGNQSPFEDTEEDKPKYEQGNIVIDIDFDSVPQIHG 38
Db      2 QNSGNQSPFEDTEEDKPKYEQGNIVIDIDFDSVPQIHG 39
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Search completed: October 22, 2005, 03:51:16
Job time : 28.8363 secs

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OM protein - protein search, using sw model

Run on: October 22, 2005, 10:49:15 / Search time 107.19 Seconds
(without alignments)
148.005 Million cell updates/sec

Title: US-10-731-238-36

Perfect score: 207
Sequence: 1 QNSGNQSFEDTIEDKPKYEQGNIVDIDFDSVPQIHG 38

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1862951 seqs, 417491010 residues

Total number of hits satisfying chosen parameters: 1862951

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

Published Applications Aa.*
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14: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
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17: /cgn2_6/ptodata/2/pubpaa/US10F_PUBCOMB.pep.*
18: /cgn2_6/ptodata/2/pubpaa/US10G_PUBCOMB.pep.*
19: /cgn2_6/ptodata/2/pubpaa/US11A_PUBCOMB.pep.*
20: /cgn2_6/ptodata/2/pubpaa/US11A_NEW_PUB.pep.*
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22: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	207	100.0	38	18	US-10-731-238-36
2	199	96.1	38	9	US-10-731-238-5
3	199	96.1	139	9	US-09-813-820-8
4	199	96.1	388	8	US-08-901-062-1
5	199	96.1	559	15	US-08-781-986A-5251
6	199	96.1	559	15	US-10-329-624-5251
7	199	96.1	767	9	US-09-815-242-5899
8	199	96.1	767	9	US-09-815-242-13140
9	199	96.1	940	17	US-10-470-048B-424
10	199	96.1	948	17	US-10-470-048B-69
11	199	96.1	961	15	US-10-282-122A-43778

12	199	96.1	1018	9	US-09-815-242-5797	Sequence 5797, Ap
13	199	96.1	1018	9	US-09-815-242-12838	Sequence 12838, A
14	199	96.1	1018	17	US-10-470-048B-68	Sequence 68, Appl
15	199	96.1	1027	8	US-08-781-986A-5254	Sequence 5254, Ap
16	199	96.1	1027	15	US-10-329-624-5254	Sequence 5254, Ap
17	199	96.1	1038	15	US-10-282-122A-43827	Sequence 43827, A
18	199	93.2	38	18	US-10-731-238-37	Sequence 37, Appl
19	199	93.2	38	18	US-10-731-238-39	Sequence 39, Appl
20	199	93.2	38	18	US-10-731-238-40	Sequence 40, Appl
21	199	93.2	38	18	US-10-731-238-41	Sequence 41, Appl
22	199	93.2	38	18	US-10-731-238-38	Sequence 38, Appl
23	199	92.8	38	18	US-10-731-238-38	Sequence 42, Appl
24	199	92.3	38	18	US-10-731-238-42	Sequence 6, Appl1
25	199	92.3	38	18	US-10-731-238-6	Sequence 43, Appl
26	199	92.3	978	9	US-09-815-242-5456	Sequence 5456, Ap
27	199	92.3	1001	9	US-09-815-242-12686	Sequence 12686, A
28	189	91.3	38	18	US-10-731-238-35	Sequence 35, Appl
29	188	91.1	38	18	US-10-731-238-35	Sequence 56, Appl
30	188	90.8	38	18	US-10-731-238-46	Sequence 46, Appl
31	185	89.4	38	18	US-10-731-238-44	Sequence 44, Appl
32	180.5	87.2	39	18	US-10-731-238-57	Sequence 57, Appl
33	180	87.0	38	18	US-10-731-238-7	Sequence 7, Appl1
34	174	84.1	38	18	US-10-731-238-47	Sequence 47, Appl
35	173	83.6	38	18	US-10-731-238-48	Sequence 48, Appl
36	172	83.1	38	18	US-10-731-238-8	Sequence 8, Appl1
37	172	83.1	38	18	US-10-731-238-49	Sequence 49, Appl
38	170	82.1	38	18	US-10-731-238-45	Sequence 45, Appl
39	166	80.2	38	18	US-10-731-238-50	Sequence 50, Appl
40	157	75.8	36	18	US-10-731-238-58	Sequence 58, Appl
41	149	72.0	30	14	US-10-731-238-59	Sequence 59, Appl
42	141	68.1	30	14	US-10-287-821-1	Sequence 2, Appl1
43	141	68.1	31	14	US-10-287-821-2	Sequence 1, Appl1
44	77.5	37.4	37	20	US-11-066-697-1134	Sequence 1134, Ap
45	74	35.7	14	18	US-10-731-238-60	Sequence 60, Appl

ALIGNMENTS

RESULT 1
US-10-731-238-36
Sequence 36, Application US/10731238
Publication No. US2005012352A1
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
Patli, Joseph M.
House-Pompeo, Karen L.
Speziale, Pietro
McGavin, Martin J.
TITLE OF INVENTION: FIBROBLAST BINDING PROTEIN COMPOSITIONS
AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESSES:
ADDRESSER: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/731,238
FILING DATE: 10-Dec-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE: 21-Jan-1998
APPLICATION NUMBER: US 60/036,139

FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAMK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 36:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
US-10-731-238-36
SEQUENCE DESCRIPTION: SEQ ID NO: 36:
Query Match 100.0%; Score 207; DB 18; Length 38;
Best Local Similarity 100.0%; Pred. No. 4.8e-20;
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 QNSGNQSFPEDEBDEKPKYEQGNIVDIDPDSVPQIHG 38
DB 1 QNSGNQSFPEDEBDEKPKYEQGNIVDIDPDSVPQIHG 38
RESULT 2
US-10-731-238-5
Sequence 5, Application US/10731238
Publication No. US20050123552A1
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
Patti, Joseph M.
House-Pompeo, Karen L.
Speziale, Pietro
Joh, Danny
McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P. O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/731,238
FILING DATE: 10-Dec-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE: 21-Jan-1998
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAMK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>

TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-10-731-238-5
Query Match 96.1%; Score 199; DB 18; Length 38;
Best Local Similarity 97.4%; Pred. No. 5.5e-19;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 QNSGNQSFPEDEBDEKPKYEQGNIVDIDPDSVPQIHG 38
DB 1 QNSGNQSFPEDEBDEKPKYEQGNIVDIDPDSVPQIHG 38
RESULT 3
US-09-813-820-8
Sequence 8, Application US/09813820
Patent No. US20020102262A1
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
Patti, Joseph M.
House-Pompeo, Karen
Sthanam, Narayana
Symersky, Jindrich
TITLE OF INVENTION: COLLAGEN BINDING PROTEIN COMPOSITIONS
AND METHODS OF USE
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P. O. Box 4433
CITY: Houston
STATE: Texas
COUNTRY: U.S.
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/813,820
FILING DATE: 22-Mar-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/856,253
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Kitchell, Barbara S.
REGISTRATION NUMBER: 33,928
REFERENCE/DOCKET NUMBER: TAMK:193
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
TELEFAX: (512) 474-7577
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 139 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
US-09-813-820-8
SEQUENCE DESCRIPTION: SEQ ID NO: 8:
Query Match 96.1%; Score 199; DB 9; Length 139;
Best Local Similarity 97.4%; Pred. No. 2.6e-18;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 QNSGNQSFPEDEBDEKPKYEQGNIVDIDPDSVPQIHG 38
DB 16 QNSGNQSFPEDEBDEKPKYEQGNIVDIDPDSVPQIHG 53
RESULT 4
US-08-901-062-1
Sequence 1, Application US/08901062

Publication No. US20020025324A1
GENERAL INFORMATION:
APPLICANT: SEALS, JONATHAN R.
TITLE OF INVENTION: RECOMBINANT BIVALENT BACTERIAL VACCINE
TITLE OF INVENTION: FOR THE PREVENTION OF MASTITIS
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: HALE AND DOR LLP
STREET: 60 State Street
CITY: Boston
STATE: MA
COUNTRY: United States Of America
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/901,062
FILING DATE: 25-JUL-1997
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Baker, Hollie L.
REGISTRATION NUMBER: 31,321
REFERENCE/DOCKET NUMBER: 106941.153
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 526-6000
TELEFAX: (617) 526-5000
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 388 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHEICAL: NO
ANTI-SENSE: NO
US-08-901-062-1

Query Match 96.1%; Score 199; DB 8; Length 388;
Best Local Similarity 97.4%; Pred. No. 8.7e-18;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ONSGNSFPEDTEEDKPKYEGGNIYVIDIDFDSVPQIHG 38
DB 265 ONSGNSFPEDTEEDKPKYEGGNIYVIDIDFDSVPQIHG 302

RESULT 5
US-08-781-986A-5251
Sequence 5251, Application US/08781986A
Publication No. US20030054436A1
GENERAL INFORMATION:
APPLICANT: Charles Kunsch
TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
NUMBER OF SEQUENCES: 5255
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COUNTRY: USA
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/781,986A
FILING DATE:
CLASSIFICATION: 435

PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Benson, Bob
REGISTRATION NUMBER: 30,446
REFERENCE/DOCKET NUMBER: PB248P
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 5251:
SEQUENCE CHARACTERISTICS:
LENGTH: 559 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-781-986A-5251

Query Match 96.1%; Score 199; DB 8; Length 559;
Best Local Similarity 97.4%; Pred. No. 1.3e-17;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ONSGNSFPEDTEEDKPKYEGGNIYVIDIDFDSVPQIHG 38
DB 301 ONSGNSFPEDTEEDKPKYEGGNIYVIDIDFDSVPQIHG 338

RESULT 6
US-10-329-624-5251
Sequence 5251, Application US/10329624
Publication No. US20040043037A1
GENERAL INFORMATION:
APPLICANT: Charles Kunsch
Gill H. Choi
Patrick S. Dillon
Craig A. Rosen
Steven C. Barash
Michael R. Farnon
TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
NUMBER OF SEQUENCES: 5256
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COUNTRY: USA
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/329,624
FILING DATE: 27-Dec-2002
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/956,171
FILING DATE: October 20, 1997
APPLICATION NUMBER: 60/009,861
FILING DATE: January 5, 1996
APPLICATION NUMBER: 08/781,986
FILING DATE: January 3, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Mark J. Hyman
REGISTRATION NUMBER: 46,789
REFERENCE/DOCKET NUMBER: PB248P1D1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (240) 314-1224
TELEFAX: (301) 309-8439
INFORMATION FOR SEQ ID NO: 5251:
SEQUENCE CHARACTERISTICS:
LENGTH: 559 amino acids

TYPE: amino acid
STRANDEDNESS: single.
TOPOLOGY: linear.
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 5251;
US-10-329-624-5251

Query Match 96.1%; Score 199; DB 15; Length 559;
Best Local Similarity 97.4%; Pred. No. 1.3e-17;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QNSGNOSFPEDETDKPKYEGGNIYDIDFDSVPQIHG 38
Db 301 QNSGNOSFPEDETDKPKYEGGNIYDIDFDSVPQIHG 338

RESULT 7

US-09-815-242-5899
; Sequence 5899, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haseibeck, Robert
; APPLICANT: Ohlsen, Kari L.
; APPLICANT: Zyekind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; FILE REFERENCE: ELITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5899
; LENGTH: 767
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-09-815-242-5899

Query Match 96.1%; Score 199; DB 9; Length 767;
Best Local Similarity 97.4%; Pred. No. 2e-17;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QNSGNOSFPEDETDKPKYEGGNIYDIDFDSVPQIHG 38
Db 682 QNSGNOSFPEDETDKPKYEGGNIYDIDFDSVPQIHG 719

RESULT 8

US-09-815-242-13140
; Sequence 13140, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haseibeck, Robert
; APPLICANT: Ohlsen, Kari L.
; APPLICANT: Zyekind, Judith W.

APPLICANT: Wall, Daniel
APPLICANT: Trawick, John D.
APPLICANT: Carr, Grant J.
APPLICANT: Yamamoto, Robert T.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in
FILE REFERENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21, 078
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 13140
LENGTH: 767
TYPE: PRT
ORGANISM: Staphylococcus aureus
US-09-815-242-13140

Query Match 96.1%; Score 199; DB 9; Length 767;
Best Local Similarity 97.4%; Pred. No. 2e-17;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QNSGNOSFPEDETDKPKYEGGNIYDIDFDSVPQIHG 38
Db 682 QNSGNOSFPEDETDKPKYEGGNIYDIDFDSVPQIHG 719

RESULT 9

US-10-470-048B-424
; Sequence 424, Application US/10470048B
; Publication No. US20050037444A1
; GENERAL INFORMATION:
; APPLICANT: MEINKE ET AL.
; TITLE OF INVENTION: A METHOD FOR IDENTIFICATION, ISOLATION AND PRODUCTION OF
; FILE REFERENCE: SONN:035US
; CURRENT APPLICATION NUMBER: US/10/470,048B
; CURRENT FILING DATE: 2003-07-25
; NUMBER OF SEQ ID NOS: 603
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 424
; LENGTH: 940
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-10-470-048B-424

Query Match 96.1%; Score 199; DB 17; Length 940;
Best Local Similarity 97.4%; Pred. No. 2.5e-17;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QNSGNOSFPEDETDKPKYEGGNIYDIDFDSVPQIHG 38
Db 682 QNSGNOSFPEDETDKPKYEGGNIYDIDFDSVPQIHG 719

RESULT 10

US-10-470-048B-69
; Sequence 69, Application US/10470048B
; Publication No. US20050037444A1

```

; GENERAL INFORMATION:
; APPLICANT: MEINKE ET AL.
; TITLE OF INVENTION: A METHOD FOR IDENTIFICATION, ISOLATION AND PRODUCTION OF
; TITLE OF INVENTION: ANTIGENS TO A SPECIFIC PATHOGEN
; FILE REFERENCE: SONN.035US
; CURRENT APPLICATION NUMBER: US/10/470.048B
; NUMBER OF SEQ ID NOS: 603
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 69
; LENGTH: 948
; TYPE: PRF
; ORGANISM: Staphylococcus aureus
; US-10-470-048B-69

Query Match      96.1%; Score 199; DB 17; Length 948;
Best Local Similarity 97.4%; Pred. No. 2.5e-17;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Cy 1 QNSGNQSFEDTEEDKPKYEQGNIVDIDFDSVPQIHG 38
    |||||
Db 690 QNSGNQSFEDTEEDKPKYEQGNIVDIDFDSVPQIHG 727

RESULT 11
US-10-282-122A-43778
; Sequence 43778, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zykkind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Foremych, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 43778
; LENGTH: 961
; TYPE: PRF
; ORGANISM: Staphylococcus aureus
; US-10-282-122A-43778
```

```

Query Match      96.1%; Score 199; DB 15; Length 961;
Best Local Similarity 97.4%; Pred. No. 2.6e-17;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Cy 1 QNSGNQSFEDTEEDKPKYEQGNIVDIDFDSVPQIHG 38
    |||||
Db 693 QNSGNQSFEDTEEDKPKYEQGNIVDIDFDSVPQIHG 730

RESULT 12
US-09-815-242-5797
; Sequence 5797, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari L.
; APPLICANT: Zykkind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; TITLE OF INVENTION: Prokaryotes
; FILE REFERENCE: ELITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5797
; LENGTH: 1018
; TYPE: PRF
; ORGANISM: Staphylococcus aureus
; US-09-815-242-5797

Query Match      96.1%; Score 199; DB 9; Length 1018;
Best Local Similarity 97.4%; Pred. No. 2.8e-17;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Cy 1 QNSGNQSFEDTEEDKPKYEQGNIVDIDFDSVPQIHG 38
    |||||
Db 746 QNSGNQSFEDTEEDKPKYEQGNIVDIDFDSVPQIHG 783

RESULT 13
US-09-815-242-12838
; Sequence 12838, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari L.
; APPLICANT: Zykkind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
```



```
/ TITLE OF INVENTION: Prokaryotes
/ FILE REFERENCE: ELITRA 011A
/ CURRENT APPLICATION NUMBER: US/09/815,242
/ CURRENT FILING DATE: 2001-03-21
/ PRIOR APPLICATION NUMBER: 60/191,078
/ PRIOR FILING DATE: 2000-03-21
/ PRIOR APPLICATION NUMBER: 60/206,848
/ PRIOR FILING DATE: 2000-05-23
/ PRIOR APPLICATION NUMBER: 60/207,727
/ PRIOR FILING DATE: 2000-05-26
/ PRIOR APPLICATION NUMBER: 60/242,578
/ PRIOR FILING DATE: 2000-10-23
/ PRIOR APPLICATION NUMBER: 60/253,625
/ PRIOR FILING DATE: 2000-11-27
/ PRIOR APPLICATION NUMBER: 60/257,931
/ PRIOR FILING DATE: 2000-12-22
/ PRIOR APPLICATION NUMBER: 60/269,308
/ PRIOR FILING DATE: 2001-02-16
/ NUMBER OF SEQ ID NOS: 14110
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 12838
/ LENGTH: 1018
/ TYPE: PRT
/ ORGANISM: Staphylococcus aureus
US-09-815-242-12838

Query Match          96.1%; Score 199; DB 9; Length 1018;
Best Local Similarity 97.4%; Pred. No. 2.8e-17;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 QNSGNSFPEDTEEDKPKYEGGNIIVDIDFDSVPQIHG 38
Db      746 QNSGNSFPEDTEEDKPKYEGGNIIVDIDFDSVPQIHG 783

RESULT 14
US-10-470-048B-68
/ Sequence 68, Application US/10470048B
/ Publication No. US20050037444A1
/ GENERAL INFORMATION:
/ APPLICANT: MEINKE ET AL.
/ TITLE OF INVENTION: A METHOD FOR IDENTIFICATION, ISOLATION AND PRODUCTION OF
/ TITLE OF INVENTION: ANTIGENS TO A SPECIFIC PATHOGEN
/ FILE REFERENCE: SOMN-035US
/ CURRENT APPLICATION NUMBER: US/10/470,048B
/ CURRENT FILING DATE: 2003-07-25
/ NUMBER OF SEQ ID NOS: 603
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 68
/ LENGTH: 1018
/ TYPE: PRT
/ ORGANISM: Staphylococcus aureus
US-10-470-048B-68

Query Match          96.1%; Score 199; DB 17; Length 1018;
Best Local Similarity 97.4%; Pred. No. 2.8e-17;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 QNSGNSFPEDTEEDKPKYEGGNIIVDIDFDSVPQIHG 38
Db      746 QNSGNSFPEDTEEDKPKYEGGNIIVDIDFDSVPQIHG 783

RESULT 15
US-08-781-986A-5254
/ Sequence 5254, Application US/08781986A
/ Publication No. US20030054436A1
/ GENERAL INFORMATION:
/ APPLICANT: Charles Kunach
/ TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
/ NUMBER OF SEQUENCES: 5255
/ CORRESPONDENCE ADDRESSES:
/ ADDRESSEE: Human Genome Sciences, Inc.
```

```
/ STREET: 9410 Key West Avenue
/ CITY: Rockville
/ STATE: Maryland
/ COUNTRY: USA
/ ZIP: 20850
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
/ COMPUTER: HP Vectra 486/33
/ OPERATING SYSTEM: MSDOS version 6.2
/ SOFTWARE: ASCII Text
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/781,986A
/ FILING DATE:
/ CLASSIFICATION: 435
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER:
/ FILING DATE:
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Benson, Bob
/ REGISTRATION NUMBER: 30,446
/ REFERENCE/DOCKET NUMBER: PB248PP
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (301) 309-8504
/ TELEFAX: (301) 309-8512
/ INFORMATION FOR SEQ ID NO: 5254:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 1027 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
US-08-781-986A-5254

Query Match          96.1%; Score 199; DB 8; Length 1027;
Best Local Similarity 97.4%; Pred. No. 2.8e-17;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 QNSGNSFPEDTEEDKPKYEGGNIIVDIDFDSVPQIHG 38
Db      755 QNSGNSFPEDTEEDKPKYEGGNIIVDIDFDSVPQIHG 792

Search completed: October 22, 2005, 11:34:46
Job time : 107.19 secs
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GenCore version 5.1.6
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OM protein - protein search, using SW model

Run on: October 22, 2005, 02:23:36 ; Search time 19.0841 Seconds
(without alignments)
191.586 Million cell updates/sec

Title: US-10-731-238-36

Perfect score: 207
Sequence: 1 QNSGNQSPFEDTEBDKPKRYEQGNIVDIDFDSVPQIHG 38

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR_79: *
1: pir1: *
2: pir2: *
3: pir3: *
4: pir4: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	199	96.1	940	2	S19702 fibronectin-binding
2	199	96.1	961	2	S19702 fibronectin-binding
3	199	96.1	1018	2	A32192 fibronectin-binding
4	199	96.1	1038	2	H90053 fibronectin-binding
5	57	27.5	1460	2	D81675 polycystic membrane
6	55.5	26.8	1273	1	TDRTLT leukocyte common a
7	55.5	26.8	1291	1	A28334 protein-tyrosine-p
8	55	26.6	636	2	AD1878 cyanoophycin synthe
9	55	26.6	837	2	T19825 fibronectin-binding
10	55	26.6	920	2	T43263 fibronectin-binding
11	55	26.6	1091	2	S33850 fibronectin-binding
12	53.5	25.8	882	1	IJHUCE cadherin 1 precurs
13	53	25.6	110	2	H75048 DNA-directed RNA p
14	53	25.6	705	2	A45508 heat shock protein
15	53	25.6	1244	2	S25327 cytoskeleton assem
16	52.5	25.4	437	2	S11925 S-locus-specific g
17	52.5	25.4	494	2	T14516 protein phosphatas
18	52.5	25.4	817	2	T03852 probable transcrip
19	52	25.1	110	2	A71112 hypochlorite prote
20	52	25.1	241	2	H97723 amino-acid ABC tra
21	52	25.1	241	2	C71725 hypochlorite prote
22	52	25.1	345	2	T33906 hypochlorite prote
23	52	25.1	413	2	T31663 hypochlorite prote
24	52	25.1	784	2	T45971 hypochlorite prote
25	52	25.1	833	2	E90577 hypochlorite prote
26	52	25.1	1369	2	S58160 hypochlorite prote
27	52	25.1	1424	2	T03851 thyroid hormone re
28	52	25.1	1817	2	T34249 hypochlorite prote
29	51.5	24.9	155	1	RNBYR6 DNA-directed RNA p

30	51.5	24.9	205	2	G69784 hypothetical prote
31	51.5	24.9	342	2	A89846 hypothetical prote
32	51.5	24.9	358	2	E86452 protein F6N18.15 [
33	51.5	24.9	375	2	C75040 alcohol dehydrogen
34	51.5	24.9	491	1	IJBOPC P-cadherin - bovin
35	51.5	24.9	540	2	B82170 peptide ABC transp
36	51.5	24.9	671	1	OKBOG protein kinase (EC
37	51.5	24.9	686	1	S05702 protein kinase (EC
38	51.5	24.9	822	1	ITMCP P-cadherin precurs
39	51.5	24.9	829	1	IJHUCP cadherin 3 precurs
40	51.5	24.9	875	2	C81209 cepa protein NME03
41	51.5	24.9	880	2	G81786 Neisseria-specific
42	51.5	24.9	880	2	G81786 leukocyte common a
43	51.5	24.9	1304	1	A46546 n-acetyl-gamma-glu
44	51	24.6	270	2	T43039 alpha-amylase (EC
45	51	24.6	330	2	D75160 alpha-amylase (EC
	51	24.6	558	2	JC5135

ALIGNMENTS

RESULT 1

S19702 fibronectin-binding protein B - Staphylococcus aureus
C:Species: Staphylococcus aureus
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
C:Accession: S19702
R:Joensen, K.; Signaes, C.; Mueller, H.P.; Lindberg, M.
Eur. J. Biochem. 202, 1041-1048, 1991
A:Title: Two different genes encode fibronectin binding proteins in Staphylococcus aureus
A:Reference number: S19702; MUID:92111475; PMID:1837266
A:Accession: S19702
A:Status: Preliminary
A:Molecule type: DNA
A:Residues: 1-940 <JOB>
A:Cross-references: UNIPROT:053682; EMBL:X62992; NID:949040; PIDN:CAA44726.1; PID:958156;
C:Keywords: fibronectin binding

Query Match 96.1%; Score 199; DB 2; Length 940;
Best Local Similarity 97.4%; Pred. No. 1.1e-17;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QNSGNQSPFEDTEBDKPKRYEQGNIVDIDFDSVPQIHG 38

DB 682 QNSGNQSPFEDTEBDKPKRYEQGNIVDIDFDSVPQIHG 719

RESULT 2

G90053 hypothetical protein fnbB [imported] - Staphylococcus aureus (strain N315)
C:Species: Staphylococcus aureus
C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
R:Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguchi, A.; Mizutani-U, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.; Imae, A.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiratsugu, K.
Lancet 357, 1225-1240, 2001
A:Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.
A:Reference number: A89758; MUID:21311952; PMID:11418146
A:Accession: G90053
A:Status: Preliminary
A:Molecule type: DNA
A:Residues: 1-961 <KUR>
A:Cross-references: UNIPROT:Q99RD3; GB:BA000018; PID:G13702452; PIDN:BA843593.1; GSPDB:G
A:Experimental source: strain N315
C:Genetics: fnbB

Query Match 96.1%; Score 199; DB 2; Length 961;
Best Local Similarity 97.4%; Pred. No. 1.2e-17;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QNSGNQSPFEDTEBDKPKRYEQGNIVDIDFDSVPQIHG 38

Db 693 QNSGNQSFEDTEBDKPKYEGGNIIVDIDPDSVPOIHG 730

RESULT 3

A32192

A:Species: Staphylococcus aureus

C/Date: 31-Jul-1989 #sequence_revision 31-Jul-1989 #text_change 16-Feb-1997

C/Accession: A32192

R/SjSnaes, C.; Raucsi, G.; Joensson, K.; Lindgren, P.E.; Anantharamaiah, G.M.; Heeoeck, M

Proc. Natl. Acad. Sci. U.S.A. 86, 699-703, 1989

A/Title: Nucleotide sequence of the gene for a fibronectin-binding protein from Staphylo

A/Reference number: A32192; MUID:89098998; PMID:2521391

A/Accession: A32192

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-1018 <SIG>

A/Cross-references: GB:J04151

C/Keywords: fibronectin binding

Query Match 96.1%; Score 199; DB 2; Length 1018;

Best Local Similarity 97.4%; Pred. No. 1.3e-17;

Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QNSGNQSFEDTEBDKPKYEGGNIIVDIDPDSVPOIHG 38

Db 746 QNSGNQSFEDTEBDKPKYEGGNIIVDIDPDSVPOIHG 783

RESULT 4

H90053

A:Species: Staphylococcus aureus (strain N315)

C/Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004

C/Accession: H90053

R/Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Ogun

ma, A.; Mutant-i-i, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.;

Lancet 357, 1225-1240, 2001

A/Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.

A/Reference number: A89758; MUID:21311952; PMID:11418146

A/Accession: H90053

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-1038 <KUR>

A/Cross-references: UNIPROT:Q99RD2; GB:BA000018; PID:g13702453; PIDN:BA843594.1; GSPDB:C

A/Experimental source: strain N315

C/Genetics:

A/Gene: fnb

Query Match 96.1%; Score 199; DB 2; Length 1038;

Best Local Similarity 97.4%; Pred. No. 1.3e-17;

Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QNSGNQSFEDTEBDKPKYEGGNIIVDIDPDSVPOIHG 38

Db 742 QNSGNQSFEDTEBDKPKYEGGNIIVDIDPDSVPOIHG 779

RESULT 5

D81675

A:Species: Chlamydia muridarum, Chlamydia trachomatis MoPn

C/Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004

C/Accession: D81675

R/Read, T.D.; Brumham, R.C.; Shen, C.; Gall, S.R.; Heideberg, J.F.; White, O.; Hickey,

C.; Dodson, R.; Gwin, M.; Nelson, W.; Deboy, R.; Kolonay, J.; McClarty, G.; Salzberg,

Nucleic Acids Res. 28, 1397-1406, 2000

A/Title: Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39.

A/Reference number: A81500; MUID:20150255; PMID:10684935

A/Accession: D81675

A/Status: preliminary

A/Molecule type: DNA
A/Residues: 1-1460 <TET>
A/Cross-references: UNIPROT:Q9PRT1; GB:AE002338; GB:AE002160; NID:g7190724; PIDN:AAF39511
A/Experimental source: strain N199 (MoPn)
C/Genetics:
A/Gene: TC0695

Query Match 27.5%; Score 57; DB 2; Length 1460;

Best Local Similarity 32.4%; Pred. No. 58;

Matches 11; Conservative 9; Mismatches 14; Indels 0; Gaps 0;

QY 2 NSGNQSFEDTEBDKPKYEGGNIIVDIDPDSVPO 35

Db 39 SSSQSFTEIIPENGAHYRVSGVPSFDFNIB 72

RESULT 6

TDRRLT

A:Species: common antigen precursor, splice form 4 - rat

N/Alternate names: CD45; L-CA; LY-5; T200

N/Contains: leukocyte common antigen precursor, splice form 1; leukocyte common antigen f

.1.3.48)

C/Species: Rattus norvegicus (Norway rat)

C/Date: 04-Dec-1986 #sequence_revision 05-May-2000 #text_change 09-Jul-2004

C/Accession: A29450; B29450; C29450; D29450; A60241; A02247; I54569; A45854

R/Barclay, A.N.; Jackson, D.I.; Willis, A.C.; Williams, A.F.

EMBO J. 6, 1259-1264, 1987

A/Title: Lymphocyte specific heterogeneity in the rat leukocyte common antigen (T200) 18

A/Reference number: A91067; MUID:87275817; PMID:2440674

A/Accession: A29450

A/Molecule type: mRNA

A/Residues: 20-30,163-218 <BAR1>

A/Cross-references: UNIPROT:Q64224; GB:M25820; GB:M24611; NID:g205153; GB:Y00065; GB:K030

A/Experimental source: splice form 1

A/Note: the translation in Genbank entry RATLCA1, PIDN:AAA41518.1, PID:g205154, release 1

A/Accession: B29450

A/Molecule type: mRNA

A/Residues: 19-30,122-218 <BAR2>

A/Cross-references: GB:M25821; GB:M24611; NID:g205155; PIDN:AAA41519.1, PID:g205156; GB:Y

A/Experimental source: splice form 2

A/Accession: C29450

A/Molecule type: mRNA

A/Residues: 20-30,73-121,163-218 <BAR3>

A/Cross-references: GB:M25822; GB:M24611; NID:g205157; PIDN:AAA41520.1, PID:g205158; GB:Y

A/Experimental source: splice form 3

A/Accession: D29450

A/Molecule type: mRNA

A/Residues: 28-218 <BAR4>

A/Cross-references: GB:M25823; GB:M24611; NID:g205159; PIDN:AAA41521.1, PID:g205160; GB:Y

A/Experimental source: splice form 4

A/Note: the sequence in Genbank entry RATLCA1V, release 113.0, has the codon AGG for 56-T

R/Barclay, A.N.; Jackson, D.I.; Willis, A.C.; Williams, A.F.

Adv. Exp. Med. Biol. 237, 3-7, 1988

A/Title: The leukocyte-common antigen (L-CA) family.

A/Reference number: A60241; MUID:89319817; PMID:2978200

A/Accession: A60241

A/Status: not compared with conceptual translation

A/Molecule type: DNA

A/Residues: 30-161 <BAR5>

R/Thomas, M.L.; Barclay, A.N.; Gagnon, J.; Williams, A.F.

Cell 41, 83-93, 1985

A/Title: Evidence from cDNA clones that the rat leukocyte-common antigen (T200) spans the

A/Reference number: A02247; MUID:85201691; PMID:3158393

A/Accession: A02247

A/Molecule type: mRNA

A/Residues: 187-189, 'K', 191-192, 'K', 208-1273 <THO>

A/Cross-references: GB:M10072; GB:M81859; NID:g205140; PIDN:AAA41513.1, PID:g205143

A/Note: the translation in Genbank entry RATLCA1, release 113.0, begins at non-initiator

R/McCall, M.N.; Shotton, D.M.; Barclay, A.N.

Immunology 76, 310-317, 1992

A/Title: Expression of soluble isoforms of rat CD45. Analysis by electron microscopy and

A/Reference number: I54569; MUID:92340120; PMID:1378817

A:Accession: I54569
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Title: Preliminary
 A:Molecule type: mRNA
 A:Residues: 1-30,163-180 <MCC>
 A:Cross-references: GB:540716; NID:9252015; PIDN:AA2648.1; PID:9252016
 R:Jackson, D.I.; Barclay, A.N.
 Immunogenetics 29, 281-287, 1989
 A:Title: The extra segments of sequence in rat leukocyte common antigen (L-CA) are derived from a gene family
 A:Reference number: A45854; MUID:89233293; PMID:2523868
 A:Accession: A45854
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 24-227, 'H', 229-305, 'Y', 307-310 <UAC>
 A:Cross-references: GB:M18347; GB:M18348; GB:M18349
 C:Comment: This glycoprotein is found on lymphoid and myeloid cell surfaces.
 C:Superfamily: leukocyte common antigen; leukocyte common antigen cytosolic domain homol
 C:Keywords: alternative splicing; duplication; glycoprotein; phosphoprotein; phosphoric
 F:1-23/Domain: signal sequence #status predicted <SIG> splice form 4 #status predicted <
 F:24-1273/Product: leukocyte common antigen precursor, splice form 2 #status predicted <MAT
 F:24-30,122-1273/Product: leukocyte common antigen, splice form 1 #status predicted <MAT
 F:24-30,163-1273/Product: leukocyte common antigen, splice form 3 #status predicted <MAT
 F:24-30,73-121,163-216/Product: leukocyte common antigen, splice form 3 #status predicted
 F:547-568/Domain: transmembrane #status predicted <TM>
 F:565-1206/Domain: leukocyte common antigen cytosolic domain homology <LAC>
 F:569-1273/Domain: intracellular #status predicted <INT>
 F:646-870/Domain: protein-tyrosine-phosphatase homology <PTP>
 F:62,142,153,169,178,200,245,271,282,327,371,374,502/Binding site: carbohydrate (asn) (C
 F:822/Active site: Cys (phosphocysteine intermediate) #status predicted
 F:828/Binding site: substrate phosphate (Asn) (covalent) #status absent
 F:1063/Binding site: carbohydrate (asn) (covalent) #status absent

Query Match 26.8%; Score 55.5; DB 1; Length 1273;
 Best Local Similarity 40.5%; Pred. No. 77;
 Matches 15; Conservative 5; Mismatches 10; Indels 7; Gaps 2;

Qy 1 QNSGNSPEDTBEDEKPKYEGGNIVDIDPSVPIH 37
 Db 929 QHIGNQ-----EENKCK-NRSNVVYPDFNRPVLMH 958

RESULT 7
 A28334
 protein-tyrosine-phosphatase (EC 3.1.3.48) Ly-5 precursor (B-cell variant) - mouse
 N:Alternate names: 200K leukocyte common antigen; B220; CD45; Ly-5 (B-cell specific); PT
 N:Contains: protein-tyrosine-phosphatase (T-cell variant)
 C:Species: Mus musculus (house mouse)
 C:Date: 10-Sep-1999 #sequence, revision 10-Sep-1999 #text change 09-Jul-2004
 C:Accession: A28334; A29381; A61180; A60933; A35522; A29075; I54450; A28335; A23329; I57
 R:Thomas, M.L.; Reynolds, P.D.; Chain, A.; Ben-Neriah, Y.; Towbirdidge, I.S.
 Proc. Natl. Acad. Sci. U.S.A. 84, 5360-5363, 1987
 A:Title: B-cell variant of mouse T200 (Ly-5): evidence for alternative mRNA splicing.
 A:Reference number: A28334; MUID:87260986; PMID:255416
 A:Accession: A28334
 A:Molecule type: mRNA
 A:Residues: 1-1291 <THO>
 A:Cross-references: UNIPROT:P06800; UNIPROT:Q61814; UNIPROT:Q61815; UNIPROT:Q61813; GB:M
 R:Sage, Y.; Tung, J.S.; Shen, F.W.; Boyse, E.A.
 Proc. Natl. Acad. Sci. U.S.A. 83, 6940-6944, 1986
 A:Title: Sequences of Ly-5 cDNA: isoform-related diversity of Ly-5 mRNA.
 A:Reference number: A29381; MUID:86313686; PMID:2944116
 A:Accession: A29381
 A:Molecule type: mRNA
 A:Residues: 1-30,170-517, 'NTT', 521-527, 'G', 529-555, 'S', 557-587, 'S', 589-905, 'Q', 907-930, '
 A:Cross-references: GB:M14442; NID:9198914; PIDN:AAA39458.1; PID:9198915
 R:Yi, T.; Cleveland, J.U.; Ihle, J.N.
 Blood 78, 2222-2228, 1991
 A:Title: Identification of novel protein tyrosine phosphatases of hematopoietic cells by
 A:Reference number: A61180; MUID:92032882; PMID:1932742
 A:Accession: A61180
 A:Status: not compared with conceptual translation
 A:Molecule type: mRNA
 A:Residues: 730-838 <YIA>

R:Gomez, L.J.; Walker, I.D.; Sandrin, M.S.; McKenzie, I.F.C.
 Immunogenetics 25, 263-266, 1987
 A:Title: High sequence conservation between rat (T200) and mouse (Ly-5) leukocyte common
 A:Reference number: A60933; MUID:87192931; PMID:3570377
 A:Accession: A60933
 A:Molecule type: protein
 A:Residues: 'R', 289-298, '329', 'V', 331-336, 'Y', 'R', 364-370, 'X', 372-375, 595-608, 638-649, 669-6
 R:Johnson, N.A.; Meyer, C.M.; Pingel, J.T.; Thomas, M.L.
 J. Biol. Chem. 264, 6220-6229, 1989
 A:Title: Sequence conservation in potential regulatory regions of the mouse and human le
 A:Reference number: A33522; MUID:89197920; PMID:2522930
 A:Accession: A33522
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-22 <OCH>
 A:Cross-references: GB:M22456; NID:9198755; PIDN:AA646374.1; PID:9554185; GB:J04640; GB:
 R:Raschke, W.C.
 Proc. Natl. Acad. Sci. U.S.A. 84, 161-165, 1987
 A:Title: Cloned murine T200 (Ly-5) cDNA reveals multiple transcripts within B- and T-lym
 A:Reference number: A29075; MUID:87092355; PMID:2948186
 A:Accession: A29075
 A:Molecule type: mRNA
 A:Residues: 961-1291 <RAS>
 A:Cross-references: GB:M15174; NID:9201105; PIDN:AAA40161.1; PID:9201106
 R:Tung, J.
 Immunogenetics 28, 271-277, 1988
 A:Title: Structural features of Ly-5 glycoproteins of the mouse and counterparts in othe
 A:Reference number: I54450; MUID:88330145; PMID:3417340
 A:Accession: I54450
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 32-73 <RES>
 A:Cross-references: GB:M23241; NID:9340850; PIDN:AAA39460.1; PID:9548174
 R:Sage, Y.; Tung, J.S.; Shen, F.W.; Boyse, E.A.
 Proc. Natl. Acad. Sci. U.S.A. 84, 5364-5368, 1987
 A:Title: Alternative use of 5' exon in the specification of Ly-5 isoforms distinguishing
 A:Reference number: A28335; MUID:87260987; PMID:3037546
 A:Accession: A28335
 A:Molecule type: mRNA
 A:Residues: 1-30,74-226 <SA2>
 A:Cross-references: GB:M14342
 R:Shen, F.W.; Sage, Y.; Littman, G.; Freeman, G.; Tung, J.S.; Cantor, H.; Boyse, E.A.
 Proc. Natl. Acad. Sci. U.S.A. 82, 7360-7363, 1985
 A:Reference number: A23329; MUID:86042655; PMID:3864163
 A:Accession: A23329
 A:Molecule type: mRNA
 A:Residues: 10-30,170-263 <SHB>
 A:Cross-references: GB:M11934; NID:9198919; PIDN:AAA39461.1; PID:9198920
 R:Sage, Y.; Tung, J.
 Mol. Cell. Biol. 8, 4889-4895, 1988
 A:Title: Organization of the Ly-5 gene.
 A:Reference number: I57644; MUID:89096862; PMID:3211131
 A:Accession: I57644
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 'MT', 1-22 <RE2>
 A:Cross-references: GB:M23354; NID:9340890; PIDN:AAA39462.1; PID:9554192
 C:Gene: Ly-5
 C:Superfamily: leukocyte common antigen; leukocyte common antigen cytosolic domain homol
 C:Keywords: alternative splicing; glycoprotein; phosphoprotein; phosphoric monoester hyd
 F:1-23/Domain: signal sequence #status predicted <SIG>
 F:24-1291/Product: protein-tyrosine-phosphatase (B-cell variant) #status predicted <MAT>
 F:24-654/Domain: extracellular #status predicted <EXT>
 F:24-30,170-1291/Product: protein-tyrosine-phosphatase (T-cell variant) #status predicted
 F:565-586/Domain: transmembrane #status predicted <TM>
 F:583-1223/Domain: leukocyte common antigen cytosolic domain homology <LAC>
 F:587-1291/Domain: intracellular #status predicted <INT>
 F:644-888/Domain: protein-tyrosine-phosphatase homology <PTP>
 F:64,150,161,207,211,218,253,258,290,311,322,347,416,427,457,489,520,556/Binding site: c
 F:840/Active site: Cys (phosphocysteine intermediate) #status predicted
 F:846/Binding site: substrate phosphate (Arg) #status predicted

Query Match 26.8%; Score 55.5; DB 1; Length 1291;
Best Local Similarity 40.5%; Pred. No. 78;
Matches 15; Conservative 5; Mismatches 10; Indels 2;
Db 947 QHIGNQ-----EENKKK-NNNSNVVPPYDFRVLK 976

RESULT 8
AD1878
cyanophycin synthetase [imported] - Nostoc sp. (strain PCC 7120)
C:Species: Nostoc sp. strain PCC 7120
A:Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C:Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004
C:Accession: AD1878
R:Kaneaki, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriuchihara, N.; Shimp, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S.
NAkazaki, N.; Shimp, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S.
DNA Rep. 8, 205-213, 2001
A:Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Anabaena PCC 7120
A:Reference number: AB1807; MUID:21595285; PMID:11759840
A:Accession: AD1878
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-636 <KUR>
A:Cross-references: UNIPROT:O8Y2A6; GB:BA000019; PIDD:BA072531.1; PTD:G17129918; GSPDB:G17129918
A:Experimental source: strain PCC 7120
C:Genetics:
A:Gene: cphA

Query Match 26.6%; Score 55; DB 2; Length 636;
Best Local Similarity 45.5%; Pred. No. 40;
Matches 10; Conservative 5; Mismatches 7; Indels 0; Gaps 0;
Db 557 YPBDTLEDCMFGQSNLVLD 578

RESULT 9
T19825
hypochemical protein C38D4.5 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T19825
R:Coles, L.
submitted to the EMBL Data Library, October 1994
A:Reference number: Z19183
A:Accession: T19825
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-837 <WIL>
A:Cross-references: UNIPROT:P46241; EMBL:Z46241; PIDD:CA06318.1; GSPDB:GN00021; CESP:C38D4
A:Experimental source: clone C38D4
C:Genetics:
A:Gene: CESP:C38D4.5
A:Map position: 3
A:Introns: 31/3; 81/2; 137/3; 277/2; 435/3; 507/3; 544/2; 604/1; 646/2; 707/1; 791/3
F:96-133/Domain: WW repeat homology <WWR>

Query Match 26.6%; Score 55; DB 2; Length 837;
Best Local Similarity 40.0%; Pred. No. 55;
Matches 12; Conservative 4; Mismatches 14; Indels 0; Gaps 0;
Db 216 SDSFTDEDEDVXKREGISIASDSDFDEP 245

RESULT 10
T13263
cell division protein dmfl/mld1 [validated] - fission yeast (Schizosaccharomyces pombe)
C:Species: Schizosaccharomyces pombe

CjDate: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 09-Jul-2004
CjAccession: T43263; T50433
R.Schramm, M.; Fankhauser, C.; Brodbeck, C.; Simanis, V.
Genes Dev. 10, 2707-2720, 1996
A>Title: The dmfl gene is essential for correct positioning of the division septum in *E. coli*
A.Reference number: 222376; PMID:8946912
A.Accession: T43263
A>Status: preliminary; translated from GB/EMBL/DBJ
A.Molecule type: mRNA
A.Residues: 1-920 <SO>
A.Cross-references: UNIPROT:P78953; EMBL:X07599; NID:G1707677; PIDN:CAA68873.1; PID:G1707677
A.Experimental source: strain 972h(-)
R.Seeger, K.; Harris, D.; McQuigall, R.C.; Rajandream, M.A.; Barrell, B.G.
Submitted to the EMBL Data Library, November 1999
A.Reference number: 225033
A.Accession: Y50433
A.Status: preliminary
A.Molecule type: DNA
A.Residues: 1-920 <SEE>
A.Cross-references: EMBL:AL132870; PIDN:CAB60689.1; GSPDB:GN00068; SPDB:SPCC4B3.15
A.Experimental source: strain 972h(-); cosmid c4B3
C.Genetics:
A.Gene: dmfl; mdl; SPDB:SPCC4B3.15
A.Map position: 3
C.Superfamily: Schizosaccharomyces pombe cell division protein dmfl/mdl

Query Match 26.6%; Score 55; DB 2; Length 920;
Best Local Similarity 39.3%; Pred. No. 61;
Matches 11; Conservative 3; Mismatches 14; Indels 0; Gaps 0;

OY 7 SPPEDTEDEKPKYEGSGNIVDIDFDSVP 34
||| ||| | : |||
Db 250 SLPKDTEDNPALKERVETTASLDMDYKP 277

RESULT 11
S33850
fibronectin-binding protein - Streptococcus dysgalactiae
C.Species: Streptococcus dysgalactiae
C.Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Jul-2004
CjAccession: S33850; S32632
R.Lindgren, P.E.; McGavin, M.J.; Signaes, C.; Guse, B.; Gurusiddappa, S.; Hoeoek, M.; Lir
Eur. J. Biochem. 214, 819-827, 1993
A>Title: Two different genes coding for fibronectin-binding proteins from Streptococcus c
A.Reference number: S33850; PMID:8319691
A.Accession: S33850
A.Status: preliminary
A.Molecule type: DNA
A.Residues: 1-1091 <LIN>
A.Cross-references: UNIPROT:O06556; EMBL:Z22150; NID:G288966; PIDN:CAA80121.1; PID:G288966

Query Match 26.6%; Score 55; DB 2; Length 1091;
Best Local Similarity 34.2%; Pred. No. 75;
Matches 13; Conservative 7; Mismatches 16; Indels 2; Gaps 1;

OY 3 SGNSGFPEDEKPKRYEG--GNIVDIDFDSVPPIHG 38
||||| : : : : :
Db 843 SGNRTVEDTQTSQEDIVLGPGQVIDFDPSQFGMSG 880

RESULT 12
IUTUCE
cadherin 1 precursor [validated] - human
N.Alternate names: ARC-1; cell CAM 120/80; E-cadherin; epithelial cadherin; L-CAM; uvomor
C.Species: Homo sapiens (man)
C.Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 09-Jul-2004
CjAccession: S37654; S31430; S05475; S31460; S06716; A51711; JC2230; I52294; I52704; S251
C.Bussemakers, M.J.G.; van Bokhoven, A.; Mees, S.G.M.; Kemler, R.; Schnalken, J.A.
Mol. Biol. Rep. 17, 123-128, 1993
A>Title: Molecular cloning and characterization of the human E-cadherin cDNA.
A.Reference number: S37654; PMID:93211394; PMID:8459805
A.Accession: S37654
A.Molecule type: mRNA

A:Residues: 1-882 <BUS>
A:Cross-references: UNIPROT:P12830; EMBL:Z13009; NID:G31072; PIDN:CAA78353.1; PID:G31073
R:Keller, W.; Warda, A.; Oda, T.; Hirohashi, S.; Kemler, R.; Birchmeier, W.
Submitted to the EMBL Data Library, December 1992
A:Description: Sequence of human E-cadherin cDNA.
A:Reference number: S31430
A:Accession: S31430
A:Molecule type: mRNA
A:Residues: 1-542, 'F', 544-882 <REL>
A:Cross-references: EMBL:Z18923; NID:G31074; PIDN:CAA79356.1; PID:G31075
R:Mansouri, A.; Spurr, N.; Goodfellow, P.N.; Kemler, R.
Differentiation 38, 67-71, 1988
A:Title: Characterization and chromosomal localization of the gene encoding the human ce
A:Reference number: S05475; MUID:89031725; PMID:3263290
A:Accession: S05475
A:Molecule type: mRNA
A:Residues: 157-311 <MAN>
A:Cross-references: EMBL:X12790
A:Note: nucleotide sequence is not complete
R:Fixen, U.H.
submitted to the EMBL Data Library, March 1990
A:Reference number: S31460
A:Accession: S31460
A:Molecule type: mRNA
A:Residues: 265-392 <FRI>
A:Cross-references: EMBL:X52279; NID:G28821; PIDN:CAA36522.1; PID:G28822
R:Wheeler, M.J.; Buck, C.A.; Bechtol, K.B.; Dameky, C.H.
J. Cell. Biochem. 34, 187-202, 1987
A:Title: Soluble 80-kd fragment of cell-CAM 120/80 disrupts cell-cell adhesion.
A:Reference number: S06716; MUID:87280410; PMID:3611200
A:Accession: S06716
A:Molecule type: protein
A:Residues: 'XQ', 157-162, 'V', 164-179 <WHB>
R:Berr, G.; Staes, K.; van Hengel, J.; Mollema, F.; Busssemakers, M.J.G.; van Bokhoven,
Genomics 26, 281-289, 1995
A:Title: Cloning and characterization of the human invasion suppressor gene E-cadherin
A:Reference number: A57171; MUID:95324920; PMID:7601454
A:Accession: A57171
A:Status: nucleic acid sequence not shown; not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 1-30, 32-882 <BBR>
A:Cross-references: GB:L34784
R:Rimm, D.L.; Morrow, J.S.
Biochem. Biophys. Res. Commun. 200, 1754-1761, 1994
A:Title: Molecular cloning of human E-cadherin suggests a novel subdivision of the cadhe
A:Reference number: J02230; MUID:94242050; PMID:8185635
A:Accession: J02230
A:Molecule type: mRNA
A:Residues: 1-9, 'G', 11-15, 'RSPFGSQERSPPCLTRELHVGAAPPEKRR', 52-67, 'I', 69, 'LTPIP', 76-94
A:Cross-references: GB:L08599; NID:G340184; PIDN:AA61259.1; PID:G340185
A:Note: the majority of differences between this and other reports represent apparent fir
A:Note: the authors translated the codon CCG for residue 868 as Arg
R:Busssemakers, M.J.G.; Girdlaid, L.A.; van Bokhoven, A.; Schalken, J.A.
Biochem. Biophys. Res. Commun. 203, 1284-1290, 1994
A:Title: Transcriptional regulation of the human E-cadherin gene in human prostate cance
A:Reference number: I52294; MUID:94380041; PMID:8093045
A:Accession: I52294
A:Status: translation not shown; translated from GB/EMBL/DBDJ
A:Molecule type: DNA
A:Residues: 1-16 <RES>
A:Cross-references: GB:L34545; NID:G509604; PIDN:AA21764.1; PID:G509605
R:Becker, K.F.; Atkinson, M.U.; Reich, U.; Becker, I.; Nekarda, H.; Stewert, J.R.; Hofle
Cancer Res. 54, 3845-3852, 1994
A:Title: E-cadherin gene mutations provide clues to diffuse type gastric carcinomas.
A:Reference number: I52704; MUID:94306394; PMID:8033105
A:Accession: I52704
A:Status: translated from GB/EMBL/DBDJ
A:Molecule type: DNA
A:Residues: 337-476 <RE2>
A:Cross-references: GB:S72492; NID:G632756; PIDN:AA14108.1; PID:G4261808
C:Comment: Cadherins mediate calcium-dependent intercellular adhesion and are thought to
C:Genetics:
A:Gene: GDB:CDH1, VVO

A:Cross-references: GDB:120484; OMIM:192090
A:Map position: 16q22.1-16q22.1
A:Introns: 379/3; 440/3
C:Superfamily: cadherin; cadherin repeat homology
C:Keywords: calcium binding; cell adhesion; duplication; glycoprotein; transmembrane prot
F:1-27/Domain: signal sequence #status predicted <SIG>
F:128-154/Domain: propeptide #status predicted <PRO>
F:155-882/Product: E-cadherin #status experimental <MAT>
F:155-697/Domain: extracellular #status predicted <EXT>
F:157-262/Domain: cadherin repeat homology <CR1>
F:232-237/Region: cadherin binding #status predicted
F:265-375/Domain: cadherin repeat homology <CR2>
F:378-486/Domain: cadherin repeat homology <CR3>
F:487-595/Domain: cadherin repeat homology <CR4>
F:596-700/Domain: cadherin repeat homology <CR5>
F:698-731/Domain: transmembrane #status predicted <TM>
F:732-882/Domain: intracellular #status predicted <INT>
F:840-853/Region: serine-rich
F:376,558,570,622,637,849/Binding site: carbohydrate (asn) (covalent) #status predicted

Query Match 25.8% Score 53.5; DB 1; Length 882;
Best Local Similarity 45.2% Pred. No. 92;
Matches 14; Conservative 3; Mismatches 11; Indels 3; Gaps 2;

QY 9 PEDTEEDKPKY--EGCGNIVDIDPDSVPOIH 37
DB 744 PEDTRDNYVYDDEGGGGEEDDFD-LSQLH 773

RESULT 13
H75048
DNA-directed RNA polymerase (EC 2.7.7.6) chain M PAB1464 - Pyrococcus abyssi (strain Ors
C:Species: Pyrococcus abyssi
C:Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004
A:Accession: H75048
R:anonymous, Genoscope
submitted to the EMBL Data Library, July 1999
A:Description: Pyrococcus abyssi genome sequence: insights into archaeal chromosome struc
A:Reference number: A75001
A:Accession: H75048
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-110 <KAN>
A:Cross-references: UNIPROT:Q9UYX7; GB:A2748287; GB:AL096836; NID:G5458657; PIDN:CAB5028;
A:Experimental source: strain Orsay
C:Genetics:
A:Gene: PAB1464
C:Superfamily: DNA-directed RNA polymerase, subunit C11/M/9
C:Keywords: nucleic acid transferase

Query Match 25.6% Score 53; DB 2; Length 110;
Best Local Similarity 40.6% Pred. No. 9.4;
Matches 13; Conservative 6; Mismatches 7; Indels 6; Gaps 1;

QY 9 PED-----TEEDKRYEQGGINVIDPDSVP 34
DB 34 PEDAKAYKTEVEKPKPDEGIVVEODPSTLP 65

RESULT 14
A45508
heat shock protein 83 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 14-May-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
A:Accession: A45508
R:Commer, T.W.; Lafayette, P.R.; Nagao, R.T.; Key, J.L.
Plant Physiol. 94, 1689-1695, 1990
A:Title: Sequence and expression of a HSP83 from Arabidopsis thaliana.
A:Reference number: A45508
A:Accession: A45508
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-705 <CON>

A/Cross-references: UNIPROT:P27323; GB:M62984; NID:G166769; PIDN:AAA32822.1; PID:G166770
 A/Note: the authors translated the codon AAA for residue 249 as Cys, and GGT for residue
 C/Superfamily: heat shock protein 90

Query Match 25.6%; Score 53; DB 2; Length 705;
 Best Local Similarity 27.6%; Pred. No. 82;
 Matches 8; Conservative 9; Mismatches 12; Indels 0; Gaps 0;

OY 1 QNSGNQSPPEPTEDDKRYEGGNIVDD 29
 Db 216 EKTTEKISDDEDEPKENEGVEEVD 244

RESULT 15

S25327

cytoskeleton assembly control protein SLA1 - yeast (Saccharomyces cerevisiae)

N/Alternate names: protein YBL007C; protein YBL0321

C/Species: Saccharomyces cerevisiae

C/Date: 23-Apr-1993 #sequence revision 23-Apr-1993 #text_change 09-Jul-2004

C/Accession: S25327; A40673; S45740; S36355; S42277

R/Delaaveau, T.; Jacq, C.; Perea, J.

Yeast 8; 761-768, 1992

A/Title: Sequence of a 12.7 kb segment of yeast chromosome II identifies a PDR-like gene

A/Reference number: S25326; MUID:93070613; PMID:1441753

A/Accession: S25327

A/Molecule type: DNA

A/Residues: 1-1244 <DE1>

A/Cross-references: UNIPROT:P32790; EMBL:S47695; NID:G259049; PIDN:AA823985.1; PID:G2590

R/Holtzman, D.A.; Yang, S.; Drubin, D.G.

J. Cell Biol. 122, 635-644, 1993

A/Title: Synthetic-lethal interactions identify two novel genes, SLA1 and SLA2, that con

A/Reference number: A40673; MUID:93328765; PMID:8335689

A/Accession: A40673

A/Molecule type: DNA

A/Residues: 1-1244 <HOL>

A/Cross-references: GB:Z22810; NID:G311410; PIDN:CAA80463.1; PID:G311411

R/Delaaveau, T.; Jacq, C.; Perea, J.

submitted to the Protein Sequence Database, August 1994

A/Reference number: S45736

A/Accession: S45740

A/Molecule type: DNA

A/Residues: 1-1244 <DE2>

A/Cross-references: EMBL:Z35768; NID:G535989; PIDN:CAA84826.1; PID:G535990; MIPS:YBL007C

C/Comment: This protein is involved in formation of cortical cytoskeleton.

C/Genetics:

A/Gene: SGD:SLA1

A/Cross-references: SGD:S0000103; MIPS:YBL007C

A/Map position: 2L

C/Keywords: cytoskeleton

F/10-65/Domain: SH3 homology <SH31>

F/76-127/Domain: SH3 homology <SH32>

F/360-410/Domain: SH3 homology <SH33>

Query Match 25.6%; Score 53; DB 2; Length 1244;

Best Local Similarity 26.3%; Pred. No. 1.6e+02;

Matches 10; Conservative 10; Mismatches 18; Indels 0; Gaps 0;

OY 1 QNSGNQSPPEPTEDDKRYEGGNIVDDPSVPOIHG 38
 Db 1029 QNTGSAMMPQTSFNAVPQITGAMMPQTSFNAVPQVGTG 1066

Search completed: October 22, 2005, 04:14:11
 Job time : 20.0841 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 22, 2005, 02:23:35 ; Search time 93.0664 Seconds
(without alignments)
209.087 Million cell updates/sec

Title: US-10-731-238-36

Perfect score: 207

Sequence: 1 ONSGNQSFEDTEEDKPKYEGGNGNIVDIDFDSVPQIHG 38

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : UniProt_03:*

1: uniprot_sprot:*

2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	199	96.1	940	2	Q53682 staphylococ
2	199	96.1	943	2	Q8NUU8 staphylococ
3	199	96.1	957	2	Q6G6H4 staphylococ
4	199	96.1	961	2	Q99RD3 staphylococ
5	199	96.1	961	2	Q7A3J8 staphylococ
6	199	96.1	1018	1	FNBA_STPAU
7	199	96.1	1038	2	Q99RD2 staphylococ
8	199	96.1	1038	2	Q7A3J7 staphylococ
9	198	95.7	965	2	Q6GDU5 staphylococ
10	191	92.3	1015	2	Q8NUU7 staphylococ
11	191	92.3	1015	2	Q6G6H3 staphylococ
12	188	90.8	152	2	Q9AEP9 staphylococ
13	62	30.0	735	2	Q948C1 Oryza sativ
14	62	30.0	735	2	Q7XGX6 Oryza sativ
15	61	29.5	981	2	Q91LJ7 white spot
16	60	29.0	260	2	Q6FYK3 candida gla
17	59	28.5	889	2	Q6CBW0 yarrowia j1
18	58.5	28.3	347	2	Q8CEZ8 staphylococ
19	58.5	28.3	999	2	Q8K5Z5 streptococ
20	58	28.0	237	2	Q8BZM9 mus musculu
21	58	28.0	455	2	Q6Z097 mus musculu
22	58	28.0	532	2	Q9D074 m mus muscu
23	58	28.0	937	2	Q6BM10 debaryomyce
24	57	27.5	467	2	Q8H8X6 Oryza sativ
25	57	27.5	533	2	Q94677 Plasmodium
26	57	27.5	572	2	Q9GSR0 plasmodium
27	57	27.5	698	2	Q71BE1 hevea brasl
28	57	27.5	703	1	HS83_IPONI
29	57	27.5	745	2	Q7SA69 neurospora
30	57	27.5	826	2	Q6CM29 kluyveromyc
31	57	27.5	1335	2	Q7NCX8 gloeobacter

32	57	27.5	1460	1	PMPC_CHLMU	Q9PJY1 chlamydia m
33	56.5	27.3	904	2	Q54374	Q54324 sulfolobus
34	56.5	27.3	975	2	Q8NZT8	Q8NZ18 streptococ
35	56	27.1	457	2	Q9GDV3	Q9GDV3 carboxotus
36	56	27.1	490	2	Q96BN8	Q96BN8 plasmodium
37	56	27.1	648	2	Q6MUJ2	Q6MUJ2 mycoplasma
38	56	27.1	674	2	Q9F1P1	Q9F1P1 arabidopsis
39	55.5	26.8	379	2	Q8VWH9	Q8VWH9 hordeum vul
40	55.5	26.8	878	2	Q8CE77	Q8CE77 mus musculu
41	55.5	26.8	962	2	Q6LDZ3	Q6LDZ3 rattus norv
42	55.5	26.8	1255	1	CD45_RAT	CD45 ratu
43	55.5	26.8	1291	2	Q61812	Q61812 mus musculu
44	55.5	26.8	1343	2	Q64730	Q64730 mus musculu
45	55	26.6	546	2	Q8G621	Q8G621 bifidobacte

ALIGNMENTS

RESULT 1

ID	Q53682	PRELIMINARY;	PRT;	940 AA.
AC	Q53682;			
DT	01-NOV-1996 (TREMBLrel. 01, Created)			
DT	01-NOV-1996 (TREMBLrel. 01, Last sequence update)			
DT	01-MAR-2004 (TREMBLrel. 26, Last annotation update)			
DE	Fibronectin binding protein B.			
GN	Name=fnbB;			
OS	Staphylococcus aureus.			
OC	Bacteria; Firmicutes; Bacillales; Staphylococcus.			
OX	NCBI_TaxId=1280;			
RN	(1)			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=8325-4;			
RX	MEDLINE=92111475; PubMed=1837266;			
RA	Johnson K., Signas C., Muller H.P., Lindberg M.,			
RT	"Two different genes encode fibronectin binding proteins in			
RT	Staphylococcus aureus. The complete nucleotide sequence and			
RT	characterization of the second gene."			
RL	Eur. J. Biochem. 202:1041-1048(1991).			
CC	-1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by			
CC	an amide bond (By similarity).			
DR	EMBL: X62992; CAA44726.1; -			
DR	PIR: S19702; S19702.			
DR	HSSP: Q53653; INET.			
DR	GO: GO:0009986; C:cell surface; IEA.			
DR	GO: GO:0005618; C:cell wall; IEA.			
DR	GO: GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.			
DR	GO: GO:0016020; C:membrane; IEA.			
DR	GO: GO:0007155; P:cell adhesion; IEA.			
DR	InterPro: IPR008966; Adhes_Bact.			
DR	InterPro: IPR005877; Gpos_YSTRK.			
DR	InterPro: IPR001899; Gram_pos_anchor.			
DR	Pfam: PF02986; Fn_bind; 2.			
DR	Pfam: PF00746; Gram_pos_anchor; 1.			
DR	Pfam: PF04650; YSTRK_signal; 1.			
DR	TIGRFAM: TIGR01167; LpxTG_anchor; 1.			
DR	TIGRFAM: TIGR01168; YSTRK_signal; 1.			
DR	PROSITE: PS50847; GRAM_POS_ANCHORING; 1.			
KW	Cell wall; Peptidoglycan-anchor.			
SQ	SEQUENCE 940 AA; 10355 MW; E35FBBCA907AE345 CRC64;			

Query Match 96.1%; Score 199; DB 2; Length 940;
Best local similarity 97.4%; Pred. No. 6.1e-16;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 ONSGNQSFEDTEEDKPKYEGGNGNIVDIDFDSVPQIHG 38
DB 682 ONSGNQSFEDTEEDKPKYEGGNGNIVDIDFDSVPQIHG 719

RESULT 2


```

Q8NU8      ID Q8NU8      PRELIMINARY;      PRT;      943 AA.
AC Q8NU8;
DT 01-OCT-2002 (TReMBLrel. 22, Created)
DT 01-OCT-2002 (TReMBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE FmbB protein.
GN Name=fmbB; OrderedLocuNames=MM2420;
OS Staphylococcus aureus (strain MM2).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=196620;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MM2;
RX MEDLINE=22040711; PubMed=12044378; DOI=10.1016/S0140-6736(02)08713-5;
RA Baba T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Oguchi A.,
RA Nagai Y., Iwama N., Asano K., Naito T., Kuroda H., Cui L.,
RA Yamamoto K., Hiramatsu K.;
RT "Genome and virulence determinants of high virulence community-
RT acquired MRSA.";
RL Lancer 359:1819-1827 (2002).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC an amide bond (By similarity).
DR HSSP; Q53653; 1N67.
DR GO; GO:0009986; C:cell surface; IEA.
DR GO; GO:0005618; C:cell wall; IEA.
DR GO; GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0007155; P:cell adhesion; IEA.
DR InterPro; IPR008966; Adhes_bact.
DR InterPro; IPR004237; Fm_bind.
DR InterPro; IPR005877; Gpos_YsIRK.
DR InterPro; IPR001899; Gram_pos_anchor.
DR Pfam; PF02986; Fm_bind; 1.
DR Pfam; PF00746; Gram_pos_anchor; 1.
DR Pfam; PF04650; YsIRK_signal; 1.
DR TIGRFAMs; TIGR01167; LPXTG_anchor; 1.
DR TIGRFAMs; TIGR01168; YsIRK_signal; 1.
DR PROSITE; PS50847; GRAM_POS_ANCHORING; 1.
DR Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ SEQUENCE 943 AA; 104537 MW; DA8A5F31947E186A CRC64;

Query Match 96.1%; Score 199; DB 2; Length 943;
Best Local Similarity 97.4%; Pred. No. 6.2e-16;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QNSGNSGFPEDEBDEKPKRYEGQGNIVDIDFDSVPQIHG 38
Db 689 QNSGNSGFPEDEBDEKPKRYEGQGNIVDIDFDSVPQIHG 726

RESULT 3
Q6G6H4 ID Q6G6H4 PRELIMINARY; PRT; 957 AA.
AC Q6G6H4;
DT 05-JUL-2004 (TReMBLrel. 27, Created)
DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TReMBLrel. 27, Last annotation update)
DE Fibronectin-binding protein.
GN Name=fmbB; OrderedLocuNames=SA52387;
OS Staphylococcus aureus (strain MSSA476).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=282459;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=1521324; DOI=10.1073/pnae.0402521101;
RA Holden M.T.G., Feil E.J., Lindsay J.A., Peacock S.J., Day N.P.J.,
RA Enright M.C., Foster T.J., Moore C.E., Hurst L., Atkin R., Barron A.,
RA Bason N., Bentley S.D., Chillingworth C., Chillingworth T.,
RA Churcher C., Clark L., Cotton C., Cronin A., Doggett J., Dowd L.,
RA Feltwell T., Hance Z., Harris B., Hauser H., Holtroyd S., Jagsels K.,
RA James K.D., Lennard N., Lane A., Mayes R., Moule S., Mungall K.,

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RA Ormond D., Quail M.A., Rabbintowisch E., Rutherford K.M., Sanders M.,
RA Sharp S., Simmonds M., Stevens K., Whitehead S., Barrell B.G.,
RA Spratt B.G., Parkhill J.;
RT "Complete genomes of two clinical Staphylococcus aureus strains:
RT evidence for the rapid evolution of virulence and drug resistance.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:9786-9791 (2004).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC an amide bond (By similarity).
DR EMBL; BX571857; CAG44201.1; -.
DR GO; GO:0009986; C:cell surface; IEA.
DR GO; GO:0005618; C:cell wall; IEA.
DR GO; GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0007155; P:cell adhesion; IEA.
DR InterPro; IPR008966; Adhes_bact.
DR InterPro; IPR004237; Fm_bind.
DR InterPro; IPR005877; Gpos_YsIRK.
DR InterPro; IPR001899; Gram_pos_anchor.
DR Pfam; PF02986; Fm_bind; 1.
DR Pfam; PF00746; Gram_pos_anchor; 1.
DR TIGRFAMs; TIGR01167; LPXTG_anchor; 1.
DR TIGRFAMs; TIGR01168; YsIRK_signal; 1.
DR PROSITE; PS50847; GRAM_POS_ANCHORING; 1.
DR Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ SEQUENCE 957 AA; 105980 MW; 28F8BA7FFDFD3EAF CRC64;

Query Match 96.1%; Score 199; DB 2; Length 957;
Best Local Similarity 97.4%; Pred. No. 6.3e-16;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QNSGNSGFPEDEBDEKPKRYEGQGNIVDIDFDSVPQIHG 38
Db 689 QNSGNSGFPEDEBDEKPKRYEGQGNIVDIDFDSVPQIHG 726

RESULT 4
Q09RD3 ID Q09RD3 PRELIMINARY; PRT; 961 AA.
AC Q09RD3;
DT 01-JUN-2001 (TReMBLrel. 17, Created)
DT 01-JUN-2001 (TReMBLrel. 17, Last sequence update)
DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)
DE Fibronectin-binding protein homolog.
GN Name=fmbB; OrderedLocuNames=SAV2502;
OS Staphylococcus aureus (strain Mu50 / ATCC 700699).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=158878;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Mu50 / ATCC 700699;
RX MEDLINE=21311952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2;
RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Iian J.-O., Ito T.,
RA Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hoshoyama A.,
RA Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Katto C.,
RA Sekimizu K., Hiramatsu H., Kuhara S., Goto S., Yabuuchi J.,
RA Kanehisa M., Yamauchi A., Oshima K., Furuya K., Yoshino C., Shiba T.,
RA Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
RT "Whole genome sequencing of methicillin-resistant Staphylococcus
RT aureus.";
RL Lancer 357:1225-1240 (2001).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC an amide bond (By similarity).
DR EMBL; AP003365; BAB58664.1; -.
DR PIR; G90053; G90053.
DR HSSP; Q53653; 1N67.
DR GO; GO:0009986; C:cell surface; IEA.
DR GO; GO:0005618; C:cell wall; IEA.
DR GO; GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0007155; P:cell adhesion; IEA.
DR InterPro; IPR008966; Adhes_bact.

```

DR InterPro: IPR004237; Fn_bind.
 DR InterPro: IPR005877; Gpos_YsIRK.
 DR InterPro: IPR001899; Gram_pos_anchor.
 DR Pfam: PF02986; Fn_bind_1.
 DR Pfam: PF00746; Gram_pos_anchor; 1.
 DR Pfam: PF04650; YsIRK_signal; 1.
 DR TIGRFAMs: TIGR01167; LPXTG_anchor; 1.
 DR TIGRFAMs: TIGR01168; YsIRK_signal; 1.
 DR PROSITE: PS50847; GRAM_POS_ANCHORING; 1.
 DR Cell wall; Complete proteome; Peptidoglycan-anchor.
 KM SEQUENCE 961 AA; 106010 MW; 364940F884EA4101 CRC64;
 SQ

Query Match 96.1%; Score 199; DB 2; Length 961;
 Best Local Similarity 97.4%; Pred. No. 6.3e-16;
 Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QNSGNQSPEDTEBDKPKYEGGNIVDIDFDSVPQIHG 38
 Db 693 QNSGNQSPEDTEBDKPKYEGGNIVDIDFDSVPQIHG 730

RESULT 5
 ID Q7A3J8 PRELIMINARY; PRT; 961 AA.
 AC Q7A3J8;
 DT 05-JUL-2004 (TREMblrel. 27, Created)
 DT 05-JUL-2004 (TREMblrel. 27, Last sequence update)
 DT 05-JUL-2004 (TREMblrel. 27, Last annotation update)
 DE FndB protein.
 OS Name=fndB; OrderedLocustNames=SA2290;
 OS Staphylococcus aureus (strain N315).
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 NCBI_TaxID=158879;

RA SEQUENCE FROM N.A.
 RP MEDLINE=21311952; Pubmed=11418146; DOI=10.1016/S0140-6736(00)04403-2;
 RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
 RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Itoh T., Ito T.,
 RA Marumori M., Matsumaru H., Murakami A., Hosoyama A.,
 RA Mutantani Y., Takahashi N.K., Sawano T., Inoue R.-I., Kato C.,
 RA Sekimizu K., Hirakawa H., Kohara S., Goto S., Yabuzaki J.,
 RA Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
 RA Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
 RT "Whole genome sequencing of methicillin-resistant Staphylococcus
 aureus".
 RL Lancet 357:1225-1240(2001).
 CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
 an amide bond (By similarity).
 CC EMBL: AP003137; BAB43593.1; -.
 DR GO: GO:0009986; C:cell surface; IEA.
 DR GO: GO:0005618; C:cell wall; IEA.
 DR GO: GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
 DR GO: GO:0016020; C:membrane; IEA.
 DR GO: GO:0007155; P:cell adhesion; IEA.
 DR InterPro: IPR008966; Adhes_bact.
 DR InterPro: IPR004237; Fn_bind.
 DR InterPro: IPR005877; Gpos_YsIRK.
 DR InterPro: IPR001899; Gram_pos_anchor.
 DR Pfam: PF02986; Fn_bind_1.
 DR Pfam: PF00746; Gram_pos_anchor; 1.
 DR Pfam: PF04650; YsIRK_signal; 1.
 DR TIGRFAMs: TIGR01167; LPXTG_anchor; 1.
 DR TIGRFAMs: TIGR01168; YsIRK_signal; 1.
 DR PROSITE: PS50847; GRAM_POS_ANCHORING; 1.
 DR Cell wall; Complete proteome; Peptidoglycan-anchor.
 KM SEQUENCE 961 AA; 106010 MW; 364940F884EA4101 CRC64;
 SQ

Query Match 96.1%; Score 199; DB 2; Length 961;
 Best Local Similarity 97.4%; Pred. No. 6.3e-16;
 Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 1 QNSGNQSPEDTEBDKPKYEGGNIVDIDFDSVPQIHG 38
 |||||

Db 693 QNSGNQSPEDTEBDKPKYEGGNIVDIDFDSVPQIHG 730

RESULT 6
 FNBA_STAAU STANDARD; PRT; 1018 AA.
 ID FNBA_STAAU
 AC P14738;
 DT 01-APR-1990 (Rel. 14, Created)
 DT 01-APR-1990 (Rel. 14, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Fibronectin-binding protein precursor (FNBP).
 GN Name=fndB;
 OS Staphylococcus aureus.
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 NCBI_TaxID=1280;
 RN [1]

RP SEQUENCE FROM N.A.
 RC STRAIN=NCCTC 8325-4;
 RX MEDLINE=89098998; Pubmed=2521391;
 RA Signaes C., Raucel G., Joensson K., Lindgren P.-E.,
 RA Anantharamiah G.M., Hocek M., Lindberg M.;
 RT "Nucleotide sequence of the gene for a fibronectin-binding protein
 from Staphylococcus aureus: use of this peptide sequence in the
 synthesis of biologically active peptides";
 RT Proc. Natl. Acad. Sci. U.S.A. 86:699-703(1989).
 RL
 CC -1- FUNCTION: The ability of bacteria to bind fibronectin has been
 proposed as a virulence factor enabling bacteria to colonize wound
 tissues and blood clots. Binding of plasma fibronectin to the
 bacterial surface might block adhesion receptors on S.aureus, thus
 representing an important defense mechanism against tissue
 invasion.
 CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
 an amide bond (potential).
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 between the Swiss Institute of Bioinformatics and the EMBL outstation -
 the European Bioinformatics Institute. There are no restrictions on its
 use by non-profit institutions as long as its content is in no way
 modified and this statement is not removed. Usage by and for commercial
 entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 or send an email to license@isb-sib.ch).

CC EMBL: J04151; AAA26632.1; -.
 DR InterPro: IPR004237; Fn_bind.
 DR InterPro: IPR005877; Gpos_YsIRK.
 DR InterPro: IPR001899; Gram_pos_anchor.
 DR Pfam: PF02986; Fn_bind_1.
 DR Pfam: PF00746; Gram_pos_anchor; 1.
 DR Pfam: PF04650; YsIRK_signal; 1.
 DR TIGRFAMs: TIGR01167; LPXTG_anchor; 1.
 DR TIGRFAMs: TIGR01168; YsIRK_signal; 1.
 DR PROSITE: PS50847; GRAM_POS_ANCHORING; 1.
 KM Cell adhesion; Cell wall; Peptidoglycan-anchor; Repeat; Signal;
 VK
 FT SIGNAL 1 36
 FT CHAIN 37 985
 FT PROPEP 986 1018
 FT REPEAT 545 574
 FT REPEAT 575 604
 FT DOMAIN 745 878
 FT REPEAT 745 782
 FT REPEAT 783 820
 FT REPEAT 821 859
 FT REPEAT 860 878
 FT DOMAIN 879 948
 FT REPEAT 879 892
 FT REPEAT 893 906
 FT REPEAT 907 920
 FT REPEAT 921 934
 FT REPEAT 935 948
 FT SITE 982 986
 FT MOD_RES 985 985

1 Fibronectin-binding protein.
 2 Removed by sortase (potential).
 3 B-1.
 4 B-2.
 5 4 X approximate tandem repeats,
 6 fibronectin-binding domain.
 7 D-1.
 8 D-2.
 9 D-3.
 10 D-4 (incomplete).
 11 5 X tandem repeats, Pro-rich (WR).
 12 WR 1.
 13 WR 2.
 14 WR 3.
 15 WR 4.
 16 WR 5.
 17 LPXTG sorting signal (potential).
 18 Pentaglycyl muerein peptidoglycan amidated

```
FT      threonine (Potential).
SQ      SEQUENCE      1018 AA; 111780 MW; 58175EB020EB81F CRC64;
Query Match      96.1%; Score 199; DB 1; Length 1018;
Best Local Similarity 97.4%; Pred. No. 6.7e-16;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY      1 QNSGNQSFPEDETEDEKPKYEGGNIYVIDPDSVPQIHG 38
DB      746 QNSGNQSFPEDETEDEKPKYEGGNIYVIDPDSVPQIHG 783

RESULT 7
ID      Q99RD2      PRELIMINARY;      PRT; 1038 AA.
AC      Q99RD2;
DT      01-JUN-2001 (TrEMBLrel. 17, Created)
DT      01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT      01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE      Fibronectin-binding protein homolog.
GN      Name=fnb; OrderedLocustNames=SAV2503;
OS      Staphylococcus aureus (strain Mu50 / ATCC 700699).
OC      Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX      NCBI_TaxId=158878;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN=Mu50 / ATCC 700699;
RX      MEDLINE=21311952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2;
RA      Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
RA      Cui L., Oguchi A., Aoki K.-I., Nagai Y., Iian J.-O., Ito T.,
RA      Kanamori M., Matsunaru H., Maruyama A., Murakami H., Hoshoyama A.,
RA      Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
RA      Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
RA      Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
RA      Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
RT      "Whole genome sequencing of methicillin-resistant Staphylococcus
RT      aureus.";
RL      Lancet 357:1225-1240(2001).
CC      -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC      an amide bond (By similarity).
DR      EMBL; AP003365; BAB58665.1; -.
DR      PIR; H90053; H90053.
DR      GO; GO:0009986; C:cell surface; IEA.
DR      GO; GO:0005618; C:cell wall; IEA.
DR      GO; GO:0009275; C:cell wall (senu Gram-positive Bacteria); IEA.
DR      GO; GO:0016020; C:membrane; IEA.
DR      GO; GO:0007155; P:cell adhesion; IEA.
DR      InterPro; IPR008966; Adhes_bact.
DR      InterPro; IPR004237; Fn_bind.
DR      InterPro; IPR005877; Gpos_YsIRK.
DR      InterPro; IPR001899; Gram_pos_anchor.
DR      Pfam; PF02986; Fn_bind_1.
DR      Pfam; PF00746; Gram_pos_anchor; 1.
DR      Pfam; PF04650; YsIRK_signal; 1.
DR      TIGRFAMs; TIGR01167; LPXTG_anchor; 1.
DR      TIGRFAMs; TIGR01168; YsIRK_signal; 1.
DR      PROSITE; PS50847; GRAM_POS_ANCHORING; 1.
KW      Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ      SEQUENCE      1038 AA; 113618 MW; 666BF6BF2BFBB12 CRC64;

Query Match      96.1%; Score 199; DB 2; Length 1038;
Best Local Similarity 97.4%; Pred. No. 6.9e-16;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY      1 QNSGNQSFPEDETEDEKPKYEGGNIYVIDPDSVPQIHG 38
DB      742 QNSGNQSFPEDETEDEKPKYEGGNIYVIDPDSVPQIHG 779

RESULT 8
ID      Q7A3J7      PRELIMINARY;      PRT; 1038 AA.
AC      Q7A3J7;
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DT      05-JUL-2004 (TrEMBLrel. 27, Created)
DT      05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT      05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE      Fnd protein.
GN      Name=fnb; OrderedLocustNames=SA2291;
OS      Staphylococcus aureus (strain N315).
OC      Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX      NCBI_TaxId=158879;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      MEDLINE=21311952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2;
RX      Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
RA      Cui L., Oguchi A., Aoki K.-I., Nagai Y., Iian J.-O., Ito T.,
RA      Kanamori M., Matsunaru H., Maruyama A., Murakami H., Hoshoyama A.,
RA      Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
RA      Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
RA      Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
RA      Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
RT      "Whole genome sequencing of methicillin-resistant Staphylococcus
RT      aureus.";
RL      Lancet 357:1225-1240(2001).
CC      -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC      an amide bond (By similarity).
DR      EMBL; AP003337; BAB43594.1; -.
DR      GO; GO:0009986; C:cell surface; IEA.
DR      GO; GO:0005618; C:cell wall; IEA.
DR      GO; GO:0009275; C:cell wall (senu Gram-positive Bacteria); IEA.
DR      GO; GO:0016020; C:membrane; IEA.
DR      GO; GO:0007155; P:cell adhesion; IEA.
DR      InterPro; IPR008966; Adhes_bact.
DR      InterPro; IPR004237; Fn_bind.
DR      InterPro; IPR005877; Gpos_YsIRK.
DR      InterPro; IPR001899; Gram_pos_anchor.
DR      Pfam; PF02986; Fn_bind_1.
DR      Pfam; PF00746; Gram_pos_anchor; 1.
DR      Pfam; PF04650; YsIRK_signal; 1.
DR      TIGRFAMs; TIGR01167; LPXTG_anchor; 1.
DR      TIGRFAMs; TIGR01168; YsIRK_signal; 1.
DR      PROSITE; PS50847; GRAM_POS_ANCHORING; 1.
KW      Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ      SEQUENCE      1038 AA; 113618 MW; 666BF6BF2BFBB12 CRC64;

Query Match      96.1%; Score 199; DB 2; Length 1038;
Best Local Similarity 97.4%; Pred. No. 6.9e-16;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY      1 QNSGNQSFPEDETEDEKPKYEGGNIYVIDPDSVPQIHG 38
DB      742 QNSGNQSFPEDETEDEKPKYEGGNIYVIDPDSVPQIHG 779

RESULT 9
ID      Q6GDUS      PRELIMINARY;      PRT; 965 AA.
AC      Q6GDUS;
DT      05-JUL-2004 (TrEMBLrel. 27, Created)
DT      05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT      05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE      Fibronectin-binding protein.
GN      Name=fnb; OrderedLocustNames=SA2580;
OS      Staphylococcus aureus (strain MRS252).
OC      Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX      NCBI_TaxId=282458;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      PubMed=15213324; DOI=10.1073/pnas.0402521101;
RX      Hoiden M.T.G., Feil E.J., Lindsay J.A., Peacock S.J., Day N.P.J.,
RA      Enright M.C., Foster T.J., Moore C.E., Hurst L., Atkin R., Barron A.,
RA      Bacon N., Bentley S.D., Chillingworth C., Chillingworth T.,
RA      Churcher C., Clark L., Cotton C., Cronin A., Doggett J., Dowd L.,
RA      Feltwell T., Hance Z., Harris B., Hauser H., Holtroyd S., Jørgels K.,
RA      James K.D., Lennard N., Line A., Mayes R., Moule S., Mungall K.,
RA      Ormond D., Quail M.A., Rabinowitsch E., Rutherford K.M., Sanders M.,
```

RA Sharp S., Simmonds M., Stevens K., Whitehead S., Barrell B.G.,
 RA Spratt B.G., Parkhill J.,
 RT "Complete genomes of two clinical *Staphylococcus aureus* strains:
 evidence for the rapid evolution of virulence and drug resistance."
 Proc. Natl. Acad. Sci. U.S.A. 101:9786-9791(2004).
 CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
 an amide bond (By similarity).
 DR EMBL: BX571856; CAC41560.1; -;
 DR GO: GO:0009986; C:cell surface; IEA.
 DR GO: GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
 DR GO: GO:0016020; C:membrane; IEA.
 DR GO: GO:0007155; P:cell adhesion; IEA.
 DR InterPro: IPR008966; Adhes_bact.
 DR InterPro: IPR004237; Fn_bind.
 DR InterPro: IPR005877; Gpos_Ysirk.
 DR Pfam: PF02986; Gram_pos_anchor.
 DR Pfam: PF00746; Gram_pos_anchor; 1.
 DR Pfam: PF04650; Ysirk_signal; 1.
 DR TIGRPFAMs: TIGR01167; LPXTG_anchor; 1.
 DR TIGRPFAMs: TIGR01168; Ysirk_signal; 1.
 DR PROSITE: PS50847; GRAM_POS_ANCHORING; 1.
 DR Cell wall; Complete proteome; Peptidoglycan-anchor.
 KW SEQUENCE 965 AA; 105691 MW; 2982E132164D0551 CRC64;
 Query Match 95.7%; Score 198; DB 2; Length 965;
 Best Local Similarity 94.7%; Pred. No. 8,4e-16;
 Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 1 QNSGNQSFEDTEBDKPKYEGCGNIVDIDPDSVPQIIG 38
 DB 749 QNSGNQSFEDTEBDKPKYEGCGNIVDIDPDSVPQIIG 786
 RESULT 10
 Q8NUU7 PRELIMINARY; PRT; 1015 AA.
 ID Q8NUU7
 AC Q8NUU7
 DT 01-OCT-2002 (TREMblrel. 22, Created)
 DT 01-OCT-2002 (TREMblrel. 22, Last sequence update)
 DT 01-OCT-2003 (TREMblrel. 25, Last annotation update)
 DE Fnb protein.
 GN Name=fnb; OrderedLocustNames=MM2421;
 OS *Staphylococcus aureus* (strain MM2).
 CC Bacteria; Firmicutes; Bacillales; *Staphylococcus*.
 CC NCBI_TaxID=196620;
 OK NCBI_TaxID=196620;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC STRAIN=MM2;
 RX MEDLINE=22040717; PubMed=12044378; DOI=10.1016/S0140-6736(02)08713-5;
 RA Babb T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Oguchi A.,
 RA Nagai Y., Iwama N., Asano K., Naito T., Kuroda H., Cui L.,
 RA Yamamoto K., Hiramatsu K.;
 RT "Genome and virulence determinants of high virulence community-
 acquired MRSA."
 RT Lancet 359:1819-1827(2002).
 CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
 an amide bond (By similarity).
 DR EMBL: AP004830; BAB96286.1; -;
 DR GO: GO:0009986; C:cell surface; IEA.
 DR GO: GO:0005618; C:cell wall; IEA.
 DR GO: GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
 DR GO: GO:0016020; C:membrane; IEA.
 DR GO: GO:0007155; P:cell adhesion; IEA.
 DR InterPro: IPR008966; Adhes_bact.
 DR InterPro: IPR004237; Fn_bind.
 DR InterPro: IPR005877; Gpos_Ysirk.
 DR InterPro: IPR001899; Gram_pos_anchor.
 DR Pfam: PF02986; Gram_pos_anchor; 1.
 DR Pfam: PF00746; Gram_pos_anchor; 1.
 DR Pfam: PF04650; Ysirk_signal; 1.
 DR TIGRPFAMs: TIGR01167; LPXTG_anchor; 1.
 DR TIGRPFAMs: TIGR01168; Ysirk_signal; 1.
 DR PROSITE: PS50847; GRAM_POS_ANCHORING; 1.
 KW Cell wall; Complete proteome; Peptidoglycan-anchor.
 SQ SEQUENCE 1015 AA; 111145 MW; D0F9281BB64D44D2 CRC64;

DR PROSITE: PS50847; GRAM_POS_ANCHORING; 1.
 DR Cell wall; Complete proteome; Peptidoglycan-anchor.
 KW SEQUENCE 1015 AA; 111145 MW; D0F9281BB64D44D2 CRC64;
 SQ SEQUENCE 1015 AA; 111145 MW; D0F9281BB64D44D2 CRC64;
 Query Match 92.3%; Score 191; DB 2; Length 1015;
 Best Local Similarity 94.7%; Pred. No. 6,7e-15;
 Matches 36; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 QNSGNQSFEDTEBDKPKYEGCGNIVDIDPDSVPQIIG 38
 DB 747 QNSGNQSFEDTEBDKPKYEGCGNIVDIDPDSVPQIIG 784
 RESULT 11
 Q6G6H3 PRELIMINARY; PRT; 1015 AA.
 ID Q6G6H3
 AC Q6G6H3
 DT 05-JUN-2004 (TREMblrel. 27, Created)
 DT 05-JUN-2004 (TREMblrel. 27, Last sequence update)
 DT 05-JUN-2004 (TREMblrel. 27, Last annotation update)
 DE Fibrinectin-binding protein.
 GN OrderedLocustNames=SA5238;
 OS *Staphylococcus aureus* (strain MSSA476).
 CC Bacteria; Firmicutes; Bacillales; *Staphylococcus*.
 CC NCBI_TaxID=282459;
 OK NCBI_TaxID=282459;
 RN (1)
 RP SEQUENCE FROM N.A.
 RX PubMed=15213324; DOI=10.1073/pnas.0402521101;
 RA Holden M.T.G., Fell E.J., Lindsay J.A., Peacock S.J., Day N.P.J.,
 RA Enright M.C., Foster T.J., Moore C.E., Hurst L., Atkin R., Barton A.,
 RA Bacon N., Bentley S.D., Chillingworth C., Chillingworth T.,
 RA Churcher C., Clark L., Cotton C., Cronin A., Doggett J., Dowd L.,
 RA Fellwell T., Hance Z., Harris B., Hauser H., Holtroyd S., Jagels K.,
 RA James K.D., Leonard N., Lane A., Mayes R., Moutie S., Mungall K.,
 RA Ormond D., Quail M.A., Rabinowitch E., Rutherford K.M., Sanders M.,
 RA Sharp S., Simmonds M., Stevens K., Whitehead S., Barrell B.G.,
 RA Spratt B.G., Parkhill J.;
 RT "Complete genomes of two clinical *Staphylococcus aureus* strains:
 evidence for the rapid evolution of virulence and drug resistance."
 RT Proc. Natl. Acad. Sci. U.S.A. 101:9786-9791(2004).
 CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
 an amide bond (By similarity).
 DR EMBL: BX571857; CAC44202.1; -;
 DR GO: GO:0009986; C:cell surface; IEA.
 DR GO: GO:0005618; C:cell wall; IEA.
 DR GO: GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
 DR GO: GO:0016020; C:membrane; IEA.
 DR GO: GO:0007155; P:cell adhesion; IEA.
 DR InterPro: IPR008966; Adhes_bact.
 DR InterPro: IPR004237; Fn_bind.
 DR InterPro: IPR005877; Gpos_Ysirk.
 DR InterPro: IPR001899; Gram_pos_anchor.
 DR Pfam: PF02986; Gram_pos_anchor; 1.
 DR Pfam: PF00746; Gram_pos_anchor; 1.
 DR Pfam: PF04650; Ysirk_signal; 1.
 DR TIGRPFAMs: TIGR01167; LPXTG_anchor; 1.
 DR TIGRPFAMs: TIGR01168; Ysirk_signal; 1.
 DR PROSITE: PS50847; GRAM_POS_ANCHORING; 1.
 KW Cell wall; Complete proteome; Peptidoglycan-anchor.
 SQ SEQUENCE 1015 AA; 111145 MW; D0F9281BB64D44D2 CRC64;
 Query Match 92.3%; Score 191; DB 2; Length 1015;
 Best Local Similarity 94.7%; Pred. No. 6,7e-15;
 Matches 36; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 QNSGNQSFEDTEBDKPKYEGCGNIVDIDPDSVPQIIG 38
 DB 747 QNSGNQSFEDTEBDKPKYEGCGNIVDIDPDSVPQIIG 784
 RESULT 12
 Q9AEP9 PRELIMINARY; PRT; 152 AA.
 ID Q9AEP9

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AC 09ABP9;
DT 01-JUN-2001 (Tremblrel. 17, Created)
DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE Fibronectin-binding protein (Fragment).
GN Name=fnb;
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1280;
RN [1]
RP SEQUENCE FROM N.A.
AC STRAIN=CMRSA-1;
RX MEDLINE=21246681; PubMed=11349044;
RX DOI=10.1128/IAI.69.6.3791-3799.2001;
RA Rice K., Huebner M., Var D., McGavin M.J.;
RT "variance in fibronectin binding and fnb locus polymorphisms in
RT Staphylococcus aureus: identification of antigenic variation in a
RT fibronectin binding protein adhesin of the epidemic CMRSA-1 strain of
RT methicillin-resistant S. aureus.";
RL Infect. Immun. 69:3791-3799(2001).
DR EMBL; AY029184; AAK31588.1; -.
FT NON_TER
FT TER
SQ SEQUENCE 152 AA; 17193 MW; CFA3913C2B11C025 CRC64;

Query Match 90.8%; Score 188; DB 2; Length 152;
Best Local Similarity 92.1%; Pred. No. 1.8e-15;
Matches 35; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 QNSGNSFPEDTEBDRKPYEGGNIYDIDPDSVPQIHG 38
    ||:|||||:|||||:|||||:|||||:|||||:
Db 1 QNTGNSFEDTEBDRKPYEGGNIYDIDPDSVPQIHG 38

RESULT 13
Q948C1 PRELIMINARY; PRT; 735 AA.
AC 0948C1;
DT 01-DEC-2001 (Tremblrel. 19, Created)
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE Putative wall-associated protein kinase.
GN Name=OSJNBa0034A02.10;
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaceae; Oryza.
OX NCBI_TaxID=4530;
RN [1]
RP SEQUENCE FROM N.A.
RA Wing R.A., Yu Y., Soderlund C., Chen M., Kim H.-R., Rambo T.,
RA Sasaki C., Henry D., Oates R., Simmons J.;
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
DR EMBL; AC079852; AA125177.1; -.
DR HSSP; P49841; 103D.
DR Gramene; Q948C1; -.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR011009; Kinase_like.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR008271; Ser_Thr_pkin_AS.
DR ProDom; PD000001; Prot_kinase.2.
DR PROSITE; PS00107; PROTEIN KINASE ATP; 2.
DR PROSITE; PSS0011; PROTEIN KINASE DOM; 2.
DR PROSITE; PSS00108; PROTEIN KINASE ST; 1.
KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 735 AA; 82500 MW; 59EB6ADCA0E77407 CRC64;

Query Match 30.0%; Score 62; DB 2; Length 735;
Best Local Similarity 36.8%; Pred. No. 54;
Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
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Matches 14; Conservative 6; Mismatches 18; Indels 0; Gaps 0;

Qy 1 QNSGNSFPEDTEBDRKPYEGGNIYDIDPDSVPQIHG 38
    :|||:||||:||||:||||:||||:
Db 390 ENFGWHLFPETONEDKESQGGTNVSSSIMAPPKAG 427

RESULT 14
Q7XGK6 PRELIMINARY; PRT; 735 AA.
AC 07XGK6;
DT 01-OCT-2003 (Tremblrel. 25, Created)
DT 01-OCT-2003 (Tremblrel. 25, Last sequence update)
DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)
DE Putative wall-associated protein kinase.
GN ORFNames=OSJNBa0034A02.10;
OS Oryza sativa (Japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaceae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
RP SEQUENCE FROM N.A.
RA The Rice Chromosome 10 Sequencing Consortium;
RA "in-depth view of structure, activity, and evolution of rice
RT chromosome 10.";
RL Science 300:1566-1569(2003).
RN [2]
RP SEQUENCE FROM N.A.
RA Bhell C.R., Wing R.A., McCombie W.R., Messing J., Yan Q.;
RL Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
DR EMBL; AE017055; AAP52081.1; -.
DR HSSP; P49841; 103D.
DR Gramene; Q7XGK6; -.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR011009; Kinase_like.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR008271; Ser_Thr_pkin_AS.
DR ProDom; PD000001; Prot_kinase.2.
DR PROSITE; PS00107; PROTEIN KINASE ATP; 2.
DR PROSITE; PSS0011; PROTEIN KINASE DOM; 2.
DR PROSITE; PSS00108; PROTEIN KINASE ST; 1.
KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 735 AA; 82500 MW; 59EB6ADCA0E77407 CRC64;

Query Match 30.0%; Score 62; DB 2; Length 735;
Best Local Similarity 36.8%; Pred. No. 54;
Matches 14; Conservative 6; Mismatches 18; Indels 0; Gaps 0;

Qy 1 QNSGNSFPEDTEBDRKPYEGGNIYDIDPDSVPQIHG 38
    :|||:||||:||||:||||:||||:
Db 390 ENFGWHLFPETONEDKESQGGTNVSSSIMAPPKAG 427

RESULT 15
Q91LJ7 PRELIMINARY; PRT; 981 AA.
AC 091LJ7;
DT 01-DEC-2001 (Tremblrel. 19, Created)
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
DT 01-JUN-2004 (Tremblrel. 27, Last annotation update)
DE ORF43 (wsv045) (WSSV102).
OS White spot syndrome virus (WSSV).
OC Viruses; dsDNA viruses, no RNA stage; Nimaviridae; Whispovirus.
OX NCBI_TaxID=22652;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21342572; PubMed=11448154; DOI=10.1006/viro.2001.1002;
RA van Hulten M.C.W., Witteveldt J., Peters S., Kloosterboer N.,
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CC streptococci, e.g. meningitis, otitis media, pneumonia, endocarditis,
CC mastitis in cattle, abortion in horses and many others. Since the
CC antibodies block binding of bacteria, they should be effective against
CC antibiotic-resistant strains, and may replace antibiotic therapy or
CC increase its effectiveness. Sequences AAW65691-700 represent a series of
CC synthetic peptides based on the D1 region of S. aureus fibronectin
CC binding protein A. They were synthesised to contain mutations
XX
SQ Sequence 38 AA;
Query Match 100.0%; Score 207; DB 2; Length 38;
Best Local Similarity 100.0%; Pred. No. 1.3e-20;
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 QNSGNQSFEPDTEBDKPKRYEGGNIVDIDFDSVPQIHG 38
DQ 1 QNSGNQSFEPDTEBDKPKRYEGGNIVDIDFDSVPQIHG 38
RESULT 2
AAW65661 standard; peptide; 38 AA.
ID AAW65661;
AC AAW65661;
AD 16-OCT-1998 (first entry)
DE Fibronectin binding protein-derived peptide #5.
DM microbial surface components recognising adhesive matrix molecule;
KM MSCRAMM; fibronectin; fibronectin-binding protein; antibody; epitope;
KM antibiotic; bacterial infection; antibiotic-resistant strain.
XX
OS Synthetic.
OS Staphylococcus aureus.
XX
PN WO9831389-A2.
XX
PD 23-JUL-1998.
XX
PF 21-JAN-1998; 98WO-US001222.
XX
PR 21-JAN-1997; 97US-0036139P.
XX
PA (TEXA ) UNIV TEXAS A & M SYSTEM.
PI Hoeoek M, Patti JM, House-Pompeo KL, Speciale P, Joh D;
PI Mcgavin MJ;
DR WPI; 1998-413816/35.
XX
PT Antibody that binds to fibronectin-binding protein, preventing its
PT binding to fibronectin - used to treat or prevent bacterial infection,
PT especially by Staphylococci and Streptococci.
XX
PS Example 2; Page 92; 201pp; English.
XX
CC The invention relates to antibodies that bind to a fibronectin-binding
CC domain of a fibronectin-binding protein, and inhibit binding of the
CC protein to fibronectin. Also claimed are: (1) isolated peptides of a
CC fibronectin-binding protein that do not bind to fibronectin; (2) fusion
CC protein containing at least one peptide of a fibronectin-binding protein
CC linked to a second amino acid sequence; (3) nucleic acid encoding the
CC isolated peptide of (1). Antibodies, the isolated peptides of (1) and the
CC nucleic acids are all useful for immunisation (active or passive) and (by
CC inhibiting binding of bacteria to fibronectin) for preventing or treating
CC infection in humans or other animals, particularly by staphylococci or
CC streptococci, e.g. meningitis, otitis media, pneumonia, endocarditis,
CC mastitis in cattle, abortion in horses and many others. Since the
CC antibodies block binding of bacteria, they should be effective against
CC antibiotic-resistant strains, and may replace antibiotic therapy or
CC increase its effectiveness. Sequences AAW65659-68 represent synthetic
CC epitopes from the fibronectin binding domains DU and D1-D4 of the S.

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CC aureus fmbA gene
XX
SQ Sequence 38 AA;
Query Match 96.1%; Score 199; DB 2; Length 38;
Best Local Similarity 97.4%; Pred. No. 1.6e-19;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 QNSGNQSFEPDTEBDKPKRYEGGNIVDIDFDSVPQIHG 38
DQ 1 QNSGNQSFEPDTEBDKPKRYEGGNIVDIDFDSVPQIHG 38
RESULT 3
AAR58806 standard; protein; 130 AA.
ID AAR58806;
AC AAR58806;
AD 25-MAR-2003 (revised)
DT 30-MAR-1995 (first entry)
DE Fibronectin binding domain D1-D4(709-838 (P838T)).
DM Fibronectin binding protein; Fbp; fibronectin binding domain;
KM monoclonal antibody; Mab; adhesion; Gram-positive bacterium; bacteremia;
KM Escherichia coli.
XX
OS Staphylococcus aureus.
XX
PN WO9418327-A1.
XX
PD 18-AUG-1994.
XX
PF 04-FEB-1994; 94WO-GB000215.
XX
PR 05-FEB-1993; 93GB-00002289.
XX
PR 20-OCT-1993; 93GB-00021592.
XX
PA (SMIK ) SMITHKLINE BEECHAM PLC.
PI Burnham MKR, Chopra I, Critchley IA, Knowles DJC;
PI WPI; 1994-279748/34.
XX
PT Fibronectin binding protein and monoclonal antibodies specific for Fbp -
PT useful to prevent adherence of Gram-positive bacteria to indwelling
PT devices or wounds.
XX
PS Disclosure; Page 30; 40pp; English.
XX
CC Polypeptides corresponding to residues G709-P86 plus PRVPP, G709-
CC P838 (P838T) and G709-P838 (AAR58805-07, respectively) of S. aureus J2385
CC (NCIMB 40532) Fbp type A fibronectin binding domain D1-D4 region
CC (AAR58808) were expressed in E. coli BL21 (DE4) and used to raise MAbs
CC specific for Fbp. (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ Sequence 130 AA;
Query Match 96.1%; Score 199; DB 2; Length 130;
Best Local Similarity 97.4%; Pred. No. 7.1e-19;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 QNSGNQSFEPDTEBDKPKRYEGGNIVDIDFDSVPQIHG 38
DQ 2 QNSGNQSFEPDTEBDKPKRYEGGNIVDIDFDSVPQIHG 39
RESULT 4
AAR58807 standard; protein; 130 AA.
ID AAR58807;
AC AAR58807;

```

```

XX 25-MAR-2003 (revised)
DT 30-MAR-1995 (first entry)
XX
DE Fibronectin binding domain D1-D4(709-838).
XX
KM Fibronectin binding protein; Fbp; fibronectin binding domain;
KM monoclonal antibody; Mab; adhesion; Gram-positive bacterium; bacteremia;
KM Escherichia coli.
XX
OS Staphylococcus aureus.
XX
XX WO9418327-A1.
XX
PD 18-AUG-1994.
XX
PF 04-FEB-1994; 94WO-GB000215.
XX
PR 05-FEB-1993; 93GB-00002289.
XX
PR 20-OCT-1993; 93GB-00021592.
XX
PA (SMIK ) SMITHKLINE BEECHAM PLC.
XX
PI Burnham MKR, Chopra I, Critchley IA, Knowles DUC;
XX
DR WPI; 1994-279748/34.
XX
PT Fibronectin binding protein and monoclonal antibodies specific for Fbp -
PT useful to prevent adherence of Gram-positive bacteria to indwelling
PT devices or wounds.
XX
PS Disclosure; Page 30; 40pp; English.
XX
CC Polypeptides corresponding to residues G709-T886 plus PRVPT. G709-
CC P838(P838T) and G709-P838 (AAR58805-07, respectively) of S. aureus J2385
CC (NCIMB 40532) Fbp type A fibronectin binding domain D1-D4 region
CC (AAR58808) were expressed in E. coli BL21 (DE4) and used to raise Mabs
CC specific for Fbp. (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ Sequence 130 AA;

Query Match 96.1%; Score 199; DB 2; Length 130;
Best Local Similarity 97.4%; Pred. No. 7.1e-19;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 QNSGNQSFEPTEEDKPKYEGGNIVDIDFDSVPQIHG 38
    |||||
DB 2 QNSGNQSFEPTEEDKPKYEGGNIVDIDFDSVPQIHG 39

RESULT 5
AAR91202
ID AAR91202 standard; peptide; 130 AA.
XX
AC AAR91202;
XX
DT 13-NOV-1996 (first entry)
XX
DE D1-D4 fibronectin binding domains.
XX
KM Fibronectin; oral hygiene; gingivitis; gum disease; adhesion;
KM periodontitis; oral pathogen; caries; calculus; candidiasis; oral surgery;
KM tissue regeneration; irrigation; toothpaste; dentifrice; mouthwash;
KM lozenge.
XX
OS Staphylococcus aureus.
XX
XX WO9604003-A1.
XX
XX 15-FEB-1996.
XX
XX 18-JUL-1995; 95WO-EP002825.
XX

```

```

PR 05-AUG-1994; 94GB-00015902.
XX
XX (SMIK ) SMITHKLINE BEECHAM PLC.
XX
PI Barnett P, Critchley IA, Dodd I;
XX
DR WPI; 1996-129122/13.
XX
PT Prevention of adherence of oral pathogens in the oral cavity, partic.
PT tooth surfaces - by application of a fibronectin binding protein or
PT polypeptide or a monoclonal antibody or fragment against it.
XX
XX Claim 5; Page 32; 41pp; English.
XX
CC Adherence of oral pathogens, particularly to tooth surfaces, can be
CC prevented by application of a fibronectin binding protein or polypeptide.
CC The fibronectin binding protein or polypeptide is useful in the
CC manufacture of oral hygiene compositions, eg. toothpaste, liquid
CC dentifrice, mouthwash or lozenge. They are useful to prevent the plaque-
CC related development of carious lesions, gingivitis, calculus or
CC periodontal disease and to combat oral cavity infections, e.g.
CC candidiasis. They may also be useful in oral surgery e.g. in guided
CC tissue regeneration procedures to prevent subsequent bacterial infection,
CC and for irrigation of periodontal pockets. This sequence corresponds to
CC amino acids 709-838 of the D1-D4 fibronectin binding domain of
CC Staphylococcus aureus
XX
SQ Sequence 130 AA;

Query Match 96.1%; Score 199; DB 2; Length 130;
Best Local Similarity 97.4%; Pred. No. 7.1e-19;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 QNSGNQSFEPTEEDKPKYEGGNIVDIDFDSVPQIHG 38
    |||||
DB 2 QNSGNQSFEPTEEDKPKYEGGNIVDIDFDSVPQIHG 39

RESULT 6
AAR91201
ID AAR91201 standard; peptide; 130 AA.
XX
AC AAR91201;
XX
DT 13-NOV-1996 (first entry)
XX
DE D1-D4 fibronectin binding domains.
XX
KM Fibronectin; oral hygiene; gingivitis; gum disease; adhesion;
KM periodontitis; oral pathogen; caries; calculus; candidiasis; oral surgery;
KM tissue regeneration; irrigation; toothpaste; dentifrice; mouthwash;
KM lozenge.
XX
OS Staphylococcus aureus.
XX
XX WO9604003-A1.
XX
XX 15-FEB-1996.
XX
XX 18-JUL-1995; 95WO-EP002825.
XX
XX 05-AUG-1994; 94GB-00015902.
XX
XX (SMIK ) SMITHKLINE BEECHAM PLC.
XX
PI Barnett P, Critchley IA, Dodd I;
XX
DR WPI; 1996-129122/13.
XX
PT Prevention of adherence of oral pathogens in the oral cavity, partic.
PT tooth surfaces - by application of a fibronectin binding protein or
PT polypeptide or a monoclonal antibody or fragment against it.
XX

```

P8 Claim 5; Page 31-32; 41pp; English.

CC Adherence of oral pathogens, particularly to tooth surfaces, can be prevented by application of a fibronectin binding protein or polypeptide.

CC The fibronectin binding protein or polypeptide is useful in the manufacture of oral hygiene compositions, eg. toothpaste, liquid dentifrice, mouthwash or lozenge. They are useful to prevent the plaque-related development of carious lesions, gingivitis, calculus or periodontal disease and to combat oral cavity infections, e.g. candidiasis. They may also be useful in oral surgery e.g. in guided tissue regeneration procedures to prevent subsequent bacterial infection, and for irrigation of periodontal pockets. This sequence corresponds to amino acids 709-838 of the Df-D4 fibronectin binding domain of *Staphylococcus aureus* with a P838T substitution

CC

XX

SQ Sequence 130 AA;

DY Query Match 96.1%; Score 199; DB 2; Length 130;
Best Local Similarity 97.4%; Pred.No.7,1e-19;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0

Dd 1 QNSGNQSEFPDTEBDKPKYEQCGNIVDIDFDSVPQIHG 38
|||
2 QNSGNQSEFPDTEBDKPKYEQCGNIVDIDFDSVPQIHG 39

RESULT 7

ID AAY29089 standard; protein; 134 AA.
AA AAY29089;
XX AAY29089;
DT 28-SEP-1999 (first entry)
DE Cloned fibronectin binding protein binding domain (FnBAB) sequence.

KW Bovine herpes virus-2; BHV-2; cytokine; immune response; immunogen; IL; interleukin; colony stimulating factor; CSF; interferon; IFN; TNF;
KM tumour necrosis factor; recombinant virus; vaccine; mucosal disease; mastitis; breast cancer; stress-induced disease; binding domain; FnBAB;
KW fibronectin binding protein.

OS *Staphylococcus aureus*.

XX

PN WO9916892-A1.
PD 08-APR-1999.
XX

PF 29-SEP-1998; 98WO-GB002927.
XX

PR 29-SEP-1997; 97GB-00020633.
XX

PA (UYBR-) UNIV BRISTOL.
PI Bradley AJ, Duffas WPJ;
DR WPI: 1999-255101/21.
XX

N-PSDB; AAX91506.
XX

PT New bovine herpes virus-2 vectors.
XX

PS Example 2; Fig 8A-B; 130pp; English.
XX

The invention provides bovine herpes virus-2 (BHV-2) based vectors that comprise at least one cytokine-encoding DNA sequence. The expression of cytokines in mammals can up-regulate immune responses to the immunogens. The cytokine is selected from interleukins (IL), colony stimulating factors (CSF), interferons (IFN) and tumour necrosis factors (TNF). The BHV-2 based vector or recombinant virus can be used as vaccines. They can be used for preventing or treating a mucosal disease in a subject, e.g. rumenitis, cattle, sheep, goats, dogs, cats, horses, or man, particularly mastitis in cows or breast cancers in humans. They can also be used for preventing or treating a stress-induced disease. The present sequence

CC	represents a S. aureus fibronectin binding protein binding domain.
CC	sequence FNAB, the gene cloned for use in this invention. The gene has
CC	97.8 percent identity when compared to the previously published sequences
CC	FNBA and FnBB
XX	
SQ	Sequence 134 AA;
Oy	
Db	1 QNSGNSFPEDTEBDKPKYEGSGNIVDIDPDSVPQING 38 2 QNSGNSFEDTBEDEKPKYEGSGNIVDIDPDSVPEQING 39
RESULT 8	
ID	AAI29088 standard; protein; 134 AA.
AC	AAI29088;
XX	
DT	28-SEP-1999 (first entry)
XX	
DB	S. aureus fibronectin binding protein B (FnBB) binding domain.
KX	Bovine herpes virus-2; BHV-2; cytokine; immune response; immunogen; IL;
KW	interleukin; colony stimulating factor; CSF; interferon; IFN; TNF;
KM	tumour necrosis factor; recombinant virus; vaccine; mucosal disease;
KM	mastitis; breast cancer; stress-induced disease; binding domain; FnBB;
XX	fibronectin binding protein.
OS	Staphylococcus aureus.
PN	MO916892-AI.
PD	08-APR-1999.
PF	29-SEP-1998; 98WO-GB002927.
PR	29-SEP-1997; 97GB-00020633.
PA	(UYBR-) UNIV BRISTOL.
P1	Bradley AJ, Duffas WPJ;
DR	WPI: 1999-255101/21.
DR	N-PSDB; AAX91505.
PT	New bovine herpes virus-2 vectors.
PS	Example 2; Fig 8A-B; 130pp; English.
XX	
CC	The invention provides bovine herpes virus-2 (BHV-2) based vectors that
CC	comprise at least one cytokine-encoding DNA sequence. The expression of
CC	cytokines in mammals can up-regulate immune responses to the immunogens.
CC	The cytokine is selected from interleukins (IL), colony stimulating
CC	factors (CSF), interferons (IFN) and tumour necrosis factors (TNF). The
CC	BHV-2 based vector or recombinant virus can be used as vaccines. They can
CC	be used for preventing or treating a mucosal disease in a subject, e.g.,
CC	ruminants, cattle, sheep, goats, dogs, cats, horses, or man, particularly
CC	mastitis in cows or breast cancers in humans. They can also be used for
CC	preventing or treating a stress-induced disease. The present sequence
CC	represents the binding domain of a previously published S. aureus
CC	fibronecin binding protein B (FnBB) sequence. The Fnb binding domain
CC	gene sequence FNAB, cloned for use in this invention has 97.8 percent
CC	identity when compared to the previously published FNBA and FnBB gene
CC	sequences
XX	
SQ	Sequence 134 AA;
Query Match	96.1%; Score 199; DB 2; Length 134;
Best Local Similarity	97.4%; Pred.No. 7.3e-19;
	Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0


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XX 25-MAR-2003 (revised)
DT 30-MAR-1995 (first entry)
XX
XX Fbp fibronectin binding domain.
DE
XX Fibronectin binding protein; Fbp; fibronectin binding domain;
KW monoclonal antibody; Mab; adhesion; Gram-positive bacterium; bacteremia;
KW Escherichia coli; pBROC531.
XX
XX Staphylococcus aureus.
OS
XX WO9418327-A1.
PN
XX 18-AUG-1994.
PD
XX 04-FEB-1994; 94WO-GB000215.
PF
XX 05-FEB-1993; 93GB-00002289.
PR 20-OCT-1993; 93GB-00021592.
XX
XX (SMIK ) SMITHKLINE BEECHAM PLC.
PA
XX Burnham MKR, Chopra I, Critchley IA, Knowles DJC;
PI WPI; 1994-279748/34.
XX N-PSDB; MAQ71838.
DR
XX Fibronectin binding protein and monoclonal antibodies specific for Fbp -
PT useful to prevent adherence of Gram-positive bacteria to indwelling
PT devices or wounds.
XX
XX Disclosure; Page 30; 40pp; English.
PS
XX The sequences of DNA encoding S. aureus Fbp type A fibronectin binding
CC domain (DI-D4) and the encoded protein are provided. DI-D4 polypeptides
CC have been expressed in E. coli BL21(DE4) and used to raise Mabs specific
CC for Fbp. (Updated on 25-MAR-2003 to correct PN field.)
CC
XX
SQ Sequence 174 AA;

Query Match          96.1%; Score 199; DB 2; Length 174;
Best Local Similarity 97.4%; Pred. No. 1e-18;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QNSGNQSFEPDTEDEKPKYEGGNIVIDIDPSVPIQHG 38
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 2 QNSGNQSFEPDTEDEKPKYEGGNIVIDIDPSVPIQHG 39

RESULT 12
AAR91203
ID AAR91203 standard; protein; 174 AA.
XX
XX AAR91203;
AC
XX 16-OCT-2003 (revised)
DT 13-NOV-1996 (first entry)
XX
XX DI-D4 fibronectin binding domain.
DE
XX Fibronectin; oral hygiene; gingivitis; gum disease; adhesion;
KW periodontitis; oral pathogen; caries; calculus; candidiasis; oral surgery;
KW tissue regeneration; irrigation; toothpaste; dentifrice; mouthwash;
KW lozenge.
XX
XX Staphylococcus aureus; J2385.
OS
XX WO9604003-A1.
PN
XX 15-FEB-1996.
PD
XX 18-JUL-1995; 95WO-EP002825.
PF

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XX 05-AUG-1994; 94GB-00015902.
PR
XX (SMIK ) SMITHKLINE BEECHAM PLC.
PA
XX Barnett P, Critchley IA, Dodd I;
PI WPI; 1996-129122/13.
XX N-PSDB; AAT18308.
DR
XX Prevention of adherence of oral pathogens in the oral cavity, partic.
PT tooth surfaces - by application of a fibronectin binding protein or
PT polypeptide or a monoclonal antibody or fragment against it.
XX
XX Claim 5; Page 32; 41pp; English.
PS
XX Adherence of oral pathogens, particularly to tooth surfaces, can be
CC prevented by application of a fibronectin binding protein or polypeptide.
CC The fibronectin binding protein or polypeptide is useful in the
CC manufacture of oral hygiene compositions, eg. toothpaste, liquid
CC dentifrice, mouthwash or lozenge. They are useful to prevent the plaque-
CC related development of carious lesions, gingivitis, calculus or
CC periodontal disease and to combat oral cavity infections, e.g.
CC candidiasis. They may also be useful in oral surgery e.g. in guided
CC tissue regeneration procedures to prevent subsequent bacterial infection,
CC and for irrigation of periodontal pockets. This sequence corresponds to
CC amino acids 709-838 of the DI-D4 fibronectin binding domain of
CC Staphylococcus aureus with a P838T substitution. (Updated on 16-OCT-2003
CC to standardise OS field)
CC
XX
SQ Sequence 174 AA;

Query Match          96.1%; Score 199; DB 2; Length 174;
Best Local Similarity 97.4%; Pred. No. 1e-18;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QNSGNQSFEPDTEDEKPKYEGGNIVIDIDPSVPIQHG 38
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 2 QNSGNQSFEPDTEDEKPKYEGGNIVIDIDPSVPIQHG 39

RESULT 13
AAR58805
ID AAR58805 standard; protein; 181 AA.
XX
XX AAR58805;
AC
XX 25-MAR-2003 (revised)
DT 30-MAR-1995 (first entry)
XX
XX Fibronectin binding domain DI-D4 (709-886) .
DE
XX Fibronectin binding protein; Fbp; fibronectin binding domain;
KW monoclonal antibody; Mab; adhesion; Gram-positive bacterium; bacteremia;
KW Escherichia coli.
XX
XX Staphylococcus aureus.
OS
XX WO9418327-A1.
PN
XX 18-AUG-1994.
PD
XX 04-FEB-1994; 94WO-GB000215.
PF
XX 05-FEB-1993; 93GB-00002289.
PR 20-OCT-1993; 93GB-00021592.
XX
XX (SMIK ) SMITHKLINE BEECHAM PLC.
PA
XX Burnham MKR, Chopra I, Critchley IA, Knowles DJC;
PI WPI; 1994-279748/34.
XX

```

PT Fibronectin binding protein and monoclonal antibodies specific for Fdp -
 PT useful to prevent adherence of Gram-positive bacteria to indwelling
 PT devices or wounds.
 XX
 PS Disclosure; Page 29-30; 40pp; English.
 XX
 CC Polypeptides corresponding to residues G709-T886 plus PPIVPT, G709-
 CC P838(P838T) and G709-P838 (AAR58805-07, respectively) of *S. aureus* J2385
 CC (NCIM 40532) Fdp type A fibronectin binding domain D1-D4 region
 CC (AAR58808) were expressed in *E. coli* BL21(DE4) and used to raise MAbs
 CC specific for Fdp. (updated on 25-MAR-2003 to correct PN field.)
 CC
 XX
 SQ Sequence 181 AA;
 Query Match 96.1%; Score 199; DB 2; Length 181;
 Best Local Similarity 97.4%; Pred. No. 1e-18;
 Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 QNSGNQSFEPDTEBDKPKYEGGNIVDIDPSVPOIHG 38
 DB 2 QNSGNQSFEPDTEBDKPKYEGGNIVDIDPSVPOIHG 39
 RESULT 14
 AAR91200
 ID AAR91200 standard; peptide; 181 AA.
 XX
 AC AAR91200;
 XX
 DT 13-NOV-1996 (first entry)
 XX
 DE D1-D4 fibronectin binding domains.
 XX
 KM Fibronectin; oral hygiene; gingivitis; gum disease; adhesion;
 KM periodontitis; oral pathogen; caries; calculus; candidiasis; oral surgery;
 KM tissue regeneration; irrigation; toothpaste; dentifrice; mouthwash;
 KM lozenge.
 KM
 XX Staphylococcus aureus.
 OS
 FN WO9604003-A1.
 XX
 PD 15-FEB-1996.
 XX
 PF 18-JUL-1995; 95WO-EP002825.
 XX
 PR 05-AUG-1994; 94GB-00015902.
 XX
 PA (SMITK) SMITHKLINE BEECHAM PLC.
 XX
 PI Barnett P, Critchley IA, Dodd I;
 XX
 DR WPI; 1996-129122/13.
 DR N-PSDB; AAT18307.
 DR
 XX Prevention of adherence of oral pathogens in the oral cavity, partic.
 PT tooth surfaces - by application of a fibronectin binding protein or
 PT polypeptide or a monoclonal antibody or fragment against it.
 XX
 PS Claim 5; Page 31; 41pp; English.
 XX
 CC Adherence of oral pathogens, particularly to tooth surfaces, can be
 CC prevented by application of a fibronectin binding protein or polypeptide.
 CC The fibronectin binding protein or polypeptide is useful in the
 CC manufacture of oral hygiene compositions, eg. toothpaste, liquid
 CC dentifrice, mouthwash or lozenge. They are useful to prevent the plaque-
 CC related development of carious lesions, gingivitis, calculus or
 CC periodontal disease and to combat oral cavity infections, e.g.
 CC candidiasis. They may also be useful in oral surgery e.g. in guided
 CC tissue regeneration procedures to prevent subsequent bacterial infection,
 CC and for irrigation of periodontal pockets. This sequence corresponds to
 CC amino acids 709-886 of the D1-D4 fibronectin binding domain of
 CC Staphylococcus aureus

XX
 SQ Sequence 181 AA;
 Query Match 96.1%; Score 199; DB 2; Length 181;
 Best Local Similarity 97.4%; Pred. No. 1e-18;
 Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 QNSGNQSFEPDTEBDKPKYEGGNIVDIDPSVPOIHG 38
 DB 2 QNSGNQSFEPDTEBDKPKYEGGNIVDIDPSVPOIHG 39
 RESULT 15
 AAM89803
 ID AAM89803 standard; protein; 559 AA.
 XX
 AC AAM89803;
 XX
 DT 16-MAR-1999 (first entry)
 XX
 DE Staphylococcus aureus protein SEQ ID #5251.
 XX
 KM Computer readable medium; vaccine; *S. aureus* infection; immunodetection;
 KM cellulitis; eyelid infection; food poisoning; osteomyelitis; therapy;
 KM skin infection; surgical wound infection; scalded skin syndrome;
 KM toxic shock syndrome.
 KM
 XX Staphylococcus aureus.
 OS
 PN EP786519-A2.
 XX
 PD 30-JUL-1997.
 XX
 PF 07-JAN-1997; 97EP-00100117.
 XX
 PR 05-JAN-1996; 96US-0009861P.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 XX
 PI Kunech CA, Choi GH, Barash SC, Dillon PJ, Fannon MR, Rosen CA;
 XX
 DR WPI; 1997-374922/35.
 XX
 PT Polynucleotide(s) and proteins derived from *Staphylococcus aureus* -
 PT stored on computer readable medium and used in the production of anti-
 PT *S. aureus* vaccines.
 XX
 PS Claim 23; Page 3259-3261; 3271pp; English.
 XX
 CC This sequence represents a *Staphylococcus aureus* protein sequence of the
 CC invention. The DNA sequences encoding the *S. aureus* proteins are recorded
 CC on a computer readable medium, preferably selected from a floppy or hard
 CC disk, random access memory (RAM), read-only memory (ROM) or CD-ROM.
 CC Homology searches using the *S. aureus* DNA sequences allows putative
 CC functions to be assigned so that protein-encoding or regulatory regions
 CC of commercial, therapeutic or industrial importance can be obtained.
 CC Specifically, sequences which are likely to encode antigens have been
 CC identified and these polypeptides can be used in a vaccine composition
 CC against *S. aureus* infection. The polypeptides can also be used in a kit
 CC for the immunodetection of *S. aureus* in a sample. *S. aureus* is implicated
 CC in numerous human diseases, including cellulitis, eyelid infections, food
 CC poisoning, osteomyelitis, skin and surgical wound infections, scalded
 CC skin syndrome, toxic shock syndrome, etc. Organisms transformed with the
 CC DNA sequences can be used for recombinant production of the polypeptides.
 CC The new DNA sequences (and their fragments) are useful as primers or
 CC probes for isolating homologues of any of the 5191 *S. aureus* DNA sequences
 CC contained on the computer readable medium
 XX
 SQ Sequence 559 AA;
 Query Match 96.1%; Score 199; DB 2; Length 559;
 Best Local Similarity 97.4%; Pred. No. 4e-18;
 Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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OM protein - protein search, using sw model

Run on: October 22, 2005, 03:51:22 ; Search time 21.1723 Seconds
(without alignments)
133.980 Million cell updates/sec

Title: US-10-731-238-37

Perfect score: 207
Sequence: 1 QNSGNQSFEPDTEBDKPKYEGGNIVIDIDFDSVPQIHG 38

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

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4: /cgn2_6/ptodata/1/1aa/6B.COMB.pep:*
5: /cgn2_6/ptodata/1/1aa/6C.COMB.pep:*
6: /cgn2_6/ptodata/1/1aa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No	Score	Query Match	Length	ID	Description
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2	199	96.1	38	1	US-08-234-622A-2
3	199	96.1	38	4	US-09-010-317-5
4	199	96.1	114	1	US-08-259-000-3
5	199	96.1	130	2	US-08-459-135A-7
6	199	96.1	130	2	US-08-459-135A-8
7	199	96.1	130	3	US-08-495-559-7
8	199	96.1	130	3	US-08-495-559-8
9	199	96.1	139	3	US-08-856-253-8
10	199	96.1	174	2	US-08-459-135A-10
11	199	96.1	174	2	US-08-459-135A-13
12	199	96.1	174	3	US-08-495-559-10
13	199	96.1	174	3	US-08-495-559-13
14	199	96.1	176	3	US-08-495-559-6
15	199	96.1	178	2	US-08-459-135A-12
16	199	96.1	178	2	US-08-495-559-12
17	199	96.1	181	2	US-08-459-135A-6
18	199	96.1	559	4	US-08-956-171E-5251
19	199	96.1	559	4	US-08-781-986A-5251
20	199	96.1	1027	4	US-08-956-171E-5254
21	199	96.1	1027	4	US-08-781-986A-5254
22	193	93.2	38	1	US-08-729-767-3
23	193	93.2	38	4	US-09-010-317-36
24	193	93.2	38	4	US-09-010-317-39
25	193	93.2	38	4	US-09-010-317-40
26	193	93.2	38	4	US-09-010-317-41
27	192	92.8	38	4	US-09-010-317-38

ALIGNMENTS

28	192	92.8	38	4	US-09-010-317-42	Sequence 42, Appl
29	191	92.3	38	4	US-09-010-317-6	Sequence 6, Appl
30	191	92.3	38	4	US-09-010-317-43	Sequence 43, Appl
31	189	91.3	38	4	US-09-010-317-35	Sequence 35, Appl
32	188.5	91.1	39	4	US-09-010-317-47	Sequence 36, Appl
33	188	90.8	38	4	US-09-010-317-47	Sequence 37, Appl
34	185	89.4	38	4	US-09-010-317-44	Sequence 44, Appl
35	180.5	87.2	39	4	US-09-010-317-57	Sequence 57, Appl
36	180	87.0	38	1	US-08-234-622A-3	Sequence 3, Appl
37	180	87.0	38	4	US-09-010-317-7	Sequence 7, Appl
38	174	84.1	38	1	US-08-729-767-4	Sequence 4, Appl
39	174	84.1	38	4	US-09-010-317-46	Sequence 46, Appl
40	173	83.6	38	4	US-09-010-317-48	Sequence 47, Appl
41	172	83.1	38	4	US-09-010-317-49	Sequence 48, Appl
42	172	83.1	38	4	US-09-010-317-45	Sequence 49, Appl
43	170	82.1	38	4	US-09-010-317-50	Sequence 45, Appl
44	166	80.2	38	4	US-09-010-317-50	Sequence 50, Appl
45	157	75.8	36	4	US-09-010-317-58	Sequence 58, Appl

RESULT 1
US-09-010-317-37
Sequence 37, Application US/09010317
Patent No. 6685943
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
APPLICANT: Patti, Joseph M.
APPLICANT: House-Pompeo, Karen L.
APPLICANT: Speziale, Pietro
APPLICANT: Joh, Danny
APPLICANT: McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
TITLE OF INVENTION: AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSER: Arnold, White & Durkee
STREET: P. O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/010.317
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hilder, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TANK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 37:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS: linear
TOPOLOGY: linear
US-09-010-317-37
Query Match 100.0%; Score 207; DB 4; Length 38;
Best Local Similarity 100.0%; Pred. No. 1.9e-21;


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Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 QNSGNSFEPDTEBDKPKYEGGNIIVDIDPDSVPQIHG 38
Db 1 QNSGNSFEPDTEBDKPKYEGGNIIVDIDPDSVPQIHG 38

RESULT 2
US-08-234-622A-2
; Sequence 2, Application US/08234622A
; Patent No. 544014
; GENERAL INFORMATION:
; APPLICANT: HOOK, Magnus
; APPLICANT: MCGAVIN, Martin
; APPLICANT: RAUCCI, Giuseppe
; TITLE OF INVENTION: A FIBRONECTIN BINDING PEPTIDE
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Burns, Doane, Swecker & Mathis
; STREET: P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/234,622A
; FILING DATE: 28-APR-1994
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: SE 9002617-0
; FILING DATE: 10-AUG-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/SE91/00534
; FILING DATE: 09-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Meuth, Donna M
; REGISTRATION NUMBER: 36,607
; REFERENCE/DOCKET NUMBER: 012885-044
; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 38 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-234-622A-2

Query Match 96.1%; Score 199; DB 1; Length 38;
Best Local Similarity 97.4%; Pred. No. 2.4e-20;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 QNSGNSFEPDTEBDKPKYEGGNIIVDIDPDSVPQIHG 38
Db 1 QNSGNSFEPDTEBDKPKYEGGNIIVDIDPDSVPQIHG 38

RESULT 3
US-09-010-317-5
; Sequence 5, Application US/09010317
; Patent No. 6685943
; GENERAL INFORMATION:
; APPLICANT: HOOK, Magnus
; APPLICANT: Patti, Joseph M.
; APPLICANT: House-Pompeo, Karen L.
; APPLICANT: Speziale, Pietro
```

```
; APPLICANT: Joh, Danny
; APPLICANT: MCGAVIN, Martin J.
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
; AND METHODS OF USE
; NUMBER OF SEQUENCES: 105
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: TX
; COUNTRY: USA
; ZIP: 77210-4433
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/010,317
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/036,139
; FILING DATE: 21-JAN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Hibler, David W.
; REGISTRATION NUMBER: 41,071
; REFERENCE/DOCKET NUMBER: TAMK:189
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 512-418-3000
; TELEFAX: 512-474-7577
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 38 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; US-09-010-317-5

Query Match 96.1%; Score 199; DB 4; Length 38;
Best Local Similarity 97.4%; Pred. No. 2.4e-20;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 QNSGNSFEPDTEBDKPKYEGGNIIVDIDPDSVPQIHG 38
Db 1 QNSGNSFEPDTEBDKPKYEGGNIIVDIDPDSVPQIHG 38

RESULT 4
US-08-259-000-3
; Sequence 3, Application US/08259000
; Patent No. 5571514
; GENERAL INFORMATION:
; APPLICANT: HOOK, Magnus
; APPLICANT: LINDBERG, Martin Kjell
; APPLICANT: SIGNAS, Lars Christer
; APPLICANT: MADSTROM, Torckel Mikael
; APPLICANT: FROMAN, Gunnar
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN AS WELL AS
; ITS PREPARATION
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Burns, Doane, Swecker & Mathis
; STREET: P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/259,000
FILING DATE: 13-JUN-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: SE 8702272-9
FILING DATE: 01-JUN-1987
ATTORNEY/AGENT INFORMATION:
NAME: Meuth, Donna M
REGISTRATION NUMBER: 36,607
REFERENCE/DOCKET NUMBER: 012885-062
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 114 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-259-000-3

Query Match 96.1%; Score 199; DB 1; Length 114;
Best Local Similarity 97.4%; Pred. No. 9e-20;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QNSGNQSFEDTDEKPKYEGGNIIVDIDFDSVPQIHG 38
Db 2 QNSGNQSFEDTDEKPKYEGGNIIVDIDFDSVPQIHG 39

RESULT 5
US-08-459-135A-7
Sequence 7, Application US/08459135A
Patent No. 5955078
GENERAL INFORMATION:
APPLICANT: BURNHAM, Martin Karl Russel
APPLICANT: CHOPRA, Ian
APPLICANT: CRITCHLEY, Ian Alfred
APPLICANT: KNOWLES, David Justin Charles
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN: MONOCLONAL ANTIBODY AND THEIR US
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
STATE: PA
COUNTRY: U.S.A.
ZIP: 19406-0939
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: Fastseq, Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/459,135A
FILING DATE: 02-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/CB/94/00215
FILING DATE: 04-Feb-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Gimm, Edward R
REGISTRATION NUMBER: 38,891
REFERENCE/DOCKET NUMBER: P30591C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-4478
TELEFAX: 610-270-5090
TELEX:
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:

LENGTH: 130 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-459-135A-7

Query Match 96.1%; Score 199; DB 2; Length 130;
Best Local Similarity 97.4%; Pred. No. 1.1e-19;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QNSGNQSFEDTDEKPKYEGGNIIVDIDFDSVPQIHG 38
Db 2 QNSGNQSFEDTDEKPKYEGGNIIVDIDFDSVPQIHG 39

RESULT 6
US-08-459-135A-8
Sequence 8, Application US/08459135A
Patent No. 5955078
GENERAL INFORMATION:
APPLICANT: BURNHAM, Martin Karl Russel
APPLICANT: CHOPRA, Ian
APPLICANT: CRITCHLEY, Ian Alfred
APPLICANT: KNOWLES, David Justin Charles
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN: MONOCLONAL ANTIBODY AND THEIR US
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
STATE: PA
COUNTRY: U.S.A.
ZIP: 19406-0939
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: Fastseq, Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/459,135A
FILING DATE: 02-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/CB/94/00215
FILING DATE: 04-Feb-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Gimm, Edward R
REGISTRATION NUMBER: 38,891
REFERENCE/DOCKET NUMBER: P30591C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-4478
TELEFAX: 610-270-5090
TELEX:
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 130 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-459-135A-8

Query Match 96.1%; Score 199; DB 2; Length 130;
Best Local Similarity 97.4%; Pred. No. 1.1e-19;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QNSGNQSFEDTDEKPKYEGGNIIVDIDFDSVPQIHG 38
Db 2 QNSGNQSFEDTDEKPKYEGGNIIVDIDFDSVPQIHG 39

RESULT 7
US-08-495-559-7

```

; Sequence 7, Application US/08495559A
; Patent No. 6054572
; GENERAL INFORMATION:
; APPLICANT: BURHAM, Martin Karl Russel
; APPLICANT: CHOPRA, Ian
; APPLICANT: CRITCHLEY, Ian Alfred
; APPLICANT: KNOWLES, David Justin Charles
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN: MONOCLONAL
; TITLE OF INVENTION: ANTIBODY AND THEIR USE IN PREVENTING BACTERIAL ADHESION
; FILE REFERENCE: P30591
; CURRENT APPLICATION NUMBER: US/08/495,559A
; CURRENT FILING DATE: 1995-08-03
; EARLIER APPLICATION NUMBER: GB 9302289.5
; EARLIER FILING DATE: 1993-02-05
; EARLIER APPLICATION NUMBER: GB 9321592.9
; EARLIER FILING DATE: 1993-10-20
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 7
; LENGTH: 130
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-08-495-559-7

Query Match      96.1%; Score 199; DB 3; Length 130;
Best Local Similarity 97.4%; Pred. No. 1.1e-19;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 QNSGNQSFEDPTEDKPKYEQGNIVDIDPDSVPQIHG 38
Db      2 QNSGNQSFEDPTEDKPKYEQGNIVDIDPDSVPQIHG 39

RESULT 8
US-08-495-559-8
; Sequence 8, Application US/08495559A
; Patent No. 6054572
; GENERAL INFORMATION:
; APPLICANT: BURHAM, Martin Karl Russel
; APPLICANT: CHOPRA, Ian
; APPLICANT: CRITCHLEY, Ian Alfred
; APPLICANT: KNOWLES, David Justin Charles
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN: MONOCLONAL
; TITLE OF INVENTION: ANTIBODY AND THEIR USE IN PREVENTING BACTERIAL ADHESION
; FILE REFERENCE: P30591
; CURRENT APPLICATION NUMBER: US/08/495,559A
; CURRENT FILING DATE: 1995-08-03
; EARLIER APPLICATION NUMBER: GB 9302289.5
; EARLIER FILING DATE: 1993-02-05
; EARLIER APPLICATION NUMBER: GB 9321592.9
; EARLIER FILING DATE: 1993-10-20
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 8
; LENGTH: 130
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-08-495-559-8

Query Match      96.1%; Score 199; DB 3; Length 130;
Best Local Similarity 97.4%; Pred. No. 1.1e-19;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 QNSGNQSFEDPTEDKPKYEQGNIVDIDPDSVPQIHG 38
Db      2 QNSGNQSFEDPTEDKPKYEQGNIVDIDPDSVPQIHG 39

RESULT 9
US-08-856-253-8
; Sequence 8, Application US/08856253
; Patent No. 6288214
; GENERAL INFORMATION:

```

```

; APPLICANT: Hook, Magnus
; APPLICANT: Partl, Joseph M.
; APPLICANT: House-Pompeo, Karen
; APPLICANT: Schanam, Narayana
; APPLICANT: Symersky, Jindrich
; TITLE OF INVENTION: COLLAGEN BINDING PROTEIN COMPOSITIONS
; TITLE OF INVENTION: AND METHODS OF USE
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: U.S.
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/856,253
; FILING DATE: Concurrently Herewith
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/017,678
; FILING DATE: 16-MAY-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Kitchell, Barbara S.
; REGISTRATION NUMBER: 33,928
; REFERENCE/DOCKET NUMBER: TAMK:193
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (512) 418-1000
; TELEFAX: (512) 474-7577
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 139 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
US-08-856-253-8

Query Match      96.1%; Score 199; DB 3; Length 139;
Best Local Similarity 97.4%; Pred. No. 1.1e-19;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 QNSGNQSFEDPTEDKPKYEQGNIVDIDPDSVPQIHG 38
Db      16 QNSGNQSFEDPTEDKPKYEQGNIVDIDPDSVPQIHG 53

RESULT 10
US-08-459-135A-10
; Sequence 10, Application US/08459135A
; Patent No. 5955078
; GENERAL INFORMATION:
; APPLICANT: BURHAM, Martin Karl Russel
; APPLICANT: CHOPRA, Ian
; APPLICANT: CRITCHLEY, Ian Alfred
; APPLICANT: KNOWLES, David Justin Charles
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN: MONOCLONAL ANTIBODY AND THEIR USE
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corporation
; STREET: 709 Swedeland Road
; CITY: King of Prussia
; STATE: PA
; COUNTRY: U.S.A.
; ZIP: 19406-0939
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS

```

SOFTWARE: FastSeq, Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/459,135A
FILING DATE: 02-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB/94/00215
FILING DATE: 04-Feb-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Gimm, Edward R
REGISTRATION NUMBER: 38,891
REFERENCE/DOCKET NUMBER: P30591C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-4478
TELEFAX: 610-270-5090
TELEX:
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 174 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: Protein
US-08-459-135A-10

Query Match 96.1%; Score 199; DB 2; Length 174;
Best Local Similarity 97.4%; Pred. No. 1.5e-19;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QNSGNQSFEDTEEDPKPYEGCGNIVDIDFDSVPQIHG 38
|||
Db 2 QNSGNQSFEDTEEDPKPYEGCGNIVDIDFDSVPQIHG 39
|||

RESULT 11
US-08-459-135A-13
Sequence 13, Application US/08459135A
Patent No. 5955078
GENERAL INFORMATION:
APPLICANT: BURHAM, Martin Karl Russel
APPLICANT: CHOPRA, Ian
APPLICANT: CRITCHLEY, Ian Alfred
APPLICANT: KNOWLES, David Justin Charles
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN: MONOCLONAL ANTIBODY AND THEIR US
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
STATE: PA
COUNTRY: U.S.A.
ZIP: 19406-0939
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq, Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/459,135A
FILING DATE: 02-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB/94/00215
FILING DATE: 04-Feb-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Gimm, Edward R
REGISTRATION NUMBER: 38,891
REFERENCE/DOCKET NUMBER: P30591C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-4478
TELEFAX: 610-270-5090
TELEX:

INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 174 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-459-135A-13

Query Match 96.1%; Score 199; DB 2; Length 174;
Best Local Similarity 97.4%; Pred. No. 1.5e-19;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QNSGNQSFEDTEEDPKPYEGCGNIVDIDFDSVPQIHG 38
|||
Db 2 QNSGNQSFEDTEEDPKPYEGCGNIVDIDFDSVPQIHG 39
|||

RESULT 12
US-08-495-559-10
Sequence 10, Application US/08495559A
Patent No. 6054572
GENERAL INFORMATION:
APPLICANT: BURHAM, Martin Karl Russel
APPLICANT: CHOPRA, Ian
APPLICANT: CRITCHLEY, Ian Alfred
APPLICANT: KNOWLES, David Justin Charles
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN: MONOCLONAL
TITLE OF INVENTION: ANTIBODY AND THEIR USE IN PREVENTING BACTERIAL ADHESION
FILE REFERENCE: P30591
CURRENT APPLICATION NUMBER: US/08/495,559A
CURRENT FILING DATE: 1995-08-03
EARLIER APPLICATION NUMBER: GB 9302289.5
EARLIER FILING DATE: 1993-02-05
EARLIER APPLICATION NUMBER: GB 9321592.9
EARLIER FILING DATE: 1993-10-20
NUMBER OF SEQ ID NOS: 13
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 10
LENGTH: 174
TYPE: PRP
ORGANISM: Staphylococcus aureus
US-08-495-559-10

Query Match 96.1%; Score 199; DB 3; Length 174;
Best Local Similarity 97.4%; Pred. No. 1.5e-19;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QNSGNQSFEDTEEDPKPYEGCGNIVDIDFDSVPQIHG 38
|||
Db 2 QNSGNQSFEDTEEDPKPYEGCGNIVDIDFDSVPQIHG 39
|||

RESULT 13
US-08-495-559-13
Sequence 13, Application US/08495559A
Patent No. 6054572
GENERAL INFORMATION:
APPLICANT: BURHAM, Martin Karl Russel
APPLICANT: CHOPRA, Ian
APPLICANT: CRITCHLEY, Ian Alfred
APPLICANT: KNOWLES, David Justin Charles
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN: MONOCLONAL
TITLE OF INVENTION: ANTIBODY AND THEIR USE IN PREVENTING BACTERIAL ADHESION
FILE REFERENCE: P30591
CURRENT APPLICATION NUMBER: US/08/495,559A
CURRENT FILING DATE: 1995-08-03
EARLIER APPLICATION NUMBER: GB 9302289.5
EARLIER FILING DATE: 1993-02-05
EARLIER APPLICATION NUMBER: GB 9321592.9
EARLIER FILING DATE: 1993-10-20
NUMBER OF SEQ ID NOS: 13
SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 13
LENGTH: 174
TYPE: PRT
ORGANISM: Staphylococcus aureus
US-08-495-559-13

Query Match 96.1%; Score 199; DB 3; Length 174;
Best Local Similarity 97.4%; Pred. No. 1.5e-19;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QNSGNQSFEDTDEKPKYEQGNIVDIDFDSVPQIHG 38
Db 2 QNSGNQSFEDTDEKPKYEQGNIVDIDFDSVPQIHG 39

RESULT 14
US-08-495-559-6
Sequence 6, Application US/08495559A
Patent No. 6054572
GENERAL INFORMATION:
APPLICANT: BURHAM, Martin Karl Russel
APPLICANT: CHOPRA, Ian
APPLICANT: CRITCHLEY, Ian Alfred
APPLICANT: KNOWLES, David Justin Charles
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN: MONOCLONAL
TITLE OF INVENTION: ANTIBODY AND THEIR USE IN PREVENTING BACTERIAL ADHESION
FILE REFERENCE: P30591
CURRENT APPLICATION NUMBER: US/08/495,559A
EARLIER FILING DATE: 1995-08-03
EARLIER APPLICATION NUMBER: GB 9302289.5
EARLIER FILING DATE: 1993-02-05
EARLIER APPLICATION NUMBER: GB 9321592.9
EARLIER FILING DATE: 1993-10-20
NUMBER OF SEQ ID NOS: 13
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 6
LENGTH: 176
TYPE: PRT
ORGANISM: Staphylococcus aureus
US-08-495-559-6

Query Match 96.1%; Score 199; DB 3; Length 176;
Best Local Similarity 97.4%; Pred. No. 1.5e-19;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QNSGNQSFEDTDEKPKYEQGNIVDIDFDSVPQIHG 38
Db 2 QNSGNQSFEDTDEKPKYEQGNIVDIDFDSVPQIHG 39

RESULT 15
US-08-459-135A-12
Sequence 12, Application US/08459135A
Patent No. 5955078
GENERAL INFORMATION:
APPLICANT: BURHAM, Martin Karl Russel
APPLICANT: CHOPRA, Ian
APPLICANT: CRITCHLEY, Ian Alfred
APPLICANT: KNOWLES, David Justin Charles
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN: MONOCLONAL ANTIBODY AND THEIR US
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
STATE: PA
COUNTRY: U.S.A.
ZIP: 19406-0939
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: Fastseq, Version 2.0

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/459,135A
FILING DATE: 02-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA: PCT/GB/94/00215
APPLICATION NUMBER: PCT/GB/94/00215
FILING DATE: 04-Feb-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Gimm, Edward R
REGISTRATION NUMBER: 38,891
REFERENCE/DOCKET NUMBER: P30591C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-4478
TELEFAX: 610-270-5090
TELEX:
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 178 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: Protein
US-08-459-135A-12

Query Match 96.1%; Score 199; DB 2; Length 178;
Best Local Similarity 97.4%; Pred. No. 1.5e-19;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QNSGNQSFEDTDEKPKYEQGNIVDIDFDSVPQIHG 38
Db 2 QNSGNQSFEDTDEKPKYEQGNIVDIDFDSVPQIHG 39

Search completed: October 22, 2005, 05:46:43
Job time : 22.2223 secs

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OM protein - protein search, using SW model

Run on: October 22, 2005, 11:35:03 ; Search time 70.1256 Seconds
(without alignments)
226.232 Million cell updates/sec

Title: US-10-731-238-37

Perfect score: 207
Sequence: 1 QNSGNQSPFPTEDKPKRYEGGNIVIDPDSVPQIHG 38

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1862951 seqs, 417491010 residues

Total number of hits satisfying chosen parameters: 1862951

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

Published Applications AA.*
1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep.*
7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
9: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep.*
10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep.*
11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep.*
12: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
13: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
14: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
15: /cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pep.*
16: /cgn2_6/ptodata/2/pubpaa/US10E_PUBCOMB.pep.*
17: /cgn2_6/ptodata/2/pubpaa/US10F_PUBCOMB.pep.*
18: /cgn2_6/ptodata/2/pubpaa/US10A_NEW_PUB.pep.*
19: /cgn2_6/ptodata/2/pubpaa/US11A_PUBCOMB.pep.*
20: /cgn2_6/ptodata/2/pubpaa/US11A_NEW_PUB.pep.*
21: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
22: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	207	100.0	38	18 US-10-731-238-37	Sequence 37, Appl
2	199	96.1	38	18 US-10-731-238-5	Sequence 3, Appl
3	199	96.1	139	9 US-09-813-820-8	Sequence 8, Appl
4	199	96.1	388	8 US-08-801-062-1	Sequence 1, Appl
5	199	96.1	559	15 US-08-781-986A-5251	Sequence 5251, Ap
6	199	96.1	559	15 US-10-329-624-5251	Sequence 5251, Ap
7	199	96.1	767	9 US-09-815-242-5899	Sequence 5899, Ap
8	199	96.1	767	9 US-09-815-242-13140	Sequence 13140, A
9	199	96.1	940	17 US-10-470-048B-424	Sequence 424, App
10	199	96.1	948	17 US-10-470-048B-69	Sequence 69, Appl
11	199	96.1	961	15 US-10-282-122A-43778	Sequence 43778, A

12	199	96.1	1018	9 US-09-815-242-5797	Sequence 5797, Ap
13	199	96.1	1018	9 US-09-815-242-12838	Sequence 12838, A
14	199	96.1	1018	17 US-10-470-048B-68	Sequence 68, Appl
15	199	96.1	1027	8 US-08-781-986A-5254	Sequence 5254, Ap
16	199	96.1	1027	15 US-10-329-624-5254	Sequence 43827, A
17	199	96.1	1038	15 US-10-282-122A-43827	Sequence 43827, A
18	199	93.2	38	18 US-10-731-238-36	Sequence 36, Appl
19	193	93.2	38	18 US-10-731-238-39	Sequence 39, Appl
20	193	93.2	38	18 US-10-731-238-40	Sequence 40, Appl
21	193	93.2	38	18 US-10-731-238-41	Sequence 41, Appl
22	192	92.8	38	18 US-10-731-238-38	Sequence 38, Appl
23	192	92.8	38	18 US-10-731-238-42	Sequence 42, Appl
24	191	92.3	38	18 US-10-731-238-6	Sequence 6, Appl
25	191	92.3	38	18 US-10-731-238-43	Sequence 43, Appl
26	191	92.3	978	9 US-09-815-242-5456	Sequence 5456, Ap
27	191	92.3	1001	9 US-09-815-242-12686	Sequence 12686, A
28	189	91.3	38	18 US-10-731-238-35	Sequence 35, Appl
29	188.5	91.1	39	18 US-10-731-238-56	Sequence 56, Appl
30	188	90.8	38	18 US-10-731-238-47	Sequence 47, Appl
31	185	89.4	38	18 US-10-731-238-44	Sequence 44, Appl
32	180.5	87.2	39	18 US-10-731-238-57	Sequence 57, Appl
33	180	87.0	38	18 US-10-731-238-7	Sequence 7, Appl
34	174	84.1	38	18 US-10-731-238-46	Sequence 46, Appl
35	173	83.6	38	18 US-10-731-238-48	Sequence 48, Appl
36	172	83.1	38	18 US-10-731-238-8	Sequence 8, Appl
37	172	83.1	38	18 US-10-731-238-49	Sequence 49, Appl
38	170	82.1	38	18 US-10-731-238-45	Sequence 45, Appl
39	166	80.2	38	18 US-10-731-238-50	Sequence 50, Appl
40	157	75.8	36	18 US-10-731-238-58	Sequence 58, Appl
41	149	72.0	36	18 US-10-731-238-59	Sequence 59, Appl
42	141	68.1	30	14 US-10-287-821-1	Sequence 1, Appl
43	141	68.1	31	14 US-10-287-821-2	Sequence 2, Appl
44	77.5	37.4	37	20 US-11-066-697-1134	Sequence 1134, Ap
45	74	35.7	14	18 US-10-731-238-60	Sequence 60, Appl

ALIGNMENTS

RESULT 1
US-10-731-238-37
Sequence 37, Appl Application US/10731238
Publication No. US2005012352A1
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
Pattl, Joseph M.
House-Pompeo, Karen L.
Speziale, Pietro
McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/731,238
FILING DATE: 10-Dec-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE: 21-Jan-1998
APPLICATION NUMBER: US 60/036,139

FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAMK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 37:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
US-10-731-238-37
SEQUENCE DESCRIPTION: SEQ ID NO: 37:
Query Match 100.0%; Score 207; DB 18; Length 38;
Best Local Similarity 100.0%; Pred. No. 6,2e-20;
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Cy 1 QNSGNQSFEPDTEBDKPKYEQGNIVDIDPDSVPQIHG 38
Db 1 QNSGNQSFEPDTEBDKPKYEQGNIVDIDPDSVPQIHG 38
RESULT 2
US-10-731-238-5
Sequence 5, Application US/10731238
Publication No. US20050123552A1
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
Patti, Joseph M.
House-Pompeo, Karen L.
Speziale, Pietro
Joh, Danny
McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/731,238
FILING DATE: 10-Dec-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE: 21-Jan-1998
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAMK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>

TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-10-731-238-5
Query Match 96.1%; Score 199; DB 18; Length 38;
Best Local Similarity 97.4%; Pred. No. 7e-19;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Cy 1 QNSGNQSFEPDTEBDKPKYEQGNIVDIDPDSVPQIHG 38
Db 1 QNSGNQSFEPDTEBDKPKYEQGNIVDIDPDSVPQIHG 38
RESULT 3
US-09-813-820-8
Sequence 8, Application US/09813820
Patent No. US20020102262A1
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
Patti, Joseph M.
House-Pompeo, Karen
Stehnam, Maryana
Symersky, Jindrich
TITLE OF INVENTION: COLLAGEN BINDING PROTEIN COMPOSITIONS
AND METHODS OF USE
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: Texas
COUNTRY: U.S.
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/813,820
FILING DATE: 22-Mar-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/856,253
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Kitchell, Bairdara S.
REGISTRATION NUMBER: 33,928
REFERENCE/DOCKET NUMBER: TAMK:193
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
TELEFAX: (512) 474-7577
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 139 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
US-09-813-820-8
SEQUENCE DESCRIPTION: SEQ ID NO: 8:
Query Match 96.1%; Score 199; DB 9; Length 139;
Best Local Similarity 97.4%; Pred. No. 3,2e-18;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Cy 1 QNSGNQSFEPDTEBDKPKYEQGNIVDIDPDSVPQIHG 38
Db 16 QNSGNQSFEPDTEBDKPKYEQGNIVDIDPDSVPQIHG 53
RESULT 4
US-08-901-062-1
Sequence 1, Application US/08901062

Publication No. US20020025324A1
GENERAL INFORMATION:
APPLICANT: SEALS, JONATHAN R.
TITLE OF INVENTION: RECOMBINANT BIVALENT BACTERIAL VACCINE
TITLE OF INVENTION: FOR THE PREVENTION OF MASTITIS
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: HALE AND DORR LLP
STREET: 60 State Street
CITY: Boston
STATE: MA
COUNTRY: United States Of America
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/901,062
FILING DATE: 25-JUL-1997
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Baker, Hollie L.
REGISTRATION NUMBER: 31,321
REFERENCE/DOCKET NUMBER: 106941.153
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 526-6000
TELEFAX: (617) 526-5000
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 388 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYDROTHERICAL: NO
ANTI-SENSE: NO
US-08-901-062-1

Query Match 96.1%; Score 199; DB 8; Length 388;
Best Local Similarity 97.4%; Pred. No. 1,1e-17;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

CY 1 ONSGNQSFEPDTEBDKPKYEGGNIIVDIDFDSVPQIHG 38
Db 265 ONSGNQSFEPDTEBDKPKYEGGNIIVDIDFDSVPQIHG 302

RESULT 5
US-08-781-986A-5251
Sequence 5251, Application US/08781986A
Publication No. US20030054436A1
GENERAL INFORMATION:
APPLICANT: Charles Kunisch
TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
NUMBER OF SEQUENCES: 5255
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COUNTRY: USA
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/781,986A
FILING DATE:
CLASSIFICATION: 435

PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Benson, Bob
REGISTRATION NUMBER: 30,446
REFERENCE/DOCKET NUMBER: PB248PP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8512
TELEFAX: (301) 309-8504
INFORMATION FOR SEQ ID NO: 5251:
SEQUENCE CHARACTERISTICS:
LENGTH: 559 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-781-986A-5251

Query Match 96.1%; Score 199; DB 8; Length 559;
Best Local Similarity 97.4%; Pred. No. 1,1e-17;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

CY 1 ONSGNQSFEPDTEBDKPKYEGGNIIVDIDFDSVPQIHG 38
Db 301 ONSGNQSFEPDTEBDKPKYEGGNIIVDIDFDSVPQIHG 338

RESULT 6
US-10-329-624-5251
Sequence 5251, Application US/10329624
Publication No. US20040043037A1
GENERAL INFORMATION:
APPLICANT: Charles Kunisch
Gill H. Choi
Patrick S. Dillon
Craig A. Rosen
Steven C. Barash
Michael R. Fannon
TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
NUMBER OF SEQUENCES: 5256
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COUNTRY: USA
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/329,624
FILING DATE: 27-Dec-2002
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/956,171
FILING DATE: October 20, 1997
APPLICATION NUMBER: 60/009,861
FILING DATE: January 5, 1996
APPLICATION NUMBER: 08/781,986
FILING DATE: January 3, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Mark J. Hyman
REGISTRATION NUMBER: 46,789
REFERENCE/DOCKET NUMBER: PB248P1D1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (240) 314-1224
TELEFAX: (301) 309-8439
INFORMATION FOR SEQ ID NO: 5251:
SEQUENCE CHARACTERISTICS:
LENGTH: 559 amino acids

TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 5251:
US-10-329-624-5251

Query Match 96.1%; Score 199; DB 15; Length 559;
Best Local Similarity 97.4%; Pred. No. 1.6e-17;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QNSGNQSFEPDTEBDKPKYEGGNIIVDIDFDSVPQIHG 38
Db 301 QNSGNQSFEPDTEBDKPKYEGGNIIVDIDFDSVPQIHG 338

RESULT 7

US-09-815-242-5899
Sequence 5899, Application US/09815242
Patent No. US20020061569A1

GENERAL INFORMATION:

APPLICANT: Haseibeck, Robert

APPLICANT: Ohlsen, Karl L.

APPLICANT: Zykkind, Judith W.

APPLICANT: Wall, Daniel

APPLICANT: Trawick, John D.

APPLICANT: Carr, Grant J.

APPLICANT: Yamamoto, Robert T.

APPLICANT: Xu, H. Howard

TITLE OF INVENTION: Identification of Essential Genes in

FILE REFERENCE: ELITRA.011A

CURRENT APPLICATION NUMBER: US/09/815,242

PRIOR FILING DATE: 2001-03-21

PRIOR APPLICATION NUMBER: 60/191,078

PRIOR FILING DATE: 2000-03-21

PRIOR APPLICATION NUMBER: 60/206,848

PRIOR FILING DATE: 2000-05-23

PRIOR APPLICATION NUMBER: 60/207,727

PRIOR FILING DATE: 2000-05-26

PRIOR APPLICATION NUMBER: 60/242,578

PRIOR FILING DATE: 2000-10-23

PRIOR APPLICATION NUMBER: 60/253,625

PRIOR FILING DATE: 2000-11-27

PRIOR APPLICATION NUMBER: 60/257,931

PRIOR FILING DATE: 2000-12-22

PRIOR APPLICATION NUMBER: 60/269,308

PRIOR FILING DATE: 2001-02-16

NUMBER OF SEQ ID NOS: 14110

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 5899

LENGTH: 767

TYPE: PRT

ORGANISM: Staphylococcus aureus

US-09-815-242-5899

Query Match 96.1%; Score 199; DB 9; Length 767;
Best Local Similarity 97.4%; Pred. No. 2.3e-17;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QNSGNQSFEPDTEBDKPKYEGGNIIVDIDFDSVPQIHG 38
Db 682 QNSGNQSFEPDTEBDKPKYEGGNIIVDIDFDSVPQIHG 719

RESULT 8

US-09-815-242-13140
Sequence 13140, Application US/09815242
Patent No. US20020061569A1

GENERAL INFORMATION:

APPLICANT: Haseibeck, Robert

APPLICANT: Ohlsen, Karl L.

APPLICANT: Zykkind, Judith W.

APPLICANT: Wall, Daniel
APPLICANT: Trawick, John D.
APPLICANT: Carr, Grant J.
APPLICANT: Yamamoto, Robert T.
APPLICANT: Xu, H. Howard

TITLE OF INVENTION: Identification of Essential Genes in

FILE REFERENCE: ELITRA.011A

CURRENT APPLICATION NUMBER: US/09/815,242

PRIOR FILING DATE: 2001-03-21

PRIOR APPLICATION NUMBER: 60/191,078

PRIOR FILING DATE: 2000-03-21

PRIOR APPLICATION NUMBER: 60/206,848

PRIOR FILING DATE: 2000-05-23

PRIOR APPLICATION NUMBER: 60/207,727

PRIOR FILING DATE: 2000-05-26

PRIOR APPLICATION NUMBER: 60/242,578

PRIOR FILING DATE: 2000-10-23

PRIOR APPLICATION NUMBER: 60/253,625

PRIOR FILING DATE: 2000-11-27

PRIOR APPLICATION NUMBER: 60/257,931

PRIOR FILING DATE: 2000-12-22

PRIOR APPLICATION NUMBER: 60/269,308

PRIOR FILING DATE: 2001-02-16

NUMBER OF SEQ ID NOS: 14110

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 13140

LENGTH: 767

TYPE: PRT

ORGANISM: Staphylococcus aureus

US-09-815-242-13140

Query Match 96.1%; Score 199; DB 9; Length 767;
Best Local Similarity 97.4%; Pred. No. 2.3e-17;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QNSGNQSFEPDTEBDKPKYEGGNIIVDIDFDSVPQIHG 38
Db 682 QNSGNQSFEPDTEBDKPKYEGGNIIVDIDFDSVPQIHG 719

RESULT 9

US-10-470-048B-424
Sequence 424, Application US/10470048B
Publication No. US20050037444A1

GENERAL INFORMATION:

APPLICANT: MEINKE ET AL.

TITLE OF INVENTION: A METHOD FOR IDENTIFICATION, ISOLATION AND PRODUCTION OF

FILE REFERENCE: SOMN:035US

CURRENT APPLICATION NUMBER: US/10/470,048B

PRIOR FILING DATE: 2003-07-25

NUMBER OF SEQ ID NOS: 603

SOFTWARE: PatentIn version 3.1

SEQ ID NO 424

LENGTH: 940

TYPE: PRT

ORGANISM: Staphylococcus aureus

US-10-470-048B-424

Query Match 96.1%; Score 199; DB 17; Length 940;
Best Local Similarity 97.4%; Pred. No. 2.9e-17;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QNSGNQSFEPDTEBDKPKYEGGNIIVDIDFDSVPQIHG 38
Db 682 QNSGNQSFEPDTEBDKPKYEGGNIIVDIDFDSVPQIHG 719

RESULT 10

US-10-470-048B-69
Sequence 69, Application US/10470048B
Publication No. US20050037444A1

```

; GENERAL INFORMATION:
; APPLICANT: MEINKE ET AL.
; TITLE OF INVENTION: A METHOD FOR IDENTIFICATION, ISOLATION AND PRODUCTION OF
; FILE OF INVENTION: ANTIGENS TO A SPECIFIC PATHOGEN
; FILE REFERENCE: SONN-035US
; CURRENT APPLICATION NUMBER: US/10/470,048B
; CURRENT FILING DATE: 2003-07-25
; NUMBER OF SEQ ID NOS: 603
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 69
; LENGTH: 948
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
; US-10-470-048B-69

Query Match      96.1%; Score 199; DB 17; Length 948;
Best Local Similarity 97.4%; Pred. No. 3e-17;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1  QNSGNQSFEPDTEBDKPKYEQGNIIVDIDFDSVPQIHG 38
Db      690  QNSGNQSFEPDTEBDKPKYEQGNIIVDIDFDSVPQIHG 727

RESULT 11
; US-10-282-122A-43778
; Sequence 43778, Application US/10282122A
; Publication NO. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 43778
; LENGTH: 961
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
; US-10-282-122A-43778
```

```

Query Match      96.1%; Score 199; DB 15; Length 961;
Best Local Similarity 97.4%; Pred. No. 3e-17;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1  QNSGNQSFEPDTEBDKPKYEQGNIIVDIDFDSVPQIHG 38
Db      693  QNSGNQSFEPDTEBDKPKYEQGNIIVDIDFDSVPQIHG 730

RESULT 12
; US-09-815-242-5797
; Sequence 5797, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; FILE REFERENCE: ELITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14410
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5797
; LENGTH: 1018
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
; US-09-815-242-5797

Query Match      96.1%; Score 199; DB 9; Length 1018;
Best Local Similarity 97.4%; Pred. No. 3.2e-17;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1  QNSGNQSFEPDTEBDKPKYEQGNIIVDIDFDSVPQIHG 38
Db      746  QNSGNQSFEPDTEBDKPKYEQGNIIVDIDFDSVPQIHG 783

RESULT 13
; US-09-815-242-12838
; Sequence 12838, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
```

```
/ TITLE OF INVENTION: Prokaryotes
/ FILE REFERENCE: ELITRA.011A
/ CURRENT APPLICATION NUMBER: US/09/815,242
/ CURRENT FILING DATE: 2001-03-21
/ PRIOR APPLICATION NUMBER: 60/191,078
/ PRIOR FILING DATE: 2000-03-21
/ PRIOR APPLICATION NUMBER: 60/206,848
/ PRIOR FILING DATE: 2000-05-23
/ PRIOR APPLICATION NUMBER: 60/207,727
/ PRIOR FILING DATE: 2000-05-26
/ PRIOR APPLICATION NUMBER: 60/242,578
/ PRIOR FILING DATE: 2000-10-23
/ PRIOR APPLICATION NUMBER: 60/253,625
/ PRIOR FILING DATE: 2000-11-27
/ PRIOR APPLICATION NUMBER: 60/257,931
/ PRIOR FILING DATE: 2000-12-22
/ PRIOR APPLICATION NUMBER: 60/269,308
/ PRIOR FILING DATE: 2001-02-16
/ NUMBER OF SEQ ID NOS: 14110
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 12838
/ LENGTH: 1018
/ TYPE: PRT
/ ORGANISM: Staphylococcus aureus
US-09-815-242-12838

Query Match          96.1%; Score 199; DB 9; Length 1018;
Best Local Similarity 97.4%; Pred. No. 3,2e-17;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QNSGNSFEPDTEEDKPKYEGGNIVIDIDFDSVPQIHG 38
Db 746 QNSGNSFEPDTEEDKPKYEGGNIVIDIDFDSVPQIHG 783

RESULT 14
US-10-470-048B-68
/ Sequence 68, Application US/10470048B
/ Publication No. US20050037444A1
/ GENERAL INFORMATION:
/ APPLICANT: MEINKE ET AL.
/ TITLE OF INVENTION: A METHOD FOR IDENTIFICATION, ISOLATION AND PRODUCTION OF
/ FILE REFERENCE: SONN:035US
/ CURRENT APPLICATION NUMBER: US/10/470,048B
/ CURRENT FILING DATE: 2003-07-25
/ NUMBER OF SEQ ID NOS: 603
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 68
/ LENGTH: 1018
/ TYPE: PRT
/ ORGANISM: Staphylococcus aureus
US-10-470-048B-68

Query Match          96.1%; Score 199; DB 17; Length 1018;
Best Local Similarity 97.4%; Pred. No. 3,2e-17;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QNSGNSFEPDTEEDKPKYEGGNIVIDIDFDSVPQIHG 38
Db 746 QNSGNSFEPDTEEDKPKYEGGNIVIDIDFDSVPQIHG 783

RESULT 15
US-08-781-986A-5254
/ Sequence 5254, Application US/08781986A
/ Publication No. US20030054436A1
/ GENERAL INFORMATION:
/ APPLICANT: Charles Kunsch
/ TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
/ NUMBER OF SEQUENCES: 5255
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Human Genome Sciences, Inc.
```

```
/ STREET: 9410 Key West Avenue
/ CITY: Rockville
/ STATE: Maryland
/ COUNTRY: USA
/ ZIP: 20850
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Diskette, 3.50 inch, 1.4MB storage
/ COMPUTER: HP Vectra 486/33
/ OPERATING SYSTEM: MSDOS version 6.2
/ SOFTWARE: ASCII Text
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/781,986A
/ FILING DATE:
/ CLASSIFICATION: 435
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER:
/ FILING DATE:
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Benson, Bob
/ REGISTRATION NUMBER: 30,446
/ REFERENCE/DOCKET NUMBER: PB248PP
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (301) 309-8504
/ TELEFAX: (301) 309-8512
/ INFORMATION FOR SEQ ID NO: 5254:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 1027 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
US-08-781-986A-5254

Query Match          96.1%; Score 199; DB 8; Length 1027;
Best Local Similarity 97.4%; Pred. No. 3,3e-17;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QNSGNSFEPDTEEDKPKYEGGNIVIDIDFDSVPQIHG 38
Db 755 QNSGNSFEPDTEEDKPKYEGGNIVIDIDFDSVPQIHG 792

Search completed: October 22, 2005, 12:09:25
Job time : 71.1256 secs
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Db 693 QNSGNQSFEDTEBDKPKYEGGNIIVDIDFDSVPQIHG 730

RESULT 3

A32192

Fibronectin-binding protein - Staphylococcus aureus

C/Species: Staphylococcus aureus

C/Date: 31-Jul-1989 #sequence_revision 31-Jul-1989 #text_change 16-Feb-1997

C/Accession: A32192

R/Sigman, C.; Raucica, G.; Joensson, K.; Lindgren, P.E.; Anantharamaiah, G.M.; Heeok, M.

Proc. Natl. Acad. Sci. U.S.A. 86, 699-703, 1989

A/Title: Nucleotide sequence of the gene for a fibronectin-binding protein from Staphylo

A/Reference number: A32192; MUID:89098998; PMID:2521391

A/Accession: A32192

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-1018 <SIG>

A/Cross-references: GB:J04151

C/Keywords: fibronectin binding

Query Match 96.1%; Score 199; DB 2; Length 1018;
Best Local Similarity 97.4%; Pred. No. 1.7e-17;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

1 QNSGNQSFEDTEBDKPKYEGGNIIVDIDFDSVPQIHG 38

Db 746 QNSGNQSFEDTEBDKPKYEGGNIIVDIDFDSVPQIHG 783

RESULT 4

H90053

hypothetical protein fnb (imported) - Staphylococcus aureus (strain N315)

C/Species: Staphylococcus aureus

C/Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004

C/Accession: H90053

R/Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Ogun

ma, A.; Mitsuhashi, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.

Lancet 357, 1225-1240, 2001

A/Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.

A/Reference number: A89758; MUID:21311952; PMID:11418146

A/Accession: H90053

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-1038 <KUR>

A/Cross-references: UNIPROT:Q9PRD2; GB:BA000018; PID:g13702453; PIDN:BAB43594.1; GSPDB:G

C/Experimental source: strain N315

C/Genetics:

A/Gene: fnb

Query Match 96.1%; Score 199; DB 2; Length 1038;
Best Local Similarity 97.4%; Pred. No. 1.7e-17;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

1 QNSGNQSFEDTEBDKPKYEGGNIIVDIDFDSVPQIHG 38

Db 742 QNSGNQSFEDTEBDKPKYEGGNIIVDIDFDSVPQIHG 779

RESULT 5

A82940

hypothetical protein U0044 (imported) - Ureaplasma urealyticum

C/Species: Ureaplasma urealyticum

C/Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000

C/Accession: A82940

R/Glass, J.I.; Letkowitz, E.J.; Glass, J.S.; Heiner, C.R.; Chen, E.Y.; Caswell, G.H.

submitted to GenBank, February 2000

A/Description: The complete sequence of Ureaplasma urealyticum: Alternate views of a mit

A/Reference number: A82940

A/Accession: A82940

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-782 <GLA>
A/Cross-references: GB:AE002104; GB:AF222894; NID:g6898990; PIDN:AAF30449.1; GSPDB:GN001;
A/Experimental source: serovar 3; biovar 1
C/Genetics:
A/Gene: U0044
A/Gene code: SGCS

Query Match 27.8%; Score 57.5; DB 2; Length 782;
Best Local Similarity 38.9%; Pred. No. 25;
Matches 14; Conservative 3; Mismatches 14; Indels 5; Gaps 1;

1 QNSGNQSFEDTEBDKPKYEGGNIIVDIDFDSVPQI 36

Db 619 QGFFGFLDHPDHKSGNSYPQG-----LDPSRVPI 649

RESULT 6

T48814

hypothetical protein 15B6.220 (imported) - Neurospora crassa

C/Species: Neurospora crassa

C/Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 09-Jul-2004

C/Accession: T48814

R/Schulte, U.; Aign, V.; Hehse, J.; Brandt, P.; Fartmann, B.; Holland, R.; Nyakatura,

submitted to the Protein Sequence Database, April 2000

A/Reference number: Z24541

A/Accession: T48814

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-1952 <SCH>

A/Cross-references: UNIPROT:Q9P6T1; EMBL:ALJ53622; GSPDB:GN00112; NCSP:15B6.220

A/Experimental source: cosmid contig 15B6; strain 74

C/Genetics:

A/Gene: NCSP:15B6.220

A/Map position: 2

A/Introns: 281/3

Query Match 27.3%; Score 56.5; DB 2; Length 1952;
Best Local Similarity 29.4%; Pred. No. 95;
Matches 10; Conservative 10; Mismatches 13; Indels 1; Gaps 1;

3 SGNSQSFEDTEBDKPKYEGGNIIVDIDFDSVPQI 36

Db 547 TGAEEYEP-ETPARRYSEGGKEMSPFESIHV 579

RESULT 7

TDR1LT

leukocyte common antigen precursor, splice form 4 - rat

N/Alternate names: CD45; L-CA; Ly-5; T200

N/Contents: leukocyte common antigen precursor, splice form 1; leukocyte common antigen f

1.3.48)

C/Species: Rattus norvegicus (Norway rat)

C/Date: 04-Dec-1986 #sequence_revision 05-May-2000 #text_change 09-Jul-2004

C/Accession: A29450; B29450; C29450; D29450; A60241; A02247; I54569; A45854

R/Bercley, A.N.; Jackson, D.I.; Willis, A.C.; Williams, A.F.

EMBO J. 6, 1259-1264, 1987

A/Title: Lymphocyte specific heterogeneity in the rat leukocyte common antigen (T200) is

A/Reference number: A31067; MUID:87275817; PMID:2440674

A/Accession: A29450

A/Molecule type: mRNA

A/Residues: 20-30,163-218 <BAR1>

A/Cross-references: UNIPROT:Q64224; GB:M25820; GB:M24611; NID:g205153; GB:Y00065; GB:K03(

A/Experimental source: splice form 1

A/Note: the translation in GenBank entry RATLCAI, PIDN:AAA41518.1, PID:g205154, release 1

A/Accession: B29450

A/Molecule type: mRNA

A/Residues: 19-30,122-218 <BAR2>

A/Cross-references: GB:M25821; GB:M24611; NID:g205155; PIDN:AAA41519.1; PID:g205156; GB:Y

A/Experimental source: splice form 2

A/Accession: C29450

A/Molecule type: mRNA

A/Residues: 20-30,73-121,163-218 <BAR3>

A/Cross-references: GB:M25822; GB:M24611; NID:g205157; PIDN:AAA41520.1; PID:g205158; GB:Y

A:Experimental source: splice form 3
A:Accession: D29450
A:Molecule type: mRNA
A:Residues: 28-218 <BAR4>
A:Cross-references: GB:M25823; GB:M24611; NID:g205159; PIDN:AAA41521.1; PID:g205160; GB:
A:Experimental source: Splice form 4
A>Note: the sequence in Genbank entry RATTCAIV, release 113.0, has the codon AGG for 56-
R:Barclay, A.N.; Jackson, D.I.; Millie, A.C.; Williams, A.F.
Adv. Exp. Med. Biol. 237, 3-7, 1988
A>Title: The leukocyte-common antigen (L-CA) family.
A:Reference number: A60241; MUID:89319817; PMID:2978200
A:Accession: A60241
A>Status: not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 30-161 <BAR5>
R:Thomas, M.L.; Barclay, A.N.; Gagnon, J.; Williams, A.F.
Cell 41, 83-93, 1985
A>Title: Evidence from cDNA clones that the rat leukocyte-common antigen (T200) spans th
A:Reference number: A02247; MUID:85201691; PMID:3158393
A:Accession: A02247
A:Molecule type: mRNA
A:Residues: 187-189, 'K', 191-192, 'K', 208-1273 <THO>
A:Cross-references: GB:M10072; GB:W8159; NID:g205140; PIDN:AAA41513.1; PID:g205143
A>Note: the translation in Genbank entry RATTCAI, release 113.0, begins at non-initiatcattc
A>Note: parts of this sequence were determined by protein sequencing
R:McCall, M.N.; Shotton, D.M.; Barclay, A.N.
Immunology 76, 310-317, 1992
A>Title: Expression of soluble isoforms of rat CD45. Analysis by electron microscopy and
A:Reference number: I54569; MUID:92340120; PMID:1378817
A:Accession: I54569
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-30, 163-180 <MCC>
A:Cross-references: GB:S40716; NID:g252015; PIDN:AAB2648.1; PID:g252016
R:Jackson, D.I.; Barclay, A.N.
Immunogenetics 29, 281-287, 1989
A>Title: The extra segments of sequence in rat leukocyte common antigen (L-CA) are deriv
A:Reference number: A45854; MUID:89233293; PMID:2523868
A:Accession: A45854
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 24-227, 'H', 229-305, 'Y', 307-310 <JAC>
A:Cross-references: GB:M18347; GB:M18348; GB:M18349
C:Comment: This glycoprotein is found on lymphoid and myeloid cell surfaces.
C:Superfamily: leukocyte common antigen; leukocyte common antigen cytosolic domain homolo
C:Keywords: alternative splicing; duplication; glycoprotein; phosphoprotein; phosphoric
F:1-23/Domain: signal sequence #status predicted <SIG>
F:24-1273/Product: leukocyte common antigen precursor, splice form 4 #status predicted <
F:24-546/Domain: extracellular #status predicted <EXT>
F:24-30, 122-1273/Product: leukocyte common antigen, splice form 2 #status predicted <MA
F:24-30, 163-1273/Product: leukocyte common antigen, splice form 1 #status predicted <MA
F:24-30, 73-121, 163-218/Product: leukocyte common antigen, splice form 3 #status predicte
F:1548-568/Domain: transmembrane #status predicted <TM>
F:1556-1206/Domain: leukocyte common antigen cytosolic domain homology <LAC>
F:1566-1273/Domain: intracellular #status predicted <INT>
F:1646-870/Domain: protein-tyrosine-phosphatase homology <PP>
F:162, 142, 155, 154, 178, 200, 245, 271, 282, 327, 371, 374, 502/Binding site: carbohydrate (Asn)
F:1822/Active site: Cys (phosphotyrosine intermediate) #status predicted
F:1828/Binding site: substrate phosphate (Arg) #status predicted
F:1053/Binding site: carbohydrate (Asn) (covalent) #status absent

Query Match 26.8%; Score 55.5; DB 1; Length 1273;
Best Local Similarity 40.5%; Pred. No. 79;
Matches 15; Conservative 5; Mismatches 10; Indels 7; Gaps 2;

QY 1 QNSGNOSFEPTDEBDPKRYEOGNIYVDDIPSPQPIH 37
| : |||| | : || : | | | : | : ||
Db 929 OHIGNQ-----EENKKK-NRSSNVYPYDKNVKPLKH 958

RESULT 8
A28334
protein-tyrosine-phosphatase (EC 3.1.3.48) ty-5 precursor (B-cell variant) - mouse

N:Alternate names: 200K leukocyte common antigen; B220; CD45; Ly-5 (B-cell specific); P19C/containing protein-tyrosine-phosphatase (T-cell variant)
C:Species: Mus musculus (house mouse)
C:Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #text_change 09-Jul-2004
C:Accession: A28334; A29381; A61180; A60933; A33522; A29075; I54450; A28335; A23329; I576
R:Thoms, M.L.; Reynolds, P.J.; Chain, A.; Ben-Neriah, Y.; Trowbridge, I.S.
Proc. Natl. Acad. Sci. U.S.A. 84, 5360-5363, 1987
A:Title: B-cell variant of mouse T200 (Ly-5): evidence for alternative mRNA splicing.
A:Reference number: A28334; MUID:87260986; PMID:295516
A:Accession: A28334
A:Molecule type: mRNA
A:Residues: 1-1291 <RTO>
A:Cross-references: UNIPROT:P06800; UNIPROT:Q61814; UNIPROT:Q61815; UNIPROT:Q61813; GB:M.
Proc. Natl. Acad. Sci. U.S.A. 83, 6940-6944, 1986
A:Title: Sequences of Ly-5 cDNA: isoform-related diversity of Ly-5 mRNA.
A:Reference number: A29381; MUID:86313686; PMID:2944116
A:Accession: A29381
A:Molecule type: mRNA
A:Residues: 1-30,170-517, 'NNT', 521-527, 'G', 529-555, 'S', 557-587, 'S', 589-905, 'Q', 907-930, 'F'
A:Cross-references: GB:M44342; NID:G198914; P1DN:AAA39458.1; PID:G198915
R:Yi, T.; Cleveland, W.J.; Ihle, J.N.
Blood 78, 2222-2228, 1991
A:Title: Identification of novel protein tyrosine phosphatases of hematopoietic cells by
A:Accession number: A61180; MUID:92032882; PMID:1932742
A:Accession: A61180
A:Status: not compared with conceptual translation
A:Status: not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 730-838 <YIA>
R:Gomez, L.J.; Walker, I.D.; Sandrin, M.S.; McKenzie, I.F.C.
Immunogenetics 25, 263-266, 1987
A:Title: High sequence conservation between rat (T200) and mouse (Ly-5) leukocyte common
A:Reference number: A60933; MUID:87192931; PMID:3570377
A:Accession: A60933
A:Molecule type: Protein
A:Residues: 'R', 289-298, '229', 'V', '331-336', 'Y', 'R', '364-370', 'X', '372-375; 595-608; 638-649; 669-6
R:Johnson, N.A.; Meyer, C.M.; Pingel, J.T.; Thomas, M.L.
J. Biol. Chem. 264, 6220-6229, 1989
A:Title: Sequence conservation in potential regulatory regions of the mouse and human leu
A:Reference number: A33522; MUID:89197920; PMID:2522930
A:Accession: A33522
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-22 <JOH>
A:Cross-references: GB:M22456; NID:G198755; P1DN:AAA6374.1; PID:G554185; GB:J04640; GB:J
R:Raachke, W.C.
Proc. Natl. Acad. Sci. U.S.A. 84, 161-165, 1987
A:Title: Cloned murine T200 (Ly-5) cDNA reveals multiple transcripts within B- and T-lym
A:Reference number: A29075; MUID:87092355; PMID:2948186
A:Accession: A29075
A:Molecule type: mRNA
A:Residues: 961-1291 <RAS>
A:Cross-references: GB:M15174; NID:G201105; P1DN:AAA40161.1; PID:G201106
R:Tung, J.
Immunogenetics 28, 271-277, 1988
A:Title: Structural features of Ly-5 glycoproteins of the mouse and counterparts in other
A:Reference number: I54450; MUID:88330145; PMID:3117740
A:Accession: I54450
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 32-73 <RES>
A:Cross-references: GB:M22241; NID:G340850; P1DN:AAA39460.1; PID:G548174
R:Saga, Y.; Tung, J.S.; Shen, F.W.; Boyse, E.A.
Proc. Natl. Acad. Sci. U.S.A. 84, 5364-5366, 1987
A:Title: Alternative use of 5' exons in the specification of Ly-5 isoforms distinguishing
A:Reference number: A28335; MUID:87260987; PMID:3037546
A:Accession: A28335
A:Molecule type: mRNA
A:Residues: 1-50,74-226 <SA2>
A:Cross-references: GB:M14342
R:Shen, F.W.; Saga, Y.; Littman, G.; Freeman, G.; Tung, J.S.; Cantor, H.; Boyse, E.A.
Proc. Natl. Acad. Sci. U.S.A. 82, 7360-7363, 1985
A:Reference number: A23329; MUID:86042665; PMID:3864163

```

A:Accession: J23329
A:Molecule type: mRNA
A:Residues: 10-30,170-263 <SHE>
A:Cross-references: GB:M1934; NID:g198919; PIDN:AAA9461.1; PID:g198920
R:Saga, Y.; Tung, J.
Mol. Cell. Biol. 8, 4889-4895, 1988
A>Title: Organization of the Ly-5 Gene.
A:Reference number: I57644; MUID:89096862; PMID:3211131
A:Accession: I57644
A>Status: preliminary; translated from GB/EMBL/DDBU
A:Molecule type: DNA
A:Residues: 'MT',1-22 <RE2>
A:Cross-references: GB:M23354; NID:g340890; PIDN:AAA9462.1; PID:g554192
C:Geneticis:
A:Gene: Ly-5
C:Superfamily: leukocyte common antigen; leukocyte common antigen cytosolic domain homology
C:Keywords: alternative splicing; glycoprotein; phosphoprotein; phosphoric monoester hydrolysis
F:1-23/Domains: signal sequence #status predicted <SIG>
F:24-129/Product: protein-tyrosine-phosphatase (B-cell variant) #status predicted <MAT>
F:24-564/Domains: extracellular #status predicted <EXT>
F:24-30,170-129/Product: protein-tyrosine-phosphatase (T-cell variant) #status predicted <INT>
F:565-566/Domains: transmembrane #status predicted <TM>
F:583-1223/Domains: leukocyte common antigen cytosolic domain homology <LAC>
F:587-1291/Domains: intracellular #status predicted <INT>
F:664-888/Domains: protein-tyrosine-phosphatase homology <PP>
F:64,150,161,207,211,218,253,258,290,311,322,347,416,427,457,489,520,556/Binding site: c
F:84/Active site: Cys (phosphotyrosine intermediate) #status predicted
F:84/Binding site: substrate phosphate (Arg) #status predicted

Query Match      26.8%   Score 55.5; DB 1; Length 1291;
Best Local Similarity 40.5%; Pred. No. 80;
Matches 15; Conservative 5; Mismatches 10; Indels 7; Gaps 2;

QY      1 QNSGNSEFPTEEDPKPYEQGNIVIDIPDSVPDIH 37
Db       947 QHIGNQ-----EENKKK-NRNSNVVPRDFRVPLKH 976
          ||| | | | | | | | | | | | | | |
          ||| | | | | | | | | | | | | | |

RESULT 9
hypochemical protein FJ3D5.5 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
C:Accession: T34249
R:Wilcox, L.
submitted to the EMBL Data Library, June 1995
A:Description: The sequence of C. elegans cosmid FJ3D5.
A:Reference number: Z21494
A:Accession: T34249
A>Status: preliminary; translated from GB/EMBL/DDBU
A:Molecule type: DNA
A:Residues: 1-1817 <ML>
A:Cross-references: UNIPROT:Q19931; EMBL:U28941; PIDN:AAC71101.1; GSPDB:GN00020; CESP:F3
A:Experimental source: strain Bristol N2; clone FJ3D5
C:Geneticis:
A:Gene: CESP:FJ3D5.5
A:Map position: 2
A:introns: 22/2; 107/2; 199/2; 291/2; 384/2; 476/2; 566/2; 648/2; 728/2; 904/2; 1047/2;

Query Match      26.6%   Score 55; DB 2; Length 1817;
Best Local Similarity 47.8%; Pred. No. 1,4e+02;
Matches 11; Conservative 3; Mismatches 9; Indels 0; Gaps 0;

QY      1 QNSGNSEFPTEEDPKPYEQCG 23
Db       1357 RNYSSESDEDDPAMEEAG 1379
          :||:| | | | | | | | | | | | | | |
          :||:| | | | | | | | | | | | | | |

RESULT 10
hypochemical protein At2g20570 [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
```

```

CjAccession: H84590
Riln, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
M.; Ko, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.;
eues, D.; Niernan, W.C.; White, O.; Eissen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.
Native 402, 761-768, 1999
A>Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A|Reference number: AB4420; MUID:20083487; PMID:10617197
A|Accession: H84590
A>Status: preliminary
A|Molecule type: DNA
A|Residues: 1-406 <STO>
A|Cross-references: UNIPROT:Q9SIV3; GB:AE002093; NID:g4512654; PID:AAD21709.1; GSPDB:GN
C|Genetics:
A|Gene: At2g20570
A|Map position: 2

Query Match          26.3%; Score 54.5; DB 2; Length 406;
Best Local Similarity 36.7%; Pred.No.28;
Matches 11; Conservative 8; Mismatches 10; Indels 1; Gaps 1;

Cy      10 PDEEDKPKYEGGNIVD-IDPDSVPQHIG 38
       |||||::|::|::|::|::|::|::|::|
Db      30 PEEREFPDFADHGDLDIIDPDFDIFGVAG 59

RESULT 11
S11925
S-locus-specific glycoprotein - wild cabbage
CjSpecies: Brassica oleracea (wild cabbage)
CjDate: 21-Nov-1993 #sequence_revision 21-Jul-1995 #text_change 09-Jul-2004
A|Accession: S11925
R|Chen, C.H.; Nasrallah, J.B.
Mol. Gen. Genet. 222, 241-248, 1990
A|Title: A new class of S sequences defined by a pollen recessive self-incompatibility al
A|Reference number: S11925; MUID:91109707; PMID:1980334
A|Accession: S11925
A>Status: preliminary
A|Molecule type: DNA
A|Residues: 1-437 <CH>
A|Cross-references: UNIPROT:Q23740
CjSuperfamily: S-locus-specific glycoprotein; S-locus-specific glycoprotein homology
C|Keywords: glycoprotein
F:42-435/Domain: S-locus-specific glycoprotein homology <SSG>

Query Match          26.3%; Score 54.5; DB 2; Length 437;
Best Local Similarity 21.7%; Pred.No.31;
Matches 10; Conservative 14; Mismatches 13; Indels 9; Gaps 1;

Cy      2 NSGNSEFPDTEEDKKPY-----EOGNGIVIDIDPSVPIHG 38
       |||||::|::|::|::|::|::|::|::|
Db      196 SSGNTTVKIDTORGLPFLINOGRIYMORSGPWGMHFGSCIEPVQG 241

RESULT 12
T14516
S-locus-specific glycoprotein Sc - wild cabbage (fragment)
CjSpecies: Brassica oleracea (wild cabbage)
CjDate: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
A|Accession: T14516
R|Pastuglia, M.; Ruffio, V.; Delorme, V.; Dumas, C.; Cock, J.M.
submitted to the EMBL Data Library, April 1997
A|Reference number: Z18121
A|Accession: T14516
A|Status: preliminary; translated from GB/EMBL/DBJ
A|Molecule type: DNA
A|Residues: 1-494 <PAS>
A|Cross-references: UNIPROT:Q23740; EMBL:Y12321; NID:e1043982; PID:e353244
A|Experimental source: variety acephala, strain p57Sc
C|Genetics:
A|Note: Intron positions not resolved (incomplete sequence)
C|Keywords: glycoprotein

```

Query Match 26.3%; Score 54.5; DB 2; Length 494;
Best Local Similarity 21.7%; Pred. No. 36;
Matches 10; Conservative 14; Mismatches 13; Indels 9; Gaps 1;
Qy 2 NSGNQSFEPPTBEDKPKYEGGNIVDIDPDSVPOIHG 38
Db 196 SSGNTYKIDTQRIPEFILNQGRYEMQSGPMNGMERSGIPEVOG 241

RESULT 13
884219
hypothetical protein Vng061sc [imported] - Halobacterium sp. NRC-1
C:Species: Halobacterium sp. NRC-1
C:Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
C:Accession: G84219
R:Ng, W.V.; Kennedy, S.P.; Mahirae, G.G.; Bergquist, B.; Pan, M.; Shukla, H.D.; Lasky, S.; Leitbauer, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Jaldic, Jung, K.H.; Alam, M.; Freitas, T.
Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000
A:Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ebhardt, H.; Lowe, T.M.; Li, A.; Title: Genome sequence of Halobacterium species NRC-1.
A:Reference number: A84160; MUID:20504483; PMID:11016950
A:Accession: G84219
A:Status: Preliminary
A:Molecule type: DNA
A:Residues: 1-545 <STO>
A:Cross-references: UNIPROT:Q9HRN5; GB:AE004437; NID:g10580209; PIDN:AA019123.1; GSPDB:C
C:Genetics:
A:Gene: VNG0615C

Query Match 26.1%; Score 54; DB 2; Length 545;
Best Local Similarity 40.0%; Pred. No. 46;
Matches 12; Conservative 5; Mismatches 13; Indels 0; Gaps 0;
Qy 9 EPTBEDKPKTEGGNIVDIDPDSVPOIHG 38
Db 141 EPDREQAILEYEDGVVHADPSVGLRG 170

RESULT 14
T47560
serine protein kinase-like - Arabidopsis thaliana
N:Alternate names: protein F8J2.200
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 09-Jul-2004
C:Accession: T47560
R:Nyakatura, G.; Fartmann, B.; Dauner, D.; Sterr, W.; Holland, R.; Weichselgartner, M.; Mayer, K.F.X.
submitted to the Protein Sequence Database, April 2000
A:Reference number: 22458
A:Accession: T47560
A:Status: Preliminary
A:Molecule type: DNA
A:Residues: 1-523 <NTA>
A:Cross-references: UNIPROT:Q9LFP89; EMBL:AL132969
A:Experimental source: cultivar Columbia; BAC clone F8J2
C:Genetics:
A:Map position: 3
A:Introns: 65/3; 370/3; 386/3
A>Note: F8J2.200
C:Superfamily: human protein kinase c1k1; protein kinase homology

Query Match 25.4%; Score 52.5; DB 2; Length 523;
Best Local Similarity 32.0%; Pred. No. 69;
Matches 16; Conservative 7; Mismatches 10; Indels 17; Gaps 2;
Qy 2 NSGNQSFEPPTBEDKPKYEGGNIVDIDPDSV 34
Db 461 NSGPRSIKSLDENSQKLTDEKRNKEBQEAIVEYMGNNVVISLDSKP 510

RESULT 15
C71609

hypothetical protein PFB0655c - malaria parasite (Plasmodium falciparum)
C:Species: Plasmodium falciparum
C:Date: 13-Nov-1998 #sequence_revision 13-Nov-1998 #text_change 09-Jul-2004
C:Accession: C71609
R:Gardner, M.J.; Tettein, H.; Carucci, D.J.; Cummings, L.M.; Aravind, L.; Koonin, E.V.; ; Perera, M.; Salzberg, S.; Zhou, L.; Sutton, G.G.; Clayton, R.; White, O.; Smith, H.O.; Science 282, 1126-1132, 1998
A:Title: Chromosome 2 sequence of the human malaria parasite Plasmodium falciparum.
A:Reference number: A71600; MUID:99021743; PMID:9804551
A:Accession: C71609
A:Status: Preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-558 <GAR>
A:Cross-references: UNIPROT:O96224; GB:AE001409; GB:AE001362; NID:g3845241; PIDN:AA071920
A:Experimental source: clone 3D7
C:Genetics:
A:Gene: PFB0655c

Query Match 25.4%; Score 52.5; DB 2; Length 558;
Best Local Similarity 40.6%; Pred. No. 74;
Matches 13; Conservative 6; Mismatches 12; Indels 1; Gaps 1;
Qy 1 NSGNQSFEPPTBEDKPKYEGGNIVDIDPDS 32
Db 448 ENNVNANENENEBEQKTEGGHYD-DEDS 478

Search completed: October 22, 2005, 06:09:43
Job time : 16.8905 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 22, 2005, 04:10:49 / Search time 69.6361 Seconds
(without alignments)
279.439 Million cell updates/sec

Title: US-10-731-238-37
Perfect score: 207
Sequence: 1 QNSGNQSFEPDTEBDKPKYEGGNIVDIDFDSVPQIHG 38

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	199	96.1	940	2	Q53682 staphylococ
2	199	96.1	943	2	Q8NUU8 staphylococ
3	199	96.1	957	2	Q6G6H4 staphylococ
4	199	96.1	961	2	Q6G6H4 staphylococ
5	199	96.1	961	2	Q7A3J8 staphylococ
6	199	96.1	1018	1	FNBA_STRAU
7	199	96.1	1038	2	Q7A3J7 staphylococ
8	199	96.1	1038	2	Q7A3J7 staphylococ
9	198	95.7	965	2	Q6G6H5 staphylococ
10	191	92.3	1015	2	Q8NUU7 staphylococ
11	191	92.3	1015	2	Q6G6H3 staphylococ
12	188	90.8	1054	2	Q9AEP9 staphylococ
13	63.5	30.7	2084	2	Q9AEP9 staphylococ
14	62.5	30.2	923	2	Q6G6H2 staphylococ
15	60	29.0	889	2	Q6G6H0 staphylococ
16	60	29.0	968	1	PKD2_HUMAN
17	60	29.0	981	2	Q9A1J7 white spot
18	58.5	28.3	101	2	Q68YU3 vacciniu
19	58	28.0	237	2	Q8BZM9 mus muscu
20	58	28.0	455	2	Q6ZC97 mus muscu
21	58	28.0	532	2	Q9D074 m mus muscu
22	58	28.0	597	2	Q6FV62 candida gla
23	58	28.0	674	2	Q9F1F1 arabisopsi
24	57.5	27.8	782	1	Y044_UREPA
25	57	27.5	533	2	Q94677 plasmodia
26	57	27.5	572	2	Q9GSR0 plasmodium
27	57	27.5	684	2	Q64YN9 bacteroides
28	57	27.5	698	2	Q71EE1 hevea bras
29	57	27.5	703	1	HS83_IPONI
30	57	27.5	745	2	Q7SA69 neuropsora
31	57	27.5	2641	2	Q9BXD4 homo sapien

32	57	27.5	2847	2	015018	015018 homo sapien
33	56.5	27.3	395	2	Q7MG85	Q7MG85 vibrio vuln
34	56.5	27.3	904	2	Q54324	Q54324 sulfoblob
35	56.5	27.3	975	2	Q8N2U8	Q8N2U8 streptococ
36	56.5	27.3	999	2	Q8K525	Q8K525 streptococ
37	56.5	27.3	1335	2	Q7NCX8	Q7NCX8 gloebacter
38	56.5	27.3	1992	2	Q9P6T1	Q9P6T1 neuropsora
39	56	27.1	514	2	Q9BYR3	Q9BYR3 homo sapien
40	56	27.1	959	2	Q8TLA5	Q8TLA5 methanosa
41	56	27.1	1626	2	Q9V5X5	Q9V5X5 drosophila
42	56	27.1	2658	2	Q8T5G0	Q8T5G0 plasmodium
43	55.5	26.8	878	2	Q8C6Q7	Q8C6Q7 mus muscu
44	55.5	26.8	962	2	Q6LDZ3	Q6LDZ3 rattus norv
45	55.5	26.8	1255	1	CD45_RAT	CD45 ratu

ALIGNMENTS

RESULT 1

ID	Q53682	PRELIMINARY;	PRT;	940 AA.
AC	Q53682;			
DT	01-NOV-1996 (TREMBLrel. 01, Created)			
DT	01-NOV-1996 (TREMBLrel. 01, Last sequence update)			
DT	01-MAR-2004 (TREMBLrel. 26, Last annotation update)			
DE	Fibronectin binding protein B.			
GN	Name=fnbB;			
OS	Staphylococcus aureus.			
OC	Bacteria; Firmicutes; Bacillales; Staphylococcus.			
OX	NCBI_TaxID=1280;			
RN	(1)			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=8325-4;			
RX	MEDLINE=9211475; PubMed=1837266;			
RA	Johnson K., Signas C., Muller H.P., Lindberg M.;			
RT	"Two different genes encode fibronectin binding proteins in Staphylococcus aureus. The complete nucleotide sequence and characterization of the second gene."			
RT	Eur. J. Biochem. 202:1041-1048 (1991).			
RL	-1 SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by an amide bond (By similarity).			
CC				
DR	EMBL: X62992; CAA4726.1; ..			
DR	PIR: S19702; S19702.			
DR	HSP: Q53653; IN67.			
DR	GO: GO:0009986; C:cell surface; IEA.			
DR	GO: GO:0005618; C:cell wall; IEA.			
DR	GO: GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.			
DR	GO: GO:0016020; C:membrane; IEA.			
DR	GO: GO:0007155; F:cell adhesion; IEA.			
DR	InterPro: IPR008966; Adhes_bact.			
DR	InterPro: IPR004237; Fn_bind.			
DR	InterPro: IPR005877; Gpos_SiRK.			
DR	InterPro: IPR01899; Gram_pos_anchor.			
DR	Pfam: PF02986; Fn_bind; 2.			
DR	Pfam: PF00746; Gram_pos_anchor; 1.			
DR	Pfam: PF04650; SiRK_signal; 1.			
DR	TIGRFAMs: TIGR01167; LpYTG_anchor; 1.			
DR	TIGRFAMs: TIGR01168; SiRK_signal; 1.			
DR	PROSITE: PS50847; GRAM_POS_ANCHORING; 1.			
KW	Cell wall; Peptidoglycan-anchor.			
SQ	SEQUENCE 940 AA; 10355 MW; E35FBCA907AE345 CRC64;			
Query Match	96.1%; Score 199; DB 2; Length 940;			
Best Local Similarity	97.4%; Pred. No. 8.7e-16;			
Matches	37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;			
QY	1 QNSGNQSFEPDTEBDKPKYEGGNIVDIDFDSVPQIHG 38			
DB	682 QNSGNQSFEPDTEBDKPKYEGGNIVDIDFDSVPQIHG 719			
RESULT 2				

```
08NUN8
ID Q8NUN8 PRELIMINARY; PRT; 943 AA.
AC Q8NUN8;
DT 01-OCT-2002 (TREMBLrel. 22, Created)
DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE FmbB protein.
GN Name=fmbB; OrderedLocNames=MW2420;
OS Staphylococcus aureus (strain MW2);
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=196620;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MW2;
RA MEDLINE=22040711; PubMed=12044378; DOI=10.1016/S0140-6736(02)08713-5;
RA Bada T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Oguchi A.,
RA Nagai Y., Iwama N., Asano K., Naito T., Kuroda H., Cui L.,
RA Yamamoto K., Hiramatsu K.;
RT "Genome and virulence determinants of high virulence community-
RT acquired MRSA.";
RL Lancet 359:1819-1827(2002).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC an amide bond (By similarity).
DR EMBL; AP004830; BAB96285.1; -.
DR HSSP; Q53653; IN67.
DR GO; GO:0009986; C:cell surface; IEA.
DR GO; GO:0005568; C:cell wall; IEA.
DR GO; GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0007155; P:cell adhesion; IEA.
DR InterPro; IPR008966; Adhes_bact.
DR InterPro; IPR004237; Fn_bind.
DR InterPro; IPR005877; Gpos_YsIRK.
DR InterPro; IPR001899; Gram_pos_anchor.
DR Pfam; PF02986; Fn_bind.1.
DR Pfam; PF00746; Gram_pos_anchor.1.
DR Pfam; PF04650; YsIRK_signal.1.
DR TIGRFAMs; TIGR01167; LPXTG_anchor.1.
DR TIGRFAMs; TIGR01168; YsIRK_signal.1.
DR PROSITE; PS50847; GRAM_POS_ANCHORING.1.
KW Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ SEQUENCE 943 AA; 104537 MW; DA8A5FF31947E1B6A CRC64;

Query Match 96.1%; Score 199; DB 2; Length 943;
Best Local Similarity 97.4%; Pred. No. 8.8e-16;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QNSGNQSFEDTDEBKPKYEGGNIVIDIPDSVPQIHG 38
DB 689 QNSGNQSFEDTDEBKPKYEGGNIVIDIPDSVPQIHG 726

RESULT 3
Q6G6H4 PRELIMINARY; PRT; 957 AA.
AC Q6G6H4;
DT 05-JUN-2004 (TREMBLrel. 27, Created)
DT 05-JUN-2004 (TREMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE Fibronectin-binding protein.
GN Name=fmbB; OrderedLocNames=SA52387;
OS Staphylococcus aureus (strain MSSA476).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=282459;
RN [1]
RP SEQUENCE FROM N.A.
RA PubMed=15213324; DOI=10.1073/pnas.0402521101;
RA Holden M.T.G., Fell E.J., Lindsay J.A., Peacock S.J., Day N.P.J.,
RA Enright M.C., Foster T.J., Moore C.E., Hurst L., Atkin R., Barton A.,
RA Baon N., Bentley S.D., Chillingworth C., Chillingworth T.,
RA Churcher C., Clark L., Cotton C., Cronin A., Doggett J., Dowd L.,
RA Feltham T., Hance Z., Harris B., Hauser H., Holtroyd S., Jørgensen K.,
RA James K.D., Lennard N., Lane A., Mayes R., Moule S., Mungall K.,
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RA Ormond D., Quail M.A., Rabinowitsch E., Rutherford K.M., Sanders M.,
RA Sharp S., Simmonds M., Stevens K., Whitehead S., Barrall B.G.,
RA Spratt B.G., Parkhill J.;
RT "Complete genomes of two clinical Staphylococcus aureus strains:
RT evidence for the rapid evolution of virulence and drug resistance.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:9786-9791(2004).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC an amide bond (By similarity).
DR EMBL; BX571857; CAG44201.1; -.
DR GO; GO:0009986; C:cell surface; IEA.
DR GO; GO:0005568; C:cell wall; IEA.
DR GO; GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0007155; P:cell adhesion; IEA.
DR InterPro; IPR008966; Adhes_bact.
DR InterPro; IPR004237; Fn_bind.
DR InterPro; IPR005877; Gpos_YsIRK.
DR InterPro; IPR001899; Gram_pos_anchor.
DR Pfam; PF02986; Fn_bind.1.
DR Pfam; PF00746; Gram_pos_anchor.1.
DR Pfam; PF04650; YsIRK_signal.1.
DR TIGRFAMs; TIGR01167; LPXTG_anchor.1.
DR TIGRFAMs; TIGR01168; YsIRK_signal.1.
DR PROSITE; PS50847; GRAM_POS_ANCHORING.1.
KW Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ SEQUENCE 957 AA; 105980 MW; 28F8BA7FFD3EAF CRC64;

Query Match 96.1%; Score 199; DB 2; Length 957;
Best Local Similarity 97.4%; Pred. No. 8.9e-16;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QNSGNQSFEDTDEBKPKYEGGNIVIDIPDSVPQIHG 38
DB 689 QNSGNQSFEDTDEBKPKYEGGNIVIDIPDSVPQIHG 726

RESULT 4
ID Q99RD3 PRELIMINARY; PRT; 961 AA.
AC Q99RD3;
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE Fibronectin-binding protein homolog.
GN Name=fmbB; OrderedLocNames=SAV2502;
OS Staphylococcus aureus (strain Mu50 / ATCC 700699).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=158878;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Mu50 / ATCC 700699;
RA MEDLINE=21311952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2;
RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Iian J.-O., Ito T.,
RA Kanamori M., Matsunaru H., Maruyama A., Murakami H., Hoshoyama A.,
RA Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
RA Sekinizu K., Hiramatsu H., Kohara S., Goto S., Yabuuchi J.,
RA Kamehisa M., Yamashita A., Ohshima K., Furuya K., Yoshino C., Shiba T.,
RA Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
RT "Whole genome sequencing of methicillin-resistant Staphylococcus
RT aureus.";
RL Lancet 357:1225-1240(2001).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC an amide bond (By similarity).
DR EMBL; AP003365; BAB58664.1; -.
DR PIR; G90053; G90053.
DR HSSP; Q53653; IN67.
DR GO; GO:0009986; C:cell surface; IEA.
DR GO; GO:0005568; C:cell wall; IEA.
DR GO; GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0007155; P:cell adhesion; IEA.
DR InterPro; IPR008966; Adhes_bact.
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DR InterPro: IPR004237; Fn_bind.
 DR InterPro: IPR005877; Gpos_YsIRK.
 DR InterPro: IPR001899; Gram_pos_anchor.
 DR Pfam: PF02986; Fn_bind; 1.
 DR Pfam: PF00746; Gram_pos_anchor; 1.
 DR Pfam: PF04650; YsIRK_signal; 1.
 DR TIGRPFAMs: TIGR01167; LPXTG_anchor; 1.
 DR TIGRPFAMs: TIGR01168; YsIRK_signal; 1.
 DR PROSITE: PS50847; GRAM_POS_ANCHORING; 1.
 KM Cell wall; Complete proteome; Peptidoglycan-anchor.
 SQ SEQUENCE 961 AA; 106010 MW; 364940F884EA4101 CRC64;

Query Match 96.1%; Score 199; DB 2; Length 961;
 Best Local Similarity 97.4%; Pred. No. 9e-16;
 Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QNSGNQSFEDTEDEKPKYEGGNIVDIDFDSVPQIHG 38
 Db 693 QNSGNQSFEDTEDEKPKYEGGNIVDIDFDSVPQIHG 730

RESULT 5
 ID 07A3J8 PRELIMINARY; PRT; 961 AA.
 AC 07A3J8;
 DT 05-JUL-2004 (TREMBlrel. 27, Created)
 DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
 DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
 DE FnBb protein.
 GN Name=FnBb; OrderedLocustNames=SA2290;
 OS Staphylococcus aureus (strain N315).
 CC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 CX NCBI_TaxID=158879;

RA SEQUENCE FROM N.A.
 RP MEDLINE=21311952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2;
 RA Kusuda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
 RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Lian J.-Q., Ito T.,
 RA Matsumori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,
 RA Mitutani Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaio C.,
 RA Sekimizu K., Hirakawa H., Kohara S., Goto S., Yabuzaki J.,
 RA Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
 RA Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
 RT "Whole genome sequencing of methicillin-resistant Staphylococcus
 aureus".
 RL Lancet 357:1225-1240(2001).
 CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
 an amide bond (By similarity).
 CC EMBL: AP003137; BAB3593.1; -.
 DR GO: GO:0009986; C:cell surface; IEA.
 DR GO: GO:0005618; C:cell wall; IEA.
 DR GO: GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
 DR GO: GO:0016020; C:membrane; IEA.
 DR GO: GO:0007155; P:cell adhesion; IEA.
 DR InterPro: IPR008966; Adhes_bact.
 DR InterPro: IPR004237; Fn_bind.
 DR InterPro: IPR005877; Gpos_YsIRK.
 DR InterPro: IPR001899; Gram_pos_anchor.
 DR Pfam: PF02986; Fn_bind; 1.
 DR Pfam: PF00746; Gram_pos_anchor; 1.
 DR Pfam: PF04650; YsIRK_signal; 1.
 DR TIGRPFAMs: TIGR01167; LPXTG_anchor; 1.
 DR TIGRPFAMs: TIGR01168; YsIRK_signal; 1.
 DR PROSITE: PS50847; GRAM_POS_ANCHORING; 1.
 KM Cell wall; Complete proteome; Peptidoglycan-anchor.
 SQ SEQUENCE 961 AA; 106010 MW; 364940F884EA4101 CRC64;

Query Match 96.1%; Score 199; DB 2; Length 961;
 Best Local Similarity 97.4%; Pred. No. 9e-16;
 Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 1 QNSGNQSFEDTEDEKPKYEGGNIVDIDFDSVPQIHG 38
 |||

Db 693 QNSGNQSFEDTEDEKPKYEGGNIVDIDFDSVPQIHG 730

RESULT 6
 FNBA_STAUV STANDARD; PRT; 1018 AA.
 ID FNBA_STAUV
 AC P14758;
 DT 01-APR-1990 (Rel. 14, Created)
 DT 01-APR-1990 (Rel. 14, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Fibronectin-binding protein precursor (FNBP).
 GN Name=Fnba;
 OS Staphylococcus aureus.
 CC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 CX NCBI_TaxID=1280;
 RN [1]

RP SEQUENCE FROM N.A.
 RP STRAIN=NCITC 8325-4;
 RC MEDLINE=89098998; PubMed=2521391;
 RX Signaes C., Raucel G., Joensen K., Lindgren P.-E.,
 RA Anantharamiah G.M., Hoelck M., Lindberg M.;
 RT "Nucleotide sequence of the gene for a fibronectin-binding protein
 from Staphylococcus aureus: use of this peptide sequence in the
 synthesis of biologically active peptides".
 RT Proc. Natl. Acad. Sci. U.S.A. 86:699-703(1989).
 RL -1- FUNCTION: The ability of bacteria to bind fibronectin has been
 proposed as a virulence factor enabling bacteria to colonize wound
 tissues and blood clots. Binding of plasma fibronectin to the
 bacterial surface might block adhesion receptors on S.aureus, thus
 representing an important defense mechanism against tissue
 invasion.

-1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
 an amide bond (potential).
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 between the Swiss Institute of Bioinformatics and the EMBL Outstation -
 the European Bioinformatics Institute. There are no restrictions on its
 use by non-profit institutions as long as its content is in no way
 modified and this statement is not removed. Usage by and for commercial/
 entities requires a license agreement (See <http://www.ebi.ac.uk/announcements> or send an email to license@ebi.ac.uk).
 CC -----

CC EMBL: J04151; AAA26632.1; -
 DR InterPro: IPR004237; Fn_bind.
 DR InterPro: IPR005877; Gpos_YsIRK.
 DR InterPro: IPR001899; Gram_pos_anchor.
 DR Pfam: PF02986; Fn_bind; 1.
 DR Pfam: PF00746; Gram_pos_anchor; 1.
 DR Pfam: PF04650; YsIRK_signal; 1.
 DR TIGRPFAMs: TIGR01167; LPXTG_anchor; 1.
 DR TIGRPFAMs: TIGR01168; YsIRK_signal; 1.
 DR PROSITE: PS50847; GRAM_POS_ANCHORING; 1.
 KM Cell adhesion; Cell wall; Peptidoglycan-anchor; Repeat; Signal;
 VM Virulence.
 FT SIGNAL 1 36
 FT CHAIN 37 985
 FT PROPEP 986 1018
 FT REPEAT 545 574
 FT REPEAT 575 604
 FT DOMAIN 745 878
 FT REPEAT 745 782
 FT REPEAT 783 820
 FT REPEAT 821 859
 FT REPEAT 860 878
 FT DOMAIN 879 948
 FT REPEAT 879 892
 FT REPEAT 893 906
 FT REPEAT 907 920
 FT REPEAT 921 934
 FT REPEAT 935 948
 FT SITE 982 986
 FT MOD_RES 985 985
 B-1. Fibronectin-binding protein.
 B-2. Removed by sortase (potential).
 B-2. 4 X approximate tandem repeats, fibronectin-binding domain.
 D-1. D-1.
 D-2. D-2.
 D-3. D-3.
 D-4 (incomplete). D-4 (incomplete).
 5 X tandem repeats, Pro-rich (WR).
 WR 1. WR 1.
 WR 2. WR 2.
 WR 3. WR 3.
 WR 4. WR 4.
 WR 5. WR 5.
 LPXTG sorting signal (potential).
 pentaglycyl murein peptidoglycan amidated

```

FT      chreonine (Potential).
SQ      SEQUENCE      1018 AA;      111780 MW;      58175BD020E81F1F CRC64;

Query Match      96.1%;      Score 199;      DB 1;      Length 1018;
Best Local Similarity      97.4%;      Pred. No. 9.5e-16;
Matches      37;      Conservative      0;      Mismatches      1;      Indels      0;      Gaps      0;

QY      1 QNSGNQSFPEPTEDKPKRYEGGNIYVIDPDSVPQIHG 38
      |||||
DB      746 QNSGNQSFPEPTEDKPKRYEGGNIYVIDPDSVPQIHG 783

RESULT 7
QY      099RD2      PRELIMINARY;      PRT;      1038 AA.
ID      099RD2
AC      099RD2;
DT      01-JUN-2001 (TrEMBLrel. 17, Created)
DT      01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT      01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE      Fibronectin-binding protein homolog.
GN      Name=fnb; OrderedLocuNames=SAV2503;
OS      Staphylococcus aureus (strain M50 / ATCC 700699).
OC      Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX      NCBI_TaxID=158878;
RN      [1]
RC      SEQUENCE FROM N.A.
RP      MEDLINE=21311952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2;
RX      Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
RA      Cui L., Oguchi A., Aoki K.-I., Nagai Y., Iian J.-Q., Ito T.,
RA      Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,
RA      Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
RA      Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
RA      Kamehira M., Yamaehita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
RA      Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
RT      "Whole genome sequencing of methicillin-resistant Staphylococcus
RT      aureus."
RL      Lancer 357:1225-1240(2001).
CC      -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC      an amide bond (By similarity).
DR      EMBL; AP003365; BAB58665.1; -.
DR      PIR; H90053; H90053.
DR      GO; GO:0009986; C:cell surface; IEA.
DR      GO; GO:0005618; C:cell wall; IEA.
DR      GO; GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR      GO; GO:0016020; C:membrane; IEA.
DR      GO; GO:0007155; P:cell adhesion; IEA.
DR      InterPro; IPR008966; Adhes_bact.
DR      InterPro; IPR004237; Fn_bind.
DR      InterPro; IPR005877; Gpos_YsIRK.
DR      InterPro; IPR001899; Gram_pos_anchor.
DR      Pfam; PF02986; Fn_bind; 1.
DR      Pfam; PF00746; Gram_pos_anchor; 1.
DR      Pfam; PF04650; YsIRK_signal; 1.
DR      TIGRFAMs; TIGR01167; LPXTG_anchor; 1.
DR      TIGRFAMs; TIGR01168; YsIRK_signal; 1.
DR      PROSITE; PSS0847; GRAM_POS_ANCHORING; 1.
KW      Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ      SEQUENCE      1038 AA;      113618 MW;      666BF6BF2FBEB12 CRC64;

Query Match      96.1%;      Score 199;      DB 2;      Length 1038;
Best Local Similarity      97.4%;      Pred. No. 9.8e-16;
Matches      37;      Conservative      0;      Mismatches      1;      Indels      0;      Gaps      0;

QY      1 QNSGNQSFPEPTEDKPKRYEGGNIYVIDPDSVPQIHG 38
      |||||
DB      742 QNSGNQSFPEPTEDKPKRYEGGNIYVIDPDSVPQIHG 779

RESULT 8
QY      07A3J7      PRELIMINARY;      PRT;      1038 AA.
ID      07A3J7
AC      07A3J7;

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DT      05-JUL-2004 (TrEMBLrel. 27, Created)
DT      05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT      05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE      Fnb protein.
GN      Name=fnb; OrderedLocuNames=SA2291;
OS      Staphylococcus aureus (strain N315).
OC      Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX      NCBI_TaxID=158879;
RN      [1]
RC      SEQUENCE FROM N.A.
RP      MEDLINE=21311952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2;
RX      Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
RA      Cui L., Oguchi A., Aoki K.-I., Nagai Y., Iian J.-Q., Ito T.,
RA      Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,
RA      Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
RA      Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
RA      Kamehira M., Yamaehita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
RA      Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
RT      "Whole genome sequencing of methicillin-resistant Staphylococcus
RT      aureus."
RL      Lancer 357:1225-1240(2001).
CC      -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC      an amide bond (By similarity).
DR      EMBL; AP003137; BAB43594.1; -.
DR      GO; GO:0009986; C:cell surface; IEA.
DR      GO; GO:0005618; C:cell wall; IEA.
DR      GO; GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR      GO; GO:0016020; C:membrane; IEA.
DR      GO; GO:0007155; P:cell adhesion; IEA.
DR      InterPro; IPR008966; Adhes_bact.
DR      InterPro; IPR004237; Fn_bind.
DR      InterPro; IPR005877; Gpos_YsIRK.
DR      InterPro; IPR001899; Gram_pos_anchor.
DR      Pfam; PF02986; Fn_bind; 1.
DR      Pfam; PF00746; Gram_pos_anchor; 1.
DR      Pfam; PF04650; YsIRK_signal; 1.
DR      TIGRFAMs; TIGR01167; LPXTG_anchor; 1.
DR      TIGRFAMs; TIGR01168; YsIRK_signal; 1.
DR      PROSITE; PSS0847; GRAM_POS_ANCHORING; 1.
KW      Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ      SEQUENCE      1038 AA;      113618 MW;      666BF6BF2FBEB12 CRC64;

Query Match      96.1%;      Score 199;      DB 2;      Length 1038;
Best Local Similarity      97.4%;      Pred. No. 9.8e-16;
Matches      37;      Conservative      0;      Mismatches      1;      Indels      0;      Gaps      0;

QY      1 QNSGNQSFPEPTEDKPKRYEGGNIYVIDPDSVPQIHG 38
      |||||
DB      742 QNSGNQSFPEPTEDKPKRYEGGNIYVIDPDSVPQIHG 779

RESULT 9
QY      06GDU5      PRELIMINARY;      PRT;      965 AA.
ID      06GDU5
AC      06GDU5;
DT      05-JUL-2004 (TrEMBLrel. 27, Created)
DT      05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT      05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE      Fibronectin-binding protein.
GN      Name=fnbA; OrderedLocuNames=SA2580;
OS      Staphylococcus aureus (strain MSA252).
OC      Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX      NCBI_TaxID=282458;
RN      [1]
RC      SEQUENCE FROM N.A.
RP      PubMed=15213324; DOI=10.1073/pnas.0403521101;
RX      Hildgen M.T.G., Fell E.J., Lindsey J.A., Peacock S.J., Day N.P.J.,
RA      Enright M.C., Foster T.J., Moore C.E., Hurst L., Atkin R., Barron A.,
RA      Bason N., Bentley S.D., Chillingworth C., Chillingworth T.,
RA      Churcher C., Clark L., Cotton C., Cronin A., Doggett J., Dowd L.,
RA      Felwell T., Hance Z., Harris B., Hauser H., Holtroyd S., Jagsis K.,
RA      James K.D., Lennard N., Line A., Mayes R., Moule S., Mungall K.,
RA      Ormond D., Quail M.A., Rabinowitsch E., Rutherford K.M., Sanders M.,

```

RA Sharp S., Simmonds M., Stevens K., Whitehead S., Barrell B.G.,
 RA Spratt B.G., Parkhill J.,
 RT "Complete genomes of two clinical *Staphylococcus aureus* strains:
 evidence for the rapid evolution of virulence and drug resistance."
 Proc. Natl. Acad. Sci. U.S.A. 101:9786-9791(2004).
 CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
 an amide bond (By similarity).
 DR EMBL: BX571856; CAC41560.1; -
 DR GO: GO:0009986; C:cell surface; IEA.
 DR GO: GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
 DR GO: GO:0016020; C:membrane; IEA.
 DR GO: GO:0007155; P:cell adhesion; IEA.
 DR InterPro: IPR008966; Adhes_bact.
 DR InterPro: IPR004237; Fn_bind.
 DR InterPro: IPR005877; Gpos_Ysirk.
 DR Pfam: PF02986; Fn_bind; 1.
 DR Pfam: PF00746; Gram_pos_anchor; 1.
 DR Pfam: PF04650; Ysirk_signal; 1.
 DR TIGRfams: TIGR01167; LPXTG_anchor; 1.
 DR TIGRfams: TIGR01168; Ysirk_signal; 1.
 DR PROSITE: PS50847; GRAM_POS_ANCHORING; 1.
 DR Cell wall; Complete proteome; Peptidoglycan-anchor.
 KW SEQUENCE 965 AA; 105691 MW; 29828132164D0551 CRC64;
 NCBI_TaxID=282459;
 Query Match 95.7%; Score 198; DB 2; Length 965;
 Best Local Similarity 94.7%; Pred. No. 1.2e-15;
 Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 1 QNSGNQSFEPDTEBDKPKYEGGNIIVDIDPDSVPQIIG 38
 DB 749 QNSGNQSFEPDTEBDKPKYEGGNIIVDIDPDSVPQIIG 786
 RESULT 10
 Q8NUU7 PRELIMINARY; PRT; 1015 AA.
 AC Q8NUU7
 DT 01-OCT-2002 (TREMBLrel. 22, Created)
 DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update)
 DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
 DE Fmb protein.
 GN Name=fmb; OrderedLocustNames=MM2421;
 OS *Staphylococcus aureus* (strain MM2).
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 OK NCBI_TaxID=196620;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=MM2;
 RX MEDLINE=22040717; PubMed=12044378; DOI=10.1016/S0140-6736(02)08713-5;
 RA Babb T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Oguchi A.,
 RA Nagai Y., Iwana N., Asano K., Naito T., Kuroda H., Cui L.,
 RA Yamamoto K., Hiramoto K.,
 RT "Genome and virulence determinants of high virulence community-
 RT acquired MRSA."
 RT Lancet 359:1819-1827(2002).
 CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
 an amide bond (By similarity).
 DR EMBL: AP004830; BAB96286.1; -
 DR GO: GO:0009986; C:cell surface; IEA.
 DR GO: GO:0005618; C:cell wall; IEA.
 DR GO: GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
 DR GO: GO:0016020; C:membrane; IEA.
 DR GO: GO:0007155; P:cell adhesion; IEA.
 DR InterPro: IPR008966; Adhes_bact.
 DR InterPro: IPR004237; Fn_bind.
 DR InterPro: IPR005877; Gpos_Ysirk.
 DR InterPro: IPR001899; Gram_pos_anchor.
 DR Pfam: PF02986; Fn_bind; 1.
 DR Pfam: PF00746; Gram_pos_anchor; 1.
 DR Pfam: PF04650; Ysirk_signal; 1.
 DR TIGRfams: TIGR01167; LPXTG_anchor; 1.
 DR TIGRfams: TIGR01168; Ysirk_signal; 1.
 DR PROSITE: PS50847; GRAM_POS_ANCHORING; 1.
 KW Cell wall; Complete proteome; Peptidoglycan-anchor.
 SEQUENCE 1015 AA; 111145 MW; D0F9281BB64D4D2 CRC64;
 NCBI_TaxID=282459;

DR PROSITE: PS50847; GRAM_POS_ANCHORING; 1.
 KW Cell wall; Complete proteome; Peptidoglycan-anchor.
 SEQUENCE 1015 AA; 111145 MW; D0F9281BB64D4D2 CRC64;
 Query Match 92.3%; Score 191; DB 2; Length 1015;
 Best Local Similarity 94.7%; Pred. No. 9.3e-15;
 Matches 36; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 QNSGNQSFEPDTEBDKPKYEGGNIIVDIDPDSVPQIIG 38
 DB 747 QNSGNQSFEPDTEBDKPKYEGGNIIVDIDPDSVPQIIG 784
 RESULT 11
 Q6G6H3 PRELIMINARY; PRT; 1015 AA.
 AC Q6G6H3
 DT 05-JUN-2004 (TREMBLrel. 27, Created)
 DT 05-JUN-2004 (TREMBLrel. 27, Last sequence update)
 DT 05-JUN-2004 (TREMBLrel. 27, Last annotation update)
 DE Fibronectin-binding protein.
 GN OrderedLocustNames=SAS2388;
 OS *Staphylococcus aureus* (strain MSSA476).
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 OK NCBI_TaxID=282459;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX PubMed=15213324; DOI=10.1073/pnas.0402521101;
 RA Holden M.T.G., Fell E.J., Lindsey J.A., Peacock S.J., Day N.P.J.,
 RA Enright M.C., Foster T.J., Moore C.E., Hurst L., Atkin R., Barron A.,
 RA Baason N., Bentley S.D., Chillingworth C., Chillingworth T.,
 RA Churcher C., Clark L., Cotton C., Cronin A., Doggett J., Dowd L.,
 RA Fellwell T., Hance Z., Harris B., Hauser H., Holtroyd S., Jagels K.,
 RA James K.D., Leonard N., Line A., Mayes R., Moulie S., Mungall K.,
 RA Ormond D., Quail M.A., Rabinowitch E., Rutherford K.M., Sanders M.,
 RA Sharp S., Simmonds M., Stevens K., Whitehead S., Barrell B.G.,
 RA Spratt B.G., Parkhill J.,
 RT "Complete genomes of two clinical *Staphylococcus aureus* strains:
 RT evidence for the rapid evolution of virulence and drug resistance."
 Proc. Natl. Acad. Sci. U.S.A. 101:9786-9791(2004).
 CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
 an amide bond (By similarity).
 DR EMBL: BX571857; CAC44202.1; -
 DR GO: GO:0009986; C:cell surface; IEA.
 DR GO: GO:0005618; C:cell wall; IEA.
 DR GO: GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
 DR GO: GO:0016020; C:membrane; IEA.
 DR GO: GO:0007155; P:cell adhesion; IEA.
 DR InterPro: IPR008966; Adhes_bact.
 DR InterPro: IPR004237; Fn_bind.
 DR InterPro: IPR005877; Gpos_Ysirk.
 DR InterPro: IPR001899; Gram_pos_anchor.
 DR Pfam: PF02986; Fn_bind; 1.
 DR Pfam: PF00746; Gram_pos_anchor; 1.
 DR Pfam: PF04650; Ysirk_signal; 1.
 DR TIGRfams: TIGR01167; LPXTG_anchor; 1.
 DR TIGRfams: TIGR01168; Ysirk_signal; 1.
 DR PROSITE: PS50847; GRAM_POS_ANCHORING; 1.
 KW Cell wall; Complete proteome; Peptidoglycan-anchor.
 SEQUENCE 1015 AA; 111145 MW; D0F9281BB64D4D2 CRC64;
 NCBI_TaxID=282459;
 Query Match 92.3%; Score 191; DB 2; Length 1015;
 Best Local Similarity 94.7%; Pred. No. 9.3e-15;
 Matches 36; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 QNSGNQSFEPDTEBDKPKYEGGNIIVDIDPDSVPQIIG 38
 DB 747 QNSGNQSFEPDTEBDKPKYEGGNIIVDIDPDSVPQIIG 784
 RESULT 12
 Q9AEP9 PRELIMINARY; PRT; 152 AA.
 ID Q9AEP9

```
AC 09ABP9;
DT 01-JUN-2001 (TReMBLrel. 17, Created)
DT 01-JUN-2001 (TReMBLrel. 17, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE Fibronectin-binding protein (Fragment).
GN Name=fnb;
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1280;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CMRSA-1;
RX MEDLINE=2124681; PubMed=1134904;
RX DOI=10.1128/IAI.69.6.3791-3799.2001;
RA Rice K., Huencia M., Vaz D., McGavin M.J.;
RT "Variance in fibronectin binding and fnb locus polymorphisms in
RT Staphylococcus aureus: identification of antigenic variation in a
RT fibronectin binding protein adhesin of the epidemic CMRSA-1 strain of
RT methicillin-resistant S. aureus.";
RL Infect. Immun. 69:3791-3799 (2001).
DR EMBL; AY029184; AAKJ1588.1; -.
FT NON_TER
FT TER
SQ SEQUENCE 152 AA; 17193 MW; CFA3913C2B11C025 CRC64;

Query Match 90.8%; Score 188; DB 2; Length 152;
Best Local Similarity 92.1%; Pred. No. 2.6e-15;
Matches 35; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 QNSGNSQSFEDTDEKPKRYEGGNIIVDIDPDSVPQIHG 38
Dy 1 QNTGNSQSFEDTDEKPKRYEGGNIIVDIDPDSVPQIQG 38

RESULT 13
Q9HEC9 PRELIMINARY; PRT; 2084 AA.
ID Q9HEC9
AC Q9HEC9;
DT 01-MAR-2001 (TReMBLrel. 16, Created)
DT 01-MAR-2001 (TReMBLrel. 16, Last sequence update)
DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)
DE Hypothetical protein 99H12.230.
GN Name=99H12.230;
OS Neurospora crassa.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.
OX NCBI_TaxID=5141;
RN [1]
RP SEQUENCE FROM N.A.
RA Schultze U., Hohelsel J., Brandt P., Fartmann B., Holland R.,
RA Nyakatura G., Mewes H.W., Mannhaupt G.;
RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA German Neurospora genome project;
RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL51018; CACI8259.1; -.
KM Hypothetical protein.
SQ SEQUENCE 2084 AA; 222490 MW; 15EB53001C70158B7 CRC64;

Query Match 30.7%; Score 63.5; DB 2; Length 2084;
Best Local Similarity 40.5%; Pred. No. 1.2e+02;
Matches 15; Conservative 5; Mismatches 8; Indels 9; Gaps 1;

Qy 7 SFEEDT-----EEDKPKRYEGGNIIVDIDPDSVP 34
Dy 1797 SYEDTTPPSKDDQDSESEKPKPKKKGPMYDDDDDFP 1833

RESULT 14
Q69L72 PRELIMINARY; PRT; 923 AA.
ID Q69L72
AC Q69L72;
```

```
DT 25-OCT-2004 (TReMBLrel. 28, Created)
DT 25-OCT-2004 (TReMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TReMBLrel. 28, Last annotation update)
DE Putative PMS2 postneurotic segregation increased 2.
GN Name=OSUNBa0016G10.12;
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaceae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
RP SEQUENCE FROM N.A.
RA Sasaki T., Matsumoto T., Katayose Y.;
RT "Oryza sativa nipponbare(GA3) genomic DNA, chromosome 2, BAC
RT clone:OSUNBa0016G10.";
RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AP005874; BAD34084.1; -.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0006298; P:mismatch repair; IEA.
DR InterPro; IPR003594; ATPbind_ATPase.
DR InterPro; IPR002099; DNA_mis_repair.
DR InterPro; IPR000102; MAP1B_neuraxin.
DR Pfam; PF01119; DNA_mis_repair; 1.
DR Pfam; PF02518; HATPase_cj_1.
DR TIGRFAMs; TIGR00585; mult1_1.
DR TIGRFAMs; TIGR00585; mult1_1.
DR PROSITE; PS00058; DNA_MISMATCH_REPAIR_1; UNKNOWN_1.
DR PROSITE; PS00230; MAP1B_NEURAXIN; UNKNOWN_1.
SQ SEQUENCE 923 AA; 101237 MW; A5FD02C047947191 CRC64;

Query Match 30.2%; Score 62.5; DB 2; Length 923;
Best Local Similarity 45.2%; Pred. No. 64;
Matches 14; Conservative 5; Mismatches 11; Indels 1; Gaps 1;

Qy 6 QSFEPDEKPKRYEGGNIIVDIDPDSVPQI 36
Dy 551 QSFVPEWEDSPQHSSEPNIVS-HRDEVPQL 580

RESULT 15
O6CBW0 PRELIMINARY; PRT; 889 AA.
ID O6CBW0
AC O6CBW0;
DT 25-OCT-2004 (TReMBLrel. 28, Created)
DT 25-OCT-2004 (TReMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TReMBLrel. 28, Last annotation update)
DE Similar to sp|P53935 Saccharomyces cerevisiae YNL091w.
GN ORFName=YAL10C150709;
OS Yarrowia lipolytica CL1899.
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Dipodascaceae; Yarrowia.
OX NCBI_TaxID=284591;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CL1899;
RG Genolevures;
RA Dujon B., Sherman D., Fischer G., Durrens P., Casaregola S.,
RA Lafontaine I., de Montigny J., Marck C., Neugeyglisse C., Talla E.,
RA Geoffard N., Frangeul L., Aigle M., Anhouard V., Babour A., Barbe V.,
RA Barney S., Blanchin S., Beckerich J.M., Beyne B., Bleykasten C.,
RA Boistrame A., Boyer J., Catullo L., Contantollet F., de Darvar A.,
RA Despons L., Fabre E., Fairhead C., Ferry-Dumazet H., Gropfi A.,
RA Hantreya F., Hennequin C., Juniaux N., Joyet P., Kachouri R.,
RA Karretet A., Koszul R., Lemaire M., Lesur I., Ma L., Muller H.,
RA Nicoud J.M., Nikolski M., Oztas S., Ozter-Kalogeropoulos O.,
RA Pellenz S., Potier S., Richard G.F., Straud M.L., Suleau A.,
RA Swenne S., Tekala S., Wesolowski-Louvel M., Weethof E., Wirth B.,
RA Zeniou-Meyer M., Zivanovic I., Bolotin-Fukuhara M., Thierry A.,
RA Bouchier C., Caudron B., Scarpelli C., Gallardin C., Weisenbach J.,
RA Mincker P., Souciet J.L.;
RT "Genome evolution in yeasts.";
RL Nature 430:35-44 (2004).
RN [2]
RP SEQUENCE FROM N.A.
```

RC STRAIN=CLIB99;
RA Genoscope;
RL Submitted (JUL-2004) to the EMBL/Genbank/DBJ databases.
DR EMBL; CR382129; CAG82165.1; -;
SQ SEQUENCE 889 AA; 100256 MW; CC1B4588BAC17363 CRC64;

Query Match 29.0%; Score 60; DB 2; Length 889;
Best Local Similarity 42.9%; Pred. No. 1.2e+02;
Matches 15; Conservative 7; Mismatches 11; Indels 2; Gaps 2;

OY 1 QNSGNQ-SFEPDTEEDKP-KYEGGNTVDIDPDSV 33
Db 230 QNIGKEIDEEDGTBDEDPYGFEGEDVQSLDVSSV 264

Search completed: October 22, 2005, 06:05:51
Job time : 75.6361 secs

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GenCore version 5.1.6
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OM protein - protein search, using SW model

Run on: October 25, 2005, 19:38:38 ; Search time 83.8325 Seconds
(without alignments)
175.313 Million cell updates/sec

Title: US-10-731-238-38
Perfect score: 206
Sequence: 1 QNSGNQSFEEPTEDKPKYEGGNIVDIDFDSVPQIHG 38

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: A_Geneseq_16Dec04:*

- 1: Geneseqp1980s:*
- 2: Geneseqp1990s:*
- 3: Geneseqp2000s:*
- 4: Geneseqp2001s:*
- 5: Geneseqp2002s:*
- 6: Geneseqp2003as:*
- 7: Geneseqp2003bs:*
- 8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	206	100.0	38	2	AAW65694
2	198	96.1	38	2	AAW65661
3	198	96.1	130	2	AAW58806
4	198	96.1	130	2	AAW58807
5	198	96.1	130	2	AAW91202
6	198	96.1	130	2	AAW91201
7	198	96.1	134	2	AAW29089
8	198	96.1	134	2	AAW29088
9	198	96.1	134	2	AAW29087
10	198	96.1	139	2	AAW31556
11	198	96.1	174	2	AAW58808
12	198	96.1	174	2	AAW91203
13	198	96.1	181	2	AAW58805
14	198	96.1	181	2	AAW91200
15	198	96.1	559	2	AAW89803
16	198	96.1	767	4	AAU34403
17	198	96.1	767	4	AAU37547
18	198	96.1	940	2	AAW07070
19	198	96.1	940	6	ABJ19111
20	198	96.1	948	6	ADA89470
21	198	96.1	948	6	ABJ18923
22	198	96.1	948	6	ABW72536
23	198	96.1	961	6	ABU15854
24	198	96.1	1018	1	AAW82115
25	198	96.1	1018	4	AAU37245

26	198	96.1	1018	4	AAU34301
27	198	96.1	1018	6	ABJ18922
28	198	96.1	1018	6	ABW72537
29	198	96.1	1027	2	AAW89806
30	198	96.1	1038	6	ABU15903
31	192	93.2	38	2	AAW65692
32	192	93.2	38	2	AAW65695
33	192	93.2	38	2	AAW65696
34	192	93.2	38	2	AAW65697
35	192	93.2	38	2	AAW65693
36	191	92.7	38	2	AAW65698
37	190	92.2	38	2	AAW65662
38	190	92.2	38	2	AAW65699
39	190	92.2	978	4	AAU37093
40	190	92.2	1001	4	AAU37093
41	189	91.7	38	1	AAW80660
42	189	91.7	38	1	AAW82116
43	188	91.3	38	2	AAW65691
44	187.5	91.0	39	2	AAW65712
45	187	90.8	38	2	AAW65704

ALIGNMENTS

RESULT 1
AAW65694 standard; peptide; 38 AA.

AC AAW65694;
DT 16-OCT-1998 (first entry)
DE Fibronectin binding protein-derived peptide #38.
XX microbial surface components recognising adhesive matrix molecule;
XX MSCRAMM; fibronectin; fibronectin-binding protein; antibody; epitope;
XX antibiotic; Bacterial infection; antibiotic-resistant strain.
OS Synthetic.
OS Staphylococcus aureus.
XX WO9831389-A2.
XX 23-JUL-1998.
XX 21-JAN-1998; 98WO-US001222.
XX 21-JAN-1997; 97US-0036139P.
XX (TEXAS) UNIV TEXAS A & M SYSTEM.
XX Hoeck M, Patti JM, House-Pompeo KL, Speziale P, Joh D;
XX McGravin MJ;
XX WPI, 1998-413816/35.
XX Antibody that binds to fibronectin-binding protein, preventing its
XX binding to fibronectin - used to treat or prevent bacterial infection,
XX especially by Staphylococci and Streptococci.
XX Example 8, Page 102, 201pp; English.

The invention relates to antibodies that bind to a fibronectin-binding domain of a fibronectin-binding protein, and inhibit binding of the protein to fibronectin. Also claimed are: (1) isolated peptides of a fibronectin-binding protein that do not bind to fibronectin; (2) fusion protein containing at least one peptide of a fibronectin-binding protein linked to a second amino acid sequence; (3) nucleic acid encoding the isolated peptide of (1). Antibodies, the isolated peptides of (1) and the nucleic acids are all useful for immunisation (active or passive) and (b) inhibiting binding of bacteria to fibronectin for preventing or treating infection in humans or other animals, particularly by staphylococci or

CC streptococci, e.g. meningitis, otitis media, pneumonia, endocarditis,
 CC mastitis in cattle, abortion in horses and many others. Since the
 CC antibodies block binding of bacteria, they should be effective against
 CC antibiotic-resistant strains, and may replace antibiotic therapy or
 CC increase its effectiveness. Sequences AAM6561-700 represent a series of
 CC synthetic peptides based on the D1 region of *S. aureus* fibronectin
 CC binding protein A. They were synthesised to contain mutations
 XX

SO Sequence 38 AA:

QY Query Match 100.0%; Score 206; DB 2; Length 38;
 Best Local Similarity 100.0%; Pred. No. 1.6e-20;
 Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 QNSGNOSFEETEDKPKYEGGNIVDIDFDSVPQIHG 38
 1 QNSGNOSFEETEDKPKYEGGNIVDIDFDSVPQIHG 38

RESULT 2
 AAM6561
 ID AAM6561 standard; peptide; 38 AA.
 XX
 AC AAM6561;
 XX
 DT 16-OCT-1998 (first entry)
 XX
 DE Fibronectin binding protein-derived peptide #5.
 XX
 KM microbial surface components recognising adhesive matrix molecule;
 KM MSCRAMM; fibronectin; fibronectin-binding protein; antibody; epitope;
 KM antibiotic; bacterial infection; antibiotic-resistant strain.
 XX
 OS Synthetic.
 OS Staphylococcus aureus.
 XX
 XX MO9831389-A2.
 XX
 PD 23-JUL-1998.
 XX
 XX 21-JAN-1998; 98MO-US001222.
 PF
 XX 21-JAN-1997; 97US-0036139P.
 PR
 XX
 XX (TEXA) UNIV TEXAS A & M SYSTEM.
 PA
 XX Hoeoek M, Patti JM, House-Pompeo KL, Speciale P, Joh D;
 PI McGavin MJ;
 PI
 XX WPI; 1998-413816/35.
 DR
 XX

PT Antibody that binds to fibronectin-binding protein, preventing its
 binding to fibronectin - used to treat or prevent bacterial infection,
 PT especially by Staphylococci and Streptococci.
 PT
 PS Example 2; Page 92; 201pp; English.

CC The invention relates to antibodies that bind to a fibronectin-binding
 CC domain of a fibronectin-binding protein, and inhibit binding of the
 CC protein to fibronectin. Also claimed are: (1) isolated peptides of a
 CC fibronectin-binding protein that do not bind to fibronectin; (2) fusion
 CC protein containing at least one peptide of a fibronectin-binding protein
 CC linked to a second amino acid sequence; (3) nucleic acid encoding the
 CC isolated peptide of (1). Antibodies, the isolated peptides of (1) and the
 CC nucleic acids are all useful for immunisation (active or passive) and (by
 CC inhibiting binding of bacteria to fibronectin) for preventing or treating
 CC infection in humans or other animals, particularly by staphylococci or
 CC streptococci, e.g. meningitis, otitis media, pneumonia, endocarditis,
 CC mastitis in cattle, abortion in horses and many others. Since the
 CC antibodies block binding of bacteria, they should be effective against
 CC antibiotic-resistant strains, and may replace antibiotic therapy or
 CC increase its effectiveness. Sequences AAM6561-700 represent synthetic
 CC epitopes from the fibronectin binding domains DU and D1-D4 of the S.

CC aureus fnda gene
 XX

SO Sequence 38 AA:

QY Query Match 96.1%; Score 198; DB 2; Length 38;
 Best Local Similarity 97.4%; Pred. No. 1.9e-19;
 Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 1 QNSGNOSFEETEDKPKYEGGNIVDIDFDSVPQIHG 38
 1 QNSGNOSFEETEDKPKYEGGNIVDIDFDSVPQIHG 38

RESULT 3
 AAR58806
 ID AAR58806 standard; protein; 130 AA.
 XX
 AC AAR58806;
 XX
 DT 25-MAR-2003 (revised)
 DT 30-MAR-1995 (first entry)
 XX
 DE Fibronectin binding domain D1-D4 (709-838 (P838T)).
 XX
 KM Fibronectin binding protein; Fbp; fibronectin binding domain;
 KM monoclonal antibody; Mab; adhesion; Gram-positive bacterium; bacteremia;
 KM *Becherichia coli*.
 XX
 OS Staphylococcus aureus.
 OS
 XX MO9418327-A1.
 XX
 PD 18-AUG-1994.
 XX
 PF 04-FEB-1994; 94MO-GB000215.
 PF
 XX 05-FEB-1993; 93GB-00002289.
 PR 20-OCT-1993; 93GB-00021592.
 PR
 XX (SMIK) SMITHKLINE BEECHAM PLC.
 PA
 XX Burnham MKR, Chopra I, Critchley IA, Knowles DJC;
 PI
 XX WPI; 1994-279748/34.
 DR
 XX
 XX Fibronectin binding protein and monoclonal antibodies specific for Fbp -
 PT useful to prevent adherence of Gram-positive bacteria to indwelling
 PT devices or wounds.
 PT
 XX
 PS Disclosure; Page 30; 40pp; English.
 PS
 XX Polypeptides corresponding to residues G709-T886 plus PIVPPT, G709-
 CC P838(P838T) and G709-P838 (AAR58805-07, respectively) of *S. aureus* J2385
 CC (NCIMB 40532) Fbp type A fibronectin binding domain D1-D4 region
 CC (AAR58808) were expressed in *E. coli* BL21(DE4) and used to raise Mabs
 CC specific for Fbp. (Updated on 25-MAR-2003 to correct PN field.)
 CC
 XX

SO Sequence 130 AA:

QY Query Match 96.1%; Score 198; DB 2; Length 130;
 Best Local Similarity 97.4%; Pred. No. 8.5e-19;
 Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 1 QNSGNOSFEETEDKPKYEGGNIVDIDFDSVPQIHG 38
 2 QNSGNOSFEETEDKPKYEGGNIVDIDFDSVPQIHG 39

RESULT 4
 AAR58807
 ID AAR58807 standard; protein; 130 AA.
 XX
 AC AAR58807;

```

XX 25-MAR-2003 (revised)
DT 30-MAR-1995 (first entry)
XX
DE Fibronectin binding domain D1-D4(709-838).
XX
KM Fibronectin binding protein; Fbp; fibronectin binding domain;
KM monoclonal antibody; Mab; adhesion; Gram-positive bacterium; bacteremia;
KM Escherichia coli.
XX
OS Staphylococcus aureus.
XX
PN WO9418327-A1.
XX
PD 18-AUG-1994.
XX
PF 04-FEB-1994; 94WO-GB000215.
XX
PR 05-FEB-1993; 93GB-00002289.
PR 20-OCT-1993; 93GB-00021592.
XX
PA (SMIK ) SMITHKLINE BEECHAM PLC.
XX
PI Burnham MKR, Chopra I, Critchley IA, Knowles DJC;
XX
DR WPI; 1994-279748/34.
XX
PT Fibronectin binding protein and monoclonal antibodies specific for Fbp -
PT useful to prevent adherence of Gram-positive bacteria to indwelling
PT devices or wounds.
XX
PS Disclosure; Page 30; 40pp; English.
XX
CC Polypeptides corresponding to residues G709-T886 plus PPIVPT, G709-
CC P838(P838T) and G709-P838 (AARS58805-07, respectively) of S. aureus J2385
CC (NCIMB 40532) Fbp type A fibronectin binding domain D1-D4 region
CC (AARS58808) were expressed in E. coli BL21(DE4) and used to raise Mabs
CC specific for Fbp. (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ Sequence 130 AA:

Query Match 96.1%; Score 198; DB 2; Length 130;
Best Local Similarity 97.4%; Pred. No. 8.5e-19;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QNSGNQSFEEPTEDDKPYEQGNIVDIDFDSVPQIHG 38
    |||||
DB 2 QNSGNQSFEEPTEDDKPYEQGNIVDIDFDSVPQIHG 39

RESULT 5
AAR91202
ID AAR91202 standard; peptide; 130 AA.
XX
AC AAR91202;
XX
DT 13-NOV-1996 (first entry)
XX
DE D1-D4 fibronectin binding domains.
XX
KM Fibronectin; oral hygiene; gingivitis; gum disease; adhesion;
KM periodontitis; oral pathogen; caries; calculus; candidiasis; oral surgery;
KM tissue regeneration; irrigation; toothpaste; dentifrice; mouthwash;
KM lozenge.
XX
OS Staphylococcus aureus.
XX
PN WO9604003-A1.
XX
PD 15-FEB-1996.
XX
PR 18-JUL-1995; 95WO-EP002825.
XX
PA (SMIK ) SMITHKLINE BEECHAM PLC.
XX
PI Barnett P, Critchley IA, Knowles DJC;
XX
DR WPI; 1996-129122/13.
XX
PT Prevention of adherence of oral pathogens in the oral cavity, partic.
PT tooth surfaces - by application of a fibronectin binding protein or
PT polypeptide or a monoclonal antibody or fragment against it.
XX
PS Claim 5; Page 32; 41pp; English.
XX
CC Adherence of oral pathogens, particularly to tooth surfaces, can be
CC prevented by application of a fibronectin binding protein or polypeptide.
CC The fibronectin binding protein or polypeptide is useful in the
CC manufacture of oral hygiene compositions, eg. toothpaste, liquid
CC dentifrice, mouthwash or lozenge. They are useful to prevent the plaque-
CC related development of carious lesions, gingivitis, calculus or
CC periodontal disease and to combat oral cavity infections, eg.
CC candidiasis. They may also be useful in oral surgery e.g. in guided
CC tissue regeneration procedures to prevent subsequent bacterial infection,
CC and for irrigation of periodontal pockets. This sequence corresponds to
CC amino acids 709-838 of the D1-D4 fibronectin binding domain of
CC Staphylococcus aureus
XX
SQ Sequence 130 AA:

Query Match 96.1%; Score 198; DB 2; Length 130;
Best Local Similarity 97.4%; Pred. No. 8.5e-19;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QNSGNQSFEEPTEDDKPYEQGNIVDIDFDSVPQIHG 38
    |||||
DB 2 QNSGNQSFEEPTEDDKPYEQGNIVDIDFDSVPQIHG 39

RESULT 6
AAR91201
ID AAR91201 standard; peptide; 130 AA.
XX
AC AAR91201;
XX
DT 13-NOV-1996 (first entry)
XX
DE D1-D4 fibronectin binding domains.
XX
KM Fibronectin; oral hygiene; gingivitis; gum disease; adhesion;
KM periodontitis; oral pathogen; caries; calculus; candidiasis; oral surgery;
KM tissue regeneration; irrigation; toothpaste; dentifrice; mouthwash;
KM lozenge.
XX
OS Staphylococcus aureus.
XX
PN WO9604003-A1.
XX
PD 15-FEB-1996.
XX
PR 18-JUL-1995; 95WO-EP002825.
XX
PA (SMIK ) SMITHKLINE BEECHAM PLC.
XX
PI Barnett P, Critchley IA, Dodd I;
XX
DR WPI; 1996-129122/13.
XX
PT Prevention of adherence of oral pathogens in the oral cavity, partic.
PT tooth surfaces - by application of a fibronectin binding protein or
PT polypeptide or a monoclonal antibody or fragment against it.
XX

```

PS Claim 5; Page 31-32; 41pp; English.

XX CC Adherence of oral pathogens, particularly to tooth surfaces, can be

CC prevented by application of a fibronectin binding protein or polypeptide.

CC The fibronectin binding protein or polypeptide is useful in the

CC manufacture of oral hygiene compositions, eg. toothpaste, liquid

CC dentifrice, mouthwash or lozenge. They are useful to prevent the plaque-

CC related development of carious lesions, gingivitis, calculus or

CC periodontal disease and to combat oral cavity infections, e.g.

CC candidiasis. They may also be useful in oral surgery e.g. in guided

CC tissue regeneration procedures to prevent subsequent bacterial infection,

CC and for irrigation of periodontal pockets. This sequence corresponds to

CC amino acids 709-838 of the D1-D4 fibronectin binding domain of

CC Staphylococcus aureus with a P838T substitution

XX SQ Sequence 130 AA;

Query Match 96.1%; Score 198; DB 2; Length 130;

Best Local Similarity 97.4%; Pred. No. 8.5e-19;

Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QNSGNQSFEEPTEDKPKYEGGNIVDIDPDSVPQIHG 38

2 QNSGNQSFEEPTEDKPKYEGGNIVDIDPDSVPQIHG 39

Db

RESULT 7

AAV29089

ID AAV29089 standard; protein; 134 AA.

XX AC AAV29089;

XX DT 28-SEP-1999 (first entry)

XX DE Cloned fibronectin binding protein binding domain (FnBAB) sequence.

XX XX Bovine herpes virus-2; BHV-2; cytokine; immune response; immunogen; IL;

XX KM Interleukin; colony stimulating factor; CSF; interferon; IFN; TNF;

XX KM tumour necrosis factor; recombinant virus; vaccine; mucosal disease;

XX KM mastitis; breast cancer; stress-induced disease; binding domain; FnBAB;

XX KM fibronectin binding protein.

XX OS Staphylococcus aureus.

XX PN MO9916892-A1.

XX PD 08-APR-1999.

XX PF 29-SEP-1998; 98MO-GB002927.

XX PR 29-SEP-1997; 97GB-00020633.

XX PT New bovine herpes virus-2 vectors.

XX PA (UYBR-) UNIV BRISTOL.

XX PI Bradley AJ, Duffas WPH;

XX DR WPI; 1999-255101/21.

XX DR N-PSDB; AAX91506.

XX PT New bovine herpes virus-2 vectors.

XX XX Example 2; Fig 8A-B; 130pp; English.

XX CC The invention provides bovine herpes virus-2 (BHV-2) based vectors that

CC comprise at least one cytokine-encoding DNA sequence. The expression of

CC cytokines in mammals can up-regulate immune responses to the immunogens.

CC The cytokine is selected from interleukins (IL), colony stimulating

CC factors (CSF), interferons (IFN) and tumour necrosis factors (TNF). The

CC BHV-2 based vector or recombinant virus can be used as vaccines. They can

CC be used for preventing or treating a mucosal disease in a subject, e.g.

CC ruminants, cattle, sheep, goats, dogs, cats, horses, or man, particularly

CC mastitis in cows or breast cancers in humans. They can also be used for

CC preventing or treating a stress-induced disease. The present sequence

CC represents a S. aureus fibronectin binding protein binding domain

CC sequence FnBAB, the gene cloned for use in this invention. The gene has

CC 97.8 percent identity when compared to the previously published sequences

CC FnBA and FnBB

XX SQ Sequence 134 AA;

Query Match 96.1%; Score 198; DB 2; Length 134;

Best Local Similarity 97.4%; Pred. No. 8.8e-19;

Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QNSGNQSFEEPTEDKPKYEGGNIVDIDPDSVPQIHG 38

2 QNSGNQSFEEPTEDKPKYEGGNIVDIDPDSVPQIHG 39

Db

RESULT 8

AAV29088

ID AAV29088 standard; protein; 134 AA.

XX AC AAV29088;

XX DT 28-SEP-1999 (first entry)

XX DE S. aureus fibronectin binding protein B (FnBB) binding domain.

XX XX Bovine herpes virus-2; BHV-2; cytokine; immune response; immunogen; IL;

XX KM Interleukin; colony stimulating factor; CSF; interferon; IFN; TNF;

XX KM tumour necrosis factor; recombinant virus; vaccine; mucosal disease;

XX KM mastitis; breast cancer; stress-induced disease; binding domain; FnBB;

XX KM fibronectin binding protein.

XX OS Staphylococcus aureus.

XX PN MO9916892-A1.

XX PD 08-APR-1999.

XX PF 29-SEP-1998; 98MO-GB002927.

XX PR 29-SEP-1997; 97GB-00020633.

XX PT New bovine herpes virus-2 vectors.

XX PA (UYBR-) UNIV BRISTOL.

XX PI Bradley AJ, Duffas WPH;

XX DR WPI; 1999-255101/21.

XX DR N-PSDB; AAX91505.

XX PT New bovine herpes virus-2 vectors.

XX XX Example 2; Fig 8A-B; 130pp; English.

XX CC The invention provides bovine herpes virus-2 (BHV-2) based vectors that

CC comprise at least one cytokine-encoding DNA sequence. The expression of

CC cytokines in mammals can up-regulate immune responses to the immunogens.

CC The cytokine is selected from interleukins (IL), colony stimulating

CC factors (CSF), interferons (IFN) and tumour necrosis factors (TNF). The

CC BHV-2 based vector or recombinant virus can be used as vaccines. They can

CC be used for preventing or treating a mucosal disease in a subject, e.g.

CC ruminants, cattle, sheep, goats, dogs, cats, horses, or man, particularly

CC mastitis in cows or breast cancers in humans. They can also be used for

CC preventing or treating a stress-induced disease. The present sequence

CC represents the binding domain of a previously published S. aureus

CC fibronectin binding protein B (FnBB) sequence. The FnB binding domain

CC gene sequence FnBAB, cloned for use in this invention has 97.8 percent

CC identity when compared to the previously published FnBA and FnBB gene

CC sequences

XX SQ Sequence 134 AA;

Query Match 96.1%; Score 198; DB 2; Length 134;

Best Local Similarity 97.4%; Pred. No. 8.8e-19;

Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QNSGNQSFEEPTEDKPKRYEGGNIVIDIDFDSVPQIHG 38
 DB 2 QNSGNQSFEEPTEDKPKRYEGGNIVIDIDFDSVPQIHG 39

RESULT 9

AAV29087
 ID AAV29087 standard; protein; 134 AA.

AC AAV29087;

DT 28-SEP-1999 (first entry)

DE S. aureus fibronectin binding protein A (FnBA) binding domain.

XX Bovine herpes virus-2; BHV-2; cytokine; immune response; immunogen; IL;

KW Interleukin; colony stimulating factor; CSF; interferon; IFN; TNF;

KW tumour necrosis factor; recombinant virus; vaccine; mucosal disease;

KW mastitis; breast cancer; stress-induced disease; binding domain; FnBA;

XX fibronectin binding protein.

OS Staphylococcus aureus.

PN MO9916892-A1.

PD 08-APR-1999.

PF 29-SEP-1998; 98WO-GB002927.

PR 29-SEP-1997; 97GB-00020633.

XX (UYBR-) UNIV BRISTOL.

XX Bradley AJ, Duffas WP;

XX WPI; 1999-255101/21.

XX N-PSDB; AAX91504.

XX New bovine herpes virus-2 vectors.

XX Example 2; Fig 8A-B; 130pp; English.

XX The invention provides bovine herpes virus-2 (BHV-2) based vectors that

XX comprise at least one cytokine-encoding DNA sequence. The expression of

XX cytokines in mammals can up-regulate immune responses to the immunogens.

XX The cytokine is selected from interleukins (IL), colony stimulating

XX factors (CSF), interferons (IFN) and tumour necrosis factors (TNF). The

XX BHV-2 based vector or recombinant virus can be used as vaccines. They can

XX be used for preventing or treating a mucosal disease in a subject, e.g.

XX mastitis in cows or breast cancers in humans. They can also be used for

XX preventing or treating a stress-induced disease. The present sequence

XX represents the binding domain of a previously published S. aureus

XX fibronectin binding protein A (FnBA) sequence. The FnB binding domain

XX gene sequence FnBAB, cloned for use in this invention has 97.8 percent

XX identity when compared to the previously published FnBA and FnBB gene

XX sequences

SQ Sequence 134 AA;

Query Match 96.1%; Score 198; DB 2; Length 134;

Best Local Similarity 97.4%; Pred. No. 8.8e-19;

Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QNSGNQSFEEPTEDKPKRYEGGNIVIDIDFDSVPQIHG 38

DB 2 QNSGNQSFEEPTEDKPKRYEGGNIVIDIDFDSVPQIHG 39

RESULT 10

AAW31556

ID AAW31556 standard; protein; 139 AA.

AC AAW31556;

DT 27-AUG-2003 (revised)

DT 25-MAR-2003 (revised)

DT 21-MAY-1998 (first entry)

DE Fibronectin-binding MSCRAMM derivative pQD.

XX Fibronectin; pQD; collagen binding protein; sepsis; infection;

KW microbial surface component recognising adhesive matrix molecule; MSCRAMM;

KW adhesin; vaccine; immunisation; diagnosis; therapy; mastitis.

XX Staphylococcus aureus.

OS Key

FT Peptide

FT 1..12

FT /note= "vector POE30-derived peptide"

PN MO9743314-A2.

PD 20-NOV-1997.

PF 14-MAY-1997; 97WO-US008210.

PR 16-MAY-1996; 96US-0017678P.

PA (TEXA) UNIV TEXAS A & M SYSTEM.

XX (UABR-) UAB RES FOUND.

XX Hoeck M, Patti JM, House-Pompeo K, Sthanam N, Symersky J;

XX WPI; 1998-008801/01.

XX Antibody that interacts with collagen binding domain of Staphylococcal

XX cna gene product - useful to prevent bacterial sepsis in animal infected

XX with Staphylococcus aureus.

XX Disclosure; Page 91; 143pp; English.

XX This protein comprises Staphylococcus aureus fibronectin-binding

XX microbial surface component recognising adhesive matrix molecule (MSCRAMM)

XX derivative pQD, plus a vector-derived N-terminal peptide. The invention

XX relates to claimed nucleic acid sequences (see A193436-38) encoding S.

XX aureus collagen binding protein (CBP) epitopes M17, M31 and M55 (see

XX AAW31552-54) that confer protection against S. aureus infection. CBP

XX protein and antigenic epitopes are contemplated for use in the treatment

XX of pathological infections, especially to prevent bacterial adhesion to

XX collagen. The epitopes are also contemplated for use in the preparation

XX of vaccines and as carrier proteins in vaccine formulations, as well as

XX in the formulation of compositions for the prevention of S. aureus

XX infection. pCP33 and pQD (see AAW31556) were used to raise anti-MSCRAMM

XX polyclonal antibodies used in passive immunisation against bovine

SQ Sequence 139 AA;

Query Match 96.1%; Score 198; DB 2; Length 139;

Best Local Similarity 97.4%; Pred. No. 9.2e-19;

Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QNSGNQSFEEPTEDKPKRYEGGNIVIDIDFDSVPQIHG 38

DB 16 QNSGNQSFEEPTEDKPKRYEGGNIVIDIDFDSVPQIHG 53

RESULT 11

AAR58808

AC AAR58808;

```

XX      25-MAR-2003 (revised)
DT      30-MAR-1995 (first entry)
DT      XX
XX      Fbp fibronectin binding domain.
DE      XX
KW      Fibronectin binding protein; Fbp; fibronectin binding domain;
KW      monoclonal antibody; MAb; adhesion; Gram-positive bacterium; bacteremia;
KW      Escherichia coli; pBAC0531.
XX      XX
OS      Staphylococcus aureus.
XX      XX
PN      MO9418327-A1.
XX      18-AUG-1994.
XX      XX
XX      04-FEB-1994; 94WO-GB000215.
XX      PF
XX      PR 05-FEB-1993; 93GB-00002289.
XX      PR 20-OCT-1993; 93GB-00021592.
XX      XX
XX      (SMIK ) SMITHKLINE BEECHAM PLC.
XX      PA
XX      Burnham MKR, Chopra I, Critchley IA, Knowles DJC;
XX      PI
XX      WPI; 1994-279748/34.
XX      DR
XX      N-PSDB; AA071838.
XX      XX
XX      Fibronectin binding protein and monoclonal antibodies specific for Fbp -
XX      PT useful to prevent adherence of Gram-positive bacteria to indwelling
XX      PT devices or wounds.
XX      XX
XX      Disclosure; Page 30; 40pp; English.
XX      PS
XX      CC The sequences of DNA encoding S. aureus Fbp type A fibronectin binding
XX      CC domain (D1-D4) and the encoded protein are provided. D1-D4 polypeptides
XX      CC have been expressed in E. coli BL21(DE4) and used to raise MBs specific
XX      CC for Fbp. (Updated on 25-MAR-2003 to correct PN field.)
XX      CC
XX      SQ Sequence 174 AA;

Query Match 96.1%; Score 198; DB 2; Length 174;
Best Local Similarity 97.4%; Pred. No. 1,2e-18;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0.

QY      1 QNSGNQSFEEPTEDDKPKYEGGNIIVDIDFDSVPQING 38
      |||||
DB      2 QNSGNQSFEEPTEDDKPKYEGGNIIVDIDFDSVPQING 39

RESULT 12
ID      AAR91203
XX      AAR91203 standard; protein; 174 AA.
XX      XX
XX      AAR91203;
XX      XX
DT      16-OCT-2003 (revised)
DT      13-NOV-1996 (first entry)
XX      XX
DE      D1-D4 fibronectin binding domains.
XX      XX
KW      Fibronectin; oral hygiene; gingivitis; gum disease; adhesion;
KW      periodontitis; oral pathogen; caries; calculus; candidiasis; oral surgery;
KW      tissue regeneration; irrigation; toothpaste; dentifrice; mouthwash;
XX      KW lozeng.
XX      XX
XX      Staphylococcus aureus; J2385.
XX      OS
XX      PN MO9604003-A1.
XX      XX
XX      15-FEB-1996.
XX      PD
XX      18-JUL-1995; 95WO-EP002825.
XX      PF

```

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XX 05-AUG-1994; 94GB-00015902.
XX
XX (SMIK ) SMITHKLINE BEECHAM PLC.
XX
XX Barnett P, Critchley IA, Dodd I;
XX
XX WPI; 1996-129122/13.
XX
XX N-PSDB; AAT18308.
XX
XX
XX Prevention of adherence of oral pathogens in the oral cavity, partic.
XX tooth surfaces - by application of a fibronectin binding protein or
XX polypeptide or a monoclonal antibody or fragment against it.
XX
XX
XX Claim 5; Page 32; 41pp; English.
XX
XX
XX Adherence of oral pathogens, particularly to tooth surfaces, can be
XX prevented by application of a fibronectin binding protein or polypeptide.
XX The fibronectin binding protein or polypeptide is useful in the
XX manufacture of oral hygiene compositions, eg. toothpaste, liquid
XX dentifrice, mouthwash or lozenge. They are useful to prevent the plaque-
XX related development of carious lesions, gingivitis, calculus or
XX periodontal disease and to combat oral cavity infections, e.g.
XX candidiasis. They may also be useful in oral surgery e.g. in guided
XX tissue regeneration procedures to prevent subsequent bacterial infection,
XX and for irrigation of periodontal pockets. This sequence corresponds to
XX amino acids 709-838 of the D1-D4 fibronectin binding domain of
XX Staphylococcus aureus with a P838F substitution. (Updated on 16-OCT-2003
XX to standardise OS field)
XX
XX
XX Sequence 174 AA:
XX
XX
XX Query Match 96.1%; Score 198; DB 2; Length 174;
XX Best Local Similarity 97.4%; Pred. No. 1.2e-18;
XX Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX
XX 1 QNSGNOSFEPTEDKPRYEGGNIVDIDPDSVPQING 38
XX |||||
XX 2 QNSGNOSFEPTEDKPRYEGGNIVDIDPDSVPQING 39
XX
XX
XX RESULT 13
XX AAR58805
XX ID AAR58805 standard; protein; 181 AA.
XX
XX AC AAR58805;
XX
XX DT 25-MAR-2003 (revised)
XX DT 30-MAR-1995 (first entry)
XX
XX DE Fibronectin binding domain D1-D4(709-886).
XX
XX KW Fibronectin binding protein; Fbp; fibronectin binding domain;
XX KW monoclonal antibody; MAb; adhesion; Gram-positive bacterium; bacteremia;
XX KW Escherichia coli.
XX
XX OS Staphylococcus aureus.
XX
XX PN WO9418327-A1.
XX
XX PD 18-AUG-1994.
XX
XX PF 04-FEB-1994; 94WO-GB0000215.
XX
XX PR 05-FEB-1993; 93GB-00002289.
XX PR 20-OCT-1993; 93GB-00021592.
XX
XX PA (SMIK ) SMITHKLINE BEECHAM PLC.
XX
XX PI Burnham MKR, Chopra I, Critchley IA, Knowles DJC;
XX
XX WPI; 1994-279746/34.
XX

```

PT Fibronectin binding protein and monoclonal antibodies specific for Fbp -
 PT useful to prevent adherence of Gram-positive bacteria to indwelling
 PT devices or wounds.
 XX
 PS Disclosure; Page 29-30; 40pp; English.
 CC
 CC Polypeptides corresponding to residues G709-T886 plus PRVYPT, G709-
 CC P836(P838T) and G709-P838 (AAR58805-07, respectively) of *S. aureus* J2385
 CC (NCIMB 40532) Fbp type A fibronectin binding domain D1-D4 region
 CC (AAR58808) were expressed in *E. coli* BL21(DE4) and used to raise Mabs
 CC specific for Fbp. (Updated on 25-MAR-2003 to correct PN field.)
 CC
 XX
 SQ Sequence 181 AA;
 Query Match 96.1%; Score 198; DB 2; Length 181;
 Best Local Similarity 97.4%; Pred. No. 1.3e-18;
 Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 QNSGNQSFEEPTBEDPKPKYEGGNIYDIDPDSVPQIHG 38
 DB 2 QNSGNQSFEEPTBEDPKPKYEGGNIYDIDPDSVPQIHG 39
 RESULT 14
 AAR91200
 ID AAR91200 standard; peptide; 181 AA.
 XX
 AC AAR91200;
 DT 13-NOV-1996 (first entry)
 DE D1-D4 fibronectin binding domains.
 XX
 KW Fibronectin: oral hygiene; gingivitis; gum disease; adhesion;
 KW periodontitis; oral pathogens; caries; calculus; candidiasis; oral surgery;
 KW tissue regeneration; irrigation; toothpaste; dentifrice; mouthwash;
 KW lozenge.
 XX
 OS Staphylococcus aureus.
 XX
 PN WO9604003-A1.
 XX
 PD 15-FEB-1996.
 XX
 PF 18-JUL-1995; 95WO-EP002825.
 XX
 PR 05-AUG-1994; 94GB-00015902.
 XX
 PA (SMIK) SMITHKLINE BEECHAM PLC.
 XX
 PI Barnett P, Critchley IA, Dodd I;
 XX
 DR WPI; 1996-129122/13.
 XX
 DR N-PSDB; AAT18307.
 XX
 PT Prevention of adherence of oral pathogens in the oral cavity, partic.
 PT tooth surfaces - by application of a fibronectin binding protein or
 PT polypeptide or a monoclonal antibody or fragment against it.
 PS
 XX Claim 5; Page 31; 41pp; English.
 XX
 CC Adherence of oral pathogens, particularly to tooth surfaces, can be
 CC prevented by application of a fibronectin binding protein or polypeptide.
 CC The fibronectin binding protein or polypeptide is useful in the
 CC manufacture of oral hygiene compositions, eg. toothpaste, liquid
 CC dentifrice, mouthwash or lozenge. They are useful to prevent the plaque-
 CC related development of carious lesions, gingivitis, calculus or
 CC candidiasis. They may also be useful in oral cavity infections, e.g.
 CC periodontitis. They may also be useful in oral surgery e.g. in guided
 CC tissue regeneration procedures to prevent subsequent bacterial infection,
 CC and for irrigation of periodontal pockets. This sequence corresponds to
 CC amino acids 709-886 of the D1-D4 fibronectin binding domain of
 CC Staphylococcus aureus

XX
 SQ Sequence 181 AA;
 Query Match 96.1%; Score 198; DB 2; Length 181;
 Best Local Similarity 97.4%; Pred. No. 1.3e-18;
 Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 QNSGNQSFEEPTBEDPKPKYEGGNIYDIDPDSVPQIHG 38
 DB 2 QNSGNQSFEEPTBEDPKPKYEGGNIYDIDPDSVPQIHG 39
 RESULT 15
 AAM89803
 ID AAM89803 standard; protein; 559 AA.
 XX
 AC AAM89803;
 DT 16-MAR-1999 (first entry)
 DE Staphylococcus aureus protein SEQ ID #5251.
 XX
 KW Computer readable medium; vaccine; *S. aureus* infection; immunodetection;
 KW cellulitis; eyelid infection; food poisoning; osteomyelitis; therapy;
 KW skin infection; surgical wound infection; scalded skin syndrome;
 KW toxic shock syndrome.
 XX
 OS Staphylococcus aureus.
 XX
 PN EP786519-A2.
 XX
 PD 30-JUL-1997.
 XX
 PF 07-JAN-1997; 97BP-00100117.
 XX
 PR 05-JAN-1996; 96US-0009861P.
 XX
 PA (HMAN-) HUMAN GENOME SCI INC.
 XX
 PI Kunsch CA, Choi GH, Barash SC, Dillon PJ, Fannon MR, Rosen CA;
 XX
 DR WPI; 1997-374922/35.
 XX
 PD Polynucleotide(s) and proteins derived from *Staphylococcus aureus* -
 PT stored on computer readable medium and used in the production of anti-
 PT *S. aureus* vaccines.
 XX
 PS Claim 23; Page 3259-3261; 3271pp; English.
 XX
 CC This sequence represents a *Staphylococcus aureus* protein sequence of the
 CC invention. The DNA sequences encoding the *S. aureus* proteins are recorded
 CC on a computer readable medium, preferably selected from a floppy or hard
 CC disk, random access memory (RAM), read-only memory (ROM) or CD-ROM.
 CC Homology searches using the *S. aureus* DNA sequences allows putative
 CC functions to be assigned so that protein-encoding or regulatory regions
 CC of commercial, therapeutic or industrial importance can be obtained.
 CC Specifically, sequences which are likely to encode antigens have been
 CC identified and these polypeptides can be used in a vaccine composition
 CC against *S. aureus* infection. The polypeptides can also be used in a kit
 CC for the immunodetection of *S. aureus* in a sample. *S. aureus* is implicated
 CC in numerous human diseases, including cellulitis, eyelid infections, food
 CC poisoning, osteomyelitis, skin and surgical wound infections, scalded
 CC skin syndrome, toxic shock syndrome, etc. Organisms transformed with the
 CC DNA sequences can be used for recombinant production of the polypeptides.
 CC The new DNA sequences (and their fragments) are useful as primers or
 CC probes for isolating homologues of any of the 5191 *S. aureus* DNA sequences
 CC contained on the computer readable medium
 XX
 SQ Sequence 559 AA;
 Query Match 96.1%; Score 198; DB 2; Length 559;
 Best Local Similarity 97.4%; Pred. No. 5e-18;
 Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 ONSGNOSFEETEDKPKYEOGNIVDIDPDSVPOIHG 38
| | | | | | | | | | | | | | | | | | | | | |
Db 301 ONSGNOSFEETEDKPKYEOGNIVDIDPDSVPOIHG 338

Search completed: October 25, 2005, 20:21:02
Job time : 83.8825 secs

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OM protein - protein search, using SW model

Run on: October 22, 2005, 03:51:22 ; Search time 21.1723 Seconds
(without alignments)
133.980 Million cell updates/sec

Title: US-10-731-238-38

Perfect score: 206
Sequence: 1 QNSGNQSFEEPTEDKPKYEQGNIVDIDFDSVPQIHG 38

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

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5: /cgn2_6/ptodata/1/1aa/6B_COMB.pep:*
6: /cgn2_6/ptodata/1/1aa/Backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	206	100.0	38	4	US-09-010-317-38 Sequence 38, Appl
2	198	96.1	38	1	US-08-234-622A-2 Sequence 2, Appl1
3	198	96.1	38	4	US-09-010-317-5 Sequence 5, Appl1
4	198	96.1	114	1	US-08-259-000-3 Sequence 3, Appl1
5	198	96.1	130	2	US-08-459-135A-7 Sequence 7, Appl1
6	198	96.1	130	2	US-08-459-135A-8 Sequence 8, Appl1
7	198	96.1	130	3	US-08-495-559-7 Sequence 7, Appl1
8	198	96.1	130	3	US-08-495-559-8 Sequence 8, Appl1
9	198	96.1	139	3	US-08-856-253-8 Sequence 8, Appl1
10	198	96.1	174	2	US-08-459-135A-10 Sequence 10, Appl1
11	198	96.1	174	2	US-08-459-135A-13 Sequence 13, Appl1
12	198	96.1	174	3	US-08-495-559-10 Sequence 10, Appl1
13	198	96.1	174	3	US-08-495-559-13 Sequence 13, Appl1
14	198	96.1	176	3	US-08-495-559-6 Sequence 6, Appl1
15	198	96.1	178	2	US-08-459-135A-12 Sequence 12, Appl1
16	198	96.1	178	3	US-08-495-559-12 Sequence 12, Appl1
17	198	96.1	181	2	US-08-459-135A-6 Sequence 6, Appl1
18	198	96.1	559	4	US-08-956-171E-5251 Sequence 5251, Ap
19	198	96.1	559	4	US-08-781-986A-5251 Sequence 5251, Ap
20	198	96.1	1027	4	US-08-956-171E-5254 Sequence 5254, Ap
21	198	96.1	1027	4	US-08-781-986A-5254 Sequence 5254, Ap
22	192	93.2	38	1	US-08-729-767-3 Sequence 3, Appl1
23	192	93.2	38	4	US-09-010-317-36 Sequence 36, Appl1
24	192	93.2	38	4	US-09-010-317-37 Sequence 37, Appl1
25	192	93.2	38	4	US-09-010-317-39 Sequence 39, Appl1
26	192	93.2	38	4	US-09-010-317-40 Sequence 40, Appl1
27	192	93.2	38	4	US-09-010-317-41 Sequence 41, Appl1

28	191	92.7	38	4	US-09-010-317-42 Sequence 42, Appl1
29	190	92.2	38	4	US-09-010-317-6 Sequence 6, Appl1
30	190	92.2	38	4	US-09-010-317-43 Sequence 43, Appl1
31	188	91.3	38	4	US-09-010-317-35 Sequence 35, Appl1
32	187.5	91.0	39	4	US-09-010-317-56 Sequence 56, Appl1
33	187	90.8	38	4	US-09-010-317-48 Sequence 48, Appl1
34	179.5	87.1	39	4	US-09-010-317-57 Sequence 57, Appl1
35	179	86.9	38	1	US-08-234-622A-3 Sequence 3, Appl1
36	179	86.9	38	4	US-09-010-317-7 Sequence 7, Appl1
37	173	84.0	38	1	US-08-729-767-4 Sequence 4, Appl1
38	173	84.0	38	4	US-09-010-317-46 Sequence 46, Appl1
39	173	84.0	38	4	US-09-010-317-47 Sequence 47, Appl1
40	171	83.0	38	4	US-09-010-317-8 Sequence 8, Appl1
41	171	83.0	38	4	US-09-010-317-49 Sequence 49, Appl1
42	170	82.5	38	4	US-09-010-317-44 Sequence 44, Appl1
43	169	82.0	38	4	US-09-010-317-45 Sequence 45, Appl1
44	156	75.7	36	4	US-09-010-317-58 Sequence 58, Appl1
45	151	73.3	38	4	US-09-010-317-50 Sequence 50, Appl1

ALIGNMENTS

RESULT 1
US-09-010-317-38
Sequence 38, Application US/09010317
Patent No. 6685943
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
APPLICANT: Patti, Joseph M.
APPLICANT: House-Pompeo, Karen L.
APPLICANT: Speziale, Pietro
APPLICANT: Joh, Danny
APPLICANT: McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
TITLE OF INVENTION: AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/010.317
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hihler, David W.
REGISTRATION NUMBER: 41,071
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 38:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-09-010-317-38
Query Match 100.0%; Score 206; DB 4; Length 38;
Best Local Similarity 100.0%; Pred. No. 1e-21;

Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ONSGNOSFEPTEDKPKYEOGNIIVDIDFDSVPQIHG 38
Db 1 ONSGNOSFEPTEDKPKYEOGNIIVDIDFDSVPQIHG 38

RESULT 2

US-08-234-622A-2
Sequence 2, Application US/08234622A
Patent No. 5440014
GENERAL INFORMATION:
APPLICANT: HOOK, Magnus
APPLICANT: MCGAVIN, Martin
APPLICANT: RAUCCI, Giuseppe
TITLE OF INVENTION: A FIBRONECTIN BINDING PEPTIDE
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Burns, Doane, Swecker & Mathis
STREET: P.O. Box 1404
CITY: Alexandria
STATE: Virginia
COUNTRY: United States
ZIP: 2213-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/234,622A
FILING DATE: 28-APR-1994
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: SE 9002617-0
FILING DATE: 10-AUG-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/SE91/00534
FILING DATE: 09-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: Meuth, Donna M
REGISTRATION NUMBER: 36,607
REFERENCE/DOCKET NUMBER: 012885-044
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-234-622A-2

Query Match 96.1%; Score 198; DB 1; Length 38;
Best Local Similarity 97.4%; Pred. No. 1.3e-20;

Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ONSGNOSFEPTEDKPKYEOGNIIVDIDFDSVPQIHG 38
Db 1 ONSGNOSFEPTEDKPKYEOGNIIVDIDFDSVPQIHG 38

RESULT 3

US-09-010-317-5
Sequence 5, Application US/09010317
Patent No. 6685943
GENERAL INFORMATION:
APPLICANT: HOOK, Magnus
APPLICANT: PATTI, Joseph M.
APPLICANT: HOUSE-POMPEO, Karen L.
APPLICANT: Speziale, Pietro

APPLICANT: Joh, Danny
APPLICANT: MCGAVIN, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TMK-189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear

US-09-010-317-5
Query Match 96.1%; Score 198; DB 4; Length 38;
Best Local Similarity 97.4%; Pred. No. 1.3e-20;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ONSGNOSFEPTEDKPKYEOGNIIVDIDFDSVPQIHG 38
Db 1 ONSGNOSFEPTEDKPKYEOGNIIVDIDFDSVPQIHG 38

RESULT 4

US-08-259-000-3
Sequence 3, Application US/08259000
Patent No. 5571514
GENERAL INFORMATION:
APPLICANT: HOOK, Magnus
APPLICANT: LINDBERG, Martin Kjell
APPLICANT: SIGNAS, Lars Christer
APPLICANT: MADSTROM, Torkel Mikael
APPLICANT: FROMAN, Gunnar
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN AS WELL AS
ITS PREPARATION
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Burns, Doane, Swecker & Mathis
STREET: P.O. Box 1404
CITY: Alexandria
STATE: Virginia
COUNTRY: United States
ZIP: 2213-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25

;;
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/259,000
;; FILING DATE: 13-JUN-1994
;; CLASSIFICATION: 435
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: SE 8702272-9
;; FILING DATE: 01-JUN-1987
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Meuth, Donna M
;; REGISTRATION NUMBER: 36,607
;; REFERENCE/DOCKET NUMBER: 012885-062
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (703) 836-6620
;; TELEFAX: (703) 836-2021
;; INFORMATION FOR SEQ ID NO: 3:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 114 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; US-08-259-000-3

Query Match 96.1%; Score 198; DB 1; Length 114;
Best Local Similarity 97.4%; Pred. No. 5.2e-20;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ONSGNSFEPTEDDKPKYEGGNIVDIDFDSVPQIHG 38
|||
DB 2 ONSGNSFEPTEDDKPKYEGGNIVDIDFDSVPQIHG 39

RESULT 5
US-08-459-135A-7
; Sequence 7, Application US/08459135A
; Patent No. 5955078
; GENERAL INFORMATION:
; APPLICANT: BURNHAM, Martin Karl Russel
; APPLICANT: CHOPRA, Ian
; APPLICANT: CRITCHLEY, Ian Alfred
; APPLICANT: KNOWLES, David Justin Charles
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN: MONOCLONAL ANTIBODY AND THEIR US
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corporation
; STREET: 709 Swedeland Road
; CITY: King of Prussia
; STATE: PA
; COUNTRY: U.S.A.
; ZIP: 19406-0939
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: Fastseq, Version 2.0.
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/459,135A
; FILING DATE: 02-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB/94/00215
; FILING DATE: 04-Feb-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Gimmil, Edward R
; REGISTRATION NUMBER: 38,891
; REFERENCE/DOCKET NUMBER: P30591C2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-270-4478
; TELEFAX: 610-270-5090
; TELEX:
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:

;; LENGTH: 130 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; US-08-459-135A-7

Query Match 96.1%; Score 198; DB 2; Length 130;
Best Local Similarity 97.4%; Pred. No. 6.1e-20;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ONSGNSFEPTEDDKPKYEGGNIVDIDFDSVPQIHG 38
|||
DB 2 ONSGNSFEPTEDDKPKYEGGNIVDIDFDSVPQIHG 39

RESULT 6
US-08-459-135A-8
; Sequence 8, Application US/08459135A
; Patent No. 5955078
; GENERAL INFORMATION:
; APPLICANT: BURNHAM, Martin Karl Russel
; APPLICANT: CHOPRA, Ian
; APPLICANT: CRITCHLEY, Ian Alfred
; APPLICANT: KNOWLES, David Justin Charles
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN: MONOCLONAL ANTIBODY AND THEIR US
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corporation
; STREET: 709 Swedeland Road
; CITY: King of Prussia
; STATE: PA
; COUNTRY: U.S.A.
; ZIP: 19406-0939
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: Fastseq, Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/459,135A
; FILING DATE: 02-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB/94/00215
; FILING DATE: 04-Feb-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Gimmil, Edward R
; REGISTRATION NUMBER: 38,891
; REFERENCE/DOCKET NUMBER: P30591C2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-270-4478
; TELEFAX: 610-270-5090
; TELEX:
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 130 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
;; US-08-459-135A-8

Query Match 96.1%; Score 198; DB 2; Length 130;
Best Local Similarity 97.4%; Pred. No. 6.1e-20;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ONSGNSFEPTEDDKPKYEGGNIVDIDFDSVPQIHG 38
|||
DB 2 ONSGNSFEPTEDDKPKYEGGNIVDIDFDSVPQIHG 39

RESULT 7
US-08-495-559-7

```

; Sequence 7, Application US/08495559A
; Patent No. 6054572
; GENERAL INFORMATION:
; APPLICANT: BURHAM, Martin Karl Russel
; APPLICANT: CHOPRA, Ian
; APPLICANT: CRITCHLEY, Ian Alfred
; APPLICANT: KNOWLES, David Justin Charles
; TITLE OF INVENTION: FIBROECTIN BINDING PROTEIN: MONOCLONAL
; TITLE OF INVENTION: ANTIBODY AND THEIR USE IN PREVENTING BACTERIAL ADHESION
; FILE REFERENCE: P30591
; CURRENT APPLICATION NUMBER: US/08/495,559A
; CURRENT FILING DATE: 1995-08-03
; EARLIER APPLICATION NUMBER: GB 9302289.5
; EARLIER FILING DATE: 1993-02-05
; EARLIER APPLICATION NUMBER: GB 9321592.9
; EARLIER FILING DATE: 1993-10-20
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 7
; LENGTH: 130
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-08-495-559-7

Query Match      96.1%; Score 198; DB 3; Length 130;
Best Local Similarity 97.4%; Pred. No. 6.1e-20;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1 QNSGNQSFEEPTEDKPKYEOGNIVIDIDPSVPOIHG 38
Db      2 QNSGNQSFEEPTEDKPKYEOGNIVIDIDPSVPOIHG 39

RESULT 8
US-08-495-559-8
; Sequence 8, Application US/08495559A
; Patent No. 6054572
; GENERAL INFORMATION:
; APPLICANT: BURHAM, Martin Karl Russel
; APPLICANT: CHOPRA, Ian
; APPLICANT: CRITCHLEY, Ian Alfred
; APPLICANT: KNOWLES, David Justin Charles
; TITLE OF INVENTION: FIBROECTIN BINDING PROTEIN: MONOCLONAL
; TITLE OF INVENTION: ANTIBODY AND THEIR USE IN PREVENTING BACTERIAL ADHESION
; FILE REFERENCE: P30591
; CURRENT APPLICATION NUMBER: US/08/495,559A
; CURRENT FILING DATE: 1995-08-03
; EARLIER APPLICATION NUMBER: GB 9302289.5
; EARLIER FILING DATE: 1993-02-05
; EARLIER APPLICATION NUMBER: GB 9321592.9
; EARLIER FILING DATE: 1993-10-20
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 8
; LENGTH: 130
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-08-495-559-8

Query Match      96.1%; Score 198; DB 3; Length 130;
Best Local Similarity 97.4%; Pred. No. 6.1e-20;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1 QNSGNQSFEEPTEDKPKYEOGNIVIDIDPSVPOIHG 38
Db      2 QNSGNQSFEEPTEDKPKYEOGNIVIDIDPSVPOIHG 39

RESULT 9
US-08-856-253-8
; Sequence 8, Application US/08856253
; Patent No. 6288214
; GENERAL INFORMATION:
```

```

; APPLICANT: Hook, Magnus
; APPLICANT: Patti, Joseph M.
; APPLICANT: House-Pompeo, Karen
; APPLICANT: Stnam, Narayana
; APPLICANT: Symesky, Jindlich
; TITLE OF INVENTION: COLLAGEN BINDING PROTEIN COMPOSITIONS
; TITLE OF INVENTION: AND METHODS OF USE
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESS: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: U.S.
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/856,253
; FILING DATE: Concurrently Herewith
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/017,678
; FILING DATE: 16-MAY-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Kitchell, Barbara S.
; REGISTRATION NUMBER: 33,928
; REFERENCE/DOCKET NUMBER: TAMK.193
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (512) 418-3000
; TELEFAX: (512) 474-7577
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 139 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
US-08-856-253-8

Query Match      96.1%; Score 198; DB 3; Length 139;
Best Local Similarity 97.4%; Pred. No. 6.6e-20;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1 QNSGNQSFEEPTEDKPKYEOGNIVIDIDPSVPOIHG 38
Db      16 QNSGNQSFEEPTEDKPKYEOGNIVIDIDPSVPOIHG 53

RESULT 10
US-08-459-135A-10
; Sequence 10, Application US/08459135A
; Patent No. 5955078
; GENERAL INFORMATION:
; APPLICANT: BURHAM, Martin Karl Russel
; APPLICANT: CHOPRA, Ian
; APPLICANT: CRITCHLEY, Ian Alfred
; APPLICANT: KNOWLES, David Justin Charles
; TITLE OF INVENTION: FIBROECTIN BINDING PROTEIN: MONOCLONAL ANTIBODY AND THEIR USE
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESS: SmithKline Beecham Corporation
; STREET: 709 Swedeland Road
; CITY: King of Prussia
; STATE: PA
; COUNTRY: U.S.A.
; ZIP: 19406-0939
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
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SOFTWARE: Fastseq, Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/459,135A
FILING DATE: 02-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB/94/00215
FILING DATE: 04-Feb-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Gimmil, Edward R
REGISTRATION NUMBER: 38,891
REFERENCE/DOCKET NUMBER: P30591C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-4478
TELEFAX: 610-270-5090
TELEX:
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 174 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: Protein
US-08-459-135A-10

Query Match 96.1%; Score 198; DB 2; Length 174;
Best Local Similarity 97.4%; Pred. No. 8.6e-20;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QNSGNQSFEEPTEDPKPYEQGNGNIVDIDFDSVPQIHG 38
Db 2 QNSGNQSFEEPTEDPKPYEQGNGNIVDIDFDSVPQIHG 39

RESULT 11
US-08-459-135A-13
Sequence 13, Application US/08459135A
Patent No. 5955078
GENERAL INFORMATION:
APPLICANT: BURNNAM, Martin Karl Russel
APPLICANT: CHOPRA, Ian
APPLICANT: CRITCHLEY, Ian Alfred
APPLICANT: KNOWLES, David Justin Charles
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN: MONOCLONAL ANTIBODY AND THEIR US
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
STATE: PA
COUNTRY: U.S.A.
ZIP: 19406-0939
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: Fastseq, Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/459,135A
FILING DATE: 02-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB/94/00215
FILING DATE: 04-Feb-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Gimmil, Edward R
REGISTRATION NUMBER: 38,891
REFERENCE/DOCKET NUMBER: P30591C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-4478
TELEFAX: 610-270-5090
TELEX:

INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 174 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-459-135A-13

Query Match 96.1%; Score 198; DB 2; Length 174;
Best Local Similarity 97.4%; Pred. No. 8.6e-20;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QNSGNQSFEEPTEDPKPYEQGNGNIVDIDFDSVPQIHG 38
Db 2 QNSGNQSFEEPTEDPKPYEQGNGNIVDIDFDSVPQIHG 39

RESULT 12
US-08-495-559-10
Sequence 10, Application US/08495559A
Patent No. 6054572
GENERAL INFORMATION:
APPLICANT: BURNNAM, Martin Karl Russel
APPLICANT: CHOPRA, Ian
APPLICANT: CRITCHLEY, Ian Alfred
APPLICANT: KNOWLES, David Justin Charles
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN: MONOCLONAL
FILE REFERENCE: P30591
CURRENT APPLICATION NUMBER: US/08/495,559A
CURRENT FILING DATE: 1995-08-03
EARLIER APPLICATION NUMBER: GB 9302289.5
EARLIER FILING DATE: 1993-02-05
EARLIER APPLICATION NUMBER: GB 9321592.9
EARLIER FILING DATE: 1993-10-20
NUMBER OF SEQ ID NOS: 13
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 10
LENGTH: 174
TYPE: PRT
ORGANISM: Staphylococcus aureus
US-08-495-559-10

Query Match 96.1%; Score 198; DB 3; Length 174;
Best Local Similarity 97.4%; Pred. No. 8.6e-20;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QNSGNQSFEEPTEDPKPYEQGNGNIVDIDFDSVPQIHG 38
Db 2 QNSGNQSFEEPTEDPKPYEQGNGNIVDIDFDSVPQIHG 39

RESULT 13
US-08-495-559-13
Sequence 13, Application US/08495559A
Patent No. 6054572
GENERAL INFORMATION:
APPLICANT: BURNNAM, Martin Karl Russel
APPLICANT: CHOPRA, Ian
APPLICANT: CRITCHLEY, Ian Alfred
APPLICANT: KNOWLES, David Justin Charles
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN: MONOCLONAL
FILE REFERENCE: P30591
CURRENT APPLICATION NUMBER: US/08/495,559A
CURRENT FILING DATE: 1995-08-03
EARLIER APPLICATION NUMBER: GB 9302289.5
EARLIER FILING DATE: 1993-02-05
EARLIER APPLICATION NUMBER: GB 9321592.9
EARLIER FILING DATE: 1993-10-20
NUMBER OF SEQ ID NOS: 13
SOFTWARE: FastSeq for Windows Version 3.0

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; SEQ ID NO 13
; LENGTH: 174
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-08-495-559-13

Query Match          96.1%; Score 198; DB 3; Length 174;
Best Local Similarity 97.4%; Pred. No. 8.6e-20;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QNSGNQSFEEPTEDDKPKYEQGNIVDIDFDSVPQIHG 38
    |||||
Db 2 QNSGNQSFEEPTEDDKPKYEQGNIVDIDFDSVPQIHG 39

RESULT 14
US-08-495-559-6
; Sequence 6, Application US/08495559A
; Patent No. 6054572
; GENERAL INFORMATION:
; APPLICANT: BURHAM, Martin Karl Russel
; APPLICANT: CHOPRA, Ian
; APPLICANT: CRITCHLEY, Ian Alfred
; APPLICANT: KNOWLES, David Justin Charles
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN: MONOCLONAL
; TITLE OF INVENTION: ANTIBODY AND THEIR USE IN PREVENTING BACTERIAL ADHESION
; FILE REFERENCE: P30591
; CURRENT APPLICATION NUMBER: US/08/495,559A
; CURRENT FILING DATE: 1995-08-03
; EARLIER APPLICATION NUMBER: GB 9302289.5
; EARLIER FILING DATE: 1993-02-05
; EARLIER APPLICATION NUMBER: GB 9321592.9
; EARLIER FILING DATE: 1993-10-20
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 176
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-08-495-559-6

Query Match          96.1%; Score 198; DB 3; Length 176;
Best Local Similarity 97.4%; Pred. No. 8.8e-20;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QNSGNQSFEEPTEDDKPKYEQGNIVDIDFDSVPQIHG 38
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Db 2 QNSGNQSFEEPTEDDKPKYEQGNIVDIDFDSVPQIHG 39

RESULT 15
US-08-459-135A-12
; Sequence 12, Application US/08459135A
; Patent No. 5955078
; GENERAL INFORMATION:
; APPLICANT: BURHAM, Martin Karl Russel
; APPLICANT: CHOPRA, Ian
; APPLICANT: CRITCHLEY, Ian Alfred
; APPLICANT: KNOWLES, David Justin Charles
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN: MONOCLONAL ANTIBODY AND THEIR US
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corporation
; STREET: 709 Swedeland Road
; CITY: King of Prussia
; STATE: PA
; COUNTRY: U.S.A.
; ZIP: 19406-0939
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: Fastseq, Version 2.0
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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/459,135A
; FILING DATE: 02-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB/94/00215
; FILING DATE: 04-Feb-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Gimmil, Edward R
; REGISTRATION NUMBER: 38,891
; REFERENCE/DOCKET NUMBER: P30591C2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-270-4478
; TELEFAX: 610-270-5090
; TELEX:
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 178 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Protein
US-08-459-135A-12

Query Match          96.1%; Score 198; DB 2; Length 178;
Best Local Similarity 97.4%; Pred. No. 8.9e-20;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QNSGNQSFEEPTEDDKPKYEQGNIVDIDFDSVPQIHG 38
    |||||
Db 2 QNSGNQSFEEPTEDDKPKYEQGNIVDIDFDSVPQIHG 39
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Search completed: October 22, 2005, 05:46:43
Job time : 21.2223 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 22, 2005, 11:35:03 ; Search time 70.1256 Seconds
(without alignments)
226.232 Million cell updates/sec

Title: US-10-731-238-38

Perfect score: 206
Sequence: 1 QNSGNQSFEEPTEDPKRYEGCGNIVDIDFDSVPQIHG 38

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1862951 seqs, 417491010 residues

Total number of hits satisfying chosen parameters: 1862951

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

Published Applications AA.*
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19: /cgn2_6/ptodata/2/pubpaa/US11A_PUBCOMB.pep.*
20: /cgn2_6/ptodata/2/pubpaa/US11A_PUBCOMB.pep.*
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22: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	198	96.1	38	18	US-10-731-238-5
3	198	96.1	139	9	US-09-813-820-8
4	198	96.1	388	8	US-08-501-062-1
5	198	96.1	559	15	US-10-329-624-5251
6	198	96.1	559	15	US-10-329-624-5251
7	198	96.1	767	9	US-09-815-242-5899
8	198	96.1	767	9	US-09-815-242-13140
9	198	96.1	940	17	US-10-470-048B-424
10	198	96.1	948	17	US-10-470-048B-69
11	198	96.1	961	15	US-10-282-122A-43778

12	198	96.1	1018	9	US-09-815-242-5797	Sequence 5797, Ap
13	198	96.1	1018	9	US-09-815-242-12838	Sequence 12838, A
14	198	96.1	1018	17	US-10-470-048B-68	Sequence 56, Appl
15	198	96.1	1027	8	US-08-781-986A-5254	Sequence 5254, Ap
16	198	96.1	1027	15	US-10-329-624-5254	Sequence 5254, Ap
17	198	96.1	1038	15	US-10-282-122A-43827	Sequence 43827, A
18	192	93.2	38	18	US-10-731-238-36	Sequence 36, Appl
19	192	93.2	38	18	US-10-731-238-37	Sequence 37, Appl
20	192	93.2	38	18	US-10-731-238-39	Sequence 39, Appl
21	192	93.2	38	18	US-10-731-238-40	Sequence 40, Appl
22	192	93.2	38	18	US-10-731-238-41	Sequence 41, Appl
23	191	92.7	38	18	US-10-731-238-42	Sequence 42, Appl
24	190	92.2	38	18	US-10-731-238-43	Sequence 43, Appl
25	190	92.2	38	18	US-10-731-238-44	Sequence 44, Appl
26	190	92.2	978	9	US-09-815-242-5456	Sequence 5456, Ap
27	190	92.2	1001	9	US-09-815-242-12686	Sequence 12686, A
28	188	91.3	38	18	US-10-731-238-35	Sequence 35, Appl
29	187.5	91.0	38	18	US-10-731-238-36	Sequence 36, Appl
30	187	90.8	38	18	US-10-731-238-48	Sequence 48, Appl
31	179.5	87.1	38	18	US-10-731-238-57	Sequence 57, Appl
32	179	86.9	38	18	US-10-731-238-7	Sequence 7, Appl
33	173	84.0	38	18	US-10-731-238-46	Sequence 46, Appl
34	173	84.0	38	18	US-10-731-238-47	Sequence 47, Appl
35	171	83.0	38	18	US-10-731-238-8	Sequence 8, Appl
36	171	83.0	38	18	US-10-731-238-49	Sequence 49, Appl
37	170	82.5	38	18	US-10-731-238-44	Sequence 44, Appl
38	169	82.0	38	18	US-10-731-238-45	Sequence 45, Appl
39	156	75.7	36	18	US-10-731-238-58	Sequence 58, Appl
40	151	73.3	38	18	US-10-731-238-50	Sequence 59, Appl
41	148	71.8	36	18	US-10-731-238-59	Sequence 1, Appl
42	140	68.0	30	14	US-10-287-821-1	Sequence 2, Appl
43	140	68.0	31	14	US-10-287-821-2	Sequence 1134, Ap
44	76.5	31.1	37	20	US-11-066-697-1134	Sequence 60, Appl
45	74	35.9	14	18	US-10-731-238-60	

ALIGNMENTS

RESULT 1
US-10-731-238-38
Sequence 38, Application US/10731238
Publication No. US20050123552A1
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
Patli, Joseph M.
House-Pompeo, Karen L.
Speziale, Pietro
Joh, Danny
McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/731,238
FILING DATE: 10-Dec-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE: 21-Jan-1998
APPLICATION NUMBER: US 60/036,139

FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAMK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 38:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 38:
US-10-731-238-38

Query Match 100.0%; Score 206; DB 18; Length 38;
Best Local Similarity 100.0%; Pred. No. 7,5e-20;
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QNSGNQSFEEPTEDKPKYEQGNIVIDIDFDSVPQIHG 38
Db 1 QNSGNQSFEEPTEDKPKYEQGNIVIDIDFDSVPQIHG 38

RESULT 2
US-10-731-238-5
Sequence 5, Application US/10731238
Publication No. US20050123552A1
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
Pattl, Joseph M.
House-Pompeo, Karen L.
Speziale, Pietro
Joh, Danny
McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/731,238
FILING DATE: 10-Dec-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE: 21-Jan-1998
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAMK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>

TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-10-731-238-5

Query Match 96.1%; Score 198; DB 18; Length 38;
Best Local Similarity 97.4%; Pred. No. 8,6e-19;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QNSGNQSFEEPTEDKPKYEQGNIVIDIDFDSVPQIHG 38
Db 1 QNSGNQSFEEPTEDKPKYEQGNIVIDIDFDSVPQIHG 38

RESULT 3
US-09-813-820-8
Sequence 8, Application US/09813820
Patent No. US2002010282A1
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
Pattl, Joseph M.
House-Pompeo, Karen
Schanam, Narayana
Symerksy, Jindrich
TITLE OF INVENTION: COLLAGEN BINDING PROTEIN COMPOSITIONS
AND METHODS OF USE
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: Texas
COUNTRY: U.S.
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/813,820
FILING DATE: 22-Mar-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/856,253
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Kitchell, Barbara S.
REGISTRATION NUMBER: 33,928
REFERENCE/DOCKET NUMBER: TAMK:193
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
TELEFAX: (512) 474-7577
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 139 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-09-813-820-8

Query Match 96.1%; Score 198; DB 9; Length 139;
Best Local Similarity 97.4%; Pred. No. 3,9e-16;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QNSGNQSFEEPTEDKPKYEQGNIVIDIDFDSVPQIHG 38
Db 16 QNSGNQSFEEPTEDKPKYEQGNIVIDIDFDSVPQIHG 53

RESULT 4
US-08-901-062-1
Sequence 1, Application US/08901062

Publication No. US20020025324A1
GENERAL INFORMATION:
APPLICANT: SEALS, JONATHAN R.
TITLE OF INVENTION: RECOMBINANT BIVALENT BACTERIAL VACCINE
TITLE OF INVENTION: FOR THE PREVENTION OF MASTITIS
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: HALE AND DORR LLP
STREET: 60 State Street
CITY: Boston
STATE: MA
COUNTRY: United States Of America
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/901,062
FILING DATE: 25-JUL-1997
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Baker, Hollie L.
REGISTRATION NUMBER: 31,321
REFERENCE/DOCKET NUMBER: 106941.153
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 526-6000
TELEFAX: (617) 526-5000
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 388 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-901-062-1

Query Match 96.1%; Score 198; DB 8; Length 388;
Best Local Similarity 97.4%; Pred. No. 1,3e-17;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

1 QNSGNSFEPTBEDPKRYEGGNIYDIDFDSVPQIHG 38
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265 QNSGNSFEPTBEDPKRYEGGNIYDIDFDSVPQIHG 302
RESULT 5
US-08-781-986A-5251
Sequence 5251, Application US/08781986A
Publication No. US20030054436A1
GENERAL INFORMATION:
APPLICANT: Charles Kunsch
TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
NUMBER OF SEQUENCES: 5255
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COUNTRY: USA
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4MB storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/781,986A
FILING DATE:
CLASSIFICATION: 435

PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Benson, Bob
REGISTRATION NUMBER: 30,446
REFERENCE/DOCKET NUMBER: PB248BP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8512
TELEFAX: (301) 309-8504
INFORMATION FOR SEQ ID NO: 5251:
SEQUENCE CHARACTERISTICS:
LENGTH: 559 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-781-986A-5251

Query Match 96.1%; Score 198; DB 8; Length 559;
Best Local Similarity 97.4%; Pred. No. 2e-17;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

1 QNSGNSFEPTBEDPKRYEGGNIYDIDFDSVPQIHG 38
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301 QNSGNSFEPTBEDPKRYEGGNIYDIDFDSVPQIHG 338

RESULT 6
US-10-329-624-5251
Sequence 5251, Application US/10329624
Publication No. US20040043037A1
GENERAL INFORMATION:
APPLICANT: Charles Kunsch
Gail H. Choi
Patrick S. Dillon
Craig A. Rosen
Steven C. Barash
Michael R. Fannon
TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
NUMBER OF SEQUENCES: 5256
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COUNTRY: USA
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4MB storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/329,624
FILING DATE: 27-Dec-2002
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/956,171
FILING DATE: October 20, 1997
APPLICATION NUMBER: 60/009,861
FILING DATE: January 5, 1996
APPLICATION NUMBER: 08/781,986
FILING DATE: January 3, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Mark J. Hyman
REGISTRATION NUMBER: 46,789
REFERENCE/DOCKET NUMBER: PB248PDI1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (240) 314-1224
TELEFAX: (301) 309-8439
INFORMATION FOR SEQ ID NO: 5251:
SEQUENCE CHARACTERISTICS:
LENGTH: 559 amino acids

TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 5251:
US-10-329-624-5251

Query Match 96.1%; Score 198; DB 15; Length 559;
Best Local Similarity 97.4%; Pred. No. 2e-17;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 QNSGNQSFEEPTEDKPKYEGGNIVIDIDPSVPOIHG 38
Db 301 QNSGNQSFEEPTEDKPKYEGGNIVIDIDPSVPOIHG 338

RESULT 7

US-09-815-242-5899
Sequence 5899, Application US/09815242
Patent No. US20020061569A1
GENERAL INFORMATION:
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Karl L.
APPLICANT: Zykkind, Judith W.
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John D.
APPLICANT: Carr, Grant J.
APPLICANT: Yamamoto, Robert T.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: US/09/815,242
PRIOR FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 5899
LENGTH: 767
TYPE: PRT
ORGANISM: Staphylococcus aureus
US-09-815-242-5899

Query Match 96.1%; Score 198; DB 9; Length 767;
Best Local Similarity 97.4%; Pred. No. 2.9e-17;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 QNSGNQSFEEPTEDKPKYEGGNIVIDIDPSVPOIHG 38
Db 682 QNSGNQSFEEPTEDKPKYEGGNIVIDIDPSVPOIHG 719

RESULT 8

US-09-815-242-13140
Sequence 13140, Application US/09815242
Patent No. US20020061569A1
GENERAL INFORMATION:
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Karl L.
APPLICANT: Zykkind, Judith W.

APPLICANT: Wall, Daniel
APPLICANT: Trawick, John D.
APPLICANT: Carr, Grant J.
APPLICANT: Yamamoto, Robert T.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: US/09/815,242
PRIOR FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 13140
LENGTH: 767
TYPE: PRT
ORGANISM: Staphylococcus aureus
US-09-815-242-13140

Query Match 96.1%; Score 198; DB 9; Length 767;
Best Local Similarity 97.4%; Pred. No. 2.9e-17;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 QNSGNQSFEEPTEDKPKYEGGNIVIDIDPSVPOIHG 38
Db 682 QNSGNQSFEEPTEDKPKYEGGNIVIDIDPSVPOIHG 719

RESULT 9

US-10-470-048B-424
Sequence 424, Application US/10470048B
Publication No. US20050037444A1
GENERAL INFORMATION:
APPLICANT: MEINKE ET AL.
TITLE OF INVENTION: A METHOD FOR IDENTIFICATION, ISOLATION AND PRODUCTION OF
FILE REFERENCE: SONN.035US
CURRENT APPLICATION NUMBER: US/10/470,048B
PRIOR FILING DATE: 2003-07-25
NUMBER OF SEQ ID NOS: 603
SOFTWARE: PatentIn version 3.1
SEQ ID NO 424
LENGTH: 940
TYPE: PRT
ORGANISM: Staphylococcus aureus
US-10-470-048B-424

Query Match 96.1%; Score 198; DB 17; Length 940;
Best Local Similarity 97.4%; Pred. No. 3.7e-17;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 QNSGNQSFEEPTEDKPKYEGGNIVIDIDPSVPOIHG 38
Db 682 QNSGNQSFEEPTEDKPKYEGGNIVIDIDPSVPOIHG 719

RESULT 10

US-10-470-048B-69
Sequence 69, Application US/10470048B
Publication No. US20050037444A1

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; GENERAL INFORMATION:
; APPLICANT: MEINKE ET AL.
; TITLE OF INVENTION: A METHOD FOR IDENTIFICATION, ISOLATION AND PRODUCTION OF
; TITLE OF INVENTION: ANTIGENS TO A SPECIFIC PATHOGEN
; FILE REFERENCE: SONN-035US
; CURRENT APPLICATION NUMBER: US/10/470,048B
; CURRENT FILING DATE: 2003-07-25
; NUMBER OF SEQ ID NOS: 603
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 69
; LENGTH: 948
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
; US-10-470-048B-69

Query Match      96.1%; Score 198; DB 17; Length 948;
Best Local Similarity 97.4%; Pred. No. 3.7e-17;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Cy      1  ONSGNQSFEEPTEDKPKYEOGNIIVDIDFDSVPQIHG 38
Db      690  ONSGNQSFEEPTEDKPKYEOGNIIVDIDFDSVPQIHG 727

RESULT 11
US-10-282-122A-43778
; Sequence 43778, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Lianguo
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zykkind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forevth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining prior Application data removed - See file wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 43778
; LENGTH: 961
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
; US-10-282-122A-43778
```

```

Query Match      96.1%; Score 198; DB 15; Length 961;
Best Local Similarity 97.4%; Pred. No. 3.8e-17;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Cy      1  ONSGNQSFEEPTEDKPKYEOGNIIVDIDFDSVPQIHG 38
Db      693  ONSGNQSFEEPTEDKPKYEOGNIIVDIDFDSVPQIHG 730

RESULT 12
US-09-815-242-5797
; Sequence 5797, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari L.
; APPLICANT: Zykkind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; TITLE OF INVENTION: Prokaryotes
; FILE REFERENCE: ELITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5797
; LENGTH: 1018
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
; US-09-815-242-5797

Query Match      96.1%; Score 198; DB 9; Length 1018;
Best Local Similarity 97.4%; Pred. No. 4e-17;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Cy      1  ONSGNQSFEEPTEDKPKYEOGNIIVDIDFDSVPQIHG 38
Db      746  ONSGNQSFEEPTEDKPKYEOGNIIVDIDFDSVPQIHG 783

RESULT 13
US-09-815-242-12838
; Sequence 12838, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari L.
; APPLICANT: Zykkind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
```

```

; TITLE OF INVENTION: Prokaryotes
; FILE REFERENCE: EUTRA.011a
; CURRENT APPLICATION NUMBER: US/09/815,242
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO: 12838
; LENGTH: 1018
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-09-815-242-12838
```

```
Query Match          96.1%; Score 198; DB 9; Length 1018;
Best Local Similarity 97.4%; Pred. No. 4e-17;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      1  QNSGNQSFEEPTEDKPKRYEGGNIVDIDPDSVPQIHG 38
          |||
```

```
Db      746  QNSGNQSFEEPTEDKPKRYEGGNIVDIDPDSVPQIHG 783
```

RESULT 14

```
US-10-470-0488-68
; Sequence 68, Application US/104700488
; Publication No. US20050037444A1
; GENERAL INFORMATION:
; APPLICANT: MEINKE ET AL.
; TITLE OF INVENTION: A METHOD FOR IDENTIFICATION, ISOLATION AND PRODUCTION OF
; FILE REFERENCE: SONN.03505
; CURRENT APPLICATION NUMBER: US/10/470,0488
; NUMBER OF SEQ ID NOS: 2003-07-25
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 68
; LENGTH: 1018
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-10-470-0488-68
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```
Query Match          96.1%; Score 198; DB 17; Length 1018;
Best Local Similarity 97.4%; Pred. No. 4e-17;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      1  QNSGNQSFEEPTEDKPKRYEGGNIVDIDPDSVPQIHG 38
          |||
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Db      746  QNSGNQSFEEPTEDKPKRYEGGNIVDIDPDSVPQIHG 783
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RESULT 15

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US-08-781-986A-5254
; Sequence 5254, Application US/08781986A
; Publication No. US20030054436A1
; GENERAL INFORMATION:
; APPLICANT: Charles Kunach
; TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
; NUMBER OF SEQUENCES: 5255
; CORRESPONDENCE ADDRESS:
; ADDRESS: Human Genome Sciences, Inc.
```

```

; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/781,986A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Benson, Bob
; REGISTRATION NUMBER: 30,446
; REFERENCE/DOCKET INFORMATION:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 5254:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1027 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-781-986A-5254
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Query Match          96.1%; Score 198; DB 8; Length 1027;
Best Local Similarity 97.4%; Pred. No. 4.1e-17;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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```
QY      1  QNSGNQSFEEPTEDKPKRYEGGNIVDIDPDSVPQIHG 38
          |||
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Db      755  QNSGNQSFEEPTEDKPKRYEGGNIVDIDPDSVPQIHG 792
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Search completed: October 22, 2005, 12:09:25
Job time : 70.1256 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 22, 2005, 04:14:19 ; Search time 13.8905 Seconds
(without alignments)
263.219 Million cell updates/sec

Title: US-10-731-238-38

Perfect score: 206
Sequence: 1 QNSGNQSFPEPTEDPKPKYEGGNIIVDIDFDSVPQIHG 38

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	198	96.1	940	2 S19702	fibronectin-binding
2	198	96.1	961	2 G90053	fibronectin-binding
3	198	96.1	1018	2 A32192	fibronectin-binding
4	198	96.1	1038	2 H90053	fibronectin-binding
5	57	27.7	413	2 T31663	isolectin-B4
6	57	27.7	1460	2 D81675	polymorphic chain 11
7	56	27.2	1199	2 T15826	hypothetical prote
8	55.5	26.9	1273	1 TDRIT	leukocyte common a
9	55.5	26.9	1291	1 A28334	protein-tyrosine-p
10	54.5	26.5	155	1 RNBYR	DNA-directed RNA p
11	54	26.2	794	2 T45971	hypothetical prote
12	54	26.2	1952	2 T48814	hypothetical prote
13	53.5	26.0	582	2 I48673	matrix metalloprot
14	53.5	26.0	582	2 I38028	matrix metalloprot
15	53.5	26.0	1300	2 I53799	kinectin 1 - huma
16	53.5	26.0	1356	2 S32763	kinectin 1 - huma
17	53	25.7	168	2 T33564	hypothetical prote
18	53	25.7	183	2 D83840	hypothetical prote
19	53	25.7	545	2 T33659	hypothetical prote
20	53	25.7	568	2 T33660	hypothetical prote
21	53	25.7	651	2 AD3057	glycogen debranchi
22	53	25.7	651	2 B98229	glycogen debranchi
23	52.5	25.5	110	2 H75048	DNA-directed RNA p
24	52.5	25.5	428	2 T32952	hypothetical prote
25	52.5	25.2	241	2 H97723	hypothetical prote
26	52	25.2	241	2 C71725	amino-acid ABC tra
27	52	25.2	339	2 S07577	legumin storage pr
28	52	25.2	335	2 S07578	legumin storage pr
29	52	25.2	335	2 S07576	legumin storage pr

30	52	25.2	484	2 A24942	legumin B4 precurs
31	52	25.2	979	2 S62459	probable transcript
32	52	25.2	1022	2 I53078	homeotic gene regu
33	52	25.2	1613	2 S39059	protein BRG1 - hum
34	52	25.2	1647	2 S45252	SNF2beta protein -
35	51.5	25.0	110	2 A71112	probable transcript
36	51.5	25.0	133	2 S62573	hypothetical prote
37	51.5	25.0	540	2 B82170	peptide ABC transp
38	51.5	25.0	558	2 C71609	hypothetical prote
39	51.5	25.0	669	2 I38029	matrix metalloprot
40	51.5	25.0	817	2 T03852	protein phosphatas
41	51.5	25.0	1304	1 A46546	leukocyte common a
42	51.5	25.0	2128	2 I52577	beta-spectrin - mo
43	51	24.8	270	2 T43039	hypothetical prote
44	51	24.8	615	2 T39758	proline-serine ric
45	51	24.8	732	2 T05448	hypothetical prote

ALIGNMENTS

RESULT 1
S19702
fibronectin-binding protein B - Staphylococcus aureus
C/Species: Staphylococcus aureus
C/Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
C/Accession: S19702
R./Jensen, K.; Signaes, C.; Mueller, H.P.; Lindberg, M.
Eur. J. Biochem. 202, 1041-1048, 1991
A./Title: Two different genes encode fibronectin binding proteins in Staphylococcus aureus
A./Reference number: S19702; MUID:92111475; PMID:1837266
A./Accession: S19702
A./Status: preliminary
A./Molecule type: DNA
A./Residues: 1-940 <JOB>
A./Cross-references: UNIPROT:Q53682; EMBL:X62992; NID:949040; PIDN:CAA44726.1; PID:958156;
C./Keywords: fibronectin binding

Query Match
Best Local Similarity 96.1%; Score 198; DB 2; Length 940;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QNSGNQSFPEPTEDPKPKYEGGNIIVDIDFDSVPQIHG 38
DB 682 QNSGNQSFPEPTEDPKPKYEGGNIIVDIDFDSVPQIHG 719

RESULT 2
G90053
hypothetical protein fnbB [imported] - Staphylococcus aureus (strain N315)
C/Species: Staphylococcus aureus
C/Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C/Accession: G90053

R./Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguc
ma, A.; Mizutani-U, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.;
C./Shib, T.; Hatcori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
A./Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.
A./Reference number: A89758; MUID:21311952; PMID:11418146

A./Accession: G90053
A./Status: preliminary
A./Molecule type: DNA
A./Residues: 1-961 <KUR>
A./Cross-references: UNIPROT:Q99RD3; GB:BA000018; PID:G13702452; PIDN:BA843593.1; GSPDB:G
A./Experimental source: strain N315
C./Genetics:
A./Gene: fnbB

Query Match
Best Local Similarity 96.1%; Score 198; DB 2; Length 961;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QNSGNQSFPEPTEDPKPKYEGGNIIVDIDFDSVPQIHG 38

Db 693 QNSGNQSFEBDEBKPKRYEGCGNIVDIDFDSVPQIHG 730

RESULT 3

A32192
fibronectin-binding protein - Staphylococcus aureus
C:Species: Staphylococcus aureus
C:Date: 31-Jul-1989 #sequence_revision 31-Jul-1989 #text_change 16-Feb-1997
C:Accession: A32192
R:Signae, C.; Raucci, G.; Joensson, K.; Lindgren, P.E.; Anantharamiah, G.M.; Hoesek, M.
Proc. Natl. Acad. Sci. U.S.A. 86, 699-703, 1989
A:Title: Nucleotide sequence of the gene for a fibronectin-binding protein from Staphylo
A:Reference number: A32192; MUID:8908998; PMID:2521391
A:Accession: A32192
A:Status: Preliminary
A:Molecule type: DNA
A:Residues: 1-1018 <SIG>
A:Cross-references: GB:J04151
C:Keywords: fibronectin binding

Query Match 96.1%; Score 198; DB 2; Length 1018;
Best Local Similarity 97.4%; Pred. No. 2.4e-17;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QNSGNQSFEBDEBKPKRYEGCGNIVDIDFDSVPQIHG 38

Db 746 QNSGNQSFEBDEBKPKRYEGCGNIVDIDFDSVPQIHG 783

RESULT 4

H90053
hypothetical protein fnb [imported] - Staphylococcus aureus (strain N315)

C:Species: Staphylococcus aureus
C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004

C:Accession: H90053

R:Kuroda, M.; Ohka, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguc
ma, A.; Mizutani-Uji, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.;
C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1245-1240, 2001

A:Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.
A:Reference number: A89758; MUID:21111952; PMID:11418146
A:Accession: H90053
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1038 <KUR>

A:Cross-references: UNIPROT:Q99RD2; GB:BA000018; PID:G13702453; PIDN:BAB43594.1; GSPDB:C
A:Experimental source: strain N315
C:Genetics:

A:Gene: fnb
Query Match 96.1%; Score 198; DB 2; Length 1038;
Best Local Similarity 97.4%; Pred. No. 2.5e-17;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QNSGNQSFEBDEBKPKRYEGCGNIVDIDFDSVPQIHG 38

Db 742 QNSGNQSFEBDEBKPKRYEGCGNIVDIDFDSVPQIHG 779

RESULT 5

T31663
Isolucine-cRNA ligase (EC 6.1.1.5) - sea squirt (Ciona intestinalis) (fragment)

C:Species: Ciona intestinalis

C:Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004

C:Accession: T31663

R:Bird, A.P.; Clark, V.; Jones, S.J.; Leitgeb, S.; Lennard, N.; Tweedie, S.
submitted to the EMBL Data Library, October 1996
A:Reference number: Z21050
A:Accession: T31663
A:Status: Preliminary
A:Molecule type: DNA

A:Residues: 1-413 <BIR>

A:Cross-references: UNIPROT:Q94425; EMBL:Z80904; NID:e1007749; PID:e276498; PIDN:CAB02584
C:Genetics:
A:Note: intron positions not resolved (incomplete sequence)
C:Keywords: ligase

Query Match 27.7%; Score 57; DB 2; Length 413;
Best Local Similarity 50.0%; Pred. No. 14;
Matches 11; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

QY 11 PTEEDKPKRYEGCGNIVDIDFDS 32

Db 213 PTQYNADEYERGRDIDIDWFD 234

RESULT 6

D81675
polymorphic membrane protein B/C family TC0695 [imported] - Chlamydia muridarum (strain
C:Species: Chlamydia muridarum, Chlamydia trachomatis MoPn
C:Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004
C:Accession: D81675
R:Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hickey, I.
C.; Dodson, R.; Gwinn, M.; Nelson, W.; Deboy, R.; Kolonay, J.; McClarty, G.; Salzberg,
Nucleic Acids Res. 28, 1397-1406, 2000

A:Title: Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39.
A:Reference number: A81500; MUID:20150255; PMID:10684935
A:Accession: D81675
A:Status: preliminary
A:Molecule type: DNA

A:Residues: 1-1460 <TET>
A:Cross-references: UNIPROT:Q99PJV; GB:AE00338; GB:AE002160; NID:g7190724; PIDN:AAF39511
A:Experimental source: strain N19g (MoPn)
C:Genetics:

A:Gene: TC0695

Query Match 27.7%; Score 57; DB 2; Length 1460;
Best Local Similarity 32.4%; Pred. No. 61;
Matches 11; Conservative 9; Mismatches 14; Indels 0; Gaps 0;

QY 2 NSGNQSFEBDEBKPKRYEGCGNIVDIDFDSVPQ 35

Db 39 SSSQSFTEIIPNGAERYVSGDVFSDFSNIP 72

RESULT 7

T15826
hypothetical protein C52E12.1 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans
C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999

C:Accession: T15826
R:Du, Z.
submitted to the EMBL Data Library, February 1996

A:Description: The sequence of C. elegans coemid C52E12.
A:Reference number: Z18412
A:Accession: T15826
A:Status: preliminary
A:Molecule type: DNA

A:Residues: 1-1199 <DUG>
A:Cross-references: EMBL:U50135; NID:g1208884; PID:g1208889; PIDN:AAA93457.1; CESP:C52E12.
C:Genetics:

A:Gene: CESP:C52E12.1
A:Introns: 58/3; 90/2; 120/3; 159/2; 208/3; 248/1; 270/3; 291/3; 309/1; 348/3; 374/3; 46;

Query Match 27.2%; Score 56; DB 2; Length 1199;
Best Local Similarity 36.7%; Pred. No. 65;
Matches 11; Conservative 6; Mismatches 13; Indels 0; Gaps 0;

QY 5 NSQFEPTEEDKPKRYEGCGNIVDIDFDSVP 34

Db 326 NSQSRQPKYDKMYKRYMISAAHNFSDIP 355

RESULT 8

TDRLT

Leukocyte common antigen precursor, splice form 4 - rat
 N:Alternate names: CD45; L-CA; Ly-5; T200
 N:Contains: leukocyte common antigen precursor, splice form 1; leukocyte common antigen
 1.3.48)
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 04-Dec-1986 #sequence revision 05-May-2000 #text_change 09-Jul-2004
 C:Accession: A29450; B29450; C29450; D29450; A60241; A02247; I54569; A45854
 R:Barclay, A.N.; Jackson, D.I.; Willis, A.C.; Williams, A.F.
 EMBL J. 6, 1259-1264, 1987
 A>Title: Lymphocyte specific heterogeneity in the rat leukocyte common antigen (T200) is
 A:Reference number: A91067; MUID:87275817; PMID:2440674
 A:Accession: A29450
 A:Molecule type: mRNA
 A:Residues: 20-30,163-218 <BAR1>
 A:Cross-references: UNIPROT:Q64224; GB:M25820; GB:M24611; NID:G205153; GB:Y0065; GB:K03
 A:Experimental source: splice form 1
 A:Note: the translation in GenBank entry RATLCAI, PIDN:AAA41518.1, PID:G205154, release
 A:Accession: B29450
 A:Molecule type: mRNA
 A:Residues: 19-30,122-218 <BAR2>
 A:Cross-references: GB:M25821; GB:M24611; NID:G205155; PIDN:AAA41519.1; PID:G205156; GB:
 A:Experimental source: splice form 2
 A:Accession: C29450
 A:Molecule type: mRNA
 A:Residues: 20-30,73-121,163-218 <BAR3>
 A:Cross-references: GB:M25822; GB:M24611; NID:G205157; PIDN:AAA41520.1; PID:G205158; GB:
 A:Experimental source: splice form 3
 A:Accession: D29450
 A:Molecule type: mRNA
 A:Residues: 28-318 <BAR4>
 A:Cross-references: GB:M25823; GB:M24611; NID:G205159; PIDN:AAA41521.1; PID:G205160; GB:
 A:Experimental source: splice form 4
 A:Note: the sequence in GenBank entry RATLCAIV, release 113.0, has the codon ACG for 56-
 R:Barclay, A.N.; Jackson, D.I.; Willis, A.C.; Williams, A.F.
 Adv. Exp. Med. Biol. 237, 3-7, 1988
 A>Title: The leukocyte-common antigen (L-CA) family.
 A:Reference number: A60241; MUID:89319817; PMID:2978200
 A:Accession: A60241
 A:Molecule type: not compared with conceptual translation
 A:Status: not compared with conceptual translation
 A:Molecule type: DNA
 A:Residues: 30-161 <BAR5>
 R:Thomas, M.L.; Barclay, A.N.; Gagnon, J.; Williams, A.F.
 Cell 41, 83-93, 1985
 A>Title: Evidence from cDNA clones that the rat leukocyte-common antigen (T200) spans th
 A:Reference number: A02247; MUID:85201691; PMID:3158393
 A:Accession: A02247
 A:Molecule type: mRNA
 A:Residues: 187-189, 'K', 191-192, 'K', 208-1273 <THO>
 A:Cross-references: GB:M10072; GB:M81859; NID:G205140; PIDN:AAA41513.1; PID:G205143
 A:Note: the translation in GenBank entry RATLCAI, release 113.0, begins at non-initiat
 A:Note: parts of this sequence were determined by protein sequencing
 R:McCall, W.N.; Shorton, D.M.; Barclay, A.N.
 Immunology 76, 310-317, 1992
 A>Title: Expression of soluble isoforms of rat CD45. Analysis by electron microscopy and
 A:Reference number: I54569; MUID:92340120; PMID:1378817
 A:Accession: I54569
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-30,163-180 <MCC>
 A:Cross-references: GB:S40716; NID:G252015; PIDN:AAB22648.1; PID:G252016
 R:Jackson, D.I.; Barclay, A.N.
 Immunogenetics 29, 281-287, 1989
 A>Title: The extra segments of sequence in rat leukocyte common antigen (L-CA) are deriv
 A:Reference number: A45854; MUID:89233293; PMID:2523868
 A:Accession: A45854
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 24-227, 'H', 229-305, 'Y', 307-310 <JAC>
 A:Cross-references: GB:M18347; GB:M18348; GB:M18349
 C:Comment: This glycoprotein is found on lymphoid and myeloid cell surfaces.
 C:Superfamily: leukocyte common antigen; leukocyte common antigen cytosolic domain homol
 C:Keyword: alternative splicing; duplication; glycoprotein; phosphoprotein; phosphoric
 F.1-23/Domain: signal sequence #status predicted <SIG>

F.24-1273/Product: leukocyte common antigen precursor, splice form 4 #status predicted <F
 F.24-546/Domain: extracellular #status predicted <EXT>
 F.24-30,122-1273/Product: leukocyte common antigen, splice form 2 #status predicted <MAT
 F.24-30,163-1273/Product: leukocyte common antigen, splice form 1 #status predicted <MAT
 F.24-30,163-1273/Product: leukocyte common antigen, splice form 3 #status predicted
 F.24-30,163-1273/Product: leukocyte common antigen, splice form 3 #status predicted
 F.547-566/Domain: transmembrane #status predicted <TM>
 F.565-1206/Domain: leukocyte common antigen cytosolic domain homology <LAC>
 F.569-1273/Domain: intracellular #status predicted <INT>
 F.646-870/Domain: protein-tyrosine-phosphatase homology <PP>
 F.62,142,153,164,178,200,245,271,282,327,371,374,502/Binding site: carbohydrate (Asn) (C
 F.822/Active site: Cys (phosphotyrosine intermediate) #status predicted
 F.826/Binding site: substrate phosphate (Arg) #status predicted
 F.1063/Binding site: carbohydrate (Asn) (covalent) #status absent

Query Match 26.9% Score 55.5; DB 1; Length 1273;
 Best Local Similarity 40.5%; Pred. No. 81;
 Matches 15; Conservative 5; Mismatches 10; Indels 7; Gaps 2;

QY 1 QNSGNQSEEPREPKRYEQGNIVDDPDSVPQIH 37
 DB 929 QHIGNQ-----ENRKK-NRNSNVYPYDFNRVPLKH 958

RESULT 9
 A28334
 protein-tyrosine-phosphatase (EC 3.1.3.48) Ly-5 precursor (B-cell variant) - mouse
 N:Alternate names: 200K leukocyte common antigen; B220; CD45; Ly-5 (B-cell specific); PT
 N:Contains: protein-tyrosine-phosphatase (T-cell variant)
 C:Species: Mus musculus (house mouse)
 C:Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #text_change 09-Jul-2004
 C:Accession: A28334; A29381; A61180; A60933; A33822; A29075; I54450; A28335; A23329; I57
 R:Thomas, M.L.; Reynolds, P.O.; Chain, A.; Ben-Neriah, Y.; Trowbridge, I.S.
 Proc. Natl. Acad. Sci. U.S.A. 84, 5360-5363, 1987
 A>Title: B-cell variant of mouse T200 (Ly-5): evidence for alternative mRNA splicing.
 A:Reference number: A28334; MUID:87260986; PMID:2955416
 A:Accession: A28334
 A:Molecule type: mRNA
 A:Residues: 1-1291 <THO>
 A:Cross-references: UNIPROT:P06800; UNIPROT:Q61814; UNIPROT:Q61815; UNIPROT:Q61813; GB:M
 R:Saga, Y.; Tung, J.S.; Shen, F.W.; Boyse, E.A.
 Proc. Natl. Acad. Sci. U.S.A. 83, 6940-6944, 1986
 A>Title: Sequences of Ly-5 cDNA: isoform-related diversity of Ly-5 mRNA.
 A:Reference number: A29381; MUID:86313686; PMID:2944116
 A:Accession: A29381
 A:Molecule type: mRNA
 A:Residues: 1-30,170-517, 'NTT', 521-527, 'G', 529-555, 'S', 557-587, 'S', 589-905, 'Q', 907-930, 'F
 A:Cross-references: GB:M14342; NID:9198914; PIDN:AAA9458.1; PID:9198915
 R:Yi, T.; Cleveland, J.L.; Ihle, J.N.
 Blood 78, 2222-2228, 1991
 A>Title: Identification of novel protein tyrosine phosphatases of hematopoietic cells by
 A:Reference number: A61180; MUID:92032882; PMID:1932742
 A:Accession: A61180
 A:Status: not compared with conceptual translation
 A:Molecule type: not compared with conceptual translation
 A:Molecule type: mRNA
 A:Residues: 730-838 <YIA>
 R:Gomez, L.U.; Walker, I.D.; Sandrin, M.S.; McKenzie, I.F.C.
 Immunogenetics 25, 263-266, 1987
 A>Title: High sequence conservation between rat (T200) and mouse (Ly-5) leukocyte common
 A:Reference number: A60933; MUID:87192931; PMID:3570377
 A:Accession: A60933
 A:Molecule type: protein
 A:Residues: 'R', 289-298; 329, 'V', 331-336, 'Y', 'R', 364-370, 'X', 372-375; 585-608; 638-649; 660-
 R:Johnson, N.A.; Meyer, C.M.; Pingel, J.T.; Thomas, M.L.
 J. Biol. Chem. 264, 6220-6229, 1989
 A>Title: Sequence conservation in potential regulatory regions of the mouse and human l
 A:Reference number: A33522; MUID:89197920; PMID:2522330
 A:Accession: A33522
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-22 <JOH>
 A:Cross-references: GB:M22456; NID:9198755; PIDN:AAB46374.1; PID:9554185; GB:J04640; GB:J
 R:Raaschke, W.C.
 Proc. Natl. Acad. Sci. U.S.A. 84, 161-165, 1987

A;Title: Cloned murine T200 (Ly-5) cDNA reveals multiple transcripts within B- and T-lym
 A;Reference number: A29075; MUID:87092355; PMID:2948186
 A;Accession: A29075
 A;Molecule type: mRNA
 A;Residues: 961-1291 <RAS>
 A;Cross-references: GB:M15174; NID:G201105; PIDN:AAA40161.1; PID:G201106
 R;Tung, J.
 Immunogenetics 28, 271-277, 1988
 A;Title: Structural features of Ly-5 glycoproteins of the mouse and counterparts in othe
 A;Reference number: 154450; MUID:86330145; PMID:3417340
 A;Accession: 154450
 A;Status: preliminary; translated from GB/EMBL/DBJ
 A;Molecule type: DNA
 A;Residues: 32-73 <RES>
 A;Cross-references: GB:M23241; NID:G340850; PIDN:AAA39460.1; PID:G548174
 R;Saga, Y.; Tung, J.S.; Shen, F.W.; Boyse, E.A.
 Proc. Natl. Acad. Sci. U.S.A. 84, 5364-5368, 1987
 A;Title: Alternative use of 5' exons in the specification of Ly-5 isoforms distinguishes
 A;Reference number: A28335; MUID:87260987; PMID:3037546
 A;Accession: A28335
 A;Molecule type: mRNA
 A;Residues: 1-50,74-226 <SA2>
 A;Cross-references: GB:M14342
 R;Shen, F.W.; Saga, Y.; Litman, G.; Freeman, G.; Tung, J.S.; Cantor, H.; Boyse, E.A.
 Proc. Natl. Acad. Sci. U.S.A. 82, 7360-7363, 1985
 A;Reference number: A23329; MUID:8604265; PMID:3864163
 A;Accession: A23329
 A;Molecule type: mRNA
 A;Residues: 10-30,170-263 <SHE>
 A;Cross-references: GB:M11934; NID:G198919; PIDN:AAA39461.1; PID:G198920
 R;Saga, Y.; Tung, J.
 Mol. Cell. Biol. 8, 4889-4895, 1988
 A;Title: Organization of the Ly-5 Gene
 A;Reference number: 157644; MUID:8909662; PMID:3211131
 A;Accession: 157644
 A;Status: preliminary; translated from GB/EMBL/DBJ
 A;Molecule type: DNA
 A;Residues: 'MT', 1-22 <RES>
 A;Cross-references: GB:M23354; NID:G340890; PIDN:AAA39462.1; PID:G554192
 C;Genetics:
 A;Gene: Ly-5
 C;Superfamily: leukocyte common antigen; leukocyte common antigen cytosolic domain homol
 C;Keywords: alternative splicing; glycoprotein; phosphoprotein; phosphoric monoester hyd
 F;1-23/Domain: signal sequence #status predicted <SIG>
 F;24-1291/Product: protein-tyrosine-phosphatase (B-cell variant) #status predicted <MAT>
 F;24-564/Domain: extracellular #status predicted <EXT>
 F;24-30,170-1291/Product: protein-tyrosine-phosphatase (T-cell variant) #status predicte
 F;565-586/Domain: transmembrane #status predicted <TM>
 F;583-1223/Domain: leukocyte common antigen cytosolic domain homology <IAC>
 F;587-1291/Domain: intracellular #status predicted <INT>
 F;664-888/Domain: protein-tyrosine-phosphatase homology <PTR>
 F;64,150,161,207,211,218,253,258,290,311,322,347,416,427,457,489,520,556/Binding site: C
 F;840/Active site: Cys (phosphotyrosine intermediate) #status predicted
 F;846/Binding site: substrate phosphate (Arg) #status predicted
 Query Match 26.9%; Score 55.5; DB 1; Length 1291;
 Best Local Similarity 40.5%; Pred. No. 82;
 Matches 15; Conservative 5; Mismatches 10; Indels 7; Gaps 2;
 QY 1 QNSGNQFEPTEDPKRYEQGNIVDIDPSVPOIH 37
 Db 947 QHIGNQ-----EENKKK-NRNSNVVPYDFNRVPLKH 976
 RESULT 10
 RNBVR6
 DNA-directed RNA polymerase (EC 2.7.7.6) chain RPO26 - yeast (Saccharomyces cerevisiae)
 N;Alternate names: DNA-directed RNA polymerase 2X chain; DNA-directed RNA polymerase II
 C;Species: Saccharomyces cerevisiae
 C;Date: 30-Sep-1992 #sequence_revision 30-Sep-1992 #text_change 09-Jul-2004
 C;Accession: S13307; A36352; B34588; A38846; S58817
 R;Archambault, J.; Schappert, K.T.; Friesen, J.D.
 Mol. Cell. Biol. 10, 6123-6131, 1990

A;Title: A suppressor of an RNA polymerase II mutation of Saccharomyces cerevisiae encodes
 A;Reference number: A36352; MUID:91061718; PMID:2247052
 A;Accession: S13307
 A;Molecule type: DNA
 A;Residues: 1-155 <ARCI>
 A;Cross-references: UNIPROT:P20435; EMBL:M33924; NID:G172452; PIDN:AAA34989.1; PID:G17245
 A;Accession: A36352
 A;Molecule type: mRNA
 A;Residues: 1-155 <ARC2>
 A;Cross-references: GB:M33924; NID:G172452; PIDN:AAA34989.1; PID:G172453
 R;Moychik, N.A.; Liao, S.M.; Kolodziej, P.A.; Young, R.A.
 Genes Dev. 4, 313-323, 1990
 A;Title: Subunits shared by eukaryotic nuclear RNA polymerases.
 A;Reference number: A34588; MUID:90249736; PMID:2186966
 A;Accession: B34588
 A;Status: not compared with conceptual translation
 A;Molecule type: DNA
 A;Residues: 1-155 <MOY1>
 A;Cross-references: GB:X53288; NID:G287823; PIDN:CAA37382.1; PID:G287824
 A;Accession: A38846
 A;Molecule type: protein
 A;Residues: 48-60,99-115 <MOY2>
 R;Miller, N.
 submitted to the EMBL Data Library, April 1995
 A;Description: The sequence of S. cerevisiae cosmid 9677.
 A;Reference number: 558816
 A;Accession: 558817
 A;Molecule type: DNA
 A;Residues: 1-155 <ML>
 A;Cross-references: EMBL:U25841; NID:G786295; PIDN:AA64616.1; PID:G786304; GSPDB:GN00014
 C;Comment: This protein is a subunit of DNA-directed RNA polymerases I, II, and III.
 C;Genetics:
 A;Gene: SGD:RPO26; RP86; MIPS:YPR187W
 A;Cross-references: SGD:S0006391; MIPS:YPR187W
 A;Map position: 16R
 A;Intons: 7/2
 C;Superfamily: DNA-directed RNA polymerase chain RPO26
 C;Keywords: nucleotidyltransferase
 F;3-42/Region: acidic
 F;65-97/Region: basic
 Query Match 26.5%; Score 54.5; DB 1; Length 155;
 Best Local Similarity 36.7%; Pred. No. 9.6;
 Matches 11; Conservative 6; Mismatches 4; Indels 9; Gaps 1;
 QY 2 NSGNQSFPE-----EPTEDPKRYEQG 22
 Db 9 NDGNENFDPDVEHFSDSETYEEKPDKDG 38
 RESULT 11
 T45971
 hypothetical protein F9D24.20 - Arabidopsis thaliana
 C;Species: Arabidopsis thaliana (mouse-ear cress)
 C;Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 09-Jul-2004
 C;Accession: T45971
 R;D'Angelo, M.; Vezzi, A.; Modesto, D.; Pigazzzi, M.; Valle, G.; Mewes, H.W.; Lemcke, K.;
 submitted to the Protein Sequence Database, January 2000
 A;Reference number: Z23011
 A;Accession: T45971
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-784 <DAN>
 A;Cross-references: UNIPROT:Q9W2K5; EMBL:AL137081
 A;Experimental source: cultivar Columbia; BAC clone F9D24
 C;Genetics:
 A;Map position: 3
 A;Note: F9D24.20
 C;Superfamily: Arabidopsis thaliana hypothetical protein F9D24.20
 Query Match 26.2%; Score 54; DB 2; Length 784;
 Best Local Similarity 32.0%; Pred. No. 72;
 Matches 16; Conservative 6; Mismatches 8; Indels 20; Gaps 2;

Matches 13; Conservative 4; Mismatches 11; Indels 1; Gaps 1;

11 PTEEDKPKY-EOGNIVDIDFDSVPQIHG 38

Db 303 PSVPDKPKNPTYGPNICDGNFDTVAMLRG 331

RESULT 15

153799

CGI protein - human

C;Species: Homo sapiens (man)

C:\Accession: 153788 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004

C; Accession: 153799
P-Print C G : Tenn

R;Print, C.G.; Leung, E.; Harrison, J.E.; Watson, J.D.; Krissansen, G.W.
Gene 144 221-228 1994

Gene 144, 221-228, 1994

A:Reference number: 153799: MUID:94314220: PMID:8039706
A>Title: Cloning of a gene encoding a human leukocyte protein characterized by extensive

A:Accession: I53799
A:Reference number: 153/99; MOLD:94514220; PMID:8055700

A;Status: Preliminary

A:molecule type: mRNA

A;Residues: 1-1300 <R

A; Cross-references: UNIP

C:\Genetics:

A;Gene: GDE

A; Cross-referen

1

Query Match	Score	DB 2	Length
26.0%	53.5		1300

Best Local Similarity 38.2%; Pred. No. 1.5e+02;

Matches 13; Conservative 5; Mismatches 7; Indels 9; Gaps 1;

11 PTEEDKPKYE-----QGGINVIDIDFDSVPQ 35

Db 49 PTKTDKKAEEKKKKKKEIQNGNLHESDSSEVPR 82

Search completed: October 22, 2005, 06:09:44

Job time : 14.8905 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 22, 2005, 04:10:49 ; Search time 69.6361 Seconds
(without alignments)
279.439 Million cell updates/sec

Title: US-10-731-238-38

Perfect score: 206

Sequence: 1 QNSGNQSFEEPTBEDPKRYEQGNIVDIDPDSVPQIHG 38

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	198	96.1	940 2 Q53682	Q53682 staphylococ
2	198	96.1	943 2 Q8NUH8	Q8NUH8 staphylococ
3	198	96.1	957 2 Q6G6H4	Q6G6H4 staphylococ
4	198	96.1	961 2 Q998D3	Q998D3 staphylococ
5	198	96.1	961 2 Q7A3J8	Q7A3J8 staphylococ
6	198	96.1	1018 1 FNBA_STPAU	F14738 staphylococ
7	198	96.1	1038 2 Q998D2	Q998D2 staphylococ
8	198	96.1	1038 2 Q7A3J7	Q7A3J7 staphylococ
9	197	95.6	965 2 Q6GDU5	Q6GDU5 staphylococ
10	190	92.2	1015 2 Q8NUU7	Q8NUU7 staphylococ
11	190	92.2	1015 2 Q6G6H3	Q6G6H3 staphylococ
12	187	90.8	152 2 Q9AEP9	Q9AEP9 staphylococ
13	61	29.6	354 2 Q7RRM0	Q7RRM0 plasmodium
14	60.5	29.4	5922 2 Q8LIN2	Q8LIN2 plasmodium
15	59	28.6	1246 2 Q7UKY7	Q7UKY7 rhodospirell
16	58.5	28.4	1015 2 Q6FRE8	Q6FRE8 candida gla
17	58	28.2	684 2 Q6CIN9	Q6CIN9 bacteroides
18	58	28.2	889 2 Q6CBW0	Q6CBW0 yarrowia ll
19	58	28.2	981 2 Q91LJ7	Q91LJ7 white spot
20	58	28.2	1335 2 Q7NCK8	Q7NCK8 gloeobacter
21	57.5	27.9	191 2 Q6BMS4	Q6BMS4 debaryomyce
22	57	27.7	237 2 Q8BZM9	Q8BZM9 mus musculu
23	57	27.7	413 1 SY1C10IN	Q94425 ciona intes
24	57	27.7	455 2 Q6Z097	Q6Z097 mus musculu
25	57	27.7	532 2 Q9D074	Q9D074 m mus muscu
26	57	27.7	745 2 Q7SA99	Q7SA99 neurospora
27	57	27.7	856 2 Q6C206	Q6C206 yarrowia ll
28	57	27.7	968 1 PKD2_HUMAN	Q13563 homo sapien
29	57	27.7	1142 1 ENAM_HUMAN	Q99101 homo sapien
30	57	27.7	1142 2 O81WP4	Q81WP4 homo sapien
31	57	27.7	1460 1 PMPC_CHLMU	Q9PJY1 chlamydia m

32	57	27.7	1848 2 Q6CNT6	Q6CNT6 kluyveromyc
33	56.5	27.4	133 2 Q9NH77	Q9NH77 plasmodium
34	56.5	27.4	1791 2 Q81HX4	Q81HX4 plasmodium
35	56	27.2	457 2 Q9GDV3	Q9GDV3 carpodrocus
36	56	27.2	610 2 Q6CJN0	Q6CJN0 kluyveromyc
37	56	27.2	925 2 Q18782	Q18782 caenorhabdi
38	56	27.2	1350 2 Q6LFP5	Q6LFP5 plasmodium
39	55.5	26.9	878 2 Q8C6Q7	Q8C6Q7 mus musculu
40	55.5	26.9	962 2 Q6LDZ3	Q6LDZ3 rattus norv
41	55.5	26.9	975 2 Q8NZJ8	Q8NZJ8 streptococc
42	55.5	26.9	999 2 Q8K5Z5	Q8K5Z5 streptococc
43	55.5	26.9	1255 1 CD45_RAT	P04157 rattus norv
44	55.5	26.9	1291 2 Q61812	Q61812 mus musculu
45	55.5	26.9	1343 2 Q64730	Q64730 mus musculu

ALIGNMENTS

RESULT 1

ID	Q53682	PRELIMINARY;	PRT;	940 AA.
AC	Q53682;			
DT	01-NOV-1996 (TREMBLrel. 01, Created)			
DT	01-NOV-1996 (TREMBLrel. 01, Last sequence update)			
DT	01-MAR-2004 (TREMBLrel. 26, Last annotation update)			
DE	Fibronectin binding protein B.			
GN	Name=fnbB;			
OS	Staphylococcus aureus.			
OC	Bacteria; Firmicutes; Bacillales; Staphylococcus.			
OX	NCBI_Taxid=1280;			
RN	(1)			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=8325-4;			
RX	MEDLINE=9211475; PubMed=1837266;			
RA	Johnson K., Signas C., Muller H.P., Lindberg M.;			
RT	"Two different genes encode fibronectin binding proteins in			
RT	staphylococcus aureus. The complete nucleotide sequence and			
RT	characterization of the second gene."			
RL	Eur. J. Biochem. 202:1041-1048 (1991).			
CC	-1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by			
CC	an amide bond (By similarity).			
DR	EMBL; X62992; CAA44726.1; -			
DR	PIR; S19702; S19702.			
DR	HSSP; Q53653; IN67.			
DR	GO; GO:0009986; C:cell surface; IEA.			
DR	GO; GO:0005618; C:cell wall; IEA.			
DR	GO; GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.			
DR	GO; GO:0016020; C:membrane; IEA.			
DR	GO; GO:007155; P:cell adhesion; IEA.			
DR	InterPro; IPR008966; Adhes_Bact.			
DR	InterPro; IPR004237; Fn_bind.			
DR	InterPro; IPR005877; Gpos_YsIRK.			
DR	InterPro; IPR001899; Gram_pos_anchor.			
DR	Pfam; PF02986; Fn_bind; 2.			
DR	Pfam; PF00746; Gram_pos_anchor; 1.			
DR	Pfam; PF04650; YsIRK_signal; 1.			
DR	TIGRPFAM; TIGR01167; LPXTG_anchor; 1.			
DR	TIGRPFAM; TIGR01168; YsIRK_signal; 1.			
DR	PROSITE; PSS0647; GRAM_POS_ANCHORING; 1.			
KW	Cell wall; Peptidoglycan-anchor.			
SQ	SEQUENCE 940 AA; 10355 MW; E35FBCA907AE345 CRC64;			

Query Match 96.1%; Score 198; DB 2; Length 940;
Best local Similarity 97.4%; Pred. No. 8.7e-16;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QNSGNQSFEEPTBEDPKRYEQGNIVDIDPDSVPQIHG 38
DB 682 QNSGNQSFEEPTBEDPKRYEQGNIVDIDPDSVPQIHG 719

RESULT 2

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Q8NU8      PRELIMINARY;      PRT;      943 AA.
ID Q8NU8
AC Q8NU8
DT 01-OCT-2002 (TREMBlrel. 22, Created)
DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE FnbB protein.
GN Name=fnbB; OrderedlocusNames=MM2420;
OS Staphylococcus aureus (strain MM2).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
CX NCBI_TaxID=196620;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MM2;
RX MEDLINE=22040717; PubMed=12044378; DOI=10.1016/S0140-6736(02)08713-5;
RA Bada T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Oguchi A.,
RA Yamamoto K., Hiramatsu K.;
RT "Genome and virulence determinants of high virulence community-
RT acquired MRSA.";
RL Lancet 359:1819-1827(2002).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC an amide bond (By similarity).
DR EMBL; AP004830; BAB96285.1; -.
DR HSSP; Q53653; 1N67.
DR GO; GO:0009986; C:cell surface; IEA.
DR GO; GO:0005618; C:cell wall; IEA.
DR GO; GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0007155; P:cell adhesion; IEA.
DR InterPro; IPR008966; Adhes_bact.
DR InterPro; IPR004237; Fn_bind.
DR InterPro; IPR005877; Gpos_YsIRK.
DR InterPro; IPR001899; Gram_pos_anchor.
DR Pfam; PF02986; Fn_bind; 1.
DR Pfam; PF00746; Gram_pos_anchor; 1.
DR TIGRFAMs; TIGR01167; LPXTG_anchor; 1.
DR TIGRFAMs; TIGR01168; YsIRK_signal; 1.
DR PROSITE; PS50847; GRAM_POS_ANCHORING; 1.
KW Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ SEQUENCE 943 AA; 104537 MW; DA8A5F31947E1B6A CRC64;

Query Match 96.1%; Score 198; DB 2; Length 943;
Best Local Similarity 97.4%; Pred. No. 8.7e-16;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QNSGNQSFEEPTEDKPKRYEGGNIIVDIDFDSVPQING 38
DB 689 QNSGNQSFEEPTEDKPKRYEGGNIIVDIDFDSVPQING 726

RESULT 3
Q6G6H4 PRELIMINARY; PRT; 957 AA.
ID Q6G6H4
AC Q6G6H4
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE Fibronectin-binding protein.
GN Name=fnbB; OrderedlocusNames=SA52387;
OS Staphylococcus aureus (strain MSSA476).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
CX NCBI_TaxID=282459;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=15213324; DOI=10.1073/pnas.0402521101;
RA Holden M.T.G., Fell E.J., Lindsay J.A., Peacock S.J., Day N.P.J.,
RA Enright M.C., Foster T.J., Moore C.E., Hurst L., Atkin R., Barron A.,
RA Baason N., Bentley S.D., Chillingworth C., Chillingworth T.,
RA Churcher C., Clark L., Corton C., Cronin A., Doggett J., Dowd L.,
RA Feltwell T., Hance Z., Harris B., Hauser H., Holroyd S., Jagsels K.,
RA James K.D., Lennard N., Line A., Mayes R., Moule S., Mungall K.,
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RA Ormond D., Quail M.A., Rabbintowlsch E., Rutherford K.M., Sanders M.,
RA Sharp S., Simmonds M., Stevens K., Whitehead S., Barrell B.G.,
RA Spratt B.G., Parkhill J.;
RT "Complete genomes of two clinical Staphylococcus aureus strains:
RT evidence for the rapid evolution of virulence and drug resistance.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:9786-9791(2004).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC an amide bond (By similarity).
DR EMBL; BX571857; CAG44201.1; -.
DR GO; GO:0009986; C:cell surface; IEA.
DR GO; GO:0005618; C:cell wall; IEA.
DR GO; GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0007155; P:cell adhesion; IEA.
DR InterPro; IPR008966; Adhes_bact.
DR InterPro; IPR004237; Fn_bind.
DR InterPro; IPR005877; Gpos_YsIRK.
DR InterPro; IPR001899; Gram_pos_anchor.
DR Pfam; PF02986; Fn_bind; 1.
DR Pfam; PF00746; Gram_pos_anchor; 1.
DR TIGRFAMs; TIGR01167; LPXTG_anchor; 1.
DR TIGRFAMs; TIGR01168; YsIRK_signal; 1.
DR PROSITE; PS50847; GRAM_POS_ANCHORING; 1.
KW Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ SEQUENCE 957 AA; 105980 MW; 28F8BA7FFDD3EAF CRC64;

QY 1 QNSGNQSFEEPTEDKPKRYEGGNIIVDIDFDSVPQING 38
DB 689 QNSGNQSFEEPTEDKPKRYEGGNIIVDIDFDSVPQING 726

RESULT 4
Q99RD3 PRELIMINARY; PRT; 961 AA.
ID Q99RD3
AC Q99RD3
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE Fibronectin-binding protein homolog.
GN Name=fnbB; OrderedlocusNames=SAV2502;
OS Staphylococcus aureus (strain Mu50 / ATCC 700699).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
CX NCBI_TaxID=158878;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Mu50 / ATCC 700699;
RX MEDLINE=21311952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2;
RA Kuroda M., Onota T., Uchiyama I., Bada T., Yuzawa H., Kobayashi I.,
RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Iian J.-Q., Ito T.,
RA Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hoshoyama A.,
RA Mizutani-Ui Y., Takehashi N.K., Sawano T., Inoue R.-I., Kaito C.,
RA Sekimizu K., Hiraoka H., Kubara S., Goto S., Yabuzaki J.,
RA Kanehisa M., Yanaishita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
RA Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
RT "Whole genome sequencing of methicillin-resistant Staphylococcus
RT aureus.";
RL Lancet 357:1225-1240(2001).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC an amide bond (By similarity).
DR EMBL; AP003365; BAB58664.1; -.
DR PIR; G90053; G90053.
DR HSSP; Q53653; 1N67.
DR GO; GO:0009986; C:cell surface; IEA.
DR GO; GO:0005618; C:cell wall; IEA.
DR GO; GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0007155; P:cell adhesion; IEA.
DR InterPro; IPR008966; Adhes_bact.
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FT          threonine (Potential).
SQ  SEQUENCE      1018 AA;  111780 MW;  5815E00208181F CRC64;
Query Match      96.1%; Score 198; DB 1; Length 1018;
Best Local Similarity 97.4%; Pred. No. 9.5e-16;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy          1  QNSGNQSFEEPTBEDKPKYEGGNIIVDIDFDSVPQIHG 38
Db          746  QNSGNQSFEEPTBEDKPKYEGGNIIVDIDFDSVPQIHG 783

RESULT 7
ID  Q099RD2      PRELIMINARY;      PRT; 1038 AA.
AC  Q099RD2;
DT  01-JUN-2001 (TREMBlrel. 17, Created)
DT  01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT  01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE  Fibronectin-binding protein homolog.
GN  Name=fnb; OrderedLocustNames=SAV2503;
OS  Staphylococcus aureus (strain Mu50 / ATCC 700699).
OC  Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX  NCBI_TaxID=158878;
[1]
RN  SEQUENCE FROM N.A.
RC  STRAINMu50 / ATCC 700699;
RX  MEDLINE=21311952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2;
RA  Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
RA  Cui L., Oguchi A., Aoki K.-I., Nagai Y., Iian J.-Q., Ito T.,
RA  Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hoshoyama A.,
RA  Mizutani U. Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
RA  Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
RA  Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
RA  Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
RT  "Whole genome sequencing of methicillin-resistant Staphylococcus
RL  aureus.";
RL  Lancet 357:1225-1240(2001).
CC  -I- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC  an amide bond (By similarity).
DR  EMBL; AP003137; BAB58665.1; -.
DR  PIR; H90053; H90053.
DR  GO; GO:0009986; C:cell surface; IEA.
DR  GO; GO:0005618; C:cell wall; IEA.
DR  GO; GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR  GO; GO:0016020; C:membrane; IEA.
DR  GO; GO:0007155; P:cell adhesion; IEA.
DR  InterPro; IPR008966; Adhes_bact.
DR  InterPro; IPR004237; Fn_bind.
DR  InterPro; IPR005877; Gpos_YsIRK.
DR  InterPro; IPR001899; Gram_pos_anchor.
DR  Pfam; PF02986; Fn_bind; 1.
DR  Pfam; PF00746; Gram_pos_anchor; 1.
DR  Pfam; PF04650; YsIRK_signal; 1.
DR  TIGRFAMs; TIGR01167; LpxTG_anchor; 1.
DR  TIGRFAMs; TIGR01168; YsIRK_signal; 1.
DR  PROSITE; PS50847; GRAM_POS_ANCHORING; 1.
KW  Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ  SEQUENCE      1038 AA;  113618 MW;  666BF6BF2BFBEB12 CRC64;

Query Match      96.1%; Score 198; DB 2; Length 1038;
Best Local Similarity 97.4%; Pred. No. 9.7e-16;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy          1  QNSGNQSFEEPTBEDKPKYEGGNIIVDIDFDSVPQIHG 38
Db          742  QNSGNQSFEEPTBEDKPKYEGGNIIVDIDFDSVPQIHG 779

RESULT 8
ID  Q07A3J7      PRELIMINARY;      PRT; 1038 AA.
AC  Q07A3J7;

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DT  05-JUL-2004 (TREMBlrel. 27, Created)
DT  05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT  05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE  Fnb protein.
GN  Name=fnb; OrderedLocustNames=SA2291;
OS  Staphylococcus aureus (strain N315).
OC  Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX  NCBI_TaxID=158879;
[1]
RN  SEQUENCE FROM N.A.
RX  MEDLINE=21311952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2;
RA  Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
RA  Cui L., Oguchi A., Aoki K.-I., Nagai Y., Iian J.-Q., Ito T.,
RA  Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hoshoyama A.,
RA  Mizutani U. Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
RA  Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
RA  Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
RA  Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
RT  "Whole genome sequencing of methicillin-resistant Staphylococcus
RL  aureus.";
RL  Lancet 357:1225-1240(2001).
CC  -I- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC  an amide bond (By similarity).
DR  EMBL; AP003137; BAB43594.1; -.
DR  GO; GO:0009986; C:cell surface; IEA.
DR  GO; GO:0005618; C:cell wall; IEA.
DR  GO; GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR  GO; GO:0016020; C:membrane; IEA.
DR  GO; GO:0007155; P:cell adhesion; IEA.
DR  InterPro; IPR008966; Adhes_bact.
DR  InterPro; IPR004237; Fn_bind.
DR  InterPro; IPR005877; Gpos_YsIRK.
DR  InterPro; IPR001899; Gram_pos_anchor.
DR  Pfam; PF02986; Fn_bind; 1.
DR  Pfam; PF00746; Gram_pos_anchor; 1.
DR  Pfam; PF04650; YsIRK_signal; 1.
DR  TIGRFAMs; TIGR01167; LpxTG_anchor; 1.
DR  TIGRFAMs; TIGR01168; YsIRK_signal; 1.
DR  PROSITE; PS50847; GRAM_POS_ANCHORING; 1.
KW  Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ  SEQUENCE      1038 AA;  113618 MW;  666BF6BF2BFBEB12 CRC64;

Query Match      96.1%; Score 198; DB 2; Length 1038;
Best Local Similarity 97.4%; Pred. No. 9.7e-16;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy          1  QNSGNQSFEEPTBEDKPKYEGGNIIVDIDFDSVPQIHG 38
Db          742  QNSGNQSFEEPTBEDKPKYEGGNIIVDIDFDSVPQIHG 779

RESULT 9
ID  Q06GDU5      PRELIMINARY;      PRT; 965 AA.
AC  Q06GDU5;
DT  05-JUL-2004 (TREMBlrel. 27, Created)
DT  05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT  05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE  Fibronectin-binding protein.
GN  Name=fnbA; OrderedLocustNames=SA2580;
OS  Staphylococcus aureus (strain MRSA252).
OC  Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX  NCBI_TaxID=282458;
[1]
RN  SEQUENCE FROM N.A.
RX  PubMed=15213324; DOI=10.1073/pnae.0402521101;
RA  Hoiden M.T.G., Feil E.J., Lindsey J.A., Peacock S.J., Day N.P.J.,
RA  Enright M.C., Foster T.J., Moore C.E., Hurst L., Atkin R., Barron A.,
RA  Bason N., Bentley S.D., Chillingworth C., Chillingworth T.,
RA  Churcher C., Clark L., Cotton C., Cronin A., Doggett J., Dowd L.,
RA  Feltham T., Hance Z., Harris B., Hauser H., Holtroyd S., Jegerle K.,
RA  James K.D., Lennard N., Line A., Mayes R., Moule S., Mungall K.,
RA  Ormond D., Quail M.A., Rabinowitsch E., Rutherford K.M., Sanders M.,

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RA Sharp S., Simmonds M., Stevens K., Whitehead S., Barrell B.G.,
RA Spratt B.G., Parkhill J.;
RT "Complete genomes of two clinical *Staphylococcus aureus* strains:
evidence for the rapid evolution of virulence and drug resistance";
RL Proc. Natl. Acad. Sci. U.S.A. 101:9786-9791(2004).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
an amide bond (By similarity).
DR EMBL: BX571856; CAG41560.1; -.
DR GO: GO:0009986; C:cell surface; IEA.
DR GO: GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO: GO:0016020; C:membrane; IEA.
DR GO: GO:007155; P:cell adhesion; IEA.
DR InterPro: IPR008966; Adhes_bact.
DR InterPro: IPR004237; Fn_bind.
DR InterPro: IPR005877; Gpos_YsIRK.
DR InterPro: IPR001899; Gram_pos_anchor.
DR Pfam: PF02986; Fn_bind; 1.
DR Pfam: PF00746; Gram_pos_anchor; 1.
DR Pfam: PF04650; YsIRK_signal; 1.
DR TIGRPFAM: TIGR01167; LPXTG_anchor; 1.
DR TIGRPFAM: TIGR01168; YsIRK_signal; 1.
DR PROSITE: PS50847; GRAM_POS_ANCHORING; 1.
KW Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ SEQUENCE 965 AA; 105651 MW; 29828132164D0551 CRC64;

Query Match 95.6%; Score 197; DB 2; Length 965;
Best Local Similarity 94.7%; Pred. No. 1.2e-15;
Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 ONSGNSFEPTBEDPKYEGCGNIVDIDFDSVPQIQG 38
Db 749 ONSGNSFEPTBEDPKYEGCGNIVDIDFDSVPQIQG 786
|||||
RESULT 10
ID Q8NUU7 PRELIMINARY; PRT; 1015 AA.
AC Q8NUU7;
DT 01-OCT-2002 (TREMblrel. 22, Created)
DT 01-OCT-2002 (TREMblrel. 22, Last sequence update)
DT 01-OCT-2003 (TREMblrel. 25, Last annotation update)
DE Fnd protein.
GN Name=fnd; OrderedLocuNames=NM2421;
OS *Staphylococcus aureus* (strain NM2).
OC Bacteria; Firmicutes; Bacillales; *Staphylococcus*.
OX NCBI_TaxId=196620;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NM2;
RX MEDLINE=22040717; PubMed=12044378; DOI=10.1016/S0140-6736(02)08713-5;
RA Baba T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Oguchi A.,
RA Nagai Y., Iwama N., Asano K., Naimi T., Kuroda H., Cui L.,
RA Yamamoto K., Hiratsutsu K.;
RT "Genome and virulence determinants of high virulence community-
acquired MRSA";
RL Lancet 359:1819-1827(2002).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
an amide bond (By similarity).
DR EMBL: AP004830; BAB96286.1; -.
DR GO: GO:0009986; C:cell surface; IEA.
DR GO: GO:0005618; C:cell wall; IEA.
DR GO: GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO: GO:0016020; C:membrane; IEA.
DR GO: GO:007155; P:cell adhesion; IEA.
DR InterPro: IPR008966; Adhes_bact.
DR InterPro: IPR004237; Fn_bind.
DR InterPro: IPR005877; Gpos_YsIRK.
DR InterPro: IPR001899; Gram_pos_anchor.
DR Pfam: PF02986; Fn_bind; 1.
DR Pfam: PF00746; Gram_pos_anchor; 1.
DR TIGRPFAM: TIGR01167; LPXTG_anchor; 1.
DR TIGRPFAM: TIGR01168; YsIRK_signal; 1.

DR PROSITE: PS50847; GRAM_POS_ANCHORING; 1.
KW Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ SEQUENCE 1015 AA; 111145 MW; D0F9281BB64D44D2 CRC64;

Query Match 92.2%; Score 190; DB 2; Length 1015;
Best Local Similarity 94.7%; Pred. No. 9.3e-15;
Matches 36; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ONSGNSFEPTBEDPKYEGCGNIVDIDFDSVPQIQG 38
Db 747 ONSGNSFEPTBEDPKYEGCGNIVDIDFDSVPQIQG 784
|||||
RESULT 11
ID Q6G6H3 PRELIMINARY; PRT; 1015 AA.
AC Q6G6H3;
DT 05-JUL-2004 (TREMblrel. 27, Created)
DT 05-JUL-2004 (TREMblrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMblrel. 27, Last annotation update)
DE Fibronectin-binding protein.
GN OrderedLocuNames=SAS2388;
OS *Staphylococcus aureus* (strain MSSA476).
OC Bacteria; Firmicutes; Bacillales; *Staphylococcus*.
OX NCBI_TaxId=282459;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=15213324; DOI=10.1073/pnas.0402521101;
RA Holden M.T.G., Fell E.J., Lindsey J.A., Peacock S.J., Day N.P.J.,
RA Enright M.C., Foster T.J., Moore C.B., Hurst L., Atkin R., Barron A.,
RA Bason N., Bentley S.D., Chillingworth C., Chillingworth T.,
RA Churcher C., Clark L., Corton C., Cronin A., Doggett J., Dowd L.,
RA Felwell T., Hance Z., Harris B., Hauser H., Holroyd S., Jagsels K.,
RA James K.D., Lennard N., Line A., Mayes R., Moutie S., Mungall K.,
RA Ormond D., Quail M.A., Rabinowitsch B., Rutherford K.M., Sanders M.,
RA Sharp S., Simmonds M., Stevens K., Whitehead S., Barrell B.G.,
RA Spratt B.G., Parkhill J.;
RT "Complete genomes of two clinical *Staphylococcus aureus* strains:
evidence for the rapid evolution of virulence and drug resistance";
RL Proc. Natl. Acad. Sci. U.S.A. 101:9786-9791(2004).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
an amide bond (By similarity).
DR EMBL: BX571857; CAG44202.1; -.
DR GO: GO:0009986; C:cell surface; IEA.
DR GO: GO:0005618; C:cell wall; IEA.
DR GO: GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO: GO:0016020; C:membrane; IEA.
DR GO: GO:007155; P:cell adhesion; IEA.
DR InterPro: IPR008966; Adhes_bact.
DR InterPro: IPR004237; Fn_bind.
DR InterPro: IPR005877; Gpos_YsIRK.
DR InterPro: IPR001899; Gram_pos_anchor.
DR Pfam: PF02986; Fn_bind; 1.
DR Pfam: PF00746; Gram_pos_anchor; 1.
DR Pfam: PF04650; YsIRK_signal; 1.
DR TIGRPFAM: TIGR01167; LPXTG_anchor; 1.
DR TIGRPFAM: TIGR01168; YsIRK_signal; 1.
DR PROSITE: PS50847; GRAM_POS_ANCHORING; 1.
KW Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ SEQUENCE 1015 AA; 111145 MW; D0F9281BB64D44D2 CRC64;

Query Match 92.2%; Score 190; DB 2; Length 1015;
Best Local Similarity 94.7%; Pred. No. 9.3e-15;
Matches 36; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ONSGNSFEPTBEDPKYEGCGNIVDIDFDSVPQIQG 38
Db 747 ONSGNSFEPTBEDPKYEGCGNIVDIDFDSVPQIQG 784
|||||
RESULT 12
ID Q9AEP9 PRELIMINARY; PRT; 152 AA.


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AC O9AEP9:
DT 01-JUN-2001 (TReMBLrel. 17, Created)
DT 01-JUN-2001 (TReMBLrel. 17, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE Fibronectin-binding protein (Fragment).
GN Name=fnb;
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1280;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CMRSA-1;
RX MEDLINE=21246681; PubMed=11349044;
DOI=10.1128/IAI.69.6.3791-3799.2001;
RA Rice K., Huebner M., Vaz D., McGavin M.J.;
RT "Variation in fibronectin binding and fnb locus polymorphisms in
Staphylococcus aureus: identification of antigenic variation in a
fibronectin binding protein adhesin of the epidemic CMRSA-1 strain of
RT methicillin-resistant S. aureus.";
RL Infect.Immun. 69:3791-3799(2001).
DR EMBL; AY029184; AACJ1588.1; -.
FT NON TER 1
FT NON TER 152
SQ SEQUENCE 152 AA; 17193 MW; CFA3913C2B11C025 CRC64;

Query Match 90.8%; Score 187; DB 2; Length 152;
Best Local Similarity 92.1%; Pred. No. 2.6e-15;
Matches 35; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Oy 1 ONSGNQSFEEPTEDKPKYEGCGNIVDIDFDSVPQIHG 38
Db 1 QNTGNQSFEDTDEBKPKYEGCGNIVDIDFDSVPQIHG 38

RESULT 13
O7RRM0 PRELIMINARY; PRT; 354 AA.
AC O7RRM0:
DT 01-MAR-2004 (TReMBLrel. 26, Created)
DT 01-MAR-2004 (TReMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)
DE Hypothetical protein.
GN Name=py00659;
OS Plasmodium yoelii yoelii.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=73239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=17XNL;
RX PubMed=12368865; DOI=10.1038/nature01099;
RA Carlton J.M., Angiolini S.V., Suh B.B., Kooil T.W., Petrea M.,
Silva J.C., Ermolaeva W.D., Allen J.E., Selengut J.D., Koo H.L.,
Peterson J.D., Pop M., Kosack D.S., Shumway M.F., Bidwell S.L.,
Shallom S.J., van Aken S.E., Riedmiller S.B., Feldblum T.V.,
Cho J.K., Quackenbush J., Sedegah M., Shoabli A., Cummings L.M.,
Florens L., Yates F.R., III, Raine J.D., Sinden R.E., Harris M.A.,
Cunningham D.A., Preiser P.R., Bergman L.W., Vaideya A.B.,
van Lin L.H., Janse C.U., Waters A.P., Smith H.O., White O.R.,
Salzberg S.L., Venter J.C., Fraser C.M., Hoffman S.L., Gardner M.J.,
Carucci D.J.;
RA "Genome sequence and comparative analysis of the model rodent malaria
RT parasite Plasmodium yoelii yoelii.";
RL Nature 419:512-519(2002).
CC -1- CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
preliminary data.
DR EMBL; AABL01000190; EAA17916.1; -.
DR InterPro; IPR007955; Byatlin.
DR Pfam; PF05291; Byatlin; 1.
RW Hypothetical protein.
SQ SEQUENCE 354 AA; 41350 MW; 4DD5424B1FFB80F CRC64;

Query Match 29.6%; Score 61; DB 2; Length 354;
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Best Local Similarity 36.7%; Pred. No. 32;
Matches 18; Conservative 6; Mismatches 11; Indels 14; Gaps 3;

Oy 1 ONSGNQSFEEPTEDKPKYEGCGNIVDIDFDSVPQ 35
Db 116 QNYMNNYSEPNIDIEDLNKINGYKGGNGNLTDSNNKLTDFDKSPE 164

RESULT 14
O8IIN2 PRELIMINARY; PRT; 5922 AA.
AC O8IIN2:
DT 01-MAR-2003 (TReMBLrel. 23, Created)
DT 01-MAR-2003 (TReMBLrel. 23, Last sequence update)
DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)
DE Hypothetical protein.
GN ORFNames=PF11_0528;
OS Plasmodium falciparum (isolate 3D7).
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=36329;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22255705; PubMed=12368864; DOI=10.1038/nature01097;
RA Gardner M.J., Hall N., Fung E., White O., Berriman M., Hyman R.W.,
Carlton J.M., Pain A., Nelson K.E., Bowman S., Paulsen I.T., James K.,
Eisen J.A., Rutherford K., Salzberg S.L., Craig A., Kyes S.,
Chen M.S., Nene V., Shallom S.J., Suh B., Peterson J., Angiolini S.,
Petrea M., Allen J., Selengut J., Haft D., Mather M.W., Vaideya A.B.,
Martin D.M., Fairlamb A.H., Fraunholz M.J., Roos D.S., Ralph S.A.,
McCadden G.I., Cummings L.M., Subramanian G.M., Mungall C.,
Venter J.C., Carucci D.J., Hoffman S.L., Newbold C., Davis R.W.,
Fraser C.M., Barrett B.;
RA "Genome sequence of the human malaria parasite Plasmodium
RT falciparum.";
RL Nature 419:498-511(2002).
DR EMBL; AB014837; AAN35722.1; -.
DR HSSP; O93IC2; IMWX.
DR InterPro; IPR011591; Botulinum.
DR Prodom; PD001963; Botulinum; 1.
KM Hypothetical protein.
SQ SEQUENCE 5922 AA; 710217 MW; 2066B6DBA448225 CRC64;

Query Match 29.4%; Score 60.5; DB 2; Length 5922;
Best Local Similarity 38.9%; Pred. No. 8.9e+02;
Matches 14; Conservative 4; Mismatches 7; Indels 11; Gaps 1;

Oy 2 NSGN-----QSFEPTEDKPKYEGCGNIV 26
Db 696 NSGNIFVHEHFNLIQKVEDPTLDEKKNKEGGKXY 731

RESULT 15
O7UKY7 PRELIMINARY; PRT; 1246 AA.
AC O7UKY7:
DT 01-OCT-2003 (TReMBLrel. 25, Created)
DT 01-OCT-2003 (TReMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)
DE 5-methyltetrahydrofolate--homocysteine methyltransferase (BC
2.1.1.13).
GN Name=metH; OrderedLocuNames=RB9857;
OS Rhodospirillum rubrum.
OC Bacteria; Planctomycetes; Planctomycetacia; Planctomycetales;
OC Planctomycetaceae; Pirellula.
OX NCBI_TaxID=117;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=1;
RX MEDLINE=22735913; PubMed=12835416; DOI=10.1073/pnas.1431443100;
RA Gloeckner F.O., Kube W., Bauer M., Teeling H., Lombardot T.,
Ludwig W., Gade D., Beck A., Borzym K., Hellmann K., Rabus R.,
Schlesner H., Aumann R., Reinhardt R.;
RA "Complete genome sequence of the marine planctomycete Pirellula sp.
```

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RT strain 1."; Acad. Sci. U.S.A. 100:8298-8303(2003).
RL Proc. Natl. Acad. Sci. U.S.A. 100:8298-8303(2003).
DR EMBL; BX294150; CAD76493.1; -.
DR HSSP; P13009; 1BMT.
DR GO; GO:0005622; C:intracellular; IEA.
DR GO; GO:0050897; F:cobalt ion binding; IEA.
DR GO; GO:0004156; F:dihydripterolate synthase activity; IEA.
DR GO; GO:0008898; F:homocysteine S-methyltransferase activity; IEA.
DR GO; GO:0008705; F:methionine synthase activity; IEA.
DR GO; GO:0008168; F:methyltransferase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0009396; F:folate acid and derivative biosynthesis; IEA.
DR GO; GO:0009086; P:methionine biosynthesis; IEA.
DR InterPro; IPR006158; B12-binding.
DR InterPro; IPR011007; B12 binding.
DR InterPro; IPR003759; CoMet synth B12.
DR InterPro; IPR000489; Dhdropt synth.
DR InterPro; IPR011005; DHP_synth_like.
DR InterPro; IPR004223; Met_synth_B12.
DR InterPro; IPR010988; M_synth_B12_like.
DR InterPro; IPR003726; S_methyl_trans.
DR Pfam; PF02310; B12-binding; 1.
DR Pfam; PF02607; B12-binding; 2; 1.
DR Pfam; PF02965; Met_synth_B12; 1.
DR Pfam; PF00809; Pterin_bind; 1.
DR Pfam; PF02574; S-methyl_trans; 1.
DR Complete proteome; Methylyltransferase; Transferase.
KW SEQUENCE 1246 AA; 139004 MW; CAF2825176B5109F CRC64;
SQ
```

Query Match 28.6%; Score 59; DB 2; Length 1246;
Best Local Similarity 33.3%; Pred. No. 2.3e+02;
Matches 9; Conservative 8; Mismatches 10; Indels 0; Gaps 0;

```
QY 5 NQSFEEPTEDKPKYEGGNTVIDIDPD 31
DB 394 NEEYDEAVEVAREQVENGATITDVNPD 420
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Search completed: October 22, 2005, 06:05:53
Job time : 71.6361 secs

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CC streptococci, e.g. meningitis, otitis media, pneumonia, endocarditis,
CC mastitis in cattle, abortion in horses and many others. Since the
CC antibodies block binding of bacteria, they should be effective against
CC antibiotic-resistant strains, and may replace antibiotic therapy or
CC increase its effectiveness. Sequences AAW6561-700 represent a series of
CC synthetic peptides based on the D1 region of S. aureus fibronectin
CC binding protein A. They were synthesised to contain mutations
XX
SQ Sequence 38 AA;
Query Match 100.0%; Score 207; DB 2; Length 38;
Best Local Similarity 100.0%; Pred. No. 4.9e-19;
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 QNSGNQSFEEDEEDKPKYEGGNIYVIDFDSVPQIHG 38
DB 1 QNSGNQSFEEDEEDKPKYEGGNIYVIDFDSVPQIHG 38
RESULT 2
AAW65661
ID AAW65661 standard; peptide; 38 AA.
AC AAW65661;
XX
XX 16-OCT-1998 (first entry)
DE Fibronectin binding protein-derived peptide #5.
XX
XX microbial surface components recognising adhesive matrix molecule;
KW MSCRAMM; fibronectin; fibronectin-binding protein; antibody; epitope;
KW antibiotic; bacterial infection; antibiotic-resistant strain.
XX
XX Synthetic.
OS Staphylococcus aureus.
XX
XX WO9831389-A2.
XX
XX 23-JUL-1998.
XX
XX 21-JAN-1998; 98WO-US001222.
XX
XX 21-JAN-1997; 97US-0036139P.
XX
XX (TEXA ) UNIV TEXAS A & M SYSTEM.
XX
XX Hosoeck M, Patti JM, House-Pompeo KI, Speciale P, Joh D;
XX Mcgavin MD;
XX
XX WPI; 1998-413816/35.
XX
XX Antibody that binds to fibronectin-binding protein, preventing its
XX binding to fibronectin - used to treat or prevent bacterial infection,
XX especially by Staphylococci and Streptococci.
XX
XX Example 2; Page 92; 201pp; English.
XX
XX The invention relates to antibodies that bind to a fibronectin-binding
XX domain of a fibronectin-binding protein, and inhibit binding of the
XX protein to fibronectin. Also claimed are: (1) isolated peptides of a
XX fibronectin-binding protein that do not bind to fibronectin; (2) fusion
XX protein containing at least one peptide of a fibronectin-binding protein
XX linked to a second amino acid sequence; (3) nucleic acid encoding the
XX isolated peptide of (1). Antibodies, the isolated peptides of (1) and the
XX nucleic acids are all useful for immunisation (active or passive) and (by
XX inhibiting binding of bacteria to fibronectin) for preventing or treating
XX infection in humans or other animals, particularly by staphylococci or
XX streptococci, e.g. meningitis, otitis media, pneumonia, endocarditis,
XX mastitis in cattle, abortion in horses and many others. Since the
XX antibodies block binding of bacteria, they should be effective against
XX antibiotic-resistant strains, and may replace antibiotic therapy or
XX increase its effectiveness. Sequences AAW6561-68 represent synthetic
XX epitopes from the fibronectin binding domains DU and D1-D4 of the S.

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CC aureus fnda gene
XX
SQ Sequence 38 AA;
Query Match 96.1%; Score 199; DB 2; Length 38;
Best Local Similarity 97.4%; Pred. No. 5.1e-18;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 1 QNSGNQSFEEDEEDKPKYEGGNIYVIDFDSVPQIHG 38
DB 1 QNSGNQSFEEDEEDKPKYEGGNIYVIDFDSVPQIHG 38
RESULT 3
AAR58806
ID AAR58806 standard; protein; 130 AA.
AC AAR58806;
XX
XX 25-MAR-2003 (revised)
XX 30-MAR-1995 (first entry)
DE Fibronectin binding domain D1-D4(709-838 (P838T)).
XX
XX Fibronectin binding protein; Fbp; fibronectin binding domain;
KW monoclonal antibody; MAb; adhesion; Gram-positive bacterium; bacteremia;
KW Escherichia coli.
XX
XX Staphylococcus aureus.
OS
XX
XX WO9418327-A1.
XX
XX 18-AUG-1994.
XX
XX 04-FEB-1994; 94WO-GB000215.
XX
XX 05-FEB-1993; 93GB-00002289.
XX
XX 20-OCT-1993; 93GB-00021592.
XX
XX (SMIK ) SMITHKLINE BEECHAM PLC.
XX
XX Burnham MKR, Chopra I, Critchley IA, Knowles DJC;
XX
XX WPI; 1994-279748/34.
XX
XX Fibronectin binding protein and monoclonal antibodies specific for Fbp -
XX useful to prevent adherence of Gram-positive bacteria to indwelling
XX devices or wounds.
XX
XX Disclosure; Page 30; 40pp; English.
XX
XX Polypeptides corresponding to residues G709-T886 plus PPIVPT, G709-
XX P838(P838T) and G709-P838 (AAR58805-07, respectively) of S. aureus J2385
XX (NCIMB 40532) Fbp type A fibronectin binding domain D1-D4 region
XX (AAR58808) were expressed in E. coli BL21 (DE4) and used to raise MAbs
XX specific for Fbp. (Updated on 25-MAR-2003 to correct PN field.)
XX
XX
SQ Sequence 130 AA;
Query Match 96.1%; Score 199; DB 2; Length 130;
Best Local Similarity 97.4%; Pred. No. 2.1e-17;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 1 QNSGNQSFEEDEEDKPKYEGGNIYVIDFDSVPQIHG 38
DB 2 QNSGNQSFEEDEEDKPKYEGGNIYVIDFDSVPQIHG 39
RESULT 4
AAR58807
ID AAR58807 standard; protein; 130 AA.
AC AAR58807;

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XX 25-MAR-2003 (revised)
DT 30-MAR-1995 (first entry)
XX
XX Fibronectin binding domain D1-D4 (709-838).
DE
XX Fibronectin binding protein; Fbp; fibronectin binding domain;
KM monoclonal antibody; MAb; adhesion; Gram-positive bacterium; bacteremia;
KW Escherichia coli.
XX
OS Staphylococcus aureus.
XX
XX WO9418327-A1.
XX
PD 18-AUG-1994.
XX
XX 04-FEB-1994; 94WO-GB000215.
XX
XX 05-FEB-1993; 93GB-00002289.
XX 20-OCT-1993; 93GB-00021592.
XX
XX (SMIK) SMITHKLINE BEECHAM PLC.
XX Burnham MKR, Chopra I, Critchley IA, Knowles DJC;
XX WPI; 1994-279748/34.
XX
XX Fibronectin binding protein and monoclonal antibodies specific for Fbp -
PT useful to prevent adherence of Gram-positive bacteria to indwelling
PT devices or wounds.
XX
XX Disclosure; Page 30; 40pp; English.
XX
XX Polypeptides corresponding to residues G709-T886 plus PPIVPT, G709-
CC P838(P838T) and G709-P838 (AAR58805-07, respectively) of S. aureus J2385
CC (NCIMB 40532) Fbp type A fibronectin binding domain D1-D4 region
CC (AAR58808) were expressed in E. coli BL21(DE4) and used to raise MAbs
CC specific for Fbp. (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ Sequence 130 AA;
Query Match 96.1%; Score 199; DB 2; Length 130;
Best Local Similarity 97.4%; Pred. No. 2.1e-17;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 QNSGNQSFEDDEDPKPKYEGGNIIVDIDFDSVPQIHG 38
DB 2 QNSGNQSFEDDEDPKPKYEGGNIIVDIDFDSVPQIHG 39
RESULT 5
AAR91202 standard; peptide; 130 AA.
XX
XX AAR91202;
XX
DT 13-NOV-1996 (first entry)
XX
XX D1-D4 fibronectin binding domains.
DE
XX Fibronectin; oral hygiene; gingivitis; gum disease; adhesion;
KM periodontitis; oral pathogen; caries; calculus; candidiasis; oral surgery;
KW tissue regeneration; irrigation; toothpaste; dentifrice; mouthwash;
lozenge.
XX
XX Staphylococcus aureus.
XX
XX WO9604003-A1.
XX
XX 15-FEB-1996.
XX
XX 18-JUL-1995; 95WO-EP002825.
XX

PR 05-AUG-1994; 94GB-00015902.
XX
XX (SMIK) SMITHKLINE BEECHAM PLC.
XX
XX Barnett P, Critchley IA, Dodd I;
XX
XX WPI; 1996-129122/13.
XX
XX Prevention of adherence of oral pathogens in the oral cavity, partic.
PT tooth surfaces - by application of a fibronectin binding protein or
PT polypeptide or a monoclonal antibody or fragment against it.
XX
XX Claim 5; Page 32; 41pp; English.
XX
XX Adherence of oral pathogens, particularly to tooth surfaces, can be
CC prevented by application of a fibronectin binding protein or polypeptide.
CC The fibronectin binding protein or polypeptide is useful in the
CC manufacture of oral hygiene compositions, eg. toothpaste, liquid
CC dentifrice, mouthwash or lozenge. They are useful to prevent the plaque-
CC related development of carious lesions, gingivitis, calculus or
CC periodontal disease and to combat oral cavity infections, e.g.
CC candidiasis. They may also be useful in oral surgery e.g. in guided
CC tissue regeneration procedures to prevent subsequent bacterial infection,
CC and for irrigation of periodontal pockets. This sequence corresponds to
CC amino acids 709-838 of the D1-D4 fibronectin binding domain of
CC Staphylococcus aureus
XX
SQ Sequence 130 AA;
Query Match 96.1%; Score 199; DB 2; Length 130;
Best Local Similarity 97.4%; Pred. No. 2.1e-17;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 QNSGNQSFEDDEDPKPKYEGGNIIVDIDFDSVPQIHG 38
DB 2 QNSGNQSFEDDEDPKPKYEGGNIIVDIDFDSVPQIHG 39
RESULT 6
AAR91201 standard; peptide; 130 AA.
XX
XX AAR91201;
XX
DT 13-NOV-1996 (first entry)
XX
XX D1-D4 fibronectin binding domains.
DE
XX Fibronectin; oral hygiene; gingivitis; gum disease; adhesion;
KM periodontitis; oral pathogen; caries; calculus; candidiasis; oral surgery;
KW tissue regeneration; irrigation; toothpaste; dentifrice; mouthwash;
lozenge.
XX
XX Staphylococcus aureus.
XX
XX WO9604003-A1.
XX
XX 15-FEB-1996.
XX
XX 18-JUL-1995; 95WO-EP002825.
XX
XX 05-AUG-1994; 94GB-00015902.
XX
XX (SMIK) SMITHKLINE BEECHAM PLC.
XX Barnett P, Critchley IA, Dodd I;
XX WPI; 1996-129122/13.
XX
XX Prevention of adherence of oral pathogens in the oral cavity, partic.
PT tooth surfaces - by application of a fibronectin binding protein or
PT polypeptide or a monoclonal antibody or fragment against it.
XX

PS Claim 5; Page 31-32; 41pp; English.

CC Adherence of oral pathogens, particularly to tooth surfaces, can be
CC prevented by application of a fibronectin binding protein or polypeptide.
CC The fibronectin binding protein or polypeptide is useful in the
CC manufacture of oral hygiene compositions, eg. toothpaste, liquid
CC dentifrice, mouthwash or lozenge. They are useful to prevent the plaque-
CC related development of carious lesions, gingivitis, calculus or
CC periodontal disease and to combat oral cavity infections, e.g.
CC candidiasis. They may also be useful in oral surgery e.g. in guided
CC tissue regeneration procedures to prevent subsequent bacterial infection,
CC and for irritation of periodontal pockets. This sequence corresponds to
CC amino acids 709-838 of the D1-D4 fibronectin binding domain of
CC Staphylococcus aureus with a P838R substitution

XX
XX
SQ Sequence 130 AA;

Query Match 96.1%; Score 199; DB 2; Length 130;
Best Local Similarity 97.4%; Pred. No. 2.1e-17;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 QNSGNQSFEEDEPKRYEQGNIVDIDPSVPOIHG 38
D6 2 QNSGNQSFEEDEPKRYEQGNIVDIDPSVPOIHG 39

RESULT 7
AAAY29089
ID AAAY29089 standard; protein; 134 AA.
XX
XX AC AAAY29089;
XX
XX DT 28-SEP-1999 (first entry)
XX
DE Cloned fibronectin binding protein binding domain (FnBAB) sequence.
XX
XX BV Bovine herpes virus-2; BHV-2; cytokine; immune response; immunogen; IL;
XX interleukin; colony stimulating factor; CSF; interferon; IFN; TNF;
XX tumour necrosis factor; recombinant virus; vaccine; mucosal disease;
XX mastitis; breast cancer; stress-induced disease; binding domain; FnBAB;
XX fibronectin binding protein.
XX
XX OS Staphylococcus aureus.
XX
XX PN WO9916892-A1.
XX
XX PD 08-APR-1999.
XX
XX PF 29-SEP-1998; 98WO-GB002927.
XX
XX PR 29-SEP-1997; 97GB-00020633.
XX
XX PA (UYBR-) UNIV BRISTOL.
XX
XX PI Bradley AJ, Duffas WPJ;
XX
XX DR WPI; 1999-255101/21.
XX
XX DR N-PSDB; AAX91505.
XX
XX PT New bovine herpes virus-2 vectors.
XX
XX PS Example 2; Fig 8A-B; 130pp; English.

CC The invention provides bovine herpes virus-2 (BHV-2) based vectors that
CC comprise at least one cytokine-encoding DNA sequence. The expression of
CC cytokines in mammals can up-regulate immune responses to the immunogens.
CC The cytokine is selected from interleukins (IL), colony stimulating
CC factors (CSF), interferons (IFN) and tumour necrosis factors (TNF). The
CC BHV-2 based vector or recombinant virus can be used as vaccines. They can
CC be used for preventing or treating a mucosal disease in a subject, e.g.
CC ruminants, cattle, sheep, goats, dogs, cats, horses, or man, particularly
CC mastitis in cows or breast cancers in humans. They can also be used for
CC preventing or treating a stress-induced disease. The present sequence

CC represents a S. aureus fibronectin binding protein binding domain
CC sequence FnBAB, the gene cloned for use in this invention. The gene has
CC 97.8 percent identity when compared to the previously published sequences
CC FnBA and FnBB

XX
XX
SQ Sequence 134 AA;

Query Match 96.1%; Score 199; DB 2; Length 134;
Best Local Similarity 97.4%; Pred. No. 2.2e-17;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 QNSGNQSFEEDEPKRYEQGNIVDIDPSVPOIHG 38
D6 2 QNSGNQSFEEDEPKRYEQGNIVDIDPSVPOIHG 39

RESULT 8
AAAY29088
ID AAAY29088 standard; protein; 134 AA.
XX
XX AC AAAY29088;
XX
XX DT 28-SEP-1999 (first entry)
XX
XX DE S. aureus fibronectin binding protein B (FnBB) binding domain.
XX
XX BV Bovine herpes virus-2; BHV-2; cytokine; immune response; immunogen; IL;
XX interleukin; colony stimulating factor; CSF; interferon; IFN; TNF;
XX tumour necrosis factor; recombinant virus; vaccine; mucosal disease;
XX mastitis; breast cancer; stress-induced disease; binding domain; FnBB;
XX fibronectin binding protein.
XX
XX OS Staphylococcus aureus.
XX
XX PN WO9916892-A1.
XX
XX PD 08-APR-1999.
XX
XX PF 29-SEP-1998; 98WO-GB002927.
XX
XX PR 29-SEP-1997; 97GB-00020633.
XX
XX PA (UYBR-) UNIV BRISTOL.
XX
XX PI Bradley AJ, Duffas WPJ;
XX
XX DR WPI; 1999-255101/21.
XX
XX DR N-PSDB; AAX91505.
XX
XX PT New bovine herpes virus-2 vectors.
XX
XX PS Example 2; Fig 8A-B; 130pp; English.

CC The invention provides bovine herpes virus-2 (BHV-2) based vectors that
CC comprise at least one cytokine-encoding DNA sequence. The expression of
CC cytokines in mammals can up-regulate immune responses to the immunogens.
CC The cytokine is selected from interleukins (IL), colony stimulating
CC factors (CSF), interferons (IFN) and tumour necrosis factors (TNF). The
CC BHV-2 based vector or recombinant virus can be used as vaccines. They can
CC be used for preventing or treating a mucosal disease in a subject, e.g.
CC ruminants, cattle, sheep, goats, dogs, cats, horses, or man, particularly
CC mastitis in cows or breast cancers in humans. They can also be used for
CC preventing or treating a stress-induced disease. The present sequence
CC represents the binding domain of a previously published S. aureus
CC fibronectin binding protein B (FnBB) sequence. The FnB binding domain
CC gene sequence FnBAB, cloned for use in this invention has 97.8 percent
CC identity when compared to the previously published FnBA and FnBB gene
CC sequences

XX
XX
SQ Sequence 134 AA;

Query Match 96.1%; Score 199; DB 2; Length 134;
Best Local Similarity 97.4%; Pred. No. 2.2e-17;

Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ONSGNQSFEEDEBDKPKYEGGNIVDIDFDSVPQIHG 38
 DB 2 ONSGNQSFEEDEBDKPKYEGGNIVDIDFDSVPQIHG 39

RESULT 9
 AAY29087
 ID AAY29087 standard; protein; 134 AA.

AC AAY29087;

DT 28-SEP-1999 (first entry)

DE S. aureus fibronectin binding protein A (FnBA) binding domain.

XX Bovine herpes virus-2; BHV-2; cytokine; immune response; immunogen; IL;
 XX interleukin; colony stimulating factor; CSF; interferon; IFN; TNF;
 XX tumour necrosis factor; recombinant virus; vaccine; mucosal disease;
 XX mastitis; breast cancer; stress-induced disease; binding domain; FnBA;
 XX fibronectin binding protein.

OS Staphylococcus aureus.

PN WO916892-A1.

XX 08-APR-1999.

XX 29-SEP-1998; 98WO-GB002927.

XX 29-SEP-1997; 97GB-00020633.

XX (UYBR-) UNIV BRISTOL.

XX Bradley AJ, Duffas WP;

XX WPI; 1999-255101/21.

XX N-PSDB; AAX91504.

XX New bovine herpes virus-2 vectors.

XX Example 2; Fig 8A-B; 130pp; English.

XX The invention provides bovine herpes virus-2 (BHV-2) based vectors that
 XX comprise at least one cytokine-encoding DNA sequence. The expression of
 XX cytokines in mammals can up-regulate immune responses to the immunogens.
 XX The cytokine is selected from interleukins (IL), colony stimulating
 XX factors (CSF), interferons (IFN) and tumour necrosis factors (TNF). The
 XX BHV-2 based vector or recombinant virus can be used as vaccines. They can
 XX be used for preventing or treating a mucosal disease in a subject, e.g.
 XX ruminants, cattle, sheep, goats, dogs, cats, horses, or man, particularly
 XX mastitis in cows or breast cancers in humans. They can also be used for
 XX preventing or treating a stress-induced disease. The present sequence
 XX represents the binding domain of a previously published S. aureus
 XX fibronectin binding protein A (FnBA) sequence. The FnB binding domain
 XX gene sequence FnBAB, cloned for use in this invention has 97.8 percent
 XX identity when compared to the previously published FnBA and FnBB gene
 XX sequences

XX Sequence 134 AA;

Query Match 96.1%; Score 199; DB 2; Length 134;
 Best Local Similarity 97.4%; Pred. No. 2.2e-17;
 Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ONSGNQSFEEDEBDKPKYEGGNIVDIDFDSVPQIHG 38
 DB 2 ONSGNQSFEEDEBDKPKYEGGNIVDIDFDSVPQIHG 39

RESULT 10
 AAW31556

ID AAW31556 standard; protein; 139 AA.

XX AAW31556;

XX 27-AUG-2003 (revised)

XX 25-MAR-2003 (revised)

XX 21-MAY-1998 (first entry)

XX Fibronectin-binding MSCRAMM derivative pOD.

XX Fibronectin; pOD; collagen binding protein; sepsis; infection;
 XX microbial surface component recognising adhesive matrix molecule; MSCRAMM;
 XX adhesin; vaccine; immunisation; diagnosis; therapy; mastitis.

XX Staphylococcus aureus.

XX Key Location/Qualifiers

XX Peptide 1..12 /note= "vector pOE30-derived peptide"

XX WO9743314-A2.

XX 20-NOV-1997.

XX 14-MAY-1997; 97WO-US008210.

XX 16-MAY-1996; 96US-0017678P.

XX (TEXA-) UNIV TEXAS A & M SYSTEM.

XX (UABR-) UAB RES FOUND.

XX Hoeck M, Patti JM, House-Pompeo K, Schanam N, Symersky J;

XX WPI; 1998-008801/01.

XX Antibody that interacts with collagen binding domain of Staphylococcal

XX cna gene product - useful to prevent bacterial sepsis in animal infected

XX with Staphylococcus aureus.

XX Disclosure; Page 91; 143pp; English.

XX This protein comprises Staphylococcus aureus fibronectin-binding
 XX microbial surface component recognising adhesive matrix molecule (MSCRAMM)
 XX derivative pOD, plus a vector-derived N-terminal peptide. The invention
 XX relates to claimed nucleic acid sequences (see AAT93436-38) encoding S.
 XX aureus collagen binding protein (CBP) epitopes M17, M31 and M55 (see
 XX AAW1552-54) that confer protection against S. aureus infection. CBP
 XX protein and antigenic epitopes are contemplated for use in the treatment
 XX of pathological infections, especially to prevent bacterial adhesion to
 XX collagen. The epitopes are also contemplated for use in the preparation
 XX of vaccines and as carrier proteins in vaccine formulations, as well as
 XX in the formulation of compositions for the prevention of S. aureus
 XX infection. pCR33 and pOD (see AAW31556) were used to raise anti-MSCRAMM
 XX polyclonal antibodies used in passive immunisation against bovine
 XX mastitis. (Updated on 25-MAR-2003 to correct PI field.) (Updated on 27-
 XX AUG-2003 to correct OS field.)

XX Sequence 139 AA;

Query Match 96.1%; Score 199; DB 2; Length 139;
 Best Local Similarity 97.4%; Pred. No. 2.3e-17;
 Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ONSGNQSFEEDEBDKPKYEGGNIVDIDFDSVPQIHG 38
 DB 16 ONSGNQSFEEDEBDKPKYEGGNIVDIDFDSVPQIHG 53

RESULT 11
 AAR58808
 ID AAR58808 standard; protein; 174 AA.

XX AAR58808;

[illegible]

```

XX 05-AUG-1994; 94GB-00015902.
PR
XX (SMIK ) SMITHKLINE BEECHAM PLC.
PA
XX Barnett P, Critchley IA, Dodd I;
PI
XX WPI; 1996-129122/13.
XX N-PSDB; AAT18308.
DR
XX
XX Prevention of adherence of oral pathogens in the oral cavity, partic.
PT tooth surfaces - by application of a fibronectin binding protein or
PR polypeptide or a monoclonal antibody or fragment against it.
XX
XX Claim 5; Page 32; 41pp; English.
PS
XX
XX Adherence of oral pathogens, particularly to tooth surfaces, can be
CC prevented by application of a fibronectin binding protein or polypeptide.
CC The fibronectin binding protein or polypeptide is useful in the
CC manufacture of oral hygiene compositions, eg. toothpaste, liquid
CC dentifrice, mouthwash or lozenges. They are useful to prevent the plaque-
CC related development of carious lesions, gingivitis, calculus or
CC periodontal disease and to combat oral cavity infections, e.g.
CC candidiasis. They may also be useful in oral surgery e.g. in guided
CC tissue regeneration procedures to prevent subsequent bacterial infection,
CC and for irrigation of periodontal pockets. This sequence corresponds to
CC amino acids 709-838 of the D1-D4 fibronectin binding domain of
CC Staphylococcus aureus with a P838T substitution. (Updated on 16-OCT-2003
CC to standardise OS field)
XX
XX Sequence 174 AA:
SQ
XX
XX Query Match 96.1%; Score 199; DB 2; Length 174;
XX Best Local Similarity 97.4%; Pred. No. 3e-17;
XX Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Oy 1 QNSGNOSFEEDPESDKPYEKGSGNIVPIDPFSVPQING 38
Db 2 QNSGNOSFEEDPESDKPYEKGSGNIVPIDPFSVPQING 39
XX
XX RESULT 13
XX AAR58805
XX ID AAR58805 standard; protein, 181 AA.
XX
XX AAR58805;
XX AC
XX 25-MAR-2003 (revised)
XX DT 30-MAR-1995 (first entry)
XX
XX Fibronectin binding domain D1-D4(709-886) .
DE
XX
XX Fibronectin binding protein; Fbp; fibronectin binding domain;
KW monoclonal antibody; Mwb; adhesion; Gram-positive bacterium; bacteremia;
KW Escherichia coli.
XX
XX Staphylococcus aureus.
XX OS
XX
XX WO9418327-A1.
XX PN
XX 18-AUG-1994.
XX PD
XX
XX 04-FEB-1994; 94WO-GB000215.
XX PF
XX
XX 05-FEB-1993; 93GB-00002289.
XX PR 20-OCT-1993; 93GB-00021592.
XX
XX (SMIK ) SMITHKLINE BEECHAM PLC.
XX PA
XX Burnham MKR, Chopra I, Critchley IA, Knowles DJC;
XX PI
XX WPI; 1994-279746/34.
XX

```

PT Fibronectin binding protein and monoclonal antibodies specific for Fbp -
 PT useful to prevent adherence of Gram-positive bacteria to indwelling
 PT devices or wounds.
 XX
 XX Disclousure: Page 29-30; 40pp; English.
 XX
 XX Polypeptides corresponding to residues G709-T886 plus PPIVPT, G709-
 CC P838(P838T) and G709-P838 (AA85805-07, respectively) of S. aureus J2385
 CC (NCIMB 40532) Fbp type A fibronectin binding domain D1-D4 region
 CC (AA85808) were expressed in E. coli BL21 (DE4) and used to raise Mabs
 CC specific for Fbp. (Updated on 25-MAR-2003 to correct PN field.)
 CC
 XX
 SQ Sequence 181 AA;
 Query Match 96.1%; Score 199; DB 2; Length 181;
 Best Local Similarity 97.4%; Pred. No. 3,1e-17;
 Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 ONSGNQSFEEDEBDPKRYEQGNGNIVDIDFDSVPQIHG 38
 |||||
 DB 2 ONSGNQSFEEDEBDPKRYEQGNGNIVDIDFDSVPQIHG 39
 RESULT 14
 AAR91200
 ID AAR91200 standard; peptide; 181 AA.
 XX
 AC AAR91200;
 XX
 DT 13-NOV-1996 (first entry)
 XX
 DE D1-D4 fibronectin binding domains.
 XX
 KM Fibronectin; oral hygiene; gingivitis; gum disease; adhesion;
 KM periodontitis; oral pathogen; caries; calculus; candidiasis; oral surgery;
 KM tissue regeneration; irrigation; toothpaste; dentifrice; mouthwash;
 KM lozenge.
 XX
 OS Staphylococcus aureus.
 XX
 PN W09604003-A1.
 XX
 PD 15-FEB-1996.
 XX
 PF 18-JUL-1995; 95WO-BP002825.
 XX
 PR 05-AUG-1994; 94GB-00015902.
 XX
 PA (SMIK) SMITHKLINE BEECHAM PLC.
 XX
 PI Barnett P, Critchley IA, Dodd I;
 XX
 XX WPI; 1996-129122/13.
 DR N-PSDB; AAT18307.
 XX
 PT Prevention of adherence of oral pathogens in the oral cavity, partic.
 PT tooth surfaces - by application of a fibronectin binding protein or
 PT polypeptide or a monoclonal antibody or fragment against it.
 XX
 XX Claim 5; Page 31; 41pp; English.
 XX
 XX Adherence of oral pathogens, particularly to tooth surfaces, can be
 CC prevented by application of a fibronectin binding protein or polypeptide.
 CC The fibronectin binding protein or polypeptide is useful in the
 CC manufacture of oral hygiene compositions, eg. toothpaste, liquid
 CC dentifrice, mouthwash or lozenge. They are useful to prevent the plaque-
 CC related development of carious lesions, gingivitis, calculus or
 CC periodontal disease and to combat oral cavity infections, e.g.
 CC candidiasis. They may also be useful in oral surgery e.g. in guided
 CC tissue regeneration procedures to prevent subsequent bacterial infection,
 CC and for irrigation of periodontal pockets. This sequence corresponds to
 CC amino acids 709-886 of the D1-D4 fibronectin binding domain of
 CC Staphylococcus aureus

XX
 SQ Sequence 181 AA;
 Query Match 96.1%; Score 199; DB 2; Length 181;
 Best Local Similarity 97.4%; Pred. No. 3,1e-17;
 Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 ONSGNQSFEEDEBDPKRYEQGNGNIVDIDFDSVPQIHG 38
 |||||
 DB 2 ONSGNQSFEEDEBDPKRYEQGNGNIVDIDFDSVPQIHG 39
 RESULT 15
 AAM89803
 ID AAM89803 standard; protein; 559 AA.
 XX
 AC AAM89803;
 XX
 DT 16-MAR-1999 (first entry)
 XX
 DE Staphylococcus aureus protein SEQ ID #5251.
 XX
 KM Computer readable medium; vaccine; S. aureus infection; immunodetection;
 KM cellulitis; eyelid infection; food poisoning; osteomyelitis; therapy;
 KM skin infection; surgical wound infection; scalded skin syndrome;
 KM toxic shock syndrome.
 XX
 OS Staphylococcus aureus.
 XX
 PN EP786519-A2.
 XX
 PD 30-JUL-1997.
 XX
 PF 07-JAN-1997; 97EP-00100117.
 XX
 PR 05-JAN-1996; 96US-0009861P.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 XX
 PI Kunsch CA, Choi GH, Barash SC, Dillon PJ, Fannon MR, Rosen CA;
 XX
 XX WPI; 1997-374922/35.
 DR
 XX
 PT Polynucleotide(s) and proteins derived from Staphylococcus aureus -
 PT stored on computer readable medium and used in the production of anti-
 PT S. aureus vaccines.
 XX
 XX Claim 23; Page 3259-3261; 3271pp; English.
 XX
 XX This sequence represents a Staphylococcus aureus protein sequence of the
 CC invention. The DNA sequences encoding the S. aureus proteins are recorded
 CC on a computer readable medium, preferably selected from a floppy or hard
 CC disk, random access memory (RAM), read-only memory (ROM) or CD-ROM.
 CC Homology searches using the S. aureus DNA sequences allows putative
 CC functions to be assigned so that protein-encoding or regulatory regions
 CC of commercial, therapeutic or industrial importance can be obtained.
 CC Specifically, sequences which are likely to encode antigens have been
 CC identified and these polypeptides can be used in a vaccine composition
 CC against S. aureus infection. The polypeptides can also be used in a kit
 CC for the immunodetection of S. aureus in a sample. S. aureus is implicated
 CC in numerous human diseases, including cellulitis, eyelid infections, food
 CC poisoning, osteomyelitis, skin and surgical wound infections, scalded
 CC skin syndrome, toxic shock syndrome, etc. Organisms transformed with the
 CC DNA sequences can be used for recombinant production of the polypeptides.
 CC The new DNA sequences (and their fragments) are useful as primers or
 CC probes for isolating homologues of any of the 5191 S. aureus DNA sequences
 CC contained on the computer readable medium
 XX
 SQ Sequence 559 AA;
 Query Match 96.1%; Score 199; DB 2; Length 559;
 Best Local Similarity 97.4%; Pred. No. 1,1e-16;
 Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QNSGNQSFEDPEEDPKPKYEOGNIVDIDPDSVPQIHG 38
| | | | | | | | | | | | | | | | | | | | | |
Db 301 QNSGNQSFEDPEEDPKPKYEOGNIVDIDPDSVPQIHG 338

Search completed: October 25, 2005, 20:21:03
Job time : 84.8825 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 22, 2005, 03:51:22 ; Search time 21.1723 Seconds
(without alignments)
133.980 Million cell updates/sec

Title: US-10-731-238-39

Perfect score: 207
Sequence: 1 ONSGNQSEFDEPDEPKPKYEGGNIVDIDFDSVPQIHG 38

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: /cgn2_6/prodata/1/iaa/5A_COMB.pep.*
2: /cgn2_6/prodata/1/iaa/5B_COMB.pep.*
3: /cgn2_6/prodata/1/iaa/5A_COMB.pep.*
4: /cgn2_6/prodata/1/iaa/5B_COMB.pep.*
5: /cgn2_6/prodata/1/iaa/PCITUS_COMB.pep.*
6: /cgn2_6/prodata/1/iaa/beckfil1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	207	100.0	38	4	US-09-010-317-39 Sequence 39, Appl
2	199	96.1	38	1	US-08-234-622A-2 Sequence 2, Appl1
3	199	96.1	38	4	US-09-010-317-5 Sequence 5, Appl1
4	199	96.1	114	1	US-08-259-000-3 Sequence 3, Appl1
5	199	96.1	130	2	US-08-459-135A-7 Sequence 7, Appl1
6	199	96.1	130	2	US-08-459-135A-8 Sequence 8, Appl1
7	199	96.1	130	3	US-08-495-559-7 Sequence 7, Appl1
8	199	96.1	130	3	US-08-495-559-8 Sequence 8, Appl1
9	199	96.1	139	3	US-08-856-253-8 Sequence 8, Appl1
10	199	96.1	174	2	US-08-459-135A-10 Sequence 10, Appl
11	199	96.1	174	2	US-08-459-135A-13 Sequence 13, Appl
12	199	96.1	174	3	US-08-495-559-10 Sequence 10, Appl
13	199	96.1	174	3	US-08-495-559-13 Sequence 13, Appl
14	199	96.1	176	3	US-08-495-559-6 Sequence 6, Appl1
15	199	96.1	178	3	US-08-459-135A-12 Sequence 12, Appl
16	199	96.1	178	3	US-08-495-559-12 Sequence 12, Appl
17	199	96.1	181	2	US-08-459-135A-6 Sequence 6, Appl1
18	199	96.1	559	4	US-08-956-171E-5251 Sequence 5251, Ap
19	199	96.1	559	4	US-08-781-986A-5251 Sequence 5251, Ap
20	199	96.1	1027	4	US-08-956-171E-5254 Sequence 5254, Ap
21	199	96.1	1027	4	US-08-781-986A-5254 Sequence 5254, Ap
22	199	93.2	38	1	US-08-729-767-3 Sequence 3, Appl1
23	199	93.2	38	4	US-09-010-317-36 Sequence 36, Appl
24	199	93.2	38	4	US-09-010-317-37 Sequence 37, Appl
25	199	93.2	38	4	US-09-010-317-40 Sequence 40, Appl
26	199	93.2	38	4	US-09-010-317-41 Sequence 41, Appl
27	192	92.8	38	4	US-09-010-317-38 Sequence 38, Appl

28	192	92.8	38	4	US-09-010-317-42	Sequence 42, Appl
29	191	92.3	38	4	US-09-010-317-6	Sequence 6, Appl
30	191	92.3	38	4	US-09-010-317-43	Sequence 43, Appl
31	189	91.3	38	4	US-09-010-317-35	Sequence 35, Appl
32	188.5	91.1	39	4	US-09-010-317-56	Sequence 56, Appl
33	180.5	87.2	39	4	US-09-010-317-57	Sequence 57, Appl
34	180	87.0	38	1	US-08-234-622A-3	Sequence 3, Appl1
35	180	87.0	38	4	US-09-010-317-7	Sequence 7, Appl1
36	174	84.1	38	1	US-08-729-767-4	Sequence 4, Appl1
37	174	84.1	38	4	US-09-010-317-46	Sequence 46, Appl
38	174	84.1	38	4	US-09-010-317-47	Sequence 47, Appl
39	173	83.6	38	4	US-09-010-317-48	Sequence 48, Appl
40	172	83.1	38	4	US-09-010-317-8	Sequence 8, Appl1
41	172	83.1	38	4	US-09-010-317-49	Sequence 49, Appl
42	171	82.6	38	4	US-09-010-317-44	Sequence 44, Appl
43	170	82.1	38	4	US-09-010-317-45	Sequence 45, Appl
44	157	75.8	36	4	US-09-010-317-58	Sequence 58, Appl
45	152	73.4	38	4	US-09-010-317-50	Sequence 50, Appl

ALIGNMENTS

RESULT 1
US-09-010-317-39
Sequence 39, Application US/09010317
Patent No. 6685943
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
APPLICANT: Patti, Joseph M.
APPLICANT: House-Pompeo, Karen L.
APPLICANT: Speziale, Pietro
APPLICANT: Joh, Danny
APPLICANT: McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
TITLE OF INVENTION: AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 39:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-09-010-317-39
Query Match 100.0%; Score 207; DB 4; Length 38;
Best Local Similarity 100.0%; Pred. No. 1.8e-20;

Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QNSGNQSFEDDEPKPKYEGGNIIVDIDFDSVPQIHG 38
Db 1 QNSGNQSFEDDEPKPKYEGGNIIVDIDFDSVPQIHG 38

RESULT 2

US-08-234-622A-2

; Sequence 2, Application US/08234622A

; Patent No. 5440014

; GENERAL INFORMATION:

; APPLICANT: HOOK, Magnus

; APPLICANT: MCGAVIN, Martin

; APPLICANT: RAUCCI, Giuseppe

; TITLE OF INVENTION: A FIBRONECTIN BINDING PEPTIDE

; NUMBER OF SEQUENCES: 4

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Burns, Doane, Swecker & Mathis

; STREET: P. O. Box 1404

; CITY: Alexandria

; STATE: Virginia

; COUNTRY: United States

; ZIP: 22313-1404

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/234,622A

; FILING DATE: 28-APR-1994

; CLASSIFICATION: 530

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: SE 9002617-0

; FILING DATE: 10-AUG-1990

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: WO PCT/SE91/00534

; FILING DATE: 09-AUG-1991

; ATTORNEY/AGENT INFORMATION:

; NAME: Meuth, Donna M

; REGISTRATION NUMBER: 36,607

; REFERENCE/DOCKET NUMBER: 012885-044

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (703) 836-6620

; TELEFAX: (703) 836-2021

; INFORMATION FOR SEQ ID NO: 2:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 38 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

US-08-234-622A-2

Query Match 96.1%; Score 199; DB 1; Length 38;
Best Local Similarity 97.4%; Pred. No. 2e-19; Indels 0; Gaps 0;
Matches 37; Conservative 0; Mismatches 1;

Qy 1 QNSGNQSFEDDEPKPKYEGGNIIVDIDFDSVPQIHG 38
Db 1 QNSGNQSFEDDEPKPKYEGGNIIVDIDFDSVPQIHG 38

RESULT 3

US-09-010-317-5

; Sequence 5, Application US/09010317

; Patent No. 6685943

; GENERAL INFORMATION:

; APPLICANT: HOOK, Magnus

; APPLICANT: PATTI, Joseph M.

; APPLICANT: House-Pompeo, Karen L.

; APPLICANT: Speziale, Pietro

APPLICANT: Joh, Danny
APPLICANT: MCGAVIN, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
TITLE OF INVENTION: AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:

; ADDRESSEE: Arnold, White & Durkee

; STREET: P. O. Box 4433

; CITY: Houston

; STATE: TX

; COUNTRY: USA

; ZIP: 77210-4433

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/010,317

; FILING DATE:

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 60/036,139

; FILING DATE: 21-JAN-1997

; ATTORNEY/AGENT INFORMATION:

; NAME: Hibler, David W.

; REGISTRATION NUMBER: 41,071

; REFERENCE/DOCKET NUMBER: TANK.189

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 512-418-5000

; TELEFAX: 512-474-7577

; INFORMATION FOR SEQ ID NO: 5:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 38 amino acids

; TYPE: amino acid

; STRANDEDNESS:

; TOPOLOGY: linear

US-09-010-317-5

Query Match 96.1%; Score 199; DB 4; Length 38;
Best Local Similarity 97.4%; Pred. No. 2e-19; Indels 0; Gaps 0;
Matches 37; Conservative 0; Mismatches 1;

Qy 1 QNSGNQSFEDDEPKPKYEGGNIIVDIDFDSVPQIHG 38
Db 1 QNSGNQSFEDDEPKPKYEGGNIIVDIDFDSVPQIHG 38

RESULT 4

US-08-259-000-3

; Sequence 3, Application US/08259000

; Patent No. 5571514

; GENERAL INFORMATION:

; APPLICANT: HOOK, Magnus

; APPLICANT: LINDBERG, Martin Kjell

; APPLICANT: SIGNAS, Lars Christer

; APPLICANT: WADSTROM, Torkel Mikael

; APPLICANT: FROWAN, Gunnar

; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN AS WELL AS

; NUMBER OF SEQUENCES: 4

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Burns, Doane, Swecker & Mathis

; STREET: P. O. Box 1404

; CITY: Alexandria

; STATE: Virginia

; COUNTRY: United States

; ZIP: 22313-1404

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.25

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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/259,000
FILING DATE: 13-JUN-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: SE 8702272-9
FILING DATE: 01-JUN-1987
ATTORNEY/AGENT INFORMATION:
NAME: Meuth, Donna M
REGISTRATION NUMBER: 36,607
REFERENCE/DOCKET NUMBER: 012885-062
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 114 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-259-000-3

Query Match          96.1%; Score 199; DB 1; Length 114;
Best Local Similarity 97.4%; Pred. No. 7,4e-19;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ONSGNQSFEDDEPKRYEGGNIIVDIDFDSVPQIHG 38
DB 2 ONSGNQSFEDDEPKRYEGGNIIVDIDFDSVPQIHG 39

RESULT 5
US-08-459-135A-7
Sequence 7, Application US/08459135A
Patent No. 5955078
GENERAL INFORMATION:
APPLICANT: BURNHAM, Martin Karl Russel
APPLICANT: CHOPRA, Ian
APPLICANT: CRITCHLEY, Ian Alfred
APPLICANT: KNOWLES, David Justin Charles
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN: MONOCLONAL ANTIBODY AND THEIR US
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSER: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
STATE: PA
COUNTRY: U.S.A.
ZIP: 19406-0939
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: Fastseq, Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/459,135A
FILING DATE: 02-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB/94/00215
FILING DATE: 04-Feb-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Gimmil, Edward R
REGISTRATION NUMBER: 38,891
REFERENCE/DOCKET NUMBER: P30591C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-4478
TELEFAX: 610-270-5090
TELFX:
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
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LENGTH: 130 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein.
US-08-459-135A-7

Query Match          96.1%; Score 199; DB 2; Length 130;
Best Local Similarity 97.4%; Pred. No. 8.6e-19;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ONSGNQSFEDDEPKRYEGGNIIVDIDFDSVPQIHG 38
DB 2 ONSGNQSFEDDEPKRYEGGNIIVDIDFDSVPQIHG 39

RESULT 6
US-08-459-135A-8
Sequence 8, Application US/08459135A
Patent No. 5955078
GENERAL INFORMATION:
APPLICANT: BURNHAM, Martin Karl Russel
APPLICANT: CHOPRA, Ian
APPLICANT: CRITCHLEY, Ian Alfred
APPLICANT: KNOWLES, David Justin Charles
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN: MONOCLONAL ANTIBODY AND THEIR US
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSER: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
STATE: PA
COUNTRY: U.S.A.
ZIP: 19406-0939
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: Fastseq, Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/459,135A
FILING DATE: 02-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB/94/00215
FILING DATE: 04-Feb-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Gimmil, Edward R
REGISTRATION NUMBER: 38,891
REFERENCE/DOCKET NUMBER: P30591C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-4478
TELEFAX: 610-270-5090
TELFX:
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 130 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-459-135A-8

Query Match          96.1%; Score 199; DB 2; Length 130;
Best Local Similarity 97.4%; Pred. No. 8.6e-19;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ONSGNQSFEDDEPKRYEGGNIIVDIDFDSVPQIHG 38
DB 2 ONSGNQSFEDDEPKRYEGGNIIVDIDFDSVPQIHG 39

RESULT 7
US-08-495-559-7
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; Sequence 7, Application US/08495559A
; Patent No. 6054572
; GENERAL INFORMATION:
; APPLICANT: BURHAM, Martin Karl Russel
; APPLICANT: CHOPRA, Ian
; APPLICANT: CRITCHLEY, Ian Alfred
; APPLICANT: KNOWLES, David Justin Charles
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN: MONOCLONAL
; TITLE OF INVENTION: ANTIBODY AND THEIR USE IN PREVENTING BACTERIAL ADHESION
; FILE REFERENCE: P30591
; CURRENT APPLICATION NUMBER: US/08/495,559A
; CURRENT FILING DATE: 1995-08-03
; EARLIER APPLICATION NUMBER: GB 9302289.5
; EARLIER FILING DATE: 1993-02-05
; EARLIER APPLICATION NUMBER: GB 9321592.9
; EARLIER FILING DATE: 1993-10-20
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 7
; LENGTH: 130
; TYPE: PR1
; ORGANISM: Staphylococcus aureus
US-08-495-559-7

Query Match          96.1%; Score 199; DB 3; Length 130;
Best Local Similarity 97.4%; Pred. No. 8.6e-19;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QNSGNQSFEEDEPKRYEQGNIVDIDFDSVPQIHG 38
Db 2 QNSGNQSFEEDEPKRYEQGNIVDIDFDSVPQIHG 39

RESULT 8
US-08-495-559-8
; Sequence 8, Application US/08495559A
; Patent No. 6054572
; GENERAL INFORMATION:
; APPLICANT: BURHAM, Martin Karl Russel
; APPLICANT: CHOPRA, Ian
; APPLICANT: CRITCHLEY, Ian Alfred
; APPLICANT: KNOWLES, David Justin Charles
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN: MONOCLONAL
; TITLE OF INVENTION: ANTIBODY AND THEIR USE IN PREVENTING BACTERIAL ADHESION
; FILE REFERENCE: P30591
; CURRENT APPLICATION NUMBER: US/08/495,559A
; CURRENT FILING DATE: 1995-08-03
; EARLIER APPLICATION NUMBER: GB 9302289.5
; EARLIER FILING DATE: 1993-02-05
; EARLIER APPLICATION NUMBER: GB 9321592.9
; EARLIER FILING DATE: 1993-10-20
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 8
; LENGTH: 130
; TYPE: PR1
; ORGANISM: Staphylococcus aureus
US-08-495-559-8

Query Match          96.1%; Score 199; DB 3; Length 130;
Best Local Similarity 97.4%; Pred. No. 8.6e-19;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QNSGNQSFEEDEPKRYEQGNIVDIDFDSVPQIHG 38
Db 2 QNSGNQSFEEDEPKRYEQGNIVDIDFDSVPQIHG 39

RESULT 9
US-08-856-253-8
; Sequence 8, Application US/08856253
; Patent No. 6288214
; GENERAL INFORMATION:
; APPLICANT: Hook, Magnus
; APPLICANT: Patti, Joseph M.
; APPLICANT: House-Pompeo, Karen
; APPLICANT: Schanham, Narayana
; APPLICANT: Symersky, Jindrich
; TITLE OF INVENTION: COLLAGEN BINDING PROTEIN COMPOSITIONS
; TITLE OF INVENTION: AND METHODS OF USE
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: U.S.
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/856,253
; FILING DATE: Concurrently Herewith
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/017,678
; FILING DATE: 16-MAY-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Kitchell, Barbara S.
; REGISTRATION NUMBER: 33,928
; REFERENCE/DOCKET NUMBER: TAMK:193
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (512) 418-3000
; TELEFAX: (512) 474-7577
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 139 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
US-08-856-253-8

Query Match          96.1%; Score 199; DB 3; Length 139;
Best Local Similarity 97.4%; Pred. No. 9.3e-19;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QNSGNQSFEEDEPKRYEQGNIVDIDFDSVPQIHG 38
Db 16 QNSGNQSFEEDEPKRYEQGNIVDIDFDSVPQIHG 53

RESULT 10
US-08-459-135A-10
; Sequence 10, Application US/08459135A
; Patent No. 5955078
; GENERAL INFORMATION:
; APPLICANT: BURHAM, Martin Karl Russel
; APPLICANT: CHOPRA, Ian
; APPLICANT: CRITCHLEY, Ian Alfred
; APPLICANT: KNOWLES, David Justin Charles
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN: MONOCLONAL ANTIBODY AND THEIR USE
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSER: SmithKline Beecham Corporation
; STREET: 709 Swedeland Road
; CITY: King of Prussia
; STATE: PA
; COUNTRY: U.S.A.
; ZIP: 19406-0939
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
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; APPLICANT: Hook, Magnus
; APPLICANT: Patti, Joseph M.
; APPLICANT: House-Pompeo, Karen
; APPLICANT: Schanham, Narayana
; APPLICANT: Symersky, Jindrich
; TITLE OF INVENTION: COLLAGEN BINDING PROTEIN COMPOSITIONS
; TITLE OF INVENTION: AND METHODS OF USE
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: U.S.
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/856,253
; FILING DATE: Concurrently Herewith
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/017,678
; FILING DATE: 16-MAY-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Kitchell, Barbara S.
; REGISTRATION NUMBER: 33,928
; REFERENCE/DOCKET NUMBER: TAMK:193
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (512) 418-3000
; TELEFAX: (512) 474-7577
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 139 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
US-08-856-253-8

Query Match          96.1%; Score 199; DB 3; Length 139;
Best Local Similarity 97.4%; Pred. No. 9.3e-19;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QNSGNQSFEEDEPKRYEQGNIVDIDFDSVPQIHG 38
Db 16 QNSGNQSFEEDEPKRYEQGNIVDIDFDSVPQIHG 53

RESULT 10
US-08-459-135A-10
; Sequence 10, Application US/08459135A
; Patent No. 5955078
; GENERAL INFORMATION:
; APPLICANT: BURHAM, Martin Karl Russel
; APPLICANT: CHOPRA, Ian
; APPLICANT: CRITCHLEY, Ian Alfred
; APPLICANT: KNOWLES, David Justin Charles
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN: MONOCLONAL ANTIBODY AND THEIR USE
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSER: SmithKline Beecham Corporation
; STREET: 709 Swedeland Road
; CITY: King of Prussia
; STATE: PA
; COUNTRY: U.S.A.
; ZIP: 19406-0939
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
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SOFTWARE: Fastseq, Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/459,135A
FILING DATE: 02-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB/94/00215
FILING DATE: 04-Feb-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Gimm, Edward R
REGISTRATION NUMBER: 38,891
REFERENCE/DOCKET NUMBER: P30591C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-4478
TELEFAX: 610-270-5090
TELEX:
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 174 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: Protein
US-08-459-135A-10

Query Match 96.1%; Score 199; DB 2; Length 174;
Best Local Similarity 97.4%; Pred. No. 1.2e-18;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QNSGNQSFEDPEDEPKPYEGGNIYVIDPDSVPQIHG 38
Db 2 QNSGNQSFEDPEDEPKPYEGGNIYVIDPDSVPQIHG 39

RESULT 11
US-08-459-135A-13
Sequence 13, Application US/08459135A
Patent No. 5955078
GENERAL INFORMATION:
APPLICANT: BURHAM, Martin Karl Russel
APPLICANT: CHOPRA, Ian
APPLICANT: CRITCHLEY, Ian Alfred
APPLICANT: KNOWLES, David Justin Charles
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN: MONOCLONAL ANTIBODY AND THEIR US
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
STATE: PA
COUNTRY: U.S.A.
ZIP: 19406-0939
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: Fastseq, Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/459,135A
FILING DATE: 02-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB/94/00215
FILING DATE: 04-Feb-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Gimm, Edward R
REGISTRATION NUMBER: 38,891
REFERENCE/DOCKET NUMBER: P30591C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-4478
TELEFAX: 610-270-5090
TELEX:

INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 174 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-459-135A-13

Query Match 96.1%; Score 199; DB 2; Length 174;
Best Local Similarity 97.4%; Pred. No. 1.2e-18;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QNSGNQSFEDPEDEPKPYEGGNIYVIDPDSVPQIHG 38
Db 2 QNSGNQSFEDPEDEPKPYEGGNIYVIDPDSVPQIHG 39

RESULT 12
US-08-495-559-10
Sequence 10, Application US/08495559A
Patent No. 6054572
GENERAL INFORMATION:
APPLICANT: BURHAM, Martin Karl Russel
APPLICANT: CHOPRA, Ian
APPLICANT: CRITCHLEY, Ian Alfred
APPLICANT: KNOWLES, David Justin Charles
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN: MONOCLONAL
TITLE OF INVENTION: ANTIBODY AND THEIR USE IN PREVENTING BACTERIAL ADHESION
FILE REFERENCE: P30591
CURRENT APPLICATION NUMBER: US/08/495,559A
CURRENT FILING DATE: 1995-08-03
EARLIER APPLICATION NUMBER: GB 9302289.5
EARLIER FILING DATE: 1993-02-05
EARLIER APPLICATION NUMBER: GB 9321592.9
EARLIER FILING DATE: 1993-10-20
NUMBER OF SEQ ID NOS: 13
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 10
LENGTH: 174
TYPE: PRT
ORGANISM: Staphylococcus aureus
US-08-495-559-10

Query Match 96.1%; Score 199; DB 3; Length 174;
Best Local Similarity 97.4%; Pred. No. 1.2e-18;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QNSGNQSFEDPEDEPKPYEGGNIYVIDPDSVPQIHG 38
Db 2 QNSGNQSFEDPEDEPKPYEGGNIYVIDPDSVPQIHG 39

RESULT 13
US-08-495-559-13
Sequence 13, Application US/08495559A
Patent No. 6054572
GENERAL INFORMATION:
APPLICANT: BURHAM, Martin Karl Russel
APPLICANT: CHOPRA, Ian
APPLICANT: CRITCHLEY, Ian Alfred
APPLICANT: KNOWLES, David Justin Charles
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN: MONOCLONAL
TITLE OF INVENTION: ANTIBODY AND THEIR USE IN PREVENTING BACTERIAL ADHESION
FILE REFERENCE: P30591
CURRENT APPLICATION NUMBER: US/08/495,559A
CURRENT FILING DATE: 1995-08-03
EARLIER APPLICATION NUMBER: GB 9302289.5
EARLIER FILING DATE: 1993-02-05
EARLIER APPLICATION NUMBER: GB 9321592.9
EARLIER FILING DATE: 1993-10-20
NUMBER OF SEQ ID NOS: 13
SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 13
LENGTH: 174
TYPE: PRT
ORGANISM: Staphylococcus aureus
US-08-495-559-13

Query Match 96.1%; Score 199; DB 3; Length 174;
Best Local Similarity 97.4%; Pred. No. 1.2e-18;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QNSGNQSFEEDEBDKPKRYEQGNIVDIDFDSVPQIHG 38
Db 2 QNSGNQSFEEDEBDKPKRYEQGNIVDIDFDSVPQIHG 39

RESULT 14
US-08-495-559-6
Sequence 6, Application US/08495559A
Patent No. 6054572
GENERAL INFORMATION:
APPLICANT: BURHAM, Martin Karl Russel
APPLICANT: CHOPRA, Ian
APPLICANT: CRITCHLEY, Ian Alfred
APPLICANT: KNOWLES, David Justin Charles
TITLE OF INVENTION: FIBROBLAST BINDING PROTEIN: MONOCLONAL
TITLE OF INVENTION: ANTIBODY AND THEIR USE IN PREVENTING BACTERIAL ADHESION
FILE REFERENCE: P30591
CURRENT FILING DATE: 1995-08-03
EARLIER APPLICATION NUMBER: GB 9302289.5
EARLIER FILING DATE: 1993-02-05
EARLIER APPLICATION NUMBER: GB 9321592.9
EARLIER FILING DATE: 1993-10-20
NUMBER OF SEQ ID NOS: 13
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 6
LENGTH: 176
TYPE: PRT
ORGANISM: Staphylococcus aureus
US-08-495-559-6

Query Match 96.1%; Score 199; DB 3; Length 176;
Best Local Similarity 97.4%; Pred. No. 1.2e-18;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QNSGNQSFEEDEBDKPKRYEQGNIVDIDFDSVPQIHG 38
Db 2 QNSGNQSFEEDEBDKPKRYEQGNIVDIDFDSVPQIHG 39

RESULT 15
US-08-459-135A-12
Sequence 12, Application US/08459135A
Patent No. 5955078
GENERAL INFORMATION:
APPLICANT: BURHAM, Martin Karl Russel
APPLICANT: CHOPRA, Ian
APPLICANT: CRITCHLEY, Ian Alfred
APPLICANT: KNOWLES, David Justin Charles
TITLE OF INVENTION: FIBROBLAST BINDING PROTEIN: MONOCLONAL ANTIBODY AND THEIR US
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
STATE: PA
COUNTRY: U.S.A.
ZIP: 19406-0939
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: Fastseq, Version 2.0

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/459,135A
FILING DATE: 02-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB/94/00215
FILING DATE: 04-Feb-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Gimmi, Edward R
REGISTRATION NUMBER: 38,891
REFERENCE/DOCKET NUMBER: P30591C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-4478
TELEFAX: 610-270-5090
TELEX:
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 178 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: Protein
US-08-459-135A-12

Query Match 96.1%; Score 199; DB 2; Length 178;
Best Local Similarity 97.4%; Pred. No. 1.2e-18;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QNSGNQSFEEDEBDKPKRYEQGNIVDIDFDSVPQIHG 38
Db 2 QNSGNQSFEEDEBDKPKRYEQGNIVDIDFDSVPQIHG 39

Search completed: October 22, 2005, 05:46:43
Job time : 21.2223 secs

GenCore version 5.1.6
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OM protein - protein search, using SW model

Run on: October 22, 2005, 11:35:03 ; Search time 70.1256 Seconds
(without alignments)
226.232 Million cell updates/sec

Title: US-10-731-238-39

Perfect score: 207
Sequence: 1 QNSGNQSPEDPEEDPKRYEGCGNIVIDPDSVPQIHG 38

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Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

Published Applications AA: *
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22: /cgn2_6/ptodata/2/pubpaa/US10L_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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2	199	96.1	38	18 US-10-731-238-5	Sequence 8, Appl
3	199	96.1	139	9 US-09-813-820-8	Sequence 1, Appl
4	199	96.1	388	8 US-08-901-062-1	Sequence 5251, Ap
5	199	96.1	559	15 US-10-329-624-5251	Sequence 5899, Ap
6	199	96.1	767	9 US-09-815-242-5899	Sequence 13140, A
7	199	96.1	767	9 US-09-815-242-13140	Sequence 424, App
8	199	96.1	940	17 US-10-470-048B-424	Sequence 69, Appl
9	199	96.1	948	17 US-10-470-048B-65	Sequence 43778, A
10	199	96.1	961	15 US-10-282-122A-43778	Sequence 5797, Ap
11	199	96.1			Sequence 12838, A
					Sequence 68, Appl
					Sequence 5254, Ap
					Sequence 43827, A
					Sequence 37, Appl
					Sequence 40, Appl
					Sequence 41, Appl
					Sequence 38, Appl
					Sequence 42, Appl
					Sequence 6, Appl
					Sequence 43, Appl
					Sequence 5456, Ap
					Sequence 12866, A
					Sequence 35, Appl
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					Sequence 47, Appl
					Sequence 48, Appl
					Sequence 49, Appl
					Sequence 44, Appl
					Sequence 45, Appl
					Sequence 58, Appl
					Sequence 59, Appl
					Sequence 2, Appl
					Sequence 114, Ap
					Sequence 60, Appl

12 199 96.1 1018 9 US-09-815-242-5797
13 199 96.1 1018 9 US-09-815-242-12838
14 199 96.1 1018 17 US-10-470-048B-68
15 199 96.1 1027 8 US-08-781-986A-5254
16 199 96.1 1027 15 US-10-329-624-5254
17 199 96.1 1038 15 US-10-282-122A-43827
18 199 93.2 38 18 US-10-731-238-36
19 199 93.2 38 18 US-10-731-238-37
20 199 93.2 38 18 US-10-731-238-40
21 199 93.2 38 18 US-10-731-238-41
22 199 92.8 38 18 US-10-731-238-38
23 199 92.8 38 18 US-10-731-238-38
24 199 92.3 38 18 US-10-731-238-42
25 199 92.3 38 18 US-10-731-238-6
26 199 92.3 38 18 US-10-731-238-43
27 199 92.3 978 9 US-09-815-242-5456
28 189 91.3 1001 9 US-09-815-242-12866
29 188.5 91.1 38 18 US-10-731-238-35
30 180.5 87.2 39 18 US-10-731-238-56
31 180 87.0 39 18 US-10-731-238-57
32 174 84.1 38 18 US-10-731-238-46
33 174 84.1 38 18 US-10-731-238-47
34 173 83.6 38 18 US-10-731-238-48
35 172 83.1 38 18 US-10-731-238-8
36 172 83.1 38 18 US-10-731-238-49
37 171 82.6 38 18 US-10-731-238-44
38 170 82.1 38 18 US-10-731-238-45
39 157 75.8 36 18 US-10-731-238-58
40 152 73.4 38 18 US-10-731-238-50
41 149 72.0 36 18 US-10-731-238-59
42 141 68.1 30 14 US-10-287-821-1
43 141 68.1 31 14 US-10-287-821-2
44 77.5 37.4 37 20 US-11-066-657-1134
45 74 35.7 14 18 US-10-731-238-60

ALIGNMENTS

Sequence 5797, Ap
Sequence 12838, A
Sequence 68, Appl
Sequence 5254, Ap
Sequence 43827, A
Sequence 37, Appl
Sequence 40, Appl
Sequence 41, Appl
Sequence 38, Appl
Sequence 42, Appl
Sequence 6, Appl
Sequence 43, Appl
Sequence 5456, Ap
Sequence 12866, A
Sequence 35, Appl
Sequence 56, Appl
Sequence 57, Appl
Sequence 7, Appl
Sequence 46, Appl
Sequence 47, Appl
Sequence 48, Appl
Sequence 49, Appl
Sequence 44, Appl
Sequence 45, Appl
Sequence 58, Appl
Sequence 59, Appl
Sequence 2, Appl
Sequence 114, Ap
Sequence 60, Appl

RESULT 1
US-10-731-238-39
; Sequence 39, Application US/10731238
; Publication No. US20050123552A1
; GENERAL INFORMATION:
; APPLICANT: Hook, Magnus
; Patti, Joseph M.
; House-Pompeo, Karen L.
; Speziale, Pietro
; John, Danny
; McGavin, Martin J.
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
; AND METHODS OF USE
; NUMBER OF SEQUENCES: 105
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: TX
; COUNTRY: USA
; ZIP: 77210-4433
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/731,238
; FILING DATE: 10-Dec-2003
; CLASSIFICATION DATA:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/010,317
; FILING DATE: 21-Jan-1998
; APPLICATION NUMBER: US 60/036,139

;; FILING DATE: 21-JAN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Hibler, David W.
; REGISTRATION NUMBER: 41,071
; REFERENCE/DOCKET NUMBER: TANK:189
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 512-418-3000
; TELEFAX: 512-474-7577
; INFORMATION FOR SEQ ID NO: 39:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 38 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; US-10-731-238-39
; SEQUENCE DESCRIPTION: SEQ ID NO: 39:

Query Match 100.0%; Score 207; DB 18; Length 38;
Best Local Similarity 100.0%; Pred. No. 3,7e-19;
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QNSGNQSFEEDEEDKPKRYEGGNIIVDIDFDSVPQIHG 38
DB 1 QNSGNQSFEEDEEDKPKRYEGGNIIVDIDFDSVPQIHG 38

RESULT 2
US-10-731-238-5
; Sequence 5, Application US/10731238
; Publication No. US20050123552A1
; GENERAL INFORMATION:
; APPLICANT: Hook, Magnus
; Patti, Joseph M.
; House-Pompeo, Karen L.
; Speciale, Pietro
; Joh, Danny
; McGavin, Martin J.
; TITLE OF INVENTION: FIBROBLAST BINDING PROTEIN COMPOSITIONS
; NUMBER OF SEQUENCES: 105
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: TX
; COUNTRY: USA
; ZIP: 77210-4433
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/731,238
; FILING DATE: 10-Dec-2003
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/010,317
; FILING DATE: 21-Jan-1998
; APPLICATION NUMBER: US 60/036,139
; FILING DATE: 21-JAN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Hibler, David W.
; REGISTRATION NUMBER: 41,071
; REFERENCE/DOCKET NUMBER: TANK:189
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 512-418-3000
; TELEFAX: 512-474-7577
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 38 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>

;; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 5:
; US-10-731-238-5
; Query Match 96.1%; Score 199; DB 18; Length 38;
; Best Local Similarity 97.4%; Pred. No. 3,9e-18;
; Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QNSGNQSFEEDEEDKPKRYEGGNIIVDIDFDSVPQIHG 38
DB 1 QNSGNQSFEEDEEDKPKRYEGGNIIVDIDFDSVPQIHG 38

RESULT 3
US-09-813-820-8
; Sequence 8, Application US/09813820
; Patent No. US20020102262A1
; GENERAL INFORMATION:
; APPLICANT: Hook, Magnus
; Patti, Joseph M.
; House-Pompeo, Karen
; Schanam, Narayana
; Symersky, Jindrich
; TITLE OF INVENTION: COLLAGEN BINDING PROTEIN COMPOSITIONS
; AND METHODS OF USE
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: U.S.
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; OPERATING SYSTEM: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/813,820
; FILING DATE: 22-Mar-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/856,253
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Kitchell, Barbara S.
; REGISTRATION NUMBER: 33,928
; REFERENCE/DOCKET NUMBER: TANK:193
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (512) 418-3000
; TELEFAX: (512) 474-7577
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 139 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; US-09-813-820-8
; SEQUENCE DESCRIPTION: SEQ ID NO: 8:

Query Match 96.1%; Score 199; DB 9; Length 139;
Best Local Similarity 97.4%; Pred. No. 1,7e-17;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QNSGNQSFEEDEEDKPKRYEGGNIIVDIDFDSVPQIHG 38
DB 16 QNSGNQSFEEDEEDKPKRYEGGNIIVDIDFDSVPQIHG 53

RESULT 4
US-08-901-062-1
; Sequence 1, Application US/08901062

Publication No. US20020025324A1
GENERAL INFORMATION:
APPLICANT: SEALS, JONATHAN R.
TITLE OF INVENTION: RECOMBINANT BIVALENT BACTERIAL VACCINE
TITLE OF INVENTION: FOR THE PREVENTION OF MASTITIS
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESSES:
ADDRESSER: HALE AND DORR LLP
STREET: 60 State Street
CITY: Boston
STATE: MA
COUNTRY: United States Of America
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/901,062
FILING DATE: 25-JUL-1997
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Baker, Hollie L.
REGISTRATION NUMBER: 31,321
REFERENCE/DOCKET NUMBER: 106941.153
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 526-6000
TELEFAX: (617) 526-5000
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 388 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-901-062-1

Query Match 96.1%; Score 199; DB 8; Length 388;
Best Local Similarity 97.4%; Pred. No. 5,6e-17;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QNSGNSFEEDPEEDKPKYEOGSGNIVDIDFDSVPQIHG 38
DB 265 QNSGNSFEEDPEEDKPKYEOGSGNIVDIDFDSVPQIHG 302

RESULT 5
US-08-781-986A-5251
Sequence 5251, Application US/08781986A
Publication No. US20030054436A1
GENERAL INFORMATION:
APPLICANT: Charles Kunesh
TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
NUMBER OF SEQUENCES: 5255
CORRESPONDENCE ADDRESSES:
ADDRESSER: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COUNTRY: USA
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4MB storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/781,986A
FILING DATE:
CLASSIFICATION: 435

PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Benson, Bob
REGISTRATION NUMBER: 30,446
REFERENCE/DOCKET NUMBER: PB248BP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8512
TELEFAX: (301) 309-8504
INFORMATION FOR SEQ ID NO: 5251:
SEQUENCE CHARACTERISTICS:
LENGTH: 559 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-781-986A-5251

Query Match 96.1%; Score 199; DB 8; Length 559;
Best Local Similarity 97.4%; Pred. No. 8,6e-17;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QNSGNSFEEDPEEDKPKYEOGSGNIVDIDFDSVPQIHG 38
DB 301 QNSGNSFEEDPEEDKPKYEOGSGNIVDIDFDSVPQIHG 338

RESULT 6
US-10-329-624-5251
Sequence 5251, Application US/10329624
Publication No. US20040043037A1
GENERAL INFORMATION:
APPLICANT: Charles Kunesh
Gill H. Choi
Patrick S. Dillon
Craig A. Rosen
Steven C. Barash
Michael R. Fannon
TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
NUMBER OF SEQUENCES: 5256
CORRESPONDENCE ADDRESSES:
ADDRESSER: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COUNTRY: USA
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4MB storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/329,624
FILING DATE: 27-Dec-2002
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/956,171
FILING DATE: October 20, 1997
APPLICATION NUMBER: 60/009,861
FILING DATE: January 5, 1996
APPLICATION NUMBER: 08/781,986
FILING DATE: January 3, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Mark J. Hyman
REGISTRATION NUMBER: 46,789
REFERENCE/DOCKET NUMBER: PB248P1D1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (240) 314-1224
TELEFAX: (301) 309-8439
INFORMATION FOR SEQ ID NO: 5251:
SEQUENCE CHARACTERISTICS:
LENGTH: 559 amino acids

TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 5251:
US-10-329-624-5251

Query Match 96.1%; Score 199; DB 15; Length 559;
Best Local Similarity 97.4%; Pred. No. 8.6e-17;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QNSGNQSFEEDEPKRYEGGNIVIDIDFDSVPQIHG 38
Db 301 QNSGNQSFEEDEPKRYEGGNIVIDIDFDSVPQIHG 338

RESULT 7
US-09-815-242-5899

; Sequence 5899, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari L.
; APPLICANT: Zykkind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; TITLE OF INVENTION: Prokaryotes
; FILE REFERENCE: ELITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5899
; LENGTH: 767
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-09-815-242-5899

Query Match 96.1%; Score 199; DB 9; Length 767;
Best Local Similarity 97.4%; Pred. No. 1.2e-16;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QNSGNQSFEEDEPKRYEGGNIVIDIDFDSVPQIHG 38
Db 682 QNSGNQSFEEDEPKRYEGGNIVIDIDFDSVPQIHG 719

RESULT 8
US-09-815-242-13140

; Sequence 13140, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari L.
; APPLICANT: Zykkind, Judith W.

; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; TITLE OF INVENTION: Prokaryotes
; FILE REFERENCE: ELITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13140
; LENGTH: 767
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-09-815-242-13140

Query Match 96.1%; Score 199; DB 9; Length 767;
Best Local Similarity 97.4%; Pred. No. 1.2e-16;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QNSGNQSFEEDEPKRYEGGNIVIDIDFDSVPQIHG 38
Db 682 QNSGNQSFEEDEPKRYEGGNIVIDIDFDSVPQIHG 719

RESULT 9
US-10-470-048B-424

; Sequence 424, Application US/10470048B
; Publication No. US20050037444A1
; GENERAL INFORMATION:
; APPLICANT: MEINKE ET AL.
; TITLE OF INVENTION: A METHOD FOR IDENTIFICATION, ISOLATION AND PRODUCTION OF
; TITLE OF INVENTION: ANTIGENS TO A SPECIFIC PATHOGEN
; FILE REFERENCE: SONN.035US
; CURRENT APPLICATION NUMBER: US/10/470,048B
; CURRENT FILING DATE: 2003-07-25
; NUMBER OF SEQ ID NOS: 603
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 424
; LENGTH: 940
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-10-470-048B-424

Query Match 96.1%; Score 199; DB 17; Length 940;
Best Local Similarity 97.4%; Pred. No. 1.6e-16;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QNSGNQSFEEDEPKRYEGGNIVIDIDFDSVPQIHG 38
Db 682 QNSGNQSFEEDEPKRYEGGNIVIDIDFDSVPQIHG 719

RESULT 10

US-10-470-048B-69
; Sequence 69, Application US/10470048B
; Publication No. US20050037444A1


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; TITLE OF INVENTION: Prokaryotes
; FILE REFERENCE: ELITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: PatSeq for Windows Version 4.0
; SEQ ID NO 12838
; LENGTH: 1018
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
; US-09-815-242-12838

Query Match          96.1%; Score 199; DB 9; Length 1018;
Best Local Similarity 97.4%; Pred. No. 1.7e-16;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY      1  QNSGNQSFEDPDEBKPKYEQGNIVDIDFDSVPQIHG 38
Db      746  QNSGNQSFEDPDEBKPKYEQGNIVDIDFDSVPQIHG 783

RESULT 14
US-10-470-0488-68
; Sequence 68, Application US/104700488
; Publication No. US20050037444A1
; GENERAL INFORMATION:
; APPLICANT: MEINKE ET AL.
; TITLE OF INVENTION: A METHOD FOR IDENTIFICATION, ISOLATION AND PRODUCTION OF
; TITLE OF INVENTION: ANTIGENS TO A SPECIFIC PATHOGEN
; FILE REFERENCE: SCMN.035US
; CURRENT APPLICATION NUMBER: US/10/470,0488
; NUMBER OF SEQ ID NOS: 603
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 68
; LENGTH: 1018
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
; US-10-470-0488-68

Query Match          96.1%; Score 199; DB 17; Length 1018;
Best Local Similarity 97.4%; Pred. No. 1.7e-16;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY      1  QNSGNQSFEDPDEBKPKYEQGNIVDIDFDSVPQIHG 38
Db      746  QNSGNQSFEDPDEBKPKYEQGNIVDIDFDSVPQIHG 783

RESULT 15
US-08-781-986A-5254
; Sequence 5254, Application US/08781986A
; Publication No. US20030054436A1
; GENERAL INFORMATION:
; APPLICANT: Charles Kunach
; TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
; NUMBER OF SEQUENCES: 5255
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
```

```

; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4MB storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/781,986A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Benson, Bob
; REGISTRATION NUMBER: 30,446
; REFERENCE/DOCKET NUMBER: PB248PP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 5254:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1027 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-781-986A-5254

Query Match          96.1%; Score 199; DB 8; Length 1027;
Best Local Similarity 97.4%; Pred. No. 1.7e-16;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY      1  QNSGNQSFEDPDEBKPKYEQGNIVDIDFDSVPQIHG 38
Db      755  QNSGNQSFEDPDEBKPKYEQGNIVDIDFDSVPQIHG 792

Search completed: October 22, 2005, 12:09:26
Job time : 71.1256 secs
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 22, 2005, 04:14:19 ; Search time 13.8905 Seconds
(without alignments)
263.219 Million cell updates/sec

Title: US-10-731-238-39

Perfect score: 207

Sequence: 1 QNSGNQSFEDPEBDPKRYEGGNIIVDIDFDSVPQIHG 38

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	199	96.1	940	2	S19702 fibronectin-binding
2	199	96.1	961	2	G90053 hypothetical prote
3	199	96.1	1018	2	A32192 fibronectin-binding
4	199	96.1	1038	2	H90053 hypothetical prote
5	58.5	28.3	817	2	T03852 protein phosphatas
6	58	28.0	1817	2	T34249 hypothetical prote
7	57	27.5	500	2	C81657 general secretion
8	57	27.5	501	2	D71499 probable gen. secr
9	56.5	27.3	968	2	T25667 hypothetical prote
10	55.5	26.8	1273	1	TDR171 leukocyte common a
11	55.5	26.8	1291	1	A28334 protein-tyrosine-p
12	55	26.6	310	2	B83331 catechol 1,2-dioxy
13	55	26.6	329	2	S07577 legumin storage pr
14	55	26.6	335	2	S07576 legumin storage pr
15	55	26.6	345	2	T33068 hypothetical prote
16	55	26.6	465	2	S69038 legumin B4 precurs
17	55	26.6	484	2	A24942 hypothetical prote
18	55	26.6	837	2	T19825 homocytic gene regu
19	55	26.6	1022	2	I51078 polymorphic membra
20	55	26.6	1460	2	D81675 protein BRG1 - hum
21	55	26.6	1613	2	S39059 SNFbeta protein -
22	55	26.6	1647	2	T43564 hypothetical prote
23	54	26.1	705	2	A45508 heat shock membrane
24	53	25.6	142	2	F70826 legumin storage pr
25	53	25.6	335	2	S07578 conserved hypothet
26	53	25.6	785	2	T18252 lipoprotein vacuol
27	53	25.6	833	2	E90577 chromosome segrega
28	53	25.6	1233	2	T40059
29	53	25.6	1233	2	T40059

30	53	25.6	1420	1	A44361 aniloride-sensitiv
31	53	25.6	1952	2	T48814 hypothetical prote
32	52.5	25.4	558	2	C71609 hypothetical prote
33	52	25.1	165	2	F95002 conserved hypothet
34	52	25.1	188	2	B97875 conserved hypothet
35	52	25.1	265	2	A43738 Endo16 protein - s
36	52	25.1	265	2	S57978 hypothetical prote
37	52	25.1	273	2	T6108 hypothetical prote
38	52	25.1	359	2	G70814 probable fat prote
39	52	25.1	425	2	T16433 hypothetical prote
40	52	25.1	442	2	H72266 asfB/chur-related
41	52	25.1	444	2	T26229 hypothetical prote
42	52	25.1	596	2	T23193 hypothetical prote
43	52	25.1	1396	2	T10627 hypothetical prote
44	52	25.1	1424	2	T03851 thyroid hormone re
45	51.5	24.9	144	2	A70411 small heat shock p

ALIGNMENTS

RESULT 1

S19702
C:Species: Staphylococcus aureus
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
C:Accession: S19702
R:Joensen, K.; Signaes, C.; Mueller, H.P.; Lindberg, M.
Eur. J. Biochem. 202, 1041-1048, 1991
A:Title: Two different genes encode fibronectin binding proteins in Staphylococcus aureus
A:Reference number: S19702; MUID:92111475; PMID:1837266
A:Accession: S19702
A:Status: Preliminary
A:Molecule type: DNA
A:Residues: 1-940 <JOB>
A:Cross-references: UNIPROT:053682; EMBL:X62992; NID:949040; PIDN:CAA44726.1; PID:958156;
C:Keywords: fibronectin binding

Query Match 96.1%; Score 199; DB 2; Length 940;
Best Local Similarity 97.4%; Pred. No. 7.3e-17;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QNSGNQSFEDPEBDPKRYEGGNIIVDIDFDSVPQIHG 38
Db 682 QNSGNQSFEDPEBDPKRYEGGNIIVDIDFDSVPQIHG 719

RESULT 2

G90053
C:Species: Staphylococcus aureus
C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C:Accession: G90053
R:Kurida, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Gai, L.; Oguchi, A.; Mizutani-Ut, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.; C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiratake, K.
Lancet 357, 1225-1240, 2001
A:Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.
A:Reference number: A89758; MUID:21311952; PMID:11418146
A:Accession: G90053
A:Status: Preliminary
A:Molecule type: DNA
A:Residues: 1-961 <KUR>
A:Cross-references: UNIPROT:099RD3; GB:BA000018; PID:G13702452; PIDN:BA843593.1; GSPDB:G
A:Experimental source: strain N315
C:Genetics: fmbB

Query Match 96.1%; Score 199; DB 2; Length 961;
Best Local Similarity 97.4%; Pred. No. 7.5e-17;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QNSGNQSFEDPEBDPKRYEGGNIIVDIDFDSVPQIHG 38

D71499
 Probable gen. secretion protein E - Chlamydia trachomatis (serotype D, strain UW3/Cx)
 C:Species: Chlamydia trachomatis
 C>Date: 13-Sep-1998 #sequence_revision 13-Sep-1998 #text_change 09-Jul-2004
 C:Accession: D71499
 R:Stefens, R.S.; Kalman, S.; Lammel, C.J.; Fan, J.; Marathe, R.; Aravind, L.; Mitchell, Science 282, 754-759, 1998
 A:Title: Genome sequence of an obligate intracellular pathogen of humans: Chlamydia trachomatis
 A:Reference number: A71570; MUID:9900809; PMID:9784136
 A:Accession: D71499
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-501 <ARN>
 A:Cross-references: UNIPROT:O84575; GB:AE001327; GB:AE001273; NID:g3328999; PIDN:AAC6817
 A:Experimental source: serotype D, strain UW-3/Cx
 C:Genetics:
 A:Gene: ggpE
 C:Superfamily: secretion protein xcpR

Query Match 27.5%; Score 57; DB 2; Length 501;
 Best Local Similarity 37.0%; Pred. No. 23;
 Matches 10; Conservative 7; Mismatches 10; Indels 0; Gaps 0;

Qy 12 PEEDKPKTEQGNIVDIPDSVPIQHG 38
 Db 188 FODGRKIKLQGGQEIEMRSTVPIVHG 214

RESULT 9
 T25667
 Hypothetical protein D2092.5 - Caenorhabditis elegans
 C:Species: Caenorhabditis elegans
 C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
 C:Accession: T25667
 R:Gutlung, S.; Maggi, L.
 submitted to the EMBL Data Library, February 1997
 A:Description: The sequence of C. elegans cosmid D2092.
 A:Reference number: Z20067
 A:Accession: T25667
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-968 <GAT>
 A:Cross-references: UNIPROT:P91193; EMBL:U88167; PIDN:AAB42225.1; GSPDB:GN00019; CESP:ID2
 C:Genetics:
 A:Experimental source: strain Bristol N2; clone D2092
 A:Gene: CESP:D2092.5
 A:Map position: 1
 A:Introns: 18/2; 42/3; 78/2; 140/3; 195/1; 221/2; 244/1; 283/2; 328/1; 345/1; 471/3; 688

Query Match 27.3%; Score 56.5; DB 2; Length 968;
 Best Local Similarity 38.7%; Pred. No. 57;
 Matches 12; Conservative 5; Mismatches 11; Indels 3; Gaps 1;

Qy 1 QNSGNQSFEDPEEDKPKTEQGNIVDIPD 31
 Db 397 KHNKNSGFSTPNDKCK--GKSRIDVMD 424

RESULT 10
 T07117
 Leukocyte common antigen precursor, splice form 4 - rat
 N:Alternate names: CD45; L-CA; Ly-5; T200
 N:Contains: leukocyte common antigen precursor, splice form 1; leukocyte common antigen
 .1.3.48)
 C:Species: Rattus norvegicus (Norway rat)
 C>Date: 04-Dec-1986 #sequence_revision 05-May-2000 #text_change 09-Jul-2004
 C:Accession: A23450; B29450; C29450; D29450; A60241; A02247; A45854
 R:Barclay, A.N.; Jackson, D.I.; Willis, A.C.; Williams, A.F.
 EMBO J. 6, 1259-1264, 1987
 A:Title: Lymphocyte specific heterogeneity in the rat leukocyte common antigen (T200) is
 A:Reference number: A91067; MUID:87275817; PMID:2440674
 A:Accession: A23450
 A:Molecule type: mRNA

A:Residues: 20-30, 163-218 <BAR1>
 A:Cross-references: UNIPROT:Q64224; GB:M25820; GB:M24611; NID:g205153; GB:Y00065; GB:K03
 A:Experimental source: splice form 1
 A>Note: the translation in Genbank entry RATLCAV, PIDN:AAA41518.1, PID:g205154, release 1
 A:Accession: B29450
 A:Molecule type: mRNA
 A:Residues: 19-30, 122-218 <BAR2>
 A:Cross-references: GB:M25821; GB:M24611; NID:g205155; PIDN:AAA41519.1; PID:g205156; GB:1
 A:Experimental source: splice form 2
 A:Accession: C29450
 A:Molecule type: mRNA
 A:Residues: 20-30, 73-121, 163-218 <BAR3>
 A:Cross-references: GB:M25822; GB:M24611; NID:g205157; PIDN:AAA41520.1; PID:g205158; GB:1
 A:Experimental source: splice form 3
 A:Accession: D29450
 A:Molecule type: mRNA
 A:Residues: 28-218 <BAR4>
 A:Cross-references: GB:M25823; GB:M24611; NID:g205159; PIDN:AAA41521.1; PID:g205160; GB:1
 A:Experimental source: splice form 4
 A>Note: the sequence in Genbank entry RATLCAV, release 113.0, has the codon ACG for 56-5
 R:Barclay, A.N.; Jackson, D.I.; Willis, A.C.; Williams, A.F.
 Adv. Exp. Med. Biol. 237, 3-7, 1988
 A:Title: The leukocyte-common antigen (L-CA) family.
 A:Reference number: A60241; MUID:89319817; PMID:2978200
 A:Accession: A60241
 A:Status: not compared with conceptual translation
 A:Molecule type: DNA
 A:Residues: 30-161 <BAR5>
 R:Thomas, M.L.; Barclay, A.N.; Gagnon, J.; Williams, A.F.
 Cell 41, 83-93, 1985
 A:Title: Evidence from cDNA clones that the rat leukocyte-common antigen (T200) spans the
 A:Reference number: A02247; MUID:85201691; PMID:3158393
 A:Accession: A02247
 A:Molecule type: mRNA
 A:Residues: 187-189, 'K', 191-192, 'K', 208-1273 <THO>
 A:Cross-references: GB:M0072; GB:M81859; NID:g205140; PIDN:AAA41513.1; PID:g205143
 A>Note: the translation in Genbank entry RATLCAV, release 113.0, begins at non-initiator
 A>Note: parts of this sequence were determined by protein sequencing
 R:McCall, M.N.; Shotton, D.M.; Barclay, A.N.
 Immunology 76, 310-317, 1992
 A:Title: Expression of soluble isoforms of rat CD45. Analysis by electron microscopy and
 A:Reference number: I54569; MUID:92340120; PMID:1378817
 A:Accession: I54569
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-30, 163-180 <MCC>
 A:Cross-references: GB:S40716; NID:g252015; PIDN:AAB22648.1; PID:g252016
 R:Jackson, D.I.; Barclay, A.N.
 Immunogenetics 29, 281-287, 1989
 A:Title: The extra segments of sequence in rat leukocyte common antigen (L-CA) are derivative
 A:Reference number: A45854; MUID:89233293; PMID:2523868
 A:Accession: A45854
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 24-227, 'H', 229-305, 'Y', 307-310 <JAC>
 A:Cross-references: GB:M18347; GB:M18348; GB:M18349
 A:Comment: This glycoprotein is found on lymphoid and myeloid cell surfaces.
 C:Superfamily: leukocyte common antigen; leukocyte common antigen cytosolic domain homolo
 C:Keywords: alternative splicing; duplication; glycoprotein; phosphoprotein; phosphoric n
 F:1-23/Domain: signal sequence #status predicted <SIG>
 F:24-1273/Product: leukocyte common antigen precursor, splice form 4 #status predicted <P
 F:24-546/Domain: extracellular #status predicted <EXT>
 F:24-30, 122-1273/Product: leukocyte common antigen, splice form 2 #status predicted <MAT
 F:24-30, 163-1273/Product: leukocyte common antigen, splice form 1 #status predicted <MAT
 F:24-30, 73-121, 163-218/Product: leukocyte common antigen, splice form 3 #status predicted
 F:547-568/Domain: transmembrane #status predicted <TM>
 F:565-1206/Domain: leukocyte common antigen cytosolic domain homology <LAC>
 F:569-1273/Domain: intracellular #status predicted <INT>
 F:568-870/Domain: protein-cytosine-phosphate homology <PPP>
 F:142, 153, 163, 178, 200, 245, 271, 282, 327, 371, 374, 502/Binding site: carbohydrate (Asn) (cc
 F:822/Active site: Cys (phosphocysteine intermediate) #status predicted
 F:828/Binding site: substrate phosphate (Arg) #status predicted
 F:1063/Binding site: carbohydrate (Asn) (covalent) #status absent

```

Query Match      26.8%; Score 55.5; DB 1; Length 1273;
Best Local Similarity 40.5%; Pred. No. 1e+02;
Matches 15; Conservative 5; Mismatches 10; Indels 7; Gaps 2;

Oy      1 QNSGNQSFEDDPKPYEGCGNIVDIDFDSVPQIH 37
      ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      929 QHIGNQ-----ENKKK-NRNSNVVPDFNRVPLKH 958

RESULT 11
A28334
A:Cross-references: EC 3.1.3.48; Ly-5 precursor (B-cell variant) - mouse
N:Alternate names: 200K leukocyte common antigen; B220; CD45; Ly-5 (B-cell specific); PT
C:Species: Mus musculus (house mouse)
C:Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #text_change 09-Jul-2004
C:Accession: A28334; A29381; A6180; A60933; A33522; A29075; I54450; A28335; A23329; I57
R:Thomas, M.L.; Reynolds, P.J.; Chain, A.; Ben-Neriah, Y.; Trowbridge, I.S.
A:Title: B-cell variant of mouse T200 (Ly-5): evidence for alternative mRNA splicing.
A:Reference number: A28334; MUID:87260986; PMID:2955416
A:Accession: A28334
A:Molecule type: mRNA
A:Residues: 1-1291 <THO>
A:Cross-references: UNIPROT:P06800; UNIPROT:Q61814; UNIPROT:Q61815; UNIPROT:Q61813; GB:M
R:Saga, Y.; Tung, J.S.; Shen, F.W.; Boyse, E.A.
Proc. Natl. Acad. Sci. U.S.A. 83, 6940-6944, 1986
A:Title: Sequences of Ly-5 cDNA: isoform-related diversity of Ly-5 mRNA.
A:Reference number: A29381; MUID:86313686; PMID:2944116
A:Accession: A29381
A:Molecule type: mRNA
A:Residues: 1-30,170-517, 'NTT', 521-527, 'G', 529-555, 'S', 557-587, 'S', 589-905, 'Q', 907-930, '
A:Cross-references: GB:M4342; NID:G198914; PIDN:AAA39458.1; PID:G198915
R:Yi, T.; Cleveland, J.L.; Ihle, J.N.
Blood 78, 2222-2228, 1991
A:Title: Identification of novel protein tyrosine phosphatases of hematopoietic cells by
A:Reference number: A61180; MUID:92032882; PMID:1932742
A:Accession: A61180
A:Status: not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 730-838 <YIA>
R:Gomez, L.J.; Walker, I.D.; Sandrin, M.S.; McKenzie, I.F.C.
Immunogenetics 25, 263-266, 1987
A:Title: High sequence conservation between rat (T200) and mouse (Ly-5) leukocyte common
A:Reference number: A60933; MUID:87192931; PMID:3570377
A:Accession: A60933
A:Molecule type: Protein
A:Residues: 'R', 289-298; '329', 'V', 331-336, 'Y', 'R', 364-370, 'X', 372-375; 595-608; 638-649; 669-
R:Johnson, N.A.; Meyer, C.M.; Pingel, J.T.; Thomas, M.L.
J. Biol. Chem. 264, 6220-6229, 1989
A:Title: Sequence conservation in potential regulatory regions of the mouse and human lg
A:Reference number: A33522; MUID:89197920; PMID:2522930
A:Accession: A33522
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-22 <JOH>
A:Cross-references: GB:M22456; NID:G198755; PIDN:AAA46374.1; PID:G554185; GB:J04640; GB:
R:Rasche, W.C.
Proc. Natl. Acad. Sci. U.S.A. 84, 161-165, 1987
A:Title: Cloned murine T200 (Ly-5) cDNA reveals multiple transcripts within B- and T-lym
A:Reference number: A29075; MUID:87092355; PMID:2948186
A:Accession: A29075
A:Molecule type: mRNA
A:Residues: 961-1291 <RAS>
A:Cross-references: GB:M15174; NID:G201105; PIDN:AAA40161.1; PID:G201106
R:Tung, J.
Immunogenetics 28, 271-277, 1988
A:Title: Structural features of Ly-5 glycoproteins of the mouse and counterparts in othe
A:Reference number: I54450; MUID:88330145; PMID:3417340
A:Accession: I54450
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA

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A:Residues: 32-73 <RES>
A:Cross-references: GB:M23241; NID:G340850; PIDN:AAA39460.1; PID:G548174
R:Saga, Y.; Tung, J.S.; Shen, F.W.; Boyse, E.A.
Proc. Natl. Acad. Sci. U.S.A. 84, 5364-5368, 1987
A:Title: Alternative use of 5' exons in the specification of Ly-5 isoforms distinguishing
A:Reference number: A28335; MUID:87260987; PMID:3037546
A:Accession: A28335
A:Molecule type: mRNA
A:Residues: 1-30, 74-226 <SA2>
A:Cross-references: GB:M14342
R:Shen, F.W.; Saga, Y.; Littman, G.; Freeman, G.; Tung, J.S.; Cantor, H.; Boyse, E.A.
Proc. Natl. Acad. Sci. U.S.A. 82, 7360-7363, 1985
A:Reference number: A23329; MUID:86042665; PMID:3864163
A:Accession: A23329
A:Molecule type: mRNA
A:Residues: 10-30,170-263 <SHE>
A:Cross-references: GB:M11934; NID:G198919; PIDN:AAA39461.1; PID:G198920
R:Saga, Y.; Tung, J.
Mol. Cell. Biol. 9, 4889-4895, 1988
A:Title: Organization of the Ly-5 Gene.
A:Reference number: I57644; MUID:89096862; PMID:3211131
A:Accession: I57644
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 'MT', 1-22 <RE2>
A:Cross-references: GB:M23354; NID:G340890; PIDN:AAA39462.1; PID:G554192
C:Genetics:
A:Gene: Ly-5
C:Superfamily: leukocyte common antigen; leukocyte common antigen cytosolic domain homolo
C:Keywords: alternative splicing; glycoprotein; phosphoprotein; phosphoric monoester hyd
F:1-23/Dominant: signal sequence #status predicted <SIG>
F:24-1291/Product: protein-tyrosine-phosphatase (B-cell variant) #status predicted <EXT>
F:24-564/Dominant: extracellular #status predicted <EXT>
F:24-30,170-1291/Product: protein-tyrosine-phosphatase (T-cell variant) #status predicted
F:565-586/Dominant: transmembrane #status predicted <TM>
F:583-1223/Dominant: leukocyte common antigen cytosolic domain homology <LAC>
F:587-1291/Dominant: intracellular #status predicted <INT>
F:664-888/Dominant: protein-tyrosine-phosphatase homology <PTP>
F:64,150,161,207,211,218,253,258,290,311,322,347,416,427,457,489,520,556/Binding site: ct
F:840/Active site: Cys (phosphocysteine intermediate) #status predicted
F:846/Binding site: substrate phosphate (Arg) #status predicted

Query Match      26.8%; Score 55.5; DB 1; Length 1291;
Best Local Similarity 40.5%; Pred. No. 1.1e+02;
Matches 15; Conservative 5; Mismatches 10; Indels 7; Gaps 2;

Oy      1 QNSGNQSFEDDPKPYEGCGNIVDIDFDSVPQIH 37
      ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      947 QHIGNQ-----ENKKK-NRNSNVVPDFNRVPLKH 976

RESULT 12
B83331
A:Title: 1,2-dioxygenase PA2507 [imported] - Pseudomonas aeruginosa (strain PAO1)
C:Species: Pseudomonas aeruginosa
C:Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004
C:Accession: B83331
R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Watterer, P.; Hickey, M.J.; Brj
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kass, A.; Lapidis, K.; Lim,
., Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A:Title: Complete genome sequence of Pseudomonas aeruginosa PAO1, an opportunistic pathog
A:Reference number: A82950; MUID:20437337; PMID:10984043
A:Accession: B83331
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-310 <STO>
A:Cross-references: UNIPROT:Q910X5; GB:AE004678; GB:AE004091; NID:G9948560; PIDN:AAG0589;
A:Experimental source: strain PAO1
C:Genetics:
A:Gene: catA; PA2507
C:Superfamily: catechol 1,2-dioxygenase

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Query Match 26.6%; Score 55; DB 2; Length 310;
 Best Local Similarity 32.1%; Pred. No. 24;
 Matches 9; Conservative 7; Mismatches 12; Indels 0; Gaps 0;

QY 4 GNQSFEDPPEEDPKPYEQGNVVDIDFD 31
 DB 260 GDLRFNDPDAARDRGVGGRAELDFD 287

RESULT 13

Legumin storage protein LeB6 - fava bean (fragment)
 C:Species: Vicia faba (fava bean)
 C:Date: 21-Nov-1993 #sequence_revision 26-Jul-1996 #text_change 09-Jul-2004

C:Accession: S07577
 R:Heim, U.; Schubert, R.; Baumelein, H.; Wobus, U.
 Plant Mol. Biol. 13, 653-663, 1989

A:Title: The legumin gene family: structure and evolutionary implications of Vicia faba
 A:Reference number: S07576; MUID:91370849; PMID:2491681
 A:Accession: S07577

A:Status: translation not shown
 A:Molecule type: DNA

A:Residues: 1-339 <HEI>
 A:Cross-references: UNIPROT:P16079; EMBL:X14240; NID:G22020; PIDN:CAA32456.1; PID:G29584
 C:Genetics:

A:Gene: LeB6
 A:Introns: 34/3; 204/3
 C:Superfamily: glycinin

C:Keywords: seed; storage protein

Query Match 26.6%; Score 55; DB 2; Length 329;
 Best Local Similarity 52.4%; Pred. No. 26;
 Matches 11; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

QY 4 GNQSFEDPPEEDPKPYEQGN 24
 DB 128 GQOEEREEERKORSEQGRN 148

RESULT 14

S07576
 Legumin storage protein LeB2 - fava bean (fragment)
 C:Species: Vicia faba (fava bean)

C:Date: 21-Nov-1993 #sequence_revision 26-May-1995 #text_change 09-Jul-2004
 C:Accession: S07576
 R:Heim, U.; Schubert, R.; Baumelein, H.; Wobus, U.
 Plant Mol. Biol. 13, 653-663, 1989

A:Title: The legumin gene family: structure and evolutionary implications of Vicia faba
 A:Reference number: S07576; MUID:91370849; PMID:2491681
 A:Accession: S07576

A:Status: translation not shown
 A:Molecule type: DNA

A:Residues: 1-335 <HEI>
 A:Cross-references: UNIPROT:P16078; EMBL:X14237; NID:G22013; PIDN:CAA32454.1; PID:G29584
 C:Genetics:

A:Gene: LeB2
 A:Introns: 34/3; 210/3
 C:Superfamily: glycinin

C:Keywords: seed; storage protein

Query Match 26.6%; Score 55; DB 2; Length 335;
 Best Local Similarity 52.4%; Pred. No. 27;
 Matches 11; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

QY 4 GNQSFEDPPEEDPKPYEQGN 24
 DB 134 GQOEEREEERKORSEQGRN 154

RESULT 15

T33906
 hypothetical protein Y25C1A.8 - Caenorhabditis elegans
 C:Species: Caenorhabditis elegans

C:Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
 C:Accession: T33906

R:Kallick, J.; Smith, A.; Gibson, A.
 submitted to the EMBL Data Library, February 1999
 A:Description: The sequence of C. elegans coemid Y25C1A.
 A:Reference number: Z21437

A:Accession: T33906
 A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA
 A:Residues: 1-345 <KAL>
 A:Cross-references: UNIPROT:Q9TYM0; EMBL:AF125459; PIDN:ADI2844.1; GSPDB:GN00020; CESP:)

A:Experimental source: strain Bristol N2; clone Y25C1A
 C:Genetics:

A:Gene: CESP:Y25C1A.8
 A:Map position: 2
 A:Introns: 45/1; 78/2; 140/3; 230/2; 304/2

Query Match 26.6%; Score 55; DB 2; Length 345;
 Best Local Similarity 34.3%; Pred. No. 27;
 Matches 12; Conservative 8; Mismatches 13; Indels 2; Gaps 1;

QY 4 GNQSFEDPPEEDPKPYEQGNVVDIDFDSPQI 36
 DB 170 GEDBADDDDEDDEDGDDGDKYKXNFDSDPEL 204

Search completed: October 22, 2005, 06:09:45
 Job time : 14.8905 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 22, 2005, 04:10:49 ; Search time 69.6361 Seconds
(without alignments)
279.439 Million cell updates/sec

Title: US-10-731-238-39
Perfect score: 207
Sequence: 1 ONSGNQSFEDPEEDPKRYEGCGNIVIDPDSVPQIHG 38

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues
Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	199	96.1	Q53682	Q53682 staphylococ
2	199	96.1	Q8NNU8	Q8NNU8 staphylococ
3	199	96.1	Q6G6H4	Q6G6H4 staphylococ
4	199	96.1	Q99RD3	Q99RD3 staphylococ
5	199	96.1	Q7A3J8	Q7A3J8 staphylococ
6	199	96.1	Q7A3J8	Q7A3J8 staphylococ
7	199	96.1	Q99RD2	Q99RD2 staphylococ
8	199	96.1	Q7A3J7	Q7A3J7 staphylococ
9	198	95.7	Q6GDU5	Q6GDU5 staphylococ
10	191	92.3	Q8NNU7	Q8NNU7 staphylococ
11	191	92.3	Q6G6H3	Q6G6H3 staphylococ
12	188	90.8	Q9AEP9	Q9AEP9 staphylococ
13	166	31.9	Q6BM10	Q6BM10 m mus muscu
14	61	29.5	Q8BG50	Q8BG50 m mus muscu
15	61	29.5	Q91LJ7	Q91LJ7 white spot
16	60.5	29.2	Q8OOG8	Q8OOG8 methanocarc
17	60	29.0	Q6FVK3	Q6FVK3 candida gla
18	60	29.0	Q6ZV47	Q6ZV47 oryza sativ
19	60	29.0	Q6ZV47	Q6ZV47 oryza sativ
20	59	28.5	PKD2_HUMAN	PKD2_HUMAN
21	59	28.5	Q6STR5	Q6STR5 manheimia
22	59	28.5	Q47942	Q47942 streptococ
23	59	28.5	Q6C206	Q6C206 yarrowia 11
24	59	28.5	Q6C206	Q6C206 yarrowia 11
25	58.5	28.3	Q6R891	Q6R891 mus muscu
26	58.5	28.3	Q6R891	Q6R891 mus muscu
27	58.5	28.3	Q8H8X6	Q8H8X6 oryza sativ
28	58	28.0	Q6W3C5	Q6W3C5 caenorhabdi
29	58	28.0	Q19931	Q19931 caenorhabdi
30	58	28.0	Q19931	Q19931 caenorhabdi
31	57.5	27.8	Q8VWH9	Q8VWH9 hordeum vul

32	57.5	27.8	666	1	PKD2_MOUSE	O35245 mus musculu
33	57.5	27.8	966	2	Q7TS17	Q7TS17 mus musculu
34	57.5	27.8	966	2	Q8BPR6	Q8BPR6 mus musculu
35	57.5	27.8	1791	2	Q81HX4	Q81HX4 plasmodium
36	57	27.5	237	2	Q8B2M9	Q8B2M9 mus musculu
37	57	27.5	455	2	Q6ZQ97	Q6ZQ97 mus musculu
38	57	27.5	500	2	Q9PJG9	Q9PJG9 chlamydia m
39	57	27.5	501	2	Q84575	Q84575 chlamydia t
40	57	27.5	532	2	Q9D074	Q9D074 m mus muscu
41	57	27.5	533	2	Q94677	Q94677 plasmodium
42	57	27.5	572	2	Q9GSR0	Q9GSR0 plasmodium
43	57	27.5	626	2	Q6D823	Q6D823 erwina car
44	57	27.5	698	2	Q71EB1	Q71EB1 hevea brasl
45	57	27.5	703	1	H583_IPOVI	P51819 ipomoea nil

ALIGNMENTS

RESULT 1	ID	Q53682	PRELIMINARY;	PRT;	940 AA.
AC	Q53682;				
DT	01-NOV-1996 (TREMBLrel. 01, Created)				
DT	01-NOV-1996 (TREMBLrel. 01, Last sequence update)				
DT	01-MAR-2004 (TREMBLrel. 26, Last annotation update)				
DE	Fibronectin binding protein B.				
GN	Name=fnbB;				
OS	Staphylococcus aureus.				
OC	Bacteria; Firmicutes; Bacillales; Staphylococcus.				
OX	NCBI_TaxID=1280;				
RN	(1)				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=8325-4;				
RX	MEDLINE=92111475; PubMed=1837266;				
RA	Jonsson K., Signas C., Muller H.P., Lindberg M.,				
RT	"Two different genes encode fibronectin binding proteins in				
RT	Staphylococcus aureus. The complete nucleotide sequence and				
RT	characterization of the second gene."				
RL	Eur. J. Biochem. 202:1041-1048(1991).				
CC	-1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by				
CC	an amide bond (By similarity).				
DR	EMBL: X62982; CAA44726.1; -				
DR	PIR: S19702; S19702.				
DR	HSSP: Q53653; IN67.				
DR	GO: GO:0009986; C:cell surface; IEA.				
DR	GO: GO:0005618; C:cell wall; IEA.				
DR	GO: GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.				
DR	GO: GO:0010200; C:membrane; IEA.				
DR	GO: GO:0007155; P:cell adhesion; IEA.				
DR	InterPro: IPR008966; Adhes_Bact.				
DR	InterPro: IPR004237; Fn_bind.				
DR	InterPro: IPR005877; Gpos_YSRK.				
DR	InterPro: IPR001899; Gram_pos_anchor.				
DR	Pfam: PF02986; Fn_bind_2.				
DR	Pfam: PF00746; Gram_pos_anchor; 1.				
DR	Pfam: PF04650; YSRK_signal; 1.				
DR	TIGRFAMS: TIGR01167; LPXTG_anchor; 1.				
DR	TIGRFAMS: TIGR01168; YSRK_signal; 1.				
DR	PROSITE: PS50847; GRAM_POS_ANCHORING; 1.				
KW	Cell wall; Peptidoglycan-anchor.				
SEQ	SEQUENCE 940 AA; 10355 MW; E35FBBCA907AE345 CRC64;				
Query Match	96.1%;	Score 199;	DB 2;	Length 940;	
Best local similarity	97.4%;	Pred. No. 8.9e-16;			
Matches 37;	Conservative 0;	Mismatches 1;	Indels 0;	Gaps 0;	
QY	1 ONSGNQSFEDPEEDPKRYEGCGNIVIDPDSVPQIHG 38				
DB	682 ONSGNQSFEDPEEDPKRYEGCGNIVIDPDSVPQIHG 719				
RESULT 2					

```
08NUT8
ID 08NUT8 PRELIMINARY; PRT: 943 AA.
AC 08NUT8;
DT 01-OCT-2002 (TREMBlrel. 22, Created)
DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Fimb protein.
GN Name=fimb; OrderedLocuNames=MS2420;
OS Staphylococcus aureus (strain MW2).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCB1_taxid=196620;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN:MW2;
RX MEDLINE=22040717; PubMed=12044378; DOI=10.1016/S0140-6736(02)08713-5;
RA Baba T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Oguchi A.,
RA Yamamoto K., Hiratsuku K.;
RT "Genome and virulence determinants of high virulence community-
acquired MRSA";
RL Lancet 359:1819-1827(2002)
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
an amide bond (By similarity).
DR EMBL: AP004830; BAB96285.1; -.
DR HSSP: Q53653; 1N67.
DR GO:00009986; C:cell surface; IEA.
DR GO:00005618; C:cell wall; IEA.
DR GO:00009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO:0016020; C:membrane; IEA.
DR GO:0007155; P:cell adhesion; IEA.
DR InterPro: IPR008966; Adhes_bact.
DR InterPro: IPR004237; Fn_bind.
DR InterPro: IPR005877; Gpos_YsIRK.
DR InterPro: IPR001899; Gram_pos_anchor.
DR Pfam: PF02986; Fn_bind.1.
DR Pfam: PF00746; Gram_pos_anchor.1.
DR TIGRFAMs: TIGR01167; LpXTG_anchor.1.
DR TIGRFAMs: TIGR01168; YsIRK_signal.1.
DR PROSITE: PS50847; GRAM_POS_ANCHORING.1.
KW Cell wall, Complete proteome; Peptidoglycan-anchor.
SQ SEQUENCE 943 AA; 104537 MW; DA8A5F31947E1B6A CRC64;

Query Match 96.1%; Score 199; DB 2; Length 943;
Best Local Similarity 97.4%; Pred. No. 8.9e-16;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 ONSGNQSFEDPEEDPKPYEGGNIIVDIDFDSVPQIHG 38
DB 689 ONSGNQSFEDPEEDPKPYEGGNIIVDIDFDSVPQIHG 726

RESULT 3
O6G6H4 PRELIMINARY; PRT: 957 AA.
AC O6G6H4;
DT 05-JUN-2004 (TREMBlrel. 27, Created)
DT 05-JUN-2004 (TREMBlrel. 27, Last sequence update)
DT 05-JUN-2004 (TREMBlrel. 27, Last annotation update)
DE Fibronectin-binding protein.
GN Name=fmbB; OrderedLocuNames=SSA2387;
OS Staphylococcus aureus (strain MSSA476).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCB1_taxid=282459;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN:M50 / ATCC 700699;
RX PubMed=15213324; DOI=10.1073/pnas.0402521101;
RA Holden M.T.G., Peil E.J., Lindsey J.A., Peacock S.J., Day N.P.J.,
RA Enright M.C., Foster T.J., Moore C.E., Hurst L., Atkin R., Barron A.,
RA Baeson N., Bentley S.D., Chillingworth C., Chillingworth T.,
RA Churcher C., Clark L., Cotton C., Cronin A., Doggett J., Dowd L.,
RA Feltwell T., Hance Z., Harris B., Hauser H., Holtroyd S., Jagsis K.,
RA James K.D., Lennard N., Line A., Mayes R., Moule S., Mungall K.,
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RA Ormond D., Quail M.A., Rabinowitsch E., Rutherford K.M., Sanders M.,
RA Sharp S., Simmonds M., Stevens K., Whitehead S., Barrell B.G.,
RA Spratt B.G., Parkhill J.;
RT "Complete genomes of two clinical Staphylococcus aureus strains:
RT evidence for the rapid evolution of virulence and drug resistance.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:9786-9791(2004).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
an amide bond (By similarity).
DR EMBL: BX571857; CAG44201.1; -.
DR GO:00009986; C:cell surface; IEA.
DR GO:00005618; C:cell wall; IEA.
DR GO:00009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO:0016020; C:membrane; IEA.
DR GO:0007155; P:cell adhesion; IEA.
DR InterPro: IPR008966; Adhes_bact.
DR InterPro: IPR004237; Fn_bind.
DR InterPro: IPR005877; Gpos_YsIRK.
DR InterPro: IPR001899; Gram_pos_anchor.
DR Pfam: PF00746; Gram_pos_anchor.1.
DR Pfam: PF02986; Fn_bind.1.
DR TIGRFAMs: TIGR01167; LpXTG_anchor.1.
DR TIGRFAMs: TIGR01168; YsIRK_signal.1.
DR PROSITE: PS50847; GRAM_POS_ANCHORING.1.
KW Cell wall, Complete proteome; Peptidoglycan-anchor.
SQ SEQUENCE 957 AA; 105980 MW; 28F8BA7FFD3EAF CRC64;

Query Match 96.1%; Score 199; DB 2; Length 957;
Best Local Similarity 97.4%; Pred. No. 9e-16;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 ONSGNQSFEDPEEDPKPYEGGNIIVDIDFDSVPQIHG 38
DB 689 ONSGNQSFEDPEEDPKPYEGGNIIVDIDFDSVPQIHG 726

RESULT 4
O99RD3 PRELIMINARY; PRT: 961 AA.
AC O99RD3;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE Fibronectin-binding protein homolog.
GN Name=fmbB; OrderedLocuNames=SAV2502;
OS Staphylococcus aureus (strain M50 / ATCC 700699).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCB1_taxid=158878;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN:M50 / ATCC 700699;
RX MEDLINE=21311952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2;
RA Kuroda M., Onota T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Iian Y.-Q., Ito T.,
RA Mizumori M., Matsumaru H., Maruyama A., Murakami H., Hoshiyama A.,
RA Kitazumi Y., Takahashi N.K., Sawano T., Inoue R.-I., Kato C.,
RA Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
RA Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
RA Hattori M., Ogasawara N., Hayashi H., Hiratsuku K.;
RT "Whole genome sequencing of methicillin-resistant Staphylococcus
aureus.";
RL Lancet 357:1225-1240(2001).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
an amide bond (By similarity).
DR EMBL: AP003365; BAB58664.1; -.
DR PIR: G90053; G90053.
DR HSSP: Q53653; 1N67.
DR GO:00009986; C:cell surface; IEA.
DR GO:00005618; C:cell wall; IEA.
DR GO:00009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO:0016020; C:membrane; IEA.
DR GO:0007155; P:cell adhesion; IEA.
DR InterPro: IPR008966; Adhes_bact.
```

DR InterPro; IPR004237; Fn_bind.
 DR InterPro; IPR005877; Gpos_YsIRK.
 DR InterPro; IPR001899; Gram_pos_anchor.
 DR Pfam; PF02986; Fn_bind; 1.
 DR Pfam; PF00746; Gram_pos_anchor; 1.
 DR Pfam; PF04650; YsIRK_signal; 1.
 DR TIGRfams; TIGR01167; LPXTG_anchor; 1.
 DR TIGRfams; TIGR01168; YsIRK_signal; 1.
 DR PROSITE; PS50847; GRAM_POS_ANCHORING; 1.
 DR Cell wall; Complete proteome; Peptidoglycan-anchor.
 KW SEQUENCE 961 AA; 106010 MW; 364940F884EA4101 CRC64;
 SQ

Query Match 96.1%; Score 199; DB 2; Length 961;
 Best Local Similarity 97.4%; Pred. No. 9.1e-16;
 Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

1 QNSGNQSFEDPDEBKPKYEGGNIVIDIDFDSVPQIHG 38
 DB 693 QNSGNQSFEDPDEBKPKYEGGNIVIDIDFDSVPQIHG 730

RESULT 5
 ID Q7A3J8 PRELIMINARY; PRT; 961 AA.
 AC Q7A3J8;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Fnb protein.
 GN Name=fnb; OrderedLocustNames=SA2299;
 OS Staphylococcus aureus (strain N315).
 CC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 OC NCBI_TaxID=158879;
 RN [1]

SEQUENCE FROM N.A.
 MEDLINE=2111952; PubMed=1118146; DOI=10.1016/S0140-6736(00)04403-2;
 RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
 RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Iian J.-Q., Ito T.,
 RA Kanamori M., Matsunari H., Maruyama A., Murakami H., Hoshoyama A.,
 RA Mizutani-U Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
 RA Sekizawa K., Hirakawa H., Kohara S., Goto S., Yabuuchi J.,
 RA Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
 RA Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
 RT "Whole genome sequencing of methicillin-resistant Staphylococcus
 aureus";
 RL Lancet 357;1225-1240(2001).
 CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
 an amide bond (By similarity).
 CC EMBL; APO03137; BAB43593.1; -;
 DR GO; GO:0009986; C:cell surface; IEA.
 DR GO; GO:0005618; C:cell wall; IEA.
 DR GO; GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0007155; P:cell adhesion; IEA.
 DR InterPro; IPR008966; Adhes_Dact.
 DR InterPro; IPR004237; Fn_bind.
 DR InterPro; IPR005877; Gpos_YsIRK.
 DR InterPro; IPR001899; Gram_pos_anchor.
 DR Pfam; PF02986; Fn_bind; 1.
 DR Pfam; PF00746; Gram_pos_anchor; 1.
 DR Pfam; PF04650; YsIRK_signal; 1.
 DR TIGRfams; TIGR01167; LPXTG_anchor; 1.
 DR TIGRfams; TIGR01168; YsIRK_signal; 1.
 DR PROSITE; PS50847; GRAM_POS_ANCHORING; 1.
 KW Cell wall; Complete proteome; Peptidoglycan-anchor.
 SQ SEQUENCE 961 AA; 106010 MW; 364940F884EA4101 CRC64;
 QY

DB 693 QNSGNQSFEDPDEBKPKYEGGNIVIDIDFDSVPQIHG 730

RESULT 6
 FNBA STAAU STANDARD; PRT; 1018 AA.
 ID FNBA STAAU
 AC P14738;
 DT 01-APR-1990 (Rel. 14, Created)
 DT 01-APR-1990 (Rel. 14, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Fibronectin-binding protein precursor (FNBp).
 GN Name=fnbA;
 OS Staphylococcus aureus.
 CC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 OC NCBI_TaxID=1280;
 RN [1]

SEQUENCE FROM N.A.
 RP STRAIN=NCIC 8325-4;
 RC MEDLINE=89098998; PubMed=2521391;
 RA Signaes C., Raucsi G., Joensson K., Lindgren P.-E.,
 RA Anantharamaiah G.M., Hoeoek M., Lindberg M.;
 RT "Nucleotide sequence of the gene for a fibronectin-binding protein
 from Staphylococcus aureus: use of this peptide sequence in the
 synthesis of biologically active peptides";
 RT Proc. Natl. Acad. Sci. U.S.A. 86:699-703(1989).
 RL

-1- FUNCTION: The ability of bacteria to bind fibronectin has been
 proposed as a virulence factor enabling bacteria to colonize wound
 tissues and blood clots. Binding of plasma fibronectin to the
 bacterial surface might block adhesion receptors on S.aureus, thus
 representing an important defense mechanism against tissue
 invasion.
 CC

-1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
 an amide bond (Potential).
 CC

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 or send an email to license@isb-sib.ch).
 CC

DR EMBL; J04151; AAA26632.1; -;
 DR InterPro; IPR004237; Fn_bind.
 DR InterPro; IPR005877; Gpos_YsIRK.
 DR InterPro; IPR001899; Gram_pos_anchor.
 DR Pfam; PF02986; Fn_bind; 1.
 DR Pfam; PF00746; Gram_pos_anchor; 1.
 DR Pfam; PF04650; YsIRK_signal; 1.
 DR TIGRfams; TIGR01167; LPXTG_anchor; 1.
 DR TIGRfams; TIGR01168; YsIRK_signal; 1.
 DR PROSITE; PS50847; GRAM_POS_ANCHORING; 1.
 KW Cell adhesion; Cell wall; Peptidoglycan-anchor; Repeat; Signal;
 VM Virulence.
 FT SIGNA 1 36
 FT CHAIN 37 985
 FT PROPEP 986 1018
 FT REPEAT 545 574
 FT REPEAT 575 604
 FT DOMAIN 745 878
 FT REPEAT 745 782
 FT REPEAT 783 820
 FT REPEAT 821 859
 FT REPEAT 860 878
 FT DOMAIN 879 948
 FT REPEAT 879 882
 FT REPEAT 893 906
 FT REPEAT 907 920
 FT REPEAT 921 934
 FT REPEAT 935 948
 FT SITE 982 986
 FT MOD_RES 985 985

Fibronectin-binding protein.
 Removed by sortase (Potential).
 B-1.
 B-2.
 4 X approximate tandem repeats,
 fibronectin-binding domain.
 D-1.
 D-2.
 D-3.
 D-4 (incomplete).
 5 X tandem repeats, Pro-rich (WR).
 WR 1.
 WR 2.
 WR 3.
 WR 4.
 WR 5.
 LPXTG sorting signal (Potential).
 Pentaglycyl murein peptidoglycan amidated


```

FT      chreonine (Potential).
SQ      SEQUENCE      1018 AA;      111780 MW;      58175E0020E81F1F CRC64;
Query Match
Best Local Similarity      96.1%;      Score 199;      DB 1;      Length 1018;
Matches      37;      Conservative      0;      Mismatches      1;      Indels      0;      Gaps      0;

QY      1  QNSGNQSFEEDEPDKPKRYEGGNIIVDIDFDSVPQIHG 38
DB      746  QNSGNQSFEEDEPDKPKRYEGGNIIVDIDFDSVPQIHG 783

RESULT 7
ID      Q99RD2      PRELIMINARY;      PRT;      1038 AA.
AC      Q99RD2;
DT      01-JUN-2001 (TReMBLrel. 17, Created)
DT      01-JUN-2001 (TReMBLrel. 17, Last sequence update)
DT      01-MAR-2004 (TReMBLrel. 26, Last annotation update)
DE      Fibronectin-binding protein homolog.
GN      Name=fnb; OrderedLocuNames=SAV2503;
OS      Staphylococcus aureus (strain Mu50 / ATCC 700699).
OC      Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX      NCBI_TaxId=158878;
RN
RP      SEQUENCE FROM N.A.
RC      STRAIN=Mu50 / ATCC 700699;
RX      MEDLINE=21311952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2;
RA      Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
RA      Cui L., Oguchi A., Aoki K.-I., Nagai Y., Iian J.-Q., Ito T.,
RA      Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hasegawa A.,
RA      Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaiko C.,
RA      Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
RA      Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
RA      Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
RT      "Whole genome sequencing of methicillin-resistant Staphylococcus
RT      aureus.";
RL      Lancel 357:1225-1240(2001).
CC      -I- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC      an amide bond (by similarity).
EMBL; AP003137; BAB58665.1; -.
DR      GO: GO:0009986; C:cell surface; IEA.
DR      GO: GO:0005618; C:cell wall; IEA.
DR      GO: GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR      GO: GO:0016020; C:membrane; IEA.
DR      GO: GO:007155; P:cell adhesion; IEA.
DR      InterPro: IPR008966; Adhes_bact.
DR      InterPro: IPR004237; Fn_bind.
DR      InterPro: IPR005877; Gpos_YsIRK.
DR      InterPro: IPR001899; Gram_pos_anchor.
DR      Pfam; PF02986; Fn_bind.1.
DR      Pfam; PF00746; Gram_pos_anchor.1.
DR      Pfam; PF04650; YsIRK_signal.1.
DR      TIGRFAMs; TIGR01167; LpxTG_anchor.1.
DR      TIGRFAMs; TIGR01168; YsIRK_signal.1.
DR      PROSITE; PS50847; GRAM_POS_ANCHORING.1.
KW      Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ      SEQUENCE      1038 AA;      113618 MW;      666BF6BF2FBBB12 CRC64;

Query Match
Best Local Similarity      96.1%;      Score 199;      DB 2;      Length 1038;
Matches      37;      Conservative      0;      Mismatches      1;      Indels      0;      Gaps      0;

QY      1  QNSGNQSFEEDEPDKPKRYEGGNIIVDIDFDSVPQIHG 38
DB      742  QNSGNQSFEEDEPDKPKRYEGGNIIVDIDFDSVPQIHG 779

RESULT 8
ID      Q7A3J7      PRELIMINARY;      PRT;      1038 AA.
AC      Q7A3J7;

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DT      05-JUL-2004 (TReMBLrel. 27, Created)
DT      05-JUL-2004 (TReMBLrel. 27, Last sequence update)
DT      05-JUL-2004 (TReMBLrel. 27, Last annotation update)
DE      Fnb protein.
GN      Name=fnb; OrderedLocuNames=SA2291;
OS      Staphylococcus aureus (strain N315).
OC      Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX      NCBI_TaxId=158879;
RN
RP      SEQUENCE FROM N.A.
RC      MEDLINE=21311952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2;
RA      Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
RA      Cui L., Oguchi A., Aoki K.-I., Nagai Y., Iian J.-Q., Ito T.,
RA      Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hasegawa A.,
RA      Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaiko C.,
RA      Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
RA      Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
RA      Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
RT      "Whole genome sequencing of methicillin-resistant Staphylococcus
RT      aureus.";
RL      Lancel 357:1225-1240(2001).
CC      -I- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC      an amide bond (by similarity).
EMBL; AP003137; BAB43594.1; -.
DR      GO: GO:0009986; C:cell surface; IEA.
DR      GO: GO:0005618; C:cell wall; IEA.
DR      GO: GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR      GO: GO:0016020; C:membrane; IEA.
DR      GO: GO:007155; P:cell adhesion; IEA.
DR      InterPro: IPR008966; Adhes_bact.
DR      InterPro: IPR004237; Fn_bind.
DR      InterPro: IPR005877; Gpos_YsIRK.
DR      InterPro: IPR001899; Gram_pos_anchor.
DR      Pfam; PF02986; Fn_bind.1.
DR      Pfam; PF00746; Gram_pos_anchor.1.
DR      Pfam; PF04650; YsIRK_signal.1.
DR      TIGRFAMs; TIGR01167; LpxTG_anchor.1.
DR      TIGRFAMs; TIGR01168; YsIRK_signal.1.
DR      PROSITE; PS50847; GRAM_POS_ANCHORING.1.
KW      Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ      SEQUENCE      1038 AA;      113618 MW;      666BF6BF2FBBB12 CRC64;

Query Match
Best Local Similarity      96.1%;      Score 199;      DB 2;      Length 1038;
Matches      37;      Conservative      0;      Mismatches      1;      Indels      0;      Gaps      0;

QY      1  QNSGNQSFEEDEPDKPKRYEGGNIIVDIDFDSVPQIHG 38
DB      742  QNSGNQSFEEDEPDKPKRYEGGNIIVDIDFDSVPQIHG 779

RESULT 9
ID      Q6GDUS      PRELIMINARY;      PRT;      965 AA.
AC      Q6GDUS;
DT      05-JUL-2004 (TReMBLrel. 27, Created)
DT      05-JUL-2004 (TReMBLrel. 27, Last sequence update)
DT      05-JUL-2004 (TReMBLrel. 27, Last annotation update)
DE      Fibronectin-binding protein.
GN      Name=fnbA; OrderedLocuNames=SA2580;
OS      Staphylococcus aureus (strain MRSA252).
OC      Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX      NCBI_TaxId=282458;
RN
RP      SEQUENCE FROM N.A.
RC      PubMed=15213324; DOI=10.1073/pnae.040252101;
RA      Holden M.T.G., Fell E.J., Lindsey J.A., Peacock S.J., Day N.P.J.,
RA      Enright M.C., Foster T.J., Moore C.E., Hurst L., Atkin R., Barron A.,
RA      Bacon N., Bentley S.D., Chillingworth C., Chillingworth T.,
RA      Churcher C., Clark L., Cotton C., Cronin A., Doggett J., Dowd L.,
RA      Feltham T., Hance Z., Harris B., Hauser H., Holtroyd S., Jørgels K.,
RA      James K.D., Lennard N., Line A., Mayes R., Moule S., Mungall K.,
RA      Ormond D., Quail M.A., Rabinowitsch E., Rutherford K.M., Sanders M.,

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RA Sharp S., Simmonds M., Stevens K., Whitehead S., Barrell B.G.,
 RA Spratt B.G., Parkhill J.;
 RT "Complete genomes of two clinical *Staphylococcus aureus* strains:
 RL Proc. Natl. Acad. Sci. U.S.A. 101:9786-9791(2004)
 CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
 an amide bond (by similarity).
 DR EMBL: BX571856; CAG41560.1; -;
 DR GO: GO:0009986; C:cell surface; IEA.
 DR GO: GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
 DR GO: GO:0016020; C:membrane; IEA.
 DR GO: GO:007155; P:cell adhesion; IEA.
 DR InterPro: IPR008966; Adhes_bact.
 DR InterPro: IPR004237; Fn_bind.
 DR InterPro: IPR005877; Gpos_YsIRK.
 DR InterPro: IPR001899; Gram_pos_anchor.
 DR Pfam: PF02986; Fn_bind; 1.
 DR Pfam: PF00746; Gram_pos_anchor; 1.
 DR Pfam: PF04650; YsIRK_signal; 1.
 DR TIGRFAMs: TIGR01167; LPXTG_anchor; 1.
 DR TIGRFAMs: TIGR01168; YsIRK_signal; 1.
 DR PROSITE: PS0847; GRAM_POS_ANCHORING; 1.
 KW Cell wall; Complete proteome; Peptidoglycan-anchor.
 OC Staphylococcus aureus (strain MSSA476).
 SQ SEQUENCE 965 AA; 105691 MW; 2982E132164D0551 CRC64;

Query Match 95.7%; Score 198; DB 2; Length 965;
 Best Local Similarity 94.7%; Pred. No. 1,2e-15;
 Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Oy 1 QNSGNQSFEDPEEDKPKYEQGNIIVDIDFDSVPQIHG 38
 Db 749 QNSGNQSFEDPEEDKPKYEQGNIIVDIDFDSVPQIHG 786

RESULT 10
 Q8NUU7 PRELIMINARY; PRT; 1015 AA.
 AC Q8NUU7;
 DT 01-OCT-2002 (TREMBLrel. 22, Created)
 DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update)
 DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
 DE Fnb protein.
 GN Name=fnb; OrderedlocusNames=MW2421;
 OS Staphylococcus aureus (strain MW2).
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 NCBI_TaxId=196620;
 RX MEDLINE=22040717; PubMed=12044378; DOI=10.1016/S0140-6736(02)08713-5;
 RA Babu T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Oguni A.,
 RA Nagai Y., Iwama N., Asano K., Naimi T., Kuroda H., Cui L.,
 RA Yamamoto K., Hiratake K.;
 RT "Genome and virulence determinants of high virulence community-
 RT acquired MRSA";
 RL Lancet 359:1819-1827(2002).
 CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
 an amide bond (by similarity).
 DR EMBL: AF004830; BAB96286.1; -;
 DR GO: GO:0009986; C:cell surface; IEA.
 DR GO: GO:0005618; C:cell wall; IEA.
 DR GO: GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
 DR GO: GO:0016020; C:membrane; IEA.
 DR GO: GO:007155; P:cell adhesion; IEA.
 DR InterPro: IPR008966; Adhes_bact.
 DR InterPro: IPR004237; Fn_bind.
 DR InterPro: IPR005877; Gpos_YsIRK.
 DR InterPro: IPR001899; Gram_pos_anchor.
 DR Pfam: PF02986; Fn_bind; 1.
 DR Pfam: PF00746; Gram_pos_anchor; 1.
 DR Pfam: PF04650; YsIRK_signal; 1.
 DR TIGRFAMs: TIGR01167; LPXTG_anchor; 1.
 DR TIGRFAMs: TIGR01168; YsIRK_signal; 1.

DR PROSITE: PS50847; GRAM_POS_ANCHORING; 1.
 KW Cell wall; Complete proteome; Peptidoglycan-anchor.
 SQ SEQUENCE 1015 AA; 111145 MW; D0F9281BB64D44D2 CRC64;

Query Match 92.3%; Score 191; DB 2; Length 1015;
 Best Local Similarity 94.7%; Pred. No. 9.5e-15;
 Matches 36; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 1 QNSGNQSFEDPEEDKPKYEQGNIIVDIDFDSVPQIHG 38
 Db 747 QNSGNQSFEDPEEDKPKYEQGNIIVDIDFDSVPQIHG 784

RESULT 11
 Q6G6H3 PRELIMINARY; PRT; 1015 AA.
 AC Q6G6H3;
 DT 05-JUL-2004 (TREMBLrel. 27, Created)
 DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
 DE Fibronectin-binding protein.
 GN OrderedlocusNames=SA52388;
 OS Staphylococcus aureus (strain MSSA476).
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 NCBI_TaxId=282459;
 RX PubMed=15213324; DOI=10.1073/pnas.0402521101;
 RA Holden M.T.G., Fell E.J., Lindsay J.A., Peacock S.J., Day N.P.J.,
 RA Enright M.C., Foster T.J., Moore C.E., Hurst E., Atkin R., Barron A.,
 RA Baeson N., Bentley S.D., Chillingworth C., Chillingworth T.,
 RA Churcher C., Clark L., Cotton C., Cronin A., Doggett J., Dowd L.,
 RA Feltham T., Hance Z., Harris B., Hauser H., Holtroyd S., Jørgensen K.,
 RA James K.D., Leonard N., Line A., Mayes R., Moutie S., Mungall K.,
 RA Ormond D., Quail M.A., Rabinowitch E., Rutherford K.M., Sanders M.,
 RA Sharp S., Simmonds M., Stevens K., Whitehead S., Barrell B.G.,
 RA Spratt B.G., Parkhill J.;
 RT "Complete genomes of two clinical *Staphylococcus aureus* strains:
 RT evidence for the rapid evolution of virulence and drug resistance.";
 RL Proc. Natl. Acad. Sci. U.S.A. 101:9786-9791(2004).
 CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
 an amide bond (by similarity).
 DR EMBL: BX571857; CAG4202.1; -;
 DR GO: GO:0009986; C:cell surface; IEA.
 DR GO: GO:0005618; C:cell wall; IEA.
 DR GO: GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
 DR GO: GO:0016020; C:membrane; IEA.
 DR GO: GO:007155; P:cell adhesion; IEA.
 DR InterPro: IPR008966; Adhes_bact.
 DR InterPro: IPR004237; Fn_bind.
 DR InterPro: IPR005877; Gpos_YsIRK.
 DR InterPro: IPR001899; Gram_pos_anchor.
 DR Pfam: PF02986; Fn_bind; 1.
 DR Pfam: PF00746; Gram_pos_anchor; 1.
 DR Pfam: PF04650; YsIRK_signal; 1.
 DR TIGRFAMs: TIGR01167; LPXTG_anchor; 1.
 DR TIGRFAMs: TIGR01168; YsIRK_signal; 1.
 DR PROSITE: PS50847; GRAM_POS_ANCHORING; 1.
 KW Cell wall; Complete proteome; Peptidoglycan-anchor.
 SQ SEQUENCE 1015 AA; 111145 MW; D0F9281BB64D44D2 CRC64;

Query Match 92.3%; Score 191; DB 2; Length 1015;
 Best Local Similarity 94.7%; Pred. No. 9.5e-15;
 Matches 36; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 1 QNSGNQSFEDPEEDKPKYEQGNIIVDIDFDSVPQIHG 38
 Db 747 QNSGNQSFEDPEEDKPKYEQGNIIVDIDFDSVPQIHG 784

RESULT 12
 Q9AEP9 PRELIMINARY; PRT; 152 AA.
 ID Q9AEP9

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AC Q9AEP9;
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Fibronectin-binding protein (Fragment).
GN Name=fnb;
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
NCBI_TaxID=1280;
RN STRAIN=CMSA-1;
RP SEQUENCE FROM N.A.
RX MEDLINE=21246681; PubMed=11349044;
DOI=10.1128/IAI.69.6.3791-3799.2001;
RA Rice K., Huebner M., Vaz D., McGavin M.J.;
RT "Variance in fibronectin binding and fnb locus polymorphisms in
RT Staphylococcus aureus: identification of antigenic variation in a
RT fibronectin binding protein adhesin of the epidemic CMSA-1 strain of
RT methicillin-resistant S. aureus.";
RL Infect. Immun. 69:3791-3799(2001).
DR EMBL; AY029184; AACJ1588.1; -.
FT NON TER 1 152
FT SEQUENCE 152 AA; 17193 MW; CFA3913C2B11C025 CRC64;
SQ SEQUENCE 152 AA; 17193 MW; CFA3913C2B11C025 CRC64;

Query Match 90.8%; Score 188; DB 2; Length 152;
Best Local Similarity 92.1%; Pred. No. 2,4e-15;
Matches 35; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Cy 1 QNSGNQSFEDPEEDKPKYEGCGNIVDIDFDSVPQIHG 38
Db 1 QNTGNSFEEDTEEDKPKYEGCGNIVDIDFDSVPQIQG 38

RESULT 13
O6BM10 PRELIMINARY; PRT; 937 AA.
AC Q6BM10;
DT 25-OCT-2004 (TREMBLrel. 28, Created)
DT 25-OCT-2004 (TREMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TREMBLrel. 28, Last annotation update)
DE Similar to CA4347|IPF3636 Candida albicans IPF3636.
GN ORNames=DEHA0F058089;
OS Debaryomyces hansenii CBS767.
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Debaryomyces.
NCBI_TaxID=284592;
RN [1]
RP SEQUENCE FROM N.A.
RL STRAIN=CBS767;
RG Genolevures;
RA Dujon B., Sherman D., Fischer G., Durrens P., Casaregola S.,
RA Lafontaine I., de Montigny J., Marck C., Neuveglise C., Talla E.,
RA Goffard N., Frangeul L., Aigle M., Anhouard V., Babour A., Barde V.,
RA Barnay S., Blanchin S., Beckerich J.M., Beyne B., Bleykasten C.,
RA Boisarane A., Boyer J., Catolico L., Contamoli F., de Darvar A.,
RA Despons L., Fabre E., Fairhead C., Ferry-Dunazet H., Groppi A.,
RA Hantreya F., Hennequin C., Jauniaux N., Joyet P., Kachouri R.,
RA Kerrest A., Koszul R., Lemaire M., Lesur I., Ma L., Muller H.,
RA Niclaud J.M., Nikolski M., Oztas S., Ozier-Kalogeropoulos O.,
RA Pellens S., Potter S., Richard G.F., Straub M.L., Sulaeu A.,
RA Swemene D., Tekala F., Wesolowski-Louvel M., Westhof E., Wirth B.,
RA Zenlou-Meyer M., Zivanovic I., Bolotin-Fukuhara M., Thierry A.,
RA Bouchier C., Caubon B., Scarpelli C., Galliard C., Weissenbach J.,
RA Wincker P., Souciet J.L.;
RT "Genome evolution in yeasts.";
RL Nature 430:35-44(2004).
RN [2]
RP SEQUENCE FROM N.A.
RL STRAIN=CBS767;
RA Genoscope;
RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; CR382138; CAG88916.1; -.

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DR GO:0005634; C:nucleus; IEA.
DR GO:0003684; F:damaged DNA binding; IEA.
DR GO:0006289; P:nucleotide-excision repair; IEA.
DR InterPro; IPR004583; Rad4.
DR Pfam; PF03835; Rad4; 1.
SQ SEQUENCE 937 AA; 107136 MW; 1DC3E795681B9BF7 CRC64;

Query Match 31.9%; Score 66; DB 2; Length 937;
Best Local Similarity 35.0%; Pred. No. 26;
Matches 14; Conservative 9; Mismatches 13; Indels 4; Gaps 2;

Cy 1 QNSGNQSFEDPEEDKPKYEG--GNIIVDIDFDSVPQIH 37
Db 772 EESGCGFVEDPEDE-AKYSQARIGGPLINVELDMDPDY 810

RESULT 14
O8BG50 PRELIMINARY; PRT; 297 AA.
AC O8BG50;
DT 01-MAR-2003 (TREMBLrel. 23, Created)
DT 01-MAR-2003 (TREMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TREMBLrel. 28, Last annotation update)
DE Mus musculus 12 days embryo embryonic body between diaphragm region
DE and neck cDNA, RIKEN full-length enriched library, clone:943063P18
DE product:hypothetical protein, full insert sequence (Mus musculus 10
DE days neonate cortex cDNA, RIKEN full-length enriched library,
DE clone:A830020B06 product:hypothetical protein, full insert
DE sequence).
GN Name=A830020B06R1k;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RL STRAIN=C57BL/6J;
RC TISSUE=Cortex, and Embryonic body between diaphragm region and neck;
RX MEDLINE=99279253; PubMed=10349635; DOI=10.1016/S0876-6879(99)03004-9;
RA Carinici P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Mech. Enzymol. 303:19-44(1999).
RN [2]
RP SEQUENCE FROM N.A.
RL STRAIN=C57BL/6J;
RC TISSUE=Cortex, and Embryonic body between diaphragm region and neck;
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA RIKEN PANTOM Consortium;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
RN [3]
RP SEQUENCE FROM N.A.
RL STRAIN=C57BL/6J;
RC TISSUE=Cortex, and Embryonic body between diaphragm region and neck;
RA The FANTOM Consortium,
RA The RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
RN [4]
RP SEQUENCE FROM N.A.
RL STRAIN=C57BL/6J;
RC TISSUE=Cortex, and Embryonic body between diaphragm region and neck;
RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carinici P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Kanno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630(2000).
RN [5]
RP SEQUENCE FROM N.A.
RL STRAIN=C57BL/6J;
RC TISSUE=Cortex, and Embryonic body between diaphragm region and neck;

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RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shihata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA Komno H., Akiyama J., Nishi K., Kitsuai T., Tashiro H., Itoh M.,
RA Suni N., Ishii Y., Nakamura S., Hazama M., Nishie T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watanishi M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.,
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771(2000).
RN [6]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J;
RC TISSUE=Cortex, and Embryonic body between diaphragm region and neck;
RA Adechi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
RA Katoh H., Kawai J., Kojima Y., Kondo S., Komno H., Koya S.,
RA Kurihara C., Matuyama T., Miyazaki A., Murata M., Nakamura M.,
RA Nihei K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
RA Sasaki D., Shihata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
RA Tagawa A., Takahashi F., Takaku-Akashira S., Takeda Y., Tanaka T.,
RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.,
RL Submitted (JUL-2001) to the EMBL/Genbank/DBJ databases.
DR EMBL; AK034935; BAC28886.1; -
DR EMBL; AK034681; BAC31618.1; -
DR MGD; MGI:2442781; A83020B06Rik.
KW Hypothetical protein.
SQ SEQUENCE 297 AA; 33424 MW; C758198DB0AB34A7 CRC64;

Query Match 29.5%; Score 61; DB 2; Length 297;
Best Local Similarity 39.4%; Pred. No. 28;
Matches 13; Conservative 7; Mismatches 9; Indels 4; Gaps 1;

QY 3 SGNQSFEDPEE---DKPKYEGGNIIVIDFD 31
DB 57 SDNEKTDPEEBSGGDRPKREBEGDFLDYPCD 89

RESULT 15
ID Q91LJ7 PRELIMINARY; PRT; 981 AA.
AC Q91LJ7;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE ORF43 (W6045) (WSSV102).
OS White spot syndrome virus (WSSV).
OC Viruses; dsDNA viruses, no RNA stage; Nimaviridae; Whispovirus.
OX NCBI_TaxID=92652;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21342572; PubMed=11448154; DOI=10.1006/viro.2001.1002;
RA van Hulten M.C.M., Witteveldt J., Peters S., Kloosterboer N.,
RA Tarchini R., Fiers W., Sandbriek H., Lankhorst R.K., Vlak J.M.;
RT "The white spot syndrome virus DNA genome sequence.";
RL Virology 286:7-22(2001).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=21548311; PubMed=11689662;
DOI=10.1128/JVI.75.23.11811-11820.2001;
RA Yang F., He J., Lin X., Li Q., Pan D., Zhang X., Xu X.;
RT "Complete genome sequence of the shrimp white spot bacilliform
RT virus.";
RL J. Virol. 75:11811-11820(2001).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=20517548; PubMed=11062040; DOI=10.1006/viro.2000.0597;
RA Teal M.F., Yu H.T., Tzeng H.F., Leu J.H., Chou C.M., Huang C.J.,
RA Wang C.H., Lin J.Y., Kou G.H., Lo C.F.;

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RT "Identification and characterization of a shrimp white spot syndrome
RT virus (WSSV) gene that encodes a novel chimeric polypeptide of
RT cellular-type thymidine kinase and thymidylate kinase.";
RL Virology 277:100-110(2000).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=21844071; PubMed=11853398; DOI=10.1006/viro.2001.1273;
RA Chen L.L., Leu J.H., Huang C.J., Chou C.M., Chen S.M., Wang C.H.,
RA Lo C.F., Kou G.H.;
RT "Identification of a nucleocapsid protein (VP35) gene of shrimp white
RT spot syndrome virus and characterization of the motif important for
RT targeting VP35 to the nuclei of transfected insect cells.";
RL Virology 293:44-53(2002).
RN [5]
RP SEQUENCE FROM N.A.
RA Lo C.-F., Kou G.-H.;
RL Submitted (OCT-2001) to the EMBL/Genbank/DBJ databases.
DR EMBL; AF369029; AAK77712.1; -
DR EMBL; AF320923; AAL33048.1; -
DR EMBL; AF440570; AAL88970.1; -
SQ SEQUENCE 981 AA; 109321 MW; 2422D60A24C61A72 CRC64;

Query Match 29.5%; Score 61; DB 2; Length 981;
Best Local Similarity 34.5%; Pred. No. 1.2e+02;
Matches 10; Conservative 9; Mismatches 10; Indels 0; Gaps 0;

QY 1 QNSGNQSFEDPEEDPKPKYEGGNIIVID 29
DB 286 ENGHEHMTSBEEDDEYEBGGCLSDID 314

Search completed: October 22, 2005, 06:05:55
Job time : 71.6361 secs

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CC streptococci, e.g. meningitis, otitis media, pneumonia, endocarditis,
CC mastitis in cattle, abortion in horses and many others. Since the
CC antibodies block binding of bacteria, they should be effective against
CC antibiotic-resistant strains, and may replace antibiotic therapy or
CC increase its effectiveness. Sequences AAW6561-700 represent a series of
CC synthetic peptides based on the D1 region of S. aureus fibronectin
CC binding protein A. They were synthesised to contain mutations
XX
SQ Sequence 38 AA;
Query Match 100.0%; Score 207; DB 2; Length 38;
Best Local Similarity 100.0%; Pred. No. 1e-20;
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 QNSGNQSFEDTPEDKPKYEGGNIIVDIDFDSVPQIHG 38
DQ 1 QNSGNQSFEDTPEDKPKYEGGNIIVDIDFDSVPQIHG 38
RESULT 2
AAW65661
ID AAW65661 standard; peptide; 38 AA.
XX
AC AAW65661;
XX
DT 16-OCT-1998 (first entry)
XX
DE Fibronectin binding protein-derived peptide #5.
XX
KW microbial surface components recognising adhesive matrix molecule;
KW MSCRAMM; fibronectin; fibronectin-binding protein; antibody; epitope;
KW antibiotic; bacterial infection; antibiotic-resistant strain.
XX
OS Synthetic.
OS Staphylococcus aureus.
XX
PN WO9831389-A2.
XX
PD 23-JUL-1998.
XX
PF 21-JAN-1998; 98WO-US001222.
XX
PR 21-JAN-1997; 97US-00361339P.
XX
PA (TEXA ) UNIV TEXAS A & M SYSTEM.
XX
PI Hoseok M, Patti JM, House-Pompeo KL, Speciale P, Joh D;
PI McGavin MJ;
XX
DR WPI; 1998-413816/35.
XX
PT Antibody that binds to fibronectin-binding protein, preventing its
PT binding to fibronectin - used to treat or prevent bacterial infection,
PT especially by Staphylococci and Streptococci.
XX
PS Example 2; Page 92; 201pp; English.
XX
CC The invention relates to antibodies that bind to a fibronectin-binding
CC domain of a fibronectin-binding protein, and inhibit binding of the
CC protein to fibronectin. Also claimed are: (1) isolated peptides of a
CC fibronectin-binding protein that do not bind to fibronectin; (2) fusion
CC protein containing at least one peptide of a fibronectin-binding protein
CC linked to a second amino acid sequence; (3) nucleic acid encoding the
CC isolated peptide of (1). Antibodies, the isolated peptides of (1) and the
CC nucleic acids are all useful for immunisation (active or passive) and (by
CC inhibiting binding of bacteria to fibronectin) for preventing or treating
CC infection in humans or other animals, particularly by staphylococci or
CC streptococci, e.g. meningitis, otitis media, pneumonia, endocarditis,
CC mastitis in cattle, abortion in horses and many others. Since the
CC antibodies block binding of bacteria, they should be effective against
CC antibiotic-resistant strains, and may replace antibiotic therapy or
CC increase its effectiveness. Sequences AAW6561-68 represent synthetic
CC epitopes from the fibronectin binding domains DU and D1-D4 of the S.
```

```
CC aureus fnBA gene
XX
SQ Sequence 38 AA;
Query Match 96.1%; Score 199; DB 2; Length 38;
Best Local Similarity 97.4%; Pred. No. 1.3e-19;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 QNSGNQSFEDTPEDKPKYEGGNIIVDIDFDSVPQIHG 38
DQ 1 QNSGNQSFEDTPEDKPKYEGGNIIVDIDFDSVPQIHG 38
RESULT 3
AAR58806
ID AAR58806 standard; protein; 130 AA.
XX
AC AAR58806;
XX
DT 25-MAR-2003 (revised)
DT 30-MAR-1995 (first entry)
XX
DE Fibronectin binding domain D1-D4(709-838 (P838T)).
XX
KW Fibronectin binding protein; Fbp; fibronectin binding domain;
KW monoclonal antibody; Mab; adhesion; Gram-positive bacterium; bacteremia;
KW Escherichia coli.
XX
OS Staphylococcus aureus.
XX
PN WO9418327-A1.
XX
PD 18-AUG-1994.
XX
PF 04-FEB-1994; 94WO-GB000215.
XX
PR 05-FEB-1993; 93GB-00002289.
PR 20-OCT-1993; 93GB-00021592.
XX
PA (SMIK ) SMITHKLINE BEECHAM PLC.
XX
PI Burnham MKR, Chopra I, Critchley IA, Knowles DJC;
XX
DR WPI; 1994-279748/34.
XX
XX
PT Fibronectin binding protein and monoclonal antibodies specific for Fbp -
PT useful to prevent adherence of Gram-positive bacteria to indwelling
PT devices or wounds.
XX
PS Disclosure; Page 30; 40pp; English.
XX
CC Polypeptides corresponding to residues G709-T886 plus PRIVPT, G709-
CC P838(P838T) and G709-P838 (AAR58805-07, respectively) of S. aureus J2385
CC (NCIMB 40532) Fbp type A fibronectin binding domain D1-D4 region
CC (AAR58808) were expressed in E. coli BL21(DE4) and used to raise Mabs
CC specific for Fbp. (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ Sequence 130 AA;
Query Match 96.1%; Score 199; DB 2; Length 130;
Best Local Similarity 97.4%; Pred. No. 5.5e-19;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 QNSGNQSFEDTPEDKPKYEGGNIIVDIDFDSVPQIHG 38
DQ 2 QNSGNQSFEDTPEDKPKYEGGNIIVDIDFDSVPQIHG 39
RESULT 4
AAR58807
ID AAR58807 standard; protein; 130 AA.
XX
AC AAR58807;
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XX 25-MAR-2003 (revised)
DT 30-MAR-1995 (first entry)
XX
DE Fibronectin binding domain D1-D4(709-838).
XX
KW Fibronectin binding protein; Fbp; fibronectin binding domain;
KW monoclonal antibody; MAb; adhesion; Gram-positive bacterium; bacteremia;
KW Escherichia coli.
XX
OS Staphylococcus aureus.
XX
PN WO9418327-A1.
XX
PD 18-AUG-1994.
XX
PP 04-FEB-1994; 94WO-GB000215.
XX
PR 05-FEB-1993; 93GB-00002289.
PR 20-OCT-1993; 93GB-00021592.
XX
PA (SMIK ) SMITHKLINE BEECHAM PLC.
XX
PI Burnham MKR, Chopra I, Critchley IA, Knowles DUC;
XX
DR WPI; 1994-279748/34.
XX
PT Fibronectin binding protein and monoclonal antibodies specific for Fbp -
PT useful to prevent adherence of Gram-positive bacteria to indwelling
PT devices or wounds.
XX
PS Disclosure; Page 30; 40pp; English.
XX
CC Polypeptides corresponding to residues G709-T886 plus PPIVPR, G709-
CC P838(P838T) and G709-P838 (AARS8805-07, respectively) of S. aureus J2385
CC (NCTMB 40532) Fbp type A fibronectin binding domain D1-D4 region
CC (AARS8808) were expressed in E. coli BL21(DE4) and used to raise MBs
CC specific for Fbp. (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ Sequence 130 AA;

Query Match          96.1%; Score 199; DB 2; Length 130;
Best Local Similarity 97.4%; Pred. No. 5.5e-19;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 QNSGNQSFEDTPEBDKPKYEQGNIIVDIDFDSVPQIHG 38
    |||||
DB 2 QNSGNQSFEDTPEBDKPKYEQGNIIVDIDFDSVPQIHG 39

RESULT 5
ID AAR91202 standard; peptide; 130 AA.
XX
AC AAR91202;
XX
DT 13-NOV-1996 (first entry)
XX
DE D1-D4 fibronectin binding domains.
XX
KW Fibronectin; oral hygiene; gingivitis; gum disease; adhesion;
KW periodontitis; oral pathogen; caries; calculus; candidiasis; oral surgery;
KW tissue regeneration; irrigation; toothpaste; dentifrice; mouthwash;
KW lozenge.
XX
OS Staphylococcus aureus.
XX
PN WO9604003-A1.
XX
PD 15-FEB-1996.
XX
PF 18-JUL-1995; 95WO-EP002825.
XX

```

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PR 05-AUG-1994; 94GB-00015902.
XX
XX (SMIK ) SMITHKLINE BEECHAM PLC.
XX
PI Barnett P, Critchley IA, Dodd I;
XX
DR WPI; 1996-129122/13.
XX
PT Prevention of adherence of oral pathogens in the oral cavity, partic.
PT tooth surfaces - by application of a fibronectin binding protein or
PT polypeptide or a monoclonal antibody or fragment against it.
XX
PS Claim 5; Page 32; 41pp; English.
XX
CC Adherence of oral pathogens, particularly to tooth surfaces, can be
CC prevented by application of a fibronectin binding protein or polypeptide.
CC The fibronectin binding protein or polypeptide is useful in the
CC manufacture of oral hygiene compositions, eg. toothpaste, liquid
CC dentifrice, mouthwash or lozenge. They are useful to prevent the plaque-
CC related development of carious lesions, gingivitis, calculus or
CC periodontal disease and to combat oral cavity infections, e.g.
CC candidiasis. They may also be useful in oral surgery e.g. in guided
CC tissue regeneration procedures to prevent subsequent bacterial infection,
CC and for irrigation of periodontal pockets. This sequence corresponds to
CC amino acids 709-838 of the D1-D4 fibronectin binding domain of
CC Staphylococcus aureus
XX
SQ Sequence 130 AA;

Query Match          96.1%; Score 199; DB 2; Length 130;
Best Local Similarity 97.4%; Pred. No. 5.5e-19;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 QNSGNQSFEDTPEBDKPKYEQGNIIVDIDFDSVPQIHG 38
    |||||
DB 2 QNSGNQSFEDTPEBDKPKYEQGNIIVDIDFDSVPQIHG 39

RESULT 6
ID AAR91201 standard; peptide; 130 AA.
XX
AC AAR91201;
XX
DT 13-NOV-1996 (first entry)
XX
DE D1-D4 fibronectin binding domains.
XX
KW Fibronectin; oral hygiene; gingivitis; gum disease; adhesion;
KW periodontitis; oral pathogen; caries; calculus; candidiasis; oral surgery;
KW tissue regeneration; irrigation; toothpaste; dentifrice; mouthwash;
KW lozenge.
XX
OS Staphylococcus aureus.
XX
PN WO9604003-A1.
XX
PD 15-FEB-1996.
XX
PF 18-JUL-1995; 95WO-EP002825.
XX
PR 05-AUG-1994; 94GB-00015902.
XX
PA (SMIK ) SMITHKLINE BEECHAM PLC.
XX
PI Barnett P, Critchley IA, Dodd I;
XX
DR WPI; 1996-129122/13.
XX
PT Prevention of adherence of oral pathogens in the oral cavity, partic.
PT tooth surfaces - by application of a fibronectin binding protein or
PT polypeptide or a monoclonal antibody or fragment against it.
XX

```


PS Claim 5; Page 31-32; 41pp; English.

CC Adherence of oral pathogens, particularly to tooth surfaces, can be

CC prevented by application of a fibronectin binding protein or polypeptide.

CC The fibronectin binding protein or polypeptide is useful in the

CC manufacture of oral hygiene compositions, eg. toothpaste, liquid

CC dentifrice, mouthwash or lozenge. They are useful to prevent the plaque-

CC related development of carious lesions, gingivitis, calculus or

CC periodontal disease and to combat oral cavity infections, e.g.

CC candidiasis. They may also be useful in oral surgery e.g. in guided

CC tissue regeneration procedures to prevent subsequent bacterial infection,

CC and for irrigation of periodontal pockets. This sequence corresponds to

CC amino acids 709-838 of the D1-D4 fibronectin binding domain of

CC Staphylococcus aureus with a P838T substitution

XX

SQ Sequence 130 AA;

Query Match 96.1%; Score 199; DB 2; Length 130;

Best Local Similarity 97.4%; Pred. No. 5.5e-19;

Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QNSGNQSFEDTPEDKPKYEGGNIVIDIDFDSVPQIHG 38

DB 2 QNSGNQSFEDTPEDKPKYEGGNIVIDIDFDSVPQIHG 39

RESULT 7

AAAY29089

ID AAY29089 standard; protein; 134 AA.

XX

AC AAY29089;

XX

DT 28-SEP-1999 (first entry)

XX

DE Cloned fibronectin binding protein binding domain (FnBAB) sequence.

XX

XX Bovine herpes virus-2; BHV-2; cytokine; immune response; immunogen; IL;

XX Interleukin; colony stimulating factor; CSF; interferon; IFN; TNF;

XX Tumour necrosis factor; recombinant virus; vaccine; mucosal disease;

XX mastitis; breast cancer; stress-induced disease; binding domain; FnBAB;

XX fibronectin binding protein.

XX

OS Staphylococcus aureus.

XX

FN W09916892-A1.

XX

PD 08-APR-1999.

XX

PF 29-SEP-1998; 98W0-GB002927.

XX

PR 29-SEP-1997; 97GB-00020633.

XX

XX (UYBR-) UNIV BRISTOL.

PA

PI Bradley AJ, Duffas WPJ;

XX WPI; 1999-255101/21.

XX

DR N-PSDB; AAX91506.

XX

PT New bovine herpes virus-2 vectors.

XX

PS Example 2; Fig 8A-B; 130pp; English.

XX

CC The invention provides bovine herpes virus-2 (BHV-2) based vectors that

CC comprise at least one cytokine-encoding DNA sequence. The expression of

CC cytokines in mammals can up-regulate immune responses to the immunogens.

CC The cytokine is selected from interleukins (IL), colony stimulating

CC factors (CSF), interferons (IFN) and tumour necrosis factors (TNF). The

CC BHV-2 based vector or recombinant virus can be used as vaccines. They can

CC be used for preventing or treating a mucosal disease in a subject, e.g.

CC runtaants, cattle, sheep, goats, dogs, cats, horses, or man, particularly

CC mastitis in cows or breast cancers in humans. They can also be used for

CC preventing or treating a stress-induced disease. The present sequence

CC represents a S. aureus fibronectin binding protein binding domain

CC sequence FnBAB, the gene cloned for use in this invention. The gene has

CC 97.8 percent identity when compared to the previously published sequences

CC FnBA and FnBB

XX

SQ Sequence 134 AA;

Query Match 96.1%; Score 199; DB 2; Length 134;

Best Local Similarity 97.4%; Pred. No. 5.7e-19;

Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QNSGNQSFEDTPEDKPKYEGGNIVIDIDFDSVPQIHG 38

DB 2 QNSGNQSFEDTPEDKPKYEGGNIVIDIDFDSVPQIHG 39

RESULT 8

AAAY29088

ID AAY29088 standard; protein; 134 AA.

XX

AC AAY29088;

XX

DT 28-SEP-1999 (first entry)

XX

DE S. aureus fibronectin binding protein B (FnBB) binding domain.

XX

XX Bovine herpes virus-2; BHV-2; cytokine; immune response; immunogen; IL;

XX Interleukin; colony stimulating factor; CSF; interferon; IFN; TNF;

XX Tumour necrosis factor; recombinant virus; vaccine; mucosal disease;

XX mastitis; breast cancer; stress-induced disease; binding domain; FnBB;

XX fibronectin binding protein.

XX

OS Staphylococcus aureus.

XX

FN W09916892-A1.

XX

PD 08-APR-1999.

XX

PF 29-SEP-1998; 98W0-GB002927.

XX

PR 29-SEP-1997; 97GB-00020633.

XX

XX (UYBR-) UNIV BRISTOL.

PA

PI Bradley AJ, Duffas WPJ;

XX WPI; 1999-255101/21.

XX

DR N-PSDB; AAX91505.

XX

PT New bovine herpes virus-2 vectors.

XX

PS Example 2; Fig 8A-B; 130pp; English.

XX

CC The invention provides bovine herpes virus-2 (BHV-2) based vectors that

CC comprise at least one cytokine-encoding DNA sequence. The expression of

CC cytokines in mammals can up-regulate immune responses to the immunogens.

CC The cytokine is selected from interleukins (IL), colony stimulating

CC factors (CSF), interferons (IFN) and tumour necrosis factors (TNF). The

CC BHV-2 based vector or recombinant virus can be used as vaccines. They can

CC be used for preventing or treating a mucosal disease in a subject, e.g.

CC runtaants, cattle, sheep, goats, dogs, cats, horses, or man, particularly

CC mastitis in cows or breast cancers in humans. They can also be used for

CC preventing or treating a stress-induced disease. The present sequence

CC represents the binding domain of a previously published S. aureus

CC fibronectin binding protein B (FnBB) sequence. The FnB binding domain

CC gene sequence FnBAB, cloned for use in this invention has 97.8 percent

CC identity when compared to the previously published FnBA and FnBB gene

CC sequences

XX

SQ Sequence 134 AA;

Query Match 96.1%; Score 199; DB 2; Length 134;

Best Local Similarity 97.4%; Pred. No. 5.7e-19;

Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QNSGNOSFEEDTPEDKPKYEGGNIYDIDFDSVPQIHG 38
 DB 2 QNSGNOSFEEDTPEDKPKYEGGNIYDIDFDSVPQIHG 39

RESULT 9

ID AAY29087
 ID AAY29087 standard; protein; 134 AA.

AC AAY29087;

DT 28-SEP-1999 (first entry)

DE S. aureus fibronectin binding protein A (Fnba) binding domain.

XX Bovine herpes virus-2; BHV-2; cytokine; immune response; immunogen; IL;
 XX Interleukin; colony stimulating factor; CSF; interferon; IFN; TNF;
 XX tumour necrosis factor; recombinant virus; vaccine; mucosal disease;
 XX mastitis; breast cancer; stress-induced disease; binding domain; Fnba;
 XX fibronectin binding protein.

XX Staphylococcus aureus.

XX WO916892-A1.

XX 08-APR-1999.

XX 29-SEP-1998; 98WO-GB002927.

XX 29-SEP-1997; 97GB-00020633.

XX (UYBR-) UNIV BRISTOL.

XX Bradley AJ, Duffas WP;

XX WPI; 1999-255101/21.

XX N-PSDB; AAX91504.

XX New bovine herpes virus-2 vectors.

XX Example 2; Fig 8A-B; 130pp; English.

CC The invention provides bovine herpes virus-2 (BHV-2) based vectors that
 CC comprise at least one cytokine-encoding DNA sequence. The expression of
 CC cytokines in mammals can up-regulate immune responses to the immunogens.
 CC The cytokine is selected from interleukins (IL), colony stimulating
 CC factors (CSF), interferons (IFN) and tumour necrosis factors (TNF). The
 CC BHV-2 based vector or recombinant virus can be used as vaccines. They can
 CC be used for preventing or treating a mucosal disease in a subject, e.g.
 CC ruminants, cattle, sheep, goats, dogs, cats, horses, or man, particularly
 CC mastitis in cows or breast cancers in humans. They can also be used for
 CC preventing or treating a stress-induced disease. The present sequence
 CC represents the binding domain of a previously published S. aureus
 CC fibronectin binding protein A (Fnba) sequence. The Fnba binding domain
 CC gene sequence FnbaB, cloned for use in this invention has 97.8 percent
 CC identity when compared to the previously published Fnba and FnbaB gene
 CC sequences

CC Sequence 134 AA;

CC Query Match 96.1%; Score 199; DB 2; Length 134;

CC Best Local Similarity 97.4%; Pred. No. 5,7e-19;

CC Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 QNSGNOSFEEDTPEDKPKYEGGNIYDIDFDSVPQIHG 38
 DB 2 QNSGNOSFEEDTPEDKPKYEGGNIYDIDFDSVPQIHG 39

RESULT 10
 AAW31556

ID AAW31556 standard; protein; 139 AA.

XX AAW31556;

XX 27-AUG-2003 (revised)

XX 25-MAR-2003 (revised)

XX 21-MAY-1998 (first entry)

XX Fibronectin-binding MSCRAMM derivative POD.

XX Fibronectin; POD; collagen binding protein; sepsis; infection;
 XX microbial surface component recognising adhesive matrix molecule; MSCRAMM;
 XX adhesin; vaccine; immunisation; diagnosis; therapy; mastitis.

XX Staphylococcus aureus.

XX Key Location/Qualifiers

XX Peptide 1..12 /note="vector pQE30-derived peptide"

XX WO9743314-A2.

XX 20-NOV-1997.

XX 14-MAY-1997; 97WO-US008210.

XX 16-MAY-1996; 96US-0017678P.

XX (TEXA) UNIV TEXAS A & M SYSTEM.

XX (UABR-) UAB RES FOUND.

XX Hoecek M, Patti JM, House-Pompeo K, Schanham N, Symersky J;

XX WPI; 1998-008801/01.

XX Antibody that interacts with collagen binding domain of Staphylococcal
 XX cna gene product - useful to prevent bacterial sepsis in animal infected
 XX with Staphylococcus aureus.

XX Disclosure; Page 91; 143pp; English.

XX This protein comprises Staphylococcus aureus fibronectin-binding
 CC microbial surface component recognising adhesive matrix molecule (MSCRAMM)
 CC derivative POD, plus a vector-derived N-terminal peptide. The invention
 CC relates to claimed nucleic acid sequences (see AAT93436-38) encoding S.
 CC aureus collagen binding protein (CBP) epitopes M17, M31 and M55 (see
 CC AAW31552-54) that confer protection against S. aureus infection. CBP
 CC protein and antigenic epitopes are contemplated for use in the treatment
 CC of pathological infections, especially to prevent bacterial adhesion to
 CC collagen. The epitopes are also contemplated for use in the preparation
 CC of vaccines and as carrier proteins in vaccine formulations, as well as
 CC in the formulation of compositions for the prevention of S. aureus
 CC infection. pCF33 and POD (see AAW31556) were used to raise anti-MSCRAMM
 CC polyclonal antibodies used in passive immunisation against bovine
 CC mastitis. (updated on 25-MAR-2003 to correct PI field.) (updated on 27-
 CC AUG-2003 to correct OS field.)

XX Sequence 139 AA;

XX Query Match 96.1%; Score 199; DB 2; Length 139;

XX Best Local Similarity 97.4%; Pred. No. 6e-19;

XX Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 QNSGNOSFEEDTPEDKPKYEGGNIYDIDFDSVPQIHG 38
 DB 16 QNSGNOSFEEDTPEDKPKYEGGNIYDIDFDSVPQIHG 53

RESULT 11

ID AAR58808 standard; protein; 174 AA.

XX AAR58808;

```
XX 25-MAR-2003 (revised)
DT 30-MAR-1995 (first entry)
XX
DE Fbp fibronectin binding domain.
XX
KW Fibronectin binding protein; Fbp; fibronectin binding domain;
KM monoclonal antibody; Mab; adhesion; Gram-positive bacterium; bacteremia;
KW Escherichia coli; pR0C531.
XX
OS Staphylococcus aureus.
XX
PN WO9418327-A1.
XX
PD 18-AUG-1994.
XX
PF 04-FEB-1994; 94WO-GB000215.
XX
PR 05-FEB-1993; 93GB-00002289.
PR 20-OCT-1993; 93GB-00021592.
XX
PA (SMIK ) SMITHKLINE BEECHAM PLC.
PI Burnham MKR, Chopra I, Critchley IA, Knowles DUC;
XX
DR WPI: 1994-279748/34.
DR N-PSDB; AA071838.
XX
PT Fibronectin binding protein and monoclonal antibodies specific for Fbp -
PT useful to prevent adherence of Gram-positive bacteria to indwelling
PT devices or wounds.
XX
PS Disclosure; Page 30; 40pp; English.
XX
CC The sequences of DNA encoding S. aureus Fbp type A fibronectin binding
CC domain (D1-D4) and the encoded protein are provided. D1-D4 polypeptides
CC have been expressed in E. coli BL21(DE4) and used to raise Mabs specific
CC for Fbp. (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ Sequence 174 AA;

Query Match          96.1%; Score 199; DB 2; Length 174;
Best Local Similarity 97.4%; Pred. No. 7.8e-19;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Cy 1 QNSGNQSFEEPTPEDKPKYEGGNIVIDIDFDSVPQING 38
    |||||
Db 2 QNSGNQSFEEPTPEDKPKYEGGNIVIDIDFDSVPQING 39

RESULT 12
AAR91203
ID AAR91203 standard; protein; 174 AA.
XX
AC AAR91203;
XX
DT 16-OCT-2003 (revised)
DT 13-NOV-1996 (first entry)
XX
DE D1-D4 fibronectin binding domains.
XX
KW Fibronectin; oral hygiene; gingivitis; gum disease; adhesion;
KW periodontitis; oral pathogen; caries; calculus; candidiasis; oral surgery;
KW tissue regeneration; irrigation; toothpaste; dentifrice; mouthwash;
KW lozenge.
XX
OS Staphylococcus aureus; J2385.
XX
PN WO9604003-A1.
XX
PD 15-FEB-1996.
XX
PF 18-JUL-1995; 95WO-EP002825.
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```
XX 05-AUG-1994; 94GB-00015902.
XX
PA (SMIK ) SMITHKLINE BEECHAM PLC.
XX
PI Barnett P, Critchley IA, Dodd I;
XX
DR WPI: 1996-129122/13.
DR N-PSDB; MAT18308.
XX
PT Prevention of adherence of oral pathogens in the oral cavity, partic.
PT tooth surfaces - by application of a fibronectin binding protein or
PT polypeptide or a monoclonal antibody or fragment against it.
XX
PS Claim 5; Page 32; 41pp; English.
XX
CC Adherence of oral pathogens, particularly to tooth surfaces, can be
CC prevented by application of a fibronectin binding protein or polypeptide.
CC The fibronectin binding protein or polypeptide is useful in the
CC manufacture of oral hygiene compositions, eg. toothpaste, liquid
CC dentifrice, mouthwash or lozenge. They are useful to prevent the plaque-
CC related development of carious lesions, gingivitis, calculus or
CC periodontal disease and to combat oral cavity infections, e.g.
CC candidiasis. They may also be useful in oral surgery e.g. in guided
CC tissue regeneration procedures to prevent subsequent bacterial infection,
CC and for irrigation of periodontal pockets. This sequence corresponds to
CC amino acids 709-838 of the D1-D4 fibronectin binding domain of
CC Staphylococcus aureus with a P838T substitution. (Updated on 16-OCT-2003
CC to standardise OS field)
XX
SQ Sequence 174 AA;

Query Match          96.1%; Score 199; DB 2; Length 174;
Best Local Similarity 97.4%; Pred. No. 7.8e-19;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Cy 1 QNSGNQSFEEPTPEDKPKYEGGNIVIDIDFDSVPQING 38
    |||||
Db 2 QNSGNQSFEEPTPEDKPKYEGGNIVIDIDFDSVPQING 39

RESULT 13
AAR58805
ID AAR58805 standard; protein; 181 AA.
XX
AC AAR58805;
XX
DT 25-MAR-2003 (revised)
DT 30-MAR-1995 (first entry)
XX
DE Fibronectin binding domain D1-D4 (709-886).
XX
KW Fibronectin binding protein; Fbp; fibronectin binding domain;
KW monoclonal antibody; Mab; adhesion; Gram-positive bacterium; bacteremia;
KW Escherichia coli.
XX
OS Staphylococcus aureus.
XX
PN WO9418327-A1.
XX
PD 18-AUG-1994.
XX
PF 04-FEB-1994; 94WO-GB000215.
XX
PR 05-FEB-1993; 93GB-00002289.
PR 20-OCT-1993; 93GB-00021592.
XX
PA (SMIK ) SMITHKLINE BEECHAM PLC.
PI Burnham MKR, Chopra I, Critchley IA, Knowles DUC;
XX
DR WPI: 1994-279748/34.
```

PT Fibronectin binding protein and monoclonal antibodies specific for Fbp -
 PT useful to prevent adherence of Gram-positive bacteria to indwelling
 PT devices or wounds.
 XX
 XX Disclousure; Page 29-30; 40pp; English.
 PS
 CC Polypeptides corresponding to residues G709-T886 plus PPIVPT, G709-
 CC P838(P838T) and G709-P838 (AAR58805-07, respectively) of S. aureus J2385
 CC (NCIMB 40532) Fbp type A fibronectin binding domain D1-D4 region
 CC (AAR58808) were expressed in E. coli BL21 (DE3) and used to raise Mabs
 CC specific for Fbp. (Updated on 25-MAR-2003 to correct PN field.)
 CC
 XX
 SQ Sequence 181 AA;
 Query Match 96.1%; Score 199; DB 2; Length 181;
 Best Local Similarity 97.4%; Pred. No. 8.2e-19;
 Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 QNSGNQSFEDTPEBKPKYEGGNIYDIDPDSVPQIHG 38
 DB 2 QNSGNQSFEDTPEBKPKYEGGNIYDIDPDSVPQIHG 39
 RESULT 14
 AAR91200
 ID AAR91200 standard; peptide; 181 AA.
 XX
 AC AAR91200;
 XX
 DT 13-NOV-1996 (first entry)
 XX
 DE D1-D4 fibronectin binding domains.
 XX
 KW Fibronectin; oral hygiene; gingivitis; gum disease; adhesion;
 KW periodontitis; oral pathogen; caries; calculus; candidiasis; oral surgery;
 KW tissue regeneration; irrigation; toothpaste; dentifrice; mouthwash;
 KW lozenge.
 KW
 OS Staphylococcus aureus.
 XX
 PN WO9604003-A1.
 XX
 PD 15-FEB-1996.
 XX
 PF 18-JUL-1995; 95WO-EP002825.
 XX
 PR 05-AUG-1994; 94GB-00015902.
 XX
 PA (SMIR) SMITHKLINE BEECHAM PLC.
 XX
 PI Barnett P, Critchley IA, Dodd I;
 XX
 DR WPI, 1996-129122/13.
 XX
 DR N-PSDB; AAT18307.
 XX
 PT Prevention of adherence of oral pathogens in the oral cavity, partic.
 PT tooth surfaces - by application of a fibronectin binding protein or
 PT polypeptide or a monoclonal antibody or fragment against it.
 XX
 PS Claim 5; Page 31; 41pp; English.
 XX
 CC Adherence of oral pathogens, particularly to tooth surfaces, can be
 CC prevented by application of a fibronectin binding protein or polypeptide.
 CC The fibronectin binding protein or polypeptide is useful in the
 CC manufacture of oral hygiene compositions, eg. toothpaste, liquid
 CC dentifrice, mouthwash or lozenge. They are useful to prevent the plaque-
 CC related development of carious lesions, gingivitis, calculus or
 CC periodontal disease and to combat oral cavity infections, e.g.
 CC candidiasis. They may also be useful in oral surgery e.g. in guided
 CC tissue regeneration procedures to prevent subsequent bacterial infection,
 CC and for irrigation of periodontal pockets. This sequence corresponds to
 CC amino acids 709-886 of the D1-D4 fibronectin binding domain of
 CC Staphylococcus aureus

XX
 SQ Sequence 181 AA;
 Query Match 96.1%; Score 199; DB 2; Length 181;
 Best Local Similarity 97.4%; Pred. No. 8.2e-19;
 Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 QNSGNQSFEDTPEBKPKYEGGNIYDIDPDSVPQIHG 38
 DB 2 QNSGNQSFEDTPEBKPKYEGGNIYDIDPDSVPQIHG 39
 RESULT 15
 AAW89803
 ID AAW89803 standard; protein; 559 AA.
 XX
 AC AAW89803;
 XX
 DT 16-MAR-1999 (first entry)
 XX
 DE Staphylococcus aureus protein SEQ ID #5251.
 XX
 KW Computer readable medium; vaccine; S. aureus infection; immunodetection;
 KW cellulitis; eyelid infection; food poisoning; osteomyelitis; therapy;
 KW skin infection; surgical wound infection; scalded skin syndrome;
 KW toxic shock syndrome.
 KW
 OS Staphylococcus aureus.
 XX
 PN EP786519-A2.
 XX
 PD 30-JUL-1997.
 XX
 PF 07-JAN-1997; 97EP-00100117.
 XX
 PR 05-JAN-1996; 96US-0009861P.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 XX
 PI Kunsch CA, Choi GH, Barash SC, Dillon PJ, Fannon MR, Rosen CA;
 XX
 DR WPI, 1997-374922/35.
 XX
 PT Polynucleotide(s) and proteins derived from Staphylococcus aureus -
 PT stored on computer readable medium and used in the production of anti-
 PT S. aureus vaccines.
 XX
 PS Claim 23; Page 3259-3261; 3271pp; English.
 XX
 CC This sequence represents a Staphylococcus aureus protein sequence of the
 CC invention. The DNA sequences encoding the S. aureus proteins are recorded
 CC on a computer readable medium, preferably selected from a floppy or hard
 CC disk, random access memory (RAM), read-only memory (ROM) or CD-ROM.
 CC Homology searches using the S. aureus DNA sequences allows putative
 CC functions to be assigned so that protein-encoding or regulatory regions
 CC of commercial, therapeutic or industrial importance can be obtained.
 CC Specifically, sequences which are likely to encode antigens have been
 CC identified and these polypeptides can be used in a vaccine composition
 CC against S. aureus infection. The polypeptides can also be used in a kit
 CC for the immunodetection of S. aureus in a sample. S. aureus is implicated
 CC in numerous human diseases, including cellulitis, eyelid infections, food
 CC poisoning, osteomyelitis, skin and surgical wound infections, scalded
 CC skin syndrome, toxic shock syndrome, etc. Organisms transformed with the
 CC DNA sequences can be used for recombinant production of the polypeptide.
 CC The new DNA sequences (and their fragments) are useful as primers or
 CC probes for isolating homologues of any of the 5191 S. aureus DNA sequences
 CC contained on the computer readable medium
 CC
 XX
 SQ Sequence 559 AA;
 Query Match 96.1%; Score 199; DB 2; Length 559;
 Best Local Similarity 97.4%; Pred. No. 3.2e-18;
 Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ONSGNQSFEDTPEPKRYEOGNIVDIDPDSVPQIHG 38
| | | | | | | | | | | | | | | | | | | | | |
Db 301 ONSGNQSFEDTPEPKRYEOGNIVDIDPDSVPQIHG 338

Search completed: October 25, 2005, 20:21:03
Job time : 83.8825 secs

GenCore version 5.1.6
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OM protein - protein search, using SW model

Run on: October 22, 2005, 03:51:22 ; Search time 21.1723 Seconds
(without alignments)
133.980 Million cell updates/sec

Title: US-10-731-238-40

Perfect score: 207
Sequence: 1 QNSGNQSPFEDTPEDKPKYEGQGNIVDIDFDSVPQIHG 38

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: /cgn2_6/prodata/1/1aa/5A_COMB.pep:*
2: /cgn2_6/prodata/1/1aa/5B_COMB.pep:*
3: /cgn2_6/prodata/1/1aa/6A_COMB.pep:*
4: /cgn2_6/prodata/1/1aa/6B_COMB.pep:*
5: /cgn2_6/prodata/1/1aa/PCITUS_COMB.pep:*
6: /cgn2_6/prodata/1/1aa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	207	100.0	38	4	US-09-010-317-40
2	199	96.1	38	1	US-08-234-622A-2
3	199	96.1	38	4	US-09-010-317-5
4	199	96.1	114	1	US-08-259-000-3
5	199	96.1	130	2	US-08-459-135A-7
6	199	96.1	130	2	US-08-459-135A-8
7	199	96.1	130	3	US-08-495-559-7
8	199	96.1	130	3	US-08-495-559-8
9	199	96.1	139	3	US-08-856-253-8
10	199	96.1	174	2	US-08-459-135A-10
11	199	96.1	174	2	US-08-459-135A-13
12	199	96.1	174	3	US-08-495-559-10
13	199	96.1	174	3	US-08-495-559-13
14	199	96.1	176	3	US-08-495-559-6
15	199	96.1	178	3	US-08-459-135A-12
16	199	96.1	178	3	US-08-495-559-12
17	199	96.1	181	4	US-08-459-135A-6
18	199	96.1	559	4	US-08-956-171E-5251
19	199	96.1	559	4	US-08-781-986A-5251
20	199	96.1	1027	4	US-08-956-171E-5254
21	199	96.1	1027	4	US-08-781-986A-5254
22	193	93.2	38	1	US-08-729-767-3
23	193	93.2	38	4	US-09-010-317-36
24	193	93.2	38	4	US-09-010-317-37
25	193	93.2	38	4	US-09-010-317-39
26	193	93.2	38	4	US-09-010-317-41
27	192	92.8	38	4	US-09-010-317-38

28	192	92.8	38	4	US-09-010-317-42	Sequence 42, Appl
29	191	92.3	38	4	US-09-010-317-6	Sequence 6, Appl
30	191	92.3	38	4	US-09-010-317-43	Sequence 43, Appl
31	189	91.3	38	4	US-09-010-317-35	Sequence 35, Appl
32	188.5	91.1	39	4	US-09-010-317-56	Sequence 56, Appl
33	180.5	87.2	39	4	US-09-010-317-57	Sequence 57, Appl
34	180	87.0	38	1	US-08-234-622A-3	Sequence 3, Appl
35	180	87.0	38	4	US-09-010-317-7	Sequence 7, Appl
36	174	84.1	38	1	US-08-729-767-4	Sequence 4, Appl
37	174	84.1	38	4	US-09-010-317-46	Sequence 46, Appl
38	174	84.1	38	4	US-09-010-317-47	Sequence 47, Appl
39	173	83.6	38	4	US-09-010-317-48	Sequence 48, Appl
40	172	83.1	38	4	US-09-010-317-8	Sequence 8, Appl
41	172	83.1	38	4	US-09-010-317-49	Sequence 49, Appl
42	171	82.6	38	4	US-09-010-317-44	Sequence 44, Appl
43	170	82.1	38	4	US-09-010-317-45	Sequence 45, Appl
44	157	75.8	36	4	US-09-010-317-58	Sequence 58, Appl
45	152	73.4	38	4	US-09-010-317-50	Sequence 50, Appl

ALIGNMENTS

RESULT 1
US-09-010-317-40
Sequence 40, Application US/09010317
Patent No. 6685943
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
APPLICANT: Patti, Joseph M.
APPLICANT: House-Pompeo, Karen L.
APPLICANT: Speziale, Pietro
APPLICANT: Joh, Danny
APPLICANT: McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
TITLE OF INVENTION: AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TANKK:189
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 40:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-09-010-317-40
Query Match 100.0% Score 207; DB 4; Length 38;
Best Local Similarity 100.0%; Pred. No. 1.3e-21;

Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QNSGNSFEEDTPEDKPKYEGGNIVDIDFDSVPQIHG 38
Db 1 QNSGNSFEEDTPEDKPKYEGGNIVDIDFDSVPQIHG 38

RESULT 2

US-08-234-622A-2

; Sequence 2, Application US/08234622A

; Patent No. 5440014

; GENERAL INFORMATION:

; APPLICANT: HOOK, Magnus

; APPLICANT: MCGAVIN, Martin

; APPLICANT: RAUCCI, Giuseppe

; TITLE OF INVENTION: A FIBRONECTIN BINDING PEPTIDE

; NUMBER OF SEQUENCES: 4

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Burns, Doane, Swecker & Mathis

; STREET: P.O. Box 1404

; CITY: Alexandria

; STATE: Virginia

; COUNTRY: United States

; ZIP: 22313-1404

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/234,622A

; FILING DATE: 28-APR-1994

; CLASSIFICATION: 530

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: SE 9002617-0

; FILING DATE: 10-AUG-1990

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: WO PCT/SE91/00534

; FILING DATE: 09-AUG-1991

; ATTORNEY/AGENT INFORMATION:

; NAME: Meuth, Donna M

; REGISTRATION NUMBER: 36,607

; REFERENCE/DOCKET NUMBER: 012885-044

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (703) 836-6620

; TELEFAX: (703) 836-2021

; INFORMATION FOR SEQ ID NO: 2:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 38 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

; US-08-234-622A-2

Query Match 96.1%; Score 199; DB 1; Length 38;
Best Local Similarity 97.4%; Pred. No. 1.6e-20;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QNSGNSFEEDTPEDKPKYEGGNIVDIDFDSVPQIHG 38
Db 1 QNSGNSFEEDTPEDKPKYEGGNIVDIDFDSVPQIHG 38

RESULT 3

US-09-010-317-5

; Sequence 5, Application US/09010317

; Patent No. 6685943

; GENERAL INFORMATION:

; APPLICANT: Hook, Magnus

; APPLICANT: Patti, Joseph M.

; APPLICANT: House-Pompeo, Karen L.

; APPLICANT: Speciale, Pietro

; US-09-010-317-5

APPLICANT: Joh, Danny
APPLICANT: McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
TITLE OF INVENTION: AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TPMK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-09-010-317-5

Query Match 96.1%; Score 199; DB 4; Length 38;
Best Local Similarity 97.4%; Pred. No. 1.6e-20;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QNSGNSFEEDTPEDKPKYEGGNIVDIDFDSVPQIHG 38
Db 1 QNSGNSFEEDTPEDKPKYEGGNIVDIDFDSVPQIHG 38

RESULT 4

US-08-259-000-3

; Sequence 3, Application US/08259000

; Patent No. 5571514

; GENERAL INFORMATION:

; APPLICANT: HOOK, Magnus

; APPLICANT: LINDBERG, Martin Kjell

; APPLICANT: SIGNAS, Lars Christer

; APPLICANT: WADSTROM, Torkel Mikael

; APPLICANT: FROMAN, Gunnar

; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN AS WELL AS

; TITLE OF INVENTION: ITS PREPARATION

; NUMBER OF SEQUENCES: 4

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Burns, Doane, Swecker & Mathis

; STREET: P.O. Box 1404

; CITY: Alexandria

; STATE: Virginia

; COUNTRY: United States

; ZIP: 22313-1404

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.25

;;
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/259,000
;; FILING DATE: 13-JUN-1994
;; CLASSIFICATION: 435
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: SE 8702272-9
;; FILING DATE: 01-JUN-1987
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Meuth, Donna M
;; REGISTRATION NUMBER: 36,607
;; REFERENCE/DOCKET NUMBER: 012865-062
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (703) 836-6620
;; TELEFAX: (703) 836-2021
;; INFORMATION FOR SEQ ID NO: 3:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 114 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; US-08-259-000-3

Query Match 96.1%; Score 199; DB 1; Length 114;
Best Local Similarity 97.4%; Pred. No. 6,1e-20;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ONSGNQSFEDTPEEDKPKYEGGNIIVDIDFDSVPQIHG 38
Db 2 ONSGNQSFEDTPEEDKPKYEGGNIIVDIDFDSVPQIHG 39

RESULT 5
US-08-459-135A-7
Sequence 7, Application US/08459135A
Patent No. 5955078
GENERAL INFORMATION:
APPLICANT: BURNHAM, Martin Karl Russel
APPLICANT: CHOPEA, Ian
APPLICANT: CRITCHLEY, Ian Alfred
APPLICANT: KNOWLES, David Justin Charles
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN: MONOCLONAL ANTIBODY AND THEIR US
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
STATE: PA
COUNTRY: U.S.A.
ZIP: 19406-0939
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: Fastseq, Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/459,135A
FILING DATE: 02-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB/94/00215
FILING DATE: 04-Feb-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Gimmil, Edward R
REGISTRATION NUMBER: 38,891
REFERENCE/DOCKET NUMBER: P30591C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-4478
TELEFAX: 610-270-5090
TELEX:
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:

;;
;; LENGTH: 130 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; US-08-459-135A-7

Query Match 96.1%; Score 199; DB 2; Length 130;
Best Local Similarity 97.4%; Pred. No. 7,2e-20;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ONSGNQSFEDTPEEDKPKYEGGNIIVDIDFDSVPQIHG 38
Db 2 ONSGNQSFEDTPEEDKPKYEGGNIIVDIDFDSVPQIHG 39

RESULT 6
US-08-459-135A-8
Sequence 8, Application US/08459135A
Patent No. 5955078
GENERAL INFORMATION:
APPLICANT: BURNHAM, Martin Karl Russel
APPLICANT: CHOPEA, Ian
APPLICANT: CRITCHLEY, Ian Alfred
APPLICANT: KNOWLES, David Justin Charles
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN: MONOCLONAL ANTIBODY AND THEIR US
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
STATE: PA
COUNTRY: U.S.A.
ZIP: 19406-0939
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: Fastseq, Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/459,135A
FILING DATE: 02-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB/94/00215
FILING DATE: 04-Feb-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Gimmil, Edward R
REGISTRATION NUMBER: 38,891
REFERENCE/DOCKET NUMBER: P30591C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-4478
TELEFAX: 610-270-5090
TELEX:
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 130 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-459-135A-8

Query Match 96.1%; Score 199; DB 2; Length 130;
Best Local Similarity 97.4%; Pred. No. 7,2e-20;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ONSGNQSFEDTPEEDKPKYEGGNIIVDIDFDSVPQIHG 38
Db 2 ONSGNQSFEDTPEEDKPKYEGGNIIVDIDFDSVPQIHG 39

RESULT 7
US-08-495-559-7


```

; Sequence 7, Application US/08495559A
; Patent No. 6054572
; GENERAL INFORMATION:
; APPLICANT: BURMAN, Martin Karl Russel
; APPLICANT: CHOPRA, Ian
; APPLICANT: CRITCHLEY, Ian Alfred
; APPLICANT: KNOWLES, David Justin Charles
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN: MONOCLONAL
; TITLE OF INVENTION: ANTIBODY AND THEIR USE IN PREVENTING BACTERIAL ADHESION
; FILE REFERENCE: P30591
; CURRENT APPLICATION NUMBER: US/08/495,559A
; CURRENT FILING DATE: 1995-08-03
; EARLIER APPLICATION NUMBER: GB 9302289.5
; EARLIER FILING DATE: 1993-02-05
; EARLIER APPLICATION NUMBER: GB 9321592.9
; EARLIER FILING DATE: 1993-10-20
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 7
; LENGTH: 130
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
; US-08-495-559-7

Query Match          96.1%; Score 199; DB 3; Length 130;
Best Local Similarity 97.4%; Pred. No. 7.2e-20;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QNSGNSFEEDTPEDKPKRYEOGNIVIDIDFDSVPQIHG 38
Db 2 QNSGNSFEEDTPEDKPKRYEOGNIVIDIDFDSVPQIHG 39

RESULT 8
US-08-495-559-8
; Sequence 8, Application US/08495559A
; Patent No. 6054572
; GENERAL INFORMATION:
; APPLICANT: BURMAN, Martin Karl Russel
; APPLICANT: CHOPRA, Ian
; APPLICANT: CRITCHLEY, Ian Alfred
; APPLICANT: KNOWLES, David Justin Charles
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN: MONOCLONAL
; TITLE OF INVENTION: ANTIBODY AND THEIR USE IN PREVENTING BACTERIAL ADHESION
; FILE REFERENCE: P30591
; CURRENT APPLICATION NUMBER: US/08/495,559A
; CURRENT FILING DATE: 1995-08-03
; EARLIER APPLICATION NUMBER: GB 9302289.5
; EARLIER FILING DATE: 1993-02-05
; EARLIER APPLICATION NUMBER: GB 9321592.9
; EARLIER FILING DATE: 1993-10-20
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 8
; LENGTH: 130
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
; US-08-495-559-8

Query Match          96.1%; Score 199; DB 3; Length 130;
Best Local Similarity 97.4%; Pred. No. 7.2e-20;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QNSGNSFEEDTPEDKPKRYEOGNIVIDIDFDSVPQIHG 38
Db 2 QNSGNSFEEDTPEDKPKRYEOGNIVIDIDFDSVPQIHG 39

RESULT 9
US-08-856-253-8
; Sequence 8, Application US/08856253
; Patent No. 6288214
; GENERAL INFORMATION:
; APPLICANT: Hook, Magnus
; APPLICANT: Patti, Joseph M.
; APPLICANT: House-Pomero, Karen
; APPLICANT: Stahanam, Narayana
; APPLICANT: Symersky, Jindrich
; TITLE OF INVENTION: COLLAGEN BINDING PROTEIN COMPOSITIONS
; TITLE OF INVENTION: AND METHODS OF USE
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: U.S.
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/856,253
; FILING DATE: Concurrently Herewith
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/017,678
; FILING DATE: 16-MAY-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Kitchell, Barbara S.
; REGISTRATION NUMBER: 33,928
; REFERENCE/DOCKET NUMBER: TAMK:193
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (512) 418-3000
; TELEFAX: (512) 474-7577
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 139 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; US-08-856-253-8

Query Match          96.1%; Score 199; DB 3; Length 139;
Best Local Similarity 97.4%; Pred. No. 7.8e-20;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QNSGNSFEEDTPEDKPKRYEOGNIVIDIDFDSVPQIHG 38
Db 16 QNSGNSFEEDTPEDKPKRYEOGNIVIDIDFDSVPQIHG 53

RESULT 10
US-08-459-135A-10
; Sequence 10, Application US/08459135A
; Patent No. 5955078
; GENERAL INFORMATION:
; APPLICANT: BURMAN, Martin Karl Russel
; APPLICANT: CHOPRA, Ian
; APPLICANT: CRITCHLEY, Ian Alfred
; APPLICANT: KNOWLES, David Justin Charles
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN: MONOCLONAL ANTIBODY AND THEIR USE
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corporation
; STREET: 709 Swedeland Road
; CITY: King of Prussia
; STATE: PA
; COUNTRY: U.S.A.
; ZIP: 19406-0939
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
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; APPLICANT: Hook, Magnus
; APPLICANT: Patti, Joseph M.
; APPLICANT: House-Pomero, Karen
; APPLICANT: Stahanam, Narayana
; APPLICANT: Symersky, Jindrich
; TITLE OF INVENTION: COLLAGEN BINDING PROTEIN COMPOSITIONS
; TITLE OF INVENTION: AND METHODS OF USE
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: U.S.
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/856,253
; FILING DATE: Concurrently Herewith
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/017,678
; FILING DATE: 16-MAY-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Kitchell, Barbara S.
; REGISTRATION NUMBER: 33,928
; REFERENCE/DOCKET NUMBER: TAMK:193
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (512) 418-3000
; TELEFAX: (512) 474-7577
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 139 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; US-08-856-253-8

Query Match          96.1%; Score 199; DB 3; Length 139;
Best Local Similarity 97.4%; Pred. No. 7.8e-20;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QNSGNSFEEDTPEDKPKRYEOGNIVIDIDFDSVPQIHG 38
Db 16 QNSGNSFEEDTPEDKPKRYEOGNIVIDIDFDSVPQIHG 53

RESULT 10
US-08-459-135A-10
; Sequence 10, Application US/08459135A
; Patent No. 5955078
; GENERAL INFORMATION:
; APPLICANT: BURMAN, Martin Karl Russel
; APPLICANT: CHOPRA, Ian
; APPLICANT: CRITCHLEY, Ian Alfred
; APPLICANT: KNOWLES, David Justin Charles
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN: MONOCLONAL ANTIBODY AND THEIR USE
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corporation
; STREET: 709 Swedeland Road
; CITY: King of Prussia
; STATE: PA
; COUNTRY: U.S.A.
; ZIP: 19406-0939
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
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SOFTWARE: FastSeq, Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/459,135A
FILING DATE: 02-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB/94/00215
FILING DATE: 04-Feb-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Gimmil, Edward R
REGISTRATION NUMBER: 38,891
REFERENCE/DOCKET NUMBER: P30591C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-4478
TELEFAX: 610-270-5090
TELEX:
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 174 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: Protein
US-08-459-135A-10

Query Match 96.1%; Score 199; DB 2; Length 174;
Best Local Similarity 97.4%; Pred. No. 1e-19;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QNSGNQSFEDTPEDEKPKYEGGNIYDIDFDSVPQIHG 38
DB 2 QNSGNQSFEDTPEDEKPKYEGGNIYDIDFDSVPQIHG 39

RESULT 11
US-08-459-135A-13
Sequence 13, Application US/08459135A
Patent No. 5955078
GENERAL INFORMATION:
APPLICANT: BURHAM, Martin Karl Russel
APPLICANT: CHOPRA, Ian
APPLICANT: CRITCHLEY, Ian Alfred
APPLICANT: KNOWLES, David Justin Charles
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN: MONOCLONAL ANTIBODY AND THEIR US
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Smithkline Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
STATE: PA
COUNTRY: U.S.A.
ZIP: 19406-0939
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq, Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/459,135A
FILING DATE: 02-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB/94/00215
FILING DATE: 04-Feb-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Gimmil, Edward R
REGISTRATION NUMBER: 38,891
REFERENCE/DOCKET NUMBER: P30591C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-4478
TELEFAX: 610-270-5090
TELEX:

INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 174 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-459-135A-13

Query Match 96.1%; Score 199; DB 2; Length 174;
Best Local Similarity 97.4%; Pred. No. 1e-19;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QNSGNQSFEDTPEDEKPKYEGGNIYDIDFDSVPQIHG 38
DB 2 QNSGNQSFEDTPEDEKPKYEGGNIYDIDFDSVPQIHG 39

RESULT 12
US-08-495-559-10
Sequence 10, Application US/08495559A
Patent No. 6054572
GENERAL INFORMATION:
APPLICANT: BURHAM, Martin Karl Russel
APPLICANT: CHOPRA, Ian
APPLICANT: CRITCHLEY, Ian Alfred
APPLICANT: KNOWLES, David Justin Charles
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN: MONOCLONAL
TITLE OF INVENTION: ANTIBODY AND THEIR USE IN PREVENTING BACTERIAL ADHESION
FILE REFERENCE: P30591
CURRENT APPLICATION NUMBER: US/08/495,559A
CURRENT FILING DATE: 1995-08-03
EARLIER APPLICATION NUMBER: GB 9302289.5
EARLIER FILING DATE: 1993-02-05
EARLIER APPLICATION NUMBER: GB 9321592.9
EARLIER FILING DATE: 1993-10-20
NUMBER OF SEQ ID NOS: 13
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 10
LENGTH: 174
TYPE: PRT
ORGANISM: Staphylococcus aureus
US-08-495-559-10

Query Match 96.1%; Score 199; DB 3; Length 174;
Best Local Similarity 97.4%; Pred. No. 1e-19;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QNSGNQSFEDTPEDEKPKYEGGNIYDIDFDSVPQIHG 38
DB 2 QNSGNQSFEDTPEDEKPKYEGGNIYDIDFDSVPQIHG 39

RESULT 13
US-08-495-559-13
Sequence 13, Application US/08495559A
Patent No. 6054572
GENERAL INFORMATION:
APPLICANT: BURHAM, Martin Karl Russel
APPLICANT: CHOPRA, Ian
APPLICANT: CRITCHLEY, Ian Alfred
APPLICANT: KNOWLES, David Justin Charles
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN: MONOCLONAL
TITLE OF INVENTION: ANTIBODY AND THEIR USE IN PREVENTING BACTERIAL ADHESION
FILE REFERENCE: P30591
CURRENT APPLICATION NUMBER: US/08/495,559A
CURRENT FILING DATE: 1995-08-03
EARLIER APPLICATION NUMBER: GB 9302289.5
EARLIER FILING DATE: 1993-02-05
EARLIER APPLICATION NUMBER: GB 9321592.9
EARLIER FILING DATE: 1993-10-20
NUMBER OF SEQ ID NOS: 13
SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 13
 LENGTH: 174
 TYPE: PRT
 ORGANISM: Staphylococcus aureus
 US-08-495-559-13

Query Match 96.1%; Score 199; DB 3; Length 174;
 Best Local Similarity 97.4%; Pred. No. 1e-19;
 Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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 Db 2 QNSGNQSFEDTPEDKPKRYEQGNIVDIDFDSVPQIHG 39

RESULT 14
 US-08-495-559-6
 Sequence 6, Application US/08495559A
 Patent No. 6054572
 GENERAL INFORMATION:
 APPLICANT: BURHAM, Martin Karl Russel
 APPLICANT: CHOPRA, Ian
 APPLICANT: CRITCHLEY, Ian Alfred
 APPLICANT: KNOWLES, David Justin Charles
 TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN: MONOCLONAL
 TITLE OF INVENTION: ANTIBODY AND THEIR USE IN PREVENTING BACTERIAL ADHESION
 FILE REFERENCE: P30591
 CURRENT FILING DATE: 1995-08-03
 EARLIER APPLICATION NUMBER: GB 9302289.5
 EARLIER FILING DATE: 1993-02-05
 EARLIER APPLICATION NUMBER: GB 9321592.9
 EARLIER FILING DATE: 1993-10-20
 NUMBER OF SEQ ID NOS: 13
 SOFTWARE: FastSeq for Windows Version 3.0
 SEQ ID NO 6
 LENGTH: 176
 TYPE: PRT
 ORGANISM: Staphylococcus aureus
 US-08-495-559-6

Query Match 96.1%; Score 199; DB 3; Length 176;
 Best Local Similarity 97.4%; Pred. No. 1e-19;
 Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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 Db 2 QNSGNQSFEDTPEDKPKRYEQGNIVDIDFDSVPQIHG 39

RESULT 15
 US-08-459-135A-12
 Sequence 12, Application US/08459135A
 Patent No. 5955078
 GENERAL INFORMATION:
 APPLICANT: BURHAM, Martin Karl Russel
 APPLICANT: CHOPRA, Ian
 APPLICANT: CRITCHLEY, Ian Alfred
 APPLICANT: KNOWLES, David Justin Charles
 TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN: MONOCLONAL ANTIBODY AND THEIR US
 NUMBER OF SEQUENCES: 15
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: SmithKline Beecham Corporation
 STREET: 709 Swedeland Road
 CITY: King of Prussia
 STATE: PA
 COUNTRY: U S A
 ZIP: 19406-0939
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: Fastseq, Version 2.0

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/459,135A
 FILING DATE: 02-JUN-1995
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: PCT/GB/94/00215
 FILING DATE: 04-Feb-1994
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Gimmil, Edward R
 REGISTRATION NUMBER: 38,891
 REFERENCE/DOCKET NUMBER: P30591C2
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 610-270-4478
 TELEFAX: 610-270-5090
 TELEX:
 INFORMATION FOR SEQ ID NO: 12:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 178 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: Protein
 US-08-459-135A-12

Query Match 96.1%; Score 199; DB 2; Length 178;
 Best Local Similarity 97.4%; Pred. No. 1e-19;
 Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QNSGNQSFEDTPEDKPKRYEQGNIVDIDFDSVPQIHG 38
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 Db 2 QNSGNQSFEDTPEDKPKRYEQGNIVDIDFDSVPQIHG 39

Search completed: October 22, 2005, 05:46:44
 Job time : 22.2223 secs

GenCore version 5.1.6
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OM protein - protein search, using SW model

Run on: October 22, 2005, 11:35:03 ; Search time 70.1256 Seconds
(without alignments)
226.232 Million cell updates/sec

Title: US-10-731-238-40

Perfect score: 207
Sequence: 1 QNSGNQSPFEDTPEDKPKYEGCGNIVDIDFDSVPQIHG 38

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1862951 seqs, 417491010 residues

Total number of hits satisfying chosen parameters: 1862951

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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22: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	199	96.1	38	18	US-10-731-238-5
3	199	96.1	139	9	US-09-813-820-8
4	199	96.1	388	8	US-08-801-062-1
5	199	96.1	559	15	US-10-329-624-5251
6	199	96.1	767	9	US-09-815-242-5899
7	199	96.1	767	9	US-09-815-242-13140
8	199	96.1	940	17	US-10-470-048B-424
9	199	96.1	948	17	US-10-470-048B-69
10	199	96.1	961	15	US-10-282-122A-43778
11	199	96.1	961	15	US-10-282-122A-43778

12	199	96.1	1018	9	US-09-815-242-5797	Sequence 5797, Ap
13	199	96.1	1018	9 <td>US-09-815-242-12838</td> <td>Sequence 12838, A</td>	US-09-815-242-12838	Sequence 12838, A
14	199	96.1	1018	17 <td>US-10-470-048B-68</td> <td>Sequence 68, Appl</td>	US-10-470-048B-68	Sequence 68, Appl
15	199	96.1	1027	8 <td>US-08-781-986A-5254</td> <td>Sequence 5254, Ap</td>	US-08-781-986A-5254	Sequence 5254, Ap
16	199	96.1	1027	15 <td>US-10-329-624-5254</td> <td>Sequence 43827, A</td>	US-10-329-624-5254	Sequence 43827, A
17	199	96.1	1038	15 <td>US-10-282-122A-43827</td> <td>Sequence 43827, A</td>	US-10-282-122A-43827	Sequence 43827, A
18	199	93.2	38	18 <td>US-10-731-238-36</td> <td>Sequence 36, Appl</td>	US-10-731-238-36	Sequence 36, Appl
19	199	93.2	38	18 <td>US-10-731-238-37</td> <td>Sequence 37, Appl</td>	US-10-731-238-37	Sequence 37, Appl
20	199	93.2	38	18 <td>US-10-731-238-39</td> <td>Sequence 39, Appl</td>	US-10-731-238-39	Sequence 39, Appl
21	199	93.2	38	18 <td>US-10-731-238-41</td> <td>Sequence 41, Appl</td>	US-10-731-238-41	Sequence 41, Appl
22	199	93.2	38	18 <td>US-10-731-238-42</td> <td>Sequence 42, Appl</td>	US-10-731-238-42	Sequence 42, Appl
23	199	92.8	38	18 <td>US-10-731-238-43</td> <td>Sequence 43, Appl</td>	US-10-731-238-43	Sequence 43, Appl
24	199	92.3	38	18 <td>US-10-731-238-44</td> <td>Sequence 44, Appl</td>	US-10-731-238-44	Sequence 44, Appl
25	199	92.3	38	18 <td>US-10-731-238-45</td> <td>Sequence 45, Appl</td>	US-10-731-238-45	Sequence 45, Appl
26	199	92.3	38	18 <td>US-10-731-238-46</td> <td>Sequence 46, Appl</td>	US-10-731-238-46	Sequence 46, Appl
27	199	92.3	38	18 <td>US-10-731-238-47</td> <td>Sequence 47, Appl</td>	US-10-731-238-47	Sequence 47, Appl
28	199	91.3	38	18 <td>US-10-731-238-48</td> <td>Sequence 48, Appl</td>	US-10-731-238-48	Sequence 48, Appl
29	188.5	91.1	39	18 <td>US-10-731-238-49</td> <td>Sequence 49, Appl</td>	US-10-731-238-49	Sequence 49, Appl
30	180.5	87.2	39	18 <td>US-10-731-238-50</td> <td>Sequence 50, Appl</td>	US-10-731-238-50	Sequence 50, Appl
31	180	87.0	38	18 <td>US-10-731-238-51</td> <td>Sequence 51, Appl</td>	US-10-731-238-51	Sequence 51, Appl
32	174	84.1	38	18 <td>US-10-731-238-52</td> <td>Sequence 52, Appl</td>	US-10-731-238-52	Sequence 52, Appl
33	174	84.1	38	18 <td>US-10-731-238-53</td> <td>Sequence 53, Appl</td>	US-10-731-238-53	Sequence 53, Appl
34	173	83.6	38	18 <td>US-10-731-238-54</td> <td>Sequence 54, Appl</td>	US-10-731-238-54	Sequence 54, Appl
35	172	83.1	38	18 <td>US-10-731-238-55</td> <td>Sequence 55, Appl</td>	US-10-731-238-55	Sequence 55, Appl
36	172	83.1	38	18 <td>US-10-731-238-56</td> <td>Sequence 56, Appl</td>	US-10-731-238-56	Sequence 56, Appl
37	171	82.6	38	18 <td>US-10-731-238-57</td> <td>Sequence 57, Appl</td>	US-10-731-238-57	Sequence 57, Appl
38	170	82.1	38	18 <td>US-10-731-238-58</td> <td>Sequence 58, Appl</td>	US-10-731-238-58	Sequence 58, Appl
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41	149	72.0	36	18 <td>US-10-731-238-61</td> <td>Sequence 61, Appl</td>	US-10-731-238-61	Sequence 61, Appl
42	141	68.1	31	14	US-10-287-821-1	Sequence 1, Appl
43	141	68.1	31	14	US-10-287-821-2	Sequence 2, Appl
44	81.5	35.4	37	20	US-11-066-697-1134	Sequence 1134, Ap
45	74	35.7	14	18	US-10-731-238-60	Sequence 60, Appl

ALIGNMENTS

RESULT 1
US-10-731-238-40
Sequence 40, Application US/10731238
Publication No. US20050123552A1
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
Patli, Joseph M.
House-Pompeo, Karen L.
Speziale, Pietro
Joh, Danny
McCaivin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/731,238
FILING DATE: 10-Dec-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE: 21-Jan-1998
APPLICATION NUMBER: US 60/036,139

FILED DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAMK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 40:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 40:
US-10-731-238-40

Query Match 100.0%; Score 207; DB 18; Length 38;
Best Local Similarity 100.0%; Pred. No. 3,7e-20;
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QNSGNQSFEDTPEDKPKRYEGGNIIVDIDFDSVPQIHG 38
1 QNSGNQSFEDTPEDKPKRYEGGNIIVDIDFDSVPQIHG 38

Db 1 QNSGNQSFEDTPEDKPKRYEGGNIIVDIDFDSVPQIHG 38

RESULT 2
US-10-731-238-5
Sequence 5, Application US/10731238
Publication No. US20050123552A1
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
Patti, Joseph M.
House-Pompeo, Karen L.
Speziale, Pietro
Joh, Danny
McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/731,238
FILING DATE: 10-Dec-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE: 21-Jan-1998
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAMK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>

TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-10-731-238-5

Query Match 96.1%; Score 199; DB 18; Length 38;
Best Local Similarity 97.4%; Pred. No. 4.3e-19;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QNSGNQSFEDTPEDKPKRYEGGNIIVDIDFDSVPQIHG 38
1 QNSGNQSFEDTPEDKPKRYEGGNIIVDIDFDSVPQIHG 38

Db 1 QNSGNQSFEDTPEDKPKRYEGGNIIVDIDFDSVPQIHG 38

RESULT 3
US-09-813-820-8
Sequence 8, Application US/09813820
Patent No. US20020102262A1
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
Patti, Joseph M.
House-Pompeo, Karen
Schanam, Narayana
Symersky, Jindrich
TITLE OF INVENTION: COLLAGEN BINDING PROTEIN COMPOSITIONS
AND METHODS OF USE
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: Texas
COUNTRY: U.S.
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/813,820
FILING DATE: 22-Mar-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/856,253
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Kitchell, Barbara S.
REGISTRATION NUMBER: 33,928
REFERENCE/DOCKET NUMBER: TAMK:193
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
TELEFAX: (512) 474-7577
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 139 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-09-813-820-8

Query Match 96.1%; Score 199; DB 9; Length 139;
Best Local Similarity 97.4%; Pred. No. 2e-18;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QNSGNQSFEDTPEDKPKRYEGGNIIVDIDFDSVPQIHG 38
1 QNSGNQSFEDTPEDKPKRYEGGNIIVDIDFDSVPQIHG 38

Db 16 QNSGNQSFEDTPEDKPKRYEGGNIIVDIDFDSVPQIHG 53

RESULT 4
US-08-901-062-1
Sequence 1, Application US/08901062

Publication No. US20020025324A1
GENERAL INFORMATION:
APPLICANT: SEALS, JONATHAN R.
TITLE OF INVENTION: RECOMBINANT BIVALENT BACTERIAL VACCINE
TITLE OF INVENTION: FOR THE PREVENTION OF MASTITIS
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESSES:
ADDRESSES: HALE AND DORR LLP
STREET: 60 State Street
CITY: Boston
STATE: MA
COUNTRY: United States Of America
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/901,062
FILING DATE: 25-JUL-1997
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Baker, Hollie L.
REGISTRATION NUMBER: 31,321
REFERENCE/DOCKET NUMBER: 106941.153
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 526-6000
TELEFAX: (617) 526-5000
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 388 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-901-062-1

Query Match 96.1%; Score 199; DB 8; Length 388;
Best Local Similarity 97.4%; Pred. No. 6, 7e-18;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

1 ONSGNSFEEDTPEDEKPKYEOGNNIVDIDFDSVPQIHG 38
265 ONSGNSFEEDTPEDEKPKYEOGNNIVDIDFDSVPQIHG 302
RESULT 5
US-08-781-986A-5251
Sequence 5251, Application US/08781986A
Publication No. US20030054436A1
GENERAL INFORMATION:
APPLICANT: Charles Kunech
TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
NUMBER OF SEQUENCES: 5255
CORRESPONDENCE ADDRESSES:
ADDRESSES: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COUNTRY: USA
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/781,986A
FILING DATE:
CLASSIFICATION: 435

PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Benson, Bob
REGISTRATION NUMBER: 30,446
REFERENCE/DOCKET NUMBER: PB248PP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8512
TELEFAX: (301) 309-8504
INFORMATION FOR SEQ ID NO: 5251:
SEQUENCE CHARACTERISTICS:
LENGTH: 559 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-781-986A-5251

Query Match 96.1%; Score 199; DB 8; Length 559;
Best Local Similarity 97.4%; Pred. No. 1e-17;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

1 ONSGNSFEEDTPEDEKPKYEOGNNIVDIDFDSVPQIHG 38
301 ONSGNSFEEDTPEDEKPKYEOGNNIVDIDFDSVPQIHG 338

RESULT 6
US-10-329-624-5251
Sequence 5251, Application US/10329624
Publication No. US20040043037A1
GENERAL INFORMATION:
APPLICANT: Charles Kunech
Gill H. Choi
Patrick S. Dillon
Craig A. Rosen
Steven C. Barash
Michael R. Fannon
TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
NUMBER OF SEQUENCES: 5256
CORRESPONDENCE ADDRESSES:
ADDRESSES: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COUNTRY: USA
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/329, 624
FILING DATE: 27-Dec-2002
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/956,171
FILING DATE: October 20, 1997
APPLICATION NUMBER: 60/009,861
FILING DATE: January 5, 1996
APPLICATION NUMBER: 08/781,986
FILING DATE: January 3, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Mark J. Hyman
REGISTRATION NUMBER: 46,789
REFERENCE/DOCKET NUMBER: PB248P1D1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (240) 314-1224
TELEFAX: (301) 309-8439
INFORMATION FOR SEQ ID NO: 5251:
SEQUENCE CHARACTERISTICS:
LENGTH: 559 amino acids

TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 5251:
US-10-329-624-5251

Query Match 96.1%; Score 199; DB 15; Length 559;
Best Local Similarity 97.4%; Pred. No. 1e-17;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QNSGNQSFEDTPEBKPKYEGGNIVIDIDFDSVPQIHG 38
Db 301 QNSGNQSFEDTPEBKPKYEGGNIVIDIDFDSVPQIHG 338

RESULT 7
US-09-815-242-5899

Sequence 5899, Application US/09815242
Patent No. US20020061569A1

GENERAL INFORMATION:

APPLICANT: Haselbeck, Robert

APPLICANT: Ohlsen, Karl L.

APPLICANT: Zykkind, Judith W.

APPLICANT: Wall, Daniel

APPLICANT: Trawick, John D.

APPLICANT: Carr, Grant J.

APPLICANT: Yamamoto, Robert T.

APPLICANT: Xu, H. Howard

TITLE OF INVENTION: Identification of Essential Genes in

FILE REFERENCE: ELITRA.011A

CURRENT APPLICATION NUMBER: US/09/815,242

CURRENT FILING DATE: 2001-03-21

PRIOR APPLICATION NUMBER: 60/191,078

PRIOR FILING DATE: 2000-03-21

PRIOR APPLICATION NUMBER: 60/206,848

PRIOR FILING DATE: 2000-05-23

PRIOR APPLICATION NUMBER: 60/207,727

PRIOR FILING DATE: 2000-05-26

PRIOR APPLICATION NUMBER: 60/242,578

PRIOR FILING DATE: 2000-10-23

PRIOR APPLICATION NUMBER: 60/253,625

PRIOR FILING DATE: 2000-11-27

PRIOR APPLICATION NUMBER: 60/257,931

PRIOR FILING DATE: 2000-12-22

PRIOR APPLICATION NUMBER: 60/269,308

PRIOR FILING DATE: 2001-02-16

NUMBER OF SEQ ID NOS: 14110

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 5899

LENGTH: 767

TYPE: PRT

ORGANISM: Staphylococcus aureus

US-09-815-242-5899

Query Match 96.1%; Score 199; DB 9; Length 767;
Best Local Similarity 97.4%; Pred. No. 1.5e-17;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QNSGNQSFEDTPEBKPKYEGGNIVIDIDFDSVPQIHG 38
Db 682 QNSGNQSFEDTPEBKPKYEGGNIVIDIDFDSVPQIHG 719

RESULT 8
US-09-815-242-13140

Sequence 13140, Application US/09815242
Patent No. US20020061569A1

GENERAL INFORMATION:

APPLICANT: Haselbeck, Robert

APPLICANT: Ohlsen, Karl L.

APPLICANT: Zykkind, Judith W.

APPLICANT: Wall, Daniel
APPLICANT: Trawick, John D.
APPLICANT: Carr, Grant J.
APPLICANT: Yamamoto, Robert T.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in
FILE REFERENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: US/09/815,242

CURRENT FILING DATE: 2001-03-21

PRIOR APPLICATION NUMBER: 60/191,078

PRIOR FILING DATE: 2000-03-21

PRIOR APPLICATION NUMBER: 60/206,848

PRIOR FILING DATE: 2000-05-23

PRIOR APPLICATION NUMBER: 60/207,727

PRIOR FILING DATE: 2000-05-26

PRIOR APPLICATION NUMBER: 60/242,578

PRIOR FILING DATE: 2000-10-23

PRIOR APPLICATION NUMBER: 60/253,625

PRIOR FILING DATE: 2000-11-27

PRIOR APPLICATION NUMBER: 60/257,931

PRIOR FILING DATE: 2000-12-22

PRIOR APPLICATION NUMBER: 60/269,308

PRIOR FILING DATE: 2001-02-16

NUMBER OF SEQ ID NOS: 14110

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 13140

LENGTH: 767

TYPE: PRT

ORGANISM: Staphylococcus aureus

US-09-815-242-13140

Query Match 96.1%; Score 199; DB 9; Length 767;
Best Local Similarity 97.4%; Pred. No. 1.5e-17;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QNSGNQSFEDTPEBKPKYEGGNIVIDIDFDSVPQIHG 38
Db 682 QNSGNQSFEDTPEBKPKYEGGNIVIDIDFDSVPQIHG 719

RESULT 9
US-10-470-048B-424

Sequence 424, Application US/10470048B
Publication No. US20050037444A1

GENERAL INFORMATION:

APPLICANT: MEINKE ET AL.

TITLE OF INVENTION: A METHOD FOR IDENTIFICATION, ISOLATION AND PRODUCTION OF

FILE REFERENCE: SONN.035US

CURRENT APPLICATION NUMBER: US/10/470,048B

CURRENT FILING DATE: 2003-07-25

NUMBER OF SEQ ID NOS: 603

SOFTWARE: PatentIn version 3.1

SEQ ID NO 424

LENGTH: 940

TYPE: PRT

ORGANISM: Staphylococcus aureus

US-10-470-048B-424

Query Match 96.1%; Score 199; DB 17; Length 940;
Best Local Similarity 97.4%; Pred. No. 1.9e-17;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QNSGNQSFEDTPEBKPKYEGGNIVIDIDFDSVPQIHG 38
Db 682 QNSGNQSFEDTPEBKPKYEGGNIVIDIDFDSVPQIHG 719

RESULT 10
US-10-470-048B-69

Sequence 69, Application US/10470048B
Publication No. US20050037444A1

```
GENERAL INFORMATION:
APPLICANT: MEINKE ET AL.
TITLE OF INVENTION: A METHOD FOR IDENTIFICATION, ISOLATION AND PRODUCTION OF
TITLE OF INVENTION: ANTIGENS TO A SPECIFIC PATHOGEN
FILE REFERENCE: SONN:035US
CURRENT APPLICATION NUMBER: US/10/470,048B
NUMBER OF SEQ ID NOS: 603
SOFTWARE: Patentin version 3.1
SEQ ID NO 69
LENGTH: 948
TYPE: PRT
ORGANISM: Staphylococcus aureus
US-10-470-048B-69

Query Match          96.1%; Score 199; DB 17; Length 948;
Best Local Similarity 97.4%; Pred. No. 1,9e-17;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QNSGNSFEEDTPEDKPKYEGGNIIVDIDFDSVPQIHG 38
Db 690 QNSGNSFEEDTPEDKPKYEGGNIIVDIDFDSVPQIHG 727

RESULT 11
US-10-282-122A-43778
Sequence 43778, Application US/10282122A
Publication No. US20040029129A1
GENERAL INFORMATION:
APPLICANT: Mang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari
APPLICANT: Zyskind, Judith
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John
APPLICANT: Carr, Grant
APPLICANT: Yamamoto, Robert
APPLICANT: Forsyth, R.
APPLICANT: Xu, H.
TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REFERENCE: ELITRA.034A
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/230,335
PRIOR FILING DATE: 2000-09-06
PRIOR APPLICATION NUMBER: 60/230,347
PRIOR FILING DATE: 2000-09-09
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/267,636
PRIOR FILING DATE: 2001-02-09
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
Remaining Prior Application data removed - See File Wrapper or PAM.
NUMBER OF SEQ ID NOS: 78614
SOFTWARE: Patentin version 3.1
SEQ ID NO 43778
LENGTH: 961
TYPE: PRT
ORGANISM: Staphylococcus aureus
US-10-282-122A-43778
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Query Match          96.1%; Score 199; DB 15; Length 961;
Best Local Similarity 97.4%; Pred. No. 1,9e-17;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QNSGNSFEEDTPEDKPKYEGGNIIVDIDFDSVPQIHG 38
Db 693 QNSGNSFEEDTPEDKPKYEGGNIIVDIDFDSVPQIHG 730

RESULT 12
US-09-815-242-5797
Sequence 5797, Application US/09815242
Patent No. US20020061569A1
GENERAL INFORMATION:
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari L.
APPLICANT: Zyskind, Judith W.
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John D.
APPLICANT: Carr, Grant J.
APPLICANT: Yamamoto, Robert T.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in
FILE REFERENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 5797
LENGTH: 1018
TYPE: PRT
ORGANISM: Staphylococcus aureus
US-09-815-242-5797

Query Match          96.1%; Score 199; DB 9; Length 1018;
Best Local Similarity 97.4%; Pred. No. 2,1e-17;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QNSGNSFEEDTPEDKPKYEGGNIIVDIDFDSVPQIHG 38
Db 746 QNSGNSFEEDTPEDKPKYEGGNIIVDIDFDSVPQIHG 783

RESULT 13
US-09-815-242-12838
Sequence 12838, Application US/09815242
Patent No. US20020061569A1
GENERAL INFORMATION:
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari L.
APPLICANT: Zyskind, Judith W.
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John D.
APPLICANT: Carr, Grant J.
APPLICANT: Yamamoto, Robert T.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in
```



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; TITLE OF INVENTION: Prokaryotes
; FILE REFERENCE: ELITRA.011a
; CURRENT APPLICATION NUMBER: US/09/815,242
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO: 12838
; LENGTH: 1018
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
; US-09-815-242-12838

Query Match      96.1%; Score 199; DB 9; Length 1018;
Best Local Similarity 97.4%; Pred. No. 2.1e-17;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY      1  ONSGNSFEEDTPEDKPKYEGGNIVIDIDFDSVPQIHG 38
Db      746  ONSGNSFEEDTPEDKPKYEGGNIVIDIDFDSVPQIHG 783

RESULT 14
US-10-470-048B-68
; Sequence 68, Application US/10470048B
; Publication No. US2005003744A1
; GENERAL INFORMATION:
; APPLICANT: MEINKE ET AL.
; TITLE OF INVENTION: A METHOD FOR IDENTIFICATION, ISOLATION AND PRODUCTION OF
; FILE REFERENCE: SONN-035US
; CURRENT APPLICATION NUMBER: US/10/470,048B
; NUMBER OF SEQ ID NOS: 603
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 68
; LENGTH: 1018
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
; US-10-470-048B-68

Query Match      96.1%; Score 199; DB 17; Length 1018;
Best Local Similarity 97.4%; Pred. No. 2.1e-17;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY      1  ONSGNSFEEDTPEDKPKYEGGNIVIDIDFDSVPQIHG 38
Db      746  ONSGNSFEEDTPEDKPKYEGGNIVIDIDFDSVPQIHG 783

RESULT 15
US-08-781-986A-5254
; Sequence 5254, Application US/08781986A
; Publication No. US20030054436A1
; GENERAL INFORMATION:
; APPLICANT: Charles Kunsch
; TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
; NUMBER OF SEQUENCES: 5255
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Human Genome Sciences, Inc.
```

```

; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/781,986A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Benson, Bob
; REGISTRATION NUMBER: 30,446
; REFERENCE/DOCKET NUMBER: PB248PP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 5254:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1027 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-781-986A-5254

Query Match      96.1%; Score 199; DB 8; Length 1027;
Best Local Similarity 97.4%; Pred. No. 2.1e-17;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY      1  ONSGNSFEEDTPEDKPKYEGGNIVIDIDFDSVPQIHG 38
Db      755  ONSGNSFEEDTPEDKPKYEGGNIVIDIDFDSVPQIHG 792

Search completed: October 22, 2005, 12:09:26
Job time : 70.1256 secs
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 22, 2005, 04:14:19 ; Search time 13.8905 Seconds
(without alignments)
263.219 Million cell updates/sec

Title: US-10-731-238-40

Perfect score: 207
Sequence: 1 QNSGNQSFEDPTPEBKPKYEGCGNIVDIDFDSVPQIHG 38

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :
1: p1r1: *
2: p1r2: *
3: p1r3: *
4: p1r4: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	199	96.1	940	2 S19702	fibronectin-binding
2	199	96.1	961	2 G90053	hypothetical prote
3	199	96.1	1018	2 A32192	fibronectin-binding
4	199	96.1	1038	2 H90053	hypothetical prote
5	65	31.4	1460	2 D81675	polymorphic membra
6	61	29.5	979	2 S62469	probable transcrip
7	61	29.5	1952	2 T48814	hypothetical prote
8	59	28.5	396	2 E84196	cell division prot
9	56.5	27.3	155	1 RNBIR6	DNA-directed RNA p
10	56.5	27.3	968	2 T25657	hypothetical prote
11	55	26.6	222	2 A26653	glutathione trans
12	55	26.6	223	1 A27848	glutathione trans
13	55	26.6	369	2 D72240	tRNA guanine trans
14	55	26.6	428	2 T32952	hypothetical prote
15	54.5	26.3	1273	1 TDRJLT	hypothetical prote
16	54.5	26.3	1291	1 A28334	protein-tyrosine-p
17	54.5	26.3	1291	1 A28334	p54/58N - human
18	53.5	25.8	500	2 C81657	general secretion
19	53.5	25.8	501	2 D71999	probable gen. secr
20	53.5	25.8	1439	2 T27110	hypothetical prote
21	53	25.6	183	2 D83840	hypothetical prote
22	52.5	25.4	817	2 T03852	protein phosphatase
23	52	25.1	222	1 XURTG	glutathione trans
24	52	25.1	241	2 H97723	hypothetical prote
25	52	25.1	241	2 C71725	amino-acid ABC tra
26	52	25.1	265	2 S57978	hypothetical prote
27	52	25.1	294	2 T50664	methyleneretraydr
28	52	25.1	346	2 D82898	hypothetical prote
29	52	25.1	837	2 T19825	hypothetical prote

30	52	25.1	1091	2 S33850	fibronectin-binding
31	52	25.1	1183	2 S65236	probable membrane
32	52	25.1	1817	2 T34249	hypothetical prote
33	52	25.1	2168	2 T30171	nuclein - mouse
34	51.5	24.9	437	2 S11925	S-locus-specific g
35	51.5	24.9	494	2 T14516	S-locus-specific g
36	51.5	24.9	832	1 S71788	P/CAF protein - hu
37	51.5	24.9	842	2 S27533	non-motile and pha
38	51.5	24.9	842	2 S27533	histidine protein
39	51.5	24.9	935	2 T50774	probable transla
40	51	24.6	168	2 T33564	hypothetical prote
41	51	24.6	195	2 A88110	protein T24E12.11
42	51	24.6	265	1 MNVN	nonstructural prot
43	51	24.6	426	2 R81835	probable periplasm
44	51	24.6	426	2 C81129	hypothetical prote
45	51	24.6	442	2 H72266	astB/cnuR-related

ALIGNMENTS

RESULT 1

S19702
C:Species: Staphylococcus aureus
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
C:Accession: S19702
R:Johansen, K.; Signaes, C.; Mueller, H.P.; Lindberg, M.
Eur. J. Biochem. 202, 1041-1048, 1991
A:Title: Two different genes encode fibronectin binding proteins in Staphylococcus aureus
A:Reference number: S19702; MUID:92111475; PMID:1837266
A:Accession: S19702
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-940 <JOB>
A:Cross-references: UNIPROT:053682; EMBL:X62992; NID:g49040; PIDN:CAA44726.1; PID:958156;
C:Keywords: fibronectin binding

Query Match 96.1%; Score 199; DB 2; Length 940;
Best Local Similarity 97.4%; Pred. No. 5.4e-18;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QNSGNQSFEDPTPEBKPKYEGCGNIVDIDFDSVPQIHG 38

DB 682 QNSGNQSFEDPTPEBKPKYEGCGNIVDIDFDSVPQIHG 719

RESULT 2

G90053
C:Species: Staphylococcus aureus

C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004

C:Accession: G90053
R:Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguchi, A.; Mizutani-U, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.;

C:Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiratsugu, K.
Lancet 357, 1225-1240, 2001

A:Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.
A:Reference number: A89758; MUID:21111952; PMID:11418146

A:Accession: G90053

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-961 <KUR>
A:Cross-references: UNIPROT:Q99RD3; GB:BA000018; PID:G13702452; PIDN:BA843593.1; GSPDB:G

A:Experimental source: strain N315

A:Gene: fnbB

Query Match 96.1%; Score 199; DB 2; Length 961;
Best Local Similarity 97.4%; Pred. No. 5.5e-18;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QNSGNQSFEDPTPEBKPKYEGCGNIVDIDFDSVPQIHG 38

Db 693 ONSGNQSFEDTPEBKPKYEGGNIIVDIDFDSVPQIHG 730

RESULT 3

A32192

fibronectin-binding protein - Staphylococcus aureus

C:Species: Staphylococcus aureus

C:Date: 31-Jul-1989 #sequence_revision 31-Jul-1989 #text_change 16-Feb-1997

C:Accession: A32192

R:Signaas, C.; Raucet, G.; Joensson, K.; Lindgren, P.E.; Anantharamaiah, G.M.; Heoek, M.

Proc. Natl. Acad. Sci. U.S.A. 86, 699-703, 1989

A:Title: Nucleotide sequence of the gene for a fibronectin-binding protein from Staphylo

A:Reference number: A32192; MUID:8909898; PMID:2521391

A:Accession: A32192

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-1018 <SIG>

A:Cross-references: GB:J04151

C:Keywords: fibronectin binding

Query Match 96.1%; Score 199; DB 2; Length 1018;
Best Local Similarity 97.4%; Pred. No. 5.9e-18;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

1 ONSGNQSFEDTPEBKPKYEGGNIIVDIDFDSVPQIHG 38

Db 746 ONSGNQSFEDTPEBKPKYEGGNIIVDIDFDSVPQIHG 783

RESULT 4

H90053

hypothetical protein fnb [imported] - Staphylococcus aureus (strain N315)

C:Species: Staphylococcus aureus

C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004

C:Accession: H90053

R:Kuroda, M.; Ohca, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguc

ma, A.; Mizutani-Uji, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.;

C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramoto, K.

Lancet 357, 1225-1240, 2001

A:Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.

A:Reference number: A89758; MUID:21311952; PMID:11418146

A:Accession: H90053

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-1038 <KUR>

A:Cross-references: UNIPROT:Q098D2; GB:BA000018; PID:g13702453; PIDN:BAB43594.1; GSPDB:G

A:Experimental source: strain N315

C:Genetics:

A:Gene: fnb

Query Match 96.1%; Score 199; DB 2; Length 1038;
Best Local Similarity 97.4%; Pred. No. 6e-18;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

1 ONSGNQSFEDTPEBKPKYEGGNIIVDIDFDSVPQIHG 38

Db 742 ONSGNQSFEDTPEBKPKYEGGNIIVDIDFDSVPQIHG 779

RESULT 5

D81675

polymorphic membrane protein B/C family TC0695 [imported] - Chlamydia muridarum (strain

C:Species: Chlamydia muridarum, Chlamydia trachomatis MoPn

C:Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004

C:Accession: D81675

R:Read, T.D.; Brumham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hickey,

Nucleic Acids Res. 28, 1397-1406, 2000

A:Title: Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39.

A:Reference number: A81500; MUID:20150255; PMID:10684935

A:Accession: D81675

A:Status: preliminary

A:Molecule type: DNA
A:Residues: 1-1460 <TET>
A:Cross-references: UNIPROT:Q09JY1; GB:AE002338; GB:AE002160; NID:g7190724; PIDN:AAF39511
A:Experimental source: strain N199 (MoPn)
C:Genetics:
A:Gene: TC0695

Query Match 31.4%; Score 65; DB 2; Length 1460;
Best Local Similarity 35.3%; Pred. No. 4.3;
Matches 12; Conservative 9; Mismatches 13; Indels 0; Gaps 0;

2 NSGNQSFEDTPEBKPKYEGGNIIVDIDFDSVPQ 35

Db 39 SSSQSFTEIIPENGAEYRVSGDVFSDFGNIPE 72

RESULT 6

S62469

probable transcription initiation factor tfl1d subunit - fission yeast (Schizosaccharomy

C:Species: Schizosaccharomyces pombe

C:Date: 16-May-1996 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004

C:Accession: J38580; S62469

R:Barcock, K.; Churcher, C.M.; Barrell, B.G.; Rajandream, M.A.; Walsh, S.V.

submitted to the EMBL Data Library, October 1995

A:Reference number: 221745

A:Accession: J38580

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-979 <BA2>

A:Cross-references: UNIPROT:Q09813; EMBL:Z54354; NID:g1019398; PIDN:CAA91179.1; PID:g101;

A:Experimental source: strain 972h-; cosmid c2G11

C:Genetics:

A:Gene: SPAC2G11.14

A:Map position: 1L

A:introns: 21/3; 212/1; 261/3

C:Keywords: transcription initiation

Query Match 29.5%; Score 61; DB 2; Length 979;
Best Local Similarity 39.4%; Pred. No. 9.1;
Matches 13; Conservative 3; Mismatches 9; Indels 8; Gaps 1;

5 NSQSFEDTPEBKPKYEGGNIIVDIDFDSVPQIH 37

Db 57 DSSFENSNPDGPNYR-----DFDFMGSIH 81

RESULT 7

T48814

hypothetical protein 15B6.220 [imported] - Neurospora crassa

C:Species: Neurospora crassa

C:Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 09-Jul-2004

C:Accession: T48814

R:Schulte, U.; Altm, V.; Heideisel, J.; Brandt, P.; Fattmann, B.; Holland, R.; Nyakatura,

submitted to the Protein Sequence Database, April 2000

A:Reference number: 224541

A:Accession: T48814

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-1952 <SCH>

A:Cross-references: UNIPROT:Q096T1; EMBL:AL353822; GSPDB:GN00112; NCSP:15B6.220

A:Experimental source: cosmid config 15B6; strain 74

C:Genetics:

A:Gene: NCSP:15B6.220

A:Map position: 2

A:introns: 281/3

Query Match 29.5%; Score 61; DB 2; Length 1952;
Best Local Similarity 34.3%; Pred. No. 20;
Matches 12; Conservative 7; Mismatches 14; Indels 2; Gaps 1;

4 GNSQSFEDTPEBKPKYEGGNIIVDIDFDSVPQI 36

Db 545 GKTGAEEYEPETPARRYSEGGKEMSPDFSIHIV 579

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RESULT 8
E84196
cell division protein [imported] - Halobacterium sp. NRC-1
C:Species: Halobacterium sp. NRC-1
C:Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
C:Accession: E84196
R:Ng, W.V.; Kennedy, S.P.; Mahatras, G.G.; Bergquist, B.; Pan, M.; Shukla, H.D.; Lasky, S.;
Leithauer, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Jablo
Jung, K.H.; Alm, M.; Freitas, T. 12176-12181, 2000
Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000
A:Author: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Edhardt, H.; Lowe, T.M.; Li
A:Title: Genome sequence of Halobacterium species NRC-1.
A:Reference number: A84160; MWID:20504483; PMID:11016950
A:Accession: E84196
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-396 <STO>
A:Cross-references: UNIPROT:Q9H571; GB:AE004437; NID:G10579993; PIDN:AA618937.1; GSPDB:G
C:Genetics:
A:Gene: fteZ1
C:Superfamily: cell division protein fteZ

Query Match 28.5%; Score 59; DB 2; Length 396;
Best Local Similarity 40.7%; Pred. No. 5.8;
Matches 11; Conservative 6; Mismatches 10; Indels 0; Gaps 0;

QY 4 GNSGSEEDTPEDKPKYEGGNIYDIDF 30
DB 368 GDGPAQESTPEPEPEPQAGSEIEDIDY 394

RESULT 9
RMBYR6
DNA-directed RNA polymerase (EC 2.7.7.6) chain RPO26 - yeast (Saccharomyces cerevisiae)
N:Alternate names: DNA-directed RNA polymerase 23k chain; DNA-directed RNA polymerase II
C:Species: Saccharomyces cerevisiae
C:Date: 30-Sep-1992 #sequence_revision 30-Sep-1992 #text_change 09-Jul-2004
C:Accession: G13307; A26352; B34588; A38846; S58817
R:Archambault, J.; Schappert, K.T.; Priesen, J.D.
Mol. Cell. Biol. 10, 6123-6131, 1990
A:Title: A suppressor of an RNA polymerase II mutation of Saccharomyces cerevisiae encod
A:Reference number: A36352; MWID:91061718; PMID:2247052
A:Accession: G13307
A:Molecule type: DNA
A:Residues: 1-155 <ARCI>
A:Cross-references: UNIPROT:P20435; EMBL:M33924; NID:G172452; PIDN:AAA34989.1; PID:G1724
A:Accession: A36352
A:Molecule type: mRNA
A:Residues: 1-155 <ARC>
A:Cross-references: GB:M33924; NID:G172452; PIDN:AAA34989.1; PID:G172453
R:Woychik, N.A.; Liao, S.W.; Kolodziej, P.A.; Young, R.A.
Genes Dev. 4, 313-323, 1990
A:Title: Subunits shared by eukaryotic nuclear RNA polymerases.
A:Reference number: A34588; MWID:90249736; PMID:2186966
A:Accession: B34588
A:Status: not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 1-155 <NOY1>
A:Cross-references: GB:X53288; NID:G287823; PIDN:CAA37382.1; PID:G287824
A:Accession: A38846
A:Molecule type: protein
A:Residues: 48-60/99-115 <NOY2>
R:Miller, N.
submitted to the EMBL Data Library, April 1995
A:Description: The sequence of S. cerevisiae cosmid 9677.
A:Reference number: S58816
A:Accession: S58817
A:Molecule type: DNA
A:Residues: 1-155 <ML>
A:Cross-references: EMBL:U25841; NID:G786295; PIDN:AA64616.1; PID:G786304; GSPDB:GN0001
C:Comment: This protein is a subunit of DNA-directed RNA polymerases I, II, and III.

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C:Genetics:
A:Gene: SGD:RPO26; RPB6; MIPS:YPR187W
A:Cross-references: SGD:S0006391; MIPS:YPR187W
A:Map position: 168
A:Introns: 7/2
C:Superfamily: DNA-directed RNA polymerase chain RPO26
C:Keywords: nucleotidyltransferase
F/3-42/Region: acidic
F/65-97/Region: basic

Query Match 27.3%; Score 56.5; DB 1; Length 155;
Best Local Similarity 36.7%; Pred. No. 4.2;
Matches 11; Conservative 7; Mismatches 3; Indels 9; Gaps 1;

QY 2 NSGNSFE-----BDTPEDKPKYQG 22
DB 9 NDGNENFEDFVEHFSDETYEKQFDG 38

RESULT 10
T25667
hypothetical protein D2092.5 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T25667
R:Gatung, S.; Maggi, L.
submitted to the EMBL Data Library, February 1997
A:Description: The sequence of C. elegans cosmid D2092.
A:Reference number: Z20067
A:Accession: T25667
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-968 <GAT>
A:Cross-references: UNIPROT:P91193; EMBL:U88167; PIDN:AA642225.1; GSPDB:GN00019; CESP:D20
A:Experimental source: strain Bristol N2; clone D2092
C:Genetics:
A:Gene: CESP:D2092.5
A:Map position: 1
A:Introns: 18/2; 42/3; 78/2; 140/3; 195/1; 221/2; 244/1; 283/2; 328/1; 345/1; 471/3; 688/

Query Match 27.3%; Score 56.5; DB 2; Length 968;
Best Local Similarity 38.7%; Pred. No. 35;
Matches 12; Conservative 5; Mismatches 11; Indels 3; Gaps 1;

QY 1 QNSGNSFEEDTPEDKPKYEGGNIYDIDF 31
DB 397 KINNGNSGFNSTPNDKK---GKSIRDVMD 424

RESULT 11
A26653
glutathione transferase (EC 2.5.1.18) class alpha chain Ya2, hepatic - rat
N:Alternate names: GHS transferase chain Ya; glutathione transferase 1'
C:Species: Rattus norvegicus (Norway rat)
C:Date: 01-Feb-1988 #sequence_revision 01-Feb-1988 #text_change 09-Jul-2004
C:Accession: A26653; I51831; S03358; S78477; S10556; I53350; A53438
R:Telakowski-Hopkins, C.A.; Rothkopf, G.S.; Pickert, C.B.
Proc. Natl. Acad. Sci. U.S.A. 83, 9393-9397, 1986
A:Title: Structural analysis of a rat liver glutathione S-transferase Ya gene.
A:Reference number: A26653; MWID:87092258; PMID:3025841
A:Accession: A26653
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-222 <TEL>
A:Cross-references: UNIPROT:P04903; GB:M14991; NID:G204524; PIDN:AAA41295.1; PID:G204526
R:Pickert, C.B.; Telakowski-Hopkins, C.A.; Ding, G.J.
Adv. Exp. Med. Biol. 197, 185-193, 1986
A:Title: Expression and sequence analysis of rat liver glutathione S-transferase genes.
A:Reference number: I51831; MWID:87022415; PMID:3766257
A:Accession: I51831
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-222 <RES>

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A:Cross-references: GB:M25891; NID:g204507; PIDN:AAA41290.1; PID:g204508
R:Wang, R.W.; Picot, C.B.; Lu, A.Y.H.
Arch. Biochem. Biophys. 269, 536-543, 1989
A>Title: Expression of a cDNA encoding a rat liver glutathione S-transferase Ya subunit
I:Reference number: S03358; MUID:89149100; PMID:2645828
J:Accession: S03358
A>Status: not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-31 <MAN>
A:Cross-references: GB:M27446; NID:g294563; PIDN:AAA41291.1; PID:g294564
A:Accession: S78477
A:Molecule type: protein
A:Residues: 2-31 <MAN>
R:Haves, J.D.; Kerr, L.A.; Harrison, D.J.; Cronshaw, A.D.; Ross, A.G.; Neal, G.E.
Biochem. J. 268, 295-302, 1990
A>Title: Preferential over-expression of the class alpha rat Ya(2) glutathione S-transferase f Ya(1) and Ya(2) with cloned class alpha glutathione S-transferase cDNA sequences.
A:Reference number: S10555; MUID:90303203; PMID:2363675
J:Accession: S10555
A:Molecule type: protein
A:Residues: 17-50;52-62;64-85;106-140;209-222 <HAY>
R:Taylor, J.B.; Craig, R.K.; Beale, D.; Ketterer, B.
Biochem. J. 219, 223-231, 1984
A>Title: Construction and characterization of a plasmid containing complementary DNA to
I:Reference number: 152350; MUID:84202896; PMID:6547043
J:Accession: 152350
A>Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: mRNA
A:Residues: 1-129 <REM>
A:Cross-references: EMBL:X00520; NID:g56329; PIDN:CMA25203.1; PID:g56330
R:Tsu, C.P.D.; Weiss, M.U.; Karakawa, W.M.; Reddy, C.C.
Nucleic Acids Res. 10, 5407-5419, 1982
A>Title: Cloning and sequence analysis of a cDNA plasmid for one of the rat liver glutathione S-transferases
I:Reference number: A93438; MUID:83064489; PMID:6292839
J:Accession: A93438
A:Molecule type: mRNA
A:Residues: 81-222 <TUC>
A:Experimental source: clone pGTR112
C:Comment: Glutathione transferases are multifunctional dimers of identical or similar Y
independent glutathione peroxidase activity toward organic hydroperoxides. In addition,
ics and azocarcinogen dyes. It is a cytosolic protein found in many mammalian tissues.
C:Function:
A>Description: catalyzes the conjugation of glutathione to electrophilic xenobiotics, in
substrate hydrophobic ligands
C:Superfamily: glutathione transferase
C:Keywords: dimer; liver; transferase
F:2-222/Product: glutathione transferase class alpha chain Ya2 #status experimental <MATH

Query Match 26.6% Score 55; DB 2; Length 222;
Best Local Similarity 40.6%; Pred. No. 10;
Matches 13; Conservative 6; Mismatches 7; Indels 6; Gaps 2;

OY 8 FEE---DPEEDKPKYEGCGNVVIDIDPDSVPOI 36
||| :||| :||| :||| :
DB 30 FEEXLIOSPEDLEKKIKDGNTLM--FDQVPVV 58

RESULT 12
A27848
glutathione transferase (EC 2.5.1.18) class alpha chain Ya1 [similarity] - mouse
C:Species: Mus musculus (house mouse)
C>Date: 20-Apr-2000 #sequence revision 20-Apr-2000 #text_change 09-Jul-2004
C:Accession: A27848; SI5851; C28946
R:Daniel, V.; Sharon, R.; Tichauer, Y.; Sarid, S.
DNA 6, 317-324, 1987
A>Title: Mouse glutathione S-transferase Ya subunit: gene structure and sequence.
A:Reference number: A27848; MUID:880003969; PMID:3652905
J:Accession: A27848
A:Molecule type: DNA
A:Residues: 1-223 <DAN>
A:Cross-references: UNIPROT:P13745; GB:M19250; NID:g193693; GB:M19251; NID:g193694; GB:M19252; NID:g193695;
GB:X06723; GB:M17336; PIDN:AA37750.1; PID:g387179
R:McClellan, L.I.; Kerr, L.A.; Cronshaw, A.D.; Haves, J.D.

Biochem. J. 276, 461-469, 1991

A>Title: Regulation of mouse glutathione S-transferases by chemoprotectors. Molecular evolution
3), in mouse liver.
A:Reference number: S15851; MUID:91264802; PMID:2049074
A:Accession: S15851
A:Molecule type: protein
A:Residues: 16-36;51-59;63-165;208-223 <MCL>
R:Pearson, W.R.; Reinhardt, J.J.; Sisk, S.C.; Anderson, K.S.; Adler, P.N.
J. Biol. Chem. 263, 13324-13332, 1988
A>Title: Tissue-specific induction of murine glutathione transferase mRNAs by butyrlated
A:Reference number: A92668; MUID:88330838; PMID:3417659
A:Accession: C28946
A:Molecule type: mRNA
A:Residues: 1-65,'V',67-95,'T',97-157,'V',159-162,'L',164-169,'L',171-207,'L',209-213,'E'
A:Cross-references: GB:J03958; NID:91936921; PIDN:AAA37749.1; PID:g309279
C:Genetics:
A:Gene: Yal1; MGI:Gatal
A:Cross-references: MGI:1095417
A:Map position: 9:43.0
C:Superfamily: glutathione transferase
C:Keywords: dimer; transferase

Query Match 26.6%; Score 55; DB 1; Length 223;
Best Local Similarity 40.6%; Pred.No.10;
Matches 13; Conservative 6; Mismatches 7; Indels 6; Gaps 2;

OY 8 FEE--DTPEDKPYEQGNIVDPDSYPQI 36
 ||| :||| |::||| :||| :
DB 30 FEERIGSPEDLEKLKDGNLM---FDQVPWV 58

RESULT 13

D72240
rRNA guanine transglycosylase - Thermotoga maritima (strain MSB8)
C:Species: Thermotoga maritima
C>Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
C:Accession: D72240
R:Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Guinn, M.L.; Dodson, R.J.; Haft, D.H.; Hickey,
Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.;
C.M.
Nature 399, 323-329, 1999
A>Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome sequ
A:Reference number: A72200; MUID:99287316; PMID:10360571
A:Accession: D72240
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-369 <ARN>
A:Cross-references: UNIPROT:Q9X1P7; GB:AB001801; GB:AE000512; NID:9482114; PIDN:AAD3662;
A:Experimental source: strain MSB8
C:Genetics:
A:Gene: TM1561
C:Superfamily: queinine tRNA-ribosyltransferase

Query Match 26.6%; Score 55; DB 2; Length 369;
Best Local Similarity 47.1%; Pred.No.18;
Matches 16; Conservative 3; Mismatches 5; Indels 10; Gaps 3;

OY 10 EDTPEDKPYEQG-----NIVD--ID-PDSV 33
 | ||||| :||| :||| :||| :
DB 230 EFLPEDKPRYFMGGSPELLILVDRCGVDMFPSV 263

RESULT 14

D72952
hydrothermal protein C15E6.1 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999
C:Accession: T32952
R:Roßling, T.; Bielowald, T.
submitted to the EMBL Data Library, February 1998
A>Description: The sequence of C. elegans comd C15E6.
A:Reference number: Z21253
A:Accession: T32952

A>Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-428 <RNA>
 A:Cross-references: EMBL:AF045636; PIDN:AA02559.1; GSPDB:GN00022; CESP:C15B6.1
 A:Experimental source: strain Bristol N2; clone C15B6
 C:Genetic8:
 A:Gene: CESP:C15B6.1
 A:Map position: 4
 A:Introns: 124/2; 196/3

Query Match 26.6%; Score 55; DB 2; Length 428;
 Best Local Similarity 36.6%; Pred. No. 22;
 Matches 15; Conservative 3; Mismatches 13; Indels 10; Gaps 2;

Qy 7 SPEED-----TPEDPKR---YEOGNIVIDIDFDSVPQIH 37
 Db 231 SHHDEBPIVMAQIPPEKPKKAIIPAFDNVADDFDMSPLH 271

RESULT 15
 TORITL
 leukocyte common antigen precursor, splice form 4 - rat
 M:Alternate names: CD45; L-CA; LY-5; T200
 N:Contains: leukocyte common antigen precursor, splice form 1; leukocyte common antigen
 1.3.48)
 C:Species: Rattus norvegicus (Norway rat)
 C>Date: 04-Dec-1986 #sequence revision 05-May-2000 #text change 09-Jul-2004
 C:Accession: A29450; B29450; C29450; A60241; A02247; I54569; A45854
 R:Barclay, A.N.; Jackson, D.I.; Willis, A.C.; Williams, A.F.
 EMBL J. 6, 1259-1264, 1987
 A>Title: Lymphocyte specific heterogeneity in the rat leukocyte common antigen (T200) is
 A:Reference number: A91067; MUID:87275817; PMID:2440674
 A:Accession: A29450
 A:Molecule type: mRNA
 A:Residues: 20-30,163-218 <BAR1>
 A:Cross-references: UNIPROT:Q64224; GB:M25820; GB:M24611; NID:G205153; GB:Y00065; GB:K03
 A:Experimental source: splice form 1
 A>Note: the translation in GenBank entry RATLCAI, PIDN:AAA41518.1, PID:G205154, release
 A:Accession: B29450
 A:Molecule type: mRNA
 A:Residues: 19-30,122-218 <BAR2>
 A:Cross-references: GB:M25821; GB:M24611; NID:G205155; PIDN:AAA41519.1; PID:G205156; GB:
 A:Experimental source: splice form 2
 A:Accession: C29450
 A:Molecule type: mRNA
 A:Residues: 20-30,73-121,163-218 <BAR3>
 A:Cross-references: GB:M25822; GB:M24611; NID:G205157; PIDN:AAA41520.1; PID:G205158; GB:
 A:Experimental source: splice form 3
 A:Accession: D29450
 A:Molecule type: mRNA
 A:Residues: 28-218 <BAR4>
 A:Cross-references: GB:M25823; GB:M24611; NID:G205159; PIDN:AAA41521.1; PID:G205160; GB:
 A:Experimental source: splice form 4
 A>Note: the sequence in GenBank entry RATLCAIV, release 113.0, has the codon AGG for 56-
 R:Barclay, A.N.; Jackson, D.I.; Willis, A.C.; Williams, A.F.
 Adv. Exp. Med. Biol. 237, 3-7, 1988
 A>Title: The leukocyte-common antigen (L-CA) family.
 A:Reference number: A60241; MUID:89319817; PMID:2978200
 A:Accession: A60241
 A:Status: not compared with conceptual translation
 A:Molecule type: DNA
 A:Residues: 30-161 <BAR5>
 R:Thomas, M.L.; Barclay, A.N.; Gagnon, J.; Williams, A.F.
 Cell 41, 83-93, 1985
 A>Title: Evidence from cDNA clones that the rat leukocyte-common antigen (T200) spans th
 A:Reference number: A02247; MUID:85201691; PMID:3158393
 A:Accession: A02247
 A:Molecule type: mRNA
 A:Residues: 187-189, 'K', 191-192, 'K', 208-1273 <THO>
 A:Cross-references: GB:M10072; GB:M81859; NID:G205140; PIDN:AAA41513.1; PID:G205143
 A>Note: the translation in GenBank entry RATLCAI, release 113.0, begins at non-initiat
 A>Note: parts of this sequence were determined by protein sequencing
 R/McCall, M.N.; Shotton, D.M.; Barclay, A.N.

Immunology 76, 310-317, 1992
 A>Title: Expression of soluble isoforms of rat CD45. Analysis by electron microscopy and
 A:Reference number: I54569; MUID:92340120; PMID:1378817
 A:Accession: I54569
 A:Molecule type: translated from GB/EMBL/DBJ
 A>Status: preliminary
 A:Residues: 1-30,163-180 <MCC>
 A:Cross-references: GB:S40716; NID:G252015; PIDN:AB22648.1; PID:G252016
 R:Jackson, D.I.; Barclay, A.N.
 Immunogenetics 29, 281-287, 1989
 A>Title: The extra segments of sequence in rat leukocyte common antigen (L-CA) are derive
 A:Reference number: A45854; MUID:89233293; PMID:2523868
 A:Accession: A45854
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 24-227,'H', 229-305,'Y', 307-310 <JAC>
 A:Cross-references: GB:M18347; GB:M18348; GB:M18349
 C:Comment: This glycoprotein is found on lymphoid and myeloid cell surfaces.
 C:Superfamily: leukocyte common antigen; leukocyte common antigen cytosolic domain homol
 C:Keywords: alternative splicing; duplication; glycoprotein; phosphoprotein; phosphoric n
 F:1-23/Domain: signal sequence #status predicted <SIG>
 F:124-1273/Product: leukocyte common antigen precursor, splice form 4 #status predicted <P
 F:24-546/Domain: extracellular #status predicted <EXT>
 F:24-30,122-1273/Product: leukocyte common antigen, splice form 1 #status predicted <MAT
 F:24-30,163-1273/Product: leukocyte common antigen, splice form 3 #status predicted
 F:24-30,73-121,163-218/Product: leukocyte common antigen, splice form 3 #status predicted
 F:547-568/Domain: transmembrane #status predicted <TM>
 F:565-1206/Domain: leukocyte common antigen cytosolic domain homology <LAC>
 F:569-1273/Domain: intracellular #status predicted <INT>
 F:566-870/Domain: protein-tyrosine-phosphatase homology <PPP>
 F:612-142,153,164,178,200,245,271,282,327,371,374,502/Binding site: carbohydrate (Asn) (cc
 F:822/Active site: Cys (phosphocysteine intermediate) #status predicted
 F:828/Binding site: substrate phosphate (Arg) #status predicted
 F:1063/Binding site: carbohydrate (Asn) (covalent) #status absent

Query Match 26.3%; Score 54.5; DB 1; Length 1273;
 Best Local Similarity 35.1%; Pred. No. 89;
 Matches 13; Conservative 5; Mismatches 12; Indels 7; Gaps 1;

Qy 1 QNSGNQSFEDTPEDPKPYEGGNIVIDIDFDSVPQIH 37
 Db 929 QHIGNQ-----ENKKKRRSSNVVPYDFNRPPLKH 958

Search completed: October 22, 2005, 06:09:47
 Job time: 15.8905 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 22, 2005, 04:10:49 ; Search time 69.6361 Seconds
(without alignments)
279.439 Million cell updates/sec

Title: US-10-731-238-40
Perfect score: 207
Sequence: 1 QNSGNQSFEDTPEEDKPKYEGGNIIVDIDFDSVPOIHG 38

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues
Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	* Query Match Length	DB ID	Description
1	199	96.1	940 2	Q53682 staphylococ
2	199	96.1	943 2	Q8NUH8 staphylococ
3	199	96.1	957 2	Q6G6H4 staphylococ
4	199	96.1	961 2	Q99RD3 staphylococ
5	199	96.1	961 2	Q7A3J8 staphylococ
6	199	96.1	1018 1	FNBA-STPAU
7	199	96.1	1038 2	Q99RD2 staphylococ
8	199	96.1	1038 2	Q7A3J7 staphylococ
9	198	95.7	965 2	Q6GDU5 staphylococ
10	191	92.3	1015 2	Q8NUU7 staphylococ
11	191	92.3	1015 2	Q6G6H3 staphylococ
12	188	90.8	152 2	Q9AEP9 staphylococ
13	165	31.4	937 2	Q6BEM10
14	65	30.2	1460 1	PMPC-CHLMU
15	62.5	30.2	923 2	PMPC-72
16	61	29.5	979 1	T111-SCHPO
17	61	29.5	1992 2	Q9PCT1
18	59	28.5	336 2	Q9H571
19	59	28.5	889 2	Q6CBW0
20	58	28.0	220 2	Q8RH75
21	58	28.0	311 2	Q8SY78
22	58	28.0	311 2	Q8SY78
23	58	28.0	311 2	Q8SY78
24	57.5	27.8	133 2	Q9NHH7
25	57.5	27.8	447 2	Q7XZQ9
26	57.5	27.8	2084 2	Q9HEC3
27	57	27.5	260 2	Q6FVK3
28	57	27.5	745 2	Q7SA69
29	57	27.5	1163 2	Q7SSD6
30	57	27.5	1848 2	Q6CML6
31	56.5	27.3	101 2	Q68YT3

32	56.5	27.3	155 1	PPB6 YEAST	P20435 baccharomyc
33	56.5	27.3	904 2	Q54324	Q54324 sulfolobus
34	56.5	27.3	951 2	P91193	P91193 caenorhabdi
35	56.5	27.3	975 2	Q8NZJ8	Q8NZJ8 streptococc
36	56.5	27.3	999 2	Q8K5Z5	Q8K5Z5 streptococc
37	56	27.1	240 2	Q8PS80	Q8PS80 methanosaar
38	56	27.1	240 2	Q8PS80	Q8PS80 rhodospseud
39	56	27.1	295 2	Q6NCO6	P90533 dictyostell
40	56	27.1	623 2	P90533	Q9E1F1 arabidopsis
41	56	27.1	674 2	Q9P1R1	Q64YN9 bacteroides
42	56	27.1	684 2	Q64YN9	Q64YN9 bacteroides
43	55.5	26.8	700 2	Q7WFF0	Q6D193 debaryomyce
44	55.5	26.8	700 2	Q7WFF0	Q7WFF0 bordetella
45	55	26.6	221 1	GTAL RAT	P04903 rattus norv
			221 1	GTAL2 MOUSE	P10648 mus musculu

ALIGNMENTS

RESULT 1	ID	Q53682	PRELIMINARY;	PRT;	940 AA.
AC	Q53682;				
DT	01-NOV-1996 (TREMBLrel. 01, Created)				
DT	01-NOV-1996 (TREMBLrel. 01, Last sequence update)				
DT	01-MAR-2004 (TREMBLrel. 26, Last annotation update)				
DE	Fibronectin binding protein B.				
GN	Name=fnbB;				
OS	Staphylococcus aureus.				
OC	Bacteria; Firmicutes; Bacillales; Staphylococcus.				
OX	NCBI_Taxid=1280;				
RN	(1)				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=8325-4;				
RX	MEDLINE=92111475; PubMed=1837266;				
RA	Johnson K., Signas C., Muller H.P., Lindberg M.,				
RT	"Two different genes encode fibronectin binding proteins in				
RT	Staphylococcus aureus. The complete nucleotide sequence and				
RT	characterization of the second gene."				
RL	Eur. J. Biochem. 202:1041-1048(1991).				
CC	-1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by				
CC	an amide bond (By similarity).				
DR	EMBL; X62992; CAA44726.1; -				
DR	PIR; S19702; S19702.				
DR	HSSP; Q53653; IN67.				
DR	GO; GO:0009986; C:cell surface; IEA.				
DR	GO; GO:0005618; C:cell wall; IEA.				
DR	GO; GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.				
DR	GO; GO:0016020; C:membrane; IEA.				
DR	GO; GO:0007155; P:cell adhesion; IEA.				
DR	InterPro; IPR008966; Adhes_bact.				
DR	InterPro; IPR004237; Fn_bind.				
DR	InterPro; IPR005877; Gpos_YsIRK.				
DR	InterPro; IPR001899; Gram_pos_anchor.				
DR	Pfam; PF02986; Fn_bind_2.				
DR	Pfam; PF00746; Gram_pos_anchor_1.				
DR	Pfam; PF04650; YsIRK_signal; 1.				
DR	TIGRFAM; TIGR01167; LpxTG_anchor; 1.				
DR	TIGRFAM; TIGR01168; YsIRK_signal; 1.				
DR	PROSITE; PS50847; GRAM_POS_ANCHORING; 1.				
KW	Cell wall; Peptidoglycan-anchor.				
SQ	SEQUENCE 940 AA; 10355 MW; E35FBBCA907AE345 CRC64;				
Query Match	96.1%;	Score 199;	DB 2;	Length 940;	
Best Local Similarity	97.4%;	Pred. No. 4.2e-16;			
Matches	37;	Conservative	0;	Mismatches 1;	Indels 0;
QY	1 QNSGNQSFEDTPEEDKPKYEGGNIIVDIDFDSVPOIHG 38				
DB	682 QNSGNQSFEDTPEEDKPKYEGGNIIVDIDFDSVPOIHG 719				
RESULT 2					


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09N0U8
ID 09N0U8      PRELIMINARY;      PRT;      943 AA.
AC 09N0U8;
DT 01-OCT-2002 (TREMBlrel. 22, Created)
DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE FnbB protein.
GN Name=fnbB; OrderedLocNames=MM2420;
OS Staphylococcus aureus (strain MM2);
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=196620;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=22040717; PubMed=12044378; DOI=10.1016/S0140-6736(02)08713-5;
RA Baba T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Oguchi A.,
RA Yamamoto K., Hiramatsu K.;
RT "Genome and virulence determinants of high virulence community-
acquired MRSA.";
RL Lancet 359:1819-1827(2002).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
an amide bond (By similarity).
DR HSSP; Q53653; 1N67.
DR GO; GO:0009986; C:cell surface; IEA.
DR GO; GO:0005618; C:cell wall; IEA.
DR GO; GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0007155; P:cell adhesion; IEA.
DR InterPro; IPR008966; Adhes_bact.
DR InterPro; IPR004237; Fn_bind.
DR InterPro; IPR005877; Gpos_YsIRK.
DR InterPro; IPR001899; Gram_pos_anchor.
DR Pfam; PF02986; Fn_bind.1.
DR Pfam; PF00746; Gram_pos_anchor.1.
DR TIGRFAMs; TIGR01167; LpxTG_anchor.1.
DR TIGRFAMs; TIGR01168; YsIRK_signal.1.
DR PROSITE; PS50847; GRAM_POS_ANCHORING.1.
DR Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ SEQUENCE 943 AA; 104537 MW; DA8A5F3194781B6A CRC64;

Query Match 96.1%; Score 199; DB 2; Length 943;
Best Local Similarity 97.4%; Pred. No. 4.2e-16;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 ONSGNSFEEDTPEDKPKYEGCGNIVDIDFDSVPQIHG 38
DB 689 ONSGNSFEEDTPEDKPKYEGCGNIVDIDFDSVPQIHG 726

RESULT 3
O6G6H4 PRELIMINARY; PRT; 957 AA.
AC O6G6H4;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE Fibronectin-binding protein.
GN Name=fnbB; OrderedLocNames=SA52387;
OS Staphylococcus aureus (strain MSSA476).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=282459;
RN [1]
RP SEQUENCE FROM N.A.
RC PubMed=15213324; DOI=10.1073/pnas.0402521101;
RA Holden M.T.G., Fell E.J., Lindsay J.A., Peacock S.J., Day N.P.J.,
RA Enright M.C., Foerster T.J., Moore C.E., Hurst L., Atkin R., Barron A.,
RA Baeson N., Bentley S.D., Chillingworth C., Chillingworth T.,
RA Churcher C., Clark L., Cotton C., Cronin A., Doggett J., Dowd L.,
RA Felwell T., Hance Z., Harris B., Hauber H., Holroyd S., Jagels K.,
RA James K.D., Lennard N., Line A., Mayes R., Moule S., Mungall K.,

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RA Ormond D., Quail M.A., Rabinowitz E., Rutherford K.M., Sanders M.,
RA Sharp S., Simmonds M., Stevens K., Whitehead S., Barrell B.G.,
RA Spratt B.G., Parkhill J.;
RT "Complete genomes of two clinical Staphylococcus aureus strains:
RT evidence for the rapid evolution of virulence and drug resistance.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:9786-9791(2004).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
an amide bond (By similarity).
DR EMBL; BX571857; CAC44201.1; -.
DR GO; GO:0009986; C:cell surface; IEA.
DR GO; GO:0005618; C:cell wall; IEA.
DR GO; GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0007155; P:cell adhesion; IEA.
DR InterPro; IPR008966; Adhes_bact.
DR InterPro; IPR004237; Fn_bind.
DR InterPro; IPR005877; Gpos_YsIRK.
DR InterPro; IPR001899; Gram_pos_anchor.
DR Pfam; PF02986; Fn_bind.1.
DR Pfam; PF00746; Gram_pos_anchor.1.
DR TIGRFAMs; TIGR01167; LpxTG_anchor.1.
DR TIGRFAMs; TIGR01168; YsIRK_signal.1.
DR PROSITE; PS50847; GRAM_POS_ANCHORING.1.
DR Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ SEQUENCE 957 AA; 105980 MW; 28F8BA7FFDFD3EAF CRC64;

OY 1 ONSGNSFEEDTPEDKPKYEGCGNIVDIDFDSVPQIHG 38
DB 689 ONSGNSFEEDTPEDKPKYEGCGNIVDIDFDSVPQIHG 726

RESULT 4
O99RD3 PRELIMINARY; PRT; 961 AA.
AC O99RD3;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE Fibronectin-binding protein homolog.
GN Name=fnbB; OrderedLocNames=SAV2502;
OS Staphylococcus aureus (strain Mu50 / ATCC 700699).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=158878;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Mu50 / ATCC 700699;
RX MEDLINE=21311952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2;
RA Kuroda M., Onita T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Iian J.-O., Ito T.,
RA Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hoooyama A.,
RA Mizutani-Ui Y., Takehashi N.K., Sawano T., Inoue R.-I., Katto C.,
RA Sekimizu K., Hiraoka H., Kubara S., Goto S., Yabuzaki J.,
RA Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
RA Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
RT "Whole genome sequencing of methicillin-resistant Staphylococcus
aureus.";
RL Lancet 357:1225-1240(2001).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
an amide bond (By similarity).
DR EMBL; AP003365; BAB58664.1; -.
DR PIR; G90053; G90053.
DR HSSP; Q53653; 1N67.
DR GO; GO:0009986; C:cell surface; IEA.
DR GO; GO:0005618; C:cell wall; IEA.
DR GO; GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0007155; P:cell adhesion; IEA.
DR InterPro; IPR008966; Adhes_bact.

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DR InterPro; IPR004237; Fn_bind.
 DR InterPro; IPR005877; Gpos_YsIRK.
 DR InterPro; IPR001899; Gram_pos_anchor.
 DR Pfam; PF02986; Fn_bind; 1.
 DR Pfam; PF00746; Gram_pos_anchor; 1.
 DR Pfam; PF04650; YsIRK_signal; 1.
 DR TIGRFAMs; TIGR01167; LpxTG_anchor; 1.
 DR TIGRFAMs; TIGR01168; YsIRK_signal; 1.
 DR PROSITE; PS50847; GRAM_POS_ANCHORING; 1.
 DR Cell wall; Complete proteome; Peptidoglycan-anchor.
 KW SEQUENCE 961 AA; 106010 MW; 364940F884EA4101 CRC64;

Query Match 96.1%; Score 199; DB 2; Length 961;
 Best Local Similarity 97.4%; Pred. No. 4.3e-16;
 Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QNSGNQSFEDTPEEDKPKYEGGNIIVDIDPDSVPQIHG 38
 DB 693 QNSGNQSFEDTPEEDKPKYEGGNIIVDIDPDSVPQIHG 730

RESULT 5
 ID Q7A3J8 PRELIMINARY; PRT; 961 AA.
 AC Q7A3J8;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE FnBb protein.
 OS Name=fNBb; OrderedLocustNames=SA2290;
 OC Staphylococcus aureus (Strain N315).
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 OX NCBI_TaxID=158879;
 RN [1]

RP SEQUENCE FROM N.A.
 RX MEDLINE=2111952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2;
 RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
 RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Iian J.-O., Ito T.,
 RA Kanamori M., Matsumaru H., Maruyama A., Marakami H., Hosoyama A.,
 RA Mizumoto-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
 RA Sekimizu K., Hirakawa H., Kunata S., Goto S., Yabuzaki J.,
 RA Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shida T.,
 RA Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
 RT "Whole genome sequencing of methicillin-resistant Staphylococcus
 aureus";
 RL Lancet 357:1225-1240(2001).
 CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
 an amide bond (By similarity).
 CC EMBL; AP003137; BAB43593.1; -;
 DR GO; GO:000986; C:cell surface; IEA.
 DR GO; GO:0005618; C:cell wall; IEA.
 DR GO; GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0007155; P:cell adhesion; IEA.
 DR InterPro; IPR008966; Adhes_Dact.
 DR InterPro; IPR004237; Fn_bind.
 DR InterPro; IPR005877; Gpos_YsIRK.
 DR InterPro; IPR001899; Gram_pos_anchor.
 DR Pfam; PF02986; Fn_bind; 1.
 DR Pfam; PF00746; Gram_pos_anchor; 1.
 DR Pfam; PF04650; YsIRK_signal; 1.
 DR TIGRFAMs; TIGR01167; LpxTG_anchor; 1.
 DR TIGRFAMs; TIGR01168; YsIRK_signal; 1.
 DR PROSITE; PS50847; GRAM_POS_ANCHORING; 1.
 KW Cell wall; Complete proteome; Peptidoglycan-anchor.
 SQ SSQUNCE 961 AA; 106010 MW; 364940F884EA4101 CRC64;

Query Match 96.1%; Score 199; DB 2; Length 961;
 Best Local Similarity 97.4%; Pred. No. 4.3e-16;
 Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 QNSGNQSFEDTPEEDKPKYEGGNIIVDIDPDSVPQIHG 38
 |||||||

DB 693 QNSGNQSFEDTPEEDKPKYEGGNIIVDIDPDSVPQIHG 730

RESULT 6
 ID FNBA_STAUV STANDARD; PRT; 1018 AA.
 AC FNBA_STAUV
 DT 01-APR-1990 (Rel. 14, Created)
 DT 01-APR-1990 (Rel. 14, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Fibronectin-binding protein precursor (FNBP).
 GN Name=fNBb;
 OS Staphylococcus aureus.
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 OX NCBI_TaxID=1280;
 RN [1]

RP SEQUENCE FROM N.A.
 RC STRAIN=NCCTC 8325-4;
 RX MEDLINE=8909898; PubMed=2521391;
 RA Signaers C., Raucet G., Joensen K., Lindgren P.-E.,
 RA Anantharamaiah G.M., Hoeck M., Lindberg M.;
 RT "Nucleotide sequence of the gene for a fibronectin-binding protein
 from Staphylococcus aureus: use of this peptide sequence in the
 synthesis of biologically active peptides";
 RT Proc. Natl. Acad. Sci. U.S.A. 86:699-703(1989).
 RL -1- FUNCTION: The ability of bacteria to bind fibronectin has been
 proposed as a virulence factor enabling bacteria to colonize wound
 tissues and blood clots. Binding of plasma fibronectin to the
 bacterial surface might block adhesion receptors on S.aureus, thus
 representing an important defense mechanism against tissue
 invasion.
 CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
 an amide bond (Potential).
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 between the Swiss Institute of Bioinformatics and the EMBL outstation -
 the European Bioinformatics Institute. There are no restrictions on its
 use by non-profit institutions as long as its content is in no way
 modified and this statement is not removed. Usage by and for commercial
 entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 or send an email to license@isb-sib.ch).

CC EMBL; J04151; AAA26632.1; -;
 DR InterPro; IPR004237; Fn_bind.
 DR InterPro; IPR005877; Gpos_YsIRK.
 DR InterPro; IPR001899; Gram_pos_anchor.
 DR Pfam; PF02986; Fn_bind; 1.
 DR Pfam; PF00746; Gram_pos_anchor; 1.
 DR Pfam; PF04650; YsIRK_signal; 1.
 DR TIGRFAMs; TIGR01167; LpxTG_anchor; 1.
 DR TIGRFAMs; TIGR01168; YsIRK_signal; 1.
 DR PROSITE; PS50847; GRAM_POS_ANCHORING; 1.
 KW Cell adhesion; Cell wall; Peptidoglycan-anchor; Repeat; Signal;
 virulence.

FT SIGNAL 1 36
 FT CHAIN 37 985
 FT PROPEP 986 1018
 FT REPEAT 545 574
 FT REPEAT 575 604
 FT DOMAIN 745 878
 FT REPEAT 745 782
 FT REPEAT 783 820
 FT REPEAT 821 859
 FT REPEAT 860 878
 FT DOMAIN 879 948
 FT REPEAT 879 892
 FT REPEAT 893 906
 FT REPEAT 907 920
 FT REPEAT 921 934
 FT REPEAT 935 948
 FT SITE 982 986
 FT MOD_RES 985 985
 Fibronectin-binding protein.
 Removed by sortase (Potential).
 B-1.
 B-2.
 4 X approximate tandem repeats,
 fibronectin-binding domain.
 D-1.
 D-2.
 D-3.
 D-4 (incomplete).
 5 X tandem repeats, Pro-rich (WR).
 WR 1.
 WR 2.
 WR 3.
 WR 4.
 WR 5.
 LpxTG sorting signal (Potential).
 Pentaglycyl murein peptidoglycan amidated

```
FT          chreonine (Potential) .
SQ  SEQUENCE      1018 AA;  111780 MW;  5815E00208B13F CRC64;
Query Match      96.1%; Score 199; DB 1; Length 1018;
Best Local Similarity 97.4%; Pred. No. 4.6e-16;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy          1  QNSGNQSFEDTPEBKRYEGGNIVIDIDPDSVPQIHG 38
Db          746  QNSGNQSFEDTPEBKRYEGGNIVIDIDPDSVPQIHG 783

RESULT 7
AC  Q99RD2      PRELIMINARY;      PRT; 1038 AA.
ID  Q99RD2
DT  01-JUN-2001 (TREMBlrel. 17, Created)
DT  01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT  01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE  Fibronectin-binding protein homolog.
CN  Name=fnb; OrderedLocusNames=SAV2503;
OS  Staphylococcus aureus (strain Mu50 / ATCC 700639) .
OC  Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX  NCBI_TaxID=158878;
RN  [1]
RC  SEQUENCE FROM N.A.
RX  STRAIN=Mu50 / ATCC 700639;
RX  MEDLINE=21311952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2;
RA  Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
RA  Cui L., Oguchi A., Aoki K.-I., Nagai Y., Iian J.-Q., Ito T.,
RA  Kanamori M., Matsumaru H., Maruyama A., Murakami H., Haseyama A.,
RA  Mizutani M., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
RA  Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
RA  Kanehisa M., Yamashita A., Oshida K., Furuya K., Yoshino C., Shiba T.,
RA  Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
RT  "Whole genome sequencing of methicillin-resistant Staphylococcus
RT  aureus.";
RL  Lancer 357:1225-1240(2001) .
CC  -I- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC  an amide bond (by similarity) .
EMBL; AP003137; BAB58665.1; -
DR  GO; GO:0009986; C:cell surface; IEA.
DR  GO; GO:0005618; C:cell wall; IEA.
DR  GO; GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR  GO; GO:0016020; C:membrane; IEA.
DR  GO; GO:007155; P:cell adhesion; IEA.
DR  InterPro; IPR008966; Adhes_bact.
DR  InterPro; IPR004237; Fn_bind.
DR  InterPro; IPR005877; Gpos_YsIRK.
DR  InterPro; IPR001899; Gram_pos_anchor.
DR  Pfam; PF02986; Fn_bind; 1.
DR  Pfam; PF00746; Gram_pos_anchor; 1.
DR  Pfam; PF04650; YsIRK_signal; 1.
DR  TIGRFAMs; TIGR01167; LpxTG_anchor; 1.
DR  TIGRFAMs; TIGR01168; YsIRK_signal; 1.
DR  PROSITE; PS50847; GRAM_POS_ANCHORING; 1.
KW  Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ  SEQUENCE      1038 AA;  113618 MW;  666BF6BF2BFB12 CRC64;

Query Match      96.1%; Score 199; DB 2; Length 1038;
Best Local Similarity 97.4%; Pred. No. 4.7e-16;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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DT  05-JUL-2004 (TREMBlrel. 27, Created)
DT  05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT  05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE  Fnb protein.
CN  Name=fnb; OrderedLocusNames=SA2291;
OS  Staphylococcus aureus (strain N315) .
OC  Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX  NCBI_TaxID=158879;
RN  [1]
RC  SEQUENCE FROM N.A.
RX  MEDLINE=21311952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2;
RA  Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
RA  Cui L., Oguchi A., Aoki K.-I., Nagai Y., Iian J.-Q., Ito T.,
RA  Kanamori M., Matsumaru H., Maruyama A., Murakami H., Haseyama A.,
RA  Mizutani M., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
RA  Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
RA  Kanehisa M., Yamashita A., Oshida K., Furuya K., Yoshino C., Shiba T.,
RA  Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
RT  "Whole genome sequencing of methicillin-resistant Staphylococcus
RT  aureus.";
RL  Lancer 357:1225-1240(2001) .
CC  -I- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC  an amide bond (by similarity) .
EMBL; AP003137; BAB43594.1; -
DR  GO; GO:0009986; C:cell surface; IEA.
DR  GO; GO:0005618; C:cell wall; IEA.
DR  GO; GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR  GO; GO:0016020; C:membrane; IEA.
DR  GO; GO:007155; P:cell adhesion; IEA.
DR  InterPro; IPR008966; Adhes_bact.
DR  InterPro; IPR004237; Fn_bind.
DR  InterPro; IPR005877; Gpos_YsIRK.
DR  InterPro; IPR001899; Gram_pos_anchor.
DR  Pfam; PF02986; Fn_bind; 1.
DR  Pfam; PF00746; Gram_pos_anchor; 1.
DR  Pfam; PF04650; YsIRK_signal; 1.
DR  TIGRFAMs; TIGR01167; LpxTG_anchor; 1.
DR  TIGRFAMs; TIGR01168; YsIRK_signal; 1.
DR  PROSITE; PS50847; GRAM_POS_ANCHORING; 1.
KW  Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ  SEQUENCE      1038 AA;  113618 MW;  666BF6BF2BFB12 CRC64;

Query Match      96.1%; Score 199; DB 2; Length 1038;
Best Local Similarity 97.4%; Pred. No. 4.7e-16;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy          1  QNSGNQSFEDTPEBKRYEGGNIVIDIDPDSVPQIHG 38
Db          742  QNSGNQSFEDTPEBKRYEGGNIVIDIDPDSVPQIHG 779

RESULT 9
ID  Q6GDUS      PRELIMINARY;      PRT; 965 AA.
AC  Q6GDUS;
DT  05-JUL-2004 (TREMBlrel. 27, Created)
DT  05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT  05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE  Fibronectin-binding protein.
CN  Name=fnbA; OrderedLocusNames=SA2580;
OS  Staphylococcus aureus (strain MRSA252) .
OC  Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX  NCBI_TaxID=282458;
RN  [1]
RC  SEQUENCE FROM N.A.
RX  PubMed=15213324; DOI=10.1073/pnae.040252101;
RA  Holden M.T.G., Fell E.J., Lindsey J.A., Peacock S.J., Day N.P.J.,
RA  Enright M.C., Foster T.J., Moore C.E., Hurst L., Atkin R., Barron A.,
RA  Baeson N., Bentley S.D., Chillingworth C., Chillingworth T.,
RA  Churcher C., Clark L., Cotton C., Cronin A., Doggett J., Dowd L.,
RA  Feltham T., Hance Z., Harris B., Hauser H., Holtroyd S., Jørgensen K.,
RA  James K.D., Lennard N., Line A., Mayes R., Moule S., Mungall K.,
RA  Ormond D., Quail M.A., Rabinowitsch E., Rutherford K.M., Sanders M.,
```


Db 39 SSSSQSFTEILIPENGAERYVSGDVGSFSPDSNIPE 72

RESULT 15

ID 069L72 PRELIMINARY; PRT; 923 AA.

AC 069L72;
 DT 25-OCT-2004 (TrEMBLrel. 28, Created)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
 DE Putative PMS2 postmeiotic segregation increased 2.
 GN Name=OSJNBa0016310.12;
 OS Oryza sativa (japonica cultivar-group).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Ehrhartoideae; Oryzaceae; Oryza.
 CX NCBI_TaxId=39947;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Sasaki T., Matsumoto T., Katayose Y.;
 RT "Oryza sativa nipponbare (GA3) genomic DNA, chromosome 2, BAC
 RT clone:OSJNBa0016310.";
 RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AP005874; BAD34084.1; -;
 DR GO; GO:0005524; F:ATP binding; IEA.
 DR GO; GO:0006298; P:mismatch repair; IEA.
 DR InterPro; IPR003594; ATPbind_ATPase.
 DR InterPro; IPR002099; DNA_mis_repair.
 DR InterPro; IPR000102; MARIb_neuraxin.
 DR Pfam; PF01119; DNA_mis_repair; 1.
 DR Pfam; PF02518; HATPase_c; 1.
 DR TIGRFAMs; TIGR00585; mutl; 1.
 DR PROSITE; PS00058; DNA_MISMATCH_REPAIR_1; UNKNOWN_1.
 DR PROSITE; PS00230; MARIb_NEURAXIN; UNKNOWN_1.
 SQ SEQUENCE 923 AA; 101237 MW; ASFD02C047947191 CRC64;

Query Match 30.2%; Score 62.5; DB 2; Length 923;
 Best Local Similarity 45.2%; Pred.No.56;
 Matches 14; Conservative 5; Mismatches 11; Indels 1; Gaps 1;

QY 6 OSFEDTPEDKRYEGGNIYVIDPDSPVQI 36
 Db 551 OSFVPEMPEDSPQSHSPNIVS-HRDEVQQL 580

Search completed: October 22, 2005, 06:05:57
 Job time : 71.6361 secs

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GenCore version 5.1.6
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OM protein - protein search, using SW model

Run on: October 25, 2005, 19:38:38 ; Search time 83.8325 Seconds
(without alignments)
175.313 Million cell updates/sec

Title: US-10-731-238-41

Perfect score: 207
 sequence: 1 QNSGNGSFEEDETPDKPKYEQGGNIVDIDFDSVPQIHG 38

Scoring table:	BLOSUM62	
	Cancer	10 0
	Cancer	0 5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

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Minimum DB seq length: 0
Maximum DB seq length: 20000000000
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Post-processing: Minimum Match 0%
                  Maximum Match 100%
                  Listing first 45 summaries
```

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Database :
A: Genesetp.16dec04: *
1: genesetqp.1980s: *
2: genesetqp.1990s: *
3: genesetqp.2000s: *
4: genesetqp.2001s: *
5: genesetqp.2002s: *
6: genesetqp.2003as: *
7: genesetqp.2003bs: *
8: genesetqp.2004s: *
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	207	100.0	38	2	AAW65697	AAW65697 Fibronect
2	199	96.1	38	2	AAW65661	AAW65661 Fibronect
3	199	96.1	130	2	AAW58806	AAW58806 Fibronect
4	199	96.1	130	2	AAW58807	AAW58807 Fibronect
5	199	96.1	130	2	AAW91202	AAW91202 D1-D4 fib
6	199	96.1	130	2	AAW91201	AAW91201 D1-D4 fib
7	199	96.1	134	2	AAW29089	AAW29089 Cloned fi
8	199	96.1	134	2	AAW29088	AAW29088 S. aureus
9	199	96.1	134	2	AAW29087	AAW29087 S. aureus
10	199	96.1	139	2	AAW31556	AAW31556 Fibronect
11	199	96.1	174	2	AAW58808	AAW58808 Fbp Fibro
12	199	96.1	174	2	AAW91203	AAW91203 D1-D4 fib
13	199	96.1	181	2	AAW58805	AAW58805 Fibronect
14	199	96.1	181	2	AAW91200	AAW91200 D1-D4 fib
15	199	96.1	559	2	AAW89803	AAW89803 Staphyloc
16	199	96.1	767	4	AAU34403	AAU34403 Staphyloc
17	199	96.1	767	4	AAU37547	AAU37547 Staphyloc
18	199	96.1	940	2	AAW07070	AAW07070 Fibronect
19	199	96.1	940	6	ABJ19111	ABJ19111 Pathogen
20	199	96.1	948	6	ADA89470	ADA89470 Staphyloc
21	199	96.1	948	6	ABJ18923	ABJ18923 Pathogen
22	199	96.1	948	6	ABM72536	ABM72536 Staphyloc
23	199	96.1	961	6	ABU15854	ABU15854 Protein e
24	199	96.1	1018	1	AAW82115	AAW82115 Fibronect
25	199	96.1	1018	4	AAU37245	AAU37245 Staphyloc

26	199	96.1	1018	4	AAU34301	StaphyLoc
27	199	96.1	1018	6	ABJ18922	Pathogen
28	199	96.1	1018	6	ABH72537	StaphyLoc
29	199	96.1	1027	6	AAH89806	StaphyLoc
30	199	99.1	1038	6	ABU15903	Protein e
31	195	94.2	978	4	AAU33960	StaphyLoc
32	195	94.2	1001	4	AAU37093	StaphyLoc
33	193	93.2	38	2	AAW65692	AAW65692 Fibronect
34	193	93.2	38	2	AAW65695	AAW65695 Fibronect
35	193	93.2	38	2	AAW65696	AAW65696 Fibronect
36	193	93.2	38	2	AAW65693	AAW65693 Fibronect
37	192	92.8	38	2	AAW65694	AAW65694 Fibronect
38	192	92.8	38	2	AAW65698	AAW65698 Fibronect
39	191	92.3	38	2	AAW65662	AAW65662 Fibronect
40	191	92.3	38	2	AAW65599	AAW65599 Protein w
41	190	91.8	38	1	AAH80660	AAH80660 Fibronect
42	190	91.8	38	1	AAH82116	AAH82116 Fibronect
43	189	91.3	39	2	AAW65691	AAW65691 Fibronect
44	188.5	91.1	39	2	AAW65712	AAW65712 Fibronect
45	184	88.9	38	2	AAW65663	AAW65663 Fibronect

ALIGNMENTS

RESULT 1
 AAM65697
 ID AAM65697 standard; peptide; 38 AA.
 XX
 AC AAM65697;
 XX
 DT 16-OCT-1998 (first entry)
 XX
 DE Fibronectin binding protein-derived peptide #41.
 XX
 KW microbial surface components recognising adhesive matrix molecule;
 KW MSCRAMM; fibronectin; fibronectin-binding protein; antibody; epitope;
 KW antibiotic; bacterial infection; antibiotic-resistant strain.
 XX
 OS Synthetic.
 OS Staphylococcus aureus.
 XX
 PN W09831389-A2.
 XX
 PD 23-JUL-1998.
 XX
 PF 21-JAN-1998; 98WO-US001222.
 XX
 PR 21-JAN-1997; 97US-0036139P.
 XX
 XX (TEXA) UNIV TEXAS A & M SYSTEM.
 PA
 PI Hoecek M, Patti JM, House-Pompeo KL, Speziale P, Joh D;
 PI McGavin MJ;
 XX
 DR WPI; 1998-413816/35.
 XX
 PT Antibody that binds to fibronectin-binding protein, preventing its
 PT binding to fibronectin - used to treat or prevent bacterial infection,
 PT especially by Staphylococci and Streptococci.
 XX
 PS Example 8; Page 102; 201pp; English.
 XX
 CC The invention relates to antibodies that bind to a fibronectin-binding
 CC domain of a fibronectin-antibinding protein, and inhibit binding of the
 CC protein to fibronectin. Also claimed are: (1) isolated peptides of a
 CC protein-antibinding protein that do not bind to fibronectin; (2) fusion
 CC protein containing at least one peptide of a fibronectin-binding protein
 CC linked to a second amino acid sequence; (3) nucleic acid encoding the
 CC isolated peptide of (1). Antibodies, the isolated peptides of (1) and the
 CC nucleic acids are all useful for immunisation (active or passive) and (by
 CC inhibiting binding of bacteria to fibronectin) for preventing or treating
 CC infection in humans or other animals, particularly by staphylococci or

CC streptococci, e.g. meningitis, otitis media, pneumonia, endocarditis,
 CC mastitis in cattle, abortion in horses and many others. Since the
 CC antibodies block binding of bacteria, they should be effective against
 CC antibiotic-resistant strains, and may replace antibiotic therapy or
 CC increase its effectiveness. Sequences AAW6561-700 represent a series of
 CC synthetic peptides based on the D1 region of *S. aureus* fibronectin
 CC binding protein A. They were synthesised to contain mutations
 XX

SO Sequence 38 AA;
 Query Match 100.0%; Score 207; DB 2; Length 38;
 Best Local Similarity 100.0%; Pred. No. 2,1e-21;
 Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 QNSGNQSFEDTEPDKPKYEGGNIVIDIDFDSVPQIHG 38
 |||
 1 QNSGNQSFEDTEPDKPKYEGGNIVIDIDFDSVPQIHG 38

DB 1 QNSGNQSFEDTEPDKPKYEGGNIVIDIDFDSVPQIHG 38

RESULT 2
 AAW65661
 ID AAW65661 standard; peptide; 38 AA.
 XX
 AC AAW65661;
 XX
 DT 16-OCT-1998 (first entry)
 XX
 DE Fibronectin binding protein-derived peptide #5.
 XX
 KW microbial surface components recognising adhesive matrix molecule;
 KW MSCRAMM; fibronectin; fibronectin-binding protein; antibody; epitope;
 KW antibiotic; bacterial infection; antibiotic-resistant strain.
 XX
 OS Synthetic.
 OS Staphylococcus aureus.
 XX
 PN WO981389-A2.
 XX
 PD 23-JUL-1998.
 XX
 PF 21-JAN-1998; 98WO-US001222.
 XX
 PR 21-JAN-1997; 97US-0036139P.
 XX
 PA (TEXA) UNIV TEXAS A & M SYSTEM.
 XX
 PI Hoeoek M, Patti JM, House-Pompeo KU, Speciale P, Joh D;
 PI McGavin MJ;
 XX
 DR WPI; 1998-413816/35.
 XX

XX Example 2; Page 92; 201pp; English.

CC The invention relates to antibodies that bind to a fibronectin-binding
 CC domain of a fibronectin-binding protein, and inhibit binding of the
 CC protein to fibronectin. Also claimed are: (1) isolated peptides of a
 CC fibronectin-binding protein that do not bind to fibronectin; (2) fusion
 CC protein containing at least one peptide of a fibronectin-binding protein
 CC linked to a second amino acid sequence; (3) nucleic acid encoding the
 CC isolated peptide of (1). Antibodies, the isolated peptides of (1) and the
 CC nucleic acids are all useful for immunisation (active or passive) and (by
 CC inhibiting binding of bacteria to fibronectin) for preventing or treating
 CC infection in humans or other animals, particularly by staphylococci or
 CC streptococci, e.g. meningitis, otitis media, pneumonia, endocarditis,
 CC mastitis in cattle, abortion in horses and many others. Since the
 CC antibodies block binding of bacteria, they should be effective against
 CC antibiotic-resistant strains, and may replace antibiotic therapy or
 CC increase its effectiveness. Sequences AAW6569-68 represent synthetic
 CC epitopes from the fibronectin binding domains DU and D1-D4 of the S.

CC aureus fmbA gene
 XX

SO Sequence 38 AA;
 Query Match 96.1%; Score 199; DB 2; Length 38;
 Best Local Similarity 97.4%; Pred. No. 2,7e-20;
 Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 QNSGNQSFEDTEPDKPKYEGGNIVIDIDFDSVPQIHG 38
 |||
 1 QNSGNQSFEDTEPDKPKYEGGNIVIDIDFDSVPQIHG 38

DB 1 QNSGNQSFEDTEPDKPKYEGGNIVIDIDFDSVPQIHG 38

RESULT 3
 AAR58806
 ID AAR58806 standard; protein; 130 AA.
 XX
 AC AAR58806;
 XX
 DT 25-MAR-2003 (revised)
 DT 30-MAR-1995 (first entry)
 XX
 DE Fibronectin binding domain D1-D4(709-838 (P838T)).
 XX
 KW Fibronectin binding protein; Fbp; fibronectin binding domain;
 KW monoclonal antibody; Mab; adhesion; Gram-positive bacterium; bacteremia;
 KW Escherichia coli.
 XX
 OS Staphylococcus aureus.
 XX
 PN WO9418327-A1.
 XX
 PD 18-AUG-1994.
 XX
 PF 04-FEB-1994; 94WO-GB000215.
 XX
 PR 05-FEB-1993; 93GB-00002289.
 PR 20-OCT-1993; 93GB-00021592.
 XX
 PA (SMIK) SMITHKLINE BEECHAM PLC.
 XX
 PI Burnham MKR, Chopra I, Critchley IA, Knowles DJC;
 DR WPI; 1994-279746/34.
 XX

XX Disclosure; Page 30; 40pp; English.

CC Polypeptides corresponding to residues G709-T886 plus PPIVPT, G709-
 CC P838(P838T) and G709-P838 (AAR58805-07, respectively) of *S. aureus* J2385
 CC (NCIMB 40532) Fbp type A fibronectin binding domain D1-D4 region
 CC (AAR58808) were expressed in *E. coli* BL21(DE4) and used to raise Mabs
 CC specific for Fbp. (Updated on 25-MAR-2003 to correct PN field.)
 XX

SO Sequence 130 AA;
 Query Match 96.1%; Score 199; DB 2; Length 130;
 Best Local Similarity 97.4%; Pred. No. 1,2e-19;
 Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 QNSGNQSFEDTEPDKPKYEGGNIVIDIDFDSVPQIHG 38
 |||
 2 QNSGNQSFEDTEPDKPKYEGGNIVIDIDFDSVPQIHG 39

DB 2 QNSGNQSFEDTEPDKPKYEGGNIVIDIDFDSVPQIHG 39

RESULT 4
 AAR58807
 ID AAR58807 standard; protein; 130 AA.
 AC AAR58807;

```

XX 25-MAR-2003 (revised)
DT 30-MAR-1995 (first entry)
XX
XX Fibronection binding domain D1-D4 (709-838).
DE
XX Fibronection binding protein; Fbp; fibronection binding domain;
KW monoclonal antibody; MAb; adhesion; Gram-positive bacterium; bacteremia;
KW Escherichia coli.
XX
OS Staphylococcus aureus.
XX
XX WO9418327-A1.
XX
XX 18-AUG-1994.
XX
XX 04-FEB-1994; 94WO-GB000215.
XX
XX 05-FEB-1993; 93GB-00002289.
XX
XX 20-OCT-1993; 93GB-00021592.
XX
XX (SMIK ) SMITHKLINE BEECHAM PLC.
XX
XX Burnham MKR, Chopra I, Critchley IA, Knowles DJC;
XX
XX WPI; 1994-279748/34.
XX
XX Fibronection binding protein and monoclonal antibodies specific for Fbp -
XX useful to prevent adherence of Gram-positive bacteria to indwelling
XX devices or wounds.
XX
XX Disclosure; Page 30; 40pp; English.
XX
XX
XX Polypeptides corresponding to residues G709-T886 plus PIVPPT, G709-
XX P838 (P838T) and G709-P838 (AARS8805-07, respectively) of S. aureus J2385
XX (NCIMB 40532) Fbp type A fibronection binding domain D1-D4 region
XX (AARS8808) were expressed in E. coli BL21 (DE4) and used to raise MAbs
XX specific for Fbp. (Updated on 25-MAR-2003 to correct PN field.)
XX
XX
XX Sequence 130 AA:
SQ
Query Match 96.1%; Score 199; DB 2; Length 130;
Best Local Similarity 97.4%; Pred. No. 1.2e-19;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 QNSGNSFEEDTEPDKPKYEGGNIYDIDFDSVPQIHG 38
DB 2 QNSGNSFEEDTEPDKPKYEGGNIYDIDFDSVPQIHG 39
RESULT 5
AAR91202 standard; peptide; 130 AA.
XX
XX AAR91202;
XX
XX 13-NOV-1996 (first entry)
XX
XX D1-D4 fibronection binding domains.
XX
XX Fibronection; oral hygiene; gingivitis; gum disease; adhesion;
XX periodontitis; oral pathogen; caries; calculus; candidiasis; oral surgery;
XX tissue regeneration; irrigation; toothpaste; dentifrice; mouthwash;
XX lozenge.
XX
XX Staphylococcus aureus.
XX
XX WO9604003-A1.
XX
XX 15-FEB-1996.
XX
XX 18-JUL-1995; 95WO-EP002825.
XX

```

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PR 05-AUG-1994; 94GB-00015902.
XX
XX (SMIK ) SMITHKLINE BEECHAM PLC.
XX
XX Barnett P, Critchley IA, Dodd I;
XX
XX WPI; 1996-129122/13.
XX
XX Prevention of adherence of oral pathogens in the oral cavity, partic.
XX tooth surfaces - by application of a fibronection binding protein or
XX polypeptide or a monoclonal antibody or fragment against it.
XX
XX
XX Claim 5; Page 32; 41pp; English.
XX
XX Adherence of oral pathogens, particularly to tooth surfaces, can be
XX prevented by application of a fibronection binding protein or polypeptide.
XX The fibronection binding protein or polypeptide is useful in the
XX manufacture of oral hygiene compositions, eg. toothpaste, liquid
XX dentifrice, mouthwash or lozenge. They are useful to prevent the plaque-
XX related development of carious lesions, gingivitis, calculus or
XX periodontal disease and to combat oral cavity infections, e.g.
XX candidiasis. They may also be useful in oral surgery e.g. in guided
XX tissue regeneration procedures to prevent subsequent bacterial infection,
XX and for irrigation of periodontal pockets. This sequence corresponds to
XX amino acids 709-838 of the D1-D4 fibronection binding domain of
XX Staphylococcus aureus
XX
XX
XX Sequence 130 AA:
SQ
Query Match 96.1%; Score 199; DB 2; Length 130;
Best Local Similarity 97.4%; Pred. No. 1.2e-19;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 QNSGNSFEEDTEPDKPKYEGGNIYDIDFDSVPQIHG 38
DB 2 QNSGNSFEEDTEPDKPKYEGGNIYDIDFDSVPQIHG 39
RESULT 6
AAR91201 standard; peptide; 130 AA.
XX
XX AAR91201;
XX
XX 13-NOV-1996 (first entry)
XX
XX D1-D4 fibronection binding domains.
XX
XX Fibronection; oral hygiene; gingivitis; gum disease; adhesion;
XX periodontitis; oral pathogen; caries; calculus; candidiasis; oral surgery;
XX tissue regeneration; irrigation; toothpaste; dentifrice; mouthwash;
XX lozenge.
XX
XX Staphylococcus aureus.
XX
XX WO9604003-A1.
XX
XX 15-FEB-1996.
XX
XX 18-JUL-1995; 95WO-EP002825.
XX
XX 05-AUG-1994; 94GB-00015902.
XX
XX (SMIK ) SMITHKLINE BEECHAM PLC.
XX
XX Barnett P, Critchley IA, Dodd I;
XX
XX WPI; 1996-129122/13.
XX
XX Prevention of adherence of oral pathogens in the oral cavity, partic.
XX tooth surfaces - by application of a fibronection binding protein or
XX polypeptide or a monoclonal antibody or fragment against it.
XX

```

PS Claim 5; Page 31-32; 41pp; English.

XX Adherence of oral pathogens, particularly to tooth surfaces, can be

CC prevented by application of a fibronectin binding protein or polypeptide.

CC The fibronectin binding protein or polypeptide is useful in the

CC manufacture of oral hygiene compositions, eg. toothpaste, liquid

CC dentifrice, mouthwash or lozenge. They are useful to prevent the plaque-

CC related development of carious lesions, gingivitis, calculus or

CC periodontal disease and to combat oral cavity infections, e.g.

CC candidiasis. They may also be useful in oral surgery e.g. in guided

CC tissue regeneration procedures to prevent subsequent bacterial infection,

CC and for irrigation of periodontal pockets. This sequence corresponds to

CC amino acids 709-838 of the D1-D4 fibronectin binding domain of

CC Staphylococcus aureus with a P838T substitution

XX

SQ Sequence 130 AA;

Query Match 96.1%; Score 199; DB 2; Length 130;

Best Local Similarity 97.4%; Pred. No. 1,2e-19;

Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QNSGNQSFEDTDPDKPKRYEGGNIVDIDPDSVPQIHG 38

Db 2 QNSGNQSFEDTDPDKPKRYEGGNIVDIDPDSVPQIHG 39

RESULT 7

AAV29089

ID AAV29089 standard; protein; 134 AA.

XX

AC AAV29089;

XX

DT 28-SEP-1999 (first entry)

DE

XX Cloned fibronectin binding protein binding domain (FnBAB) sequence.

XX

XX Bovine herpes virus-2; BHV-2; cytokine; immune response; immunogen; IL;

KM interleukin; colony stimulating factor; CSF; interferon; IFN; TNF;

KM tumour necrosis factor; recombinant virus; vaccine; mucosal disease;

KM mastitis; breast cancer; stress-induced disease; binding domain; FnBAB;

KM fibronectin binding protein.

XX

OS Staphylococcus aureus.

XX

PN WO9916892-A1.

XX

PD 08-APR-1999.

XX

PF 29-SEP-1998; 98WO-GB002927.

XX

PR 29-SEP-1997; 97GB-00020633.

XX

PA (UYBR-) UNIV BRISTOL.

XX

PI Bradley AJ, Duffas WPB;

XX

XX WPI; 1999-255101/21.

DR N-PSDB; AAX91506.

XX

XX New bovine herpes virus-2 vectors.

XX

PS Example 2; Fig 8A-B; 130pp; English.

XX

XX The invention provides bovine herpes virus-2 (BHV-2) based vectors that

CC comprise at least one cytokine-encoding DNA sequence. The expression of

CC cytokines in mammals can up-regulate immune responses to the immunogens.

CC The cytokine is selected from interleukins (IL), colony stimulating

CC factors (CSF), interferons (IFN) and tumour necrosis factors (TNF). The

CC BHV-2 based vector or recombinant virus can be used as vaccines. They can

CC be used for preventing or treating a mucosal disease in a subject, e.g.

CC runtaunts, cattle, sheep, goats, dogs, cats, horses, or man, particularly

CC mastitis in cows or breast cancers in humans. They can also be used for

CC preventing or treating a stress-induced disease. The present sequence

CC represent a S. aureus fibronectin binding protein binding domain

CC sequence FnBAB, the gene cloned for use in this invention. The gene has

CC 97.8 percent identity when compared to the previously published sequences

CC FnBA and FnBB

XX

SQ Sequence 134 AA;

Query Match 96.1%; Score 199; DB 2; Length 134;

Best Local Similarity 97.4%; Pred. No. 1,3e-19;

Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QNSGNQSFEDTDPDKPKRYEGGNIVDIDPDSVPQIHG 38

Db 2 QNSGNQSFEDTDPDKPKRYEGGNIVDIDPDSVPQIHG 39

RESULT 8

AAV29088

ID AAV29088 standard; protein; 134 AA.

XX

AC AAV29088;

XX

DT 28-SEP-1999 (first entry)

DE

XX S. aureus fibronectin binding protein B (FnBB) binding domain.

XX

XX Bovine herpes virus-2; BHV-2; cytokine; immune response; immunogen; IL;

KM interleukin; colony stimulating factor; CSF; interferon; IFN; TNF;

KM tumour necrosis factor; recombinant virus; vaccine; mucosal disease;

KM mastitis; breast cancer; stress-induced disease; binding domain; FnBB;

KM fibronectin binding protein.

XX

OS Staphylococcus aureus.

XX

PN WO9916892-A1.

XX

PD 08-APR-1999.

XX

PF 29-SEP-1998; 98WO-GB002927.

XX

PR 29-SEP-1997; 97GB-00020633.

XX

PA (UYBR-) UNIV BRISTOL.

XX

PI Bradley AJ, Duffas WPB;

XX

XX WPI; 1999-255101/21.

DR N-PSDB; AAX91505.

XX

XX New bovine herpes virus-2 vectors.

XX

PS Example 2; Fig 8A-B; 130pp; English.

XX

XX The invention provides bovine herpes virus-2 (BHV-2) based vectors that

CC comprise at least one cytokine-encoding DNA sequence. The expression of

CC cytokines in mammals can up-regulate immune responses to the immunogens.

CC The cytokine is selected from interleukins (IL), colony stimulating

CC factors (CSF), interferons (IFN) and tumour necrosis factors (TNF). The

CC BHV-2 based vector or recombinant virus can be used as vaccines. They can

CC be used for preventing or treating a mucosal disease in a subject, e.g.

CC runtaunts, cattle, sheep, goats, dogs, cats, horses, or man, particularly

CC mastitis in cows or breast cancers in humans. They can also be used for

CC preventing or treating a stress-induced disease. The present sequence

CC represents the binding domain of a previously published S. aureus

CC fibronectin binding protein B (FnBB) sequence. The FnB binding domain

CC gene sequence FnBAB, cloned for use in this invention has 97.8 percent

CC identity when compared to the previously published FnBA and FnBB gene

CC sequences

XX

SQ Sequence 134 AA;

Query Match 96.1%; Score 199; DB 2; Length 134;

Best Local Similarity 97.4%; Pred. No. 1,3e-19;

Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QNSGNQSFEDTEPDKPKYEGGNIYDIDFDSVPQIHG 38
 |||||
 DB 2 QNSGNQSFEDTEPDKPKYEGGNIYDIDFDSVPQIHG 39

RESULT 9

AAV29087
 ID AAV29087 standard; protein; 134 AA.

AC AAV29087;
 XX

DT 28-SEP-1999 (first entry)
 XX

DE S. aureus fibronectin binding protein A (Fnba) binding domain.
 XX

XX Bovine herpes virus-2; BHV-2; cytokine; immune response; immunogen; IL;
 KM interleukin; colony stimulating factor; CSF; interferon; IFN; TNF;
 KM tumour necrosis factor; recombinant virus; vaccine; mucosal disease;
 KM mastitis; breast cancer; stress-induced disease; binding domain; Fnba;
 KM fibronectin binding protein.

XX Staphylococcus aureus.
 OS

PN WO916892-A1.
 XX

PD 08-APR-1999.
 XX

PF 29-SEP-1998; 98WO-GB002927.
 XX

PR 29-SEP-1997; 97GB-00020633.
 XX

PA (UVR-) UNIV BRISTOL.
 XX

PI Bradley AJ, Duffas WP;
 XX

DR WPI; 1999-255101/21.
 XX

DR N-PSDB; AAX91504.
 XX

PS New bovine herpes virus-2 vectors.

XX Example 2; Fig 8A-B; 130pp; English.

CC The invention provides bovine herpes virus-2 (BHV-2) based vectors that
 CC comprise at least one cytokine-encoding DNA sequence. The expression of
 CC cytokines in mammals can up-regulate immune responses to the immunogens.
 CC The cytokine is selected from interleukins (IL), colony stimulating
 CC factors (CSF), interferons (IFN) and tumour necrosis factors (TNF). The
 CC BHV-2 based vector or recombinant virus can be used as vaccines. They can
 CC be used for preventing or treating a mucosal disease in a subject, e.g.
 CC tumours, cattle, sheep, goats, dogs, cats, horses, or man, particularly
 CC mastitis in cows or breast cancers in humans. They can also be used for
 CC preventing or treating a stress-induced disease. The present sequence
 CC represents the binding domain of a previously published S. aureus
 CC fibronectin binding protein A (Fnba) sequence. The Fnba binding domain
 CC gene sequence FNBA1, cloned for use in this invention has 97.8 percent
 CC identity when compared to the previously published Fnba and Fnba gene
 CC sequences
 CC

XX Sequence 134 AA;
 SQ

Query Match 96.1%; Score 199; DB 2; Length 134;
 Best Local Similarity 97.4%; Pred. No. 1.3e-19;

Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QNSGNQSFEDTEPDKPKYEGGNIYDIDFDSVPQIHG 38
 |||||
 DB 2 QNSGNQSFEDTEPDKPKYEGGNIYDIDFDSVPQIHG 39

RESULT 10
 AAW31556

ID AAW31556 standard; protein; 139 AA.

XX AAW31556;
 AC

XX 27-AUG-2003 (revised)
 DT

DT 25-MAR-2003 (revised)
 DT

DT 21-MAY-1998 (first entry)
 XX

DE Fibronectin-binding MSCRAM derivative POD.
 XX

XX Fibronectin; POD; collagen binding protein; sepsis; infection;
 KM microbial surface component recognising adhesive matrix molecule; MSCRAM;
 KM adhesin; vaccine; immunisation; diagnosis; therapy; mastitis.

XX Staphylococcus aureus.
 OS

XX Key Location/Qualifiers
 FH 1..12
 FT Peptide /note="vector pQE30-derived peptide"

PN WO9743314-A2.
 XX

PD 20-NOV-1997.
 XX

PF 14-MAY-1997; 97WO-US008210.
 XX

PR 16-MAY-1996; 96US-0017678P.
 XX

PA (TEXA) UNIV TEXAS A & M SYSTEM.
 XX

PA (UABR) UAB RES FOUND.
 XX

PI Hoeck M, Patti JM, House-Pompeo K, Schanham N, Symersky J;
 PI

PI WPI; 1998-008801/01.
 DR

PT Antibody that interacts with collagen binding domain of Staphylococcal
 PT cna gene product - useful to prevent bacterial sepsis in animal infected
 PT with Staphylococcus aureus.

PS Disclosure; Page 91; 143pp; English.

XX This protein comprises Staphylococcus aureus fibronectin-binding
 CC microbial surface component recognising adhesive matrix molecule (MSCRAM)
 CC derivative POD, plus a vector-derived N-terminal peptide. The invention
 CC relates to claimed nucleic acid sequences (see AAT93436-38) encoding S.
 CC aureus collagen binding protein (CBP) epitopes M17, M31 and M55 (see
 CC AAW1552-54) that confer protection against S. aureus infection. CBP
 CC protein and antigenic epitopes are contemplated for use in the treatment
 CC of pathological infections, especially to prevent bacterial adhesion to
 CC collagen. The epitopes are also contemplated for use in the preparation
 CC of vaccines and as carrier proteins in vaccine formulations, as well as
 CC in the formulation of compositions for the prevention of S. aureus
 CC infection. pCF33 and POD (see AAW31556) were used to raise anti-MSCRAM
 CC polyclonal antibodies used in passive immunisation against bovine
 CC mastitis. (Updated on 25-MAR-2003 to correct PI field.) (Updated on 27-
 CC AUG-2003 to correct OS field.)
 CC

XX Sequence 139 AA;
 SQ

Query Match 96.1%; Score 199; DB 2; Length 139;
 Best Local Similarity 97.4%; Pred. No. 1.3e-19;

Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QNSGNQSFEDTEPDKPKYEGGNIYDIDFDSVPQIHG 38
 |||||
 DB 16 QNSGNQSFEDTEPDKPKYEGGNIYDIDFDSVPQIHG 53

RESULT 11
 AAR58808
 ID AAR58808 standard; protein; 174 AA.
 XX
 AC AAR58808;

```
XX
DT 25-MAR-2003 (revised)
DT 30-MAR-1995 (first entry)
XX
DE Fbp fibronectin binding domain.
XX
KW Fibronectin binding protein; Fbp; fibronectin binding domain;
KW monoclonal antibody; MAb; adhesion; Gram-positive bacterium; bacteremia;
KW Escherichia coli; p8OC531.
XX
OS Staphylococcus aureus.
XX
PN WO9418327-A1.
XX
PD 18-AUG-1994.
XX
PF 04-FEB-1994; 94WO-GB000215.
XX
PR 05-FEB-1993; 93GB-00002289.
PR 20-OCT-1993; 93GB-00021592.
XX
PA (SMIK ) SMITHKLINE BEECHAM PLC.
XX
PI Burnham MKR, Chopra I, Critchley IA, Knowles DIC;
XX
DR WPI; 1994-279748/34.
DR N-PSDB; AA071838.
XX
PT Fibronectin binding protein and monoclonal antibodies specific for Fbp -
PT useful to prevent adherence of Gram-positive bacteria to indwelling
PT devices or wounds.
XX
PS Disclosure: Page 30; 40pp; English.
XX
CC The sequences of DNA encoding S. aureus Fbp type A fibronectin binding
CC domain (D1-D4) and the encoded protein are provided. D1-D4 polypeptides
CC have been expressed in E. coli BL21(DE4) and used to raise MAbs specific
CC for Fbp. (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ Sequence 174 AA;

Query Match 96.1%; Score 199; DB 2; Length 174;
Best Local Similarity 97.4%; Pred. No. 1.7e-19;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QNSGNQSFEDTDPKPKYEGGNIVIDIDFDSVPQIHG 38
DB 2 QNSGNQSFEDTDPKPKYEGGNIVIDIDFDSVPQIHG 39

RESULT 12
AAR91203
ID AAR91203 standard; protein; 174 AA.
XX
AC AAR91203;
XX
DT 16-OCT-2003 (revised)
DT 13-NOV-1996 (first entry)
XX
DE D1-D4 fibronectin binding domains.
XX
KW Fibronectin; oral hygiene; gingivitis; gum disease; adhesion;
KW periodontitis; oral pathogen; caries; calculus; candidiasis; oral surgery;
KW tissue regeneration; irrigation; toothpaste; dentifrice; mouthwash;
KW lozenge.
XX
OS Staphylococcus aureus; J2385.
XX
PN WO9604003-A1.
XX
PD 15-FEB-1996.
XX
DR 18-JUL-1995; 95WO-EP002825.
```

```
XX
PR 05-AUG-1994; 94GB-00015902.
XX
PA (SMIK ) SMITHKLINE BEECHAM PLC.
XX
PI Barnett P, Critchley IA, Dodd I;
XX
DR WPI; 1996-129122/13.
DR N-PSDB; AAT18308.
XX
PT Prevention of adherence of oral pathogens in the oral cavity, partic.
PT tooth surfaces - by application of a fibronectin binding protein or
PT polypeptide or a monoclonal antibody or fragment against it.
XX
BS Claim 5; Page 32; 41pp; English.
XX
CC Adherence of oral pathogens, particularly to tooth surfaces, can be
CC prevented by application of a fibronectin binding protein or polypeptide.
CC The fibronectin binding protein or polypeptide is useful in the
CC manufacture of oral hygiene compositions, eg. toothpaste, liquid
CC dentifrice, mouthwash or lozenge. They are useful to prevent the plaque-
CC related development of carious lesions, gingivitis, calculus or
CC periodontal disease and to combat oral cavity infections, e.g.
CC candidiasis. They may also be useful in oral surgery e.g. in guided
CC tissue regeneration procedures to prevent subsequent bacterial infection,
CC and for irrigation of periodontal pockets. This sequence corresponds to
CC amino acids 709-838 of the D1-D4 fibronectin binding domain of
CC Staphylococcus aureus with a P838T substitution. (Updated on 16-OCT-2003
CC to standardise OS field)
XX
SQ Sequence 174 AA;

Query Match 96.1%; Score 199; DB 2; Length 174;
Best Local Similarity 97.4%; Pred. No. 1.7e-19;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QNSGNQSFEDTDPKPKYEGGNIVIDIDFDSVPQIHG 38
DB 2 QNSGNQSFEDTDPKPKYEGGNIVIDIDFDSVPQIHG 39

RESULT 13
AAR58805
ID AAR58805 standard; protein; 181 AA.
XX
AC AAR58805;
XX
DT 25-MAR-2003 (revised)
DT 30-MAR-1995 (first entry)
XX
DE Fibronectin binding domain D1-D4(709-886).
XX
KW Fibronectin binding protein; Fbp; fibronectin binding domain;
KW monoclonal antibody; MAb; adhesion; Gram-positive bacterium; bacteremia;
KW Escherichia coli.
XX
OS Staphylococcus aureus.
XX
PN WO9418327-A1.
XX
PD 18-AUG-1994.
XX
PF 04-FEB-1994; 94WO-GB000215.
XX
PR 05-FEB-1993; 93GB-00002289.
PR 20-OCT-1993; 93GB-00021592.
XX
PA (SMIK ) SMITHKLINE BEECHAM PLC.
XX
PI Burnham MKR, Chopra I, Critchley IA, Knowles DIC;
XX
DR WPI; 1994-279748/34.
```

PT Fibronection binding protein and monoclonal antibodies specific for Fbp -
 PT useful to prevent adherence of Gram-positive bacteria to indwelling
 PT devices or wounds.
 XX
 PS Disclosure: Page 29-30; 40pp; English.
 CC
 CC Polypeptides corresponding to residues G709-T886 plus PPIVPT, G709-
 CC P838(P838T) and G709-P838 (AAR58805-07, respectively) of S. aureus J2395
 CC (NCIMB 40532) Fbp type A fibronection binding domain D1-D4 region
 CC (AAR58808) were expressed in E. coli BL21 (DE4) and used to raise Mabs
 CC specific for Fbp. (Updated on 25-MAR-2003 to correct PN field.)
 XX
 SQ Sequence 181 AA;
 Query Match 96.1%; Score 199; DB 2; Length 181;
 Best Local Similarity 97.4%; Pred. No. 1.8e-19;
 Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 ONSGNQSFEDTEPPDKPKYEGCGNIVDIDFDSVPQIHG 38
 DB 2 ONSGNQSFEDTEPPDKPKYEGCGNIVDIDFDSVPQIHG 39
 RESULT 14
 AAR91200
 ID AAR91200 standard; peptide; 181 AA.
 XX
 AC AAR91200;
 XX
 DT 13-NOV-1996 (first entry)
 XX
 DE D1-D4 fibronection binding domains.
 XX
 KM Fibronection; oral hygiene; gingivitis; gum disease; adhesion;
 KM periodontitis; oral pathogen; caries; calculus; candidiasis; oral surgery;
 KM tissue regeneration; irrigation; toothpaste; dentifrice; mouthwash;
 KM lozenge.
 XX
 OS Staphylococcus aureus.
 XX
 XX
 XX WO9604003-A1.
 XX
 PD 15-FEB-1996.
 XX
 XX 18-JUL-1995; 95WO-EP002825.
 XX
 XX 05-AUG-1994; 94GB-00015902.
 XX
 XX (SMIK) SMITHKLINE BEECHAM PLC.
 XX
 XX Barnett P, Critchley IA, Dodd I;
 XX WPI, 1996-129122/13.
 XX N-PSDB; AAT18307.
 DR
 XX Prevention of adherence of oral pathogens in the oral cavity, partic.
 PT tooth surfaces - by application of a fibronection binding protein or
 PT polypeptide or a monoclonal antibody or fragment against it.
 XX
 XX Claim 5; Page 31; 41pp; English.
 XX
 XX Adherence of oral pathogens, particularly to tooth surfaces, can be
 CC prevented by application of a fibronection binding protein or polypeptide.
 CC The fibronection binding protein or polypeptide is useful in the
 CC manufacture of oral hygiene compositions, eg. toothpaste, liquid
 CC dentifrice, mouthwash or lozenge. They are useful to prevent the plaque-
 CC related development of carious lesions, gingivitis, calculus or
 CC periodontal disease and to combat oral cavity infections, e.g.
 CC candidiasis. They may also be useful in oral surgery e.g. in guided
 CC tissue regeneration procedures to prevent subsequent bacterial infection,
 CC and for irrigation of periodontal pockets. This sequence corresponds to
 CC amino acids 709-886 of the D1-D4 fibronection binding domain of
 CC Staphylococcus aureus

XX
 SQ Sequence 181 AA;
 Query Match 96.1%; Score 199; DB 2; Length 181;
 Best Local Similarity 97.4%; Pred. No. 1.8e-19;
 Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 ONSGNQSFEDTEPPDKPKYEGCGNIVDIDFDSVPQIHG 38
 DB 2 ONSGNQSFEDTEPPDKPKYEGCGNIVDIDFDSVPQIHG 39
 RESULT 15
 AAM89803
 ID AAM89803 standard; protein; 559 AA.
 XX
 AC AAM89803;
 XX
 DT 16-MAR-1999 (first entry)
 XX
 DE Staphylococcus aureus protein SEQ ID #5251.
 XX
 KM Computer readable medium; vaccine; S. aureus infection; immunodetection;
 KM cellulitis; eyelid infection; food poisoning; osteomyelitis; therapy;
 KM skin infection; surgical wound infection; scalded skin syndrome;
 KM toxic shock syndrome.
 XX
 OS Staphylococcus aureus.
 XX
 XX EP766519-A2.
 XX
 PD 30-JUL-1997.
 XX
 XX 07-JAN-1997; 97EP-00100117.
 PF
 XX 05-JAN-1996; 96US-0009861P.
 PR
 XX (HUMA-) HUMAN GENOME SCI INC.
 PA
 XX Kunech CA, Choi GH, Barash SC, Dillon PJ, Fannon MR, Rosen CA;
 XX WPI, 1997-374922/35.
 DR
 XX Polynucleotide(s) and proteins derived from Staphylococcus aureus -
 PT stored on computer readable medium and used in the production of anti-
 PT S. aureus vaccines.
 XX
 XX Claim 23; Page 3259-3261; 3271pp; English.
 PS
 XX This sequence represents a Staphylococcus aureus protein sequence of the
 CC invention. The DNA sequences encoding the S. aureus proteins are recorded
 CC on a computer readable medium, preferably selected from a floppy or hard
 CC disk, random access memory (RAM), read-only memory (ROM) or CD-ROM.
 CC Homology searches using the S. aureus DNA sequences allows putative
 CC functions to be assigned so that protein-encoding or regulatory regions
 CC of commercial, therapeutic or industrial importance can be obtained.
 CC Specifically, sequences which are likely to encode antigens have been
 CC identified and these polypeptides can be used in a vaccine composition
 CC against S. aureus infection. The polypeptides can also be used in a kit
 CC for the immunodetection of S. aureus in a sample. S. aureus is implicated
 CC in numerous human diseases, including cellulitis, eyelid infections, food
 CC poisoning, osteomyelitis, skin and surgical wound infections, scalded
 CC skin syndrome, toxic shock syndrome, etc. Organisms transformed with the
 CC DNA sequences can be used for recombinant production of the polypeptides.
 CC The new DNA sequences (and their fragments) are useful as primers or
 CC probes for isolating homologues of any of the 5191 S. aureus DNA sequences
 CC contained on the computer readable medium
 XX
 SQ Sequence 559 AA;
 Query Match 96.1%; Score 199; DB 2; Length 559;
 Best Local Similarity 97.4%; Pred. No. 7.2e-19;
 Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

GenCore version 5.1.6
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OM protein - protein search, using SW model

Run on: October 22, 2005, 03:51:22 ; Search time 21.1723 Seconds
(without alignments)
133.980 Million cell updates/sec

Title: US-10-731-238-41

Perfect score: 207
Sequence: 1 QNSGNQSFEDTPEPKRYEGQGNIVIDFDSVPQIHG 38

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: /cgn2_6/ptodata/1/1aa/5A.COMB.pep:*
2: /cgn2_6/ptodata/1/1aa/5B.COMB.pep:*
3: /cgn2_6/ptodata/1/1aa/6A.COMB.pep:*
4: /cgn2_6/ptodata/1/1aa/6B.COMB.pep:*
5: /cgn2_6/ptodata/1/1aa/6C.COMB.pep:*
6: /cgn2_6/ptodata/1/1aa/6D.COMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	207	100.0	38	4	US-09-010-317-41
2	199	96.1	38	1	US-08-234-622A-2
3	199	96.1	38	4	US-09-010-317-5
4	199	96.1	114	1	US-08-259-000-3
5	199	96.1	130	2	US-08-459-135A-7
6	199	96.1	130	2	US-08-459-135A-8
7	199	96.1	130	3	US-08-495-559-7
8	199	96.1	130	3	US-08-495-559-8
9	199	96.1	130	3	US-08-495-559-8
10	199	96.1	174	2	US-08-459-135A-10
11	199	96.1	174	2	US-08-459-135A-13
12	199	96.1	174	3	US-08-495-559-13
13	199	96.1	174	3	US-08-495-559-13
14	199	96.1	176	3	US-08-495-559-6
15	199	96.1	178	2	US-08-459-135A-12
16	199	96.1	178	3	US-08-495-559-12
17	199	96.1	181	2	US-08-459-135A-6
18	199	96.1	559	4	US-08-956-171E-5251
19	199	96.1	559	4	US-08-956-171E-5251
20	199	96.1	1027	4	US-08-956-171E-5254
21	199	96.1	1027	4	US-08-956-171E-5254
22	193	93.2	38	1	US-08-729-767-3
23	193	93.2	38	4	US-09-010-317-36
24	193	93.2	38	4	US-09-010-317-37
25	193	93.2	38	4	US-09-010-317-39
26	193	93.2	38	4	US-09-010-317-40
27	192	92.8	38	4	US-09-010-317-38

28	192	92.8	38	4	US-09-010-317-42	Sequence 42, Appl
29	191	92.3	38	4	US-09-010-317-6	Sequence 6, Appl
30	191	92.3	38	4	US-09-010-317-43	Sequence 43, Appl
31	189	91.3	38	4	US-09-010-317-35	Sequence 35, Appl
32	188.5	91.1	39	4	US-09-010-317-56	Sequence 56, Appl
33	184	88.9	38	1	US-08-234-622A-3	Sequence 3, Appl
34	184	88.9	38	4	US-09-010-317-7	Sequence 7, Appl
35	180.5	87.2	39	4	US-09-010-317-57	Sequence 57, Appl
36	178	86.0	38	1	US-08-729-767-4	Sequence 4, Appl
37	178	86.0	38	4	US-09-010-317-46	Sequence 46, Appl
38	178	86.0	38	4	US-09-010-317-47	Sequence 47, Appl
39	177	85.5	38	4	US-09-010-317-48	Sequence 48, Appl
40	176	85.0	38	4	US-09-010-317-8	Sequence 8, Appl
41	176	85.0	38	4	US-09-010-317-49	Sequence 49, Appl
42	174	84.1	38	4	US-09-010-317-45	Sequence 45, Appl
43	171	82.6	38	4	US-09-010-317-44	Sequence 44, Appl
44	161	77.8	36	4	US-09-010-317-58	Sequence 58, Appl
45	156	75.4	38	4	US-09-010-317-50	Sequence 50, Appl

ALIGNMENTS

RESULT 1
US-09-010-317-41
Sequence 41, Application US/09010317
Patent No. 6685943
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
APPLICANT: Patti, Joseph M.
APPLICANT: House-Pompeo, Karen L.
APPLICANT: Speziale, Pietro
APPLICANT: Joh, Danny
APPLICANT: McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
TITLE OF INVENTION: AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSER: Arnold, White & Durkee
STREET: P. O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TANK:189
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 41:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-09-010-317-41
Query Match 100.0%; Score 207; DB 4; Length 38;
Best Local Similarity 100.0%; Pred. No. 8.7e-22;

Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QNSGNQSFEEDETPDKPKRYEQQGNIVDIDFDSVPQIHG 38
Db 1 QNSGNQSFEEDETPDKPKRYEQQGNIVDIDFDSVPQIHG 38

RESULT 2
US-08-234-622A-2
; Sequence 2, Application US/08234622A
; Patent No. 5440014
; GENERAL INFORMATION:
; APPLICANT: HOOK, Magnus
; APPLICANT: MCGAVIN, Martin
; APPLICANT: RAUCCI, Giuseppe
; TITLE OF INVENTION: A FIBRONECTIN BINDING PEPTIDE
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Doane, Swecker & Mathis
; STREET: P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 2213-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/234,622A
; FILING DATE: 28-APR-1994
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: SE 9002617-0
; FILING DATE: 10-AUG-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/SE91/00534
; FILING DATE: 09-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Meuth, Donna M
; REGISTRATION NUMBER: 36,607
; REFERENCE/DOCKET NUMBER: 012885-044
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 38 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-234-622A-2

Query Match 96.1%; Score 199; DB 1; Length 38;
Best Local Similarity 97.4%; Pred. No. 1.1e-20;

Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QNSGNQSFEEDETPDKPKRYEQQGNIVDIDFDSVPQIHG 38
Db 1 QNSGNQSFEEDETPDKPKRYEQQGNIVDIDFDSVPQIHG 38

RESULT 3
US-09-010-317-5
; Sequence 5, Application US/09010317
; Patent No. 6685943
; GENERAL INFORMATION:
; APPLICANT: Hook, Magnus
; APPLICANT: Patti, Joseph M.
; APPLICANT: House-Pompeo, Karen L.
; APPLICANT: Speciale, Pietro

APPLICANT: Joh, Danny
APPLICANT: McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
TITLE OF INVENTION: AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TDMK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-09-010-317-5

Query Match 96.1%; Score 199; DB 4; Length 38;
Best Local Similarity 97.4%; Pred. No. 1.1e-20;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QNSGNQSFEEDETPDKPKRYEQQGNIVDIDFDSVPQIHG 38
Db 1 QNSGNQSFEEDETPDKPKRYEQQGNIVDIDFDSVPQIHG 38

RESULT 4
US-08-259-000-3
; Sequence 3, Application US/08259000
; Patent No. 5571514
; GENERAL INFORMATION:
; APPLICANT: HOOK, Magnus
; APPLICANT: LINDBERG, Martin Kjell
; APPLICANT: SIGNAS, Lars Christer
; APPLICANT: WADSTROM, Torkel Mikael
; APPLICANT: FROMAN, Gunnar
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN AS WELL AS
; NUMBER OF SEQUENCES: 4
; INFORMATION FOR SEQ ID NO: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Doane, Swecker & Mathis
; STREET: P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 2213-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25

;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/259,000
;; FILING DATE: 13-JUN-1994
;; CLASSIFICATION: 435
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: SE 8702272-9
;; FILING DATE: 01-JUN-1987
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Neuth, Donna M
;; REGISTRATION NUMBER: 36,607
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (703) 836-6620
;; TELEFAX: (703) 836-2021
;; INFORMATION FOR SEQ ID NO: 3:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 114 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; US-08-259-000-3

Query Match 96.1%; Score 199; DB 1; Length 114;
Best Local Similarity 97.4%; Pred. No. 4,2e-20;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ONSGNQSFEDTPEPKPKYEGGNIVDIDFDSVPQIHG 38
DB 2 ONSGNQSFEDTPEPKPKYEGGNIVDIDFDSVPQIHG 39

RESULT 5
US-08-459-135A-7
Sequence 7, Application US/08459135A
Patent No. 5955078
GENERAL INFORMATION:
APPLICANT: BURNHAM, Martin Karl Russel
APPLICANT: CHOPRA, Ian
APPLICANT: CRITCHLEY, Ian Alfred
APPLICANT: KNOWLES, David Justin Charles
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN: MONOCLONAL ANTIBODY AND THEIR US
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSER: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
STATE: PA
COUNTRY: U.S.A.
ZIP: 19406-0939
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: Fastseq, Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/459,135A
FILING DATE: 02-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB/94/00215
FILING DATE: 04-Feb-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Gimm, Edward R
REGISTRATION NUMBER: 38,891
REFERENCE/DOCKET NUMBER: P30591C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-4478
TELEFAX: 610-270-5090
TELEX:
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:

;; LENGTH: 130 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; US-08-459-135A-7

Query Match 96.1%; Score 199; DB 2; Length 130;
Best Local Similarity 97.4%; Pred. No. 4,9e-20;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ONSGNQSFEDTPEPKPKYEGGNIVDIDFDSVPQIHG 38
DB 2 ONSGNQSFEDTPEPKPKYEGGNIVDIDFDSVPQIHG 39

RESULT 6
US-08-459-135A-8
Sequence 8, Application US/08459135A
Patent No. 5955078
GENERAL INFORMATION:
APPLICANT: BURNHAM, Martin Karl Russel
APPLICANT: CHOPRA, Ian
APPLICANT: CRITCHLEY, Ian Alfred
APPLICANT: KNOWLES, David Justin Charles
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN: MONOCLONAL ANTIBODY AND THEIR US
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSER: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
STATE: PA
COUNTRY: U.S.A.
ZIP: 19406-0939
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: Fastseq, Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/459,135A
FILING DATE: 02-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB/94/00215
FILING DATE: 04-Feb-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Gimm, Edward R
REGISTRATION NUMBER: 38,891
REFERENCE/DOCKET NUMBER: P30591C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-4478
TELEFAX: 610-270-5090
TELEX:
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 130 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-459-135A-8

Query Match 96.1%; Score 199; DB 2; Length 130;
Best Local Similarity 97.4%; Pred. No. 4,9e-20;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ONSGNQSFEDTPEPKPKYEGGNIVDIDFDSVPQIHG 38
DB 2 ONSGNQSFEDTPEPKPKYEGGNIVDIDFDSVPQIHG 39

RESULT 7
US-08-495-559-7

```

; Sequence 7, Application US/08495559A
; Patent No. 6054572
; GENERAL INFORMATION:
; APPLICANT: BURHAM, Martin Karl Russel
; APPLICANT: CHOPRA, Ian
; APPLICANT: CRITCHLEY, Ian Alfred
; APPLICANT: KNOWLES, David Justin Charles
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN: MONOCLONAL
; TITLE OF INVENTION: ANTIBODY AND THEIR USE IN PREVENTING BACTERIAL ADHESION
; FILE REFERENCE: P30591
; CURRENT APPLICATION NUMBER: US/08/495,559A
; CURRENT FILING DATE: 1995-08-03
; EARLIER APPLICATION NUMBER: GB 9302289.5
; EARLIER FILING DATE: 1993-02-05
; EARLIER APPLICATION NUMBER: GB 9321592.9
; EARLIER FILING DATE: 1993-10-20
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 7
; LENGTH: 130
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
; US-08-495-559-7

Query Match          96.1%; Score 199; DB 3; Length 130;
Best Local Similarity 97.4%; Pred. No. 4.9e-20;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QNSGNQSFEDTPEPKRYEQGNIVDIDFDSVPQIHG 38
Db 2 QNSGNQSFEDTPEPKRYEQGNIVDIDFDSVPQIHG 39

RESULT 8
US-08-495-559-8
; Sequence 8, Application US/08495559A
; Patent No. 6054572
; GENERAL INFORMATION:
; APPLICANT: BURHAM, Martin Karl Russel
; APPLICANT: CHOPRA, Ian
; APPLICANT: CRITCHLEY, Ian Alfred
; APPLICANT: KNOWLES, David Justin Charles
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN: MONOCLONAL
; TITLE OF INVENTION: ANTIBODY AND THEIR USE IN PREVENTING BACTERIAL ADHESION
; FILE REFERENCE: P30591
; CURRENT APPLICATION NUMBER: US/08/495,559A
; CURRENT FILING DATE: 1995-08-03
; EARLIER APPLICATION NUMBER: GB 9302289.5
; EARLIER FILING DATE: 1993-02-05
; EARLIER APPLICATION NUMBER: GB 9321592.9
; EARLIER FILING DATE: 1993-10-20
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 8
; LENGTH: 130
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
; US-08-495-559-8

Query Match          96.1%; Score 199; DB 3; Length 130;
Best Local Similarity 97.4%; Pred. No. 4.9e-20;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QNSGNQSFEDTPEPKRYEQGNIVDIDFDSVPQIHG 38
Db 2 QNSGNQSFEDTPEPKRYEQGNIVDIDFDSVPQIHG 39

RESULT 9
US-08-856-253-8
; Sequence 8, Application US/08856253
; Patent No. 6288214
; GENERAL INFORMATION:
```

```

; APPLICANT: Hook, Magnus
; APPLICANT: Patti, Joseph M.
; APPLICANT: House-Pomero, Karen
; APPLICANT: Stenham, Narayana
; APPLICANT: Symersky, Jindrich
; TITLE OF INVENTION: COLLAGEN BINDING PROTEIN COMPOSITIONS
; TITLE OF INVENTION: AND METHODS OF USE
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESS: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: U.S.
; ZIP: 77210

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/856,253
; FILING DATE: Concurrently Herewith
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/017,678
; FILING DATE: 16-MAY-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Kitchell, Barbara S.
; REGISTRATION NUMBER: 33,928
; REFERENCE/DOCKET NUMBER: TAMK:193
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (512) 418-3000
; TELEFAX: (512) 474-7577
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 139 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; US-08-856-253-8

Query Match          96.1%; Score 199; DB 3; Length 139;
Best Local Similarity 97.4%; Pred. No. 5.4e-20;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QNSGNQSFEDTPEPKRYEQGNIVDIDFDSVPQIHG 38
Db 16 QNSGNQSFEDTPEPKRYEQGNIVDIDFDSVPQIHG 53

RESULT 10
US-08-459-135A-10
; Sequence 10, Application US/08459135A
; Patent No. 5955078
; GENERAL INFORMATION:
; APPLICANT: BURHAM, Martin Karl Russel
; APPLICANT: CHOPRA, Ian
; APPLICANT: CRITCHLEY, Ian Alfred
; APPLICANT: KNOWLES, David Justin Charles
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN: MONOCLONAL ANTIBODY AND THEIR USE
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESS: SmithKline Beecham Corporation
; STREET: 709 Swedeland Road
; CITY: King of Prussia
; STATE: PA
; COUNTRY: U.S.A.
; ZIP: 19406-0939
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
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SOFTWARE: Fastseq, Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/459,135A
FILING DATE: 02-JUN-1995
CLASSIFICATION: 435
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: PCT/GB/94/00215
FILING DATE: 04-FEB-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Gimmil, Edward R
REGISTRATION NUMBER: 38,891
REFERENCE/DOCKET NUMBER: P30591C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-4478
TELEFAX: 610-270-5090
TELEX:
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 174 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: Protein
US-08-459-135A-10

Query Match 96.1%; Score 199; DB 2; Length 174;
Best Local Similarity 97.4%; Pred. No. 7e-20;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QNSGNSFEEDTEPDKPKYEGGNIIVDIDFDSVPQIHG 38
DB 2 QNSGNSFEEDTEPDKPKYEGGNIIVDIDFDSVPQIHG 39

RESULT 11
US-08-459-135A-13
Sequence 13, Application US/08459135A
Patent No. 5955078
GENERAL INFORMATION:
APPLICANT: BURHAM, Martin Karl Russel
APPLICANT: CHOPRA, Ian
APPLICANT: CRITCHLEY, Ian Alfred
APPLICANT: KNOWLES, David Justin Charles
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN: MONOCLONAL ANTIBODY AND THEIR US
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
STATE: PA
COUNTRY: U.S.A.
ZIP: 19406-0939
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: Fastseq, Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/459,135A
FILING DATE: 02-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB/94/00215
FILING DATE: 04-FEB-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Gimmil, Edward R
REGISTRATION NUMBER: 38,891
REFERENCE/DOCKET NUMBER: P30591C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-4478
TELEFAX: 610-270-5090
TELEX:

INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 174 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-459-135A-13

Query Match 96.1%; Score 199; DB 2; Length 174;
Best Local Similarity 97.4%; Pred. No. 7e-20;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QNSGNSFEEDTEPDKPKYEGGNIIVDIDFDSVPQIHG 38
DB 2 QNSGNSFEEDTEPDKPKYEGGNIIVDIDFDSVPQIHG 39

RESULT 12
US-08-495-559-10
Sequence 10, Application US/08495559A
Patent No. 6054572
GENERAL INFORMATION:
APPLICANT: BURHAM, Martin Karl Russel
APPLICANT: CHOPRA, Ian
APPLICANT: CRITCHLEY, Ian Alfred
APPLICANT: KNOWLES, David Justin Charles
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN: MONOCLONAL
TITLE OF INVENTION: ANTIBODY AND THEIR USE IN PREVENTING BACTERIAL ADHESION
FILE REFERENCE: P30591
CURRENT APPLICATION NUMBER: US/08/495,559A
CURRENT FILING DATE: 1995-08-03
EARLIER APPLICATION NUMBER: GB 9302289.5
EARLIER FILING DATE: 1993-02-05
EARLIER APPLICATION NUMBER: GB 9321592.9
EARLIER FILING DATE: 1993-10-20
NUMBER OF SEQ ID NOS: 13
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 10
LENGTH: 174
TYPE: PRT
ORGANISM: Staphylococcus aureus
US-08-495-559-10

Query Match 96.1%; Score 199; DB 3; Length 174;
Best Local Similarity 97.4%; Pred. No. 7e-20;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QNSGNSFEEDTEPDKPKYEGGNIIVDIDFDSVPQIHG 38
DB 2 QNSGNSFEEDTEPDKPKYEGGNIIVDIDFDSVPQIHG 39

RESULT 13
US-08-495-559-13
Sequence 13, Application US/08495559A
Patent No. 6054572
GENERAL INFORMATION:
APPLICANT: BURHAM, Martin Karl Russel
APPLICANT: CHOPRA, Ian
APPLICANT: CRITCHLEY, Ian Alfred
APPLICANT: KNOWLES, David Justin Charles
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN: MONOCLONAL
TITLE OF INVENTION: ANTIBODY AND THEIR USE IN PREVENTING BACTERIAL ADHESION
FILE REFERENCE: P30591
CURRENT APPLICATION NUMBER: US/08/495,559A
CURRENT FILING DATE: 1995-08-03
EARLIER APPLICATION NUMBER: GB 9302289.5
EARLIER FILING DATE: 1993-02-05
EARLIER APPLICATION NUMBER: GB 9321592.9
EARLIER FILING DATE: 1993-10-20
NUMBER OF SEQ ID NOS: 13
SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 13
LENGTH: 174
TYPE: PRT
ORGANISM: Staphylococcus aureus
US-08-495-559-13

Query Match 96.1%; Score 199; DB 3; Length 174;
Best Local Similarity 97.4%; Pred. No. 7e-20;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QNSGNQSFEDTEPDKPKRYEQGNIVDIDFDSVPQIHG 38
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Db 2 QNSGNQSFEDTEPDKPKRYEQGNIVDIDFDSVPQIHG 39

RESULT 14
US-08-495-559-6
Sequence 6, Application US/08495559A
Patent No. 6054572
GENERAL INFORMATION:
APPLICANT: BURHAM, Martin Karl Russel
APPLICANT: CHOPEA, Ian
APPLICANT: CRITCHLEY, Ian Alfred
APPLICANT: KNOWLES, David Justin Charles
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN: MONOCLONAL
TITLE OF INVENTION: ANTIBODY AND THEIR USE IN PREVENTING BACTERIAL ADHESION
FILE REFERENCE: P30591
CURRENT FILING DATE: 1995-08-03
EARLIER APPLICATION NUMBER: GB 9302289.5
EARLIER FILING DATE: 1993-02-05
EARLIER APPLICATION NUMBER: GB 9321592.9
EARLIER FILING DATE: 1993-10-20
NUMBER OF SEQ ID NOS: 13
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 6
LENGTH: 176
TYPE: PRT
ORGANISM: Staphylococcus aureus
US-08-495-559-6

Query Match 96.1%; Score 199; DB 3; Length 176;
Best Local Similarity 97.4%; Pred. No. 7.1e-20;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QNSGNQSFEDTEPDKPKRYEQGNIVDIDFDSVPQIHG 38
|||
Db 2 QNSGNQSFEDTEPDKPKRYEQGNIVDIDFDSVPQIHG 39

RESULT 15
US-08-459-135A-12
Sequence 12, Application US/08459135A
Patent No. 5955078
GENERAL INFORMATION:
APPLICANT: BURHAM, Martin Karl Russel
APPLICANT: CHOPEA, Ian
APPLICANT: CRITCHLEY, Ian Alfred
APPLICANT: KNOWLES, David Justin Charles
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN: MONOCLONAL ANTIBODY AND THEIR USE
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
STATE: PA
COUNTRY: U.S.A.
ZIP: 19406-0939
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: Fastseq, Version 2.0

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/459,135A
FILING DATE: 02-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB/94/00215
FILING DATE: 04-Feb-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Gimmi, Edward R
REGISTRATION NUMBER: 38,891
REFERENCE/DOCKET NUMBER: P30591C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-4478
TELEFAX: 610-270-5090
TELEX:
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 178 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: Protein
US-08-459-135A-12

Query Match 96.1%; Score 199; DB 2; Length 178;
Best Local Similarity 97.4%; Pred. No. 7.2e-20;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QNSGNQSFEDTEPDKPKRYEQGNIVDIDFDSVPQIHG 38
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Db 2 QNSGNQSFEDTEPDKPKRYEQGNIVDIDFDSVPQIHG 39

Search completed: October 22, 2005, 05:46:44
Job time : 21.2223 secs

GenCore version 5.1.6
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OM protein - protein search, using SW model

Run on: October 22, 2005, 11:35:03 ; Search time 70.1256 Seconds
(without alignments)
226.232 Million cell updates/sec

Title: US-10-731-238-41

Perfect score: 207
Sequence: 1 ONSGNQSFEDTEPDKPKYEGGNIVDIDFDSVPQING 38

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1862951 seqs, 417491010 residues

Total number of hits satisfying chosen parameters: 1862951

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

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2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
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19: /cgn2_6/ptodata/2/pubpaa/US11_PUBCOMB.pep:*
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21: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*
22: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	207	100.0	38	US-10-731-238-41	Sequence 41, Appl
2	199	96.1	38	US-10-731-238-5	Sequence 5, Appl
3	199	96.1	139	US-09-813-820-8	Sequence 8, Appl
4	199	96.1	388	US-08-901-062-1	Sequence 1, Appl
5	199	96.1	559	US-08-781-986A-5251	Sequence 5251, Ap
6	199	96.1	559	US-10-329-624-5251	Sequence 5251, Ap
7	199	96.1	767	US-09-815-242-5899	Sequence 5899, Ap
8	199	96.1	767	US-09-815-242-13140	Sequence 13140, A
9	199	96.1	940	US-10-470-048B-424	Sequence 424, App
10	199	96.1	948	US-10-470-048B-65	Sequence 65, Appl
11	199	96.1	961	US-10-282-122A-43778	Sequence 43778, A

12	199	96.1	1018	US-09-815-242-5797	Sequence 5797, Ap
13	199	96.1	1018	US-09-815-242-12838	Sequence 12838, A
14	199	96.1	1018	US-10-470-048B-68	Sequence 68, Appl
15	199	96.1	1027	US-08-781-986A-5254	Sequence 5254, Ap
16	199	96.1	1027	US-10-329-624-5254	Sequence 5254, Ap
17	199	96.1	1038	US-10-282-122A-43827	Sequence 43827, A
18	199	94.2	978	US-09-815-242-5456	Sequence 5456, Ap
19	195	94.2	1001	US-09-815-242-12686	Sequence 12686, A
20	193	93.2	38	US-10-731-238-36	Sequence 36, Appl
21	193	93.2	38	US-10-731-238-37	Sequence 37, Appl
22	193	93.2	38	US-10-731-238-39	Sequence 39, Appl
23	193	93.2	38	US-10-731-238-40	Sequence 40, Appl
24	192	92.8	38	US-10-731-238-48	Sequence 48, Appl
25	192	92.8	38	US-10-731-238-42	Sequence 42, Appl
26	191	92.3	38	US-10-731-238-6	Sequence 6, Appl
27	191	92.3	38	US-10-731-238-43	Sequence 43, Appl
28	189	91.3	38	US-10-731-238-35	Sequence 35, Appl
29	189.5	91.1	39	US-10-731-238-56	Sequence 56, Appl
30	184	88.9	38	US-10-731-238-7	Sequence 7, Appl
31	180.5	87.2	39	US-10-731-238-57	Sequence 57, Appl
32	178	86.0	38	US-10-731-238-46	Sequence 46, Appl
33	177	85.5	38	US-10-731-238-47	Sequence 47, Appl
34	176	85.0	38	US-10-731-238-48	Sequence 48, Appl
35	176	85.0	38	US-10-731-238-8	Sequence 8, Appl
36	176	85.0	38	US-10-731-238-49	Sequence 49, Appl
37	174	84.1	38	US-10-731-238-45	Sequence 45, Appl
38	171	82.6	38	US-10-731-238-44	Sequence 44, Appl
39	161	77.8	36	US-10-731-238-58	Sequence 58, Appl
40	156	75.4	38	US-10-731-238-50	Sequence 50, Appl
41	153	73.9	36	US-10-731-238-59	Sequence 59, Appl
42	145	70.0	30	US-10-287-821-1	Sequence 1, Appl
43	145	70.0	31	US-10-287-821-2	Sequence 2, Appl
44	81.5	39.4	37	US-11-066-657-1134	Sequence 1134, Ap
45	74	35.7	14	US-10-731-238-60	Sequence 60, Appl

ALIGNMENTS

RESULT 1
US-10-731-238-41
Sequence 41, Application US/10731238
Publication No. US20050123552A1
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
Patti, Joseph M.
House-Pompeo, Karen L.
John, Danny
McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSER: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/731,238
FILING DATE: 10-Dec-2003
CLASSIFICATION DATA: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE: 21-Jan-1998
APPLICATION NUMBER: US 60/036,139

FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAMK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 41:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 41:
US-10-731-238-41

Query Match 100.0%; Score 207; DB 18; Length 38;
Best Local Similarity 100.0%; Pred. No. 3,76-20;
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ONSGNQSFEDTPEPKPYEGGNIVIDIDPSVPOIHG 38
Db 1 ONSGNQSFEDTPEPKPYEGGNIVIDIDPSVPOIHG 38

RESULT 2
US-10-731-238-5
Sequence 5, Application US/10731238
Publication No. US20050123552A1
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
Patti, Joseph M.
House-Pompeo, Karen L.
Speziale, Pietro
Joh, Danny
McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/731,238
FILING DATE: 10-Dec-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE: 21-Jan-1998
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAMK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>

TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-10-731-238-5

Query Match 96.1%; Score 199; DB 18; Length 38;
Best Local Similarity 97.4%; Pred. No. 4,36-19;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ONSGNQSFEDTPEPKPYEGGNIVIDIDPSVPOIHG 38
Db 1 ONSGNQSFEDTPEPKPYEGGNIVIDIDPSVPOIHG 38

RESULT 3
US-09-813-820-8
Sequence 8, Application US/09813820
Patent No. US20020102262A1
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
Patti, Joseph M.
House-Pompeo, Karen
Schanam, Narayana
Sytersky, Jindrich
TITLE OF INVENTION: COLLAGEN BINDING PROTEIN COMPOSITIONS
AND METHODS OF USE
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: Texas
COUNTRY: U.S.
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/813,820
FILING DATE: 22-Mar-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/856,253
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Kitchell, Barbara S.
REGISTRATION NUMBER: 33,928
REFERENCE/DOCKET NUMBER: TAMK:193
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
TELEFAX: (512) 474-7577
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 139 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-09-813-820-8

Query Match 96.1%; Score 199; DB 9; Length 139;
Best Local Similarity 97.4%; Pred. No. 1,9e-18;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ONSGNQSFEDTPEPKPYEGGNIVIDIDPSVPOIHG 38
Db 16 ONSGNQSFEDTPEPKPYEGGNIVIDIDPSVPOIHG 53

RESULT 4
US-08-901-062-1
Sequence 1, Application US/08901062

Publication No. US20020025324A1
GENERAL INFORMATION:
APPLICANT: SEALS, JONATHAN R.
TITLE OF INVENTION: RECOMBINANT BIVALENT BACTERIAL VACCINE
TITLE OF INVENTION: FOR THE PREVENTION OF MASTITIS
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: HALE AND DORR LLP
STREET: 60 State Street
CITY: Boston
STATE: MA
COUNTRY: United States of America
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/901,062
FILING DATE: 25-JUL-1997
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Baker, Hollie L.
REGISTRATION NUMBER: 31,321
REFERENCE/DOCKET NUMBER: 106941.153
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 526-6000
TELEFAX: (617) 526-5000
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 388 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHEICAL: NO
ANTI-SENSE: NO
US-08-901-062-1

Query Match 96.1%; Score 199; DB 8; Length 388;
Best Local Similarity 97.4%; Pred. No. 6,4e-18;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ONSGNOSFEEDTBPDPKPKYEOGNGNIVDIDPDSVPQIHG 38
Db 265 ONSGNOSFEEDTBPDPKPKYEOGNGNIVDIDPDSVPQIHG 302

RESULT 5
US-08-781-986A-5251
Sequence 5251, Application US/08781986A
Publication No. US20030054436A1
GENERAL INFORMATION:
APPLICANT: Charles Kunsch
TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
NUMBER OF SEQUENCES: 5255
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COUNTRY: USA
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4MB storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/781,986A
FILING DATE:
CLASSIFICATION: 435

PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Benson, Bob
REGISTRATION NUMBER: 30,446
REFERENCE/DOCKET NUMBER: PB248BP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 5251:
SEQUENCE CHARACTERISTICS:
LENGTH: 559 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-781-986A-5251

Query Match 96.1%; Score 199; DB 8; Length 559;
Best Local Similarity 97.4%; Pred. No. 9,8e-18;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ONSGNOSFEEDTBPDPKPKYEOGNGNIVDIDPDSVPQIHG 38
Db 301 ONSGNOSFEEDTBPDPKPKYEOGNGNIVDIDPDSVPQIHG 338

RESULT 6
US-10-329-624-5251
Sequence 5251, Application US/10329624
Publication No. US20040043037A1
GENERAL INFORMATION:
APPLICANT: Charles Kunsch
GIL H. Choi
Patrick S. Dillon
Craig A. Rosen
Steven C. Barash
Michael R. Fannon
TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
NUMBER OF SEQUENCES: 5256
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COUNTRY: USA
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4MB storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/329,624
FILING DATE: 27-Dec-2002
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/956,171
FILING DATE: October 20, 1997
APPLICATION NUMBER: 60/009,861
FILING DATE: January 5, 1996
APPLICATION NUMBER: 08/781,986
FILING DATE: January 3, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Mark J. Hyman
REGISTRATION NUMBER: 46,789
REFERENCE/DOCKET NUMBER: PB248P1D1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (240) 314-1224
TELEFAX: (301) 309-8439
INFORMATION FOR SEQ ID NO: 5251:
SEQUENCE CHARACTERISTICS:
LENGTH: 559 amino acids

TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 5251:
US-10-329-624-5251

Query Match 96.1%; Score 199; DB 15; Length 559;
Best Local Similarity 97.4%; Pred. No. 9.8e-18;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 QNSGNQSFEDTPEPKPYEGGNIIVDIDPDSVPQIHG 38
Db 301 QNSGNQSFEDTPEPKPYEGGNIIVDIDPDSVPQIHG 338

RESULT 7
US-09-815-242-5899

Sequence 5899, Application US/09815242
Parent No. US2002061569A1

GENERAL INFORMATION:

APPLICANT: Haselbeck, Robert

APPLICANT: Ohlsen, Kari L.

APPLICANT: Zykend, Judith W.

APPLICANT: Wall, Daniel

APPLICANT: Trawick, John D.

APPLICANT: Carr, Grant J.

APPLICANT: Yamamoto, Robert T.

TITLE OF INVENTION: Identification of Essential Genes in

FILE REFERENCE: ELITRA.011A

CURRENT APPLICATION NUMBER: US/09/815,242

PRIOR FILING DATE: 2001-03-21

PRIOR APPLICATION NUMBER: 60/191,078

PRIOR FILING DATE: 2000-03-21

PRIOR APPLICATION NUMBER: 60/206,848

PRIOR FILING DATE: 2000-05-23

PRIOR APPLICATION NUMBER: 60/207,727

PRIOR FILING DATE: 2000-05-26

PRIOR APPLICATION NUMBER: 60/242,578

PRIOR FILING DATE: 2000-10-23

PRIOR APPLICATION NUMBER: 60/253,625

PRIOR FILING DATE: 2000-11-27

PRIOR APPLICATION NUMBER: 60/257,931

PRIOR FILING DATE: 2000-12-22

PRIOR APPLICATION NUMBER: 60/269,308

PRIOR FILING DATE: 2001-02-16

NUMBER OF SEQ ID NOS: 14110

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 5899

LENGTH: 767

TYPE: PRT

ORGANISM: Staphylococcus aureus

US-09-815-242-5899

Query Match 96.1%; Score 199; DB 9; Length 767;
Best Local Similarity 97.4%; Pred. No. 1.4e-17;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 QNSGNQSFEDTPEPKPYEGGNIIVDIDPDSVPQIHG 38
Db 682 QNSGNQSFEDTPEPKPYEGGNIIVDIDPDSVPQIHG 719

RESULT 8
US-09-815-242-13140

Sequence 13140, Application US/09815242
Parent No. US2002061569A1

GENERAL INFORMATION:

APPLICANT: Haselbeck, Robert

APPLICANT: Ohlsen, Kari L.

APPLICANT: Zykend, Judith W.

APPLICANT: Wall, Daniel
APPLICANT: Trawick, John D.
APPLICANT: Carr, Grant J.
APPLICANT: Yamamoto, Robert T.

APPLICANT: Xu, H. Howard

TITLE OF INVENTION: Identification of Essential Genes in

FILE REFERENCE: ELITRA.011A

CURRENT APPLICATION NUMBER: US/09/815,242

PRIOR FILING DATE: 2001-03-21

PRIOR APPLICATION NUMBER: 60/191,078

PRIOR FILING DATE: 2000-03-21

PRIOR APPLICATION NUMBER: 60/206,848

PRIOR FILING DATE: 2000-05-23

PRIOR APPLICATION NUMBER: 60/207,727

PRIOR FILING DATE: 2000-05-26

PRIOR APPLICATION NUMBER: 60/242,578

PRIOR FILING DATE: 2000-10-23

PRIOR APPLICATION NUMBER: 60/253,625

PRIOR FILING DATE: 2000-11-27

PRIOR APPLICATION NUMBER: 60/257,931

PRIOR FILING DATE: 2000-12-22

PRIOR APPLICATION NUMBER: 60/269,308

PRIOR FILING DATE: 2001-02-16

NUMBER OF SEQ ID NOS: 14110

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 13140

LENGTH: 767

TYPE: PRT

ORGANISM: Staphylococcus aureus

US-09-815-242-13140

Query Match 96.1%; Score 199; DB 9; Length 767;
Best Local Similarity 97.4%; Pred. No. 1.4e-17;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 QNSGNQSFEDTPEPKPYEGGNIIVDIDPDSVPQIHG 38
Db 682 QNSGNQSFEDTPEPKPYEGGNIIVDIDPDSVPQIHG 719

RESULT 9
US-10-470-048B-424

Sequence 424, Application US/10470048B
Publication No. US20050037444A1

GENERAL INFORMATION:

APPLICANT: MEINKE ET AL.

TITLE OF INVENTION: A METHOD FOR IDENTIFICATION, ISOLATION AND PRODUCTION OF

FILE REFERENCE: SONN.035US

CURRENT APPLICATION NUMBER: US/10/470,048B

PRIOR FILING DATE: 2003-07-25

NUMBER OF SEQ ID NOS: 603

SOFTWARE: PatentIn version 3.1

SEQ ID NO 424

LENGTH: 940

TYPE: PRT

ORGANISM: Staphylococcus aureus

US-10-470-048B-424

Query Match 96.1%; Score 199; DB 17; Length 940;
Best Local Similarity 97.4%; Pred. No. 1.8e-17;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 QNSGNQSFEDTPEPKPYEGGNIIVDIDPDSVPQIHG 38
Db 682 QNSGNQSFEDTPEPKPYEGGNIIVDIDPDSVPQIHG 719

RESULT 10

US-10-470-048B-69

Sequence 69, Application US/10470048B

Publication No. US20050037444A1

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; GENERAL INFORMATION:
; APPLICANT: MEINKE ET AL.
; TITLE OF INVENTION: A METHOD FOR IDENTIFICATION, ISOLATION AND PRODUCTION OF
; TITLE OF INVENTION: ANTIGENS TO A SPECIFIC PATHOGEN
; FILE REFERENCE: SONN-035US
; CURRENT APPLICATION NUMBER: US/10/470,048B
; NUMBER OF SEQ ID NOS: 603
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 69
; LENGTH: 948
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
; US-10-470-048B-69

Query Match      96.1%; Score 199; DB 17; Length 948;
Best Local Similarity 97.4%; Pred. No. 1,8e-17;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1  QNSGNSFEEDTEPDKPKYEGGNIIVDIDFDSVPQIHG 38
        |||||
Db      690 QNSGNSFEEDTEPDKPKYEGGNIIVDIDFDSVPQIHG 727

RESULT 11
US-10-282-122A-43778
; Sequence 43778, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Lianguo
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zykkind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Foreyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 43778
; LENGTH: 961
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
; US-10-282-122A-43778
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Query Match      96.1%; Score 199; DB 15; Length 961;
Best Local Similarity 97.4%; Pred. No. 1,8e-17;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1  QNSGNSFEEDTEPDKPKYEGGNIIVDIDFDSVPQIHG 38
        |||||
Db      693 QNSGNSFEEDTEPDKPKYEGGNIIVDIDFDSVPQIHG 730

RESULT 12
US-09-815-242-5797
; Sequence 5797, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari L.
; APPLICANT: Zykkind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; TITLE OF INVENTION: Prokaryotes
; FILE REFERENCE: ELITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: faSeq for Windows Version 4.0
; SEQ ID NO 5797
; LENGTH: 1018
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
; US-09-815-242-5797

Query Match      96.1%; Score 199; DB 9; Length 1018;
Best Local Similarity 97.4%; Pred. No. 2e-17;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1  QNSGNSFEEDTEPDKPKYEGGNIIVDIDFDSVPQIHG 38
        |||||
Db      746 QNSGNSFEEDTEPDKPKYEGGNIIVDIDFDSVPQIHG 783

RESULT 13
US-09-815-242-12838
; Sequence 12838, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari L.
; APPLICANT: Zykkind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
```

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; TITLE OF INVENTION: Prokaryotes
; FILE REFERENCE: ELITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO: 12838
; LENGTH: 1018
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-09-815-242-12838

Query Match          96.1%; Score 199; DB 9; Length 1018;
Best Local Similarity 97.4%; Pred. No. 2e-17;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1  QNSGNSFEEDTEPDKPKRYEKGNIVIDIDFDSVPQIHG 38
Db      746  QNSGNSFEEDTEPDKPKRYEKGNIVIDIDFDSVPQIHG 783

RESULT 14
US-10-470-048B-68
; Sequence 68, Application US/10470048B
; Publication No. US20050037444A1
; GENERAL INFORMATION:
; APPLICANT: MEINKE ET AL.
; TITLE OF INVENTION: A METHOD FOR IDENTIFICATION, ISOLATION AND PRODUCTION OF
; FILE REFERENCE: SONN:035US
; CURRENT APPLICATION NUMBER: US/10/470,048B
; CURRENT FILING DATE: 2003-07-25
; NUMBER OF SEQ ID NOS: 603
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 68
; LENGTH: 1018
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-10-470-048B-68

Query Match          96.1%; Score 199; DB 17; Length 1018;
Best Local Similarity 97.4%; Pred. No. 2e-17;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1  QNSGNSFEEDTEPDKPKRYEKGNIVIDIDFDSVPQIHG 38
Db      746  QNSGNSFEEDTEPDKPKRYEKGNIVIDIDFDSVPQIHG 783

RESULT 15
US-08-781-986A-5254
; Sequence 5254, Application US/08781986A
; Publication No. US20030054436A1
; GENERAL INFORMATION:
; APPLICANT: Charles Kunach
; TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
; NUMBER OF SEQUENCES: 5255
; CORRESPONDENCE ADDRESS:
; ADDRESS: Human Genome Sciences, Inc.
;
```

```

; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4mb storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/781,986A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Benson, Bob
; REGISTRATION NUMBER: 30,446
; REFERENCE/DOCKET NUMBER: PB248PP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 5254:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1027 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-781-986A-5254

Query Match          96.1%; Score 199; DB 8; Length 1027;
Best Local Similarity 97.4%; Pred. No. 2e-17;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1  QNSGNSFEEDTEPDKPKRYEKGNIVIDIDFDSVPQIHG 38
Db      755  QNSGNSFEEDTEPDKPKRYEKGNIVIDIDFDSVPQIHG 792

Search completed: October 22, 2005, 12:09:26
Job time : 70.1256 secs
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GenCore version 5.1.6
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OM protein - protein search, using sw. model

Run on: October 22, 2005, 04:14:19 ; Search time 13.8905 Seconds
(without alignments)
263.219 Million cell updates/sec

Title: US-10-731-238-41

Perfect score: 207
Sequence: 1 QNSGNQSFEDTPEDPKRYEQGNGNIVDIDFDSVPQIHG 38

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	199	96.1	940	2	S19702 fibronectin-binding
2	199	96.1	961	2	S19702 fibronectin-binding
3	199	96.1	1018	2	A32192 fibronectin-binding
4	199	96.1	1038	2	H90053 fibronectin-binding
5	57.5	27.8	168	2	T33564 fibronectin-binding
6	55.5	26.8	582	2	I48673 fibronectin-binding
7	55.5	26.8	582	2	I38028 fibronectin-binding
8	55	26.6	345	2	T33906 fibronectin-binding
9	55	26.6	1091	2	S33850 fibronectin-binding
10	54.5	26.3	528	2	C84110 fibronectin-binding
11	53.5	25.8	1952	2	T48814 fibronectin-binding
12	53	25.6	142	2	F70826 fibronectin-binding
13	53	25.6	326	2	A41732 fibronectin-binding
14	53	25.6	386	1	S22315 fibronectin-binding
15	53	25.6	1025	2	S69790 fibronectin-binding
16	53	25.6	1369	2	S58160 fibronectin-binding
17	52.5	25.4	437	2	S11925 fibronectin-binding
18	52.5	25.4	494	2	T14516 fibronectin-binding
19	52.5	25.4	582	2	I84471 fibronectin-binding
20	52.5	25.4	817	2	T03852 fibronectin-binding
21	52	25.1	195	2	A88110 fibronectin-binding
22	52	25.1	241	2	H97723 fibronectin-binding
23	52	25.1	241	2	C71725 fibronectin-binding
24	52	25.1	833	2	E90577 fibronectin-binding
25	52	25.1	1817	2	T34249 fibronectin-binding
26	51.5	24.9	155	1	RNBYR6 fibronectin-binding
27	51.5	24.9	227	2	UC6572 fibronectin-binding
28	51.5	24.9	461	2	G75598 fibronectin-binding
29	51.5	24.9	540	2	B82170 fibronectin-binding

30	51.5	24.9	875	2	C91209	capA protein NMB03
31	51.5	24.9	880	2	G81786	Neisseria-specific
32	51.5	24.9	1263	2	T19472	hypothetical prote
33	51	24.6	183	2	D83840	hypothetical prote
34	51	24.6	511	1	S31308	aldohyde dehydroge
35	51	24.6	596	2	T23193	hypothetical prote
36	51	24.6	599	2	A26100	genome polypeptid
37	51	24.6	769	2	T27550	hypothetical prote
38	51	24.6	784	2	T45971	hypothetical prote
39	51	24.6	1460	2	D81675	polymorphic membra
40	51	24.6	1536	1	RGBY63	regulatory protein
41	51	24.6	1977	2	S54771	sodium channel alp
42	51	24.6	2303	1	GNNYTP	genome polypeptid
43	51	24.6	2303	2	S13554	genome polypeptid
44	50.5	24.4	402	2	UC7199	mRNA (guanine-N7-)
45	50.5	24.4	1056	2	E96748	hypothetical prote

ALIGNMENTS

RESULT 1
S19702
fibronectin-binding protein B - Staphylococcus aureus
C:Species: Staphylococcus aureus
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
C:Accession: S19702
R:Johansen, K.; Signaes, C.; Mueller, H.P.; Lindberg, M.
Eur. J. Biochem. 202, 1041-1048, 1991
A:Title: Two different genes encode fibronectin binding proteins in Staphylococcus aureus
A:Reference number: S19702; MUID:92111475; PMID:1837266
A:Accession: S19702
A:Status: Preliminary
A:Molecule type: DNA
A:Residues: 1-940 <JOB>
A:Cross-references: UNIPROT:Q53682; EMBL:X62392; NID:949040; PIDN:CAA44726.1; PID:958156;
C:Keywords: fibronectin binding

Query Match 96.1%; Score 199; DB 2; Length 940;
Best Local Similarity 97.4%; Pred. No. 4.8e-18;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QNSGNQSFEDTPEDPKRYEQGNGNIVDIDFDSVPQIHG 38
DB 682 QNSGNQSFEDTPEDPKRYEQGNGNIVDIDFDSVPQIHG 719

RESULT 2

G90053
hypothetical protein fmbB (imported) - Staphylococcus aureus (strain N315)
C:Species: Staphylococcus aureus
C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
R:Kurdoz, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguchi, A.; Mizutani-U, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.; Ima, A.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiratsugu, K.
Lancet 357, 1225-1240, 2001
A:Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.
A:Reference number: A89758; MUID:21311952; PMID:11418146
A:Accession: G90053
A:Status: Preliminary
A:Molecule type: DNA
A:Residues: 1-961 <KUR>
A:Cross-references: UNIPROT:Q99RD3; GB:BA000018; PID:G13702452; PIDN:BAR43593.1; GSPDB:G
A:Experimental source: strain N315
C:Genetics:
A:Gene: fmbB

Query Match 96.1%; Score 199; DB 2; Length 961;
Best Local Similarity 97.4%; Pred. No. 4.9e-18;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QNSGNQSFEDTPEDPKRYEQGNGNIVDIDFDSVPQIHG 38

```
Db 693 ONSGNQSFEDTEBDKPKYEGCGNIVDIDFDSVPQIHG 730
|||||
RESULT 3
A32192
fibronectin-binding protein - Staphylococcus aureus
C:Species: Staphylococcus aureus
C:Date: 31-Jul-1989 #sequence_revision 31-Jul-1989 #text_change 16-Feb-1997
C:Accession: A32192
R:Signaas, C.; Raucot, G.; Joensson, K.; Lindgren, P.E.; Anantharamaiah, G.M.; Hoeoek, M
Proc. Natl. Acad. Sci. U.S.A. 86, 699-703, 1989
A:Title: Nucleotide sequence of the gene for a fibronectin-binding protein from Staphylo
A:Reference number: A32192; MUID:89089898; PMID:2521391
A:Accession: A32192
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1018 <SIG>
A:Cross-references: GB:J04151
C:Keywords: fibronectin binding

Query Match 96.1%; Score 199; DB 2; Length 1018;
Best Local Similarity 97.4%; Pred. No. 5,3e-18;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 ONSGNQSFEDTEBDKPKYEGCGNIVDIDFDSVPQIHG 38
|||||
Db 746 ONSGNQSFEDTEBDKPKYEGCGNIVDIDFDSVPQIHG 783
|||||

RESULT 4
H90053
hypothetical protein fnb [imported] - Staphylococcus aureus (strain N315)
C:Species: Staphylococcus aureus
C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C:Accession: H90053
R:Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguc
ma, A.; Mizutani-U, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kato, C.; Sekimizu, K.;
C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramoto, K.
Lancet 357, 1255-1240, 2001
A:Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.
A:Reference number: A89758; MUID:21311952; PMID:11418146
A:Accession: H90053
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1038 <KUR>
A:Cross-references: UNIPROT:Q99RD2; GB:BA000018; PID:G13702453; PIDN:BA843594.1; GSPDB:G
A:Experimental source: strain N315
C:Genetics:
A:Gene: fnb

Query Match 96.1%; Score 199; DB 2; Length 1038;
Best Local Similarity 97.4%; Pred. No. 5,4e-18;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 ONSGNQSFEDTEBDKPKYEGCGNIVDIDFDSVPQIHG 38
|||||
Db 742 ONSGNQSFEDTEBDKPKYEGCGNIVDIDFDSVPQIHG 779
|||||

RESULT 5
T33564
hypothetical protein R160.4 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
C:Accession: T33564
R:Nelson, J.; Gattung, S.
Submitted to the EMBL Data Library, October 1998
A:Description: The sequence of C. elegans comid R160.
A:Reference number: 221370
A:Accession: T33564
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
```

```
A:Residues: 1-168 <NEL>
A:Cross-references: UNIPROT:Q9TZD4; EMBL:AF099001; PIDN:AA66735.1; GSPDB:GN00028; CESP:
A:Experimental source: strain Bristol N2; clone R160
C:Genetics:
A:Gene: CESP:R160.4
A:Map position: X
A:Introns: 19/2; 74/3; 100/2
C:Superfamily: Caenorhabditis elegans hypothetical protein R160.4

Query Match 27.8%; Score 57.5; DB 2; Length 168;
Best Local Similarity 30.3%; Pred. No. 3.2;
Matches 10; Conservative 9; Mismatches 9; Indels 5; Gaps 1;

OY 6 OSFEDTEBDKPKYEGCGNIVDIDFDSVPQIHG 38
|||||
Db 39 ERFDEDEBSPKPO-----GFVSLDVEQLDQVHG 66
|||||

RESULT 6
I48673
matrix metalloproteinase (EC 3.4.24.-) membrane type precursor - mouse
C:Species: Mus musculus (house mouse)
C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 22-Jun-1999
C:Accession: I48673
R:Okada, A.; Bellocq, J.P.; Rouyer, N.; Chenard, M.P.; Rio, M.C.; Chambon, P.; Baasat, P.
Proc. Natl. Acad. Sci. U.S.A. 92, 2730-2734, 1995
A:Title: Membrane-type matrix metalloproteinase (MT-MMP) gene is expressed in stromal cel
A:Reference number: I38046; MUID:95224014; PMID:7708715
A:Accession: I48673
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-582 <RES>
A:Cross-references: EMBL:X83536; NID:9804999; PIDN:CAA58520.1; PID:9805000
C:Superfamily: Interstitial collagenase; hemopexin repeat homology; matrix metalloprotein
C:Keywords: hydrolase; metalloproteinase; zinc; zymogen
F:1-33/Domain: signal sequence #status predicted <SIG>
F:24-97/Domain: activation peptide #status predicted <PRO>
F:61-284/Domain: matrix metalloproteinase homology <MMP>
F:313-508/Domain: hemopexin repeat homology <PNX>
F:93,239,243,249/Binding site: zinc, catalytic (His, His, His, His) (inhibited) #status p
F:239,243,249/Binding site: zinc, catalytic (His) (active) #status predicted
F:240/Active site: Glu #status predicted

Query Match 26.8%; Score 55.5; DB 2; Length 582;
Best Local Similarity 50.0%; Pred. No. 25;
Matches 13; Conservative 3; Mismatches 9; Indels 1; Gaps 1;

OY 14 PDKPKY-EOGGINVIDIDFDSVPQIHG 38
|||||
Db 306 PDKPKYAGPNCIDGNFTVAMLRG 331
|||||

RESULT 7
I18028
matrix metalloproteinase 14 (EC 3.4.24.-) membrane type precursor - human
N:Alternate names: matrix metalloproteinase MMP14; membrane type matrix metalloproteinase
C:Species: Homo sapiens (man)
C:Date: 17-May-1996 #sequence_revision 17-May-1996 #text_change 09-Jul-2004
C:Accession: I18028; G02274; I18046; S78011; S45341; S71384
R:Will, H.; Hinemann, B.
Eur. J. Biochem. 231, 602-608, 1995
A:Title: cDNA sequence and mRNA tissue distribution of a novel human matrix metalloprote
A:Reference number: I18028; MUID:95377289; PMID:7649159
A:Accession: I18028
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-582 <WILL>
A:Cross-references: UNIPROT:P50281; EMBL:Z48481; NID:9963053; PIDN:CAA80372.1; PID:99630;
R:Liu, G.
Submitted to the EMBL Data Library, November 1995
A:Reference number: H00963
A:Accession: G02274
A:Status: preliminary; translated from GB/EMBL/DBJ
```

A:Molecule type: mRNA
A:Residues: 1-582 <LNU>
A:Cross-references: EMBL:U41078; NID:91127836; PIDN:AAA83770.1; PID:91127837
Proc. Natl. Acad. Sci. U.S.A. 92, 2730-2734, 1995
A:Title: Membrane-type matrix metalloproteinase (MT-MMP) gene is expressed in stromal cells
A:Reference number: 138046; MUID:95224014; PMID:7708735
A:Accession: 138046
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-7,'S','9-582 <OKA>
A:Cross-references: EMBL:X83535; NID:9804993; PIDN:CAA58519.1; PID:9804994
R:Seiki, M.
submitted to the EMBL Data Library, January 1994
A:Reference number: S78011
A:Accession: S78011
A:Molecule type: mRNA
A:Residues: 1-7,'S','9-337,'K',339-582 <SEI>
A:Cross-references: EMBL:D26512; NID:9793762; PIDN:BA05519.1; PID:9793763
R:Sato, H.; Takino, T.; Okada, Y.; Cao, J.; Shinagawa, A.; Yamamoto, E.; Seiki, M.
Nature 370, 61-65, 1994
A:Title: A matrix metalloproteinase expressed on the surface of invasive tumour cells.
A:Reference number: S45341; MUID:94286011; PMID:8015608
A:Accession: S45341
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-7,'S','9-188,'R',190,'A',192-267,'K',269-272,'H','275,'P',277-285,'KQ',288
A:Cross-references: EMBL:D26512
R:Sato, H.; Kinoshita, T.; Takino, T.; Nakayama, K.; Seiki, M.
FEBS Lett. 393, 101-104, 1996
A:Title: Activation of a recombinant membrane type 1-matrix metalloproteinase (MT1-MMP)
A:Reference number: S71384; MUID:96397540; PMID:8804434
A:Accession: S71384
A:Molecule type: protein
A:Residues: 112-116 <SAM>
C:Genetics:
A:Gene: GDB:MMP14; MT1-MMP
A:Cross-references: GDB:375731; OMTM:600754
A:Map position: 14q11-14q12
C:Species: interstitial collagenase; hemopexin repeat homology; matrix metalloprote
C:Keywords: glycoprotein; hydrolysis; metalloproteinase; zinc; zymogen
F:1-33/Domain: signal sequence #status predicted <HNO>
F:24-97/Domain: activation peptide #status predicted <PRO>
F:61-284/Domain: matrix metalloproteinase homology <MMP>
F:98-582/Product: matrix metalloproteinase 14 membrane type #status predicted <MAT>
F:285-313/Domain: hinge #status predicted <HNO>
F:314-508/Domain: hemopexin repeat homology <EPX>
F:539-566/Domain: transmembrane #status predicted <TM>
F:193,239,243,249/Binding site: zinc, catalytic (Cys, His, His, His) (inhibited) #status
F:130/Binding site: carboxylate (Asn) (covalent) #status predicted
F:239,243,249/Binding site: zinc, catalytic (His) (active) #status predicted
F:240/Active site: Glu #status predicted
F:319-508/Disulfide bonds: #status predicted

Query Match	26.8%;	Score 55.5;	DB 2;	Length 582;
Best Local Similarity	50.0%;	Pred. No. 25;		
Matches 13;	Conservative 3;	Mismatches 9;	Indels 1;	Gaps 1;

14 PDKPKY-EGGKIVDIDPSVQING 38
||||| ||||| ||||| |||||
306 PDKPKPYGPNICDGNFDTVAMLRK 331

RESULT 8
T33906
hypothetical protein Y25C1A.8 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
C:Accession: T33906
R:Kalicki, J.; Smith, A.; Gibson, A.
submitted to the EMBL Data Library, February 1999
A:Description: The sequence of C. elegans cosmid Y25C1A.
A:Reference number: Z21437

[illegible]

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RESULT 11
T48814
hypothetical protein 15E6.220 [imported] - Neurospora crassa
C:Species: Neurospora crassa
C:Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 09-Jul-2004
C:Accession: T48814
R:Schulze, U.; Aign, V.; Hohsies, J.; Brandt, P.; Farctmann, B.; Holland, R.; Nyakatura,
submitted to the Protein Sequence Database, April 2000
A:Reference number: 224541
A:Accession: T48814
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1952 <SCH>
A:Cross-references: UNIPROT:Q9PFT1, EMBL:AL353822, GSPDB:GN00112, NCSP:15E6.220
A:Experimental source: cosmid contig 15E6; strain 74
C:Genetics:
A:Gene: NCSP:15E6.220
A:Map position: 2
A:Introns: 281/3

Query Match 25.8%; Score 53.5; DB 2; Length 1952;
Best Local Similarity 26.5%; Pred. No. 1.9e+02;
Matches 9; Conservative 11; Mismatches 13; Indels 1; Gaps 1;

OY 3 GNSGFEDTPDKKRYEGGNIIVDDPSVQI 36
DB 547 TGAEEFEETPAR-RYSEGGKEMSFDESHDV 579

RESULT 12
F70826
probable membrane protein - Mycobacterium tuberculosis (strain H37RV)
C:Species: Mycobacterium tuberculosis
C:Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 09-Jul-2004
C:Accession: F70826
R:Coile, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.;
Connors, R.; Davies, R.; Devlin, K.; Felwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.;
Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.;
Nature 393, 537-544, 1998
A:Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A:Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome
A:Reference number: AT0500; MUID:98295987; PMID:9634230
A:Accession: F70826
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-142 <COU>
A:Cross-references: UNIPROT:O53785; GB:AL021943; GB:AL123456; NID:G3261530; PIDN:CAA1746
A:Experimental source: strain H37RV
C:Genetics:
A:Gene: mmp95
C:Superfamily: Mycobacterium tuberculosis probable membrane protein mmp95

Query Match 25.6%; Score 53; DB 2; Length 142;
Best Local Similarity 41.7%; Pred. No. 10;
Matches 15; Conservative 3; Mismatches 10; Indels 8; Gaps 2;

OY 8 FEEDTEPDKPK---YEGG-----NIYDIDFDSVPQ 35
DB 44 FADDEPDPKVEYEVGSGSYVINYLDDAKQ 79

RESULT 13
A11732
heterogeneous ribonuclear particle protein hrp36 - fruit fly (Drosophila melanogaster)
N:Alternate names: heterogeneous nuclear RNP protein hrp36
C:Species: Drosophila melanogaster
C:Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004
C:Accession: A11732
R:Matunis, E.L.; Matunis, M.J.; Dreyfuss, G.;
J. Cell Biol. 116, 257-269, 1992
A:Title: Characterization of the major hnRNP proteins from Drosophila melanogaster.
A:Reference number: A11732; MUID:92112968; PMID:1730754

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A:Accession: A11732
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-326 <MAT>
A:Cross-references: UNIPROT:P48810, GB:X62636, NID:G11035, PIDN:CAA44502.1, PID:G11036
A:Note: sequence extracted from NCBI backbone (NCBI:76634, NCBI:P:76635)
C:Genetics:
A:Gene: FlyBase:Hrb87F
A:Cross-references: FlyBase:FBgn0004237
C:Superfamily: helix-decabilizing protein; ribonucleoprotein repeat homology
C:Keywords: DNA binding
F:25-91/Domain: ribonucleoprotein repeat homology <RNM1>
F:116-182/Domain: ribonucleoprotein repeat homology <RNM2>

Query Match 25.6%; Score 53; DB 2; Length 326;
Best Local Similarity 30.0%; Pred. No. 27;
Matches 15; Conservative 6; Mismatches 7; Indels 22; Gaps 2;

OY 1 QNSGNQSF---EEDTEPD-----KPKYEGGNIIVDI 28
DB 4 QNDSNGNYDDGEETTPBQLKLFITGGLDYRTTDDGLKAHEKKNIVDV 53

RESULT 14
S22315
snRNP-associated protein P11 - fruit fly (Drosophila melanogaster)
N:Alternate names: heterogeneous ribonuclear particle (hnRNP) protein A1 homolog; hnRNP I
C:Species: Drosophila melanogaster
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C:Accession: S22315; S65539; S13731
R:Hovemann, B.T.; Deessen, E.; Mechler, H.; Mack, E.
Nucleic Acids Res. 19, 4909-4914, 1991
A:Title: Drosophila snRNP associated protein P11 which specifically binds to heat shock I
A:Reference number: S22315; MUID:92020124; PMID:1717937
A:Accession: S22315
A:Molecule type: DNA
A:Residues: 1-386 <HOV>
A:Cross-references: UNIPROT:P48810, EMBL:X59691
R:Reiner, B.
submitted to the EMBL Data Library, August 1991
A:Reference number: S65539
A:Accession: S65539
A:Molecule type: DNA
A:Residues: 1-270, 'T', 272-386 <REI>
A:Cross-references: EMBL:X59691; NID:98317; PIDN:CAA42212.1; PID:98318
R:Haynes, S.R.; Johnson, D.; Raychaudhuri, G.; Beyer, A.L.
Nucleic Acids Res. 19, 25-31, 1991
A:Title: The Drosophila Hrb87F gene encodes a new member of the A and B hnRNP protein gr
A:Reference number: S13731; MUID:91187645; PMID:1849257
A:Accession: S13731
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-386 <HAY>
A:Cross-references: EMBL:X54803; NID:98093; PIDN:CAA38574.1; PID:98094
C:Genetics:
A:Gene: FlyBase:Hrb87F
A:Cross-references: FlyBase:FBgn0004237
A:Introns: 16/3
C:Superfamily: helix-decabilizing protein; ribonucleoprotein repeat homology
F:25-91/Domain: ribonucleoprotein repeat homology <RNM1>
F:116-182/Domain: ribonucleoprotein repeat homology <RNM2>

Query Match 25.6%; Score 53; DB 1; Length 386;
Best Local Similarity 30.0%; Pred. No. 33;
Matches 15; Conservative 6; Mismatches 7; Indels 22; Gaps 2;

OY 1 QNSGNQSF---EEDTEPD-----KPKYEGGNIIVDI 28
DB 4 QNDSNGNYDDGEETTPBQLKLFITGGLDYRTTDDGLKAHEKKNIVDV 53

RESULT 15
S69790

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OM protein - protein search, using SW model

Run on: October 22, 2005, 04:10:49 ; Search time 69.6361 Seconds
(without alignments)
279,439 Million cell updates/sec

Title: US-10-731-238-41
Perfect score: 207
Sequence: 1 QNSGNQSFEDTPEPKPKYEGCGNIYDIDPDSVPQIHG 38

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues
Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	* Query Match Length	DB ID	Description
1	199	96.1	940 2 Q53682	Q53682 staphylococ
2	199	96.1	943 2 Q8NNU8	Q8NNU8 staphylococ
3	199	96.1	957 2 Q6G6H4	Q6G6H4 staphylococ
4	199	96.1	961 2 Q99RD3	Q99RD3 staphylococ
5	199	96.1	961 2 Q7A3U8	Q7A3U8 staphylococ
6	199	96.1	1018 1 FNBA_STPAU	FNBA_STPAU
7	199	96.1	1038 2 Q99RD2	Q99RD2 staphylococ
8	199	96.1	1038 2 Q7A3J7	Q7A3J7 staphylococ
9	198	95.7	965 2 Q6GDU5	Q6GDU5 staphylococ
10	195	94.2	1015 2 Q8NNU7	Q8NNU7 staphylococ
11	195	94.2	1015 2 Q6G6H3	Q6G6H3 staphylococ
12	188	90.8	152 2 Q9AEP9	Q9AEP9 staphylococ
13	66	31.9	937 2 Q6BWI0	Q6BWI0 debaryomyce
14	60	29.0	999 2 Q8K5Z5	Q8K5Z5 streptococc
15	59	28.5	539 2 Q89PZ3	Q89PZ3 bradyrhizob
16	59	28.5	889 2 Q6CBW0	Q6CBW0 yarrowia 11
17	58.5	28.3	745 2 Q7SA69	Q7SA69 neustropora
18	58	28.0	651 2 Q9AGE9	Q9AGE9 streptococc
19	58	28.0	1246 2 Q7UKY7	Q7UKY7 rhodospirill
20	58	28.0	1335 2 Q7NCKX8	Q7NCKX8 gloeobacter
21	57.5	27.8	168 2 Q9TSD4	Q9TSD4 caenorhabdi
22	57.5	27.8	454 2 Q9JHK1	Q9JHK1 rattus norv
23	57	27.5	101 2 Q68IT3	Q68IT3 vaccinium c
24	57	27.5	215 2 Q8GBU1	Q8GBU1 uncultured
25	57	27.5	237 2 Q8BZM9	Q8BZM9 mus musculu
26	57	27.5	455 2 Q6ZQ97	Q6ZQ97 mus musculu
27	57	27.5	457 2 Q9GDV3	Q9GDV3 carpoibrotus
28	57	27.5	532 2 Q9D074	Q9D074 m mus muscu
29	57	27.5	684 2 Q64YR9	Q64YR9 bacteroides
30	57	27.5	856 2 Q6C206	Q6C206 yarrowia 11
31	57	27.5	1226 2 Q7UL12	Q7UL12 rhodospirill

32	56.5	27.3	904 2 Q54324	Q54324 sulfolobus
33	56	27.1	225 2 Q757L6	Q757L6 ashbya gos9
34	56	27.1	251 2 Q9VFD6	Q9VFD6 drosophila
35	56	27.1	626 2 Q8KPN4	Q8KPN4 streptococc
36	56	27.1	923 2 Q9S3T2	Q9S3T2 streptococc
37	56	27.1	954 2 Q6YBU6	Q6YBU6 streptococc
38	56	27.1	1013 2 Q93T52	Q93T52 streptococc
39	56	27.1	1013 2 Q91953	Q91953 streptococc
40	56	27.1	1015 2 Q93T50	Q93T50 streptococc
41	56	27.1	1023 2 Q93T53	Q93T53 streptococc
42	56	27.1	1029 2 Q9X2V2	Q9X2V2 streptococc
43	56	27.1	1046 2 Q84941	Q84941 plasmodium
44	56	27.1	1350 2 Q6LFP5	Q6LFP5 plasmodium
45	55.5	26.8	133 2 Q9NHN7	Q9NHN7 plasmodium

ALIGNMENTS

RESULT 1	ID	Q53682	PRELIMINARY;	PRT;	940 AA.
AC	Q53682;				
DT	01-NOV-1996 (TREMBLrel. 01, Created)				
DT	01-NOV-1996 (TREMBLrel. 01, Last sequence update)				
DE	01-MAR-2004 (TREMBLrel. 26, Last annotation update)				
GN	Fibronectin binding protein B.				
OS	Staphylococcus aureus.				
OC	Bacteria; Firmicutes; Bacillales; Staphylococcus.				
OX	NCBI_TaxId=1280;				
RN	(1)				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=8325-4;				
RX	MEDLINE=92111475; PubMed=1837266;				
RA	Jonsson K., Signas C., Muller H.P., Lindberg M.;				
RT	Two different genes encode fibronectin binding proteins in				
RT	Staphylococcus aureus. The complete nucleotide sequence and				
RT	characterization of the second gene."				
RL	Eur. J. Biochem. 202:1041-1048 (1991).				
CC	-1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by				
CC	an amide bond (By similarity).				
DR	EMBL; X62992; CAA44726.1; -.				
DR	PIR; S19702; S19702.				
DR	HSSP; Q53682; IN67.				
DR	GO; GO:0009986; C:cell surface; IEA.				
DR	GO; GO:0005618; C:cell wall; IEA.				
DR	GO; GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.				
DR	GO; GO:0016020; C:membrane; IEA.				
DR	GO; GO:007155; P:cell adhesion; IEA.				
DR	InterPro; IPR008966; Adhes_Dact.				
DR	InterPro; IPR004237; Fn_bind.				
DR	InterPro; IPR005877; Gpos_YsIRK.				
DR	InterPro; IPR001899; Gram_pos_anchor.				
DR	Pfam; PF02986; Fn_bind; 2.				
DR	Pfam; PF00746; Gram_pos_anchor; 1.				
DR	Pfam; PF04650; YsIRK_signal; 1.				
DR	TIGRfam; TIGR01167; LpXTG_anchor; 1.				
DR	TIGRfam; TIGR01168; YsIRK_signal; 1.				
DR	PROSITE; PS50847; GRAM_POS_ANCHORING; 1.				
DR	Cell wall; Peptidoglycan-anchor.				
DR	Cell wall; Peptidoglycan-anchor.				
DR	SEQUENCE 940 AA; 103555 MW; E35FBQCA907AE345 CRC64;				
QY	1 QNSGNQSFEDTPEPKPKYEGCGNIYDIDPDSVPQIHG 38				
DB	682 QNSGNQSFEDTPEPKPKYEGCGNIYDIDPDSVPQIHG 719				
RESULT 2					

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Q8NU8      PRELIMINARY; PRT: 943 AA.
ID Q8NU8.
AC Q8NU8.
DT 01-OCT-2002 (TREMBlrel. 22, Created)
DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Fimb protein.
GN Name=fmbB; OrderedlocusNames=MW2420;
OS Staphylococcus aureus (strain MW2)
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=196620;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NMW2;
RX MEDLINE=22040717; PubMed=12044378; DOI=10.1016/S0140-6736(02)08713-5;
RA Baba T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Oguchi A.,
RA Yamamoto K., Hiramatsu K.;
RA "Genome and virulence determinants of high virulence community-
RT acquired MRSA.";
RL Lancet 359:1819-1827(2002).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC an amide bond (By similarity).
DR EMBL; AP004830; BAB96285.1; -.
DR HSSP; Q53653; 1N67.
DR GO; GO:0009986; C:cell surface; IEA.
DR GO; GO:0005618; C:cell wall; IEA.
DR GO; GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0007155; P:cell adhesion; IEA.
DR InterPro; IPR008966; Adhes_bact.
DR InterPro; IPR004237; Fn_bind.
DR InterPro; IPR005877; Gpos_YsIRK.
DR InterPro; IPR001899; Gram_pos_anchor.
DR Pfam; PF02986; Fn_bind_1.
DR Pfam; PF00746; Gram_pos_anchor; 1.
DR Pfam; PF04650; YsIRK_signal; 1.
DR TIGRFAMs; TIGR01167; LpxTG_anchor; 1.
DR TIGRFAMs; TIGR01168; YsIRK_signal; 1.
DR PROSITE; PS50847; GRAM_POS_ANCHORING; 1.
DR Cell wall, Complete proteome; Peptidoglycan-anchor.
KW SEQUENCE 943 AA; 104537 MW; DA8A5F31947E1B6A CRC64;

Query Match 96.1%; Score 199; DB 2; Length 943;
Best Local Similarity 97.4%; Pred. No. 1.7e-16;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QNSGNQSFEDTEPDPKPYEGCGNIVDIDFDSVPQING 38
DB 689 QNSGNQSFEDTEPDPKPYEGCGNIVDIDFDSVPQING 726

RESULT 3
Q6G6H4 PRELIMINARY; PRT: 957 AA.
ID Q6G6H4.
AC Q6G6H4.
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE Fibronectin-binding protein.
GN Name=fmbB; OrderedlocusNames=SA52387;
OS Staphylococcus aureus (strain MSSA476).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=282459;
RN [1]
RP SEQUENCE FROM N.A.
RX Holden M.T.G., Fell E.J., Lindsey J.A., Peacock S.J., Day N.P.J.,
RA Enright M.C., Foster T.J., Moore C.E., Hurst L., Atkin R., Barron A.,
RA Baeson N., Bentley S.D., Chillingworth C., Chillingworth T.,
RA Churcher C., Clark L., Corson C., Cronin A., Doggett J., Dowd L.,
RA Feltwell T., Hance Z., Harris B., Hauser H., Holtroyd S., Jagsals K.,
RA James K.D., Lennard N., Line A., Mayes R., Moule S., Mungall K.,
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RA Ormond D., Quail M.A., Rabbintwitsch E., Rutherford K.M., Sanders M.,
RA Sharp S., Simmonds M., Stevens K., Whitehead S., Barrell B.G.,
RA Spratt B.G., Parkhill J.;
RT "Complete genomes of two clinical Staphylococcus aureus strains:
RT evidence for the rapid evolution of virulence and drug resistance.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:9786-9791(2004).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC an amide bond (By similarity).
DR EMBL; BX571857; CAG44201.1; -.
DR GO; GO:0009986; C:cell surface; IEA.
DR GO; GO:0005618; C:cell wall; IEA.
DR GO; GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0007155; P:cell adhesion; IEA.
DR InterPro; IPR008966; Adhes_bact.
DR InterPro; IPR004237; Fn_bind.
DR InterPro; IPR005877; Gpos_YsIRK.
DR InterPro; IPR001899; Gram_pos_anchor.
DR Pfam; PF02986; Fn_bind_1.
DR Pfam; PF00746; Gram_pos_anchor; 1.
DR Pfam; PF04650; YsIRK_signal; 1.
DR TIGRFAMs; TIGR01167; LpxTG_anchor; 1.
DR TIGRFAMs; TIGR01168; YsIRK_signal; 1.
DR PROSITE; PS50847; GRAM_POS_ANCHORING; 1.
DR Cell wall, Complete proteome; Peptidoglycan-anchor.
KW SEQUENCE 957 AA; 105980 MW; 28F8BA7FFD3EAF CRC64;

Query Match 96.1%; Score 199; DB 2; Length 957;
Best Local Similarity 97.4%; Pred. No. 1.7e-16;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QNSGNQSFEDTEPDPKPYEGCGNIVDIDFDSVPQING 38
DB 689 QNSGNQSFEDTEPDPKPYEGCGNIVDIDFDSVPQING 726

RESULT 4
Q99RD3 PRELIMINARY; PRT: 961 AA.
ID Q99RD3.
AC Q99RD3.
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE Fibronectin-binding protein homolog.
GN Name=fmbB; OrderedlocusNames=SAV2502;
OS Staphylococcus aureus (strain Mu50 / ATCC 700699).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=158878;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Mu50 / ATCC 700699;
RX MEDLINE=21311952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2;
RA Kuroda M., Onota T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Iian Y.-Q., Ito T.,
RA Kanamori M., Matsumaru H., Maruyama A., Murakami H., Horiyama A.,
RA Mizutani-Ui Y., Takehashi N.K., Sawano T., Inoue R.-I., Kato C.,
RA Sekimizu K., Hiraoka H., Kubara S., Goto S., Yabuzaki J.,
RA Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shibata T.,
RA Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
RT "Whole genome sequencing of methicillin-resistant Staphylococcus
RT aureus.";
RL Lancet 357:1225-1240(2001).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC an amide bond (By similarity).
DR EMBL; AP003365; BAB58664.1; -.
DR PIR; G90053; G90053.
DR HSSP; Q53653; 1N67.
DR GO; GO:0009986; C:cell surface; IEA.
DR GO; GO:0005618; C:cell wall; IEA.
DR GO; GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0007155; P:cell adhesion; IEA.
DR InterPro; IPR008966; Adhes_bact.
```

DR InterPro: IPR004237; Fn_bind.
 DR InterPro: IPR005877; Gpos_YsIRK.
 DR InterPro: IPR001899; Gram_pos_anchor.
 DR Pfam: PF02986; Fn_bind; 1.
 DR Pfam: PF00746; Gram_pos_anchor; 1.
 DR Pfam: PF04650; YsIRK_signal; 1.
 DR TIGRPFAM: TIGR01167; LPXTG_anchor; 1.
 DR TIGRPFAM: TIGR01168; YsIRK_signal; 1.
 DR PROSITE: PS00847; GRAM_POS_ANCHORING; 1.
 KW Cell wall; Complete proteome; Peptidoglycan-anchor.
 SQ SEQUENCE 961 AA; 106010 MW; 364940F884EA4101 CRC64;

Query Match 96.1%; Score 199; DB 2; Length 961;
 Best Local Similarity 97.4%; Pred. No. 1.7e-16;
 Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 ONSGNQSFEDTEBDKPKYEGCGNIVDIDFDSVPQIHG 38
 DB 693 ONSGNQSFEDTEBDKPKYEGCGNIVDIDFDSVPQIHG 730

RESULT 5
 ID Q7A3J8 PRELIMINARY; PRT; 961 AA.
 AC Q7A3J8;
 DT 05-JUL-2004 (TRMBLrel. 27, Created)
 DT 05-JUL-2004 (TRMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TRMBLrel. 27, Last annotation update)
 DE FnBb protein.
 GN Name=fnBb; Ordered locus names=Sa2290;
 OS Staphylococcus aureus (strain N315).
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 OX NCBI_TaxID=158879;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=2111952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2;
 RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
 RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Ito T.,
 RA Kanamori M., Matsunari H., Maruyama A., Murakami H., Hosoyama A.,
 RA Mizunuma-Uji Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
 RA Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
 RA Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
 RA Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.,
 RT "Whole genome sequencing of methicillin-resistant Staphylococcus
 aureus".
 RL Lancet 357:1225-1240(2001).
 RL -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
 an amide bond (By similarity).
 CC EMBL: AP003137; BAB43593.1; -
 CC GO: GO:0009986; C:cell surface; IEA.
 CC GO: GO:0005618; C:cell wall; IEA.
 CC GO: GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
 CC GO: GO:007155; P:cell adhesion; IEA.
 DR InterPro: IPR008966; Adhes_Dact.
 DR InterPro: IPR004237; Fn_bind.
 DR InterPro: IPR005877; Gpos_YsIRK.
 DR InterPro: IPR001899; Gram_pos_anchor.
 DR Pfam: PF02986; Fn_bind; 1.
 DR Pfam: PF00746; Gram_pos_anchor; 1.
 DR Pfam: PF04650; YsIRK_signal; 1.
 DR TIGRPFAM: TIGR01167; LPXTG_anchor; 1.
 DR TIGRPFAM: TIGR01168; YsIRK_signal; 1.
 DR PROSITE: PS00847; GRAM_POS_ANCHORING; 1.
 KW Cell wall; Complete proteome; Peptidoglycan-anchor.
 SQ SEQUENCE 961 AA; 106010 MW; 364940F884EA4101 CRC64;

Query Match 96.1%; Score 199; DB 2; Length 961;
 Best Local Similarity 97.4%; Pred. No. 1.7e-16;
 Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 ONSGNQSFEDTEBDKPKYEGCGNIVDIDFDSVPQIHG 38
 DB 693 ONSGNQSFEDTEBDKPKYEGCGNIVDIDFDSVPQIHG 730

DB 693 ONSGNQSFEDTEBDKPKYEGCGNIVDIDFDSVPQIHG 730

RESULT 6
 ID FNBA_STA0U STANDARD; PRT; 1018 AA.
 AC P14738;
 DT 01-APR-1990 (Rel. 14, Created)
 DT 01-APR-1990 (Rel. 14, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Fibronectin-binding protein precursor (FNBP).
 DE Name=fnBa;
 GN Staphylococcus aureus.
 OS Bacteria; Firmicutes; Bacillales; Staphylococcus.
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 OX NCBI_TaxID=1280;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=NCIC 8325-4;
 RX MEDLINE=89098998; PubMed=2521391;
 RA Signaes C., Raucet G., Joensson K., Lindgren P.-E.,
 RA Anantharamiah G.M., Hoeoek M., Lindberg M.,
 RT "Nucleotide sequence of the gene for a fibronectin-binding protein
 from Staphylococcus aureus: use of this peptide sequence in the
 synthesis of biologically active peptides".
 RT Proc. Natl. Acad. Sci. U.S.A. 86:699-703(1989).
 RL -1- FUNCTION: The ability of bacteria to bind fibronectin has been
 proposed as a virulence factor enabling bacteria to colonize wound
 tissues and blood clots. Binding of plasma fibronectin to the
 bacterial surface might block adhesion receptors on S.aureus, thus
 representing an important defense mechanism against tissue
 invasion.
 CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
 an amide bond (Potential).
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 between the Swiss Institute of Bioinformatics and the EMBL outstation -
 the European Bioinformatics Institute. There are no restrictions on its
 use by non-profit institutions as long as its content is in no way
 modified and this statement is not removed. Usage by and for commercial
 entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 or send an email to license@sib-sib.ch).
 CC EMBL: J04151; AAA26632.1; -
 CC InterPro: IPR004237; Fn_bind.
 CC InterPro: IPR005877; Gpos_YsIRK.
 CC InterPro: IPR001899; Gram_pos_anchor.
 CC Pfam: PF02986; Fn_bind; 1.
 CC Pfam: PF00746; Gram_pos_anchor; 1.
 CC Pfam: PF04650; YsIRK_signal; 1.
 CC TIGRPFAM: TIGR01167; LPXTG_anchor; 1.
 CC TIGRPFAM: TIGR01168; YsIRK_signal; 1.
 CC PROSITE: PS00847; GRAM_POS_ANCHORING; 1.
 KW Cell adhesion; Cell wall; Peptidoglycan-anchor; Repeat; Signal;
 virulence.
 FT SIGNAL 1 36
 FT CHAIN 37 985
 FT PROPEP 986 1018
 FT REPEAT 545 574
 FT REPEAT 575 604
 FT DOMAIN 745 878
 FT REPEAT 745 782
 FT REPEAT 783 820
 FT REPEAT 821 859
 FT REPEAT 860 878
 FT REPEAT 879 948
 FT DOMAIN 879 892
 FT REPEAT 893 906
 FT REPEAT 907 920
 FT REPEAT 921 934
 FT REPEAT 935 948
 FT SITE 982 986
 FT MOD_RES 985 985

Fibronectin-binding protein.
 Removed by sortase (Potential).
 B-1.
 B-2.
 4 X approximate tandem repeats,
 fibronectin-binding domain.
 D-1.
 D-2.
 D-3.
 D-4 (incomplete).
 5 X tandem repeats, Pro-rich (WR).
 WR 1.
 WR 2.
 WR 3.
 WR 4.
 WR 5.
 LPXTG sorting signal (Potential).
 Pentaglycyl murein peptidoglycan amidated

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PT          chreonine (Potential) .
SQ SEQUENCE 1018 AA; 111780 MW; 58175E00208B1F1F CRC64;
Query Match 96.1%; Score 199; DB 1; Length 1018;
Best Local Similarity 97.4%; Pred. No. 1.9e-16;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY          1 QNSGNQSFEDTDPKPKYEGGNIIVDIDFDSVPQIHG 38
Db          746 QNSGNQSFEDTDPKPKYEGGNIIVDIDFDSVPQIHG 763

RESULT 7
ID Q99RD2 PRELIMINARY; PRT; 1038 AA.
AC Q99RD2;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Fibronectin-binding protein homolog.
GN Name=Fnb; OrderedLocustNames=SAV2503;
OS Staphylococcus aureus (strain MU50 / ATCC 700639) .
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=158878;
[1]
RP SEQUENCE FROM N. A.
RC MEDLINE=21311952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2;
RX Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Iian J.-Q., Ito T.,
RA Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hoshoyama A.,
RA Mitutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
RA Sekimizu K., Hiraoka H., Kuhara S., Goto S., Yabuzaki J.,
RA Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shibata T.,
RA Hattori M., Ogasawara N., Hayashi H., Hiratsuka K.;
RA "Whole genome sequencing of methicillin-resistant Staphylococcus
RT aureus."
RL Lancel 357:1225-1240(2001) .
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
an amide bond (by similarity) .
EMBL; AP003365; BAB58665.1; -.
DR PIR; H90053; H90053.
DR GO; GO:0009986; C:cell surface; IEA.
DR GO; GO:0005618; C:cell wall; IEA.
DR GO; GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR InterPro; IPR008966; Adhes_Bact.
DR InterPro; IPR004237; Fn_bind.
DR InterPro; IPR001897; Gpos_YsIRK.
DR InterPro; IPR001899; Gram_pos_anchor.
DR Pfam; PF02986; Fn_bind; 1.
DR Pfam; PF00746; Gram_pos_anchor; 1.
DR Pfam; PF04650; YsIRK_signal; 1.
DR TIGRFAMs; TIGR01167; LPXTG_anchor; 1.
DR TIGRFAMs; TIGR01168; YsIRK_signal; 1.
DR PROSITE; PS50847; GRAM_POS_ANCHORING; 1.
KW Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ SEQUENCE 1038 AA; 113618 MW; 666BF6BF2BFBEB12 CRC64;

Query Match 96.1%; Score 199; DB 2; Length 1038;
Best Local Similarity 97.4%; Pred. No. 1.9e-16;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Fnb protein.
GN Name=Fnb; OrderedLocustNames=SA2291;
OS Staphylococcus aureus (strain N315) .
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=158879;
[1]
RP SEQUENCE FROM N. A.
RC MEDLINE=21311952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2;
RX Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Iian J.-Q., Ito T.,
RA Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hoshoyama A.,
RA Mitutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
RA Sekimizu K., Hiraoka H., Kuhara S., Goto S., Yabuzaki J.,
RA Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shibata T.,
RA Hattori M., Ogasawara N., Hayashi H., Hiratsuka K.;
RA "Whole genome sequencing of methicillin-resistant Staphylococcus
RT aureus."
RL Lancel 357:1225-1240(2001) .
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
an amide bond (by similarity) .
EMBL; AP003137; BAB3594.1; -.
DR GO; GO:0009986; C:cell surface; IEA.
DR GO; GO:0005618; C:cell wall; IEA.
DR GO; GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0007155; P:cell adhesion; IEA.
DR InterPro; IPR008966; Adhes_Bact.
DR InterPro; IPR004237; Fn_bind.
DR InterPro; IPR005877; Gpos_YsIRK.
DR InterPro; IPR001899; Gram_pos_anchor.
DR Pfam; PF02986; Fn_bind; 1.
DR Pfam; PF00746; Gram_pos_anchor; 1.
DR Pfam; PF04650; YsIRK_signal; 1.
DR TIGRFAMs; TIGR01167; LPXTG_anchor; 1.
DR TIGRFAMs; TIGR01168; YsIRK_signal; 1.
DR PROSITE; PS50847; GRAM_POS_ANCHORING; 1.
KW Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ SEQUENCE 1038 AA; 113618 MW; 666BF6BF2BFBEB12 CRC64;

Query Match 96.1%; Score 199; DB 2; Length 1038;
Best Local Similarity 97.4%; Pred. No. 1.9e-16;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY          1 QNSGNQSFEDTDPKPKYEGGNIIVDIDFDSVPQIHG 38
Db          742 QNSGNQSFEDTDPKPKYEGGNIIVDIDFDSVPQIHG 779

RESULT 9
ID Q6GDUS PRELIMINARY; PRT; 965 AA.
AC Q6GDUS;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Fibronectin-binding protein.
GN Name=Fbna; OrderedLocustNames=SA2580;
OS Staphylococcus aureus (strain MRSA252) .
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=282458;
[1]
RP SEQUENCE FROM N. A.
RC PubMed=15213324; DOI=10.1073/pnas.0402521101;
RX Holden M.T.G., Feil E.J., Lindsay J.A., Peacock S.J., Day N.P.J.,
RA Enright M.C., Foster T.J., Moore C.E., Hurst L., Acklin R., Barron A.,
RA Baason N., Bentley S.D., Chillingworth C., Chillingworth T.,
RA Churcher C., Clark L., Cotton C., Cronin A., Doggett J., Dowd L.,
RA Feltham T., Hance Z., Harris B., Hauser H., Holtroyd S., Jagsels K.,
RA James K.D., Lennard N., Line A., Mayes R., Moule S., Mungall K.,
RA Ormond D., Quail M.A., Rabinowitch E., Rutherford K.M., Sanders M.,

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RA Sharp S., Simmonds M., Stevens K., Whitehead S., Barrell B.G.,
 RA Spratt B.G., Parkhill J.,
 RT "Complete genomes of two clinical *Staphylococcus aureus* strains:
 RT evidence for the rapid evolution of virulence and drug resistance";
 RL Proc. Natl. Acad. Sci. U.S.A. 101:9786-9791(2004).
 CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
 CC an amide bond (By similarity).
 DR EMBL: BX571856; CAG41560.1; -.
 DR GO: GO:0009986; C:cell surface; IEA.
 DR GO: GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
 DR GO: GO:0016020; C:membrane; IEA.
 DR GO: GO:0007155; P:cell adhesion; IEA.
 DR InterPro: IPR008966; Adhes_bact.
 DR InterPro: IPR004237; Fn_bind.
 DR InterPro: IPR005877; Gpos_YsIRK.
 DR Pfam: PF02986; Fn_bind_1.
 DR Pfam: PF00746; Gram_pos_anchor_1.
 DR Pfam: PF04650; YsIRK_signal_1.
 DR TIGRFAMs: TIGR01167; LpxTG_anchor; 1.
 DR TIGRFAMs: TIGR01168; YsIRK_signal; 1.
 DR PROSITE: PS50847; GRAM_POS_ANCHORING; 1.
 DR Cell wall; Complete proteome; Peptidoglycan-anchor.
 KW Staphylococcus aureus (strain MM2).
 SQ SEQUENCE 965 AA; 105691 MW; 2982E132164D0551 CRC64;

Query Match 95.7%; Score 198; DB 2; Length 965;
 Best Local Similarity 94.1%; Pred. No. 2, 4e-16;
 Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 QNSNGSFEDTEPDPKRYEKGNGNIVDIDFDSVPQIHG 38
 Db 749 QNSNGSFEDTEPDPKRYEKGNGNIVDIDFDSVPQIHG 786

RESULT 10
 ID Q8NUU7 PRELIMINARY; PRT; 1015 AA.
 AC Q8NUU7;
 DT 01-OCT-2002 (T-EMBLrel. 22, Created)
 DT 01-OCT-2002 (T-EMBLrel. 22, Last sequence update)
 DT 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)
 DE Fnb protein.
 GN Name=fnb; OrderedLocustNames=MM2421;
 OS *Staphylococcus aureus* (strain MM2).
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 OX NCBI_TaxID=196620;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC STRAIN=MM2;
 RX MEDLINE=22040717; PubMed=12044378; DOI=10.1016/S0140-6736(02)08713-5;
 RA Baba T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Oguchi A.,
 RA Nagai Y., Iwama N., Asano K., Naito T., Kuroda H., Cui L.,
 RA Yamamoto K., Hiratsuka K.,
 RT "Genome and virulence determinants of high virulence community-
 RT acquired MRSA";
 RL Lancet 359:1819-1827(2002).
 CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
 CC an amide bond (By similarity).
 DR EMBL: AP004830; BAB96286.1; -.
 DR GO: GO:0009986; C:cell surface; IEA.
 DR GO: GO:0005618; C:cell wall; IEA.
 DR GO: GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
 DR GO: GO:0016020; C:membrane; IEA.
 DR GO: GO:0007155; P:cell adhesion; IEA.
 DR InterPro: IPR008966; Adhes_bact.
 DR InterPro: IPR004237; Fn_bind.
 DR InterPro: IPR005877; Gpos_YsIRK.
 DR InterPro: IPR001899; Gram_pos_anchor.
 DR Pfam: PF02986; Fn_bind_1.
 DR Pfam: PF00746; Gram_pos_anchor_1.
 DR Pfam: PF04650; YsIRK_signal_1.
 DR TIGRFAMs: TIGR01167; LpxTG_anchor; 1.
 DR TIGRFAMs: TIGR01168; YsIRK_signal; 1.

DR PROSITE: PS50847; GRAM_POS_ANCHORING; 1.
 KW Cell wall; Complete proteome; Peptidoglycan-anchor.
 SQ SEQUENCE 1015 AA; 111145 MW; D0F9281BB64D4D2 CRC64;

Query Match 94.2%; Score 195; DB 2; Length 1015;
 Best Local Similarity 92.1%; Pred. No. 6e-16;
 Matches 35; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 QNSNGSFEDTEPDPKRYEKGNGNIVDIDFDSVPQIHG 38
 Db 785 QNSNGSFEDTEPDPKRYEKGNGNIVDIDFDSVPQIHG 822

RESULT 11
 ID Q6G6H3 PRELIMINARY; PRT; 1015 AA.
 AC Q6G6H3;
 DT 05-JUL-2004 (T-EMBLrel. 27, Created)
 DT 05-JUL-2004 (T-EMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (T-EMBLrel. 27, Last annotation update)
 DE Fibronectin-binding protein.
 GN OrderedLocustNames=SAS2388;
 OS *Staphylococcus aureus* (strain MSSA476).
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 OX NCBI_TaxID=282459;
 RN (1)
 RP SEQUENCE FROM N.A.
 RX PubMed=15213324; DOI=10.1073/pnas.0402521101;
 RA Holden M.T.G., Fell E.J., Lindsey J.A., Peacock S.J., Day N.P.J.,
 RA Enright M.C., Foster T.J., Moore C.E., Hurst L., Atkin R., Barton A.,
 RA Baason N., Bentley S.D., Chillingworth C., Chillingworth T.,
 RA Churcher C., Clark L., Cotton C., Cronin A., Doggett J., Dowd L.,
 RA Felwell T., Hance Z., Harris B., Hauser H., Holtroyd S., Jagels K.,
 RA James K.D., Leonard N., Line A., Mayes R., Moutle S., Mungall K.,
 RA Ormond D., Quail M.A., Rabinowitch E., Rutherford K.M., Sanders M.,
 RA Sharp S., Simmonds M., Stevens K., Whitehead S., Barrell B.G.,
 RA Spratt B.G., Parkhill J.,
 RT "Complete genomes of two clinical *Staphylococcus aureus* strains:
 RT evidence for the rapid evolution of virulence and drug resistance";
 RL Proc. Natl. Acad. Sci. U.S.A. 101:9786-9791(2004).
 CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
 CC an amide bond (By similarity).
 DR EMBL: BX571857; CAG44202.1; -.
 DR GO: GO:0009986; C:cell surface; IEA.
 DR GO: GO:0005618; C:cell wall; IEA.
 DR GO: GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
 DR GO: GO:0016020; C:membrane; IEA.
 DR GO: GO:0007155; P:cell adhesion; IEA.
 DR InterPro: IPR008966; Adhes_bact.
 DR InterPro: IPR004237; Fn_bind.
 DR InterPro: IPR005877; Gpos_YsIRK.
 DR InterPro: IPR001899; Gram_pos_anchor.
 DR Pfam: PF02986; Fn_bind_1.
 DR Pfam: PF00746; Gram_pos_anchor_1.
 DR Pfam: PF04650; YsIRK_signal_1.
 DR TIGRFAMs: TIGR01167; LpxTG_anchor; 1.
 DR TIGRFAMs: TIGR01168; YsIRK_signal; 1.
 DR PROSITE: PS50847; GRAM_POS_ANCHORING; 1.
 KW Cell wall; Complete proteome; Peptidoglycan-anchor.
 SQ SEQUENCE 1015 AA; 111145 MW; D0F9281BB64D4D2 CRC64;

Query Match 94.2%; Score 195; DB 2; Length 1015;
 Best Local Similarity 92.1%; Pred. No. 6e-16;
 Matches 35; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 QNSNGSFEDTEPDPKRYEKGNGNIVDIDFDSVPQIHG 38
 Db 785 QNSNGSFEDTEPDPKRYEKGNGNIVDIDFDSVPQIHG 822

RESULT 12
 ID Q9AEP9 PRELIMINARY; PRT; 152 AA.

```
AC O9AEP9;
DT 01-JUN-2001 (TReMBLrel. 17, Last Created)
DT 01-JUN-2001 (TReMBLrel. 17, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE Fibronectin-binding protein (Fragment).
GN Name=fnb;
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
CX NCBI_TaxId=1280;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CMRSA-1;
RX DOI=10.1128/IAI.69.6.3791-3799.2001;
RA Rice K., Huebner M., Vaz D., McGavin M.J.;
RT "Variance in fibronectin binding and fnb locus polymorphisms in
RT Staphylococcus aureus: identification of antigenic variation in a
RT fibronectin binding protein adhesin of the epidemic CMRSA-1 strain of
RT methicillin-resistant S. aureus.";
RL Infect. Immun. 69:3791-3799(2001).
DR EMBL, AY029184; AAK31588.1; -.
FT NON_TER 1 152
FT TER 1 152
SQ SEQUENCE 152 AA; 17193 MW; CFA3913C2B11C025 CRC64;

Query Match 90.8%; Score 188; DB 2; Length 152;
Best Local Similarity 92.1%; Pred. No. 4, 9e-16;
Matches 35; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 QNSGNQSFEDTEPDKPYEQGNIVDIDFDSVPQIHG 38
DB 1 QNTGNGSFEDTEBDKPKYEGGNIIVDIDFDSVPQIG 38

RESULT 13
O6BM10 PRELIMINARY; PRT; 937 AA.
ID O6BM10;
AC O6BM10;
DT 25-OCT-2004 (TReMBLrel. 28, Created)
DT 25-OCT-2004 (TReMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TReMBLrel. 28, Last annotation update)
DE Similiar to CA4347|IPF3636 Candida albicans IPF3636.
GN ORFNames=DEHAOF058089;
OS Debaryomyces hansenii CBS767.
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Debaryomycetes.
CX NCBI_TaxId=284592;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CBS767;
RG Genolevures;
RA Dujon B., Sherman D., Fischer G., Durrens P., Casaregola S.,
RA Lafontaine I., de Montigny J., Marcq C., Neuvéglise C., Talla E.,
RA Goffard N., Frangeul L., Aigle M., Anthouard V., Babour A., Barbe V.,
RA Baray S., Blanchin S., Beckerich J.M., Beyne E., Bleykaeten C.,
RA Batsarme A., Boyer J., Catolico L., Confalonieri F., de Darvar A.,
RA Deepons L., Fabre E., Fairhead C., Ferry-Dumazet H., Groppi A.,
RA Hantrege F., Hemequin C., Jauniaux N., Joyet P., Kachouri R.,
RA Kerrest A., Kozul R., Lemaire M., Lesur I., Ma L., Muller H.,
RA Nicolaud J.M., Nikolski M., Oztas S., Ozler-Kalogeropoulos O.,
RA Pellens S., Potier S., Richard G.F., Straub M.L., Suleau A.,
RA Swenne D., Tekala F., Wesolowski-Louvel M., Westhof E., Wirth B.,
RA Zentou-Meyer M., Zivanovic I., Bolotin-Pukhara M., Thierry A.,
RA Bouchier C., Caudron B., Scarpelli C., Gaillardin C., Weissenbach J.,
RA Winkler P., Souclet J.L.;
RT "Genome evolution in yeasts.";
RL Nature 430:35-44(2004).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=CBS767;
RA Genoscope;
RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL, CR382138; CAG88916.1; -.
```

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DR GO:0005634; C:nucleus; IEA.
DR GO:0003684; F:damaged DNA binding; IEA.
DR GO:0006289; P:nucleotide-excision repair; IEA.
DR InterPro; IPR004583; Rad4.
DR Pfam; PF03835; Rad4; 1.
SQ SEQUENCE 937 AA; 107136 MW; 1DC3E795681B9BF7 CRC64;

Query Match 31.9%; Score 66; DB 2; Length 937;
Best Local Similarity 35.0%; Pred. No. 17;
Matches 14; Conservative 9; Mismatches 13; Indels 4; Gaps 2;

QY 1 QNSGNQSFEDTEPDKPYEQ--GNIIVDIDFDSVPQIH 37
DB 772 EESGCGFVEDPEDE- AKYSQARIGGLINVELDMEDPY 810

RESULT 14
O8K525 PRELIMINARY; PRT; 999 AA.
ID O8K525;
AC O8K525; Q79YE5;
DT 01-OCT-2002 (TReMBLrel. 22, Created)
DT 01-OCT-2002 (TReMBLrel. 22, Last sequence update)
DT 25-OCT-2004 (TReMBLrel. 28, Last annotation update)
DE Putative secreted endoglycosidase (Hypothetical protein SP80299).
GN Name=ndos; OrderedLocustNames=SP80299, Spym3_1568;
OS Streptococcus pyogenes (serotype M3).
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
CX NCBI_TaxId=198466;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MGAS315; Serotype M3;
RX MEDLINE=22133808; PubMed=12122206; DOI=10.1073/pnas.152298499;
RA Beres S.B., Sylva G.L., Barbican K.D., Lei B., Hoff J.S.,
RA Mammarella N.D., Liu W.-Y., Smoot J.C., Porcella S.F., Parkins L.D.,
RA Campbell D.S., Smith T.M., McCormick J.K., Leung D.Y.M.,
RA Schlievert P.M., Messer J.M.;
RT "Genome sequence of a serotype M3 strain of group A Streptococcus:
RT phage-encoded toxins, the high-virulence phenotype, and clone
RT emergence.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:10078-10083(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=SSI-1;
RX MEDLINE=22683278; PubMed=12799345; DOI=10.1101/gr.1096703;
RA Nakagawa T., Kurokawa K., Yamashita A., Nakata M., Tomiyasu Y.,
RA Okahashi N., Kawabata S., Yamazaki K., Shida T., Yasunaga T.,
RA Hayashi H., Hattori M., Hamada S.;
RT "Genome sequence of an M3 strain of Streptococcus pyogenes reveals a
RT large-scale genomic rearrangement in invasive strains and new insights
RT into phage evolution.";
RL Genome Res. 13:1042-1055(2003).
DR EMBL; AE014166; AM80175.1; -.
DR EMBL; AP005142; BAC3394.1; -.
DR GO:0001678; F:hydrolase activity, acting on glycosyl bonds; IEA.
DR GO:0005975; P:carbohydrate metabolism; IEA.
DR InterPro; IPR001579; Glyco_hydro_18AS.
DR InterPro; IPR001611; LBR.
DR PRINTS; PR00019; LBRICRPR.
DR PROSITE; PS01095; CHITINASE_18; UNKNOWN_1.
KW Hypothetical protein; Glycosidase; Complete proteome.
SQ SEQUENCE 999 AA; 112123 MW; 6BFBD6A47093FE CRC64;

Query Match 29.0%; Score 60; DB 2; Length 999;
Best Local Similarity 28.8%; Pred. No. 1, 1e+02;
Matches 15; Conservative 7; Mismatches 12; Indels 18; Gaps 2;

QY 5 NQSFEDTE--PDKP-----KYEQGNIVDIDFDSVPQIHG 38
DB 192 NSGIAEDTSKPYNTPEGNKALAKAIVDEYVYKIVLDDGVDEVDSDIPKVG 243

RESULT 15
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089PZ3
ID Q89PZ3 PRELIMINARY; PRT; 539 AA.
AC Q89PZ3;
DT 01-JUN-2003 (TRMBLrel. 24, Created)
DT 01-JUN-2003 (TRMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TRMBLrel. 26, Last annotation update)
DE ABC transporter substrate-binding protein.
GN Ordered locus names=blj3337;
OS Bradyrhizobium japonicum.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Bradyrhizobiaceae; Bradyrhizobium.
OX NCBI_TaxID=375;
[1]
RN SEQUENCE FROM N.A.
RP STRAIN=USDA110;
RC MEDLINE=2248498; PubMed=12597275;
RA Kaneko T., Nakamura Y., Sato S., Minamisawa K., Uchiyama T.,
RA Sasamoto S., Watanabe A., Idesawa K., Iriyuchi M., Kawashima K.,
RA Kohara M., Matsumoto M., Shimo S., Teurloka H., Wada T., Yamada M.,
RA Tabata S.;
RT "Complete genomic sequence of nitrogen-fixing symbiotic bacterium
RT Bradyrhizobium japonicum USDA110."
RL DNA Rep. 9:189-197(2002).
CC -1- SIMILARITY: Belongs to the bacterial extracellular solute-binding
CC protein family 5.
CC EMBL: AP005947; BAC48602.1;
DR GO; GO:0005215; P:transporter activity; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR000914; SBP_bac_5;
DR Pfam; PF00496; SBP_bac_5; 1.
KW Complete proteome.
SQ SEQUENCE 539 AA; 59719 MW; E8D9C95D1F83D33F CRC64;

Query Match 28.5%; Score 59; DB 2; Length 539;
Best Local Similarity 34.0%; Pred. No. 68;
Matches 17; Conservative 5; Mismatches 12; Indels 16; Gaps 2;

QY 3 SGNQSF-----EEDTEPPDKPKYEQGNIVD-IDFDSVPOI 36
DB 456 TGNQRMNYSINNPELAATAQEARFEPDAXKYEDDGKLNALHFESEWPOI 505

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Search completed: October 22, 2005, 06:05:59
 Job time : 71.6361 secs

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CC streptococci, e.g. meningitis, otitis media, pneumonia, endocarditis,
CC mastitis in cattle, abortion in horses and many others. Since the
CC antibodies block binding of bacteria, they should be effective against
CC antibiotic-resistant strains, and may replace antibiotic therapy or
CC increase its effectiveness. Sequences AAW65691-700 represent a series of
CC synthetic peptides based on the D1 region of S. aureus fibronectin
CC binding protein A. They were synthesised to contain mutations
XX
SQ Sequence 38 AA;
Query Match 100.0%; Score 206; DB 2; Length 38;
Best Local Similarity 100.0%; Pred. No. 9,1e-21;
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ONSGNQSFEDTTEPKPKYEGGNIVIDIDFDSVPQIHG 38
DB 1 ONSGNQSFEDTTEPKPKYEGGNIVIDIDFDSVPQIHG 38

RESULT 2
AAW65661
ID AAW65661 standard; peptide; 38 AA.
AC AAW65661;
XX
XX 16-OCT-1998 (first entry)
DT
DE Fibronectin binding protein-derived peptide #5.
XX
XX microbial surface components recognising adhesive matrix molecule;
XX MSCRAMM; fibronectin; fibronectin-binding protein; antibody; epitope;
XX antibiotic; bacterial infection; antibiotic-resistant strain.
XX
XX Synthetic.
XX OS Staphylococcus aureus.
XX
XX WO9831389-A2.
XX
XX 23-JUL-1998.
XX
XX 21-JAN-1998; 98WO-US001222.
XX
XX 21-JAN-1997; 97US-0036139P.
XX
XX (TEXA ) UNIV TEXAS A & M SYSTEM.
XX
XX Hoseok M, Patli JM, House-Pompeo KU, Speciale P, Joh D;
XX Mcgavin WJ;
XX
XX WPI, 1998-413816/35.
XX
XX Antibody that binds to fibronectin-binding protein, preventing its
XX binding to fibronectin - used to treat or prevent bacterial infection,
XX especially by Staphylococci and Streptococci.
XX
XX Example 2; Page 92; 201pp; English.
XX
XX The invention relates to antibodies that bind to a fibronectin-binding
XX domain of a fibronectin-binding protein, and inhibit binding of the
XX protein to fibronectin. Also claimed are: (1) isolated peptides of a
XX fibronectin-binding protein that do not bind to fibronectin; (2) fusion
XX protein containing at least one peptide of a fibronectin-binding protein
XX linked to a second amino acid sequence; (3) nucleic acid encoding the
XX isolated peptide of (1). Antibodies, the isolated peptides of (1) and the
XX nucleic acids are all useful for immunisation (active or passive) and (by
XX inhibiting binding of bacteria to fibronectin) for preventing or treating
XX infection in humans or other animals, particularly by staphylococci or
XX streptococci, e.g. meningitis, otitis media, pneumonia, endocarditis,
XX mastitis in cattle, abortion in horses and many others. Since the
XX antibodies block binding of bacteria, they should be effective against
XX antibiotic-resistant strains, and may replace antibiotic therapy or
XX increase its effectiveness. Sequences AAW65659-68 represent synthetic
XX epitopes from the fibronectin binding domains DV and D1-D4 of the S.

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CC aureus fnbA gene
XX
SQ Sequence 38 AA;
Query Match 96.1%; Score 198; DB 2; Length 38;
Best Local Similarity 97.4%; Pred. No. 1,1e-19;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 ONSGNQSFEDTTEPKPKYEGGNIVIDIDFDSVPQIHG 38
DB 1 ONSGNQSFEDTTEPKPKYEGGNIVIDIDFDSVPQIHG 38

RESULT 3
AAR58806
ID AAR58806 standard; protein; 130 AA.
AC AAR58806;
XX
XX 25-MAR-2003 (revised)
DT 30-MAR-1995 (first entry)
XX
XX Fibronectin binding domain D1-D4(709-838 (P838T)).
DE
XX Fibronectin binding protein; Fbp; fibronectin binding domain;
XX monoclonal antibody; Mab; adhesion; Gram-positive bacterium; bacteremia;
XX Escherichia coli.
XX
XX Staphylococcus aureus.
XX
XX WO9418327-A1.
XX
XX 18-AUG-1994.
XX
XX 04-FEB-1994; 94WO-GB000215.
XX
XX 05-FEB-1993; 93GB-00002289.
XX
XX 20-OCT-1993; 93GB-00021592.
XX
XX (SMIK ) SMITHKLINE BEECHAM PLC.
XX
XX Burnham MKR, Chopra I, Critchley IA, Knowles DJC;
XX
XX WPI, 1994-279748/34.
XX
XX Fibronectin binding protein and monoclonal antibodies specific for Fbp -
XX useful to prevent adherence of Gram-positive bacteria to indwelling
XX devices or wounds.
XX
XX Disclosure; Page 30; 40pp; English.
XX
XX Polypeptides corresponding to residues G709-T886 plus PPIVPT, G709-
XX P838(P838T) and G709-P838 (AAR58805-07, respectively) of S. aureus J2385
XX (NCIMB 40532) Fbp type A fibronectin binding domain D1-D4 region
XX (AAR58808) were expressed in E. coli BL21 (DE4) and used to raise Mabs
XX specific for Fbp. (Updated on 25-MAR-2003 to correct PN field.)
XX
XX
SQ Sequence 130 AA;
Query Match 96.1%; Score 198; DB 2; Length 130;
Best Local Similarity 97.4%; Pred. No. 5e-19;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 ONSGNQSFEDTTEPKPKYEGGNIVIDIDFDSVPQIHG 38
DB 2 ONSGNQSFEDTTEPKPKYEGGNIVIDIDFDSVPQIHG 39

RESULT 4
AAR58807
ID AAR58807 standard; protein; 130 AA.
AC AAR58807;

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XX 25-MAR-2003 (revised)
DT 30-MAR-1995 (first entry)
XX
DE Fibronectin binding domain D1-D4(709-838).
XX
XX Fibronectin binding protein; Fbp; fibronectin binding domain;
KM monoclonal antibody; Mab; adhesion; Gram-positive bacterium; bacteremia;
KM Escherichia coli.
XX
OS Staphylococcus aureus.
XX
XX WO9418327-A1.
XX
XX 18-AUG-1994.
XX
XX 04-FEB-1994; 94WO-GB000215.
XX
XX 05-FEB-1993; 93GB-00002289.
XX
XX 20-OCT-1993; 93GB-00021592.
XX
XX (SMIK ) SMITHKLINE BEECHAM PLC.
XX
XX Burnham MKR, Chopra I, Critchley IA, Knowles DJC;
XX
XX WPI; 1994-279748/34.
XX
XX Fibronectin binding protein and monoclonal antibodies specific for Fbp -
PT useful to prevent adherence of Gram-positive bacteria to indwelling
PT devices or wounds.
XX
XX Disclosure; Page 30; 40pp; English.
XX
XX Polypeptides corresponding to residues G709-T886 plus PPIVPT, G709-
CC P838(P838T) and G709-P838 (AAR58805-07, respectively) of S. aureus J2385
CC (NCIMB 40532) Fbp type A fibronectin binding domain D1-D4 region Mabs
CC (AAR58808) were expressed in E. coli BL21(DE4) and used to raise Mabs
CC specific for Fbp. (Updated on 25-MAR-2003 to correct PN field.)
XX
XX
XX Sequence 130 AA;
SQ
Query Match 96.1%; Score 198; DB 2; Length 130;
Best Local Similarity 97.4%; Pred. No. Se-19;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 QNSGNQSFEDTEBPKEKYEQGNIVDIDFDSVPOIHG 38
DB 2 QNSGNQSFEDTEBPKEKYEQGNIVDIDFDSVPOIHG 39
RESULT 5
AAR91202
ID AAR91202 standard; peptide; 130 AA.
XX
XX AAR91202;
XX
XX 13-NOV-1996 (first entry)
XX
XX D1-D4 fibronectin binding domains.
XX
XX Fibronectin; oral hygiene; gingivitis; gum disease; adhesion;
KM periodontitis; oral pathogen; caries; calculus; candidiasis; oral surgery;
KM tissue regeneration; irrigation; toothpaste; dentifrice; mouthwash;
KM lozenge.
XX
XX Staphylococcus aureus.
XX
XX WO9604003-A1.
XX
XX 15-FEB-1996.
XX
XX 18-JUL-1995; 95WO-EP002825.
XX

```

```

PR 05-AUG-1994; 94GB-00015902.
XX
XX (SMIK ) SMITHKLINE BEECHAM PLC.
XX
XX Barnett P, Critchley IA, Dodd I;
XX
XX WPI; 1996-129122/13.
XX
XX Prevention of adherence of oral pathogens in the oral cavity, partic.
PT tooth surfaces - by application of a fibronectin binding protein or
PT polypeptide or a monoclonal antibody or fragment against it.
XX
XX Claim 5; Page 32; 41pp; English.
XX
XX Adherence of oral pathogens, particularly to tooth surfaces, can be
CC prevented by application of a fibronectin binding protein or polypeptide.
CC The fibronectin binding protein or polypeptide is useful in the
CC manufacture of oral hygiene compositions, eg. toothpaste, liquid
CC dentifrice, mouthwash or lozenge. They are useful to prevent the plaque-
CC related development of carious lesions, gingivitis, calculus or
CC periodontal disease and to combat oral cavity infections, e.g.
CC candidiasis. They may also be useful in oral surgery e.g. in guided
CC tissue regeneration procedures to prevent subsequent bacterial infection,
CC and for irrigation of periodontal pockets. This sequence corresponds to
CC amino acids 709-838 of the D1-D4 fibronectin binding domain of
CC Staphylococcus aureus
XX
XX
XX Sequence 130 AA;
SQ
Query Match 96.1%; Score 198; DB 2; Length 130;
Best Local Similarity 97.4%; Pred. No. Se-19;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 QNSGNQSFEDTEBPKEKYEQGNIVDIDFDSVPOIHG 38
DB 2 QNSGNQSFEDTEBPKEKYEQGNIVDIDFDSVPOIHG 39
RESULT 6
AAR91201
ID AAR91201 standard; peptide; 130 AA.
XX
XX AAR91201;
XX
XX 13-NOV-1996 (first entry)
XX
XX D1-D4 fibronectin binding domains.
XX
XX Fibronectin; oral hygiene; gingivitis; gum disease; adhesion;
KM periodontitis; oral pathogen; caries; calculus; candidiasis; oral surgery;
KM tissue regeneration; irrigation; toothpaste; dentifrice; mouthwash;
KM lozenge.
XX
XX Staphylococcus aureus.
XX
XX WO9604003-A1.
XX
XX 15-FEB-1996.
XX
XX 18-JUL-1995; 95WO-EP002825.
XX
XX 05-AUG-1994; 94GB-00015902.
XX
XX (SMIK ) SMITHKLINE BEECHAM PLC.
XX
XX Barnett P, Critchley IA, Dodd I;
XX
XX WPI; 1996-129122/13.
XX
XX Prevention of adherence of oral pathogens in the oral cavity, partic.
PT tooth surfaces - by application of a fibronectin binding protein or
PT polypeptide or a monoclonal antibody or fragment against it.
XX

```

PS Claim 5; Page 31-32; 41pp; English.

XX Adherence of oral pathogens, particularly to tooth surfaces, can be

CC prevented by application of a fibronectin binding protein or polypeptide.

CC The fibronectin binding protein or polypeptide is useful in the

CC manufacture of oral hygiene compositions, eg. toothpaste, liquid

CC dentifrice, mouthwash or lozenge. They are useful to prevent the plaque-

CC related development of carious lesions, gingivitis, calculus or

CC periodontal disease and to combat oral cavity infections, e.g.

CC candidiasis. They may also be useful in oral surgery e.g. in guided

CC tissue regeneration procedures to prevent subsequent bacterial infection,

CC and for irrigation of periodontal pockets. This sequence corresponds to

CC amino acids 709-738 of the D1-D4 fibronectin binding domain of

CC Staphylococcus aureus with a P938R substitution

XX

SQ Sequence 130 AA;

Query Match 96.1%; Score 198; DB 2; Length 130;

Best Local Similarity 97.4%; Pred. No. 56-19;

Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 QNSGNQSFEDTEEDPKPYEGGNIVIDIDFDSVPQIHG 38

DB 2 QNSGNQSFEDTEEDPKPYEGGNIVIDIDFDSVPQIHG 39

RESULT 7

AAAY29089

ID AAY29089 standard; protein; 134 AA.

XX

AC AAY29089;

DT 28-SEP-1999 (first entry)

XX

DE Cloned fibronectin binding protein binding domain (FnBAB) sequence.

XX

KW Bovine herpes virus-2; BHV-2; cytokine; immune response; immunogen; IL;

KW interleukin; colony stimulating factor; CSF; interferon; IFN; TNF;

KW tumour necrosis factor; recombinant virus; vaccine; mucosal disease;

KW mastitis; breast cancer; stress-induced disease; binding domain; FnBAB;

XX

OS Staphylococcus aureus.

XX

PN WO9916892-A1.

XX

PD 08-APR-1999.

XX

PF 29-SEP-1998; 98WO-GB002927.

XX

PR 29-SEP-1997; 97GB-00020633.

XX

PA (UYBR-) UNIV BRISTOL.

XX

PI Bradley AJ, Duffas WPJ;

XX

DR WPI; 1999-255101/21.

XX

DR N-PSDB; AAX91506.

XX

PT New bovine herpes virus-2 vectors.

XX

PS Example 2; Fig 8A-B; 130pp; English.

XX

CC The invention provides bovine herpes virus-2 (BHV-2) based vectors that

CC comprise at least one cytokine-encoding DNA sequence. The expression of

CC cytokines in mammals can up-regulate immune responses to the immunogen.

CC The cytokine is selected from interleukins (IL), colony stimulating

CC factors (CSF), interferons (IFN) and tumour necrosis factors (TNF). The

CC BHV-2 based vector or recombinant virus can be used as vaccines. They can

CC be used for preventing or treating a mucosal disease in a subject, e.g.

CC ruminants, cattle, sheep, goats, dogs, cats, horses, or man, particularly

CC mastitis in cows or breast cancers in humans. They can also be used for

CC preventing or treating a stress-induced disease. The present sequence

CC represent a S. aureus fibronectin binding protein binding domain

CC sequence FnBAB, the gene cloned for use in this invention. The gene has

CC 97.8 percent identity when compared to the previously published sequences

CC FnBA and FnBB

XX

SQ Sequence 134 AA;

Query Match 96.1%; Score 198; DB 2; Length 134;

Best Local Similarity 97.4%; Pred. No. 5,26-19;

Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 QNSGNQSFEDTEEDPKPYEGGNIVIDIDFDSVPQIHG 38

DB 2 QNSGNQSFEDTEEDPKPYEGGNIVIDIDFDSVPQIHG 39

RESULT 8

AAAY29088

ID AAY29088 standard; protein; 134 AA.

XX

AC AAY29088;

DT 28-SEP-1999 (first entry)

XX

DE S. aureus fibronectin binding protein B (FnBB) binding domain.

XX

KW Bovine herpes virus-2; BHV-2; cytokine; immune response; immunogen; IL;

KW interleukin; colony stimulating factor; CSF; interferon; IFN; TNF;

KW tumour necrosis factor; recombinant virus; vaccine; mucosal disease;

KW mastitis; breast cancer; stress-induced disease; binding domain; FnBB;

XX

OS Staphylococcus aureus.

XX

PN WO9916892-A1.

XX

PD 08-APR-1999.

XX

PF 29-SEP-1998; 98WO-GB002927.

XX

PR 29-SEP-1997; 97GB-00020633.

XX

PA (UYBR-) UNIV BRISTOL.

XX

PI Bradley AJ, Duffas WPJ;

XX

DR WPI; 1999-255101/21.

XX

DR N-PSDB; AAX91505.

XX

PT New bovine herpes virus-2 vectors.

XX

PS Example 2; Fig 8A-B; 130pp; English.

XX

CC The invention provides bovine herpes virus-2 (BHV-2) based vectors that

CC comprise at least one cytokine-encoding DNA sequence. The expression of

CC cytokines in mammals can up-regulate immune responses to the immunogen.

CC The cytokine is selected from interleukins (IL), colony stimulating

CC factors (CSF), interferons (IFN) and tumour necrosis factors (TNF). The

CC BHV-2 based vector or recombinant virus can be used as vaccines. They can

CC be used for preventing or treating a mucosal disease in a subject, e.g.

CC ruminants, cattle, sheep, goats, dogs, cats, horses, or man, particularly

CC mastitis in cows or breast cancers in humans. They can also be used for

CC preventing or treating a stress-induced disease. The present sequence

CC represents the binding domain of a previously published S. aureus

CC fibronectin binding protein B (FnBB) sequence. The FnB binding domain

CC gene sequence FnBAB, cloned for use in this invention has 97.8 percent

CC identity when compared to the previously published FnBA and FnBB gene

CC sequences

XX

SQ Sequence 134 AA;

Query Match 96.1%; Score 198; DB 2; Length 134;

Best Local Similarity 97.4%; Pred. No. 5,26-19;

Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QNSGNOSFEEDTEEPKPYEGGNIYDIDPDSVPQIHG 38
 |||||
 DB 2 QNSGNOSFEEDTEEDKPKYEGGNIYDIDPDSVPQIHG 39

RESULT 9

AAV29087
 ID AAV29087 standard; protein; 134 AA.

XX AAV29087;
 AC AAV29087;
 XX
 XX

DT 28-SEP-1999 (first entry)
 XX

DE S. aureus fibronectin binding protein A (FnBA) binding domain.

XX Bovine herpes virus-2; BHV-2; cytokine; immune response; immunogen; IL;
 XX Interleukin; colony stimulating factor; CSF; interferon; IFN; TNF;
 XX tumour necrosis factor; recombinant virus; vaccine; mucosal disease;
 XX mastitis; breast cancer; stress-induced disease; binding domain; FnBA;
 XX fibronectin binding protein.

OS Staphylococcus aureus.

XX WO9116892-A1.
 XX

PN 08-APR-1999.
 XX

PD 29-SEP-1998; 98WO-GH02927.
 XX

PF 29-SEP-1997; 97GB-00020633.
 XX

PR (UYBR-) UNITV BRISTOL.
 XX

PI Bradley AJ, Duffas WP;
 XX

DR MPI; 1999-255101/21.
 XX

DR N-PSDB; AAX91504.
 XX

XX New bovine herpes virus-2 vectors.

XX Example 2; Fig 8A-B; 130pp; English.

CC The invention provides bovine herpes virus-2 (BHV-2) based vectors that
 CC comprise at least one cytokine-encoding DNA sequence. The expression of
 CC cytokines in mammals can up-regulate immune responses to the immunogens.
 CC The cytokine is selected from interleukins (IL), colony stimulating
 CC factors (CSF), interferons (IFN) and tumour necrosis factors (TNF). The
 CC BHV-2 based vector or recombinant virus can be used as vaccines. They can
 CC be used for preventing or treating a mucosal disease in a subject, e.g.
 CC mastitis in cows or breast cancers in humans. They can also be used for
 CC preventing or treating a stress-induced disease. The present sequence
 CC represents the binding domain of a previously published S. aureus
 CC fibronectin binding protein A (FnBA) sequence. The FnB binding domain
 CC gene sequence FNBA, cloned for use in this invention has 97.6 percent
 CC identity when compared to the previously published FNBA and FNBB gene
 CC sequences
 CC
 XX
 XX
 SQ Sequence 134 AA;

Query Match 96.1%; Score 198; DB 2; Length 134;
 Best Local Similarity 97.4%; Pred. No. 5.2e-19;
 Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QNSGNOSFEEDTEEPKPYEGGNIYDIDPDSVPQIHG 38
 |||||
 DB 2 QNSGNOSFEEDTEEDKPKYEGGNIYDIDPDSVPQIHG 39

RESULT 10
 AAW31556

ID AAW31556 standard; protein; 139 AA.

XX AAW31556;
 AC AAW31556;
 XX

DT 27-AUG-2003 (revised)
 DT 25-MAR-2003 (revised)
 DT 21-MAY-1998 (first entry)

XX Fibronectin-binding MSCRAMM derivative POD.

XX Fibronectin; POD; collagen binding protein; sepsis; infection;
 XX microbial surface component recognising adhesive matrix molecule; MSCRAMM;
 XX adhesin; vaccine; immunisation; diagnosis; therapy; mastitis.

XX Staphylococcus aureus.

OS Staphylococcus aureus.

XX Key Location/Qualifiers
 XX Peptide 1..12
 XX /note="vector pQE30-derived peptide"

PN WO9743314-A2.
 XX

PD 20-NOV-1997.
 XX

PF 14-MAY-1997; 97WO-US008210.
 XX

PR 16-MAY-1996; 96US-0017678P.
 XX

PA (TEXA) UNITV TEXAS A & M SYSTEM.
 XX

PA (UABR-) UAB RES POUND.
 XX

PI Hoeek M, Patti JM, House-Pompeo K, Schanam N, Symersky J;
 XX

DR MPI; 1998-008801/01.
 XX

PT Antibody that interacts with collagen binding domain of Staphylococcal
 PT cna gene product - useful to prevent bacterial sepsis in animal infected
 PT with Staphylococcus aureus.

PS Disclosure; Page 91; 143pp; English.

XX This protein comprises Staphylococcus aureus fibronectin-binding
 CC microbial surface component recognising adhesive matrix molecule (MSCRAMM)
 CC derivative POD, plus a vector-derived N-terminal peptide. The invention
 CC relates to claimed nucleic acid sequences (see AAY3436-38) encoding S.
 CC aureus collagen binding protein (CBP) epitopes M17, M31 and M55 (see
 CC AAW31552-54) that confer protection against S. aureus infection. CBP
 CC protein and antigenic epitopes are contemplated for use in the treatment
 CC of pathological infections, especially to prevent bacterial adhesion to
 CC collagen. The epitopes are also contemplated for use in the preparation
 CC of vaccines and as carrier proteins in vaccine formulations, as well as
 CC in the formulation of compositions for the prevention of S. aureus
 CC infection. pCE33 and POD (see AAW31556) were used to raise anti-MSCRAMM
 CC polyclonal antibodies used in passive immunisation against bovine
 CC mastitis. (Updated on 25-MAR-2003 to correct PI field.) (Updated on 27-
 CC AUG-2003 to correct OS field.)
 XX
 XX
 SQ Sequence 139 AA;

Query Match 96.1%; Score 198; DB 2; Length 139;
 Best Local Similarity 97.4%; Pred. No. 5.5e-19;
 Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QNSGNOSFEEDTEEPKPYEGGNIYDIDPDSVPQIHG 38
 |||||
 DB 16 QNSGNOSFEEDTEEDKPKYEGGNIYDIDPDSVPQIHG 53

RESULT 11
 AAR58808
 ID AAR58808 standard; protein; 174 AA.
 XX
 AC AAR58808;

```
XX 25-MAR-2003 (revised)
DT 30-MAR-1995 (first entry)
XX
DE Fbp fibronectin binding domain.
XX
KW Fibronectin binding protein; Fbp; fibronectin binding domain;
KM monoclonal antibody; MAb; adhesion; Gram-positive bacterium; bacteremia;
XX Escherichia coli; P838C31.
XX
OS Staphylococcus aureus.
XX
PN MO9418327-A1.
XX
PD 18-AUG-1994.
XX
PF 04-FEB-1994; 94WO-GB000215.
XX
PR 05-FEB-1993; 93GB-00002289.
PR 20-OCT-1993; 93GB-00021592.
XX
PA (SMIK ) SMITHKLINE BEECHAM PLC.
XX
PI Burnham MKR, Chopra I, Critchley IA, Knowles DJC;
XX
DR WPI; 1994-279748/34.
DR N-PSDB; AA071838.
XX
PT Fibronectin binding protein and monoclonal antibodies specific for Fbp -
PT useful to prevent adherence of Gram-positive bacteria to indwelling
PT devices or wounds.
XX
PS Disclosure; Page 30; 40pp; English.
XX
CC The sequences of DNA encoding S. aureus Fbp type A fibronectin binding
CC domain (D1-D4) and the encoded protein are provided. D1-D4 polypeptides
CC have been expressed in E. coli BL21(DB4) and used to raise MAbs specific
CC for Fbp. (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ Sequence 174 AA;

Query Match 96.1%; Score 198; DB 2; Length 174;
Best Local Similarity 97.4%; Pred. No. 7.2e-19;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QNSGNQSFEDTTEPKPYEGCGNIVDIDFDSVPQIHG 38
DB 2 QNSGNQSFEDTTEPKPYEGCGNIVDIDFDSVPQIHG 39

RESULT 12
AAR91203
ID AAR91203 standard; protein; 174 AA.
XX
AC AAR91203;
XX
DT 16-OCT-2003 (revised)
DT 13-NOV-1996 (first entry)
XX
DE D1-D4 fibronectin binding domains.
XX
KW Fibronectin; oral hygiene; gingivitis; gum disease; adhesion;
KW periodontitis; oral pathogen; caries; calculus; candidiasis; oral surgery;
KW tissue regeneration; irrigation; toothpaste; dentifrice; mouthwash;
XX lozenge.
XX
OS Staphylococcus aureus; J2385.
XX
PN MO9604003-A1.
XX
PD 15-FEB-1996.
XX
DR 18-JUL-1995; 95WO-EP002825.
```

```
XX 05-AUG-1994; 94GB-00015902.
XX
PA (SMIK ) SMITHKLINE BEECHAM PLC.
XX
PI Barnett P, Critchley IA, Dodd I;
XX
DR WPI; 1996-129122/13.
DR N-PSDB; AAT18308.
XX
PT Prevention of adherence of oral pathogens in the oral cavity, partic.
PT tooth surfaces - by application of a fibronectin binding protein or
PT polypeptide or a monoclonal antibody or fragment against it.
XX
PS Claim 5; Page 32; 41pp; English.
XX
CC Adherence of oral pathogens, particularly to tooth surfaces, can be
CC prevented by application of a fibronectin binding protein or polypeptide.
CC The fibronectin binding protein or polypeptide is useful in the
CC manufacture of oral hygiene compositions, eg. toothpaste, liquid
CC dentifrice, mouthwash or lozenge. They are useful to prevent the plaque-
CC related development of carious lesions, gingivitis, calculus or
CC periodontal disease and to combat oral cavity infections, e.g.
CC candidiasis. They may also be useful in oral surgery e.g. in guided
CC tissue regeneration procedures to prevent subsequent bacterial infection,
CC and for irrigation of periodontal pockets. This sequence corresponds to
CC amino acids 709-838 of the D1-D4 fibronectin binding domain of
CC Staphylococcus aureus with a P838T substitution. (Updated on 16-OCT-2003
CC to standardise OS field)
XX
SQ Sequence 174 AA;

Query Match 96.1%; Score 198; DB 2; Length 174;
Best Local Similarity 97.4%; Pred. No. 7.2e-19;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QNSGNQSFEDTTEPKPYEGCGNIVDIDFDSVPQIHG 38
DB 2 QNSGNQSFEDTTEPKPYEGCGNIVDIDFDSVPQIHG 39

RESULT 13
AAR58805
ID AAR58805 standard; protein; 181 AA.
XX
AC AAR58805;
XX
DT 25-MAR-2003 (revised)
DT 30-MAR-1995 (first entry)
XX
DE Fibronectin binding domain D1-D4(709-886).
XX
KW Fibronectin binding protein; Fbp; fibronectin binding domain;
KW monoclonal antibody; MAb; adhesion; Gram-positive bacterium; bacteremia;
XX Escherichia coli.
XX
OS Staphylococcus aureus.
XX
PN MO9418327-A1.
XX
PD 18-AUG-1994.
XX
PF 04-FEB-1994; 94WO-GB000215.
XX
PR 05-FEB-1993; 93GB-00002289.
PR 20-OCT-1993; 93GB-00021592.
XX
PA (SMIK ) SMITHKLINE BEECHAM PLC.
XX
PI Burnham MKR, Chopra I, Critchley IA, Knowles DJC;
XX
DR WPI; 1994-279748/34.
```

PT Fibronectin binding protein and monoclonal antibodies specific for Fbp -
 PT useful to prevent adherence of Gram-positive bacteria to indwelling
 PT devices or wounds.
 XX
 PS Disclosure: Page 29-30; 40pp; English.
 CC
 XX Polypeptides corresponding to residues G709-T886 plus PPIVPT, G709-
 CC P838(P838T) and G709-P838 (AAR58805-07, respectively) of S. aureus J2385
 CC (NCIMB 40532) Fbp type A fibronectin binding domain D1-D4 region
 CC (AAR58808) were expressed in E. coli BL21 (DE3) and used to raise Mabs
 CC specific for Fbp. (Updated on 25-MAR-2003 to correct PN field.)
 CC
 XX
 SQ Sequence 181 AA;
 Query Match 96.1%; Score 198; DB 2; Length 181;
 Best Local Similarity 97.4%; Pred. No. 7.5e-19;
 Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 ONSGNQSFEDTEEPKPKYEGGNIYDIDFDSVPQIHG 38
 DB 2 ONSGNQSFEDTEEPKPKYEGGNIYDIDFDSVPQIHG 39
 RESULT 14
 AAR91200
 ID AAR91200 standard; peptide; 181 AA.
 XX
 AC AAR91200;
 XX
 DT 13-NOV-1996 (first entry)
 XX
 DE D1-D4 fibronectin binding domains.
 XX
 KW Fibronectin; oral hygiene; gingivitis; gum disease; adhesion;
 KW periodontitis; oral pathogen; caries; calculus; candidiasis; oral surgery;
 KW tissue regeneration; irrigation; toothpaste; dentifrice; mouthwash;
 KW lozenge.
 XX
 OS Staphylococcus aureus.
 XX
 PN WO9604003-A1.
 XX
 PD 15-FEB-1996.
 XX
 PF 18-JUL-1995; 95WO-EP002825.
 XX
 PR 05-AUG-1994; 94GB-00015902.
 XX
 PA (SMIK) SMITHKLINE BEECHAM PLC.
 XX
 PI Barnett P, Critchley IA, Dodd I;
 XX
 XX WPI; 1996-129122/13.
 DR N-PSDB; AAT18307.
 XX
 PT Prevention of adherence of oral pathogens in the oral cavity, partic.
 PT tooth surfaces - by application of a fibronectin binding protein or
 PT polypeptide or a monoclonal antibody or fragment against it.
 XX
 PS Claim 5; Page 31; 41pp; English.
 XX
 CC Adherence of oral pathogens, particularly to tooth surfaces, can be
 CC prevented by application of a fibronectin binding protein or polypeptide.
 CC The fibronectin binding protein or polypeptide is useful in the
 CC manufacture of oral hygiene compositions, eg. toothpaste, liquid
 CC dentifrice, mouthwash or lozenge. They are useful to prevent the plaque-
 CC related development of carious lesions, gingivitis, calculus or
 CC periodontal disease and to combat oral cavity infections, e.g.
 CC candidiasis. They may also be useful in oral surgery e.g. in guided
 CC tissue regeneration procedures to prevent subsequent bacterial infection,
 CC and for irrigation of periodontal pockets. This sequence corresponds to
 CC amino acids 709-886 of the D1-D4 fibronectin binding domain of
 CC Staphylococcus aureus

XX
 SQ Sequence 181 AA;
 Query Match 96.1%; Score 198; DB 2; Length 181;
 Best Local Similarity 97.4%; Pred. No. 7.5e-19;
 Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 ONSGNQSFEDTEEPKPKYEGGNIYDIDFDSVPQIHG 38
 DB 2 ONSGNQSFEDTEEPKPKYEGGNIYDIDFDSVPQIHG 39
 RESULT 15
 AAM89803
 ID AAM89803 standard; protein; 559 AA.
 XX
 AC AAM89803;
 XX
 DT 16-MAR-1999 (first entry)
 XX
 DE Staphylococcus aureus protein SEQ ID #5251.
 XX
 KW Computer readable medium; vaccine; S. aureus infection; immunodetection;
 KW cellulitis; eyelid infection; food poisoning; osteomyelitis; therapy;
 KW skin infection; surgical wound infection; scalded skin syndrome;
 KW toxic shock syndrome.
 XX
 OS Staphylococcus aureus.
 XX
 PN EP766519-A2.
 XX
 PD 30-JUL-1997.
 XX
 PF 07-JAN-1997; 97EP-00100117.
 XX
 PR 05-JAN-1996; 96US-0009861P.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 XX
 PI Kunsch CA, Choi GH, Barash SC, Dillon PJ, Fannon MR, Rosen CA;
 XX
 XX WPI; 1997-374922/35.
 DR
 XX
 PT Polynucleotide(s) and proteins derived from Staphylococcus aureus -
 PT stored on computer readable medium and used in the production of anti-
 PT S. aureus vaccines.
 XX
 PS Claim 23; Page 3259-3261; 3271pp; English.
 XX
 CC This sequence represents a Staphylococcus aureus protein sequence of the
 CC invention. The DNA sequences encoding the S. aureus proteins are recorded
 CC on a computer readable medium, preferably selected from a floppy or hard
 CC disk, random access memory (RAM), read-only memory (ROM) or CD-ROM.
 CC Homology searches using the S. aureus DNA sequences allows putative
 CC functions to be assigned so that protein-encoding or regulatory regions
 CC of commercial, therapeutic or industrial importance can be obtained.
 CC Specifically, sequences which are likely to encode antigens have been
 CC identified and these polypeptides can be used in a vaccine composition
 CC against S. aureus infection. The polypeptides can also be used in a kit
 CC for the immunodetection of S. aureus in a sample. S. aureus is implicated
 CC in numerous human diseases, including cellulitis, eyelid infections, food
 CC poisoning, osteomyelitis, skin and surgical wound infections, scalded
 CC skin syndrome, toxic shock syndrome, etc. Organisms transformed with the
 CC DNA sequences can be used for recombinant production of the polypeptides.
 CC The new DNA sequences (and their fragments) are useful as primers or
 CC probes for isolating homologues of any of the 5191 S. aureus DNA sequences
 CC contained on the computer readable medium
 XX
 SQ Sequence 559 AA;
 Query Match 96.1%; Score 198; DB 2; Length 559;
 Best Local Similarity 97.4%; Pred. No. 2.9e-18;
 Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 ONSGNQSFEDTEBPCKYBOGNIVDIDFDSVPQIHG 38
|||
Db 301 ONSGNQSFEDTEBPCKYBOGNIVDIDFDSVPQIHG 338
|||

Search completed: October 25, 2005, 20:21:04
Job time : 84.8825 sec8

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 22, 2005, 03:51:22 ; Search time 21.1723 Seconds
(without alignments)
133.980 Million cell updates/sec

Title: US-10-731-238-42

Perfect score: 206

Sequence: 1 USGNGSFEEDTEEPKRYEQGNIYDIDFDSVPQIHG 38

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 7464964 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

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3: /cgn2_6/prodata/1/1aa/5A_COMB.pep:*
4: /cgn2_6/prodata/1/1aa/5B_COMB.pep:*
5: /cgn2_6/prodata/1/1aa/PCTUS_COMB.pep:*
6: /cgn2_6/prodata/1/1aa/backfill.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	206	100.0	38	4	US-09-010-317-42
2	198	96.1	38	1	US-08-234-622A-2
3	198	96.1	38	4	US-09-010-317-5
4	198	96.1	114	1	US-08-259-000-3
5	198	96.1	130	2	US-08-459-135A-7
6	198	96.1	130	2	US-08-459-135A-8
7	198	96.1	130	3	US-08-495-559-7
8	198	96.1	130	3	US-08-495-559-8
9	198	96.1	139	3	US-08-856-253-8
10	198	96.1	174	2	US-08-459-135A-10
11	198	96.1	174	2	US-08-459-135A-13
12	198	96.1	174	3	US-08-495-559-13
13	198	96.1	174	3	US-08-495-559-13
14	198	96.1	176	3	US-08-495-559-6
15	198	96.1	178	2	US-08-459-135A-12
16	198	96.1	178	2	US-08-495-559-12
17	198	96.1	181	2	US-08-459-135A-6
18	198	96.1	559	4	US-08-956-171E-5251
19	198	96.1	559	4	US-08-781-986A-5251
20	198	96.1	1027	4	US-08-956-171E-5254
21	198	96.1	1027	4	US-08-781-986A-5254
22	192	93.2	38	1	US-08-729-767-3
23	192	93.2	38	4	US-09-010-317-36
24	192	93.2	38	4	US-09-010-317-37
25	192	93.2	38	4	US-09-010-317-39
26	192	93.2	38	4	US-09-010-317-40
27	192	93.2	38	4	US-09-010-317-41

28	191	92.7	38	4	US-09-010-317-38	Sequence 38, Appl
29	190	92.2	38	4	US-09-010-317-6	Sequence 6, Appl
30	190	92.2	38	4	US-09-010-317-43	Sequence 43, Appl
31	188	91.3	38	4	US-09-010-317-35	Sequence 35, Appl
32	187.5	91.0	39	4	US-09-010-317-56	Sequence 56, Appl
33	179.5	87.1	39	4	US-09-010-317-57	Sequence 57, Appl
34	179	86.9	38	1	US-08-234-622A-3	Sequence 3, Appl
35	179	86.9	38	4	US-09-010-317-7	Sequence 7, Appl
36	173	84.0	38	1	US-08-729-767-4	Sequence 4, Appl
37	173	84.0	38	4	US-09-010-317-46	Sequence 46, Appl
38	173	84.0	38	4	US-09-010-317-47	Sequence 47, Appl
39	172	83.5	38	4	US-09-010-317-48	Sequence 48, Appl
40	172	83.0	38	4	US-09-010-317-8	Sequence 8, Appl
41	171	83.0	38	4	US-09-010-317-49	Sequence 49, Appl
42	170	82.5	38	4	US-09-010-317-45	Sequence 45, Appl
43	169	82.0	38	4	US-09-010-317-45	Sequence 45, Appl
44	160	77.7	36	4	US-09-010-317-58	Sequence 58, Appl
45	152	73.8	36	4	US-09-010-317-59	Sequence 59, Appl

ALIGNMENTS

RESULT 1
US-09-010-317-42
Sequence 42, Application US/09010317
Patent No. 6685943
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
APPLICANT: Patti, Joseph M.
APPLICANT: House-Pompeo, Karen L.
APPLICANT: Speziale, Pietro
APPLICANT: Joh, Danny
APPLICANT: McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
TITLE OF INVENTION: AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSES: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE:
CLASSIFICATION:
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 42:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-09-010-317-42
Query Match 100.0%; Score 206; DB 4; Length 38;
Best Local Similarity 100.0%; Pred. No. 2.5e-21;

Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 QNSGNQSFEDTEEPKPKYEOGNIIVDIDPDSVPQIHG 38
Db 1 QNSGNQSFEDTEEPKPKYEOGNIIVDIDPDSVPQIHG 38

RESULT 2
US-08-234-622A-2

; Sequence 2, Application US/08234622A
; Patent No. 5440014
; GENERAL INFORMATION:
; APPLICANT: HOOK, Magnus
; APPLICANT: MCGAVIN, Martin
; APPLICANT: RAUCCI, Giuseppe
; TITLE OF INVENTION: A FIBRONECTIN BINDING PEPTIDE
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Doane, Swecker & Mathis
; STREET: P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/234,622A
; FILING DATE: 28-APR-1994
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: SE 9002617-0
; FILING DATE: 10-AUG-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/SE91/00534
; FILING DATE: 09-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Meuth, Donna M
; REGISTRATION NUMBER: 36,607
; REFERENCE/DOCKET NUMBER: 012885-044
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 38 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-234-622A-2

Query Match 96.1%; Score 198; DB 1; Length 38;
Best Local Similarity 97.4%; Pred. No. 3.1e-20;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 QNSGNQSFEDTEEPKPKYEOGNIIVDIDPDSVPQIHG 38
Db 1 QNSGNQSFEDTEEPKPKYEOGNIIVDIDPDSVPQIHG 38

RESULT 3
US-09-010-317-5

; Sequence 5, Application US/09010317
; Patent No. 6685943
; GENERAL INFORMATION:
; APPLICANT: Hook, Magnus
; APPLICANT: Patti, Joseph M.
; APPLICANT: House-Pompeo, Karen L.
; APPLICANT: Speziale, Pietro

; APPLICANT: Joh, Danny
; APPLICANT: MCGAVIN, Martin J.
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
; TITLE OF INVENTION: AND METHODS OF USE
; NUMBER OF SEQUENCES: 105
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: TX
; COUNTRY: USA
; ZIP: 77210-4433

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/010,317
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/036,139
; FILING DATE: 21-JAN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Hibler, David W.
; REGISTRATION NUMBER: 41,071
; REFERENCE/DOCKET NUMBER: TMK:189
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 512-418-3000
; TELEFAX: 512-474-7577

; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 38 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; US-09-010-317-5

Query Match 96.1%; Score 198; DB 4; Length 38;
Best Local Similarity 97.4%; Pred. No. 3.1e-20;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 QNSGNQSFEDTEEPKPKYEOGNIIVDIDPDSVPQIHG 38
Db 1 QNSGNQSFEDTEEPKPKYEOGNIIVDIDPDSVPQIHG 38

RESULT 4
US-08-259-000-3

; Sequence 3, Application US/08259000
; Patent No. 5571514
; GENERAL INFORMATION:
; APPLICANT: HOOK, Magnus
; APPLICANT: LINDBERG, Martin Kjell
; APPLICANT: SIGNAS, Lars Christer
; APPLICANT: WADSTROM, Torkel Mikael
; APPLICANT: FROMAN, Gunnar
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN AS WELL AS
; TITLE OF INVENTION: ITS PREPARATION
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Doane, Swecker & Mathis
; STREET: P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25

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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/259,000
FILING DATE: 13-JUN-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: SE 8702272-9
FILING DATE: 01-JUN-1987
ATTORNEY/AGENT INFORMATION:
NAME: Meuth, Donna M
REGISTRATION NUMBER: 36,607
REFERENCE/DOCKET NUMBER: 012885-062
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 114 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-259-000-3

Query Match      96.1%; Score 198; DB 1; Length 114;
Best Local Similarity 97.4%; Pred. No. 1,2e-19;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1  QNSGNSFEEDTEBPCKYEGGNIYDIDFDSVPQIHG 38
Db      2  QNSGNSFEEDTEBPCKYEGGNIYDIDFDSVPQIHG 39

RESULT 5
US-08-459-135A-7
Sequence 7, Application US/08459135A
Patent No. 5955078
GENERAL INFORMATION:
APPLICANT: BURNHAM, Martin Karl Russel
APPLICANT: CHOPRA, Ian
APPLICANT: CRITCHLEY, Ian Alfred
APPLICANT: KNOWLES, David Justin Charles
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN: MONOCLONAL ANTIBODY AND THEIR US
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
STATE: PA
COUNTRY: U.S.A.
ZIP: 19406-0939
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: Fastseq, Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/459,135A
FILING DATE: 02-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB/94/00215
FILING DATE: 04-Feb-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Gimm, Edward R
REGISTRATION NUMBER: 38,891
REFERENCE/DOCKET NUMBER: P30591C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-4478
TELEFAX: 610-270-5090
TELEX:
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
```

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LENGTH: 130 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-459-135A-7

Query Match      96.1%; Score 198; DB 2; Length 130;
Best Local Similarity 97.4%; Pred. No. 1,4e-19;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1  QNSGNSFEEDTEBPCKYEGGNIYDIDFDSVPQIHG 38
Db      2  QNSGNSFEEDTEBPCKYEGGNIYDIDFDSVPQIHG 39

RESULT 6
US-08-459-135A-8
Sequence 8, Application US/08459135A
Patent No. 5955078
GENERAL INFORMATION:
APPLICANT: BURNHAM, Martin Karl Russel
APPLICANT: CHOPRA, Ian
APPLICANT: CRITCHLEY, Ian Alfred
APPLICANT: KNOWLES, David Justin Charles
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN: MONOCLONAL ANTIBODY AND THEIR US
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
STATE: PA
COUNTRY: U.S.A.
ZIP: 19406-0939
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: Fastseq, Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/459,135A
FILING DATE: 02-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB/94/00215
FILING DATE: 04-Feb-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Gimm, Edward R
REGISTRATION NUMBER: 38,891
REFERENCE/DOCKET NUMBER: P30591C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-4478
TELEFAX: 610-270-5090
TELEX:
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 130 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-459-135A-8

Query Match      96.1%; Score 198; DB 2; Length 130;
Best Local Similarity 97.4%; Pred. No. 1,4e-19;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1  QNSGNSFEEDTEBPCKYEGGNIYDIDFDSVPQIHG 38
Db      2  QNSGNSFEEDTEBPCKYEGGNIYDIDFDSVPQIHG 39

RESULT 7
US-08-495-559-7
```

```
Sequence 7, Application US/08495559A
Patent No. 6054572
GENERAL INFORMATION:
APPLICANT: BURMAN, Martin Karl Russel
APPLICANT: CHOPRA, Ian
APPLICANT: CRITCHLEY, Ian Alfred
APPLICANT: KNOWLES, David Justin Charles
TITLE OF INVENTION: FIBROBLAST BINDING PROTEIN: MONOCLONAL
TITLE OF INVENTION: ANTIBODY AND THEIR USE IN PREVENTING BACTERIAL ADHESION
FILE REFERENCE: P30591
CURRENT FILING DATE: 1995-08-03
EARLIER FILING DATE: 1993-02-05
EARLIER FILING DATE: 1993-10-20
NUMBER OF SEQ ID NOS: 13
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 7
LENGTH: 130
TYPE: PRT
ORGANISM: Staphylococcus aureus
US-08-495-559-7

Query Match      96.1%; Score 198; DB 3; Length 130;
Best Local Similarity 97.4%; Pred. No. 1.4e-19;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ONSGNQSFEDTEEDPKPKYEGCGNIVDIDFDSVPQIHG 38
Db 2 ONSGNQSFEDTEEDPKPKYEGCGNIVDIDFDSVPQIHG 39

RESULT 8
US-08-495-559-8
Sequence 8, Application US/08495559A
Patent No. 6054572
GENERAL INFORMATION:
APPLICANT: BURMAN, Martin Karl Russel
APPLICANT: CHOPRA, Ian
APPLICANT: CRITCHLEY, Ian Alfred
APPLICANT: KNOWLES, David Justin Charles
TITLE OF INVENTION: FIBROBLAST BINDING PROTEIN: MONOCLONAL
TITLE OF INVENTION: ANTIBODY AND THEIR USE IN PREVENTING BACTERIAL ADHESION
FILE REFERENCE: P30591
CURRENT FILING DATE: 1995-08-03
EARLIER FILING DATE: 1993-02-05
EARLIER FILING DATE: 1993-10-20
NUMBER OF SEQ ID NOS: 13
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 8
LENGTH: 130
TYPE: PRT
ORGANISM: Staphylococcus aureus
US-08-495-559-8

Query Match      96.1%; Score 198; DB 3; Length 130;
Best Local Similarity 97.4%; Pred. No. 1.4e-19;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ONSGNQSFEDTEEDPKPKYEGCGNIVDIDFDSVPQIHG 38
Db 2 ONSGNQSFEDTEEDPKPKYEGCGNIVDIDFDSVPQIHG 39

RESULT 9
US-08-856-253-8
Sequence 8, Application US/08856253
Patent No. 6288214
GENERAL INFORMATION:
```

```
APPLICANT: Hook, Magnus
APPLICANT: Patti, Joseph M.
APPLICANT: House-Pompeo, Karen
APPLICANT: Schanum, Narayana
APPLICANT: Symerky, Jindrich
TITLE OF INVENTION: COLLAGEN BINDING PROTEIN COMPOSITIONS
TITLE OF INVENTION: AND METHODS OF USE
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: Texas
COUNTRY: U.S.
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/856,253
FILING DATE: Concurrently Herewith
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/017,678
FILING DATE: 16-MAY-1996
ATTORNEY/AGENT INFORMATION:
NAME: Kitchell, Barbara S.
REGISTRATION NUMBER: 33,928
REFERENCE/DOCKET NUMBER: TAMK.193
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
TELEFAX: (512) 474-7577
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 139 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-08-856-253-8

Query Match      96.1%; Score 198; DB 3; Length 139;
Best Local Similarity 97.4%; Pred. No. 1.5e-19;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ONSGNQSFEDTEEDPKPKYEGCGNIVDIDFDSVPQIHG 38
Db 16 ONSGNQSFEDTEEDPKPKYEGCGNIVDIDFDSVPQIHG 53

RESULT 10
US-08-459-135A-10
Sequence 10, Application US/08459135A
Patent No. 5955078
GENERAL INFORMATION:
APPLICANT: BURMAN, Martin Karl Russel
APPLICANT: CHOPRA, Ian
APPLICANT: CRITCHLEY, Ian Alfred
APPLICANT: KNOWLES, David Justin Charles
TITLE OF INVENTION: FIBROBLAST BINDING PROTEIN: MONOCLONAL ANTIBODY AND THEIR USE
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
STATE: PA
COUNTRY: U.S.A.
ZIP: 19406-0939
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
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SOFTWARE: Fastseq, Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/459,135A
FILING DATE: 02-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB/94/00215
FILING DATE: 04-Feb-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Gimmil, Edward R
REGISTRATION NUMBER: 38,891
REFERENCE/DOCKET NUMBER: P30591C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-4478
TELEFAX: 610-270-5090
TELEX:
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 174 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: Protein
US-08-459-135A-10

Query Match 96.1%; Score 198; DB 2; Length 174;
Best Local Similarity 97.4%; Pred. No. 1.9e-19;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QNSGNSFEEDTEEPKPYEQGNIIVDIDPSVPOIHG 38
Db 2 QNSGNSFEEDTEEDKPYEQGNIIVDIDPSVPOIHG 39

RESULT 11
US-08-459-135A-13
Sequence 13, Application US/08459135A
Patent No. 5955078
GENERAL INFORMATION:
APPLICANT: BURHAM, Martin Karl Russel
APPLICANT: CHOPRA, Ian
APPLICANT: CRITCHLEY, Ian Alfred
APPLICANT: KNOWLES, David Justin Charles
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN: MONOCLONAL ANTIBODY AND THEIR USE
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
STATE: PA
COUNTRY: U.S.A.
ZIP: 19406-0939
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: Fastseq, Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/459,135A
FILING DATE: 02-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB/94/00215
FILING DATE: 04-Feb-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Gimmil, Edward R
REGISTRATION NUMBER: 38,891
REFERENCE/DOCKET NUMBER: P30591C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-4478
TELEFAX: 610-270-5090
TELEX:

INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 174 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-459-135A-13

Query Match 96.1%; Score 198; DB 2; Length 174;
Best Local Similarity 97.4%; Pred. No. 1.9e-19;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QNSGNSFEEDTEEPKPYEQGNIIVDIDPSVPOIHG 38
Db 2 QNSGNSFEEDTEEDKPYEQGNIIVDIDPSVPOIHG 39

RESULT 12
US-08-495-559-10
Sequence 10, Application US/08495559A
Patent No. 6054572
GENERAL INFORMATION:
APPLICANT: BURHAM, Martin Karl Russel
APPLICANT: CHOPRA, Ian
APPLICANT: CRITCHLEY, Ian Alfred
APPLICANT: KNOWLES, David Justin Charles
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN: MONOCLONAL ANTIBODY AND THEIR USE IN PREVENTING BACTERIAL ADHESION
FILE REFERENCE: P30591
CURRENT APPLICATION NUMBER: US/08/495,559A
CURRENT FILING DATE: 1995-08-03
EARLIER APPLICATION NUMBER: GB 9302289.5
EARLIER FILING DATE: 1993-02-05
EARLIER APPLICATION NUMBER: GB 9321592.9
EARLIER FILING DATE: 1993-10-20
NUMBER OF SEQ ID NOS: 13
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 10
LENGTH: 174
TYPE: PRT
ORGANISM: Staphylococcus aureus
US-08-495-559-10

Query Match 96.1%; Score 198; DB 3; Length 174;
Best Local Similarity 97.4%; Pred. No. 1.9e-19;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QNSGNSFEEDTEEPKPYEQGNIIVDIDPSVPOIHG 38
Db 2 QNSGNSFEEDTEEDKPYEQGNIIVDIDPSVPOIHG 39

RESULT 13
US-08-495-559-13
Sequence 13, Application US/08495559A
Patent No. 6054572
GENERAL INFORMATION:
APPLICANT: BURHAM, Martin Karl Russel
APPLICANT: CHOPRA, Ian
APPLICANT: CRITCHLEY, Ian Alfred
APPLICANT: KNOWLES, David Justin Charles
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN: MONOCLONAL ANTIBODY AND THEIR USE IN PREVENTING BACTERIAL ADHESION
FILE REFERENCE: P30591
CURRENT APPLICATION NUMBER: US/08/495,559A
CURRENT FILING DATE: 1995-08-03
EARLIER APPLICATION NUMBER: GB 9302289.5
EARLIER FILING DATE: 1993-02-05
EARLIER APPLICATION NUMBER: GB 9321592.9
EARLIER FILING DATE: 1993-10-20
NUMBER OF SEQ ID NOS: 13
SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 13
LENGTH: 174
TYPE: PRT
ORGANISM: Staphylococcus aureus
US-08-495-559-13

Query Match 96.1%; Score 198; DB 3; Length 174;
Best Local Similarity 97.4%; Pred. No. 1.9e-19;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QNSGNQSFEDTDEPKPKYEGGNIVIDIDFDSVPQIHG 38
DB 2 QNSGNQSFEDTDEPKPKYEGGNIVIDIDFDSVPQIHG 39

RESULT 14
US-08-495-559-6
Sequence 6, Application US/08495559A
Patent No. 6054572
GENERAL INFORMATION:
APPLICANT: BURHAM, Martin Karl Russel
APPLICANT: CHOPRA, Ian
APPLICANT: CRITCHLEY, Ian Alfred
APPLICANT: KNOWLES, David Justin Charles
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN: MONOCLONAL
FILE REFERENCE: P30591
CURRENT APPLICATION NUMBER: US/08/495,559A
CURRENT FILING DATE: 1995-08-03
EARLIER APPLICATION NUMBER: GB 9302289.5
EARLIER FILING DATE: 1993-02-05
EARLIER APPLICATION NUMBER: GB 9321592.9
EARLIER FILING DATE: 1993-10-20
NUMBER OF SEQ ID NOS: 13
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 6
LENGTH: 176
TYPE: PRT
ORGANISM: Staphylococcus aureus
US-08-495-559-6

Query Match 96.1%; Score 198; DB 3; Length 176;
Best Local Similarity 97.4%; Pred. No. 2e-19;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QNSGNQSFEDTDEPKPKYEGGNIVIDIDFDSVPQIHG 38
DB 2 QNSGNQSFEDTDEPKPKYEGGNIVIDIDFDSVPQIHG 39

RESULT 15
US-08-459-135A-12
Sequence 12, Application US/08459135A
Patent No. 5955078
GENERAL INFORMATION:
APPLICANT: BURHAM, Martin Karl Russel
APPLICANT: CHOPRA, Ian
APPLICANT: CRITCHLEY, Ian Alfred
APPLICANT: KNOWLES, David Justin Charles
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN: MONOCLONAL ANTIBODY AND THEIR US
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
STATE: PA
COUNTRY: U.S.A.
ZIP: 19406-0939
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: Fastseq, Version 2.0

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/459,135A
FILING DATE: 02-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB/94/00215
FILING DATE: 04-Feb-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Glimmi, Edward R
REGISTRATION NUMBER: 38,891
REFERENCE/DOCKET NUMBER: P30591C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-4478
TELEFAX: 610-270-5090
TELEX:
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 178 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: Protein
US-08-459-135A-12

Query Match 96.1%; Score 198; DB 2; Length 178;
Best Local Similarity 97.4%; Pred. No. 2e-19;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QNSGNQSFEDTDEPKPKYEGGNIVIDIDFDSVPQIHG 38
DB 2 QNSGNQSFEDTDEPKPKYEGGNIVIDIDFDSVPQIHG 39

Search completed: October 22, 2005, 05:46:44
Job time : 21.2223 secs

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OM protein - protein search, using sw model

Run on: October 22, 2005, 11:35:03 ; Search time 70.1256 Seconds
(without alignments)
226.232 Million cell updates/sec

Title: US-10-731-238-42

Perfect score: 206
Sequence: 1 ONSGNSFEDTEPRKPKYGGGNIIVIDFDSVPIHG 38

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1862951 seqs, 417491010 residues

Total number of hits satisfying chosen parameters: 1862951

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA.*
1: /cgn2_6/ptodata/2/pubppa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/2/pubppa/PCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/2/pubppa/US06_NEW_PUB.pep.*
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6: /cgn2_6/ptodata/2/pubppa/PCTUS_PUBCOMB.pep.*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysts of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	206	100.0	38	18	US-10-731-238-42
2	198	96.1	38	18	US-10-731-238-5
3	198	96.1	139	9	US-08-813-820-8
4	198	96.1	388	8	US-08-901-062-1
5	198	96.1	559	8	US-08-781-986A-5251
6	198	96.1	559	15	US-10-329-624-5251
7	198	96.1	767	9	US-09-815-242-5899
8	198	96.1	767	9	US-09-815-242-13140
9	198	96.1	940	17	US-10-470-048B-424
10	198	96.1	948	17	US-10-470-048B-69
11	198	96.1	961	15	US-10-282-122A-43778

12	198	96.1	1018	9	US-09-815-242-5797
13	198	96.1	1018	9	US-09-815-242-12838
14	198	96.1	1018	17	US-10-470-048B-68
15	198	96.1	1027	8	US-08-781-986A-5254
16	198	96.1	1027	15	US-10-329-624-5254
17	198	96.1	1038	15	US-10-282-122A-43827
18	192	93.2	38	18	US-10-731-238-36
19	192	93.2	38	18	US-10-731-238-37
20	192	93.2	38	18	US-10-731-238-39
21	192	93.2	38	18	US-10-731-238-40
22	192	93.2	38	18	US-10-731-238-41
23	191	92.7	38	18	US-10-731-238-38
24	190	92.2	38	18	US-10-731-238-6
25	190	92.2	38	18	US-10-731-238-43
26	190	92.2	978	9	US-09-815-242-5456
27	190	92.2	1001	9	US-09-815-242-12686
28	188	91.3	38	18	US-10-731-238-35
29	187.5	91.0	39	18	US-10-731-238-56
30	179.5	87.1	39	18	US-10-731-238-57
31	179	86.9	38	18	US-10-731-238-7
32	173	84.0	38	18	US-10-731-238-46
33	173	84.0	38	18	US-10-731-238-47
34	172	83.5	38	18	US-10-731-238-48
35	171	83.0	38	18	US-10-731-238-8
36	171	83.0	38	18	US-10-731-238-49
37	170	82.5	38	18	US-10-731-238-44
38	169	82.0	38	18	US-10-731-238-45
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44	76.5	37.1	37	20	US-11-066-697-1134
45	74	35.9	14	18	US-10-731-238-60

ALIGNMENTS

Sequence 5797, Ap
Sequence 12838, A
Sequence 68, Appl
Sequence 5254, Ap
Sequence 5254, Ap
Sequence 43827, A
Sequence 36, Appl
Sequence 37, Appl
Sequence 39, Appl
Sequence 40, Appl
Sequence 41, Appl
Sequence 38, Appl
Sequence 6, Appl
Sequence 43, Appl
Sequence 5456, Ap
Sequence 12686, A
Sequence 35, Appl
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Sequence 57, Appl
Sequence 7, Appl
Sequence 46, Appl
Sequence 47, Appl
Sequence 48, Appl
Sequence 49, Appl
Sequence 44, Appl
Sequence 45, Appl
Sequence 58, Appl
Sequence 59, Appl
Sequence 50, Appl
Sequence 2, Appl
Sequence 1134, Ap
Sequence 60, Appl

RESULT 1
US-10-731-238-42
Sequence 42, Application US/10731238
Publication No. US20050123552A1
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
Pacifi, Joseph M.
House-Pompeo, Karen L.
Speziale, Pietro
Job, Danny
McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/731,238
FILING DATE: 10-Dec-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE: 21-Jan-1998
APPLICATION NUMBER: US 60/036,139

FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAMK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 42:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 42:
US-10-731-238-42

Query Match 100.0%; Score 206; DB 18; Length 38;
Best Local Similarity 100.0%; Pred. No. 1e-19;
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ONSGNQSFEDTDEPKPYEQGNIIVDIDFDSVPQIHG 38
Db 1 ONSGNQSFEDTDEPKPYEQGNIIVDIDFDSVPQIHG 38

RESULT 2
US-10-731-238-5
Sequence 5, Application US/10731238
Publication No. US20050123552A1
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
Patti, Joseph M.
House-Pompeo, Karen L.
Speziale, Pietro
Joh, Danny
McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/731,238
FILING DATE: 10-Dec-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE: 21-Jan-1998
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAMK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>

TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-10-731-238-5

Query Match 96.1%; Score 198; DB 18; Length 38;
Best Local Similarity 97.4%; Pred. No. 1.2e-18;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ONSGNQSFEDTDEPKPYEQGNIIVDIDFDSVPQIHG 38
Db 1 ONSGNQSFEDTDEPKPYEQGNIIVDIDFDSVPQIHG 38

RESULT 3
US-09-813-820-8
Sequence 8, Application US/09813820
Patent No. US2002010262A1
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
Patti, Joseph M.
House-Pompeo, Karen
Schanam, Narayana
Syamersky, Jindrich
TITLE OF INVENTION: COLLAGEN BINDING PROTEIN COMPOSITIONS
AND METHODS OF USE
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: Texas
COUNTRY: U.S.
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/813,820
FILING DATE: 22-Mar-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/856,253
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Kitchell, Barbara S.
REGISTRATION NUMBER: 33,928
REFERENCE/DOCKET NUMBER: TAMK:193
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
TELEFAX: (512) 474-7577
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 139 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-09-813-820-8

Query Match 96.1%; Score 198; DB 9; Length 139;
Best Local Similarity 97.4%; Pred. No. 5.2e-18;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ONSGNQSFEDTDEPKPYEQGNIIVDIDFDSVPQIHG 38
Db 16 ONSGNQSFEDTDEPKPYEQGNIIVDIDFDSVPQIHG 53

RESULT 4
US-08-901-062-1
Sequence 1, Application US/08901062

Publication No. US20020025324A1
GENERAL INFORMATION:
APPLICANT: SEALS, JONATHAN R.
TITLE OF INVENTION: RECOMBINANT BIVALENT BACTERIAL VACCINE
TITLE OF INVENTION: FOR THE PREVENTION OF MASTITIS
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: HALR AND DORR LLP
STREET: 60 State Street
CITY: Boston
STATE: MA
COUNTRY: United States of America
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/901,062
FILING DATE: 25-JUL-1997
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Baker, Hollie L.
REGISTRATION NUMBER: 31,321
REFERENCE/DOCKET NUMBER: 106941.153
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 526-6000
TELEFAX: (617) 526-5000
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 388 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-901-062-1

Query Match 96.1%; Score 198; DB 8; Length 388;
Best Local Similarity 97.4%; Pred. No. 1,7e-17;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ONSGNSFEEDTEBPKEKYEQGNIVDIDFDSVPQIHG 38
Db 265 ONSGNSFEEDTEBPKEKYEQGNIVDIDFDSVPQIHG 302

RESULT 5
US-08-781-986A-5251
Sequence 5251, Application US/08781986A
Publication No. US20030054436A1
GENERAL INFORMATION:
APPLICANT: Charles Kunsch
TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
NUMBER OF SEQUENCES: 5255
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COUNTRY: USA
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4MB storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/781,986A
FILING DATE:
CLASSIFICATION: 435

PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Benson, Bob
REGISTRATION NUMBER: 30,446
REFERENCE/DOCKET NUMBER: PB248BP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8512
TELEFAX: (301) 309-8504
INFORMATION FOR SEQ ID NO: 5251:
SEQUENCE CHARACTERISTICS:
LENGTH: 559 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-781-986A-5251

Query Match 96.1%; Score 198; DB 8; Length 559;
Best Local Similarity 97.4%; Pred. No. 2.6e-17;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Db 301 ONSGNSFEEDTEBPKEKYEQGNIVDIDFDSVPQIHG 338

RESULT 6
US-10-329-624-5251
Sequence 5251, Application US/10329624
Publication No. US20040043037A1
GENERAL INFORMATION:
APPLICANT: Charles Kunsch
GIL H. Choi
Patrick S. Dillon
Craig A. Rosen
Steven C. Barash
Michael R. Farnon
TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
NUMBER OF SEQUENCES: 5256
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COUNTRY: USA
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4MB storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/329,624
FILING DATE: 27-Dec-2002
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/956,171
FILING DATE: October 20, 1997
APPLICATION NUMBER: 60/009,861
FILING DATE: January 5, 1996
APPLICATION NUMBER: 08/781,986
FILING DATE: January 3, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Mark J. Hyman
REGISTRATION NUMBER: 46,789
REFERENCE/DOCKET NUMBER: PB248P1D1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (240) 314-1224
TELEFAX: (301) 309-8439
INFORMATION FOR SEQ ID NO: 5251:
SEQUENCE CHARACTERISTICS:
LENGTH: 559 amino acids

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; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 5251:
US-10-329-624-5251

Query Match      96.1%; Score 198; DB 15; Length 559;
Best Local Similarity 97.4%; Pred. No. 2.6e-17;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 ONSGNSFEEDTEEPKPYEQGNIVIDIDFDSVPQIHG 38
DB 301 ONSGNSFEEDTEEDKPKYEQGNIVIDIDFDSVPQIHG 338

RESULT 7
US-09-815-242-5899
; Sequence 5899, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Karl L.
; APPLICANT: Zykkind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; FILE REFERENCE: ELITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2001-02-16
; PRIOR APPLICATION NUMBER: 60/269,308
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5899
; LENGTH: 767
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-09-815-242-5899

Query Match      96.1%; Score 198; DB 9; Length 767;
Best Local Similarity 97.4%; Pred. No. 3.8e-17;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 ONSGNSFEEDTEEPKPYEQGNIVIDIDFDSVPQIHG 38
DB 682 ONSGNSFEEDTEEDKPKYEQGNIVIDIDFDSVPQIHG 719

RESULT 8
US-09-815-242-13140
; Sequence 13140, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Karl L.
; APPLICANT: Zykkind, Judith W.
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; FILE REFERENCE: ELITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13140
; LENGTH: 767
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-09-815-242-13140

Query Match      96.1%; Score 198; DB 9; Length 767;
Best Local Similarity 97.4%; Pred. No. 3.8e-17;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 ONSGNSFEEDTEEPKPYEQGNIVIDIDFDSVPQIHG 38
DB 682 ONSGNSFEEDTEEDKPKYEQGNIVIDIDFDSVPQIHG 719

RESULT 9
US-10-470-048B-424
; Sequence 424, Application US/10470048B
; Publication No. US2005003744A1
; GENERAL INFORMATION:
; APPLICANT: MEINKE ET AL.
; TITLE OF INVENTION: A METHOD FOR IDENTIFICATION, ISOLATION AND PRODUCTION OF
; FILE REFERENCE: SORN:035US
; CURRENT APPLICATION NUMBER: US/10/470,048B
; PRIOR FILING DATE: 2003-07-25
; CURRENT APPLICATION NUMBER: US/10/470,048B
; NUMBER OF SEQ ID NOS: 603
; SOFTWARE: Patent version 3.1
; SEQ ID NO 424
; LENGTH: 940
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-10-470-048B-424

Query Match      96.1%; Score 198; DB 17; Length 940;
Best Local Similarity 97.4%; Pred. No. 4.8e-17;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 ONSGNSFEEDTEEPKPYEQGNIVIDIDFDSVPQIHG 38
DB 682 ONSGNSFEEDTEEDKPKYEQGNIVIDIDFDSVPQIHG 719

RESULT 10
US-10-470-048B-69
; Sequence 69, Application US/10470048B
; Publication No. US2005003744A1
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; GENERAL INFORMATION:
; APPLICANT: MEINKE ET AL.
; TITLE OF INVENTION: A METHOD FOR IDENTIFICATION, ISOLATION AND PRODUCTION OF
; TITLE OF INVENTION: ANTIGENS TO A SPECIFIC PATHOGEN
; FILE REFERENCE: SOINN:03505
; CURRENT APPLICATION NUMBER: US/10/470,048B
; CURRENT FILING DATE: 2003-07-25
; NUMBER OF SEQ ID NOS: 603
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 69
; LENGTH: 948
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
; US-10-470-048B-69

Query Match      96.1%; Score 198; DB 17; Length 948;
Best Local Similarity 97.4%; Pred. No. 4,9e-17;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy      1  ONSGNQSFEDTPEPKYKXEGGNTVIDIDFDSVPQIHG 38
Db      690  ONSGNQSFEDTPEPKYKXEGGNTVIDIDFDSVPQIHG 727

RESULT 11
US-10-282-122A-43778
; Sequence 43778, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining prior application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 43778
; LENGTH: 961
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
; US-10-282-122A-43778

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Query Match      96.1%; Score 198; DB 15; Length 961;
Best Local Similarity 97.4%; Pred. No. 5e-17;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy      1  ONSGNQSFEDTPEPKYKXEGGNTVIDIDFDSVPQIHG 38
Db      693  ONSGNQSFEDTPEPKYKXEGGNTVIDIDFDSVPQIHG 730

RESULT 12
US-09-815-242-5797
; Sequence 5797, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; FILE REFERENCE: ELITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5797
; LENGTH: 1018
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
; US-09-815-242-5797

Query Match      96.1%; Score 198; DB 9; Length 1018;
Best Local Similarity 97.4%; Pred. No. 5.3e-17;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy      1  ONSGNQSFEDTPEPKYKXEGGNTVIDIDFDSVPQIHG 38
Db      746  ONSGNQSFEDTPEPKYKXEGGNTVIDIDFDSVPQIHG 783

RESULT 13
US-09-815-242-12838
; Sequence 12838, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in

```

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; TITLE OF INVENTION: Prokaryotes
; FILE REFERENCE: ELITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO: 12838
; LENGTH: 1018
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
; US-09-815-242-12838

Query Match          96.1%; Score 198; DB 9; Length 1018;
Best Local Similarity 97.4%; Pred. No. 5.3e-17;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1  ONSGNQSFEDTEBPKPKYEOGNIIVDIDFDSVPOIHG 38
DB      746  ONSGNQSFEDTEBPKPKYEOGNIIVDIDFDSVPOIHG 783

RESULT 14
US-10-470-0488-68
; Sequence 68, Application US/104700488
; Publication No. US2005003744A1
; GENERAL INFORMATION:
; APPLICANT: MEINKE ET AL.
; TITLE OF INVENTION: A METHOD FOR IDENTIFICATION, ISOLATION AND PRODUCTION OF
; FILE REFERENCE: SOUN-035US
; CURRENT APPLICATION NUMBER: US/10/470,0488
; NUMBER OF SEQ ID NOS: 603
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 68
; LENGTH: 1018
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
; US-10-470-0488-68

Query Match          96.1%; Score 198; DB 17; Length 1018;
Best Local Similarity 97.4%; Pred. No. 5.3e-17;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1  ONSGNQSFEDTEBPKPKYEOGNIIVDIDFDSVPOIHG 38
DB      746  ONSGNQSFEDTEBPKPKYEOGNIIVDIDFDSVPOIHG 783

RESULT 15
US-08-781-986A-5254
; Sequence 5254, Application US/08781986A
; Publication No. US20030054436A1
; GENERAL INFORMATION:
; APPLICANT: Charles Kunach
; TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
; NUMBER OF SEQUENCES: 5255
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
```

```

; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4mb storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/781,986A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Benson, Bob
; REGISTRATION NUMBER: 30,446
; REFERENCE/DOCKET NUMBER: PB248PP
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 5254:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1027 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-781-986A-5254

Query Match          96.1%; Score 198; DB 8; Length 1027;
Best Local Similarity 97.4%; Pred. No. 5.4e-17;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1  ONSGNQSFEDTEBPKPKYEOGNIIVDIDFDSVPOIHG 38
DB      755  ONSGNQSFEDTEBPKPKYEOGNIIVDIDFDSVPOIHG 792
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Search completed: October 22, 2005, 12:09:27
Job time : 71.1256 secs

GenCore version 5.1.6
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OM protein - protein search, using SW model

Run on: October 22, 2005, 04:14:19 ; Search time 13.8905 Seconds
(without alignments)
263.219 Million cell updates/sec

Title: US-10-731-238-42
Perfect score: 206
Sequence: 1 QNSGNQSFEDTDEPKPKYEGCGNIVDIDFDSVPQIHG 38

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	198	96.1	940	2	S19702 fibronectin-binding
2	198	96.1	961	2	G90053 hypothetical prote
3	198	96.1	1018	2	A32192 fibronectin-binding
4	198	96.1	1038	2	H90053 hypothetical prote
5	59	28.6	396	2	B84196 cell division prot
6	56.5	27.4	1952	2	T48814 hypothetical prote
7	56	27.2	1369	2	S58160 hypothetical prote
8	54.5	26.5	155	1	RNBR6 DNA-directed RNA p
9	54.5	26.5	428	2	T32952 hypothetical prote
10	54.5	26.5	633	2	H84854 probable ATP-depen
11	54.5	26.5	875	2	C81209 tspa protein NMB03
12	54.5	26.5	880	2	G81786 Neisseria-specific
13	54	26.2	578	2	D82053 fibronectin-binding
14	54	26.2	1091	2	S33850 polymorphic membra
15	54	26.2	1460	2	D81675 S-locus-specific g
16	53.5	26.0	437	2	S11925 S-locus-specific g
17	53.5	26.0	494	2	T14516 hypothetical prote
18	53.5	26.0	1658	2	S55101 hypothetical prote
19	53	25.7	183	2	D83840 hypothetical prote
20	53	25.7	790	2	S61587 transcription acti
21	53	25.7	833	2	E90577 lipoprotein vasc
22	53	25.7	1233	2	T40059 chromosome segrega
23	52.5	25.5	328	2	AH2128 iron(III) diclrat
24	52.5	25.5	375	2	C75040 alcohol dehydrogen
25	52.5	25.5	422	1	M2MR2 E2 protein - bovin
26	52.5	25.5	1273	1	TDRPRT leukocyte common a
27	52.5	25.5	1291	1	A28334 protein-tyrosine-p
28	52	25.2	195	2	A88110 protein T24E12.11
29	52	25.2	265	2	A43738 Endo16 protein - s

30	52	25.2	306	1	M2MLEB E2 protein - bovin
31	52	25.2	329	2	S07577 legumin storage pr
32	52	25.2	335	2	S07576 legumin storage pr
33	52	25.2	425	2	T16433 hypothetical prote
34	52	25.2	484	2	A24942 legumin B4 precurs
35	52	25.2	701	2	H95039 hypothetical prote
36	52	25.2	701	2	C97910 ATP-dependent prot
37	52	25.2	1022	2	T53078 homeotic gene regu
38	52	25.2	1056	2	E86748 hypothetical prote
39	52	25.2	1536	1	R8BY63 regulatory protein
40	52	25.2	1560	2	T30282 calcium-binding pr
41	52	25.2	1613	2	S39059 protein BRG1 - hum
42	52	25.2	1647	2	S45252 SRF-beta protein -
43	51.5	25.0	558	2	C71609 hypothetical prote
44	51.5	25.0	671	1	OKBOG protein kinase (BC
45	51.5	25.0	686	1	S05702 protein kinase (BC

ALIGNMENTS

RESULT 1

S19702
C:Species: Staphylococcus aureus
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
C:Accession: S19702
R:Johansson, K.; Signaes, C.; Mueller, H.P.; Lindberg, M.
Eur. J. Biochem. 202, 1041-1048, 1991
A:Title: Two different genes encode fibronectin binding proteins in Staphylococcus aureus
A:Reference number: S19702; MUID:92111475; PMID:1837266
A:Residues: 1-940 <JOB>
A:Status: preliminary
A:Molecule type: DNA
A:Cross-references: UNIPROT:Q53682; EMBL:X62992; NID:949040; PIDN:CAA44726.1; PID:958156;
C:Keywords: fibronectin binding

Query Match 96.1%; Score 198; DB 2; Length 940;
Best Local Similarity 97.4%; Pred. No. 2.2e-17;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QNSGNQSFEDTDEPKPKYEGCGNIVDIDFDSVPQIHG 38
DB 682 QNSGNQSFEDTDEPKPKYEGCGNIVDIDFDSVPQIHG 719

RESULT 2

G90053
C:Species: Staphylococcus aureus
C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C:Accession: G90053
R:Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguchi, A.; Mizutani-U, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.; C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiratsuku, K.
Lancet 357, 1225-1240, 2001
A:Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.
A:Reference number: AB9758; MUID:21311952; PMID:1148146
A:Accession: G90053
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-961 <MUR>
A:Cross-references: UNIPROT:Q99RD3; GB:BA000018; PID:G13702452; PIDN:BA843593.1; GSPDB:G
C:Experimental source: strain N315
C:Genetics:
A:Gene: fmbB

Query Match 96.1%; Score 198; DB 2; Length 961;
Best Local Similarity 97.4%; Pred. No. 2.2e-17;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QNSGNQSFEDTDEPKPKYEGCGNIVDIDFDSVPQIHG 38

```
Db 693 QNSGNQSFEDTEBPKRYEGCGNIVDIDFDSVPQIHG 730
|||||
RESULT 3
A32192
fibronectin-binding protein - Staphylococcus aureus
C:Species: Staphylococcus aureus
C:Date: 31-Jul-1989 #sequence_revision 31-Jul-1989 #text_change 16-Feb-1997
C:Accession: A32192
R:Signaes, C.; Raucel, G.; Joensson, K.; Lindgren, P.E.; Anantharamiah, G.M.; Hoesek, M.
Proc. Natl. Acad. Sci. U.S.A. 86, 699-703, 1989
A:Title: Nucleotide sequence of the gene for a fibronectin-binding protein from Staphylococcus aureus
A:Reference number: A32192; MUID:89098998; PMID:2521391
A:Accession: A32192
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1018 <SIG>
A:Cross-references: GB:J04151
C:Keywords: fibronectin binding

Query Match 96.1%; Score 198; DB 2; Length 1018;
Best Local Similarity 97.4%; Pred. No. 2.4e-17;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Cy 1 QNSGNQSFEDTEBPKRYEGCGNIVDIDFDSVPQIHG 38
|||||
Db 746 QNSGNQSFEDTEBPKRYEGCGNIVDIDFDSVPQIHG 783
|||||

RESULT 4
H90053
hypothetical protein fmb [imported] - Staphylococcus aureus (strain N315)
C:Species: Staphylococcus aureus
C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C:Accession: H90053
R:Kuroda, M.; Ohba, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguma, A.; Mizutani-U, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.; C.; Shiba, T.; Hartori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1235-1240, 2001
A:Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.
A:Reference number: A89758; MUID:21111952; PMID:11418146
A:Accession: H90053
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1038 <KUR>
A:Cross-references: UNIPROT:Q998D2; GB:BA000018; PID:G13702453; PIDN:BAB43594.1; GSPDB:C
A:Experimental source: strain N315
C:Genetics:
A:Gene: fmb

Query Match 96.1%; Score 198; DB 2; Length 1038;
Best Local Similarity 97.4%; Pred. No. 2.4e-17;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Cy 1 QNSGNQSFEDTEBPKRYEGCGNIVDIDFDSVPQIHG 38
|||||
Db 742 QNSGNQSFEDTEBPKRYEGCGNIVDIDFDSVPQIHG 779
|||||

RESULT 5
B84196
cell division protein [imported] - Halobacterium sp. NRC-1
C:Species: Halobacterium sp. NRC-1
C:Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
C:Accession: B84196
R:Ng, W.V.; Kennedy, S.P.; Mahatras, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Lasky, S.; Leitner, K.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Madocke, D.G.; Jablo, Jung, K.H.; Alam, M.; Freitas, T.
Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000
A:Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ehardt, H.; Lowe, T.M.; Li
A:Title: Genome sequence of Halobacterium species NRC-1.
A:Reference number: A84160; MUID:20504483; PMID:11016950
```

```
A:Accession: B84196
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-536 <STO>
A:Cross-references: UNIPROT:Q9HS71; GB:AE004437; NID:G10579993; PIDN:AAI18937.1; GSPDB:G
A:Genetics:
A:Gene: ftsZ1
C:Superfamily: cell division protein ftsZ

Query Match 28.6%; Score 59; DB 2; Length 396;
Best Local Similarity 40.7%; Pred. No. 7.3;
Matches 11; Conservative 6; Mismatches 10; Indels 0; Gaps 0;

Cy 4 GNQSFEDTEBPKRYEGCGNIVDIDF 30
|||||
Db 368 GDGPAQSTPEBPKRYEGCGNIVDIDF 394
|||||

RESULT 6
T48814
hypothetical protein 15B6.220 [imported] - Neurospora crassa
C:Species: Neurospora crassa
C:Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 09-Jul-2004
C:Accession: T48814
R:Schulze, U.; Aign, V.; Hohelsel, J.; Brandt, P.; Fartmann, B.; Holland, R.; Nyakatura,
submitted to the Protein Sequence Database, April 2000
A:Reference number: Z24541
A:Accession: T48814
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1952 <SCH>
A:Cross-references: UNIPROT:Q9PET1; EMBL:AL353822; GSPDB:GN00112; NCSP:15B6.220
A:Experimental source: cosmid contig 15B6; strain 74
C:Genetics:
A:Gene: NCSP:15B6.220
A:Map position: 2
A:Introns: 281/3

Query Match 27.4%; Score 56.5; DB 2; Length 1952;
Best Local Similarity 29.4%; Pred. No. 97;
Matches 10; Conservative 10; Mismatches 13; Indels 1; Gaps 1;

Cy 3 SGNQSFEDTEBPKRYEGCGNIVDIDFDSVPQI 36
|||||
Db 547 TGAEVEPE-ETPARVSEGGKEMSFDESITHV 579
|||||

RESULT 7
S58160
hypothetical protein SPAC2F7.16c - fission yeast (Schizosaccharomyces pombe)
C:Species: Schizosaccharomyces pombe
C:Date: 13-Jan-1996 #sequence_revision 01-Mar-1996 #text_change 09-Jul-2004
C:Accession: T38564; S58160
R:Gentile, S.; Churcher, C.M.; Barrell, B.G.; Rajandream, M.A.; Walsh, S.V.
submitted to the EMBL Data Library, July 1995
A:Reference number: Z21799
A:Accession: T38564
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-1369 <GB2>
A:Cross-references: UNIPROT:Q09706; EMBL:Z50142; NID:G1052783; PIDN:CAA90503.1; PID:G105;
A:Experimental source: strain 972h; cosmid c2F7
C:Genetics:
A:Gene: SPAC2F7.16c
A:Map position: 1
C:Superfamily: phospholipase D, hPLD1 type

Query Match 27.2%; Score 56; DB 2; Length 1369;
Best Local Similarity 38.1%; Pred. No. 75;
Matches 16; Conservative 6; Mismatches 16; Indels 4; Gaps 2;

Cy 1 QNSGNQSFED--TEBPKRYEGCGNIVD--IDFDSVPQIHG 38
|||||
```

Db 1295 QSGNTSASEDSKTEKPKRTNNGIQLVDPKRVVYDLNGIRG 1336

RESULT 8

KBHNR6 DNA-directed RNA polymerase (EC 2.7.7.6) chain RPO26 - yeast (*Saccharomyces cerevisiae*)

N:Alternate names: DNA-directed RNA polymerase 23K chain; DNA-directed RNA polymerase II

C:Species: *Saccharomyces cerevisiae*

C>Date: 30-Sep-1992 #sequence_revision 30-Sep-1992 #text_change 09-Jul-2004

C:Accession: S13307; A36352; B34588; A38846; S58817

R:Archambault, J.; Schappert, K.T.; Friesen, J.D.

Mol. Cell. Biol. 10, 6123-6131, 1990

A:Title: A suppressor of an RNA polymerase II mutation of *Saccharomyces cerevisiae* encodes

A:Reference number: A36352; MUID:91061718; PMID:2247052

A:Accession: S13307

A:Molecule type: DNA

A:Residues: 1-155 <ARCI>

A:Cross-references: UNIPROT:P20435; EMBL:M33924; NID:G172452; PIDN:AAA34989.1; PID:G1724

A:Accession: A36352

A:Molecule type: mRNA

A:Residues: 1-155 <ARCI>

A:Cross-references: GB:M33924; NID:G172452; PIDN:AAA34989.1; PID:G172453

R:Woychik, N.A.; Liao, S.W.; Kolodziej, P.A.; Young, R.A.

Gene Dev. 4, 313-323, 1990

A:Title: Subunits shared by eukaryotic nuclear RNA polymerases.

A:Reference number: A34588; MUID:90249736; PMID:2186966

A:Accession: B34588

A:Status: not compared with conceptual translation

A:Molecule type: DNA

A:Residues: 1-155 <WOY1>

A:Cross-references: GB:X53288; NID:G287823; PIDN:CAA37382.1; PID:G287824

A:Accession: A38846

A:Molecule type: protein

A:Residues: 48-60/99-115 <WOY2>

R:Miller, N.

submitted to the EMBL Data Library, April 1995

A:Description: The sequence of *S. cerevisiae* cosmid 9677.

A:Reference number: S58816

A:Accession: S58817

A:Molecule type: DNA

A:Residues: 1-155 <MIL>

A:Cross-references: EMBL:U5841; NID:G786295; PIDN:AA64616.1; PID:G786304; GSPDB:GN0001

C:Comment: This protein is a subunit of DNA-directed RNA polymerase I, II, and III.

C:Genetics:

A:Gene: SGD:RPO26; RPB6; MIPS:YPR187W

A:Cross-references: SGD:S0006391; MIPS:YPR187W

A:Map position: 16R

A:Introns: 7/2

C:Superfamily: DNA-directed RNA polymerase chain RPO26

C:Keywords: nucleotidyltransferase

F:3-42/Region: acidic

F:65-97/Region: basic

Query Match 26.5%; Score 54.5; DB 1; Length 155;

Best Local Similarity 36.7%; Pred. No. 9.4;

Matches 11; Conservative 6; Mismatches 4; Indels 9; Gaps 1;

QY 2 NSGNQSFRE-----EDDEPRPKKEOG 22

DB 9 NDGNENFEDVDFHFSDEETYEKPQPKDG 38

RESULT 9

T32952

hypothetical protein C15B6.1 - *Caenorhabditis elegans*

C:Species: *Caenorhabditis elegans*

C>Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999

C:Accession: T32952

R:Rolling, T.; Biewald, T.

submitted to the EMBL Data Library, February 1998

A:Description: The sequence of *C. elegans* cosmid C15B6.

A:Reference number: Z21253

A:Accession: T32952

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-428 <ROH>

A:Cross-references: EMBL:AF045636; PIDN:AAC02359.1; GSPDB:GN00022; CESP:C15B6.1

A:Experimental source: strain Bristol N2; clone C15B6

C:Genetics:

A:Gene: CESP:C15B6.1

A:Map position: 4

A:Introns: 124/2; 196/3

Query Match 26.5%; Score 54.5; DB 2; Length 428;

Best Local Similarity 46.2%; Pred. No. 31;

Matches 12; Conservative 3; Mismatches 10; Indels 1; Gaps 1;

QY 13 EEPKPK-YEQQNIYDIDFDSVPQIH 37

DB 246 EKPKEKAIKPAFDNAYDADFNPSPLH 271

RESULT 10

H84854

probable ATP-dependent RNA helicase [imported] - *Arabidopsis thaliana*

C:Species: *Arabidopsis thaliana* (mouse-ear cress)

C>Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004

C:Accession: H84854

R:Lin, X.; Kaul, S.; Rounsaey, S.D.; Shea, T.P.; Bentol, M.I.; Town, C.D.; Fujii, C.Y.;

M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Venkatesh, S.E.; Umayam, L.; Tallon, L.

enes, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.

Nature 402, 761-768, 1999

A:Title: Sequence and analysis of chromosome 2 of the plant *Arabidopsis thaliana*.

A:Reference number: A84420; MUID:20083487; PMID:10617197

A:Accession: H84854

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-633 <STO>

A:Cross-references: UNIPROT:Q9SIN6; GB:AE002093; NID:G4559339; PIDN:AA23001.1; GSPDB:GN0

C:Genetics:

A:Gene: At2g42520

A:Map position: 2

C:Superfamily: ATP-dependent RNA helicase DBPI

Query Match 26.5%; Score 54.5; DB 2; Length 633;

Best Local Similarity 41.4%; Pred. No. 48;

Matches 12; Conservative 5; Mismatches 11; Indels 1; Gaps 1;

QY 8 FEEDTEPRKPKYEQGNIVDIDFDSVPQI 36

DB 118 FENDSEPEPAPFTQDNV-INDAYEDI 145

RESULT 11

C81209

tspp protein NMB0341 [imported] - *Neisseria meningitidis* (strain MCS8 serogroup B)

C:Species: *Neisseria meningitidis*

C>Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004

C:Accession: C81209

R:Teitelin, H.; Saunders, N.J.; Heideberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.A.

Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.;

ri, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Maignani, V.; Piazza, M.

Science 287, 1809-1815, 2000

A:Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; Ver

A:Title: Complete genome sequence of *Neisseria meningitidis* serogroup B strain MCS8.

A:Reference number: A81000; MUID:20157535; PMID:10710307

A:Accession: C81209

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-875 <TET>

A:Cross-references: UNIPROT:Q9K147; GB:AE002391; GB:AE002098; NID:G7225561; PIDN:AAF40784

A:Experimental source: serogroup B, strain MCS8

C:Genetics:

A:Gene: NMB0341

Query Match 26.5%; Score 54.5; DB 2; Length 875;

OY

Best Local Similarity 35.5%; Pred. No. 70; Matches 11; Conservative 7; Mismatches 6; Indels 7; Gaps 1;

Db

3 SGNOSFEEDTEEPKPYEQGNIIVIDFDSV 33
| | : : : | | : : ||||:
460 SAKOTFDVETDTP-----SNRIDLDFDSL 483

RESULT 12

G81796
Neisseria-specific antigen protein, Tspa NMA2146 [imported] - Neisseria meningitidis (strain C)
CDate: 05-May-2000 #sequence_revision 05-May-2000 #text_change 09-Jul-2004
Accession: G81786
R.Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morel, R.; Holtzoyd, S.; Jagoele, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandream, Nature 404, 502-506, 2000
A>Title: Complete DNA sequence of a serogroup A strain of Neisseria meningitidis Z2491.
A:Reference number: AB1775; PMID:2022256; PMID:10761919
A:Accession: G81786
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-880 <PAR>
A:Cross-references: UNIPROT:Q9JST3; GB:A1162758; GB:A1157959; NID:g7380672; PIDN:CA88533
A:Experimental source: serogroup A, strain Z2491
A:Genetics:

A:Gene: tspa; NMA2146

Query Match

Best Local Similarity 35.5%; Score 54.5; DB 2; Length 880; Matches 11; Conservative 7; Mismatches 6; Indels 7; Gaps 1;

OY

3 SGNOSFEEDTEEPKPYEQGNIIVIDFDSV 33
| | : : : | | : : ||||:
456 SAKOTFDVETDTP-----SNRIDLDFDSL 479

RESULT 13

D82053
fibrial assembly protein VCB2630 [imported] - Vibrio cholerae (strain N16961 serogroup C)
CDate: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
Accession: D82053
R.Heldberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwin, M.L.; Dodson, R.J.; charadon, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoti, I.; Sellere, F. l., R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M. Nature 406, 477-483, 2000
A>Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A:Reference number: AB2035; PMID:2040683; PMID:10952301
A:Accession: D82053
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-578 <HEI>
A:Cross-references: UNIPROT:Q9KNV0; GB:AE004329; GB:AE003852; NID:g9657211; PIDN:AAF9577577
A:Experimental source: serogroup O1; strain N16961; biotype El Tor
A:Genetics:

A:Gene: VCB2630
A:Map position: 1

Query Match

Best Local Similarity 41.7%; Score 54; DB 2; Length 578; Matches 10; Conservative 6; Mismatches 6; Indels 2; Gaps 1;

OY

13 EEPKPK--YEQGNIIVIDFDSVP 34
|:||||| |: |: |:| :
151 EKPRKSYLEKGKLISINFODIP 174

RESULT 14

S31850
fibrinectin-binding protein - Streptococcus dysgalactiae
CDate: 06-Jan-1995 #sequence revision 06-Jan-1995 #text change 09-Jul-2004
SDate: 06-Jan-1995 #sequence revision 06-Jan-1995 #text change 09-Jul-2004

```

C:Accession: S33850; S32632
R:Rindgren, P.E.; McGavin, M.J.; Signaes, C.; Guse, B.; Gurusiddappa, S.; Hoeoek, M.; Lih
Eur. J. Biochem. 214, 819-827, 1993
A>Title: Two different genes coding for fibronectin-binding proteins from Streptococcus c
A:Reference number: S33850; MUID:93307299; PMID:8319691
A:Accession: S33850
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1091 <LIN>
A:Cross-references: UNIPROT:006556; EMBL:Z22150; NID:g288968; PIDN:CAA80121.1; PID:g288968

Query Match          26.2%  Score 54;  DB 2;  Length 1091;
Beet Local Similarity 34.2%  Pred. No. 1e+02;
Matches 13;  Conservative 7;  Mismatches 16;  Indels 2;  Gaps 1;

QY      3  SGNQSFEDTTEPKPKYEQG--GNIVDIDFDSVPQIHG 38
      |||::|||::|::|::|::|::|::|::|::|
DB      843  SGNETVVEDTQTSQEDIVLGGPQGVIDFTEDSGPGMSG 880

RESULT 15
DB1675
polymorphic membrane protein B/C family TC0695 [imported] - Chlamydia muridarum (strain
C:Species: Chlamydia muridarum, Chlamydia trachomatis Mopn
C:Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004
C:Accession: DB1675
R:Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hickey,
, C.; Dodson, R.; Gwinn, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salzberg,
Nucleic Acids Res. 28, 1397-1406, 2000
A>Title: Genome sequences of Chlamydia trachomatis Mopn and Chlamydia pneumoniae AR39.
A:Reference number: AB1500; MUID:20150255; PMID:10684935
A:Accession: DB1675
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1460 <TEP>
A:Cross-references: UNIPROT:Q9PJY1; GB:AE002338; GB:AE002160; NID:g7190724; PIDN:AAF39511
A:Experimental source: strain N199 (Mopn)
C:Genetics:
A:Gene: TC0695

Query Match          26.2%  Score 54;  DB 2;  Length 1460;
Beet Local Similarity 32.4%  Pred. No. 1.5e+02;
Matches 11;  Conservative 8;  Mismatches 15;  Indels 0;  Gaps 0;

QY      2  NSGNQSFEDTTEPKPKYEQGNIIVDIDFDSVPQ 35
      |:|::|||::|::|::|::|::|::|::|
DB      39  SSSSQSFTEIIPENGAEYRVSGDVSFSDSNIDE 72

Search completed: October 22, 2005, 06:09:48
Job time : 13.8905 secs

```

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 22, 2005, 04:10:49 ; Search time 69.6361 Seconds
(without alignments)
279.439 Million cell updates/sec

Title: US-10-731-238-42
Perfect score: 206
Sequence: 1 QNSGNQSFEDTDEPKYKYGCGNIVDIDFDSVPQIHG 38

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	* Query Match Length	DB ID	Description
1	198	96.1	940 2 Q53682	Q53682 staphylococ
2	198	96.1	943 2 Q8NTU8	Q8NTU8 staphylococ
3	198	96.1	957 2 Q6G6H4	Q6G6H4 staphylococ
4	198	96.1	961 2 Q99RD3	Q99RD3 staphylococ
5	198	96.1	961 2 Q7A3J8	Q7A3J8 staphylococ
6	198	96.1	1018 1 FNBA_STRAU	FNBA_STRAU
7	198	96.1	1038 2 Q99RD2	Q99RD2 staphylococ
8	198	96.1	1038 2 Q7A3J7	Q7A3J7 staphylococ
9	197	95.6	965 2 Q6GDU5	Q6GDU5 staphylococ
10	190	92.2	1015 2 Q8NTU7	Q8NTU7 staphylococ
11	190	92.2	1015 2 Q6G6H3	Q6G6H3 staphylococ
12	187	90.8	152 2 Q9AEP9	Q9AEP9 staphylococ
13	65	31.6	937 2 Q6BM10	Q6BM10 debaryomyce
14	64.5	31.3	191 2 Q6BWS4	Q6BWS4 debaryomyce
15	60	29.1	745 2 Q7SA69	Q7SA69 neurospora
16	59	28.6	396 2 Q9HS71	Q9HS71 halobacteri
17	59	28.6	849 2 Q8CGV1	Q8CGV1 mus musculu
18	59	28.6	852 2 Q8OV99	Q8OV99 mus musculu
19	59	28.6	853 2 Q8BK66	Q8BK66 mus musculu
20	59	28.6	853 2 Q8CUC3	Q8CUC3 mus musculu
21	59	28.6	1246 2 Q7UKY7	Q7UKY7 rhodospirill
22	58.5	28.4	1015 2 Q6FRF8	Q6FRF8 candida gla
23	58	28.2	457 2 Q9GDV3	Q9GDV3 carboxibrotu
24	58	28.2	889 2 Q6CBW0	Q6CBW0 yarrowia 11
25	58	28.2	933 1 NP43_HUMAN	NP43_HUMAN
26	58	28.2	981 2 Q91LJ7	Q91LJ7 white spot
27	57.5	27.9	1791 2 Q8IH44	Q8IH44 plasmodium
28	57	27.7	154 2 Q7OKZ7	Q7OKZ7 anopheles g
29	57	27.7	499 2 Q7QGF7	Q7QGF7 anopheles g
30	57	27.7	565 2 Q6PUB5	Q6PUB5 anopheles g
31	57	27.7	968 1 PRD2_HUMAN	PRD2_HUMAN

32	57	27.7	2641 2 Q9BXD4	Q9BXD4 homo sapien
33	57	27.7	2847 2 Q15018	Q15018 homo sapien
34	56.5	27.4	441 1 S18_THREAC	S18_THREAC
35	56.5	27.4	1992 2 Q9P6T1	Q9P6T1 neurospora
36	56	27.2	312 2 Q6VSH9	Q6VSH9 staphylococ
37	56	27.2	1369 1 YAZG_SCHPO	YAZG_SCHPO
38	56	27.2	1848 2 Q6CNT6	Q6CNT6 kluyveromyc
39	55.5	26.9	101 2 Q68YU3	Q68YU3 vaccinium c
40	55.5	26.9	469 2 Q9KMT3	Q9KMT3 vibrio algi
41	55.5	26.9	667 2 Q7X994	Q7X994 oryza sativ
42	55	26.7	81 2 Q8AK01	Q8AK01 human immun
43	55	26.7	81 2 Q8AK10	Q8AK10 human immun
44	55	26.7	674 2 Q9FIF1	Q9FIF1 arabidopsis
45	55	26.7	677 2 Q9YVC7	Q9YVC7 drosophila

ALIGNMENTS

RESULT 1	Q53682	PRELIMINARY;	PRT;	940 AA.
ID	Q53682			
AC	Q53682			
DT	01-NOV-1996 (TREMBLrel. 01, Created)			
DT	01-NOV-1996 (TREMBLrel. 01, Last sequence update)			
DE	01-MAR-2004 (TREMBLrel. 26, Last annotation update)			
DE	Fibronectin binding protein B.			
GN	Name=fnbB;			
OS	Staphylococcus aureus.			
OC	Bacteria; Firmicutes; Bacillales; Staphylococcus.			
OX	NCBI_TaxID=1280;			
RN	(1)			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=8325-4;			
RX	MEDLINE=92111475; PubMed=1837266;			
RA	Johnson K., Signas C., Muller H.P., Lindberg M.;			
RT	"Two different genes encode fibronectin binding proteins in			
RT	Staphylococcus aureus. The complete nucleotide sequence and			
RT	characterization of the second gene."			
RL	Eur. J. Biochem. 202:1041-1048 (1991).			
CC	-1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by			
CC	an amide bond (By similarity).			
DR	EMBL: X62992; CAA44726.1; -			
DR	PIR: S19702; S19702.			
DR	HSSP: Q53653; IN67.			
DR	GO: GO:0009986; C:cell surface; IEA.			
DR	GO: GO:0005618; C:cell wall; IEA.			
DR	GO: GO:0009775; C:cell wall (sensu Gram-positive Bacteria); IEA.			
DR	GO: GO:0016020; C:membrane; IEA.			
DR	GO: GO:0007155; P:cell adhesion; IEA.			
DR	InterPro: IPR008966; Adhes_Dact.			
DR	InterPro: IPR004237; Fn_Bind.			
DR	InterPro: IPR005877; Gpos_YsIRK.			
DR	InterPro: IPR001899; Gram_pos_anchor.			
DR	Pfam: PF02986; Fn_Bind; 2.			
DR	Pfam: PF00746; Gram_pos_anchor; 1.			
DR	Pfam: PF04650; YsIRK_signal; 1.			
DR	TIGRFAMs: TIGR01167; LPXTG_anchor; 1.			
DR	TIGRFAMs: TIGR01168; YsIRK_signal; 1.			
DR	PROSITE: PSS0847; GRAM_POS_ANCHORING; 1.			
DR	Cell wall; peptidoglycan-anchor.			
KW	SEQUENCE 940 AA; 103555 MW; E35FBBCA907AE345 CRC64;			
QY	Query Match	96.1%;	Score 198;	DB 2; Length 940;
Db	Best Local Similarity	97.4%;	Pred. No. 5.2e-16;	
	Matches 37; Conservative	0;	Mismatches 1;	Indels 0; Gaps 0;
	1 QNSGNQSFEDTDEPKYKYGCGNIVDIDFDSVPQIHG 38			
	682 QNSGNQSFEDTDEPKYKYGCGNIVDIDFDSVPQIHG 719			
RESULT 2				

```
Q8NTU8      O8NTU8      PRELIMINARY;      PRT;      943 AA.
AC      O8NTU8.
DT      01-OCT-2002 (TReMBLrel. 22, Created)
DT      01-OCT-2002 (TReMBLrel. 22, Last annotation update)
DT      01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE      FndB protein.
GN      Name=fndB; OrderedLocusNames=MM2420;
OS      Staphylococcus aureus (strain MM2).
OC      Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX      NCBI_TaxID=196620;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN=MM2;
RX      MEDLINE=22040717; PubMed=12044378; DOI=10.1016/S0140-6736(02)08713-5;
RA      Baba T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Oguchi A.,
RA      Yamamoto K., Hiramatsu K.;
RT      "Genome and virulence determinants of high virulence community-
RT      acquired MRSA.";
RL      Lancet 359:1819-1827(2002).
CC      -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC      an amide bond (By similarity).
DR      HSSP; Q53653; 1n67.
DR      GO; GO:0009986; C:cell surface; IEA.
DR      GO; GO:0005618; C:cell wall; IEA.
DR      GO; GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR      GO; GO:0016020; C:membrane; IEA.
DR      GO; GO:007155; P:cell adhesion; IEA.
DR      InterPro; IPR008966; Adhes_bact.
DR      InterPro; IPR004237; Fn_bind.
DR      InterPro; IPR005877; Gpos_YsIRK.
DR      InterPro; IPR001899; Gram_pos_anchor.
DR      Pfam; PF02986; Fn_bind; 1.
DR      Pfam; PF00746; Gram_pos_anchor; 1.
DR      TIGRFAMs; TIGR01167; LpxTG_anchor; 1.
DR      TIGRFAMs; TIGR01168; YsIRK_signal; 1.
DR      PROSITE; PS50847; GRAM_POS_ANCHORING; 1.
KW      Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ      SEQUENCE 943 AA; 104537 MW; DA8A5F31947B1B6A CRC64;

Query Match      96.1%; Score 198; DB 2; Length 943;
Best Local Similarity 97.4%; Pred. No. 5.2e-16;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 QNSGNQSFEDTPEPKPYEQGNIIVIDFDSVPQIHG 38
DB      689 QNSGNQSFEDTPEPKPYEQGNIIVIDFDSVPQIHG 726

RESULT 3
Q6G6H4      PRELIMINARY;      PRT;      957 AA.
AC      Q6G6H4.
DT      05-JUN-2004 (TReMBLrel. 27, Created)
DT      05-JUN-2004 (TReMBLrel. 27, Last sequence update)
DT      05-JUN-2004 (TReMBLrel. 27, Last annotation update)
DE      Fibronectin-binding protein.
GN      Name=fnbB; OrderedLocusNames=SA52387;
OS      Staphylococcus aureus (strain MSS4476).
OC      Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX      NCBI_TaxID=282459;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      PubMed=15213324; DOI=10.1073/pnas.0402521101;
RA      Holden M.T.G., Fell J.E.J., Lindsay J.A., Peacock S.J., Day N.P.J.,
RA      Enright M.C., Foster T.J., Moore C.E., Hurst L., Atkin R., Barron A.,
RA      Bacon N., Bentley S.D., Chillingworth C., Chillingworth T.,
RA      Churcher C., Clark L., Cotton C., Cronin A., Doggett J., Dowd L.,
RA      Felwell T., Hance Z., Harris B., Hauser H., Holtroyd S., Jagsels K.,
RA      James K.D., Lennard N., Line A., Mayes R., Moule S., Mungall K.,
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RA      Ormond D., Quail M.A., Rabinowitsch E., Rutherford K.M., Sanders M.,
RA      Sharp S., Simmonds M., Stevens K., Whitehead S., Barrell B.G.,
RT      "Complete genomes of two clinical Staphylococcus aureus strains:
RT      evidence for the rapid evolution of virulence and drug resistance.";
RL      Proc. Natl. Acad. Sci. U.S.A. 101:9786-9791(2004).
CC      -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC      an amide bond (By similarity).
DR      EMBL; BX571857; CAG44201.1; -.
DR      GO; GO:0009986; C:cell surface; IEA.
DR      GO; GO:0005618; C:cell wall; IEA.
DR      GO; GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR      GO; GO:0016020; C:membrane; IEA.
DR      GO; GO:007155; P:cell adhesion; IEA.
DR      InterPro; IPR008966; Adhes_bact.
DR      InterPro; IPR004237; Fn_bind.
DR      InterPro; IPR005877; Gpos_YsIRK.
DR      InterPro; IPR001899; Gram_pos_anchor.
DR      Pfam; PF02986; Fn_bind; 1.
DR      Pfam; PF00746; Gram_pos_anchor; 1.
DR      TIGRFAMs; TIGR01167; LpxTG_anchor; 1.
DR      TIGRFAMs; TIGR01168; YsIRK_signal; 1.
DR      PROSITE; PS50847; GRAM_POS_ANCHORING; 1.
KW      Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ      SEQUENCE 957 AA; 105980 MW; 28F8BA7FFDFD3EAF CRC64;

Query Match      96.1%; Score 198; DB 2; Length 957;
Best Local Similarity 97.4%; Pred. No. 5.3e-16;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 QNSGNQSFEDTPEPKPYEQGNIIVIDFDSVPQIHG 38
DB      689 QNSGNQSFEDTPEPKPYEQGNIIVIDFDSVPQIHG 726

RESULT 4
Q99RD3      PRELIMINARY;      PRT;      961 AA.
AC      Q99RD3.
DT      01-JUN-2001 (TReMBLrel. 17, Created)
DT      01-JUN-2001 (TReMBLrel. 17, Last sequence update)
DT      01-JUN-2003 (TReMBLrel. 24, Last annotation update)
DE      Fibronectin-binding protein homolog.
GN      Name=fnbB; OrderedLocusNames=SAV2502;
OS      Staphylococcus aureus (strain Mu50 / ATCC 700699).
OC      Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX      NCBI_TaxID=158878;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN=Mu50 / ATCC 700699;
RX      MEDLINE=21311952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2;
RA      Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
RA      Cui L., Oguchi A., Aoki K.-I., Nagai Y., Iian J.-O., Ito T.,
RA      Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,
RA      Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
RA      Sekimizu K., Hiramatsu H., Kuhara S., Goto S., Yabuzaki J.,
RA      Kanehisa M., Yamashta A., Oshima K., Furuya K., Yoshino C., Shiba T.,
RA      Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
RT      "Whole genome sequencing of methicillin-resistant Staphylococcus
RT      aureus.";
RL      Lancet 357:1225-1240(2001).
CC      -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC      an amide bond (By similarity).
DR      EMBL; AP003365; BAB58664.1; -.
DR      PIR; G90053; G90053.
DR      HSSP; Q53653; 1n67.
DR      GO; GO:0009986; C:cell surface; IEA.
DR      GO; GO:0005618; C:cell wall; IEA.
DR      GO; GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR      GO; GO:0016020; C:membrane; IEA.
DR      GO; GO:007155; P:cell adhesion; IEA.
DR      InterPro; IPR008966; Adhes_bact.
```

```

DR InterPro; IPR004237; Fn_bind.
DR InterPro; IPR005877; Gpos_YsIRK.
DR InterPro; IPR001899; Gram_pos_anchor.
DR Pfam; PF02986; Fn_bind; 1.
DR Pfam; PF00746; Gram_pos_anchor; 1.
DR Pfam; PF04650; YsIRK_signal; 1.
DR TIGRFAMs; TIGR01167; LpXTG_anchor; 1.
DR TIGRFAMs; TIGR01168; YsIRK_signal; 1.
DR PROSITE; PS50847; GRAM_POS_ANCHORING; 1.
DR Cell wall; Complete proteome; Peptidoglycan-anchor.
KW Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ SEQUENCE 961 AA; 106010 MW; 364940F884EA4101 CRC64;

Query Match 96.1%; Score 198; DB 2; Length 961;
Best Local Similarity 97.4%; Pred. No. 5.3e-16;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QNSGNQSFEDTEBPKRYEGCGNIVDIDFDSVPQIHG 38
DB 693 QNSGNQSFEDTEBPKRYEGCGNIVDIDFDSVPQIHG 730

RESULT 5
ID 07A3J8 PRELIMINARY; PRT; 961 AA.
AC 07A3J8;
DT 05-JUL-2004 (TReMBLrel. 27, Created)
DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TReMBLrel. 27, Last annotation update)
DE FnBb protein.
OS Name=fnBb; OrderedLocustNames=SA2290;
OC Staphylococcus aureus (strain N315).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_Taxid=158879;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=2111952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2;
RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Iian J.-Q., Ito T.,
RA Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,
RA Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
RA Sekimizu K., Hirakawa H., Kohara S., Goto S., Yabuuchi J.,
RA Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
RA Hattori M., Ogasawara N., Hayashi H., Hiratake K.,
RT "Whole genome sequencing of methicillin-resistant Staphylococcus
RT aureus";
RL Lancel 357:1225-1240(2001).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC an amide bond (By similarity).
CC EMBL; AP003137; BAB43593.1; -.
DR GO; GO:000986; C:cell surface; IEA.
DR GO; GO:0005618; C:cell wall; IEA.
DR GO; GO:000975; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0007155; P:cell adhesion; IEA.
DR InterPro; IPR008966; Adhes_Dact.
DR InterPro; IPR004237; Fn_bind.
DR InterPro; IPR005877; Gpos_YsIRK.
DR InterPro; IPR001899; Gram_pos_anchor.
DR Pfam; PF02986; Fn_bind; 1.
DR Pfam; PF00746; Gram_pos_anchor; 1.
DR Pfam; PF04650; YsIRK_signal; 1.
DR TIGRFAMs; TIGR01167; LpXTG_anchor; 1.
DR TIGRFAMs; TIGR01168; YsIRK_signal; 1.
DR PROSITE; PS50847; GRAM_POS_ANCHORING; 1.
KW Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ SEQUENCE 961 AA; 106010 MW; 364940F884EA4101 CRC64;

Query Match 96.1%; Score 198; DB 2; Length 961;
Best Local Similarity 97.4%; Pred. No. 5.3e-16;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QNSGNQSFEDTEBPKRYEGCGNIVDIDFDSVPQIHG 38
DB 693 QNSGNQSFEDTEBPKRYEGCGNIVDIDFDSVPQIHG 730

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DB 693 QNSGNQSFEDTEBPKRYEGCGNIVDIDFDSVPQIHG 730

RESULT 6
ID FNBA_STAAU STANDARD; PRT; 1018 AA.
AC P14738;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Fibronectin-binding protein precursor (FNBP).
GN Name=fnBA;
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_Taxid=1280;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NCTC 8325-4;
RX MEDLINE=89098998; PubMed=2521391;
RA Signas C., Raucel G., Joensson K., Lindgren P.-E.,
RA Anantharamaiah G.M., Hoesek M., Lindberg M.;
RT "Nucleotide sequence of the gene for a fibronectin-binding protein
RT from Staphylococcus aureus: use of this peptide sequence in the
RT synthesis of biologically active peptides.";
RL Proc. Natl. Acad. Sci. U.S.A. 86:699-703(1989).
CC -1- FUNCTION: The ability of bacteria to bind fibronectin has been
CC proposed as a virulence factor enabling bacteria to colonize wound
CC tissues and blood clots. Binding of plasma fibronectin to the
CC bacterial surface might block adhesion receptors on S.aureus, thus
CC representing an important defense mechanism against tissue
CC invasion.
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC an amide bond (Potential).
CC CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement and its license agreement (See
CC http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC CC
DR EMBL; J04151; AAA26632.1; -.
DR InterPro; IPR004237; Fn_bind.
DR InterPro; IPR005877; Gpos_YsIRK.
DR InterPro; IPR001899; Gram_pos_anchor.
DR Pfam; PF02986; Fn_bind; 1.
DR Pfam; PF00746; Gram_pos_anchor; 1.
DR Pfam; PF04650; YsIRK_signal; 1.
DR TIGRFAMs; TIGR01167; LpXTG_anchor; 1.
DR TIGRFAMs; TIGR01168; YsIRK_signal; 1.
DR PROSITE; PS50847; GRAM_POS_ANCHORING; 1.
KW Cell adhesion; Cell wall; Peptidoglycan-anchor; Repeat; Signal;
KW Virulence.
FT SIGNAL 1 36
FT CHAIN 37 985
FT PROPEP 986 1018
FT REPEAT 545 574
FT REPEAT 575 604
FT DOMAIN 745 878
FT REPEAT 745 782
FT REPEAT 783 820
FT REPEAT 821 859
FT REPEAT 860 878
FT DOMAIN 879 948
FT REPEAT 879 892
FT REPEAT 893 906
FT REPEAT 907 920
FT REPEAT 921 934
FT REPEAT 935 948
FT SITE 982 985
FT MOD_RES 985 985

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Pentaglycyl murein peptidoglycan amidated
 LpXTG sorting signal (Potential).
 WR 4.
 WR 5.
 WR 3.
 WR 2.
 WR 1.
 D-4 (incomplete).
 D-3.
 D-2.
 B-1.
 B-2.
 4 X approximate tandem repeats,
 fibronectin-binding domain.
 D-1.
 Removed by sortase (Potential).
 Fibronectin-binding protein.
 1.

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FT          chreonine (Potential).
SQ  SEQUENCE      1018 AA;  11780 MW;  58175E0020881F CRC64;
Query Match      96.1%; Score 198; DB 1; Length 1018;
Best Local Similarity 97.4%; Pred. No. 5.7e-16;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy          1  QNSGNQSFEDTEBPKRYEGGNIIVDIDFDSVPQIHG 38
Db          746  QNSGNQSFEDTEBPKRYEGGNIIVDIDFDSVPQIHG 783

RESULT 7
ID  Q099RD2      PRELIMINARY;      PRT; 1038 AA.
AC  Q099RD2;
DT  01-JUN-2001 (TREMBLrel. 17, Created)
DT  01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT  01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE  Fibronectin-binding protein homolog.
GN  Name=fnb; OrderedLocustNames=SAV2503;
OC  Staphylococcus aureus (strain Mu50 / ATCC 700699).
OC  Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX  NCBI_TaxID=158878;

RN  [1]
RP  SEQUENCE FROM N.A.
RC  STRAIN=mu50 / ATCC 700699;
RX  MEDLINE=21311952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2;
RA  Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
RA  Cui L., Oguchi A., Aoki K.-I., Nagai Y., Iian J.-Q., Ito T.,
RA  Kanamori M., Matsumaru H., Maruyama A., Murakami H., Haseyama A.,
RA  Mizutani M., Takahashi N.K., Sawano T., Inoue R.-I., Kato C.,
RA  Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
RA  Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
RA  Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
RT  "Whole genome sequencing of methicillin-resistant Staphylococcus
RT  aureus.";
RL  Lancer 357:1225-1240(2001).
CC  -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC  an amide bond (by similarity).
DR  EMBL; AP003365; BAB58665.1; -.
DR  PIR; H90053; H90053.
DR  GO; GO:0009986; C:cell surface; IEA.
DR  GO; GO:0005618; C:cell wall; IEA.
DR  GO; GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR  GO; GO:0016020; C:membrane; IEA.
DR  GO; GO:007155; P:cell adhesion; IEA.
DR  InterPro; IPR008966; Adhes_bact.
DR  InterPro; IPR004237; Fn_bind.
DR  InterPro; IPR005877; Gpos_YsIRK.
DR  InterPro; IPR001899; Gram_pos_anchor.
DR  Pfam; PF02986; Fn_bind; 1.
DR  Pfam; PF00746; Gram_pos_anchor; 1.
DR  Pfam; PF04650; YsIRK_signal; 1.
DR  TIGRfams; TIGR01167; LPXTG_anchor; 1.
DR  TIGRfams; TIGR01168; YsIRK_signal; 1.
DR  PROSITE; PS50847; GRAM_POS_ANCHORING; 1.
KW  Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ  SEQUENCE 1038 AA; 113618 MW; 6668F6BF2BFBB12 CRC64;

Query Match      96.1%; Score 198; DB 2; Length 1038;
Best Local Similarity 97.4%; Pred. No. 5.9e-16;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy          1  QNSGNQSFEDTEBPKRYEGGNIIVDIDFDSVPQIHG 38
Db          742  QNSGNQSFEDTEBPKRYEGGNIIVDIDFDSVPQIHG 779

RESULT 8
ID  Q7A3J7      PRELIMINARY;      PRT; 1038 AA.
AC  Q7A3J7;

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DT  05-JUL-2004 (TREMBLrel. 27, Created)
DT  05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DT  05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE  Fnb protein.
GN  Name=fnb; OrderedLocustNames=SA2291;
OS  Staphylococcus aureus (strain N315).
OC  Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX  NCBI_TaxID=158879;

RN  [1]
RP  SEQUENCE FROM N.A.
RC  MEDLINE=21311952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2;
RA  Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
RA  Cui L., Oguchi A., Aoki K.-I., Nagai Y., Iian J.-Q., Ito T.,
RA  Kanamori M., Matsumaru H., Maruyama A., Murakami H., Haseyama A.,
RA  Mizutani M., Takahashi N.K., Sawano T., Inoue R.-I., Kato C.,
RA  Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
RA  Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
RA  Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
RT  "Whole genome sequencing of methicillin-resistant Staphylococcus
RT  aureus.";
RL  Lancer 357:1225-1240(2001).
CC  -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC  an amide bond (by similarity).
DR  EMBL; AP003137; BAB43594.1; -.
DR  GO; GO:0009986; C:cell surface; IEA.
DR  GO; GO:0005618; C:cell wall; IEA.
DR  GO; GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR  GO; GO:0016020; C:membrane; IEA.
DR  GO; GO:007155; P:cell adhesion; IEA.
DR  InterPro; IPR008966; Adhes_bact.
DR  InterPro; IPR004237; Fn_bind.
DR  InterPro; IPR005877; Gpos_YsIRK.
DR  InterPro; IPR001899; Gram_pos_anchor.
DR  Pfam; PF02986; Fn_bind; 1.
DR  Pfam; PF00746; Gram_pos_anchor; 1.
DR  Pfam; PF04650; YsIRK_signal; 1.
DR  TIGRfams; TIGR01167; LPXTG_anchor; 1.
DR  TIGRfams; TIGR01168; YsIRK_signal; 1.
DR  PROSITE; PS50847; GRAM_POS_ANCHORING; 1.
KW  Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ  SEQUENCE 1038 AA; 113618 MW; 6668F6BF2BFBB12 CRC64;

Query Match      96.1%; Score 198; DB 2; Length 1038;
Best Local Similarity 97.4%; Pred. No. 5.9e-16;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy          1  QNSGNQSFEDTEBPKRYEGGNIIVDIDFDSVPQIHG 38
Db          742  QNSGNQSFEDTEBPKRYEGGNIIVDIDFDSVPQIHG 779

RESULT 9
ID  Q6GDUS      PRELIMINARY;      PRT; 965 AA.
AC  Q6GDUS;
DT  05-JUL-2004 (TREMBLrel. 27, Created)
DT  05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DT  05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE  Fibronectin-binding protein.
GN  Name=fnbA; OrderedLocustNames=SA2580;
OS  Staphylococcus aureus (strain MRSA252).
OC  Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX  NCBI_TaxID=282458;

RN  [1]
RP  SEQUENCE FROM N.A.
RC  PubMed=15213324; DOI=10.1073/pnas.0402521101;
RX  Holden M.T.G., Feil E.J., Lindsay J.A., Peacock S.J., Day N.P.J.,
RA  Enright M.C., Foster T.J., Moore C.E., Hurst L., Atkin R., Barron A.,
RA  Baason N., Bentley S.D., Chillingworth C., Chillingworth T.,
RA  Churcher C., Clark L., Cotton C., Cronin A., Doggett J., Dowd L.,
RA  Felwell T., Hance Z., Harris B., Hauser H., Holtroyd S., Jagels K.,
RA  James K.D., Lennard N., Line A., Mayes R., Moule S., Mungall K.,
RA  Ormond D., Quail M.A., Rabinowitsch E., Rutherford K.M., Sanders M.,

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RA Sharp S., Simmonds M., Stevens K., Whitehead S., Barrell B.G.,
 RA Spratt B.G., Parkhill J.;
 RT "Complete genomes of two clinical *Staphylococcus aureus* strains:
 RT evidence for the rapid evolution of virulence and drug resistance";
 RL Proc. Natl. Acad. Sci. U.S.A. 101:9786-9791(2004).
 CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
 CC an amide bond (By similarity).
 DR EMBL: BX571856; CAG41560.1; -;
 DR GO: GO:0009986; C:cell surface; IEA.
 DR GO: GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
 DR GO: GO:0016020; C:membrane; IEA.
 DR GO: GO:0007155; P:cell adhesion; IEA.
 DR InterPro: IPR008966; Adhes_bact.
 DR InterPro: IPR004237; Fn_bind.
 DR InterPro: IPR005877; Gpos_YsIRK.
 DR InterPro: IPR001899; Gram_pos_anchor.
 DR Pfam: PF02986; Fn_bind; 1.
 DR Pfam: PF00746; Gram_pos_anchor; 1.
 DR Pfam: PF04650; YsIRK_signal; 1.
 DR TIGRFAMs: TIGR01167; LPXTG_anchor; 1.
 DR TIGRFAMs: TIGR01168; YsIRK_signal; 1.
 DR PROSITE: PS50847; GRAM_POS_ANCHORING; 1.
 KM Cell wall; Complete proteome; Peptidoglycan-anchor.
 SQ SEQUENCE 965 AA; 105691 MW; 2382E132164D0551 CRC64;
 Query Match 95.6%; Score 197; DB 2; Length 965;
 Best Local Similarity 94.7%; Pred. No. 7.2e-16;
 Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 1 QNSGNQSFEDTEBPKEQGGNIVDIDFDSVPQIIG 38
 DB 749 QNSGNQSFEDTEBPKEQGGNIVDIDFDSVPQIIG 786
 RESULT 10
 Q8NUU7 PRELIMINARY; PRT; 1015 AA.
 AC Q8NUU7;
 DT 01-OCT-2002 (TREMBlrel. 22, Created)
 DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
 DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
 DE Fnb protein.
 GN Name=fnb; OrderedlocusNames=MM2421;
 OS *Staphylococcus aureus* (strain MM2).
 OC Bacteria; Firmicutes; Bacillales; *Staphylococcus*.
 OX NCBI_TaxID=196620;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC STRAIN=MM2;
 RX MEDLINE=22040717; PubMed=12044378; DOI=10.1016/S0140-6736(02)08713-5;
 RA Baba T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Oguchi A.,
 RA Nagai Y., Iwana N., Asano K., Naimi T., Kuroda H., Cui L.,
 RA Yamamoto K., Hiratacu K.;
 RT "Genome and virulence determinants of high virulence community-
 RT acquired MRSA";
 RL Lancet 359:1819-1827(2002).
 CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
 CC an amide bond (By similarity).
 DR EMBL: AF004830; BAB96286.1; -;
 DR GO: GO:0009986; C:cell surface; IEA.
 DR GO: GO:0005618; C:cell wall; IEA.
 DR GO: GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
 DR GO: GO:0016020; C:membrane; IEA.
 DR GO: GO:0007155; P:cell adhesion; IEA.
 DR InterPro: IPR008966; Adhes_bact.
 DR InterPro: IPR004237; Fn_bind.
 DR InterPro: IPR005877; Gpos_YsIRK.
 DR InterPro: IPR001899; Gram_pos_anchor.
 DR Pfam: PF02986; Fn_bind; 1.
 DR Pfam: PF00746; Gram_pos_anchor; 1.
 DR Pfam: PF04650; YsIRK_signal; 1.
 DR TIGRFAMs: TIGR01167; LPXTG_anchor; 1.
 DR TIGRFAMs: TIGR01168; YsIRK_signal; 1.

DR PROSITE: PS50847; GRAM_POS_ANCHORING; 1.
 KM Cell wall; Complete proteome; Peptidoglycan-anchor.
 SQ SEQUENCE 1015 AA; 111145 MW; D0F9281BB64D44D2 CRC64;
 Query Match 92.2%; Score 190; DB 2; Length 1015;
 Best Local Similarity 94.7%; Pred. No. 5.8e-15;
 Matches 36; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 QNSGNQSFEDTEBPKEQGGNIVDIDFDSVPQIIG 38
 DB 747 QNSGNQSFEDTEBPKEQGGNIVDIDFDSVPQIIG 784
 RESULT 11
 Q6G6H3 PRELIMINARY; PRT; 1015 AA.
 AC Q6G6H3;
 DT 05-JUL-2004 (TREMBlrel. 27, Created)
 DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
 DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
 DE Fibronectin-binding protein.
 GN OrderedlocusNames=5A52388;
 OS *Staphylococcus aureus* (strain MSSA476).
 OC Bacteria; Firmicutes; Bacillales; *Staphylococcus*.
 OX NCBI_TaxID=282459;
 RN (1)
 RP SEQUENCE FROM N.A.
 RX PubMed=15213324; DOI=10.1073/pnas.0402521101;
 RA Holden M.T.G., Foster T.J., Moore C.E., Peacock S.J., Day N.P.J.,
 RA Enright M.C., Foster T.J., Moore C.E., Hurst L., Atkin R., Barron A.,
 RA Baason N., Bentley S.D., Chillingworth T., Chillingworth T.,
 RA Churcher C., Clark L., Cotton C., Cronin A., Doggett J., Dowd L.,
 RA Feltham T., Hance Z., Harris B., Hauser H., Holtroyd S., Jagsals K.,
 RA James K.D., Lennard N., Line A., Mayes R., Moutie S., Mungall K.,
 RA Ormond D., Quail M.A., Rabinowitch E., Rutherford K.M., Sanders M.,
 RA Sharp S., Simmonds M., Stevens K., Whitehead S., Barrell B.G.,
 RA Spratt B.G., Parkhill J.;
 RT "Complete genomes of two clinical *Staphylococcus aureus* strains:
 RT evidence for the rapid evolution of virulence and drug resistance";
 RL Proc. Natl. Acad. Sci. U.S.A. 101:9786-9791(2004).
 CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
 CC an amide bond (By similarity).
 DR EMBL: BX571857; CAG44202.1; -;
 DR GO: GO:0009986; C:cell surface; IEA.
 DR GO: GO:0005618; C:cell wall; IEA.
 DR GO: GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
 DR GO: GO:0016020; C:membrane; IEA.
 DR GO: GO:0007155; P:cell adhesion; IEA.
 DR InterPro: IPR008966; Adhes_bact.
 DR InterPro: IPR004237; Fn_bind.
 DR InterPro: IPR005877; Gpos_YsIRK.
 DR InterPro: IPR001899; Gram_pos_anchor.
 DR Pfam: PF02986; Fn_bind; 1.
 DR Pfam: PF00746; Gram_pos_anchor; 1.
 DR Pfam: PF04650; YsIRK_signal; 1.
 DR TIGRFAMs: TIGR01167; LPXTG_anchor; 1.
 DR TIGRFAMs: TIGR01168; YsIRK_signal; 1.
 DR PROSITE: PS50847; GRAM_POS_ANCHORING; 1.
 KM Cell wall; Complete proteome; Peptidoglycan-anchor.
 SQ SEQUENCE 1015 AA; 111145 MW; D0F9281BB64D44D2 CRC64;
 Query Match 92.2%; Score 190; DB 2; Length 1015;
 Best Local Similarity 94.7%; Pred. No. 5.8e-15;
 Matches 36; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 QNSGNQSFEDTEBPKEQGGNIVDIDFDSVPQIIG 38
 DB 747 QNSGNQSFEDTEBPKEQGGNIVDIDFDSVPQIIG 784
 RESULT 12
 Q9AEP9 PRELIMINARY; PRT; 152 AA.
 ID Q9AEP9

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AC 09AEP9;
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Fibronectin-binding protein (Fragment).
GN Name=fnb;
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
CX NCBI_TaxId=1280;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CMRSA-1;
RX MEDLINE=21246681; PubMed=11349044;
RX DOI=10.1128/IAI.69.6.3791-3799.2001;
RA Rice K., Huebner M., Vaz D., McGavin M.J.;
RA "Variance in fibronectin binding and fnb locus polymorphisms in
RT Staphylococcus aureus: identification of antigenic variation in a
RT fibronectin binding protein adhesion of the epidemic CMRSA-1 strain of
RT methicillin-resistant S. aureus."
RL Infect. Immun. 69:3791-3799(2001).
FT EMBL; AY029184; AAK31588.1; -.
FT NON TER 1 152
FT SEQUENCE 152 AA; 17193 MW; CFA3913C2B11C025 CRC64;
SQ
Query Match 90.8%; Score 187; DB 2; Length 152;
Best Local Similarity 92.1%; Pred. No. 1.5e-15;
Matches 35; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
Qy 1 QNSGNOSFEEDTEBPKEPKYEGGNIIVDIDFDSVPQIHG 38
Db 1 QNTGNSGFEEDTEBPKEPKYEGGNIIVDIDFDSVPQIHG 38
RESULT 13
ID 06BMT0 PRELIMINARY; PRT; 937 AA.
AC 06BMT0;
DT 25-OCT-2004 (TREMBLrel. 28, Created)
DT 25-OCT-2004 (TREMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TREMBLrel. 28, Last annotation update)
DE Similar to CA4347|IPF3636 Candida albicans IPF3636.
GN ORFNames=DEHA0F058089;
OS Debaryomyces hansenii CBS767.
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Debaryomycetes.
CX NCBI_TaxId=284592;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CBS767;
RG Genolevures;
RA Dujon B., Sherman D., Fischer G., Durrens P., Casaregola S.,
RA Lafontaine I., de Montigny J., Marck C., Neuveglise C., Talla E.,
RA Goffard N., Frangeul L., Aigle M., Anthouard V., Babour A., Barbe V.,
RA Barnay S., Blanchin S., Beckerich J.M., Beyne E., Bleykasten C.,
RA Boismarie A., Boyer J., Cattolico L., Confaniolieri F., de Daruvar A.,
RA Deepons L., Fabre E., Fairhead C., Ferry-Dumazet H., Groppi A.,
RA Hantaye F., Hennequin C., Jauniaux N., Joyet P., Kachouri R.,
RA Kerrest A., Koszul R., Lemaitre M., Lesur I., Ma L., Muller H.,
RA Nicaud J.M., Nikolski M., Oztas S., Ozler-Kalogeropoulos O.,
RA Pellenz S., Potier S., Richard G.F., Straub M.L., Suleau A.,
RA Swennene D., Tekala F., Wesolowski-Louvel M., Westhof E., Wirth B.,
RA Zentou-Meyer M., Zivanovic I., Bolotin-Pukhara M., Thierry A.,
RA Bouchier C., Caudron B., Scarpelli C., Gallardin C., Weissenbach J.,
RA Wincker P., Souciet J.L.;
RA "Genome evolution in yeasts.";
RL Nature 430:35-44(2004).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=CBS767;
RG Genoscope;
RA Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; CR382134; CAG88916.1; -.
EMBL; CR382138; CAG88916.1; -.
DR
```

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DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003684; F:damaged DNA binding; IEA.
DR GO; GO:0006289; P:nucleotide-excision repair; IEA.
DR InterPro; IPR004583; Rad4.
DR Pfam; PF03835; Rad4; 1.
SQ SEQUENCE 937 AA; 107136 MW; 1DC3E795681B9BF7 CRC64;
Query Match 31.6%; Score 65; DB 2; Length 937;
Best Local Similarity 35.0%; Pred. No. 28;
Matches 14; Conservative 9; Mismatches 13; Indels 4; Gaps 2;
Qy 1 QNSGNOSFEEDTEBPKEPKYEG--GGNIIVDIDFDSVPQIH 37
Db 772 EESGGFVED-PEPEAKYSQARIGGLINVELDMDPEYV 810
RESULT 14
ID 06BWS4 PRELIMINARY; PRT; 191 AA.
AC 06BWS4;
DT 25-OCT-2004 (TREMBLrel. 28, Created)
DT 25-OCT-2004 (TREMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TREMBLrel. 28, Last annotation update)
DE Similar to CA0628|IPF3878 Candida albicans IPF3878 unknown
DE function.
GN ORFNames=DEHA0B089879;
OS Debaryomyces hansenii CBS767.
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Debaryomycetes.
CX NCBI_TaxId=284592;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CBS767;
RG Genolevures;
RA Dujon B., Sherman D., Fischer G., Durrens P., Casaregola S.,
RA Lafontaine I., de Montigny J., Marck C., Neuveglise C., Talla E.,
RA Goffard N., Frangeul L., Aigle M., Anthouard V., Babour A., Barbe V.,
RA Barnay S., Blanchin S., Beckerich J.M., Beyne E., Bleykasten C.,
RA Boismarie A., Boyer J., Cattolico L., Confaniolieri F., de Daruvar A.,
RA Deepons L., Fabre E., Fairhead C., Ferry-Dumazet H., Groppi A.,
RA Hantaye F., Hennequin C., Jauniaux N., Joyet P., Kachouri R.,
RA Kerrest A., Koszul R., Lemaitre M., Lesur I., Ma L., Muller H.,
RA Nicaud J.M., Nikolski M., Oztas S., Ozler-Kalogeropoulos O.,
RA Pellenz S., Potier S., Richard G.F., Straub M.L., Suleau A.,
RA Swennene D., Tekala F., Wesolowski-Louvel M., Westhof E., Wirth B.,
RA Zentou-Meyer M., Zivanovic I., Bolotin-Pukhara M., Westhof E., Wirth B.,
RA Bouchier C., Caudron B., Scarpelli C., Gallardin C., Weissenbach J.,
RA Wincker P., Souciet J.L.;
RA "Genome evolution in yeasts.";
RL Nature 430:35-44(2004).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=CBS767;
RG Genoscope;
RA Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; CR382134; CAG85349.1; -.
SQ SEQUENCE 191 AA; 21401 MW; 4E57B3E62DB943A4C CRC64;
Query Match 31.3%; Score 64.5; DB 2; Length 191;
Best Local Similarity 46.9%; Pred. No. 5;
Matches 15; Conservative 6; Mismatches 10; Indels 1; Gaps 1;
Qy 2 NSGNOSFEEDTEBPKEPKYEGGNIIVDIDFDS 32
Db 39 SSSDSMDAAEPEPKYETKTSINIDIDIDS 70
RESULT 15
ID 07SA69 PRELIMINARY; PRT; 745 AA.
AC 07SA69;
DT 01-MAR-2004 (TREMBLrel. 26, Created)
DT 01-MAR-2004 (TREMBLrel. 26, Last sequence update)
DR
```


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GenCore version 5.1.6
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OM protein - protein search, using SW model

Run on: October 25, 2005, 19:38:38 ; Search time 83.8325 Seconds
(without alignments)
175.313 Million cell updates/sec

Title: US-10-731-238-43

Perfect score: 206
Sequence: 1 QNSGNQSFEDTBDKPKYEQGNIVDIDFDSVPQIHG 38

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_1dDec04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003s:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	206	100.0	38	2	AAW65699
2	197	95.6	38	2	AAW65661 Fibronect
3	197	95.6	130	2	AAW65806 Fibronect
4	197	95.6	130	2	AAW65807 Fibronect
5	197	95.6	130	2	AAW65808 Fibronect
6	197	95.6	130	2	AAW65809 Fibronect
7	197	95.6	134	2	AAW65808 S. aureus
8	197	95.6	134	2	AAW65808 S. aureus
9	197	95.6	134	2	AAW65808 S. aureus
10	197	95.6	139	2	AAW65808 S. aureus
11	197	95.6	174	2	AAW65808 S. aureus
12	197	95.6	174	2	AAW65808 S. aureus
13	197	95.6	181	2	AAW65808 S. aureus
14	197	95.6	181	2	AAW65808 S. aureus
15	197	95.6	559	2	AAW65808 S. aureus
16	197	95.6	767	4	AAU34403 Staphyloc
17	197	95.6	767	4	AAU34403 Staphyloc
18	197	95.6	940	6	AAU34403 Staphyloc
19	197	95.6	940	6	AAU34403 Staphyloc
20	197	95.6	948	6	AAU34403 Staphyloc
21	197	95.6	948	6	AAU34403 Staphyloc
22	197	95.6	948	6	AAU34403 Staphyloc
23	197	95.6	961	6	AAU34403 Staphyloc
24	197	95.6	1018	1	AAU34403 Staphyloc
25	197	95.6	1018	4	AAU34403 Staphyloc

26	197	95.6	1018	4	AAU34301	AAU34301 Staphyloc
27	197	95.6	1018	6	ABJ18922	ABJ18922 Staphyloc
28	197	95.6	1018	6	ABJ18922	ABJ18922 Staphyloc
29	197	95.6	1027	6	ABJ18922	ABJ18922 Staphyloc
30	197	95.6	1038	6	ABJ18922	ABJ18922 Staphyloc
31	197	95.6	1038	6	ABJ18922	ABJ18922 Staphyloc
32	197	95.6	1038	6	ABJ18922	ABJ18922 Staphyloc
33	197	95.6	1038	6	ABJ18922	ABJ18922 Staphyloc
34	197	95.6	1038	6	ABJ18922	ABJ18922 Staphyloc
35	197	95.6	1038	6	ABJ18922	ABJ18922 Staphyloc
36	197	95.6	1038	6	ABJ18922	ABJ18922 Staphyloc
37	197	95.6	1038	6	ABJ18922	ABJ18922 Staphyloc
38	197	95.6	1038	6	ABJ18922	ABJ18922 Staphyloc
39	197	95.6	1038	6	ABJ18922	ABJ18922 Staphyloc
40	197	95.6	1038	6	ABJ18922	ABJ18922 Staphyloc
41	197	95.6	1038	6	ABJ18922	ABJ18922 Staphyloc
42	197	95.6	1038	6	ABJ18922	ABJ18922 Staphyloc
43	197	95.6	1038	6	ABJ18922	ABJ18922 Staphyloc
44	197	95.6	1038	6	ABJ18922	ABJ18922 Staphyloc
45	197	95.6	1038	6	ABJ18922	ABJ18922 Staphyloc

ALIGNMENTS

RESULT 1
AAW65699 standard; peptide; 38 AA.
AAW65699;
16-OCT-1998 (first entry)
Fibronectin binding protein-derived peptide #43.
microbial surface components recognising adhesive matrix molecule;
MSCRAM, fibronectin; fibronectin-binding protein; antibody; epitope;
antibiotic; bacterial infection; antibiotic-resistant strain.
Synthetic.
Staphylococcus aureus.
WO9831389-A2.
23-JUL-1998.
21-JAN-1998; 98WO-US001222.
21-JAN-1997; 97US-0036139P.
(TEXAS) UNIT TEXAS A & M SYSTEM.
Hoeck M, Patti JM, House-Pompeo KL, Speziale P, Joh D;
McGavin MJ;
WPI, 1998-413816/35.
Antibody that binds to fibronectin-binding protein, preventing its
binding to fibronectin - used to treat or prevent bacterial infection,
especially by Staphylococci and Streptococci.
Example 8, Page 102, 201pp, English.
The invention relates to antibodies that bind to a fibronectin-binding
domain of a fibronectin-binding protein, and inhibit binding of the
protein to fibronectin. Also claimed are: (1) isolated peptides of a
fibronectin-binding protein that do not bind to fibronectin; (2) fusion
protein containing at least one peptide of a fibronectin-binding protein
linked to a second amino acid sequence; (3) nucleic acid encoding the
isolated peptide of (1). Antibodies, the isolated peptides of (1) and the
nucleic acids are all useful for immunisation (active or passive) and (b)
inhibiting binding of bacteria to fibronectin for preventing or treating
infection in humans or other animals, particularly by staphylococci or

```
CC streptococci, e.g. meningitis, otitis media, pneumonia, endocarditis,
CC mastitis in cattle, abortion in horses and many others. Since the
CC antibodies block binding of bacteria, they should be effective against
CC antibiotic-resistant strains, and may replace antibiotic therapy or
CC increase its effectiveness. Sequences AAW65691-700 represent a series of
CC synthetic peptides based on the D1 region of S. aureus fibronectin
CC binding protein A. They were synthesised to contain mutations
XX
SQ Sequence 38 AA;
Query Match 100.0%; Score 206; DB 2; Length 38;
Best Local Similarity 100.0%; Pred. No. 2,6e-20;
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 QNSGNQSFEDTEEDKPKYEQGNIVDIDFDSVPQIHG 38
DB 1 QNSGNQSFEDTEEDKPKYEQGNIVDIDFDSVPQIHG 38
RESULT 2
AAW65661 AAW65661 standard; peptide; 38 AA.
AC AAW65661;
XX
XX 16-OCT-1998 (first entry)
DE Fibronectin binding protein-derived peptide #5.
XX
XX microbial surface components recognising adhesive matrix molecule;
XX MSCRAMM; fibronectin; fibronectin-binding protein; antibody; epitope;
XX antibiotic; bacterial infection; antibiotic-resistant strain.
XX
XX Synthetic.
XX OS Staphylococcus aureus.
XX
XX WO9831389-A2.
XX
XX 23-JUL-1998.
XX
XX 21-JAN-1998; 98WO-US001222.
XX
XX 21-JAN-1997; 97US-0036139P.
XX
XX (TEXA ) UNIV TEXAS A & M SYSTEM.
XX
XX Hoeoek M, Patti JM, House-Pompeo KL, Speciale P, Joh D;
XX Mcgavin WJ;
XX
XX WPI; 1998-413816/35.
XX
XX Antibody that binds to fibronectin-binding protein, preventing its
XX binding to fibronectin - used to treat or prevent bacterial infection,
XX especially by Staphylococci and Streptococci.
XX
XX Example 2; Page 92; 201pp; English.
XX
XX The invention relates to antibodies that bind to a fibronectin-binding
XX domain of a fibronectin-binding protein, and inhibit binding of the
XX protein to fibronectin. Also claimed are: (1) isolated peptides of a
XX fibronectin-binding protein that do not bind to fibronectin; (2) fusion
XX protein containing at least one peptide of a fibronectin-binding protein
XX linked to a second amino acid sequence; (3) nucleic acid encoding the
XX isolated peptide of (1). Antibodies, the isolated peptides of (1) and the
XX nucleic acids are all useful for immunisation (active or passive) and (by
XX inhibiting binding of bacteria to fibronectin) for preventing or treating
XX infection in humans or other animals, particularly by staphylococci or
XX streptococci, e.g. meningitis, otitis media, pneumonia, endocarditis,
XX mastitis in cattle, abortion in horses and many others. Since the
XX antibodies block binding of bacteria, they should be effective against
XX antibiotic-resistant strains, and may replace antibiotic therapy or
XX increase its effectiveness. Sequences AAW65659-68 represent synthetic
XX epitopes from the fibronectin binding domains DU and DI-D4 of the S.
```

```
CC aureus fnbA gene
XX
XX Sequence 38 AA;
SQ
Query Match 95.6%; Score 197; DB 2; Length 38;
Best Local Similarity 97.4%; Pred. No. 4,2e-19;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 1 QNSGNQSFEDTEEDKPKYEQGNIVDIDFDSVPQIHG 38
DB 1 QNSGNQSFEDTEEDKPKYEQGNIVDIDFDSVPQIHG 38
RESULT 3
AAR58805 AAR58805 standard; protein; 130 AA.
AC AAR58805;
XX
XX 25-MAR-2003 (revised)
XX 30-MAR-1995 (first entry)
DE Fibronectin binding domain DI-D4(709-838 (P838T)).
XX
XX Fibronectin binding protein; Fbp; fibronectin binding domain;
XX monoclonal antibody; Mab; adhesion; Gram-positive bacterium; bacteremia;
XX Escherichia coli.
XX
XX Staphylococcus aureus.
XX
XX OS
XX PM WO9418327-A1.
XX
XX 18-AUG-1994.
XX
XX 04-FEB-1994; 94WO-GB000215.
XX
XX 05-FEB-1993; 93GB-00002289.
XX 20-OCT-1993; 93GB-00021592.
XX
XX (SMIK ) SMITHKLINE BEECHAM PLC.
XX
XX Burnham MKR, Chopra I, Critchley IA, Knowles DJC;
XX
XX WPI; 1994-279748/34.
XX
XX Fibronectin binding protein and monoclonal antibodies specific for Fbp -
XX useful to prevent adherence of Gram-positive bacteria to indwelling
XX devices or wounds.
XX
XX Disclosure; Page 30; 40pp; English.
XX
XX Polypeptides corresponding to residues G709-T886 plus PRIVPT, G709-
XX P838(P838T) and G709-P838 (AAR58805-07, respectively) of S. aureus J2385
XX (NCIMB 40532) Fbp type A fibronectin binding domain DI-D4 region
XX (AAR58808) were expressed in E. coli BL21(DE4) and used to raise Mabs
XX specific for Fbp. (updated on 25-MAR-2003 to correct PN field.)
XX
XX SQ Sequence 130 AA;
Query Match 95.6%; Score 197; DB 2; Length 130;
Best Local Similarity 97.4%; Pred. No. 1,8e-18;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 1 QNSGNQSFEDTEEDKPKYEQGNIVDIDFDSVPQIHG 38
DB 2 QNSGNQSFEDTEEDKPKYEQGNIVDIDFDSVPQIHG 39
RESULT 4
AAR58807 AAR58807 standard; protein; 130 AA.
AC AAR58807;
```

```

XX 25-MAR-2003 (revised)
DT 30-MAR-1995 (first entry)
XX
DE Fibronectin binding domain D1-D4 (709-838).
XX
KW Fibronectin binding protein; Fbp; fibronectin binding domain;
KW monoclonal antibody; Mab; adhesion; Gram-positive bacterium; bacteremia;
KW Escherichia coli.
XX
OS Staphylococcus aureus.
XX
PN WO9418327-A1.
XX
PD 18-AUG-1994.
XX
PF 04-FEB-1994; 94WO-GB000215.
XX
PR 05-FEB-1993; 93GB-00002289.
PR 20-OCT-1993; 93GB-00021592.
XX
PA (SMIK ) SMITHKLINE BEECHAM PLC.
XX
PI Burnham MKR, Chopra I, Critchley IA, Knowles DUC;
XX
DR WPI; 1994-279748/34.
XX
PT Fibronectin binding protein and monoclonal antibodies specific for Fbp -
PT useful to prevent adherence of Gram-positive bacteria to indwelling
PT devices or wounds.
XX
PS Disclosure; Page 30; 40pp; English.
XX
CC Polypeptides corresponding to residues 6709-7886 plus PPIVPR, 6709-
CC P8381(P8381) and 6709-P838 (AAR58805-07, respectively) of S. aureus J2385
CC (NCIMB 40532) Fbp type A fibronectin binding domain D1-D4 region
CC (AAR58808) were expressed in E. coli BL21(DE4) and used to raise Mabs
CC specific for Fbp. (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ Sequence 130 AA;
XX
Query Match 95.6%; Score 197; DB 2; Length 130;
Best Local Similarity 97.4%; Pred. No. 1.8e-18;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 QNSGNQSFEDTREDKPKYEGGNIVDIDFDSVPQIHG 38
DB 2 QNSGNQSFEDTREDKPKYEGGNIVDIDFDSVPQIHG 39
XX
RESULT 5
AAR91202
ID AAR91202 standard; peptide; 130 AA.
XX
AC AAR91202;
XX
DT 13-NOV-1996 (first entry)
XX
DE D1-D4 fibronectin binding domains.
XX
KW Fibronectin; oral hygiene; gingivitis; gum disease; adhesion;
KW periodontitis; oral pathogen; caries; calculus; candidiasis; oral surgery;
KW tissue regeneration; irrigation; toothpaste; dentifrice; mouthwash;
KW lozenge.
XX
OS Staphylococcus aureus.
XX
PN WO9604003-A1.
XX
PD 15-FEB-1996.
XX
PF 18-JUL-1995; 95WO-EP002825.
XX

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```

PR 05-AUG-1994; 94GB-00015902.
XX
PA (SMIK ) SMITHKLINE BEECHAM PLC.
XX
PI Barnett P, Critchley IA, Dodd I;
XX
DR WPI; 1996-129122/13.
XX
PT Prevention of adherence of oral pathogens in the oral cavity, partic.
PT tooth surfaces - by application of a fibronectin binding protein or
PT polypeptide or a monoclonal antibody or fragment against it.
XX
PS Claim 5; Page 32; 41pp; English.
XX
CC Adherence of oral pathogens, particularly to tooth surfaces, can be
CC prevented by application of a fibronectin binding protein or polypeptide.
CC The fibronectin binding protein or polypeptide is useful in the
CC manufacture of oral hygiene compositions, eg. toothpaste, liquid
CC dentifrice, mouthwash or lozenge. They are useful to prevent the plaque-
CC related development of carious lesions, gingivitis, calculus or
CC periodontal disease and to combat oral cavity infections, e.g.
CC candidiasis. They may also be useful in oral surgery e.g. in guided
CC tissue regeneration procedures to prevent subsequent bacterial infection,
CC and for irrigation of periodontal pockets. This sequence corresponds to
CC amino acids 709-838 of the D1-D4 fibronectin binding domain of
CC Staphylococcus aureus
XX
SQ Sequence 130 AA;
XX
Query Match 95.6%; Score 197; DB 2; Length 130;
Best Local Similarity 97.4%; Pred. No. 1.8e-18;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 QNSGNQSFEDTREDKPKYEGGNIVDIDFDSVPQIHG 38
DB 2 QNSGNQSFEDTREDKPKYEGGNIVDIDFDSVPQIHG 39
XX
RESULT 6
AAR91201
ID AAR91201 standard; peptide; 130 AA.
XX
AC AAR91201;
XX
DT 13-NOV-1996 (first entry)
XX
DE D1-D4 fibronectin binding domains.
XX
KW Fibronectin; oral hygiene; gingivitis; gum disease; adhesion;
KW periodontitis; oral pathogen; caries; calculus; candidiasis; oral surgery;
KW tissue regeneration; irrigation; toothpaste; dentifrice; mouthwash;
KW lozenge.
XX
OS Staphylococcus aureus.
XX
PN WO9604003-A1.
XX
PD 15-FEB-1996.
XX
PF 18-JUL-1995; 95WO-EP002825.
XX
PR 05-AUG-1994; 94GB-00015902.
XX
PA (SMIK ) SMITHKLINE BEECHAM PLC.
XX
PI Barnett P, Critchley IA, Dodd I;
XX
DR WPI; 1996-129122/13.
XX
PT Prevention of adherence of oral pathogens in the oral cavity, partic.
PT tooth surfaces - by application of a fibronectin binding protein or
PT polypeptide or a monoclonal antibody or fragment against it.
XX

```

PS Claim 5; Page 31-32; 41pp; English.

XX Adherence of oral pathogens, particularly to tooth surfaces, can be

CC prevented by application of a fibronectin binding protein or polypeptide.

CC The fibronectin binding protein or polypeptide is useful in the

CC manufacture of oral hygiene compositions, eg. toothpaste, liquid

CC dentifrice, mouthwash or lozenge. They are useful to prevent the plaque-

CC related development of carious lesions, gingivitis, calculus or

CC periodontal disease and to combat oral cavity infections, e.g. candidiasis.

CC They may also be useful in oral surgery e.g. in guided

CC tissue regeneration procedures to prevent subsequent bacterial infection,

CC and for irrigation of periodontal pockets. This sequence corresponds to

CC amino acids 709-838 of the D1-D4 fibronectin binding domain of

CC Staphylococcus aureus with a P838T substitution

XX

SO Sequence 130 AA;

Query Match 95.6%; Score 197; DB 2; Length 130;

Best Local Similarity 97.4%; Pred. No. 1.9e-18;

Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QNSGNQSFEDTDEKPKRYEGGNIVDIDPDSVPQIHG 38

DB 2 QNSGNQSFEDTDEKPKRYEGGNIVDIDPDSVPQIHG 39

RESULT 7

AY23089

ID AAY29089 standard; protein; 134 AA.

XX

AC AAY29089;

XX

DT 28-SEP-1999 (first entry)

XX

DE Cloned fibronectin binding protein binding domain (FnBAB) sequence.

XX

KW Bovine herpes virus-2; BHV-2; cytokine; immune response; immunogen; IL;

KW interleukin; colony stimulating factor; CSF; interferon; IFN; TNF;

KW tumour necrosis factor; recombinant virus; vaccine; mucosal disease;

KW mastitis; breast cancer; stress-induced disease; binding domain; FnBAB;

KW fibronectin binding protein.

XX

OS Staphylococcus aureus.

XX

FN W09916892-A1.

XX

PD 08-APR-1999.

XX

PF 29-SEP-1998; 98WO-GB002927.

XX

PR 29-SEP-1997; 97GB-00020633.

XX

PA (UYBR-) UNIV BRISTOL.

XX

PI Bradley AJ, Duffas WPJ;

XX

DR WPI; 1999-255101/21.

XX

DR N-PSDB; AAX91505.

XX

PT New bovine herpes virus-2 vectors.

XX

PS Example 2; Fig 8A-B; 130pp; English.

XX

CC The invention provides bovine herpes virus-2 (BHV-2) based vectors that

CC comprise at least one cytokine-encoding DNA sequence. The expression of

CC cytokines in mammals can up-regulate immune responses to the immunogens.

CC The cytokine is selected from interleukins (IL), colony stimulating

CC factors (CSF), interferons (IFN) and tumour necrosis factors (TNF). The

CC BHV-2 based vector or recombinant virus can be used as vaccines. They can

CC be used for preventing or treating a mucosal disease in a subject, e.g.

CC ruminants, cattle, sheep, goats, dogs, cats, horses, or man, particularly

CC mastitis in cows or breast cancers in humans. They can also be used for

CC preventing or treating a stress-induced disease. The present sequence

CC represents a S. aureus fibronectin binding protein binding domain

CC sequence FnBAB, the gene cloned for use in this invention. The gene has

CC 97.8 percent identity when compared to the previously published sequences

CC FnBA and FnBB

XX

SO Sequence 134 AA;

Query Match 95.6%; Score 197; DB 2; Length 134;

Best Local Similarity 97.4%; Pred. No. 1.9e-18;

Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QNSGNQSFEDTDEKPKRYEGGNIVDIDPDSVPQIHG 38

DB 2 QNSGNQSFEDTDEKPKRYEGGNIVDIDPDSVPQIHG 39

RESULT 8

AY29088

ID AAY29088 standard; protein; 134 AA.

XX

AC AAY29088;

XX

DT 28-SEP-1999 (first entry)

XX

DE S. aureus fibronectin binding protein B (FnBB) binding domain.

XX

KW Bovine herpes virus-2; BHV-2; cytokine; immune response; immunogen; IL;

KW interleukin; colony stimulating factor; CSF; interferon; IFN; TNF;

KW tumour necrosis factor; recombinant virus; vaccine; mucosal disease;

KW mastitis; breast cancer; stress-induced disease; binding domain; FnBB;

KW fibronectin binding protein.

XX

OS Staphylococcus aureus.

XX

FN W09916892-A1.

XX

PD 08-APR-1999.

XX

PF 29-SEP-1998; 98WO-GB002927.

XX

PR 29-SEP-1997; 97GB-00020633.

XX

PA (UYBR-) UNIV BRISTOL.

XX

PI Bradley AJ, Duffas WPJ;

XX

DR WPI; 1999-255101/21.

XX

DR N-PSDB; AAX91505.

XX

PT New bovine herpes virus-2 vectors.

XX

PS Example 2; Fig 8A-B; 130pp; English.

XX

CC The invention provides bovine herpes virus-2 (BHV-2) based vectors that

CC comprise at least one cytokine-encoding DNA sequence. The expression of

CC cytokines in mammals can up-regulate immune responses to the immunogens.

CC The cytokine is selected from interleukins (IL), colony stimulating

CC factors (CSF), interferons (IFN) and tumour necrosis factors (TNF). The

CC BHV-2 based vector or recombinant virus can be used as vaccines. They can

CC be used for preventing or treating a mucosal disease in a subject, e.g.

CC ruminants, cattle, sheep, goats, dogs, cats, horses, or man, particularly

CC mastitis in cows or breast cancers in humans. They can also be used for

CC preventing or treating a stress-induced disease. The present sequence

CC represents the binding domain of a previously published S. aureus

CC fibronectin binding protein B (FnBB) sequence. The FnB binding domain

CC gene sequence FnBAB, cloned for use in this invention has 97.8 percent

CC identity when compared to the previously published FnBA and FnBB gene

CC sequences

XX

SO Sequence 134 AA;

Query Match 95.6%; Score 197; DB 2; Length 134;

Best Local Similarity 97.4%; Pred. No. 1.9e-18;


```

XX 25-MAR-2003 (revised)
DT 30-MAR-1995 (first entry)
XX
XX Fbp fibronectin binding domain.
DE
XX Fibronectin binding protein; Fbp; fibronectin binding domain;
KW monoclonal antibody; Mab; adhesion; Gram-positive bacterium; bacteremia;
KW Escherichia coli; pBRCS31.
XX
OS Staphylococcus aureus.
XX
XX WO9418327-A1.
XX
XX 18-AUG-1994.
XX
XX 04-FEB-1994; 94WO-GB000215.
XX
XX 05-FEB-1993; 93GB-00002289.
XX
XX 20-OCT-1993; 93GB-00021592.
XX
XX (SMIK ) SMITHKLINE BEECHAM PLC.
XX
XX Burnham MKR, Chopra I, Critchley IA, Knowles DJC;
PI
XX WPI; 1994-279748/34.
XX
XX N-PSDB; AAO71838.
XX
XX Fibronectin binding protein and monoclonal antibodies specific for Fbp -
PT useful to prevent adherence of Gram-positive bacteria to indwelling
PT devices or wounds.
XX
XX
XX Disclosure; Page 30; 40pp; English.
XX
XX The sequences of DNA encoding S. aureus Fbp type A fibronectin binding
CC domain (D1-D4) and the encoded protein are provided. D1-D4 polypeptides
CC have been expressed in E. coli BL21(DE4) and used to raise Mabs specific
CC for Fbp. (Updated on 25-MAR-2003 to correct PN field.)
XX
XX
XX Sequence 174 AA;
SQ
Query Match 95.6%; Score 197; DB 2; Length 174;
Best Local Similarity 97.4%; Pred. No. 2.6e-18;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 QNSGNQSFEDTDEBKRYEGGNIVDIDFDSVPQIHG 38
Db 2 QNSGNQSFEDTDEBKRYEGGNIVDIDFDSVPQIHG 39
RESULT 12
ID AAR91203 standard; protein; 174 AA.
XX
XX AAR91203;
XX
XX 16-OCT-2003 (revised)
DT 13-NOV-1996 (first entry)
XX
XX D1-D4 fibronectin binding domains.
XX
XX Fibronectin; oral hygiene; gingivitis; gum disease; adhesion;
KW periodontis; oral pathogen; caries; calculus; candidiasis; oral surgery;
KW tissue regeneration; irrigation; toothpaste; dentifrice; mouthwash;
KW lozenge.
XX
XX Staphylococcus aureus; J2385.
XX
XX WO9604003-A1.
XX
XX 15-FEB-1996.
XX
XX 18-JUL-1995; 95WO-EP002825.

```

```

XX 05-AUG-1994; 94GB-00015902.
XX
XX (SMIK ) SMITHKLINE BEECHAM PLC.
XX
XX Barnett P, Critchley IA, Dodd I;
PI
XX WPI; 1996-129122/13.
XX
XX N-PSDB; AAT18308.
XX
XX Prevention of adherence of oral pathogens in the oral cavity, partic.
PT tooth surfaces - by application of a fibronectin binding protein or
PT polypeptide or a monoclonal antibody or fragment against it.
XX
XX
XX Claim 5; Page 32; 41pp; English.
XX
XX Adherence of oral pathogens, particularly to tooth surfaces, can be
CC prevented by application of a fibronectin binding protein or polypeptide.
CC The fibronectin binding protein or polypeptide is useful in the
CC manufacture of oral hygiene compositions, eg. toothpaste, liquid
CC dentifrice, mouthwash or lozenge. They are useful to prevent the plaque-
CC related development of carious lesions, gingivitis, calculus or
CC periodontal disease and to combat oral cavity infections, eg.
CC candidiasis. They may also be useful in oral surgery e.g. in guided
CC tissue regeneration procedures to prevent subsequent bacterial infection,
CC and for irrigation of periodontal pockets. This sequence corresponds to
CC amino acids 709-838 of the D1-D4 fibronectin binding domain of
CC Staphylococcus aureus with a P838T substitution. (Updated on 16-OCT-2003
CC to standardise OS field)
XX
XX
XX Sequence 174 AA;
SQ
Query Match 95.6%; Score 197; DB 2; Length 174;
Best Local Similarity 97.4%; Pred. No. 2.6e-18;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 QNSGNQSFEDTDEBKRYEGGNIVDIDFDSVPQIHG 38
Db 2 QNSGNQSFEDTDEBKRYEGGNIVDIDFDSVPQIHG 39
RESULT 13
ID AAR58805 standard; protein; 181 AA.
XX
XX AAR58805;
XX
XX 25-MAR-2003 (revised)
DT 30-MAR-1995 (first entry)
XX
XX Fibronectin binding domain D1-D4(709-886).
XX
XX Fibronectin binding protein; Fbp; fibronectin binding domain;
KW monoclonal antibody; Mab; adhesion; Gram-positive bacterium; bacteremia;
KW Escherichia coli.
XX
XX Staphylococcus aureus.
XX
XX WO9418327-A1.
XX
XX 18-AUG-1994.
XX
XX 04-FEB-1994; 94WO-GB000215.
XX
XX 05-FEB-1993; 93GB-00002289.
XX
XX 20-OCT-1993; 93GB-00021592.
XX
XX (SMIK ) SMITHKLINE BEECHAM PLC.
XX
XX Burnham MKR, Chopra I, Critchley IA, Knowles DJC;
PI
XX WPI; 1994-279748/34.
XX

```

PT Fibronectin binding protein and monoclonal antibodies specific for Fbp -
 PT useful to prevent adherence of Gram-positive bacteria to indwelling
 PT devices or wounds.
 XX
 PS Disclosure: Page 29-30; 40pp; English.
 CC
 CC Polypeptides corresponding to residues G709-T886 plus PPIVPT, G709-
 CC P838(P838T) and G709-P838 (AAR58805-07, respectively) of S. aureus J2385
 CC (NCIMB 40532) Fbp type A fibronectin binding domain D1-D4 region
 CC (AAR58808) were expressed in E. coli BL21(DE4) and used to raise Mabs
 CC specific for Fbp. (Updated on 25-MAR-2003 to correct PN field.)
 XX
 SQ Sequence 181 AA;
 Query Match 95.6%; Score 197; DB 2; Length 181;
 Best Local Similarity 97.4%; Pred. No. 2,7e-18;
 Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 OY 1 ONSGNQSFEEEDTEEDKPKYEQGNIVDIDFDSVPOIHG 38
 DB 2 ONSGNQSFEEEDTEEDKPKYEQGNIVDIDFDSVPOIHG 39
 RESULT 14
 AAR91200
 ID AAR91200 standard; peptide; 181 AA.
 AC AAR91200;
 DT 13-NOV-1996 (first entry)
 DE D1-D4 fibronectin binding domains.
 XX
 XX Fibronectin; oral hygiene; gingivitis; gum disease; adhesion;
 KM periodontitis; oral pathogen; caries; calculus; candidiasis; oral surgery;
 KM tissue regeneration; irrigation; toothpaste; dentifrice; mouthwash;
 KM lozenge.
 XX
 OS Staphylococcus aureus.
 XX
 PN WO9604003-A1.
 XX
 PD 15-FEB-1996.
 XX
 PF 18-JUL-1995; 95MO-EP002825.
 XX
 PR 05-AUG-1994; 94GB-00015902.
 XX
 PA (SMIK) SMITHKLINE BEECHAM PLC.
 XX
 PI Barnett P, Critchley IA, Dodd I;
 XX
 DR WPI; 1996-129122/13.
 DR N-PSDB; AAT18307.
 XX
 PT Prevention of adherence of oral pathogens in the oral cavity, partic.
 PT tooth surfaces - by application of a fibronectin binding protein or
 PT polypeptide or a monoclonal antibody or fragment against it.
 XX
 PS Claim 5; Page 31; 41pp; English.
 XX
 CC Adherence of oral pathogens, particularly to tooth surfaces, can be
 CC prevented by application of a fibronectin binding protein or polypeptide.
 CC The fibronectin binding protein or polypeptide is useful in the
 CC manufacture of oral hygiene compositions, eg. toothpaste, liquid
 CC dentifrice, mouthwash or lozenge. They are useful to prevent the plaque-
 CC related development of carious lesions, gingivitis, calculus or
 CC periodontal disease and to combat oral cavity infections, e.g.
 CC candidiasis. They may also be useful in oral surgery e.g. in guided
 CC tissue regeneration procedures to prevent subsequent bacterial infection,
 CC and for irrigation of periodontal pockets. This sequence corresponds to
 CC amino acids 709-886 of the D1-D4 fibronectin binding domain of
 CC Staphylococcus aureus

XX
 SQ Sequence 181 AA;
 Query Match 95.6%; Score 197; DB 2; Length 181;
 Best Local Similarity 97.4%; Pred. No. 2,7e-18;
 Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 OY 1 ONSGNQSFEEEDTEEDKPKYEQGNIVDIDFDSVPOIHG 38
 DB 2 ONSGNQSFEEEDTEEDKPKYEQGNIVDIDFDSVPOIHG 39
 RESULT 15
 AAM89803
 ID AAM89803 standard; procein; 559 AA.
 AC AAM89803;
 DT 16-MAR-1999 (first entry)
 DE Staphylococcus aureus protein SEQ ID #5251.
 XX
 XX Computer readable medium; vaccine; S.aureus infection; immunodetection;
 KM cellulitis; eyelid infection; food poisoning; osteomyelitis; therapy;
 KM skin infection; surgical wound infection; scalded skin syndrome;
 KM toxic shock syndrome.
 XX
 OS Staphylococcus aureus.
 XX
 PN EP766519-A2.
 PD 30-JUL-1997.
 XX
 PF 07-JAN-1997; 97EP-00100117.
 XX
 PR 05-JAN-1996; 96US-0009861P.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 XX
 PI Kunsch CA, Choi GH, Barash SC, Dillon PJ, Fannon MR, Rosen CA;
 XX
 DR WPI; 1997-374922/35.
 XX
 PT Polynucleotide(s) and proteins derived from Staphylococcus aureus -
 PT stored on computer readable medium and used in the production of anti-
 PT S.aureus vaccines.
 XX
 PS Claim 23; Page 3259-3261; 3271pp; English.
 XX
 CC This sequence represents a Staphylococcus aureus protein sequence of the
 CC invention. The DNA sequences encoding the S.aureus proteins are recorded
 CC on a computer readable medium, preferably selected from a floppy or hard
 CC disk, random access memory (RAM), read-only memory (ROM) or CD-ROM.
 CC Homology searches using the S.aureus DNA sequences allows putative
 CC functions to be assigned so that protein-encoding or regulatory regions
 CC of commercial, therapeutic or industrial importance can be obtained.
 CC Specifically, sequences which are likely to encode antigens have been
 CC identified and these polypeptides can be used in a vaccine composition
 CC against S.aureus infection. The polypeptides can also be used in a kit
 CC for the immunodetection of S.aureus in a sample. S.aureus is implicated
 CC in numerous human diseases, including cellulitis, eyelid infections, food
 CC poisoning, osteomyelitis, skin and surgical wound infections, scalded
 CC skin syndrome, toxic shock syndrome, etc. Organisms transformed with the
 CC DNA sequences can be used for recombinant production of the polypeptides.
 CC The new DNA sequences (and their fragments) are useful as primers or
 CC probes for isolating homologues of any of the 5191 S.aureus DNA sequences
 CC contained on the computer readable medium
 XX
 SQ Sequence 559 AA;
 Query Match 95.6%; Score 197; DB 2; Length 559;
 Best Local Similarity 97.4%; Pred. No. 1e-17;
 Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 ONSGNQSPFEDTREDKPKYEOGNIVDIDFDSVPQIHG 38
|||
Db 301 ONSGNQSPFEDTREDKPKYEOGNIVDIDFDSVPQIHG 338
|||

Search completed: October 25, 2005, 20:21:04
Job time : 83.8825 secs

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OM protein - protein search, using SW model

Run on: October 22, 2005, 03:51:22 ; Search time 21.1723 Seconds
(without alignments)
133.980 Million cell updates/sec

Title: US-10-731-238-43

Perfect score: 206
Sequence: 1 QNSGNQSFEDTEEDPKRYEQPNVIDIDFDSVPQIHG 38

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :
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3: /cgn2_6/ptodata/1/1aa/6A.COMB.pep:*
4: /cgn2_6/ptodata/1/1aa/6B.COMB.pep:*
5: /cgn2_6/ptodata/1/1aa/6C.COMB.pep:*
6: /cgn2_6/ptodata/1/1aa/Backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	206	100.0	38	4	US-09-010-317-43 Sequence 43, Appl
2	197	95.6	38	1	US-08-234-622A-2 Sequence 2, Appl
3	197	95.6	38	4	US-09-010-317-5 Sequence 5, Appl
4	197	95.6	114	1	US-08-259-000-3 Sequence 3, Appl
5	197	95.6	130	2	US-08-459-135A-7 Sequence 7, Appl
6	197	95.6	130	2	US-08-459-135A-8 Sequence 8, Appl
7	197	95.6	130	3	US-08-495-559-7 Sequence 7, Appl
8	197	95.6	130	3	US-08-495-559-8 Sequence 8, Appl
9	197	95.6	139	3	US-08-856-253-8 Sequence 8, Appl
10	197	95.6	174	2	US-08-459-135A-10 Sequence 10, Appl
11	197	95.6	174	2	US-08-459-135A-11 Sequence 10, Appl
12	197	95.6	174	3	US-08-495-559-10 Sequence 10, Appl
13	197	95.6	174	3	US-08-495-559-13 Sequence 13, Appl
14	197	95.6	176	3	US-08-495-559-6 Sequence 6, Appl
15	197	95.6	178	2	US-08-459-135A-12 Sequence 12, Appl
16	197	95.6	178	3	US-08-495-559-12 Sequence 12, Appl
17	197	95.6	181	2	US-08-459-135A-6 Sequence 6, Appl
18	197	95.6	559	4	US-08-956-171E-5251 Sequence 5251, Ap
19	197	95.6	559	4	US-08-781-986A-5251 Sequence 5251, Ap
20	197	95.6	1027	4	US-08-956-171E-5254 Sequence 5254, Ap
21	197	95.6	1027	4	US-08-781-986A-5254 Sequence 5254, Ap
22	191	92.7	38	1	US-08-729-767-3 Sequence 3, Appl
23	191	92.7	38	4	US-09-010-317-36 Sequence 36, Appl
24	191	92.7	38	4	US-09-010-317-37 Sequence 37, Appl
25	191	92.7	38	4	US-09-010-317-39 Sequence 39, Appl
26	191	92.7	38	4	US-09-010-317-40 Sequence 40, Appl
27	191	92.7	38	4	US-09-010-317-41 Sequence 41, Appl

28	190	92.2	38	4	US-09-010-317-38 Sequence 38, Appl
29	190	92.2	38	4	US-09-010-317-42 Sequence 42, Appl
30	189	91.7	38	4	US-09-010-317-45 Sequence 45, Appl
31	187	90.8	38	4	US-09-010-317-35 Sequence 35, Appl
32	187	90.8	38	4	US-09-010-317-49 Sequence 49, Appl
33	186.5	90.5	39	4	US-09-010-317-56 Sequence 56, Appl
34	186	90.3	38	4	US-09-010-317-44 Sequence 44, Appl
35	178.5	86.7	39	4	US-09-010-317-57 Sequence 57, Appl
36	178	86.4	38	1	US-08-234-622A-3 Sequence 3, Appl
37	178	86.4	38	4	US-09-010-317-7 Sequence 7, Appl
38	172	83.5	38	1	US-08-729-767-4 Sequence 4, Appl
39	172	83.5	38	4	US-09-010-317-46 Sequence 46, Appl
40	172	83.5	38	4	US-09-010-317-47 Sequence 47, Appl
41	171	83.0	38	4	US-09-010-317-48 Sequence 48, Appl
42	170	82.5	38	4	US-09-010-317-8 Sequence 8, Appl
43	168	81.6	38	4	US-09-010-317-45 Sequence 45, Appl
44	167	81.1	38	4	US-09-010-317-50 Sequence 50, Appl
45	155	75.2	36	4	US-09-010-317-58 Sequence 58, Appl

ALIGNMENTS

RESULT 1
US-09-010-317-43
Sequence 43, Application US/09010317
Patent No. 6685943
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
APPLICANT: Patti, Joseph M.
APPLICANT: House-Pompeo, Karen L.
APPLICANT: Speziale, Pietro
APPLICANT: Joh, Danny
APPLICANT: McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
TITLE OF INVENTION: AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hihler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TANK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 43:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-09-010-317-43
Query Match 100.0%; Score 206; DB 4; Length 38;
Best Local Similarity 100.0%; Pred. No. 4e-21;

Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QNSGNSFEEDTEEDKPKYEQGNIVDIDFDSVPQIHG 38
Db 1 QNSGNSFEEDTEEDKPKYEQGNIVDIDFDSVPQIHG 38

RESULT 2
US-08-234-622A-2
Sequence 2, Application US/08234622A

Patent No. 5440014
GENERAL INFORMATION:
APPLICANT: HOOK, Magnus
APPLICANT: MCGAVIN, Martin
APPLICANT: RAUCCI, Giuseppe
TITLE OF INVENTION: A FIBRONECTIN BINDING PEPTIDE
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Burns, Doane, Swecker & Mathis
STREET: P.O. Box 1404
CITY: Alexandria
STATE: Virginia
COUNTRY: United States
ZIP: 2213-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/234,622A
FILING DATE: 28-APR-1994
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: SE 9002617-0
FILING DATE: 10-AUG-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/SE91/00534
FILING DATE: 09-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: Meuch, Donna M
REGISTRATION NUMBER: 36,607
REFERENCE/DOCKET NUMBER: 012885-044
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-234-622A-2

Query Match 95.6%; Score 197; DB 1; Length 38;
Best Local Similarity 97.4%; Pred. No. 6.7e-20;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QNSGNSFEEDTEEDKPKYEQGNIVDIDFDSVPQIHG 38
Db 1 QNSGNSFEEDTEEDKPKYEQGNIVDIDFDSVPQIHG 38

RESULT 3
US-09-010-317-5
Sequence 5, Application US/09010317

Patent No. 6685943
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
APPLICANT: Patil, Joseph M.
APPLICANT: House-Pompeo, Karen L.
APPLICANT: Speciale, Pietro

APPLICANT: Joh, Danny
APPLICANT: MCGAVIN, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
TITLE OF INVENTION: AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TRMK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-5000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-09-010-317-5

Query Match 95.6%; Score 197; DB 4; Length 38;
Best Local Similarity 97.4%; Pred. No. 6.7e-20;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QNSGNSFEEDTEEDKPKYEQGNIVDIDFDSVPQIHG 38
Db 1 QNSGNSFEEDTEEDKPKYEQGNIVDIDFDSVPQIHG 38

RESULT 4
US-08-259-000-3
Sequence 3, Application US/08259000

Patent No. 5571514
GENERAL INFORMATION:
APPLICANT: HOOK, Magnus
APPLICANT: LINDBERG, Martin Kjell
APPLICANT: SIGNAS, Lars Christer
APPLICANT: WADSTROM, Torkel Mikael
APPLICANT: FROMAN, Gunnar
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN AS WELL AS
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Burns, Doane, Swecker & Mathis
STREET: P.O. Box 1404
CITY: Alexandria
STATE: Virginia
COUNTRY: United States
ZIP: 2213-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/259,000
FILING DATE: 13-JUN-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: SE 8702272-9
FILING DATE: 01-JUN-1987
ATTORNEY/AGENT INFORMATION:
NAME: Meuch, Donna M
REGISTRATION NUMBER: 36,607
REFERENCE/DOCKET NUMBER: 012885-062
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 114 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-259-000-3

Query Match 95.6%; Score 197; DB 1; Length 114;
Best Local Similarity 97.4%; Pred. No. 2.5e-19;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ONSGNQSFEDTEEDKPKYEGQPNIVDIDFDSVPQIHG 38
|||
DB 2 ONSGNQSFEDTEEDKPKYEGQGNIVDIDFDSVPQIHG 39

RESULT 5
US-08-459-135A-7
Sequence 7, Application US/08459135A
Patent No. 5955078
GENERAL INFORMATION:
APPLICANT: BURNHAM, Martin Karl Russel
APPLICANT: CHOPRA, Ian
APPLICANT: CRITCHLEY, Ian Alfred
APPLICANT: KNOWLES, David Justin Charles
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN: MONOCLONAL ANTIBODY AND THEIR US
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
STATE: PA
COUNTRY: U.S.A.
ZIP: 19406-0939
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: Fastseq, Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/459,135A
FILING DATE: 02-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB/94/00215
FILING DATE: 04-Feb-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Gimm, Edward R
REGISTRATION NUMBER: 38,891
REFERENCE/DOCKET NUMBER: P30591C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-4478
TELEFAX: 610-270-5090
TELEX:
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:

LENGTH: 130 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-459-135A-7

Query Match 95.6%; Score 197; DB 2; Length 130;
Best Local Similarity 97.4%; Pred. No. 3e-19;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ONSGNQSFEDTEEDKPKYEGQPNIVDIDFDSVPQIHG 38
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DB 2 ONSGNQSFEDTEEDKPKYEGQGNIVDIDFDSVPQIHG 39

RESULT 6
US-08-459-135A-8
Sequence 8, Application US/08459135A
Patent No. 5955078
GENERAL INFORMATION:
APPLICANT: BURNHAM, Martin Karl Russel
APPLICANT: CHOPRA, Ian
APPLICANT: CRITCHLEY, Ian Alfred
APPLICANT: KNOWLES, David Justin Charles
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN: MONOCLONAL ANTIBODY AND THEIR US
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
STATE: PA
COUNTRY: U.S.A.
ZIP: 19406-0939
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: Fastseq, Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/459,135A
FILING DATE: 02-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB/94/00215
FILING DATE: 04-Feb-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Gimm, Edward R
REGISTRATION NUMBER: 38,891
REFERENCE/DOCKET NUMBER: P30591C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-4478
TELEFAX: 610-270-5090
TELEX:
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 130 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-459-135A-8

Query Match 95.6%; Score 197; DB 2; Length 130;
Best Local Similarity 97.4%; Pred. No. 3e-19;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ONSGNQSFEDTEEDKPKYEGQPNIVDIDFDSVPQIHG 38
|||
DB 2 ONSGNQSFEDTEEDKPKYEGQGNIVDIDFDSVPQIHG 39

RESULT 7
US-08-495-559-7

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; Sequence 7, Application US/08495559A
; Patent No. 6054572
; GENERAL INFORMATION:
; APPLICANT: BURHAM, Martin Karl Russel
; APPLICANT: CHOPRA, Ian
; APPLICANT: CRITCHLEY, Ian Alfred
; APPLICANT: KNOWLES, David Justin Charles
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN: MONOCLONAL
; TITLE OF INVENTION: ANTIBODY AND THEIR USE IN PREVENTING BACTERIAL ADHESION
; FILE REFERENCE: P30591
; CURRENT APPLICATION NUMBER: US/08/495,559A
; CURRENT FILING DATE: 1995-08-03
; EARLIER APPLICATION NUMBER: GB 9302289.5
; EARLIER FILING DATE: 1993-02-05
; EARLIER APPLICATION NUMBER: GB 9321592.9
; EARLIER FILING DATE: 1993-10-20
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 7
; LENGTH: 130
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
; US-08-495-559-7

Query Match      95.6%; Score 197; DB 3; Length 130;
Best Local Similarity 97.4%; Pred. No. 3e-19;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1  QNSGNQSFEDTDEBKPKYEGQPNIVIDIDFDSVPQIHG 38
Db      2  QNSGNQSFEDTDEBKPKYEGQGNIVIDIDFDSVPQIHG 39

RESULT 8
; Sequence 8, Application US/08495559A
; Patent No. 6054572
; GENERAL INFORMATION:
; APPLICANT: BURHAM, Martin Karl Russel
; APPLICANT: CHOPRA, Ian
; APPLICANT: CRITCHLEY, Ian Alfred
; APPLICANT: KNOWLES, David Justin Charles
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN: MONOCLONAL
; TITLE OF INVENTION: ANTIBODY AND THEIR USE IN PREVENTING BACTERIAL ADHESION
; FILE REFERENCE: P30591
; CURRENT APPLICATION NUMBER: US/08/495,559A
; CURRENT FILING DATE: 1995-08-03
; EARLIER APPLICATION NUMBER: GB 9302289.5
; EARLIER FILING DATE: 1993-02-05
; EARLIER APPLICATION NUMBER: GB 9321592.9
; EARLIER FILING DATE: 1993-10-20
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 8
; LENGTH: 130
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
; US-08-495-559-8

Query Match      95.6%; Score 197; DB 3; Length 130;
Best Local Similarity 97.4%; Pred. No. 3e-19;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1  QNSGNQSFEDTDEBKPKYEGQPNIVIDIDFDSVPQIHG 38
Db      2  QNSGNQSFEDTDEBKPKYEGQGNIVIDIDFDSVPQIHG 39

RESULT 9
; Sequence 8, Application US/08456253
; Patent No. 6288214
; GENERAL INFORMATION:
; APPLICANT: BURHAM, Martin Karl Russel
; APPLICANT: CHOPRA, Ian
; APPLICANT: CRITCHLEY, Ian Alfred
; APPLICANT: KNOWLES, David Justin Charles
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN: MONOCLONAL
; TITLE OF INVENTION: ANTIBODY AND THEIR USE IN PREVENTING BACTERIAL ADHESION
; FILE REFERENCE: P30591
; CURRENT APPLICATION NUMBER: US/08/456,253
; CURRENT FILING DATE: 1995-08-03
; EARLIER APPLICATION NUMBER: GB 9302289.5
; EARLIER FILING DATE: 1993-02-05
; EARLIER APPLICATION NUMBER: GB 9321592.9
; EARLIER FILING DATE: 1993-10-20
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 9
; LENGTH: 130
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
; US-08-456-253-8

Query Match      95.6%; Score 197; DB 3; Length 130;
Best Local Similarity 97.4%; Pred. No. 3e-19;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1  QNSGNQSFEDTDEBKPKYEGQPNIVIDIDFDSVPQIHG 38
Db      2  QNSGNQSFEDTDEBKPKYEGQGNIVIDIDFDSVPQIHG 39

RESULT 10
; Sequence 10, Application US/08459135A
; Patent No. 5955078
; GENERAL INFORMATION:
; APPLICANT: BURHAM, Martin Karl Russel
; APPLICANT: CHOPRA, Ian
; APPLICANT: CRITCHLEY, Ian Alfred
; APPLICANT: KNOWLES, David Justin Charles
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN: MONOCLONAL
; TITLE OF INVENTION: ANTIBODY AND THEIR USE IN PREVENTING BACTERIAL ADHESION
; FILE REFERENCE: P30591
; CURRENT APPLICATION NUMBER: US/08/459,135A
; CURRENT FILING DATE: 1995-08-03
; EARLIER APPLICATION NUMBER: GB 9302289.5
; EARLIER FILING DATE: 1993-02-05
; EARLIER APPLICATION NUMBER: GB 9321592.9
; EARLIER FILING DATE: 1993-10-20
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 10
; LENGTH: 130
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
; US-08-459-135A-10

Query Match      95.6%; Score 197; DB 3; Length 139;
Best Local Similarity 97.4%; Pred. No. 3.2e-19;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1  QNSGNQSFEDTDEBKPKYEGQPNIVIDIDFDSVPQIHG 38
Db      16 QNSGNQSFEDTDEBKPKYEGQGNIVIDIDFDSVPQIHG 53
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; APPLICANT: Hook, Magnus
; APPLICANT: Patti, Joseph M.
; APPLICANT: House-Pomero, Karen
; APPLICANT: Stenham, Narayana
; APPLICANT: Symersky, Jindrich
; TITLE OF INVENTION: COLLAGEN BINDING PROTEIN COMPOSITIONS
; TITLE OF INVENTION: AND METHODS OF USE
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: U.S.
; ZIP: 77210

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/856,253
; FILING DATE: Concurrently Herewith
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/017,678
; FILING DATE: 16-MAY-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Kitchell, Barbara S.
; REGISTRATION NUMBER: 33,928
; REFERENCE/DOCKET NUMBER: TAMK:193
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (512) 418-3000
; TELEFAX: (512) 474-7577
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 139 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; US-08-856-253-8

Query Match      95.6%; Score 197; DB 3; Length 139;
Best Local Similarity 97.4%; Pred. No. 3.2e-19;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1  QNSGNQSFEDTDEBKPKYEGQPNIVIDIDFDSVPQIHG 38
Db      16 QNSGNQSFEDTDEBKPKYEGQGNIVIDIDFDSVPQIHG 53

RESULT 10
; Sequence 10, Application US/08459135A
; Patent No. 5955078
; GENERAL INFORMATION:
; APPLICANT: BURHAM, Martin Karl Russel
; APPLICANT: CHOPRA, Ian
; APPLICANT: CRITCHLEY, Ian Alfred
; APPLICANT: KNOWLES, David Justin Charles
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN: MONOCLONAL
; TITLE OF INVENTION: ANTIBODY AND THEIR USE IN PREVENTING BACTERIAL ADHESION
; FILE REFERENCE: P30591
; CURRENT APPLICATION NUMBER: US/08/459,135A
; CURRENT FILING DATE: 1995-08-03
; EARLIER APPLICATION NUMBER: GB 9302289.5
; EARLIER FILING DATE: 1993-02-05
; EARLIER APPLICATION NUMBER: GB 9321592.9
; EARLIER FILING DATE: 1993-10-20
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corporation
; STREET: 709 Swedeland Road
; CITY: King of Prussia
; STATE: PA
; COUNTRY: U.S.A.
; ZIP: 19406-0939
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
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SOFTWARE: FastSeq, Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/459,135A
FILING DATE: 02-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB/94/00215
FILING DATE: 04-Feb-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Gimmil, Edward R
REGISTRATION NUMBER: 38,891
REFERENCE/DOCKET NUMBER: P30591C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-4478
TELEFAX: 610-270-5090
TELEX:
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 174 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: Protein
US-08-459-135A-10

Query Match 95.6%; Score 197; DB 2; Length 174;
Best Local Similarity 97.4%; Pred. No. 4.2e-19;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ONSGNQSFEDTDEDPKPYEQGNIVDIDFDSVPQIHG 38
Db 2 ONSGNQSFEDTDEDPKPYEQGNIVDIDFDSVPQIHG 39

RESULT 11
US-08-459-135A-13
Sequence 13, Application US/08459135A
Patent No. 5955078
GENERAL INFORMATION:
APPLICANT: BURHAM, Martin Karl Russel
APPLICANT: CHOPRA, Ian
APPLICANT: CRITCHLEY, Ian Alfred
APPLICANT: KNOWLES, David Justin Charles
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN: MONOCLONAL ANTIBODY AND THEIR US
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSER: Smithkline Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
STATE: PA
COUNTRY: U.S.A.
ZIP: 19406-0939
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: Fastseq, Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/459,135A
FILING DATE: 02-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB/94/00215
FILING DATE: 04-Feb-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Gimmil, Edward R
REGISTRATION NUMBER: 38,891
REFERENCE/DOCKET NUMBER: P30591C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-4478
TELEFAX: 610-270-5090
TELEX:

INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 174 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-459-135A-13

Query Match 95.6%; Score 197; DB 2; Length 174;
Best Local Similarity 97.4%; Pred. No. 4.2e-19;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ONSGNQSFEDTDEDPKPYEQGNIVDIDFDSVPQIHG 38
Db 2 ONSGNQSFEDTDEDPKPYEQGNIVDIDFDSVPQIHG 39

RESULT 12
US-08-495-559-10
Sequence 10, Application US/08495559A
Patent No. 6054572
GENERAL INFORMATION:
APPLICANT: BURHAM, Martin Karl Russel
APPLICANT: CHOPRA, Ian
APPLICANT: CRITCHLEY, Ian Alfred
APPLICANT: KNOWLES, David Justin Charles
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN: MONOCLONAL
FILE REFERENCE: P30591
CURRENT APPLICATION NUMBER: US/08/495,559A
CURRENT FILING DATE: 1995-08-03
EARLIER APPLICATION NUMBER: GB 9302289.5
EARLIER FILING DATE: 1993-02-05
EARLIER APPLICATION NUMBER: GB 9321592.9
EARLIER FILING DATE: 1993-10-20
NUMBER OF SEQ ID NOS: 13
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 10
LENGTH: 174
TYPE: PRP
ORGANISM: Staphylococcus aureus
US-08-495-559-10

Query Match 95.6%; Score 197; DB 3; Length 174;
Best Local Similarity 97.4%; Pred. No. 4.2e-19;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ONSGNQSFEDTDEDPKPYEQGNIVDIDFDSVPQIHG 38
Db 2 ONSGNQSFEDTDEDPKPYEQGNIVDIDFDSVPQIHG 39

RESULT 13
US-08-495-559-13
Sequence 13, Application US/08495559A
Patent No. 6054572
GENERAL INFORMATION:
APPLICANT: BURHAM, Martin Karl Russel
APPLICANT: CHOPRA, Ian
APPLICANT: CRITCHLEY, Ian Alfred
APPLICANT: KNOWLES, David Justin Charles
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN: MONOCLONAL
FILE REFERENCE: P30591
CURRENT APPLICATION NUMBER: US/08/495,559A
CURRENT FILING DATE: 1995-08-03
EARLIER APPLICATION NUMBER: GB 9302289.5
EARLIER FILING DATE: 1993-02-05
EARLIER APPLICATION NUMBER: GB 9321592.9
EARLIER FILING DATE: 1993-10-20
NUMBER OF SEQ ID NOS: 13
SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 13
LENGTH: 174
TYPE: PRT
ORGANISM: Staphylococcus aureus
US-08-495-559-13

Query Match 95.6%; Score 197; DB 3; Length 174;
Best Local Similarity 97.4%; Pred. No. 4,3e-19;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QNSGNQSFEDTDEKPKRYEGGPNIVIDFDSVPQIHG 38
Db 2 QNSGNQSFEDTDEKPKRYEGGPNIVIDFDSVPQIHG 39

RESULT 14
US-08-495-559-6
Sequence 6, Application US/08495559A
Patent No. 6054572
GENERAL INFORMATION:
APPLICANT: BURHAM, Martin Karl Russel
APPLICANT: CHOPRA, Ian
APPLICANT: CRITCHLEY, Ian Alfred
APPLICANT: KNOWLES, David Justin Charles
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN: MONOCLONAL
TITLE OF INVENTION: ANTIBODY AND THEIR USE IN PREVENTING BACTERIAL ADHESION
FILE REFERENCE: P30591
CURRENT APPLICATION NUMBER: US/08/495,559A
EARLIER FILING DATE: 1995-08-03
EARLIER APPLICATION NUMBER: GB 9302289.5
EARLIER FILING DATE: 1993-02-05
EARLIER APPLICATION NUMBER: GB 9321592.9
EARLIER FILING DATE: 1993-10-20
NUMBER OF SEQ ID NOS: 13
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 6
LENGTH: 176
TYPE: PRT
ORGANISM: Staphylococcus aureus
US-08-495-559-6

Query Match 95.6%; Score 197; DB 3; Length 176;
Best Local Similarity 97.4%; Pred. No. 4,3e-19;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QNSGNQSFEDTDEKPKRYEGGPNIVIDFDSVPQIHG 38
Db 2 QNSGNQSFEDTDEKPKRYEGGPNIVIDFDSVPQIHG 39

RESULT 15
US-08-459-135A-12
Sequence 12, Application US/08459135A
Patent No. 5955078
GENERAL INFORMATION:
APPLICANT: BURHAM, Martin Karl Russel
APPLICANT: CHOPRA, Ian
APPLICANT: CRITCHLEY, Ian Alfred
APPLICANT: KNOWLES, David Justin Charles
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN: MONOCLONAL ANTIBODY AND THEIR US
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Smithkline Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
STATE: PA
COUNTRY: U.S.A.
ZIP: 19406-0939
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: Fastseq, Version 2.0

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/459,135A
FILING DATE: 02-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB/94/00215
FILING DATE: 04-Feb-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Gimm, Edward R
REGISTRATION NUMBER: 38,891
REFERENCE/DOCKET NUMBER: P30591C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-4478
TELEFAX: 610-270-5090
TELEX:
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 178 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: Protein
US-08-459-135A-12

Query Match 95.6%; Score 197; DB 2; Length 178;
Best Local Similarity 97.4%; Pred. No. 4,3e-19;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QNSGNQSFEDTDEKPKRYEGGPNIVIDFDSVPQIHG 38
Db 2 QNSGNQSFEDTDEKPKRYEGGPNIVIDFDSVPQIHG 39

Search completed: October 22, 2005, 05:46:45
Job time : 22.2223 secs

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OM protein - protein search, using SW model

Run on: October 22, 2005, 11:35:03 ; Search time 70.1256 Seconds
(without alignments)
226.232 Million cell updates/sec

Title: US-10-731-238-43

Perfect score: 206
Sequence: 1 ONSGNSFEDTEEDKPKYEGQPNIVIDFDSVPQIHG 38

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Total number of hits satisfying chosen parameters: 1862951

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

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22: /cgn2_6/ptodata/2/pubppaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysts of the total score distribution.

SUMMARIES

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4	197	95.6	388	8	US-08-901-062-1
5	197	95.6	559	15	US-10-329-624-5251
6	197	95.6	559	15	US-08-781-986A-5251
7	197	95.6	767	9	US-09-815-242-5899
8	197	95.6	767	9	US-09-815-242-13140
9	197	95.6	940	17	US-10-470-048B-424
10	197	95.6	948	17	US-10-470-048B-65
11	197	95.6	961	15	US-10-282-122A-43778

12	197	95.6	1018	9	US-09-815-242-5797
13	197	95.6	1018	9	US-09-815-242-12838
14	197	95.6	1018	17	US-10-470-048B-68
15	197	95.6	1027	8	US-08-781-986A-5254
16	197	95.6	1027	15	US-10-329-624-5254
17	197	95.6	1038	15	US-10-282-122A-43827
18	197	95.6	1038	18	US-10-731-238-16
19	191	92.7	38	18	US-10-731-238-17
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21	191	92.7	38	18	US-10-731-238-40
22	191	92.7	38	18	US-10-731-238-41
23	190	92.2	38	18	US-10-731-238-38
24	190	92.2	38	18	US-10-731-238-42
25	189	91.7	38	18	US-10-731-238-6
26	189	91.7	978	9	US-09-815-242-5556
27	189	91.7	1001	9	US-09-815-242-12686
28	187	90.8	38	18	US-10-731-238-35
29	187	90.8	38	18	US-10-731-238-49
30	186.5	90.3	39	18	US-10-731-238-56
31	186	90.3	38	18	US-10-731-238-44
32	178.5	86.7	39	18	US-10-731-238-57
33	178	86.4	38	18	US-10-731-238-51
34	172	83.5	38	18	US-10-731-238-46
35	172	83.5	38	18	US-10-731-238-47
36	171	83.0	38	18	US-10-731-238-48
37	170	82.5	38	18	US-10-731-238-8
38	168	81.6	38	18	US-10-731-238-45
39	167	81.1	38	18	US-10-731-238-50
40	155	75.2	36	18	US-10-731-238-58
41	147	71.4	36	18	US-10-731-238-59
42	139	67.5	30	14	US-10-287-821-1
43	139	67.5	31	14	US-10-287-821-2
44	76.5	37.1	37	20	US-11-066-657-1134
45	76	36.9	14	18	US-10-731-238-105

ALIGNMENTS

RESULT 1
US-10-731-238-43
Sequence 43, Application US/10731238
Publication No. US20050123552A1
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
Patti, Joseph M.
House-Pompeo, Karen L.
Speziale, Pietro
John, Danny
McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/731,238
FILING DATE: 10-Dec-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE: 21-Jan-1998
APPLICATION NUMBER: US 60/036,139

FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAMK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 43:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 43:
US-10-731-238-43

Query Match 100.0%; Score 206; DB 18; Length 38;
Best Local Similarity 100.0%; Pred. No. 4,2e-19;
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ONSGNQSFEDTDEDKPYEGGPNIVDIDFDSVPQIHG 38
Db 1 ONSGNQSFEDTDEDKPYEGGPNIVDIDFDSVPQIHG 38

RESULT 2
US-10-731-238-5
Sequence 5, Application US/10731238
Publication No. US20050123552A1
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
Pattl, Joseph M.
House-Pompeo, Karen L.
Speziale, Pietro
Joh, Danny
McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/731,238
FILING DATE: 10-Dec-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE: 21-Jan-1998
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAMK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>

TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-10-731-238-5

Query Match 95.6%; Score 197; DB 18; Length 38;
Best Local Similarity 97.4%; Pred. No. 6,1e-18;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ONSGNQSFEDTDEDKPYEGGPNIVDIDFDSVPQIHG 38
Db 1 ONSGNQSFEDTDEDKPYEGGPNIVDIDFDSVPQIHG 38

RESULT 3
US-09-813-820-8
Sequence 8, Application US/09813820
Patent No. US20020102262A1
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
Pattl, Joseph M.
House-Pompeo, Karen
Shanam, Narayana
Syemsky, Jindrich
TITLE OF INVENTION: COLLAGEN BINDING PROTEIN COMPOSITIONS
AND METHODS OF USE
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: Texas
COUNTRY: U.S.
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/813,820
FILING DATE: 22-Mar-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/856,253
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Kitchell, Barbara S.
REGISTRATION NUMBER: 33,928
REFERENCE/DOCKET NUMBER: TAMK:193
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
TELEFAX: (512) 474-7577
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 139 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-09-813-820-8

Query Match 95.6%; Score 197; DB 9; Length 139;
Best Local Similarity 97.4%; Pred. No. 2,7e-17;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ONSGNQSFEDTDEDKPYEGGPNIVDIDFDSVPQIHG 38
Db 16 ONSGNQSFEDTDEDKPYEGGPNIVDIDFDSVPQIHG 53

RESULT 4
US-08-901-062-1
Sequence 1, Application US/08901062

Publication No. US20020025324A1
GENERAL INFORMATION:
APPLICANT: SEALS, JONATHAN R.
TITLE OF INVENTION: RECOMBINANT BIVALENT BACTERIAL VACCINE
TITLE OF INVENTION: FOR THE PREVENTION OF MASTITIS
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESSES:
ADDRESSEE: HALE AND DORR LLP
STREET: 60 State Street
CITY: Boston
STATE: MA
COUNTRY: United States Of America
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/901,062
FILING DATE: 25-JUL-1997
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Baker, Hollie L.
REGISTRATION NUMBER: 31,321
REFERENCE/DOCKET NUMBER: 106941.153
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 526-6000
TELEFAX: (617) 526-5000
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 388 amino acids
TYPE: amino acid
STRADEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-901-062-1

Query Match 95.6%; Score 197; DB 8; Length 388;
Best Local Similarity 97.4%; Pred. No. 8.7e-17;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QNSGNOSFEEDTEEDKPKYEGGNIVDIDFDSVPQIHG 38
DB 265 QNSGNOSFEEDTEEDKPKYEGGNIVDIDFDSVPQIHG 302

RESULT 5
US-08-781-986A-5251
Sequence 5251, Application US/08781986A
Publication No. US20030054436A1
GENERAL INFORMATION:
APPLICANT: Charles Kunsch
TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
NUMBER OF SEQUENCES: 5255
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COUNTRY: USA
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/781,986A
FILING DATE:
CLASSIFICATION: 435

PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Benson, Bob
REGISTRATION NUMBER: 30,446
REFERENCE/DOCKET NUMBER: PB248BP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8512
TELEFAX: (301) 309-8504
INFORMATION FOR SEQ ID NO: 5251:
SEQUENCE CHARACTERISTICS:
LENGTH: 559 amino acids
TYPE: amino acid
STRADEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-781-986A-5251

Query Match 95.6%; Score 197; DB 8; Length 559;
Best Local Similarity 97.4%; Pred. No. 1.3e-16;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QNSGNOSFEEDTEEDKPKYEGGNIVDIDFDSVPQIHG 38
DB 301 QNSGNOSFEEDTEEDKPKYEGGNIVDIDFDSVPQIHG 338

RESULT 6
US-10-329-624-5251
Sequence 5251, Application US/10329624
Publication No. US20040043037A1
GENERAL INFORMATION:
APPLICANT: Charles Kunsch
GIL H. Choi
Patrick S. Dillon
Craig A. Rosen
Steven C. Barash
Michael R. Fannon
TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
NUMBER OF SEQUENCES: 5256
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COUNTRY: USA
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/329,624
FILING DATE: 27-Dec-2002
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/956,171
FILING DATE: October 20, 1997
APPLICATION NUMBER: 60/009,861
FILING DATE: January 5, 1996
APPLICATION NUMBER: 08/781,986
FILING DATE: January 3, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Mark J. Hyman
REGISTRATION NUMBER: 46,789
REFERENCE/DOCKET NUMBER: PB248P1D1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (240) 314-1224
TELEFAX: (301) 309-8439
INFORMATION FOR SEQ ID NO: 5251:
SEQUENCE CHARACTERISTICS:
LENGTH: 559 amino acids

TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 5251;
US-10-329-624-5251

Query Match 95.6%; Score 197; DB 15; Length 559;
Best Local Similarity 97.4%; Pred. No. 1,3e-16;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QNSGNQSFEDTDEDKPKYEGQPNIVIDIDFDSVPQIHG 38
Db 301 QNSGNQSFEDTDEDKPKYEGQGNIVIDIDFDSVPQIHG 338

RESULT 7
US-09-815-242-5899
Sequence 5899, Application US/09815242
Patent No. US20020061569A1
GENERAL INFORMATION:

APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Karl L.
APPLICANT: Zyskind, Judith W.
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John D.
APPLICANT: Carr, Grant J.
APPLICANT: Yamamoto, Robert T.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in
FILE REFERENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: US/09/815,242

PRIOR FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 5899
LENGTH: 767
TYPE: PRT
ORGANISM: Staphylococcus aureus
US-09-815-242-5899

Query Match 95.6%; Score 197; DB 9; Length 767;
Best Local Similarity 97.4%; Pred. No. 1.9e-16;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QNSGNQSFEDTDEDKPKYEGQPNIVIDIDFDSVPQIHG 38
Db 682 QNSGNQSFEDTDEDKPKYEGQGNIVIDIDFDSVPQIHG 719

RESULT 8
US-09-815-242-13140
Sequence 13140, Application US/09815242
Patent No. US20020061569A1
GENERAL INFORMATION:

APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Karl L.
APPLICANT: Zyskind, Judith W.

APPLICANT: Wall, Daniel
APPLICANT: Trawick, John D.
APPLICANT: Carr, Grant J.
APPLICANT: Yamamoto, Robert T.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in
FILE REFERENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: US/09/815,242

PRIOR FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 13140
LENGTH: 767
TYPE: PRT
ORGANISM: Staphylococcus aureus
US-09-815-242-13140

Query Match 95.6%; Score 197; DB 9; Length 767;
Best Local Similarity 97.4%; Pred. No. 1.9e-16;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QNSGNQSFEDTDEDKPKYEGQPNIVIDIDFDSVPQIHG 38
Db 682 QNSGNQSFEDTDEDKPKYEGQGNIVIDIDFDSVPQIHG 719

RESULT 9
US-10-470-048B-424
Sequence 424, Application US/10470048B
Publication No. US20050037444A1
GENERAL INFORMATION:
APPLICANT: MEINKE ET AL.
TITLE OF INVENTION: A METHOD FOR IDENTIFICATION, ISOLATION AND PRODUCTION OF
FILE REFERENCE: SONN:035US
CURRENT APPLICATION NUMBER: US/10/470,048B
PRIOR FILING DATE: 2003-07-25
NUMBER OF SEQ ID NOS: 603
SOFTWARE: PatentIn version 3.1
SEQ ID NO 424
LENGTH: 940
TYPE: PRT
ORGANISM: Staphylococcus aureus
US-10-470-048B-424

Query Match 95.6%; Score 197; DB 17; Length 940;
Best Local Similarity 97.4%; Pred. No. 2.4e-16;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QNSGNQSFEDTDEDKPKYEGQPNIVIDIDFDSVPQIHG 38
Db 682 QNSGNQSFEDTDEDKPKYEGQGNIVIDIDFDSVPQIHG 719

RESULT 10
US-10-470-048B-69
Sequence 69, Application US/10470048B
Publication No. US20050037444A1

```

; GENERAL INFORMATION:
; APPLICANT: MEINKE ET AL.
; TITLE OF INVENTION: A METHOD FOR IDENTIFICATION, ISOLATION AND PRODUCTION OF
; TITLE OF INVENTION: ANTIGENS TO A SPECIFIC PATHOGEN
; FILE REFERENCE: SONN.035US
; CURRENT APPLICATION NUMBER: US/10/470.0488
; NUMBER OF SEQ ID NOS: 603
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 69
; LENGTH: 948
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
; US-10-470-0488-69

Query Match      95.6%; Score 197; DB 17; Length 948;
Best Local Similarity 97.4%; Pred. No. 2.4e-16;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy      1  QNSGNQSFEDTDEDPKPYEQGPNIVDIDFDSVPQIHG 38
        |||
Db      690  QNSGNQSFEDTDEDPKPYEQGPNIVDIDFDSVPQIHG 727

RESULT 11
US-10-282-122A-43778
; Sequence 43778, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining prior Application data removed - See file Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 43778
; LENGTH: 961
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
; US-10-282-122A-43778
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Query Match      95.6%; Score 197; DB 15; Length 961;
Best Local Similarity 97.4%; Pred. No. 2.5e-16;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy      1  QNSGNQSFEDTDEDPKPYEQGPNIVDIDFDSVPQIHG 38
        |||
Db      693  QNSGNQSFEDTDEDPKPYEQGPNIVDIDFDSVPQIHG 730

RESULT 12
US-09-815-242-5797
; Sequence 5797, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; FILE REFERENCE: ELITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5797
; LENGTH: 1018
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
; US-09-815-242-5797

Query Match      95.6%; Score 197; DB 9; Length 1018;
Best Local Similarity 97.4%; Pred. No. 2.6e-16;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy      1  QNSGNQSFEDTDEDPKPYEQGPNIVDIDFDSVPQIHG 38
        |||
Db      746  QNSGNQSFEDTDEDPKPYEQGPNIVDIDFDSVPQIHG 783

RESULT 13
US-09-815-242-12838
; Sequence 12838, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
```

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; TITLE OF INVENTION: Prokaryotes
; FILE REFERENCE: ELITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12838
; LENGTH: 1018
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
; US-09-815-242-12838

Query Match          95.6%; Score 197; DB 9; Length 1018;
Best Local Similarity 97.4%; Pred. No. 2.6e-16;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 QNSGNQSFEEDEEDKPKYEQGPNIVDIDFDSVPQIHG 38
Db      746 QNSGNQSFEEDEEDKPKYEQGPNIVDIDFDSVPQIHG 783

RESULT 14
US-10-470-048B-68
; Sequence 68, Application US/10470048B
; Publication No. US20050037444A1
; GENERAL INFORMATION:
; APPLICANT: MEINKE ET AL.
; TITLE OF INVENTION: A METHOD FOR IDENTIFICATION, ISOLATION AND PRODUCTION OF
; FILE REFERENCE: S0NN:035US
; CURRENT APPLICATION NUMBER: US/10/470,048B
; CURRENT FILING DATE: 2003-07-25
; NUMBER OF SEQ ID NOS: 603
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 68
; LENGTH: 1018
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
; US-10-470-048B-68

Query Match          95.6%; Score 197; DB 17; Length 1018;
Best Local Similarity 97.4%; Pred. No. 2.6e-16;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 QNSGNQSFEEDEEDKPKYEQGPNIVDIDFDSVPQIHG 38
Db      746 QNSGNQSFEEDEEDKPKYEQGPNIVDIDFDSVPQIHG 783

RESULT 15
US-08-781-986A-5254
; Sequence 5254, Application US/08781986A
; Publication No. US20030054436A1
; GENERAL INFORMATION:
; APPLICANT: Charles Kunach
; TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
; NUMBER OF SEQUENCES: 5255
; CORRESPONDENCE ADDRESS:
; ADDRESS: Human Genome Sciences, Inc.
```

```

; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4mb storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/781,986A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Benson, Bob
; REGISTRATION NUMBER: 30,446
; REFERENCE/DOCKET NUMBER: PB248PP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 5254:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1027 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-781-986A-5254

Query Match          95.6%; Score 197; DB 8; Length 1027;
Best Local Similarity 97.4%; Pred. No. 2.7e-16;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 QNSGNQSFEEDEEDKPKYEQGPNIVDIDFDSVPQIHG 38
Db      755 QNSGNQSFEEDEEDKPKYEQGPNIVDIDFDSVPQIHG 792
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Search completed: October 22, 2005, 12:09:27
Job time : 70.1256 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 22, 2005, 04:14:19 ; Search time 13.8905 Seconds
(without alignments)
263.219 Million cell updates/sec

Title: US-10-731-238-43

Perfect score: 206
Sequence: 1 QNSGNQSFEDTDEDPKPKYEGGNIVDIDFDSVPQIHG 38

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :
1: p1r1: *
2: p1r2: *
3: p1r3: *
4: p1r4: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	197	95.6	940	2	S19702 fibronectin-binding
2	197	95.6	961	2	G90053 fibronectin-binding
3	197	95.6	1018	2	A32192 fibronectin-binding
4	197	95.6	1038	2	H90053 fibronectin-binding
5	61	29.6	1613	2	S39059 protein Brg1 - hum
6	60	29.1	511	1	S31308 aldehyde dehydroge
7	59	28.6	1647	2	S45252 SNF2beta protein -
8	59	28.6	1022	2	S15078 homeotic gene regu
9	58	28.2	720	1	A48723 replication licens
10	57.5	27.9	155	1	RNBTR6 DNA-directed RNA p
11	57.5	27.9	582	2	I48673 matrix metalloprot
12	57.5	27.9	582	2	I38028 matrix metalloprot
13	57.5	27.9	817	2	T03852 protein phosphatas
14	56	27.2	345	2	T33906 fibronectin-binding
15	56	27.2	465	2	S69038 fibronectin-binding
16	55.5	26.9	528	2	C84110 xylan beta-1,4-xy
17	55.5	26.9	1042	2	S42511 RAG-1 protein - ra
18	55.5	26.9	1615	2	JC6510 RAG-1 protein - ra
19	55	26.7	339	2	S07578 legumin storage pr
20	55	26.7	335	2	S07576 legumin storage pr
21	55	26.7	484	2	A24942 legumin B4 precurs
22	55	26.7	669	2	I38029 matrix metalloprot
23	55	26.7	1817	2	T34249 matrix metalloprot
24	54.5	26.5	482	2	T32952 fibronectin-binding
25	54.5	26.5	582	2	I84471 matrix metalloprot
26	54.5	26.5	1273	1	TDR17T leukocyte common a
27	54.5	26.5	1291	1	A28334 protein-tyrosine-p
28	54	26.2	168	2	T33564 fibronectin-binding
29	54	26.2	346	2	S49963 fibronectin-binding

30	54	26.2	596	2	T23193 fibronectin-binding
31	54	26.2	837	2	T19825 fibronectin-binding
32	54	26.2	2500	2	G71605 fibronectin-binding
33	53.5	26.0	5138	2	B96695 fibronectin-binding
34	53	25.7	273	2	T46108 fibronectin-binding
35	53	25.7	335	2	S07578 legumin storage pr
36	53	25.7	335	2	S07576 legumin storage pr
37	53	25.7	1369	2	S58160 fibronectin-binding
38	53	25.7	1536	1	RGRY33 regulatory protein
39	53	25.7	2207	2	T42759 Munc13-3 protein -
40	52.5	25.5	361	2	T51078 related to homeoti
41	52.5	25.5	540	2	B82170 peptide ABC transp
42	52	25.2	195	2	A68110 protein T24E12.11
43	52	25.2	258	2	I53021 tropomyosin T - hum
44	52	25.2	349	2	A68197 protein ZK1127.4 [
45	52	25.2	732	2	T05448 fibronectin-binding

ALIGNMENTS

RESULT 1
S19702
fibronectin-binding protein B - Staphylococcus aureus
C:Species: Staphylococcus aureus
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
C:Accession: S19702
R:Joensen, K.; Signaess, C.; Mueller, H.P.; Lindberg, M.
Eur. J. Biochem. 202, 1041-1048, 1991
A:Title: Two different genes encode fibronectin binding proteins in Staphylococcus aureus
A:Reference number: S19702; MUID:92111475; PMID:1837266
A:Accession: S19702
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-940 <JOB>
A:Cross-references: UNIPROT:053682; EMBL:X62992; NID:949040; PIDN:CAA44726.1; PID:958156;
C:Keywords: fibronectin binding

Query Match 95.6%; Score 197; DB 2; Length 940;
Best Local Similarity 97.4%; Pred. No. 4.4e-17;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QNSGNQSFEDTDEDPKPKYEGGNIVDIDFDSVPQIHG 38
DB 682 QNSGNQSFEDTDEDPKPKYEGGNIVDIDFDSVPQIHG 719

RESULT 2

G90053
fibronectin-binding protein fmbB [imported] - Staphylococcus aureus (strain N315)
C:Species: Staphylococcus aureus
C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
R:Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguchi, M.; Mizutani, U.; Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.; Shibata, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiratsuku, K.
Lancet 357, 1225-1240, 2001
A:Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.
A:Reference number: A89758; MUID:21311952; PMID:1148146
A:Accession: G90053
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-961 <KUR>
A:Cross-references: UNIPROT:Q99RD3; GB:BA000018; PID:G13702452; PIDN:BA843593.1; GSPDB:G
C:Experimental source: strain N315
C:Genetics: fmbB
A:Gene: fmbB

Query Match 95.6%; Score 197; DB 2; Length 961;
Best Local Similarity 97.4%; Pred. No. 4.5e-17;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QNSGNQSFEDTDEDPKPKYEGGNIVDIDFDSVPQIHG 38

Db 693 QNSGNQSFEDTEEDKPKYEGGNIYDIDFDSVPQIHG 730

RESULT 3

A32192
A:Title: fibronectin-binding protein - *Staphylococcus aureus*
C:Species: *Staphylococcus aureus*
C:Date: 31-Jul-1989 #sequence_revision 31-Jul-1989 #text_change 16-Feb-1997
C:Accession: A32192
R:Sjognaas, C.; Raucci, G.; Joensen, K.; Lindgren, P.E.; Anantharamaiah, G.M.; Hoeseck, M.
Proc. Natl. Acad. Sci. U.S.A. 86, 659-703, 1989
A:Title: Nucleotide sequence of the gene for a fibronectin-binding protein from *Staphylo-*
A:Reference number: A32192; MUID:8909898; PMID:2521391
A:Accession: A32192
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1018 <SIG>
A:Cross-references: GB:J04151
C:Keywords: fibronectin binding

Query Match 95.6%; Score 197; DB 2; Length 1018;
Best Local Similarity 97.4%; Pred. No. 4, 8e-17;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 QNSGNQSFEDTEEDKPKYEGGNIYDIDFDSVPQIHG 38
Db 746 QNSGNQSFEDTEEDKPKYEGGNIYDIDFDSVPQIHG 783

RESULT 4

H90053
A:Title: hypothetical protein fnb [imported] - *Staphylococcus aureus* (strain N315)
C:Species: *Staphylococcus aureus*
C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C:Accession: H90053
R:Kuroda, M.; Ohca, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguma, A.; Mizutani-U, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.;
C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramoto, K.
Lancet 357, 1225-1240, 2001
A:Title: Whole genome sequencing of methicillin-resistant *Staphylococcus aureus*.
A:Reference number: A69758; MUID:21311952; PMID:11418146
A:Accession: H90053
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1038 <KUR>
A:Cross-references: UNIPROT:Q99RD2; GB:BA000018; PID:G13702453; PIDN:BA043594.1; GSPDB:C
A:Experimental source: strain N315
C:Genetics:
A:Gene: fnb

Query Match 95.6%; Score 197; DB 2; Length 1038;
Best Local Similarity 97.4%; Pred. No. 4, 9e-17;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 QNSGNQSFEDTEEDKPKYEGGNIYDIDFDSVPQIHG 38
Db 742 QNSGNQSFEDTEEDKPKYEGGNIYDIDFDSVPQIHG 779

RESULT 5

S39059
A:Title: protein BRG1 - human
C:Species: *Homo sapiens* (man)
C:Date: 25-Feb-1994 #sequence_revision 17-Nov-1995 #text_change 09-Jul-2004
C:Accession: S39059
R:Khavari, P.A.; Peterson, C.L.; Tamkun, J.W.; Mendel, D.B.; Crabtree, G.R.
Nature 366, 170-174, 1993
A:Title: BRG1 contains a conserved domain of the SWI2/SNF2 family necessary for normal m
A:Reference number: S39059; MUID:94050144; PMID:8232556
A:Accession: S39059
A:Status: preliminary
A:Molecule type: mRNA

A:Residues: 1-1613 <KHA>
A:Cross-references: UNIPROT:Q9HBD3
C:Superfamily: human SNF2alpha protein; bromodomain homology
F:1451-1506/Domain: bromodomain homology <BRO>

Query Match 29.6%; Score 61; DB 2; Length 1613;
Best Local Similarity 31.8%; Pred. No. 22;
Matches 14; Conservative 9; Mismatches 13; Indels 8; Gaps 1;

OY 1 QNSGNQSFEDTEEDKPKYEGGNIYDIDFDSVPQI 36
Db 657 EBSGSSEEBEBSBEPQAPPTLVPEKKKKIPDSDVSEV 700

RESULT 6

S31308
A:Title: aldehyde dehydrogenase (NAD) (EC 1.2.1.3) 2 precursor, mitochondrial - yeast (*Saccharomy-*
C:Species: *Saccharomyces cerevisiae*
C:Date: 28-May-1993 #sequence_revision 31-Jan-1997 #text_change 09-Jul-2004
C:Accession: S31308
R:Thielen, J.
Submitted to the EMBL Data Library, October 1992
A:Reference number: S31308
A:Accession: S31308
A:Molecule type: DNA
A:Residues: 1-511 <THI>
A:Cross-references: UNIPROT:P32872; EMBL:Z17314; NID:G3361; PIDN:CAA78962.1; PID:G3362
C:Comment: This form is probably mitochondrial.
A:Gene: ALD2
C:Function:
A:Description: catalyzes the oxidation of an aldehyde to an acid using NAD+ and water
A>Note: enzymes with this activity are involved in diverse metabolic pathways in various
C:Superfamily: NAD-dependent aldehyde dehydrogenase; aldehyde dehydrogenase homology
C:Keywords: alcohol metabolism; mitochondrion; NAD; oxidoreductase
F:1-21/Domain: trans peptide (mitochondrion) #status predicted <TMP>
F:22-511/Product: aldehyde dehydrogenase (NAD+) 2 #status predicted <MAT>
F:80-351/Domain: aldehyde dehydrogenase homology <ALD>
F:297-331/Active site: Glu, Cys #status predicted
F:483/Binding site: NAD (Cys) #status predicted

Query Match 29.1%; Score 60; DB 1; Length 511;
Best Local Similarity 42.4%; Pred. No. 7, 6;
Matches 14; Conservative 5; Mismatches 6; Indels 8; Gaps 2;

OY 4 GNSQSFEDTEEDKPKYEGGNIYDIDFDSVPQI 36
Db 361 GN-PFESDT-----RYGQILKIEFDSIPRL 385

RESULT 7

S45252
A:Title: SNF2beta protein - human
C:Species: *Homo sapiens* (man)
C:Date: 10-Dec-1994 #sequence_revision 17-Nov-1995 #text_change 09-Jul-2004
C:Accession: S45252
R:Chiba, H.; Muramatsu, M.; Nomoto, A.; Kato, H.
Nucleic Acids Res. 22, 1815-1820, 1994
A:Title: Two human homologues of *Saccharomyces cerevisiae* SWI2/SNF2 and *Drosophila* brhma
A:Reference number: S45251; MUID:94268902; PMID:8208605
A:Accession: S45252
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-1647 <CHI>
A:Cross-references: UNIPROT:P51532; GB:D66156; NID:G505087; PIDN:BA05143.1; PID:G505088
C:Superfamily: human SNF2alpha protein; bromodomain homology
F:1485-1540/Domain: bromodomain homology <BRO>

Query Match 29.1%; Score 60; DB 2; Length 1647;
Best Local Similarity 31.8%; Pred. No. 30;
Matches 14; Conservative 9; Mismatches 13; Indels 8; Gaps 1;

OY 1 QNSGNQSFEDTEEDKPKYEGGNIYDIDFDSVPQI 36

Db 658 EESGSEEESEEEBQPOAQPPLPVEKKKIPDPDSDDVSEV 701

RESULT 8

153078 homeotic gene regulator - mouse (fragment)

C/Species: Mus sp. (mouse)

C/Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 09-Jul-2004

C/Accession: 153078

R/Randazzo, P.M.; Khavari, P.; Crabtree, G.; Tankun, J.; Rossant, J.

Dev. Biol. 161, 229-242, 1994

A/Title: bryl: a putative murine homologue of the Drosophila braham gene, a homeotic gene

A/Reference number: 153078; MUID:94123856; PMID:7904967

A/Accession: 153078

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: mRNA

A/Residues: 1-1022 <RES>

A/Cross-references: UNIPROT:Q63928; GB:S68108; NID:9545017; PIDN:AA60670.1; PID:9545018

A/Genes: bryl

C/Superfamily: human SNF2alpha protein; bromodomain homology

F:860-915/Domain: bromodomain homology <BRO>

Query Match 28.6%; Score 59; DB 2; Length 1022;

Best Local Similarity 31.8%; Pred. No. 23;

Matches 14; Conservative 9; Mismatches 13; Indels 8; Gaps 1;

1 NSGNQSFEDTEEDKPKYEQG-----NIVIDFDSVQI 36

Db 66 EESGSEEESEEEBQPOAQPPLPVEKKKIPDPDSDDVSEV 109

RESULT 9

A88723 replication licensing factor MCM5 - fission yeast (Schizosaccharomyces pombe)

N/Alternate names: cell division control protein CDC46; cell division control protein nd

C/Species: Schizosaccharomyces pombe

C/Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 09-Jul-2004

C/Accession: A48723; T38702

R/Miyake, S.; Okishio, N.; Samejima, I.; Hiraoka, Y.; Toda, T.; Satoh, I.; Yanagida, M.

Mol. Biol. Cell 4, 1003-1015, 1993

A/Title: Fission yeast genes nda4(+) and nda4(+), mutations of which lead to S-phase blo

A/Reference number: A48723; MUID:94129084; PMID:8298187

A/Accession: A48723

A/Molecule type: DNA

A/Residues: 1-720 <MTY>

A/Cross-references: UNIPROT:P41389; GB:S68467; NID:9545210; PIDN:AA60568.1; PID:9545211

R/Murphy, L.; Harrie, D.; Barrett, B.G.; Rajandream, M.A.; Walsh, S.V.

submitted to the EMBL Data Library, February 1996

A/Reference number: Z21807

A/Accession: T38702

A/Molecule type: DNA

A/Residues: 72-460, 'A', 462-584, 'R', 586-699, 'L', 701-720 <MUR>

A/Cross-references: EMBL:Z69359; PIDN:CAA9329.1; GSPDB:GN00066; SPDB:SPAC3F10.01

C/Comment: The complex of six MCM proteins is one of several proteins that must be bound

phosphorylated and dissociate from the chromatin.

C/Genetics:

A/Genes: nda4+

C/Complex: The predominant form is a heterohexamer of MCM2, MCM3, MCM4, MCM5, MCM6, and

C/Function:

A/Description: part of the replication licensing system that permits DNA replication to

C/Superfamily: replication licensing factor MCM5; MCM homology

C/Keywords: cell cycle control; DNA replication initiation; nucleus

F:132-636/Domain: MCM homology <MCM>

Query Match 28.2%; Score 58; DB 1; Length 720;

Best Local Similarity 36.6%; Pred. No. 20;

Matches 15; Conservative 10; Mismatches 12; Indels 4; Gaps 2;

2 NSGNQSFEDTEEDKPKYEQGPNIVIDFDSV-QIING 38

Db 296 NDGSKSTPLFSSEEEBFLISRTPLNLIISNSISPAIVG 336

RESULT 10

RNBRY6

DNA-directed RNA polymerase (EC 2.7.7.6) chain RPO26 - yeast (Saccharomyces cerevisiae)

N/Alternate names: DNA-directed RNA polymerase 23k chain; DNA-directed RNA polymerase II

C/Species: Saccharomyces cerevisiae

C/Date: 30-Sep-1992 #sequence_revision 30-Sep-1992 #text_change 09-Jul-2004

C/Accession: S13307; A36352; B34588; A38846; S58817

R/Archambault, J.; Schappert, K.T.; Friesen, J.D.

Mol. Cell. Biol. 10, 6123-6131, 1990

A/Title: A suppressor of an RNA polymerase II mutation of Saccharomyces cerevisiae encodes

A/Reference number: A36352; MUID:91061718; PMID:2247052

A/Accession: S13307

A/Molecule type: DNA

A/Residues: 1-155 <ARC1>

A/Cross-references: UNIPROT:P20435; EMBL:M33924; NID:g172452; PIDN:AAA4989.1; PID:g1724;

A/Accession: A36352

A/Molecule type: mRNA

A/Residues: 1-155 <ARC2>

A/Cross-references: GB:M33924; NID:g172452; PIDN:AAA4989.1; PID:g172453

R/Woychik, N.A.; Liao, S.M.; Kolodziej, P.A.; Young, R.A.

Genes Dev. 4, 313-323, 1990

A/Title: Subunits shared by eukaryotic nuclear RNA polymerases.

A/Reference number: A34588; MUID:90249736; PMID:2186966

A/Accession: B34588

A/Status: not compared with conceptual translation

A/Molecule type: DNA

A/Residues: 1-155 <WOY1>

A/Cross-references: GB:X53288; NID:g287823; PIDN:CAA37382.1; PID:g287824

A/Accession: A38846

A/Molecule type: protein

A/Residues: 48-60;99-115 <WOY2>

R/Miller, N.

submitted to the EMBL Data Library, April 1995

A/Description: The sequence of S. cerevisiae cosmid 9677.

A/Reference number: S58816

A/Accession: S58817

A/Molecule type: DNA

A/Residues: 1-155 <MTL>

A/Cross-references: EMBL:U25841; NID:g786295; PIDN:AAB64616.1; PID:g786304; GSPDB:GN00016

C/Comment: This protein is a subunit of DNA-directed RNA polymerases I, II, and III.

C/Genetics:

A/Genes: SGD:RPO26; RPB6; MIPS:YPR187w

A/Cross-references: SGD:S0006391; MIPS:YPR187w

A/Map position: 16R

A/Introns: 7/2

C/Superfamily: DNA-directed RNA polymerase chain RPO26

C/Keywords: nucleotidyltransferase

F:3-42/Region: acidic

F:65-97/Region: basic

Query Match 27.9%; Score 57.5; DB 1; Length 155;

Best Local Similarity 36.7%; Pred. No. 4;

Matches 11; Conservative 7; Mismatches 3; Indels 9; Gaps 1;

2 NSGNQSFEDTEEDKPKYEQG 22

Db 9 NSGNQSFEDTEEDKPKYEQG 38

RESULT 11

I48673 matrix metalloproteinase (EC 3.4.24.-) membrane type precursor - mouse

C/Species: Mus musculus (house mouse)

C/Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 22-Jun-1999

C/Accession: I48673

R/Okada, A.; Bellioq, J.P.; Rouyer, N.; Chenard, M.P.; Rio, M.C.; Chambon, P.; Basset, P.

Proc. Natl. Acad. Sci. U.S.A. 92, 2730-2734, 1995

A/Title: Membrane-type matrix metalloproteinase (MT-MMP) gene is expressed in stromal cel

A/Reference number: I38046; MUID:95224014; PMID:7708715

A/Accession: I48673

A/Status: preliminary; translated from GB/EMBL/DBJ

A: Molecule type: mRNA
A: Residues: 1-582 <RES>
A: Cross-references: EMBL:X83536; NID:9804999; PIDN:CAA58520.1; PID:9805000
C: Species: Homo sapiens (man)
C: Keywords: hydrolyase; metalloproteinase; zinc; zymogen
F:1-23/Domain: signal sequence #status predicted <SIG>
F:24-97/Domain: activation peptide #status predicted <PRO>
F:61-284/Domain: matrix metalloproteinase homology <MP>
F:313-508/Domain: hemopexin repeat homology <PXN>
F:933-233,243,249/binding site: zinc, catalytic (Cys, His, His, His) (inhibited) #status
F:239,243,249/binding site: zinc, catalytic (His) (active) #status predicted
F:240/Active site: Glu #status predicted

Query Match 27.9%; Score 57.5; DB 2; Length 582;
Best Local Similarity 52.0%; Pred. No. 19;
Matches 13; Conservative 3; Mismatches 8; Indels 1; Gaps 1;

Db 307 DKPKPAYPNICDGNFDTVALRG 331

15 DKPKY-ECGPNIVDDPSVQPIHG 38
||||| ||||| :|||: :
Db 307 DKPKPAYPNICDGNFDTVALRG 331

RESULT 12

138028
matrix metalloproteinase 14 (EC 3.4.24.-) membrane type precursor - human
N: Alternate names: matrix metalloproteinase MMP14; membrane type matrix metalloproteinase
C: Species: Homo sapiens (man)
C: Date: 17-May-1996 #sequence revision 17-May-1996 #text change 09-Jul-2004
C: Accession: I38028; G02274; I38046; S78011; S45341; S71384
R: Will, H.; Hinzmann, B.
Eur. J. Biochem. 231, 602-608, 1995
A: Title: cDNA sequence and mRNA tissue distribution of a novel human matrix metalloproteinase
A: Accession: I38028
A: Reference number: I38028; MUID:95377289; PMID:7649159

A: Molecule type: mRNA
A: Status: preliminary; translated from GB/EMBL/DBJ
A: Residues: 1-582 <WILL>
A: Cross-references: UNIPROT:P50281; EMBL:Z48481; NID:9963053; PIDN:CAA88372.1; PID:9963053
R: Luo, G.
submitted to the EMBL Data Library, November 1995
A: Reference number: H00963

A: Accession: G02274
A: Status: preliminary; translated from GB/EMBL/DBJ
A: Molecule type: mRNA
A: Residues: 1-582 <LUO>
A: Cross-references: EMBL:U41078; NID:q1127836; PIDN:AAA83770.1; PID:q1127837
R: Okada, A.; Bellio, J.P.; Rouyer, N.; Chénard, M.P.; Rio, M.C.; Chambon, P.; Basset, B.
Proc. Natl. Acad. Sci. U.S.A. 92, 2730-2734, 1995
A: Title: Membrane-type matrix metalloproteinase (MT-MMP) gene is expressed in stromal cells
A: Reference number: I38046; MUID:95224014; PMID:7708715

A: Accession: I38046
A: Status: translated from GB/EMBL/DBJ
A: Molecule type: mRNA
A: Residues: 1-7, 'S', '9-582 <OKA>
A: Cross-references: EMBL:X83535; NID:9804993; PIDN:CAA58519.1; PID:9804994
R: Seiki, M.
submitted to the EMBL Data Library, January 1994
A: Reference number: S78011

A: Accession: S78011
A: Molecule type: mRNA
A: Residues: 1-7, 'S', '9-337, 'K', '339-582 <SET>
A: Cross-references: EMBL:D26512; NID:q793762; PIDN:BA05519.1; PID:q793763
R: Sato, H.; Takino, T.; Okada, Y.; Cao, J.; Shinagawa, A.; Yamamoto, E.; Seiki, M.
Nature 370, 61-65, 1994
A: Title: A matrix metalloproteinase expressed on the surface of invasive tumour cells.
A: Reference number: S45341; MUID:94286011; PMID:8015608

A: Accession: S45341
A: Status: nucleic acid sequence not shown
A: Molecule type: mRNA
A: Residues: 1-7, 'S', '9-188, 'R', '190, 'A', '192-267, 'K', '269-272, 'HV', '275, 'P', '277-285, 'KQ', '288,
A: Cross-references: EMBL:D26512
R: Sato, H.; Kishimoto, T.; Takino, T.; Nakayama, K.; Seiki, M.
EBBS Lett. 393, 101-104, 1996

A:Title: Activation of a recombinant membrane type 1-matrix metalloproteinase (MT1-MMP)
A:Reference number: S71384; MUID:96397540; PMID:8804434
A:Accession: S71384
A:Molecule type: protein
A:Residues: 112-116 <S>AW>
C:Genetics:
A:Gene: GDB:TMMP14; MT1-MMP
A:Cross-references: GDB:375731; OMIM:600754
A:Map position: 14q11-14q12
C:Species: Caenorhabditis elegans
C:Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
C:Accession: T33906
R:Kaizaki, J., Smith, A., Gibson, A.
Submitted to the EMBL Data Library, February 1999
A:Description: The sequence of C. elegans cosmid Y25C1A.
A:Reference number: Z21437
A:Accession: T33906
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-345 <K>AL>
A:Cross-references: UNIPROT:O9TYW0; EMBL:AF125459; PIDD:AA012844.1; GSPDB:GN00020; CESP:\>

A:Experimental source: strain Bristol N2; clone Y25C1A
C:Genetics:

A:Gene: CESP:Y25C1A.8

A:Map position: 2

A:introns: 45/1; 78/2; 140/3; 230/2; 304/2

Query Match 27.2%; Score 56; DB 2; Length 345;

Best Local Similarity 34.3%; Pred. No. 16;

Matches 12; Conservative 8; Mismatches 13; Indels 2; Gaps 1;

QY 4 NGQSFEDTTERDPRKKEQGNF--VDIDPSVPOI 36

DB 170 GEDEADEDEDEDEDESDLGKYNFDPDDEL 204

RESULT 15

S69038

hypothetical protein YPR152c - yeast (Saccharomyces cerevisiae)

C:Species: Saccharomyces cerevisiae

C:Date: 22-Aug-1996 #sequence_revision 06-Sep-1996 #text_change 09-Jul-2004

C:Accession: S69038

R:Pulson: L.

submitted to the EMBL Data Library, November 1995

A:Description: The sequence of S. cerevisiae cosmid 9659.

A:Reference number: S69022

A:Accession: S69038

A:Molecule type: DNA

A:Residues: 1-465 <FUL>

A:Cross-references: UNIPROT:Q06525; EMBL:U40829; NID:G1066476; PID:G1066497; GSPDB:GN000

C:Genetics:

A:Gene: MIPS:YPR152c

A:Cross-references: SGD:S0006356

A:Map position: 16R

C:Superfamily: formin binding protein; WW repeat homology

F:1-36/Domain: WW repeat homology #status atypical <WW1>

Query Match 27.2%; Score 56; DB 2; Length 465;

Best Local Similarity 38.1%; Pred. No. 22;

Matches 16; Conservative 6; Mismatches 12; Indels 8; Gaps 2;

QY 2 NSGNQSFEDTTERDPRKKEQGNF---IYD---IDPSVPO 35

DB 174 SSGEDDEDEDEDEDENEQIVNQDISIIDLNLRIIDYDIDE 215

Search completed: October 22, 2005, 06:09:49
Job time : 14.8905 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 22, 2005, 04:10:49 ; Search time 69.6361 Seconds
(without alignments)
279.439 Million cell updates/sec

Title: US-10-731-238-43
Perfect score: 206
Sequence: 1 QNSGNQSFEDTIEDPKRYEQGNIVIDIPDSVPQIHG 38

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : UniProt_03:*
1: uniprot_prot:*
2: uniprot_trembl:*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	197	95.6	940 2 Q53682	Q53682 staphylococ
2	197	95.6	943 2 Q8NNU8	Q8NNU8 staphylococ
3	197	95.6	957 2 Q6G6H4	Q6G6H4 staphylococ
4	197	95.6	961 2 Q99RD3	Q99RD3 staphylococ
5	197	95.6	961 2 Q7A3J8	Q7A3J8 staphylococ
6	197	95.6	1018 1 FNB8_STPAU	F14738 staphylococ
7	197	95.6	1038 2 Q99RD2	Q99RD2 staphylococ
8	197	95.6	1038 2 Q7A3J7	Q7A3J7 staphylococ
9	196	95.1	965 2 Q6GDU5	Q6GDU5 staphylococ
10	189	91.7	1015 2 Q8NNU7	Q8NNU7 staphylococ
11	189	91.7	1015 2 Q6G6H3	Q6G6H3 staphylococ
12	186	90.3	152 2 Q9AEP9	Q9AEP9 staphylococ
13	67.5	32.8	1015 2 Q6FRE8	Q6FRE8 candida gla
14	66	32.0	2 Q6CBW0	Q6CBW0 oryza sativ
15	63.5	30.8	923 2 Q6BWM2	Q6BWM2 oryza sativ
16	61	29.6	237 2 Q8BZM9	Q8BZM9 mus musculu
17	61	29.6	455 2 Q6Z097	Q6Z097 mus musculu
18	61	29.6	532 2 Q9D074	Q9D074 mus musculu
19	60.5	29.4	337 2 Q6BWH6	Q6BWH6 debaryomyce
20	60	29.1	311 2 Q9VDY7	Q9VDY7 drosophila
21	60	29.1	467 2 Q8H8X6	Q8H8X6 oryza sativ
22	60	29.1	511 1 DHAY_YEAST	DHAY_YEAST
23	60	29.1	1647 1 SN24_HUMAN	SN24_HUMAN
24	60	29.1	1647 2 Q9HBD3	Q9HBD3 homo sapien
25	60	29.1	1679 2 Q9HBD4	Q9HBD4 homo sapien
26	59	28.6	311 2 Q8SY78	Q8SY78 drosophila
27	59	28.6	311 2 Q9VIO6	Q9VIO6 drosophila
28	59	28.6	684 2 Q64YN9	Q64YN9 bacteroides
29	59	28.6	689 2 Q979U9	Q979U9 thermoplasma
30	59	28.6	1022 2 Q63928	Q63928 mus sp. big
31	59	28.6	1348 2 Q6PAL9	Q6PAL9 mus musculu

32	59	28.6	1613 2 Q8K1P7	Q8K1P7 rattus norv
33	59	28.6	1614 2 Q6AXG8	Q6AXG8 mus musculu
34	58.5	28.4	454 2 Q9JHK1	Q9JHK1 rattus norv
35	58	28.2	230 2 Q918U9	Q918U9 brachydanio
36	58	28.2	533 2 Q94677	Q94677 plasmodium
37	58	28.2	572 2 Q9GSR0	Q9GSR0 plasmodium
38	58	28.2	720 1 MCM5_SCHPO	P41389 echizosacch
39	57.5	27.9	155 1 RPB6_YEAST	P20435 saccharomyc
40	57.5	27.9	191 2 Q6BWS4	Q6BWS4 debaryomyce
41	57.5	27.9	261 2 Q9XS17	Q9XS17 bos taurus
42	57.5	27.9	262 2 Q9BGL3	Q9BGL3 ovis aries
43	57.5	27.9	580 1 MM14_PIG	Q9X190 sus scrofa
44	57.5	27.9	582 1 MM14_HUMAN	P50281 homo sapien
45	57.5	27.9	582 1 MM14_MOUSE	P53690 mus musculu

ALIGNMENTS

```

RESULT 1
Q53682 PRELIMINARY; PRT; 940 AA.
AC Q53682;
DT 01-NOV-1996 (TREMblrel. 01, Created)
DT 01-NOV-1996 (TREMblrel. 01, Last sequence update)
DE 01-MAR-2004 (TREMblrel. 26, Last annotation update)
DE Fibronectin binding protein B.
GN Name=fnbB;
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1280;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=8325-4;
RX MEDLINE=92111475; PubMed=1837266;
RA Jonsson K., Signas C., Muller H.P., Lindberg M.;
RT "Two different genes encode fibronectin binding proteins in
RT Staphylococcus aureus. The complete nucleotide sequence and
RT characterization of the second gene."
RL Eur. J. Biochem. 202:1041-1048(1991).
CC -!- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC an amide bond (By similarity).
DR EMBL: X62992; CAA44726.1; -.
DR PIR: S19702; S19702.
DR HSSP: Q53653; 1N67.
DR GO: GO:0009986; C:cell surface; IEA.
DR GO: GO:0005618; C:cell wall; IEA.
DR GO: GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO: GO:0016020; C:membrane; IEA.
DR GO: GO:0007155; P:cell adhesion; IEA.
DR InterPro: IPR008966; Adhes_Dact.
DR InterPro: IPR004237; Fn_bind.
DR InterPro: IPR005877; Gpos_YsIRK.
DR InterPro: IPR001899; Gram_pos_anchor.
DR Pfam: PF02986; Fn_bind; 2.
DR Pfam: PF00746; Gram_pos_anchor; 1.
DR Pfam: PF04650; YsIRK_signal; 1.
DR TIGRPFAM: TIGR01167; LpxTG_anchor; 1.
DR TIGRPFAM: TIGR01168; YsIRK_signal; 1.
DR PROSITE: PS50847; GRAM_POS_ANCHORING; 1.
KW Cell wall; Peptidoglycan-anchor.
SQ SEQUENCE 940 AA; 103555 MW; E35FBBCA907AE345 CRC64;

Query Match 95.6%; Score 197; DB 2; Length 940;
Best Local Similarity 97.4%; Pred. No. 3.6e-15;
Matches 37; Conservatve 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QNSGNQSFEDTIEDPKRYEQGNIVIDIPDSVPQIHG 38
Db 682 QNSGNQSFEDTIEDPKRYEQGNIVIDIPDSVPQIHG 719

RESULT 2

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08NTUB
ID 08NTUB      PRELIMINARY;      PRT:      943 AA.
RA 08NTUB:
RT 01-OCT-2002 (TReMBLrel. 22, Created)
DT 01-OCT-2002 (TReMBLrel. 22, Last annotation update)
DE 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE FndB protein.
GN Name=fndB; OrderedLocustNames=MM2420;
OS Staphylococcus aureus (strain MM2).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=196620;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MM2;
RA MEDLINE=22040717; PubMed=12044378; DOI=10.1016/S0140-6736(02)08713-5;
RA Baba T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Oguchi A.,
RA Yamamoto K., Hiramatsu K.;
RA "Genome and virulence determinants of high virulence community-
RT acquired MRSA.";
RL Lancet 359:1819-1827(2002).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
an amide bond (by similarity).
DR EMBL; AP004830; BAB96285.1; -.
DR HSSP; Q53653; 1n67.
DR GO; GO:0009986; C:cell surface; IEA.
DR GO; GO:0005618; C:cell wall; IEA.
DR GO; GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0007155; P:cell adhesion; IEA.
DR InterPro; IPR008966; Adhes_bact.
DR InterPro; IPR004237; Fn_bind.
DR InterPro; IPR005877; Gpos_YsIRK.
DR Pfam; PF02986; Fn_bind; 1.
DR Pfam; PF00746; Gram_pos_anchor; 1.
DR TIGRFAMs; TIGR01167; LpxTG_anchor; 1.
DR TIGRFAMs; TIGR01168; YsIRK_signal; 1.
DR PROSITE; PS50847; GRAM_POS_ANCHORING; 1.
DR Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ SEQUENCE 943 AA; 104537 MW; DA8A5F31947E1B6A CRC64;

Query Match      95.6%; Score 197; DB 2; Length 943;
Best Local Similarity 97.4%; Pred. No. 3.6e-15;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QNSGNQSFEDTDEDPKPYEGQPNIVDIDFDSVPQING 38
DB 689 QNSGNQSFEDTDEDPKPYEGQGNIVDIDFDSVPQIHG 726

RESULT 3
O6G6H4 PRELIMINARY;      PRT:      957 AA.
ID O6G6H4:
AC O6G6H4:
RT 05-JUN-2004 (TReMBLrel. 27, Created)
DT 05-JUN-2004 (TReMBLrel. 27, Last annotation update)
DE Fibronectin-binding protein.
GN Name=fnbB; OrderedLocustNames=SA52387;
OS Staphylococcus aureus (strain MSSA476).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=282459;
RN [1]
RP SEQUENCE FROM N.A.
RC PubMed=15213324; DOI=10.1073/pnas.0402521101;
RA Holden M.T.G., Fell E.J., Lindsay J.A., Peacock S.J., Day N.P.J.,
RA Enright M.C., Foster T.J., Moore C.E., Hurst L., Atkin R., Barron A.,
RA Baason N., Bentley S.D., Chillingworth C., Chillingworth T.,
RA Churcher C., Clark L., Cotton C., Cronin A., Doggett J., Dowd L.,
RA Feltham T., Hance Z., Harris B., Hauser H., Holtroyd S., Jagels K.,
RA James K.D., Lennard N., Line A., Mayes R., Moule S., Mungall K.,
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RA Ormond D., Quail M.A., Rabinowitsch E., Rutherford K.M., Sanders M.,
RA Sharp S., Simmonds M., Stevens K., Whitehead S., Barrall B.G.,
RA Spratt B.G., Parkhill J.;
RT "Complete genomes of two clinical Staphylococcus aureus strains:
RT evidence for the rapid evolution of virulence and drug resistance.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:9786-9791(2004).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
an amide bond (by similarity).
DR EMBL; BX571857; CAG44201.1; -.
DR GO; GO:0009986; C:cell surface; IEA.
DR GO; GO:0005618; C:cell wall; IEA.
DR GO; GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0007155; P:cell adhesion; IEA.
DR InterPro; IPR008966; Adhes_bact.
DR InterPro; IPR004237; Fn_bind.
DR InterPro; IPR005877; Gpos_YsIRK.
DR InterPro; IPR001899; Gram_pos_anchor.
DR Pfam; PF02986; Fn_bind; 1.
DR Pfam; PF00746; Gram_pos_anchor; 1.
DR TIGRFAMs; TIGR01167; LpxTG_anchor; 1.
DR TIGRFAMs; TIGR01168; YsIRK_signal; 1.
DR PROSITE; PS50847; GRAM_POS_ANCHORING; 1.
DR Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ SEQUENCE 957 AA; 105980 MW; 28F8BA7FFDD3EAF CRC64;
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QY 1 QNSGNQSFEDTDEDPKPYEGQPNIVDIDFDSVPQING 38
DB 689 QNSGNQSFEDTDEDPKPYEGQGNIVDIDFDSVPQIHG 726

RESULT 4
O99RD3 PRELIMINARY;      PRT:      961 AA.
ID O99RD3:
AC O99RD3:
RT 01-JUN-2001 (TReMBLrel. 17, Created)
DT 01-JUN-2001 (TReMBLrel. 17, Last sequence update)
DE Fibronectin-binding protein homolog.
GN Name=fnbB; OrderedLocustNames=SAV2502;
OS Staphylococcus aureus (strain Mu50 / ATCC 700699).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=158878;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Mu50 / ATCC 700699;
RA MEDLINE=21311952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2;
RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Itoh T.,
RA Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hoshiyama A.,
RA Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kato C.,
RA Sekimizu K., Hiramatsu H., Kuhara S., Goto S., Yabuzaki J.,
RA Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
RA Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
RT "Whole genome sequencing of methicillin-resistant Staphylococcus
RT aureus.";
RL Lancet 357:1225-1240(2001).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
an amide bond (by similarity).
DR EMBL; AP003365; BAB58664.1; -.
DR PIR; G90053; G90053.
DR HSSP; Q53653; 1n67.
DR GO; GO:0009986; C:cell surface; IEA.
DR GO; GO:0005618; C:cell wall; IEA.
DR GO; GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0007155; P:cell adhesion; IEA.
DR InterPro; IPR008966; Adhes_bact.
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DR InterPro; IPR004237; Fn_bind.
DR InterPro; IPR005877; Gpos_YsIRK.
DR InterPro; IPR001899; Gram_pos_anchor.
DR Pfam; PF02986; Fn_bind; 1.
DR Pfam; PF00746; Gram_pos_anchor; 1.
DR Pfam; PF04650; YsIRK_signal; 1.
DR TIGRfams; TIGR01167; LPXTG_anchor; 1.
DR TIGRfams; TIGR01168; YsIRK_signal; 1.
DR PROSITE; PS50847; GRAM_POS_ANCHORING; 1.
KW Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ SEQUENCE 961 AA; 106010 MW; 364940F884EA4101 CRC64;

Query Match 95.6%; Score 197; DB 2; Length 961;
Best Local Similarity 97.4%; Pred. No. 3.7e-15;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QNSGNQSFEDTBDKPKYEGQGNIVDIDFDSVPQIHG 38
DB 693 QNSGNQSFEDTBDKPKYEGQGNIVDIDFDSVPQIHG 730

RESULT 5
ID Q7A3J8 PRELIMINARY; PRT; 961 AA.
AC Q7A3J8;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE FnBb protein.
OS Name=FnBb; OrderedLocustNames=SA2290;
OC Staphylococcus aureus (Strain N315).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
NCBI_Taxid=158879;

RP SEQUENCE FROM N.A.
RX MEDLINE=2111952; PubMed=1118146; DOI=10.1016/S0140-6736(00)04403-2;
RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Lian J.-Q., Ito T.,
RA Kanamori M., Matsunari H., Maruyama A., Murakami H., Hosoyama A.,
RA Mizutani-Uji Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
RA Sekimizu K., Hirakawa H., Kohara S., Goto S., Yabuuchi J.,
RA Kanehisa M., Yamashita A., Oshino K., Furuya K., Yoshino C., Shiba T.,
RA Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.,
RT "Whole genome sequencing of methicillin-resistant Staphylococcus
RT aureus";
RL Lancet 357:1225-1240(2001).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC an amide bond (By similarity).

CC EMBL; AP003137; BAB43593.1; -;
DR GO; GO:0009986; C:cell surface; IEA.
DR GO; GO:0005618; C:cell wall; IEA.
DR GO; GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR InterPro; IPR008966; Adhes_Dact.
DR InterPro; IPR004237; Fn_bind.
DR InterPro; IPR005877; Gpos_YsIRK.
DR InterPro; IPR001899; Gram_pos_anchor.
DR Pfam; PF02986; Fn_bind; 1.
DR Pfam; PF00746; Gram_pos_anchor; 1.
DR Pfam; PF04650; YsIRK_signal; 1.
DR TIGRfams; TIGR01167; LPXTG_anchor; 1.
DR TIGRfams; TIGR01168; YsIRK_signal; 1.
DR PROSITE; PS50847; GRAM_POS_ANCHORING; 1.
KW Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ SEQUENCE 961 AA; 106010 MW; 364940F884EA4101 CRC64;

Query Match 95.6%; Score 197; DB 2; Length 961;
Best Local Similarity 97.4%; Pred. No. 3.7e-15;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QNSGNQSFEDTBDKPKYEGQGNIVDIDFDSVPQIHG 38

DB 693 QNSGNQSFEDTBDKPKYEGQGNIVDIDFDSVPQIHG 730

RESULT 6
ID FNB_A STAAU STANDARD; PRT; 1018 AA.
AC P14738;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Fibronectin-binding protein precursor (FNBp).
GN Name=fnbA;
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
NCBI_Taxid=1280;

RP SEQUENCE FROM N.A.
RX STRAIN=NCTC 8325-4;
RX MEDLINE=89098998; PubMed=2521391;
RA Stignas C., Raucet G., Joensson K., Lindgren P.-E.,
RA Anantharamaiah G.M., Hoeck M., Lindberg M.,
RT "Nucleotide sequence of the gene for a fibronectin-binding protein
RT from Staphylococcus aureus: use of this peptide sequence in the
RT synthesis of biologically active peptides";
Proc. Natl. Acad. Sci. U.S.A. 86:699-703(1989).

-1- FUNCTION: The ability of bacteria to bind fibronectin has been
proposed as a virulence factor enabling bacteria to colonize wound
tissues and blood clots. Binding of plasma fibronectin to the
bacterial surface might block adhesion receptors on S.aureus, thus
representing an important defense mechanism against tissue
invasion.

-1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
an amide bond (Potential).

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CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).

CC EMBL; J04151; AAA26632.1; -;
DR InterPro; IPR004237; Fn_bind.
DR InterPro; IPR005877; Gpos_YsIRK.
DR InterPro; IPR001899; Gram_pos_anchor.
DR Pfam; PF02986; Fn_bind; 1.
DR Pfam; PF00746; Gram_pos_anchor; 1.
DR Pfam; PF04650; YsIRK_signal; 1.
DR TIGRfams; TIGR01167; LPXTG_anchor; 1.
DR TIGRfams; TIGR01168; YsIRK_signal; 1.
DR PROSITE; PS50847; GRAM_POS_ANCHORING; 1.
KW Cell adhesion; Cell wall; Peptidoglycan-anchor; Repeat; Signal;
KW Virulence.

FT SIGNAL 1 36
FT CHAIN 37 985
FT PROPEP 986 1018
FT REPEAT 545 574
FT REPEAT 575 604
FT DOMAIN 745 878
FT REPEAT 745 878
FT REPEAT 745 878
FT REPEAT 783 820
FT REPEAT 821 859
FT REPEAT 860 878
FT DOMAIN 879 948
FT REPEAT 879 892
FT REPEAT 893 906
FT REPEAT 907 920
FT REPEAT 921 934
FT REPEAT 935 948
FT SITE 982 986
FT MOD_RES 985 985

Fibronectin-binding protein.
Removed by sortase (Potential).
B-1.
B-2.
4 X approximate tandem repeats,
fibronectin-binding domain.
D-1.
D-2.
D-3.
D-4 (incomplete).
5 X tandem repeats, Pro-rich (WR).
WR 1.
WR 2.
WR 3.
WR 4.
WR 5.
LPXTG sorting signal (Potential).
Pentaglycyl murein peptidoglycan amidated

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FT          chreonine (Potential) .
SQ SEQUENCE 1018 AA; 111780 MW; 5815E0020B811F CRC64;
Query Match 95.6%; Score 197; DB 1; Length 1018;
Best Local Similarity 97.4%; Pred. No. 3.9e-15;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QNSGNQSFEDTEBDKPKYEGGPNIVDIDFDSVPQIHG 38
DB 746 QNSGNQSFEDTEBDKPKYEGGPNIVDIDFDSVPQIHG 783

RESULT 7
ID Q99RD2 PRELIMINARY; PRT; 1038 AA.
AC Q99RD2;
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Fibronectin-binding protein homolog.
GN Name=fnb; OrderedLocustNames=SA2503;
OS Staphylococcus aureus (strain Mu50 / ATCC 700699).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=158878;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Mu50 / ATCC 700699;
RX MEDLINE=21311952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2;
RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Iian J.-Q., Ito T.,
RA Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hoshoyama A.,
RA Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
RA Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
RA Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
RA Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
RT "Whole genome sequencing of methicillin-resistant Staphylococcus
RT aureus.";
RL Lancel 357:1225-1240(2001).
CC -I- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC an amide bond (by similarity).
DR EMBL; AP003365; BABS8665.1; -.
DR PIR; H90053; H90053.
DR GO; GO:0009986; C:cell surface; IEA.
DR GO; GO:0005618; C:cell wall; IEA.
DR GO; GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:007155; P:cell adhesion; IEA.
DR InterPro; IPR008966; Adhes_bact.
DR InterPro; IPR004237; Fn_bind.
DR InterPro; IPR005877; Gpos_YsIRK.
DR InterPro; IPR001899; Gram_pos_anchor.
DR Pfam; PF02986; Fn_bind; 1.
DR Pfam; PF00746; Gram_pos_anchor; 1.
DR Pfam; PF04650; YsIRK_signal; 1.
DR TIGRFAMs; TIGR01167; LpxTG_anchor; 1.
DR TIGRFAMs; TIGR01168; YsIRK_signal; 1.
DR PROSITE; PS50847; GRAM_POS_ANCHORING; 1.
KW Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ SEQUENCE 1038 AA; 113618 MW; 666BF6BF2FBBE12 CRC64;

Query Match 95.6%; Score 197; DB 2; Length 1038;
Best Local Similarity 97.4%; Pred. No. 4e-15;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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DT 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE Fnb protein.
GN Name=fnb; OrderedLocustNames=SA2291;
OS Staphylococcus aureus (strain N315).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=158879;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=21311952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2;
RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Iian J.-Q., Ito T.,
RA Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hoshoyama A.,
RA Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
RA Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
RA Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
RA Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
RT "Whole genome sequencing of methicillin-resistant Staphylococcus
RT aureus.";
RL Lancel 357:1225-1240(2001).
CC -I- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC an amide bond (by similarity).
DR EMBL; AP003137; BAB43594.1; -.
DR GO; GO:0009986; C:cell surface; IEA.
DR GO; GO:0005618; C:cell wall; IEA.
DR GO; GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:007155; P:cell adhesion; IEA.
DR InterPro; IPR008966; Adhes_bact.
DR InterPro; IPR004237; Fn_bind.
DR InterPro; IPR005877; Gpos_YsIRK.
DR InterPro; IPR001899; Gram_pos_anchor.
DR Pfam; PF02986; Fn_bind; 1.
DR Pfam; PF00746; Gram_pos_anchor; 1.
DR Pfam; PF04650; YsIRK_signal; 1.
DR TIGRFAMs; TIGR01167; LpxTG_anchor; 1.
DR TIGRFAMs; TIGR01168; YsIRK_signal; 1.
DR PROSITE; PS50847; GRAM_POS_ANCHORING; 1.
KW Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ SEQUENCE 1038 AA; 113618 MW; 666BF6BF2FBBE12 CRC64;

Query Match 95.4%; Score 197; DB 2; Length 1038;
Best Local Similarity 97.4%; Pred. No. 4e-15;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QNSGNQSFEDTEBDKPKYEGGPNIVDIDFDSVPQIHG 38
DB 742 QNSGNQSFEDTEBDKPKYEGGPNIVDIDFDSVPQIHG 779

RESULT 9
ID Q6GDUS PRELIMINARY; PRT; 965 AA.
AC Q6GDUS;
DT 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE Fibronectin-binding protein.
GN Name=fnbA; OrderedLocustNames=SA2580;
OS Staphylococcus aureus (strain MRSA252).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=282458;
RN [1]
RP SEQUENCE FROM N.A.
RC PubMed=15213324; DOI=10.1073/pnae.0402521101;
RA Holden M.T.G., Feil E.J., Lindsay J.A., Peacock S.J., Day N.P.J.,
RA Enright M.C., Foster T.J., Moore C.E., Hurst L., Atkin R., Barton A.,
RA Bacon N., Bentley S.D., Chillingworth C., Chillingworth T.,
RA Churcher C., Clark L., Cotton C., Cronin A., Doggett J., Dowd L.,
RA Feltwell T., Hance Z., Harris B., Hauser H., Holtby S., Jagsels K.,
RA James K.D., Lennard N., Line A., Mayes R., Moule S., Mungall K.,
RA Ormond D., Quail M.A., Rabinowitsch E., Rutherford K.M., Sanders M.,

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RA Sharp S., Simmonds M., Stevens K., Whitehead S., Barrell B.G.,
RA Spratt B.G., Parkhill J.;
RT "Complete genomes of two clinical *Staphylococcus aureus* strains:
RT evidence for the rapid evolution of virulence and drug resistance";
RL Proc. Natl. Acad. Sci. U.S.A. 101:9786-9791(2004).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC an amide bond (By similarity).
DR EMBL: BX571856; CAG41560.1; -;
DR GO: GO:0009986; C:cell surface; IEA.
DR GO: GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO: GO:0016020; C:membrane; IEA.
DR GO: GO:0007155; P:cell adhesion; IEA.
DR InterPro: IPR008966; Adhes_bact.
DR InterPro: IPR004237; Fn_bind.
DR InterPro: IPR005877; Gpos_YsIRK.
DR InterPro: IPR001899; Gram_pos_anchor.
DR Pfam: PF02986; Fn_bind; 1.
DR Pfam: PF00746; Gram_pos_anchor; 1.
DR TIGRFAMs: TIGR01167; LPXTG_anchor; 1.
DR TIGRFAMs: TIGR01168; YsIRK_signal; 1.
DR PROSITE: PS50847; GRAM_POS_ANCHORING; 1.
KW Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ SEQUENCE 965 AA; 105691 MW; 2982E132164D0551 CRC64;

Query Match 95.1%; Score 196; DB 2; Length 965;
Best Local Similarity 94.7%; Pred. No. 4.9e-15;
Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 QNSGNSFEEDTEEDKPKYEGGNIVDIDFDSVPIQG 38
Db 749 QNSGNSFEEDTEEDKPKYEGGNIVDIDFDSVPIQG 786
|||||
RESULT 10
Q8NTU7 PRELIMINARY; PRT; 1015 AA.
ID Q8NTU7
AC Q8NTU7
DT 01-OCT-2002 (TREMblrel. 22, Created)
DT 01-OCT-2002 (TREMblrel. 22, Last sequence update)
DT 01-OCT-2003 (TREMblrel. 25, Last annotation update)
DE Rnb protein.
GN Name=FnD; OrderedLocuNames=MW2421;
OS *Staphylococcus aureus* (strain MW2).
OC Bacteria; Firmicutes; Bacillales; *Staphylococcus*.
OX NCBI_Taxid=196620;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22040717; PubMed=12044378; DOI=10.1016/S0140-6736(02)08713-5;
RX Baba T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Oguchi A.,
RA Nagai Y., Iwano N., Asano K., Naimi T., Kuroda H., Cui L.,
RA Yamamoto K., Hiramatsu K.;
RT "Genome and virulence determinants of high virulence community-
RT acquired MRSA";
RL Lancet 359:1819-1827(2002).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC an amide bond (By similarity).
DR EMBL: AF004830; BAB96286.1; -;
DR GO: GO:0009986; C:cell surface; IEA.
DR GO: GO:0005618; C:cell wall; IEA.
DR GO: GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO: GO:0016020; C:membrane; IEA.
DR GO: GO:0007155; P:cell adhesion; IEA.
DR InterPro: IPR008966; Adhes_bact.
DR InterPro: IPR004237; Fn_bind.
DR InterPro: IPR005877; Gpos_YsIRK.
DR InterPro: IPR001899; Gram_pos_anchor.
DR Pfam: PF02986; Fn_bind; 1.
DR Pfam: PF00746; Gram_pos_anchor; 1.
DR TIGRFAMs: TIGR01167; LPXTG_anchor; 1.
DR TIGRFAMs: TIGR01168; YsIRK_signal; 1.
DR TIGRFAMs: TIGR01169; YsIRK_signal; 1.

DR PROSITE: PS50847; GRAM_POS_ANCHORING; 1.
KW Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ SEQUENCE 1015 AA; 111145 MW; D0F9281BB64D44D2 CRC64;

Query Match 91.7%; Score 189; DB 2; Length 1015;
Best Local Similarity 94.7%; Pred. No. 3.7e-14;
Matches 36; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 QNSGNSFEEDTEEDKPKYEGGNIVDIDFDSVPIQG 38
Db 747 QNSGNSFEEDTEEDKPKYEGGNIVDIDFDSVPIQG 784
|||||
RESULT 11
Q6G6H3 PRELIMINARY; PRT; 1015 AA.
ID Q6G6H3
AC Q6G6H3
DT 05-JUL-2004 (TREMblrel. 27, Created)
DT 05-JUL-2004 (TREMblrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMblrel. 27, Last annotation update)
DE Fibronectin-binding protein.
GN OrderedLocuNames=SAS2388;
OS *Staphylococcus aureus* (strain MSSA476).
OC Bacteria; Firmicutes; Bacillales; *Staphylococcus*.
OX NCBI_Taxid=282459;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=15213324; DOI=10.1073/pnas.0402521101;
RA Holden M.T.G., Foster T.J., Moore C.E., Hurst L., Atkin R., Barron A.,
RA Enright M.C., Foster T.J., Moore C.E., Hurst L., Atkin R., Barron A.,
RA Bason N., Bentley S.D., Chillingworth C., Chillingworth T., Dowd L.,
RA Churcher C., Clark L., Corton A., Doggett J., Dowd L.,
RA Felwell T., Hance Z., Harris B., Hauser H., Holtroyd S., Jagels K.,
RA James K.D., Leonard N., Line A., Mayes R., Mouton S., Mungall K.,
RA Ormond D., Quail M.A., Rabinowitch E., Rutherford K.M., Sanders M.,
RA Sharp S., Simmonds M., Stevens K., Whitehead S., Barrell B.G.,
RA Spratt B.G., Parkhill J.;
RT "Complete genomes of two clinical *Staphylococcus aureus* strains:
RT evidence for the rapid evolution of virulence and drug resistance";
RL Proc. Natl. Acad. Sci. U.S.A. 101:9786-9791(2004).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC an amide bond (By similarity).
DR EMBL: BX571857; CAG44202.1; -;
DR GO: GO:0009986; C:cell surface; IEA.
DR GO: GO:0005618; C:cell wall; IEA.
DR GO: GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO: GO:0016020; C:membrane; IEA.
DR GO: GO:0007155; P:cell adhesion; IEA.
DR InterPro: IPR008966; Adhes_bact.
DR InterPro: IPR004237; Fn_bind.
DR InterPro: IPR005877; Gpos_YsIRK.
DR InterPro: IPR001899; Gram_pos_anchor.
DR Pfam: PF02986; Fn_bind; 1.
DR Pfam: PF00746; Gram_pos_anchor; 1.
DR TIGRFAMs: TIGR01167; LPXTG_anchor; 1.
DR TIGRFAMs: TIGR01168; YsIRK_signal; 1.
DR PROSITE: PS50847; GRAM_POS_ANCHORING; 1.
KW Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ SEQUENCE 1015 AA; 111145 MW; D0F9281BB64D44D2 CRC64;

Query Match 91.7%; Score 189; DB 2; Length 1015;
Best Local Similarity 94.7%; Pred. No. 3.7e-14;
Matches 36; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 QNSGNSFEEDTEEDKPKYEGGNIVDIDFDSVPIQG 38
Db 747 QNSGNSFEEDTEEDKPKYEGGNIVDIDFDSVPIQG 784
|||||
RESULT 12
Q9AEP9 PRELIMINARY; PRT; 152 AA.
ID Q9AEP9


```
AC O9AEP9;
DT 01-JUN-2001 (TReMBLrel. 17, Created)
DT 01-JUN-2001 (TReMBLrel. 17, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE Fibronectin-binding protein (Fragment).
GN Name=fnb;
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
CX NCBI_TaxID=1280;
O6FRE8
RP SEQUENCE FROM N.A.
RC STRAIN=CMRSA-1;
RX MEDLINE=21246681; PubMed=11349044;
RX DOI=10.1128/IAI.69.6.3791-3799.2001;
RA Rice K., Huebner M., Vaz D., McGavin M.J.;
RT "Variance in fibronectin binding and fmb locus polymorphisms in
RT Staphylococcus aureus: identification of antigenic variation in a
RT fibronectin binding protein adhesin of the epidemic CMRSA-1 strain of
RT methicillin-resistant S. aureus."
RL Infect. Immun. 69:3791-3799(2001).
DR EMBL, AY029184; AAK31588.1; -.
FT NON_TER
FT NON_TER
SQ SEQUENCE 152 AA; 17193 MW; CFA3913C2B11C025 CRC64;

Query Match 90.3%; Score 186; DB 2; Length 152;
Best Local Similarity 92.1%; Pred. No. 9.8e-15;
Matches 35; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 QNSGNQSFEDTEEDKPKYEGQPNIVDIDFDSVPQIHG 38
Db 1 QNTGNGSFEDTEEDKPKYEGQGNIVDIDFDSVPQIQG 38

RESULT 13
O6FRE8 PRELIMINARY; PRT; 1015 AA.
AC O6FRE8;
DT 05-JUL-2004 (TReMBLrel. 27, Created)
DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TReMBLrel. 27, Last annotation update)
DE Similarities with sp|P36044 Saccharomyces cerevisiae YKL201c
MN4.
GN ORFNames=CAGL0H09130G;
OS Candida glabrata CBS138.
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; mitosporic Saccharomycetales; Candida.
OX NCBI_TaxID=284593;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CBS138;
RG Genolevures;
RA Dujon B., Sherman D., Fischer G., Durrens P., Casaregola S.,
RA Lafontaine I., de Montigny J., Marck C., Neuvéglise C., Talla E.,
RA Goffard N., Frangeul L., Aigle M., Anthouard V., Babour A., Barbe V.,
RA Barney S., Blanchin S., Beckerich J.M., Beyne E., Bleykasten C.,
RA Boisarne A., Boyer J., Catcolico L., Confantolieri F., de Darvar A.,
RA Despons L., Fabre E., Fairhead C., Ferry-Dumazet H., Groppi A.,
RA Hantaye F., Hennequin C., Jauniaux N., Joyet P., Kachouri R.,
RA Kerrest A., Koszul R., Lemaire M., Lesur I., Ma L., Muller H.,
RA Nicaud J.M., Nikolski M., Oztas S., Ozier-Kalogeropoulos O.,
RA Pellenz S., Potier S., Richard G.F., Straub M.L., Suleau A.,
RA Swennene D., Tekala F., Wesolowski-Louvel M., Westhof E., Wirth B.,
RA Zenlou-Meyer M., Zivanovic I., Bolotin-Fukuhara M., Thierry A.,
RA Bouchier C., Caudron B., Scarpelli C., Galliard C., Weissenbach J.,
RA Wincker P., Souciet J.L.;
RT "Genome evolution in yeasts."
RL Nature 430:35-44(2004)
DR EMBL, CR380954; CAG60129.1; -.
OX NCBI_TaxID=39947;
SQ SEQUENCE 1015 AA; 118060 MW; F32341DA13FA3BB CRC64;

Query Match 32.8%; Score 67.5; DB 2; Length 1015;
Best Local Similarity 41.2%; Pred. No. 21;
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Matches 14; Conservative 7; Mismatches 12; Indels 1; Gaps 1;

OY 1 QNSGNQSFEDTEEDKPKYEGQPNIVDIDFDSV 33
Db 345 QNFVNNRTEETEQMKAKWQDNDIDIVERDHI 378

RESULT 14
O6CBW0 PRELIMINARY; PRT; 889 AA.
AC O6CBW0;
DT 25-OCT-2004 (TReMBLrel. 28, Created)
DT 25-OCT-2004 (TReMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TReMBLrel. 28, Last annotation update)
DE Similar to sp|P53935 Saccharomyces cerevisiae YNL091w.
GN ORFNames=YAL10C15070G;
OS Yarrowia lipolytica CLT189.
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Dipodascaceae; Yarrowia.
OX NCBI_TaxID=284591;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CLT189;
RG Genolevures;
RA Dujon B., Sherman D., Fischer G., Durrens P., Casaregola S.,
RA Lafontaine I., de Montigny J., Marck C., Neuvéglise C., Talla E.,
RA Goffard N., Frangeul L., Aigle M., Anthouard V., Babour A., Barbe V.,
RA Barney S., Blanchin S., Beckerich J.M., Beyne E., Bleykasten C.,
RA Boisarne A., Boyer J., Catcolico L., Confantolieri F., de Darvar A.,
RA Despons L., Fabre E., Fairhead C., Ferry-Dumazet H., Groppi A.,
RA Hantaye F., Hennequin C., Jauniaux N., Joyet P., Kachouri R.,
RA Kerrest A., Koszul R., Lemaire M., Lesur I., Ma L., Muller H.,
RA Nicaud J.M., Nikolski M., Oztas S., Ozier-Kalogeropoulos O.,
RA Pellenz S., Potier S., Richard G.F., Straub M.L., Suleau A.,
RA Swennene D., Tekala F., Wesolowski-Louvel M., Westhof E., Wirth B.,
RA Zenlou-Meyer M., Zivanovic I., Bolotin-Fukuhara M., Thierry A.,
RA Bouchier C., Caudron B., Scarpelli C., Galliard C., Weissenbach J.,
RA Wincker P., Souciet J.L.;
RT "Genome evolution in yeasts."
RL Nature 430:35-44(2004).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=CLT189;
RG Genoscope;
RA Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL, CR382129; CAG82165.1; -.
SQ SEQUENCE 889 AA; 100256 MW; CCL184588BAC17363 CRC64;

Query Match 32.0%; Score 66; DB 2; Length 889;
Best Local Similarity 45.7%; Pred. No. 28;
Matches 16; Conservative 7; Mismatches 10; Indels 2; Gaps 2;

OY 1 QNSGNQSFEDTEEDKPKYEGQPNIVDIDFDSV 33
Db 230 QNLGKEIDEGDTEDEYGFEBGSDVQSLDVSSV 264

RESULT 15
O69L72 PRELIMINARY; PRT; 923 AA.
AC O69L72;
DT 25-OCT-2004 (TReMBLrel. 28, Created)
DT 25-OCT-2004 (TReMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TReMBLrel. 28, Last annotation update)
DE Putative PMS2 postmeiotic segregation increased 2.
GN Name=OSUNBA0016G10.12;
OS Eukarya activa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Rosaceae;
OC Euphorbiaceae; Oryzae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
RP SEQUENCE FROM N.A.
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RA Sasaki T., Matsunoto T., Katayose Y.;
RT "Oryza sativa nipponbare(GAS) genomic DNA, chromosome 2, BAC
RT clone:OSJNBa0016G10.";
RU Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AP005874; BAD34084.1; -.
DR GO; GO:0005524; P:ATP binding; IEA.
DR GO; GO:0006298; P:mismatch repair; IEA.
DR InterPro; IPR003594; ATPbind_ATPase.
DR InterPro; IPR002099; DNA_mis_repair.
DR InterPro; IPR000102; MAP1B_neuraxin.
DR Pfam; PF01119; DNA_mis_repair; 1.
DR Pfam; PF02518; HATPase_C; 1.
DR TIGRFAMs; TIGR00585; mutL; 1.
DR PROSITE; PS00058; DNA_MISMATCH_REPAIR_1; UNKNOWN_1.
DR PROSITE; PS00230; MAP1B_NEURAXIN; UNKNOWN_1.
SQ SEQUENCE 923 AA; 101237 MW; ASFD02C047947191 CRC64;

Query Match 30.8%; Score 63.5; DB 2; Length 923;
Best Local Similarity 45.2%; Pred. No. 58;
Matches 14; Conservative 5; Mismatches 11; Indels 1; Gaps 1;

QY 6 OSFEEDTEEDKPKYEGGNIVIDIDPSVPOI 36
DB 551 QSFVPMPEPDSPOHSEPPNIVS-HRDEVFQL 580

```

Search completed: October 22, 2005, 06:06:02
 Job time : 70.6361 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: October 25, 2005, 19:38:38 ; Search time 83.8325 Seconds
(without alignments)
175.313 Million cell updates/sec

Title: US-10-731-238-44

Sequence: 1 QNSGNQSPPTEDKPKYEQPNIVDIDFDSVPQIHG 38

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :
1: A_Geneseq_16Dec04:*
2: geneseqp1980s:*
3: geneseqp1990s:*
4: geneseqp2000s:*
5: geneseqp2001s:*
6: geneseqp2002s:*
7: geneseqp2003as:*
8: geneseqp2003bs:*
9: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	211	100.0	38	2	AAW65700
2	192	91.0	38	2	AAW65706
3	186	88.2	38	2	AAW65662
4	186	88.2	38	2	AAW65699
5	185	87.7	38	2	AAW65692
6	185	87.7	38	2	AAW65693
7	177	83.9	38	2	AAW65661
8	177	83.9	130	2	AAW65806
9	177	83.9	130	2	AAW65807
10	177	83.9	130	2	AAW65807
11	177	83.9	130	2	AAW65807
12	177	83.9	134	2	AAW65808
13	177	83.9	134	2	AAW65808
14	177	83.9	134	2	AAW65808
15	177	83.9	139	2	AAW65808
16	177	83.9	174	2	AAW65808
17	177	83.9	174	2	AAW65808
18	177	83.9	181	2	AAW65808
19	177	83.9	181	2	AAW65808
20	177	83.9	559	2	AAW65808
21	177	83.9	767	4	AAU34403
22	177	83.9	767	4	AAU34403
23	177	83.9	940	6	AAU34403
24	177	83.9	940	6	AAU34403
25	177	83.9	948	6	AAU34403

25	177	83.9	948	6	ABJ18923	ABJ18923
27	177	83.9	948	6	ABW72536	ABW72536
28	177	83.9	961	6	ABU15854	ABU15854
29	177	83.9	1018	1	AAW65713	AAW65713
30	177	83.9	1018	4	AAU34403	AAU34403
31	177	83.9	1018	4	AAU34403	AAU34403
32	177	83.9	1018	6	ABJ18922	ABJ18922
33	177	83.9	1018	6	ABW72537	ABW72537
34	177	83.9	1027	2	AAW65806	AAW65806
35	177	83.9	1038	6	ABU15903	ABU15903
36	175.5	83.2	39	2	AAW65713	AAW65713
37	171	81.0	38	2	AAW65695	AAW65695
38	171	81.0	38	2	AAW65696	AAW65696
39	171	81.0	38	2	AAW65697	AAW65697
40	170	80.6	38	2	AAW65698	AAW65698
41	170	80.6	38	2	AAW65698	AAW65698
42	169	80.1	978	4	AAU33960	AAU33960
43	169	80.1	1001	4	AAU37093	AAU37093
44	168	79.6	38	1	AAW65694	AAW65694
45	168	79.6	38	1	AAW65694	AAW65694

ALIGNMENTS

RESULT 1
AAW65700
ID AAW65700 standard; peptide; 38 AA.

AAW65700;

16-OCT-1998 (first entry)

Fibronectin binding protein-derived peptide #44.

microbial surface components recognising adhesive matrix molecule;

MSCRAMM; fibronectin; fibronectin-binding protein; antibody; epitope;

antibiotic; bacterial infection; antibiotic-resistant strain.

Synthetic.

Staphylococcus aureus.

W09831369-AA.

23-JUL-1998.

21-JAN-1998; 98MO-US001222.

21-JAN-1997; 97US-0036139P.

(TEXA) UNIV TEXAS A & M SYSTEM.

Hoeok M, Patti JW, House-Pompeo KL, Speziale P, Joh D;

Megavlin MJ;

WPI; 1998-413816/35.

Example 8; Page 102; 201PP; English.

The invention relates to antibodies that bind to a fibronectin-binding

domain of a fibronectin-binding protein, and inhibit binding of the

protein to fibronectin. Also claimed are: (1) isolated peptides of a

fibronectin-binding protein that do not bind to fibronectin; (2) fusion

protein containing at least one peptide of a fibronectin-binding protein

linked to a second amino acid sequence; (3) nucleic acid encoding the

isolated peptide of (1). Antibodies, the isolated peptides of (1) and the

nucleic acids are all useful for immunisation (active or passive) and (by

inhibiting binding of bacteria to fibronectin) for preventing or treating

infection in humans or other animals, particularly by staphylococci or

CC streptococci, e.g. meningitis, otitis media, pneumonia, endocarditis,
 CC mastitis in cattle, abortion in horses and many others. Since the
 CC antibodies block binding of bacteria, they should be effective against
 CC antibiotic-resistant strains, and may replace antibiotic therapy or
 CC increase its effectiveness. Sequences AAW65691-700 represent a series of
 CC synthetic peptides based on the D1 region of *S. aureus* fibronectin
 CC binding protein A. They were synthesised to contain mutations
 XX

SQ Sequence 38 AA;

QY Query Match 100.0%; Score 211; DB 2; Length 38;
 Best Local Similarity 100.0%; Pred. No. 6.2e-19;
 Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 ONSGNQSPPTEDPKPKYEQPNIVDIDFDSVPQIHG 38
 1 ONSGNQSPPTEDPKPKYEQPNIVDIDFDSVPQIHG 38

RESULT 2
 ID AAW65706 standard; peptide, 38 AA.
 XX AAW65706;
 AC AAW65706;
 XX 16-OCT-1998 (first entry)
 DT
 XX Fibronectin binding protein-derived peptide #50.
 DE
 XX microbial surface components recognising adhesive matrix molecule;
 KM MSCRAMM; fibronectin; fibronectin-binding protein; antibody; epitope;
 KW antibiotic; bacterial infection; antibiotic-resistant strain.
 XX
 OS Synthetic.
 OS *Staphylococcus aureus*.
 XX WO9831389-A2.
 XX 23-JUL-1998.
 PD
 XX 21-JAN-1998; 98WO-US001222.
 PF
 XX 21-JAN-1997; 97US-0036139P.
 PR
 XX (TEXA) UNIV TEXAS A & M SYSTEM.
 PA
 XX Hoecek M, Patti JM, House-Pompeo KL, Speciale P, Joh D;
 PI Mcgavin MJ;
 PT WPI; 1998-413816/35.
 XX

XX Antibody that binds to fibronectin-binding protein, preventing its
 PT binding to fibronectin - used to treat or prevent bacterial infection,
 PT especially by *Staphylococci* and *Streptococci*.
 PS Example 8; Page 102; 201pp; English.

CC The invention relates to antibodies that bind to a fibronectin-binding
 CC domain of a fibronectin-binding protein, and inhibit binding of the
 CC protein to fibronectin. Also claimed are: (1) isolated peptides of a
 CC fibronectin-binding protein that do not bind to fibronectin; (2) fusion
 CC protein containing at least one peptide of a fibronectin-binding protein
 CC linked to a second amino acid sequence; (3) nucleic acid encoding the
 CC isolated peptide of (1). Antibodies, the isolated peptides of (1) and the
 CC nucleic acids are all useful for immunisation (active or passive) and (by
 CC inhibiting binding of bacteria to fibronectin) for preventing or treating
 CC infection in humans or other animals, particularly by *staphylococci* or
 CC *streptococci*, e.g. meningitis, otitis media, pneumonia, endocarditis,
 CC mastitis in cattle, abortion in horses and many others. Since the
 CC antibodies block binding of bacteria, they should be effective against
 CC antibiotic-resistant strains, and may replace antibiotic therapy or
 CC increase its effectiveness. Sequences AAW65701-706 represent a series of
 CC synthetic peptides based on the D2 region of *S. aureus* fibronectin

CC binding protein A. They were synthesised to contain mutations
 XX

SQ Sequence 38 AA;

QY Query Match 91.0%; Score 192; DB 2; Length 38;
 Best Local Similarity 86.8%; Pred. No. 1.4e-16;
 Matches 33; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Db 1 ONSGNQSPPTEDPKPKYEQPNIVDIDFDSVPQIHG 38
 1 ONSGNQSPPTEDPKPKYEQPNIVDIDFDSVPQIHG 38

RESULT 3
 ID AAW65662 standard; peptide, 38 AA.
 XX AAW65662;
 AC AAW65662;
 XX 16-OCT-1998 (first entry)
 DT
 XX Fibronectin binding protein-derived peptide #6.
 DE
 XX microbial surface components recognising adhesive matrix molecule;
 KM MSCRAMM; fibronectin; fibronectin-binding protein; antibody; epitope;
 KW antibiotic; bacterial infection; antibiotic-resistant strain.
 XX
 OS Synthetic.
 OS *Staphylococcus aureus*.
 XX WO9831389-A2.
 XX 23-JUL-1998.
 PD
 XX 21-JAN-1998; 98WO-US001222.
 PF
 XX 21-JAN-1997; 97US-0036139P.
 PR
 XX (TEXA) UNIV TEXAS A & M SYSTEM.
 PA
 XX Hoecek M, Patti JM, House-Pompeo KL, Speciale P, Joh D;
 PI Mcgavin MJ;
 PT WPI; 1998-413816/35.
 XX

XX Antibody that binds to fibronectin-binding protein, preventing its
 PT binding to fibronectin - used to treat or prevent bacterial infection,
 PT especially by *Staphylococci* and *Streptococci*.
 PS Example 2; Page 92; 201pp; English.

CC The invention relates to antibodies that bind to a fibronectin-binding
 CC domain of a fibronectin-binding protein, and inhibit binding of the
 CC protein to fibronectin. Also claimed are: (1) isolated peptides of a
 CC fibronectin-binding protein that do not bind to fibronectin; (2) fusion
 CC protein containing at least one peptide of a fibronectin-binding protein
 CC linked to a second amino acid sequence; (3) nucleic acid encoding the
 CC isolated peptide of (1). Antibodies, the isolated peptides of (1) and the
 CC nucleic acids are all useful for immunisation (active or passive) and (by
 CC inhibiting binding of bacteria to fibronectin) for preventing or treating
 CC infection in humans or other animals, particularly by *staphylococci* or
 CC *streptococci*, e.g. meningitis, otitis media, pneumonia, endocarditis,
 CC mastitis in cattle, abortion in horses and many others. Since the
 CC antibodies block binding of bacteria, they should be effective against
 CC antibiotic-resistant strains, and may replace antibiotic therapy or
 CC increase its effectiveness. Sequences AAW65659-68 represent synthetic
 CC epitopes from the fibronectin binding domains DU and D1-D4 of the *S.*
 CC *aureus* fnbA gene

SQ Sequence 38 AA;

QY Query Match 88.2%; Score 186; DB 2; Length 38;
 Best Local Similarity 92.1%; Pred. No. 8e-16;

Matches 35; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 QNSGNOSFPPTTEEDPKRYEQPPNIVDIDFDSVPQIHG 38
 ID |||||
 XX |||||
 AC |||||
 XX |||||
 XX |||||
 DT 1 QNSGNOSFPEDTEEDPKRYEQPGNIVDIDFDSVPQIHG 38
 XX |||||

RESULT 4

AAW65699 standard; peptide; 38 AA.

16-OCT-1998 (first entry)

Fibronectin binding protein-derived peptide #43.

microbial surface components recognising adhesive matrix molecule;
 MSCRAM; fibronectin; fibronectin-binding protein; antibody; epitope;
 antibiotic; bacterial infection; antibiotic-resistant strain.

Synthetic.
 Staphylococcus aureus.

WO9831389-A2.

23-JUL-1998.

21-JAN-1998; 98WO-US001222.

21-JAN-1997; 97US-0036139P.

(TEXA) UNIV TEXAS A & M SYSTEM.

Hoeeck M, Patti JM, House-Pompeo KL, Speziale P, Joh D;
 Mcgavin MJ;

WPI; 1998-413816/35.

Antibody that binds to fibronectin-binding protein, preventing its
 binding to fibronectin - used to treat or prevent bacterial infection,
 especially by Staphylococci and Streptococci.

Example 8; Page 102; 201pp; English.

The invention relates to antibodies that bind to a fibronectin-binding
 domain of a fibronectin-binding protein, and inhibit binding of the
 protein to fibronectin. Also claimed are: (1) isolated peptides of a
 fibronectin-binding protein that do not bind to fibronectin; (2) fusion
 protein containing at least one peptide of a fibronectin-binding protein
 linked to a second amino acid sequence; (3) nucleic acid encoding the
 isolated peptide of (1). Antibodies, the isolated peptides of (1) and the
 nucleic acids are all useful for immunisation (active or passive) and (by
 inhibiting binding of bacteria to fibronectin) for preventing or treating
 infection in humans or other animals, particularly by staphylococci or
 streptococci, e.g. meningitis, otitis media, pneumonia, endocarditis,
 sepsitis in cattle, abortion in horses and many others. Since the
 antibodies block binding of bacteria, they should be effective against
 antibiotic-resistant strains, and may replace antibiotic therapy or
 increase its effectiveness. Sequences AAW65691-700 represent a series of
 synthetic peptides based on the DI region of S. aureus fibronectin
 binding protein A. They were synthesised to contain mutations

Sequence 38 AA;

Query Match 88.2%; Score 186; DB 2; Length 38;
 Best Local Similarity 92.1%; Pred. No. 8e-16;
 Matches 35; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 QNSGNOSFPPTTEEDPKRYEQPPNIVDIDFDSVPQIHG 38
 ID |||||
 XX |||||
 AC |||||
 XX |||||
 XX |||||
 DT 1 QNSGNOSFPEDTEEDPKRYEQPGNIVDIDFDSVPQIHG 38
 XX |||||

RESULT 5

AAW65692 standard; peptide; 38 AA.

16-OCT-1998 (first entry)

Fibronectin binding protein-derived peptide #36.

microbial surface components recognising adhesive matrix molecule;
 MSCRAM; fibronectin; fibronectin-binding protein; antibody; epitope;
 antibiotic; bacterial infection; antibiotic-resistant strain.

Synthetic.
 Staphylococcus aureus.

WO9831389-A2.

23-JUL-1998.

21-JAN-1998; 98WO-US001222.

21-JAN-1997; 97US-0036139P.

(TEXA) UNIV TEXAS A & M SYSTEM.

Hoeeck M, Patti JM, House-Pompeo KL, Speziale P, Joh D;
 Mcgavin MJ;

WPI; 1998-413816/35.

Antibody that binds to fibronectin-binding protein, preventing its
 binding to fibronectin - used to treat or prevent bacterial infection,
 especially by Staphylococci and Streptococci.

Example 8; Page 101; 201pp; English.

The invention relates to antibodies that bind to a fibronectin-binding
 domain of a fibronectin-binding protein, and inhibit binding of the
 protein to fibronectin. Also claimed are: (1) isolated peptides of a
 fibronectin-binding protein that do not bind to fibronectin; (2) fusion
 protein containing at least one peptide of a fibronectin-binding protein
 linked to a second amino acid sequence; (3) nucleic acid encoding the
 isolated peptide of (1). Antibodies, the isolated peptides of (1) and the
 nucleic acids are all useful for immunisation (active or passive) and (by
 inhibiting binding of bacteria to fibronectin) for preventing or treating
 infection in humans or other animals, particularly by staphylococci or
 streptococci, e.g. meningitis, otitis media, pneumonia, endocarditis,
 sepsitis in cattle, abortion in horses and many others. Since the
 antibodies block binding of bacteria, they should be effective against
 antibiotic-resistant strains, and may replace antibiotic therapy or
 increase its effectiveness. Sequences AAW65691-700 represent a series of
 synthetic peptides based on the DI region of S. aureus fibronectin
 binding protein A. They were synthesised to contain mutations

Sequence 38 AA;

Query Match 87.7%; Score 185; DB 2; Length 38;
 Best Local Similarity 92.1%; Pred. No. 1.1e-15;
 Matches 35; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 QNSGNOSFPPTTEEDPKRYEQPPNIVDIDFDSVPQIHG 38
 ID |||||
 XX |||||
 AC |||||
 XX |||||
 XX |||||
 DT 1 QNSGNOSFPEDTEEDPKRYEQPGNIVDIDFDSVPQIHG 38
 XX |||||

RESULT 6

AAW65693 standard; peptide; 38 AA.

AAW65693;

[illegible]

KM	MSCRAMM; fibronectin; fibronectin-binding protein; antibody; epitope;
KW	antibiotic; bacterial infection; antibiotic-resistant strain.
XX	
XX	Synthetic.
OS	Staphylococcus aureus.
PN	MO9631389-A2.
XX	
XX	23-JUL-1998.
PD	
XX	
PF	21-JAN-1998; 98WO-US001222.
XX	
PR	21-JAN-1997; 97US-0036139P.
XX	
PA	(TEXA) UNIV TEXAS A & M SYSTEM.
XX	
PI	Hoeek M, Patti JM, House-Pompeo KL, Speziale P, Joh D;
PI	McGavin WJ;
XX	
XX	WPI; 1998-413816/35.
DR	
XX	
XX	Antibody that binds to fibronectin-binding protein, preventing its
PT	binding to fibronectin - used to treat or prevent bacterial infection,
PT	especially by staphylococci and Streptococci.
XX	
PS	Example 2; Page 92; 201pp; English.
XX	
CC	The invention relates to antibodies that bind to a fibronectin-binding
CC	domain of a fibronectin-binding protein, and inhibit binding of the
CC	protein to fibronectin. Also claimed are: (1) isolated peptides of a
CC	fibronectin-binding protein that do not bind to fibronectin; (2) fusion
CC	protein containing at least one peptide of a fibronectin-binding protein
CC	linked to a second amino acid sequence; (3) nucleic acid encoding the
CC	isolated peptide of (1). Antibodies, the isolated peptides of (1) and the
CC	nucleic acids are all useful for immunisation (active or passive) and (by
CC	inhibiting binding of bacteria to fibronectin) for preventing or treating
CC	infection in humans or other animals, particularly by staphylococci or
CC	streptococci, e.g. meningitis, otitis media, pneumonia, endocarditis,
CC	mastitis in cattle, abortion in horses and many others. Since the
CC	antibodies block binding of bacteria, they should be effective against
CC	antibiotic-resistant strains, and may replace antibiotic therapy or
CC	increase its effectiveness. Sequences AM65659-68 represent synthetic
CC	epitopes from the fibronectin binding domains DU and D1-D4 of the S.
CC	aureus ftnA gene
XX	
XX	
SQ	Sequence 38 AA;
XX	
Query Match	83.9%; Score 177; DB 2; Length 38;
Best Local Similarity	89.5%; Pred. No. 1e-14;
Matches	34; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY	1 QNSGNOSFPPTEDKPYEOPNIVIDPVSFQING 38
DB	1 QNSGNOSFEEDTBDKFKYEGGNIVIDPDSVFQING 38
RESULT 8	
AA58806	AA58806 standard; protein, 130 AA.
XX	
AC	AA58806;
XX	
DT	25-MAR-2003 (revised)
DT	30-MAR-1995 (first entry)
XX	
XX	Fibronectin binding domain D1-D4(709-838(P938T)).
XX	
KX	Fibronectin binding protein; Fbp; fibronectin binding domain;
KW	monoclonal antibody; Mab; adhesion; Gram-positive bacterium; bacteremia;
KW	Escherichia coli.
XX	
OS	Staphylococcus aureus.
XX	

PN MO9418327-A1.
XX 18-AUG-1994.
XX 04-FEB-1994; 94WO-GB000215.
XX 05-FEB-1993; 93GB-00002289.
XX 20-OCT-1993; 93GB-00021592.
XX (SMIK) SMITHKLINE BEECHAM PLC.
XX Burnham MKR, Chopra I, Critchley IA, Knowles DJC;
XX WPI; 1994-279748/34.
XX Fibronection binding protein and monoclonal antibodies specific for Fbp -
XX useful to prevent adherence of Gram-positive bacteria to indwelling
XX devices or wounds.
XX Disclosure; Page 30; 40pp; English.
XX Polypeptides corresponding to residues G709-T886 plus PPIVPT, G709-
XX P838(P838T) and G709-P838 (AAR58805-07, respectively) of S. aureus J2385
XX (NCIMB 40532) Fbp type A fibronection binding domain D1-D4 region
XX (AAR58808) were expressed in E. coli BL21 (DE4) and used to raise Mabs
XX specific for Fbp. (Updated on 25-MAR-2003 to correct PN field.)
XX Sequence 130 AA;
SQ
Query Match 83.9%; Score 177; DB 2; Length 130;
Best Local Similarity 89.5%; Pred. No. 4e-14;
Matches 34; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
Qy 1 QNSGNQSPPTDEBDKPKYEQPPNIVDIDFDSVPQIHG 38
Db 2 QNSGNQSFEDTDEBDKPKYEQGNGNIVDIDFDSVPQIHG 39
RESULT 9
AAR58807
ID AAR58807 standard; protein; 130 AA.
XX AAR58807;
XX 25-MAR-2003 (revised)
XX 30-MAR-1995 (first entry)
XX Fibronection binding domain D1-D4 (709-838).
XX Fibronection binding protein; Fbp; fibronection binding domain;
XX monoclonal antibody; Mab; adhesion; Gram-positive bacterium; bacteremia;
XX Escherichia coli.
XX Staphylococcus aureus.
XX WO9418327-A1.
XX 18-AUG-1994.
XX 04-FEB-1994; 94WO-GB000215.
XX 05-FEB-1993; 93GB-00002289.
XX 20-OCT-1993; 93GB-00021592.
XX (SMIK) SMITHKLINE BEECHAM PLC.
XX Burnham MKR, Chopra I, Critchley IA, Knowles DJC;
XX WPI; 1994-279748/34.
XX Fibronection binding protein and monoclonal antibodies specific for Fbp -
XX useful to prevent adherence of Gram-positive bacteria to indwelling
XX devices or wounds.

XX Disclosure; Page 30; 40pp; English.
XX Polypeptides corresponding to residues G709-T886 plus PPIVPT, G709-
XX P838(P838T) and G709-P838 (AAR58805-07, respectively) of S. aureus J2385
XX (NCIMB 40532) Fbp type A fibronection binding domain D1-D4 region
XX (AAR58808) were expressed in E. coli BL21 (DE4) and used to raise Mabs
XX specific for Fbp. (Updated on 25-MAR-2003 to correct PN field.)
XX Sequence 130 AA;
SQ
Query Match 83.9%; Score 177; DB 2; Length 130;
Best Local Similarity 89.5%; Pred. No. 4e-14;
Matches 34; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
Qy 1 QNSGNQSPPTDEBDKPKYEQPPNIVDIDFDSVPQIHG 38
Db 2 QNSGNQSFEDTDEBDKPKYEQGNGNIVDIDFDSVPQIHG 39
RESULT 10
AAR91202
ID AAR91202 standard; peptide; 130 AA.
XX AAR91202;
XX 13-NOV-1996 (first entry)
XX D1-D4 fibronection binding domains.
XX Fibronection; oral hygiene; gingivitis; gum disease; adhesion;
XX periodontitis; oral pathogen; caries; calculus; candidiasis; oral surgery;
XX tissue regeneration; irrigation; toothpaste; dentifrice; mouthwash;
XX lozenge.
XX Staphylococcus aureus.
XX WO9604003-A1.
XX 15-FEB-1996.
XX 18-JUL-1995; 95WO-EP002825.
XX 05-AUG-1994; 94GB-00015902.
XX (SMIK) SMITHKLINE BEECHAM PLC.
XX Barnett P, Critchley IA, Dodd I;
XX WPI; 1996-129122/13.
XX Prevention of adherence of oral pathogens in the oral cavity, partic.
XX tooth surfaces - by application of a fibronection binding protein or
XX polypeptide or a monoclonal antibody or fragment against it.
XX Claim 5; Page 32; 41pp; English.
XX Adherence of oral pathogens, particularly to tooth surfaces, can be
XX prevented by application of a fibronection binding protein or polypeptide.
XX The fibronection binding protein or polypeptide is useful in the
XX manufacture of oral hygiene compositions, eg. toothpaste, liquid
XX dentifrice, mouthwash or lozenge. They are useful to prevent the plaque-
XX related development of carious lesions, gingivitis, calculus or
XX periodontal disease and to combat oral cavity infections, e.g.
XX candidiasis. They may also be useful in oral surgery e.g. in guided
XX tissue regeneration procedures to prevent subsequent bacterial infection,
XX and for irrigation of periodontal pockets. This sequence corresponds to
XX amino acids 709-838 of the D1-D4 fibronection binding domain of
XX Staphylococcus aureus
XX Sequence 130 AA;
SQ
Query Match 83.9%; Score 177; DB 2; Length 130;

Best Local Similarity 89.5%; Pred. No. 4e-14;
Matches 34; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 1 ONSGNQSPPTDEBDKPKYEQPNIVDIDFDSVPQIHG 38
 |||||
 DB 2 ONSGNQSPFEDTDEBDKPKYEQGNIVDIDFDSVPQIHG 39
 |||||

RESULT 11

ID AAR91201 standard; peptide, 130 AA.

XX AAR91201;

DT 13-NOV-1996 (first entry)

DE D1-D4 fibronectin binding domains.

XX Fibronectin; oral hygiene; gingivitis; gum disease; adhesion;

KW periodontitis; oral pathogen; caries; calculus; candidiasis; oral surgery;

KW tissue regeneration; irrigation; toothpaste; dentifrice; mouthwash;

XX lozenge.

XX Staphylococcus aureus.

XX WO9604003-A1.

XX 15-FEB-1996.

XX 18-JUL-1995; 95WO-EP002825.

XX 05-AUG-1994; 94GB-00015902.

XX (SMIK) SMITHKLINE BEECHAM PLC.

XX Barnett P, Critchley IA, Dodd I;

XX WPI, 1996-129122/13.

XX Prevention of adherence of oral pathogens in the oral cavity, partic.

XX tooth surfaces - by application of a fibronectin binding protein or

XX polypeptide or a monoclonal antibody or fragment against it.

XX Claim 5; Page 31-32; 41pp; English.

XX Adherence of oral pathogens, particularly to tooth surfaces, can be

XX prevented by application of a fibronectin binding protein or polypeptide.

XX The fibronectin binding protein or polypeptide is useful in the

XX manufacture of oral hygiene compositions, eg. toothpaste, liquid

XX dentifrice, mouthwash or lozenge. They are useful to prevent the plaque-

XX related development of carious lesions, gingivitis, calculus or

XX periodontal disease and to combat oral cavity infections, e.g.

XX candidiasis. They may also be useful in oral surgery e.g. in guided

XX tissue regeneration procedures to prevent subsequent bacterial infection,

XX and for irrigation of periodontal pockets. This sequence corresponds to

XX amino acids 709-738 of the D1-D4 fibronectin binding domain of

XX Staphylococcus aureus with a P838T substitution

XX Sequence 130 AA;

XX Query Match 83.9%; Score 177; DB 2; Length 130;

XX Best Local Similarity 89.5%; Pred. No. 4e-14;

XX Matches 34; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

AC AAY29089;
 XX 28-SEP-1999 (first entry)

XX Cloned fibronectin binding protein binding domain (FnBAB) sequence.

XX Bovine herpes virus-2; BHV-2; cytokine; immune response; immunogen; IL;

KW interleukin; colony stimulating factor; CSF; interferon; IFN; TNF;

KW tumour necrosis factor; recombinant virus; vaccine; mucosal disease;

KW mastitis; breast cancer; stress-induced disease; binding domain; FnBAB;

XX fibronectin binding protein.

XX Staphylococcus aureus.

XX WO916892-A1.

XX 08-APR-1999.

XX 29-SEP-1998; 98WO-GB002927.

XX 29-SEP-1997; 97GB-00020633.

XX (UWBR-) UNIV BRISTOL.

XX Bradley AJ, Duffas WP;

XX WPI; 1999-255101/21.

XX N-PSDB; AAX91506.

XX New bovine herpes virus-2 vectors.

XX Example 2; Fig 8A-B; 130pp; English.

XX The invention provides bovine herpes virus-2 (BHV-2) based vectors that

XX comprise at least one cytokine-encoding DNA sequence. The expression of

XX cytokines in mammals can up-regulate immune responses to the immunogen.

XX The cytokine is selected from interleukins (IL), colony stimulating

XX factors (CSF), interferons (IFN) and tumour necrosis factors (TNF). The

XX BHV-2 based vector or recombinant virus can be used as vaccines. They can

XX be used for preventing or treating a mucosal disease in a subject, e.g.

XX ruminants, cattle, sheep, goats, dogs, cats, horses, or man, particularly

XX mastitis in cows or breast cancers in humans. They can also be used for

XX preventing or treating a stress-induced disease. The present sequence

XX represents a S. aureus fibronectin binding protein binding domain

XX sequence FnBAB, the gene cloned for use in this invention. The gene has

XX 97.8 percent identity when compared to the previously published sequences

XX FnBA and FnBB

XX Sequence 134 AA;

XX Query Match 83.9%; Score 177; DB 2; Length 134;

XX Best Local Similarity 89.5%; Pred. No. 4.2e-14;

XX Matches 34; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

XX 1 ONSGNQSPPTDEBDKPKYEQPNIVDIDFDSVPQIHG 38

XX 2 ONSGNQSPFEDTDEBDKPKYEQGNIVDIDFDSVPQIHG 39

XX RESULT 13

XX AAY29088

XX ID AAY29088 standard; protein, 134 AA.

XX AAY29088;

XX 28-SEP-1999 (first entry)

XX S. aureus fibronectin binding protein B (FnBB) binding domain.

XX Bovine herpes virus-2; BHV-2; cytokine; immune response; immunogen; IL;

KW interleukin; colony stimulating factor; CSF; interferon; IFN; TNF;

KW tumour necrosis factor; recombinant virus; vaccine; mucosal disease;

KW mastitis; breast cancer; stress-induced disease; binding domain; FnBB;

KW fibronectin binding protein.
 XX
 OS Staphylococcus aureus.
 XX
 XX WO916892-A1.
 XX
 PD 08-APR-1999.
 XX
 PF 29-SEP-1998; 96WO-GB002927.
 XX
 PR 29-SEP-1997; 97GB-00020633.
 XX
 PA (UYBR-) UNIV BRISTOL.
 XX
 PI Bradley AJ, Duffas WPJ;
 XX
 PI WPI, 1999-255101/21.
 XX
 DR N-PSDB; AAX91505.
 XX
 PT New bovine herpes virus-2 vectors.
 XX
 PS Example 2; Fig 8A-B; 130pp; English.
 XX
 CC The invention provides bovine herpes virus-2 (BHV-2) based vectors that
 CC comprise at least one cytokine-encoding DNA sequence. The expression of
 CC cytokines in mammals can up-regulate immune responses to the immunogens.
 CC The cytokine is selected from interleukins (IL), colony stimulating
 CC factors (CSF), interferons (IFN) and tumour necrosis factors (TNF). The
 CC BHV-2 based vector or recombinant virus can be used as vaccines. They can
 CC be used for preventing or treating a mucosal disease in a subject, e.g.
 CC ruminants, cattle, sheep, goats, dogs, cats, horses, or man, particularly
 CC mastitis in cows or breast cancers in humans. They can also be used for
 CC preventing or treating a stress-induced disease. The present sequence
 CC represents the binding domain of a previously published S. aureus
 CC fibronectin binding protein B (FnBB) sequence. The FnB binding domain
 CC gene sequence FnBBB, cloned for use in this invention has 97.8 percent
 CC identity when compared to the previously published FnBA and FnBB gene
 CC sequences
 XX
 SQ Sequence 134 AA;
 SQ
 Query Match 83.9%; Score 177; DB 2; Length 134;
 Best Local Similarity 89.5%; Pred. No. 4.2e-14;
 Matches 34; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 QY 1 QNSGNOSFPPTDEDPKRYEQRPNIIVDIDFDSVPQIHG 38
 DB 2 QNSGNOSFPEDTEDEPKRYEQGNIVDIDFDSVPQIHG 39
 RESULT 14
 AAY29087
 ID AAY29087 standard; protein; 134 AA.
 XX
 AC AAY29087;
 XX
 DT 28-SEP-1999 (first entry)
 XX
 DE S. aureus fibronectin binding protein A (FnBA) binding domain.
 XX
 KW Bovine herpes virus-2; BHV-2; cytokine; immune response; immunogen; IL;
 KW interleukin; colony stimulating factor; CSF; interferon; IFN; TNF;
 KW tumour necrosis factor; recombinant virus; vaccine; mucosal disease;
 KW mastitis; breast cancer; stress-induced disease; binding domain; FnBA;
 KW fibronectin binding protein.
 XX
 OS Staphylococcus aureus.
 XX
 PN WO916892-A1.
 XX
 PD 08-APR-1999.
 XX
 PF 29-SEP-1998; 98WO-GB002927.

XX
 PR 29-SEP-1997; 97GB-00020633.
 XX
 PA (UYBR-) UNIV BRISTOL.
 XX
 PI Bradley AJ, Duffas WPJ;
 XX
 PI WPI, 1999-255101/21.
 XX
 DR N-PSDB; AAX91504.
 XX
 PT New bovine herpes virus-2 vectors.
 XX
 PS Example 2; Fig 8A-B; 130pp; English.
 XX
 CC The invention provides bovine herpes virus-2 (BHV-2) based vectors that
 CC comprise at least one cytokine-encoding DNA sequence. The expression of
 CC cytokines in mammals can up-regulate immune responses to the immunogens.
 CC The cytokine is selected from interleukins (IL), colony stimulating
 CC factors (CSF), interferons (IFN) and tumour necrosis factors (TNF). The
 CC BHV-2 based vector or recombinant virus can be used as vaccines. They can
 CC be used for preventing or treating a mucosal disease in a subject, e.g.
 CC ruminants, cattle, sheep, goats, dogs, cats, horses, or man, particularly
 CC mastitis in cows or breast cancers in humans. They can also be used for
 CC preventing or treating a stress-induced disease. The present sequence
 CC represents the binding domain of a previously published S. aureus
 CC fibronectin binding protein A (FnBA) sequence. The FnB binding domain
 CC gene sequence FnBBB, cloned for use in this invention has 97.8 percent
 CC identity when compared to the previously published FnBA and FnBB gene
 CC sequences
 XX
 SQ Sequence 134 AA;
 SQ
 Query Match 83.9%; Score 177; DB 2; Length 134;
 Best Local Similarity 89.5%; Pred. No. 4.2e-14;
 Matches 34; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 QY 1 QNSGNOSFPPTDEDPKRYEQRPNIIVDIDFDSVPQIHG 38
 DB 2 QNSGNOSFPEDTEDEPKRYEQGNIVDIDFDSVPQIHG 39
 RESULT 15
 AAW31556
 ID AAW31556 standard; protein; 139 AA.
 XX
 AC AAW31556;
 XX
 DT 27-AUG-2003 (revised)
 DT 25-MAR-2003 (revised)
 DT 21-MAY-1998 (first entry)
 XX
 DE Fibronectin-binding MSCRAMM derivative POD.
 XX
 KW Fibronectin; POD; collagen binding protein; sepsis; infection;
 KW microbial surface component recognising adhesive matrix molecule; MSCRAMM;
 KW adhesin; vaccine; immunisation; diagnosis; therapy; mastitis.
 XX
 OS Staphylococcus aureus.
 XX
 FH Key Location/Qualifiers
 FT Peptide 1..12
 PN /note="vector POE30-derived peptide"
 PN WO9743314-A2.
 XX
 PD 20-NOV-1997.
 XX
 PF 14-MAY-1997; 97WO-US008210.
 XX
 PR 16-MAY-1996; 96US-0017678P.
 XX
 PA (TEXA) UNIV TEXAS A & M SYSTEM.
 PA (UABR-) UAB RES FOUND.

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OW protein - protein search, using sw model

Run on: October 22, 2005, 03:51:22 ; Search time 21.1723 Seconds
(without alignments)
133.980 Million cell updates/sec

Title: US-10-731-238-44

Perfect score: 211
Sequence: 1 QNSGNQSFPPDTEEDPKRQEPNIVDIDFDSVPQING 38

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: /cgn2_6/prodata/1/1aa/5A_COMB.pep:*
2: /cgn2_6/prodata/1/1aa/5B_COMB.pep:*
3: /cgn2_6/prodata/1/1aa/6A_COMB.pep:*
4: /cgn2_6/prodata/1/1aa/6B_COMB.pep:*
5: /cgn2_6/prodata/1/1aa/CTUS_COMB.pep:*
6: /cgn2_6/prodata/1/1aa/Backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	211	100.0	38	4	US-09-010-317-44 Sequence 44, Appl
2	192	91.0	38	4	US-09-010-317-50 Sequence 50, Appl
3	186	88.2	38	4	US-09-010-317-6 Sequence 6, Appl1
4	186	88.2	38	4	US-09-010-317-43 Sequence 43, Appl
5	185	87.7	38	4	US-09-010-317-36 Sequence 36, Appl
6	185	87.7	38	4	US-09-010-317-37 Sequence 37, Appl
7	177	83.9	38	1	US-08-234-622A-2 Sequence 2, Appl1
8	177	83.9	38	4	US-09-010-317-5 Sequence 5, Appl1
9	177	83.9	114	1	US-08-259-000-3 Sequence 3, Appl1
10	177	83.9	130	2	US-08-459-135A-7 Sequence 7, Appl1
11	177	83.9	130	2	US-08-459-135A-8 Sequence 8, Appl1
12	177	83.9	130	3	US-08-495-559-7 Sequence 7, Appl1
13	177	83.9	130	3	US-08-495-559-8 Sequence 8, Appl1
14	177	83.9	139	3	US-08-856-253-8 Sequence 8, Appl1
15	177	83.9	174	2	US-08-459-135A-10 Sequence 10, Appl
16	177	83.9	174	2	US-08-459-135A-13 Sequence 13, Appl
17	177	83.9	174	3	US-08-495-559-10 Sequence 10, Appl
18	177	83.9	174	3	US-08-495-559-13 Sequence 13, Appl
19	177	83.9	176	3	US-08-495-559-6 Sequence 6, Appl1
20	177	83.9	178	3	US-08-459-135A-12 Sequence 12, Appl
21	177	83.9	181	2	US-08-495-559-12 Sequence 12, Appl
22	177	83.9	181	2	US-08-459-135A-6 Sequence 6, Appl1
23	177	83.9	559	4	US-08-956-171E-5251 Sequence 5251, Ap
24	177	83.9	559	4	US-08-781-986A-5251 Sequence 5251, Ap
25	177	83.9	1027	4	US-08-956-171E-5254 Sequence 5254, Ap
26	177	83.9	1027	4	US-08-781-986A-5254 Sequence 5254, Ap
27	175.5	83.2	39	4	US-09-010-317-57 Sequence 57, Appl

28	171	81.0	38	1	US-08-729-767-3 Sequence 3, Appl1
29	171	81.0	38	4	US-09-010-317-39 Sequence 39, Appl
30	171	81.0	38	4	US-09-010-317-40 Sequence 40, Appl
31	171	81.0	38	4	US-09-010-317-41 Sequence 41, Appl
32	170	80.6	38	4	US-09-010-317-38 Sequence 38, Appl
33	170	80.6	38	4	US-09-010-317-42 Sequence 42, Appl
34	167	79.1	38	4	US-09-010-317-8 Sequence 8, Appl1
35	167	79.1	38	4	US-09-010-317-35 Sequence 35, Appl
36	167	79.1	38	4	US-09-010-317-49 Sequence 49, Appl
37	166.5	78.9	39	4	US-09-010-317-56 Sequence 56, Appl
38	166	78.7	38	4	US-09-010-317-46 Sequence 46, Appl
39	166	78.7	38	4	US-09-010-317-47 Sequence 47, Appl
40	158	74.9	38	1	US-08-234-622A-3 Sequence 3, Appl1
41	158	74.9	38	4	US-09-010-317-7 Sequence 7, Appl1
42	152	72.0	38	1	US-08-729-767-4 Sequence 4, Appl1
43	151	71.6	38	4	US-09-010-317-48 Sequence 48, Appl
44	148	70.1	38	4	US-09-010-317-45 Sequence 45, Appl
45	144	68.2	36	4	US-09-010-317-59 Sequence 59, Appl

ALIGNMENTS

RESULT 1
US-09-010-317-44
Sequence 44, Application US/09010317
Patent No. 6685943
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
APPLICANT: Patti, Joseph M.
APPLICANT: House-Pompeo, Karen L.
APPLICANT: Speziale, Pietro
APPLICANT: Joh, Danny
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
TITLE OF INVENTION: AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TANK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 44:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS: linear
TOPOLOGY: linear
US-09-010-317-44
Query Match 100.0%; Score 211; DB 4; Length 38;
Best Local Similarity 100.0%; Pred. No. 4,7e-21;

Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QNSGNSFPPTDEBKPKYEOPPNIVDIDFDSVPQIHG 38
DB 1 QNSGNSFPPTDEBKPKYEOPPNIVDIDFDSVPQIHG 38

RESULT 2

US-09-010-317-50
; Sequence 50, Application US/09010317
; Patent No. 6685943
; GENERAL INFORMATION:
; APPLICANT: Hook, Magnus
; APPLICANT: Patti, Joseph M.
; APPLICANT: House-Pompeo, Karen L.
; APPLICANT: Speziale, Pietro
; APPLICANT: Joh, Danny
; APPLICANT: McGavin, Martin J.
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
; TITLE OF INVENTION: AND METHODS OF USE
; NUMBER OF SEQUENCES: 105
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: TX
; COUNTRY: USA
; ZIP: 77210-4433
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/010.317
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/036,139
; FILING DATE: 21-JAN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Hibler, David W.
; REGISTRATION NUMBER: 41, 071
; REFERENCE/DOCKET NUMBER: TANK:189
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 512-418-3000
; TELEFAX: 512-474-7577
; INFORMATION FOR SEQ ID NO: 50:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 38 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
US-09-010-317-50

Query Match 91.0%; Score 192; DB 4; Length 38;
Best Local Similarity 86.8%; Pred. No. 1.5e-18;
Matches 33; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 QNSGNSFPPTDEBKPKYEOPPNIVDIDFDSVPQIHG 38
DB 1 QNSGNSFPPTDEBKPKYEOPPNIVDIDFDSVPQIHG 38

RESULT 3

US-09-010-317-6
; Sequence 6, Application US/09010317
; Patent No. 6685943
; GENERAL INFORMATION:
; APPLICANT: Hook, Magnus
; APPLICANT: Patti, Joseph M.
; APPLICANT: House-Pompeo, Karen L.
; APPLICANT: Speziale, Pietro

APPLICANT: Joh, Danny
APPLICANT: McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
TITLE OF INVENTION: AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/010.317
FILING DATE:
CLASSIFICATION:

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41, 071
REFERENCE/DOCKET NUMBER: TANK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577

INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-09-010-317-6

Query Match 88.2%; Score 186; DB 4; Length 38;
Best Local Similarity 92.1%; Pred. No. 9.3e-18;
Matches 35; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 QNSGNSFPPTDEBKPKYEOPPNIVDIDFDSVPQIHG 38
DB 1 QNSGNSFPPTDEBKPKYEOPPNIVDIDFDSVPQIHG 38

RESULT 4

US-09-010-317-43
; Sequence 43, Application US/09010317
; Patent No. 6685943
; GENERAL INFORMATION:
; APPLICANT: Hook, Magnus
; APPLICANT: Patti, Joseph M.
; APPLICANT: House-Pompeo, Karen L.
; APPLICANT: Speziale, Pietro
; APPLICANT: Joh, Danny
; APPLICANT: McGavin, Martin J.
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
; TITLE OF INVENTION: AND METHODS OF USE
; NUMBER OF SEQUENCES: 105
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: TX
; COUNTRY: USA
; ZIP: 77210-4433
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAMK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 43:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-09-010-317-43

Query Match 88.2%; Score 186; DB 4; Length 38;
Best Local Similarity 92.1%; Pred. No. 9.3e-18;
Matches 35; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 QNSGNSFPDTEEDKPKYEQPPNIVIDIDFDSVPQIHG 38
Db 1 QNSGNSFPDTEEDKPKYEQGNIVIDIDFDSVPQIHG 38

RESULT 5
US-09-010-317-36
Sequence 36, Application US/09010317
Patent No. 6685943
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
APPLICANT: Patti, Joseph M.
APPLICANT: House-Pompeo, Karen L.
APPLICANT: Speziale, Pietro
APPLICANT: McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
TITLE OF INVENTION: AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CURRENT APPLICATION DATA:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAMK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 36:

SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-09-010-317-36

Query Match 87.7%; Score 185; DB 4; Length 38;
Best Local Similarity 92.1%; Pred. No. 1.3e-17;
Matches 35; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 QNSGNSFPDTEEDKPKYEQPPNIVIDIDFDSVPQIHG 38
Db 1 QNSGNSFPDTEEDKPKYEQGNIVIDIDFDSVPQIHG 38

RESULT 6
US-09-010-317-37
Sequence 37, Application US/09010317
Patent No. 6685943
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
APPLICANT: Patti, Joseph M.
APPLICANT: House-Pompeo, Karen L.
APPLICANT: Speziale, Pietro
APPLICANT: McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
TITLE OF INVENTION: AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CURRENT APPLICATION DATA:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAMK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 37:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-09-010-317-37

Query Match 87.7%; Score 185; DB 4; Length 38;
Best Local Similarity 92.1%; Pred. No. 1.3e-17;
Matches 35; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 QNSGNSFPDTEEDKPKYEQPPNIVIDIDFDSVPQIHG 38
Db 1 QNSGNSFPDTEEDKPKYEQGNIVIDIDFDSVPQIHG 38

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RESULT 7
US-08-234-622A-2
; Sequence 2, Application US/08234622A
; Patent No. 5440014
; GENERAL INFORMATION:
; APPLICANT: HOOK, Magnus
; APPLICANT: MCGAVIN, Martin
; APPLICANT: RAUCCI, Giuseppe
; TITLE OF INVENTION: A FIBRONECTIN BINDING PEPTIDE
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Burns, Doane, Swecker & Mathis
; STREET: P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Releasee #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/234,622A
; FILING DATE: 28-APR-1994
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: SE 9002617-0
; FILING DATE: 10-AUG-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/SE91/00534
; FILING DATE: 09-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Meuth, Donna M
; REGISTRATION NUMBER: 36,607
; REFERENCE/DOCKET NUMBER: 012885-044
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 38 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-234-622A-2

Query Match      83.9%; Score 177; DB 1; Length 38;
Best Local Similarity 89.5%; Pred. No. 1,4e-16;
Matches 34; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Oy 1 ONSGNQSFPPDTEEDKPKYEQPNIVIDIDFDSVPOIHG 38
Db 1 ONSGNQSFPPDTEEDKPKYEQPNIVIDIDFDSVPOIHG 38

RESULT 8
US-09-010-317-5
; Sequence 5, Application US/09010317
; Patent No. 6685943
; GENERAL INFORMATION:
; APPLICANT: Hook, Magnus
; APPLICANT: Patil, Joseph M.
; APPLICANT: House-Pompeo, Karen L.
; APPLICANT: Speziale, Pietro
; APPLICANT: Joh, Danny
; APPLICANT: McGavin, Martin J.
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
; NUMBER OF SEQUENCES: 105
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Arnold, White & Durkee
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STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Releasee #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/010,317
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/036,139
; FILING DATE: 21-JAN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Hblber, David W.
; REGISTRATION NUMBER: 41,071
; REFERENCE/DOCKET NUMBER: TAMK.189
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 512-418-3000
; TELEFAX: 512-474-7577
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 38 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; US-09-010-317-5

Query Match      83.9%; Score 177; DB 4; Length 38;
Best Local Similarity 89.5%; Pred. No. 1,4e-16;
Matches 34; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Oy 1 ONSGNQSFPPDTEEDKPKYEQPNIVIDIDFDSVPOIHG 38
Db 1 ONSGNQSFPPDTEEDKPKYEQPNIVIDIDFDSVPOIHG 38

RESULT 9
US-08-259-000-3
; Sequence 3, Application US/08259000
; Patent No. 5571514
; GENERAL INFORMATION:
; APPLICANT: HOOK, Magnus
; APPLICANT: LINDBERG, Martin Kjell
; APPLICANT: SIGNAS, Lars Christer
; APPLICANT: WADSTROM, Torkel Mikael
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN AS WELL AS
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Burns, Doane, Swecker & Mathis
; STREET: P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Releasee #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/259,000
; FILING DATE: 13-JUN-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: SE 8702272-9
; FILING DATE: 01-JUN-1987
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ATTORNEY/AGENT INFORMATION:
NAME: Neuth, Donna M
REGISTRATION NUMBER: 36,607
REFERENCE/DOCKET NUMBER: 012885-062
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 114 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-259-000-3

Query Match 83.9%; Score 177; DB 1; Length 114;
Best Local Similarity 89.5%; Pred. No. 5,1e-16;
Matches 34; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 QNSGNSFPPTDEDKPKYEQPPNIVDIDFDSVPQIHG 38
DB 2 QNSGNSFEDTDEDKPKYEQGNIVDIDFDSVPQIHG 39

RESULT 10
US-08-459-135A-7
Sequence 7, Application US/08459135A
Patent No. 5955078
GENERAL INFORMATION:
APPLICANT: BURHAM, Martin Karl Russel
APPLICANT: CHOPRA, Ian
APPLICANT: CRITCHLEY, Ian Alfred
APPLICANT: KNOWLES, David Justin Charles
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN: MONOCLONAL ANTIBODY AND THEIR US
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
STATE: PA
COUNTRY: U.S.A.
ZIP: 19406-0939
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: Fastseq, Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/459,135A
FILING DATE: 02-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB/94/00215
FILING DATE: 04-Feb-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Gimmil, Edward R
REGISTRATION NUMBER: 38,891
REFERENCE/DOCKET NUMBER: P30591C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-4478
TELEFAX: 610-270-5090
TELEX:
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 130 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-459-135A-7

Query Match 83.9%; Score 177; DB 2; Length 130;

Best Local Similarity 89.5%; Pred. No. 6e-16;
Matches 34; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 QNSGNSFPPTDEDKPKYEQPPNIVDIDFDSVPQIHG 38
DB 2 QNSGNSFEDTDEDKPKYEQGNIVDIDFDSVPQIHG 39

RESULT 11
US-08-459-135A-8
Sequence 8, Application US/08459135A
Patent No. 5955078
GENERAL INFORMATION:
APPLICANT: BURHAM, Martin Karl Russel
APPLICANT: CHOPRA, Ian
APPLICANT: CRITCHLEY, Ian Alfred
APPLICANT: KNOWLES, David Justin Charles
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN: MONOCLONAL ANTIBODY AND THEIR US
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
STATE: PA
COUNTRY: U.S.A.
ZIP: 19406-0939
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: Fastseq, Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/459,135A
FILING DATE: 02-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB/94/00215
FILING DATE: 04-Feb-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Gimmil, Edward R
REGISTRATION NUMBER: 38,891
REFERENCE/DOCKET NUMBER: P30591C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-4478
TELEFAX: 610-270-5090
TELEX:
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 130 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-459-135A-8

Query Match 83.9%; Score 177; DB 2; Length 130;
Best Local Similarity 89.5%; Pred. No. 6e-16;
Matches 34; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 QNSGNSFPPTDEDKPKYEQPPNIVDIDFDSVPQIHG 38
DB 2 QNSGNSFEDTDEDKPKYEQGNIVDIDFDSVPQIHG 39

RESULT 12
US-08-495-559-7
Sequence 7, Application US/08495559A
Patent No. 6054572
GENERAL INFORMATION:
APPLICANT: BURHAM, Martin Karl Russel
APPLICANT: CHOPRA, Ian
APPLICANT: CRITCHLEY, Ian Alfred
APPLICANT: KNOWLES, David Justin Charles


```

; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN: MONOCLONAL
; FILE REFERENCE: P30591
; CURRENT APPLICATION NUMBER: US/08/495,559A
; CURRENT FILING DATE: 1995-08-03
; EARLIER APPLICATION NUMBER: GB 9302289.5
; EARLIER FILING DATE: 1993-02-05
; EARLIER APPLICATION NUMBER: GB 9321592.9
; EARLIER FILING DATE: 1993-10-20
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 7
; LENGTH: 130
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-08-495-559-7

Query Match      83.9%; Score 177; DB 3; Length 130;
Best Local Similarity 89.5%; Pred. No. 66-16;
Matches 34; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      1  QNSGNQSPPTDEDPKPKYEQEPNIVDIDFDSVPQIHG 38
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Db      2  QNSGNQSFEDTDEDPKPKYEQGNIVIDIDFDSVPQIHG 39

RESULT 13
US-08-495-559-8
; Sequence 8, Application US/08495559A
; Patent No. 6054572
; GENERAL INFORMATION:
; APPLICANT: BURHAM, Martin Karl Russel
; APPLICANT: CHOPRA, Ian
; APPLICANT: CRITCHLEY, Ian Alfred
; APPLICANT: KNOWLES, David Justin Charles
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN: MONOCLONAL
; FILE REFERENCE: P30591
; CURRENT APPLICATION NUMBER: US/08/495,559A
; CURRENT FILING DATE: 1995-08-03
; EARLIER APPLICATION NUMBER: GB 9302289.5
; EARLIER FILING DATE: 1993-02-05
; EARLIER APPLICATION NUMBER: GB 9321592.9
; EARLIER FILING DATE: 1993-10-20
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 8
; LENGTH: 130
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-08-495-559-8

Query Match      83.9%; Score 177; DB 3; Length 130;
Best Local Similarity 89.5%; Pred. No. 66-16;
Matches 34; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      1  QNSGNQSPPTDEDPKPKYEQEPNIVDIDFDSVPQIHG 38
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Db      2  QNSGNQSFEDTDEDPKPKYEQGNIVIDIDFDSVPQIHG 39

RESULT 14
US-08-856-253-8
; Sequence 8, Application US/08856253
; Patent No. 6288214
; GENERAL INFORMATION:
; APPLICANT: HOOK, Magnus
; APPLICANT: PATTI, Joseph M.
; APPLICANT: HOUSE, Pompeo, Karen
; APPLICANT: SCHAMAM, Narayana
; APPLICANT: SYMERASKY, Jindrich
; TITLE OF INVENTION: COLLAGEN BINDING PROTEIN COMPOSITIONS
; TITLE OF INVENTION: AND METHODS OF USE
```

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; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: U.S.
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/856,253
; FILING DATE: Concurrently Herewith
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/017,678
; FILING DATE: 16-MAY-1996
; TELECOMMUNICATION INFORMATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Kitchell, Barbara S.
; REGISTRATION NUMBER: 33,928
; REFERENCE/DOCKET NUMBER: TAWK:193
; TELEPHONE: (512) 418-3000
; TELEFAX: (512) 474-7577
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 139 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
US-08-856-253-8

Query Match      83.9%; Score 177; DB 3; Length 139;
Best Local Similarity 89.5%; Pred. No. 65e-16;
Matches 34; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      1  QNSGNQSPPTDEDPKPKYEQEPNIVDIDFDSVPQIHG 38
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Db      16 QNSGNQSFEDTDEDPKPKYEQGNIVIDIDFDSVPQIHG 53

RESULT 15
US-08-459-135A-10
; Sequence 10, Application US/08459135A
; Patent No. 5955078
; GENERAL INFORMATION:
; APPLICANT: BURHAM, Martin Karl Russel
; APPLICANT: CHOPRA, Ian
; APPLICANT: CRITCHLEY, Ian Alfred
; APPLICANT: KNOWLES, David Justin Charles
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN: MONOCLONAL ANTIBODY AND THEIR US
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corporation
; STREET: 709 Swedeland Road
; CITY: King of Prussia
; STATE: PA
; COUNTRY: U.S.A.
; ZIP: 19406-0939
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq, Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/459,135A
; FILING DATE: 02-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB/94/00215
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FILING DATE: 04-Feb-1994
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Gimm, Edward R
 REGISTRATION NUMBER: 38,891
 REFERENCE/DOCKET NUMBER: P30591C2
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 610-270-4478
 TELEFAX: 610-270-5090
 TELEX:
 INFORMATION FOR SEQ ID NO: 10:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 174 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: Protein
 US-08-459-135A-10

Query Match 83.9%; Score 177; DB 2; Length 174;
 Best Local Similarity 89.5%; Pred. No. 8.4e-16;
 Matches 34; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 QNSGNOSPPDTEBDKPKYEQPNIVDIDPDSVPQIHG 38
 |||||
 Db 2 QNSGNOSPPDTEBDKPKYEQGNIVDIDPDSVPQIHG 39

Search completed: October 22, 2005, 05:46:45
 Job time : 21.2223 secs

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OM protein - protein search, using sw model

Run on: October 22, 2005, 11:35:03 ; Search time 70.1256 Seconds
(without alignments)
226.232 Million cell updates/sec

Title: US-10-731-238-44

Perfect score: 211
Sequence: 1 USGNGSFPPDTEBDKPKYEQPNIVIDIDFDSVPQIHG 38Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1862951 seqs, 417491010 residues

Total number of hits satisfying chosen parameters: 1862951

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22: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysts of the total score distribution.

SUMMARIES

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3	186	88.2	38	18	US-10-731-238-6
4	186	88.2	38	18	US-10-731-238-43
5	185	87.7	38	18	US-10-731-238-36
6	185	87.7	38	18	US-10-731-238-37
7	177	83.9	38	18	US-10-731-238-5
8	177	83.9	139	9	US-09-813-820-8
9	177	83.9	388	8	US-08-901-062-1
10	177	83.9	559	8	US-08-781-986A-5251
11	177	83.9	559	15	US-10-329-624-5251

12	177	83.9	767	9	US-09-815-242-5899
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14	177	83.9	940	17	US-10-470-048B-424
15	177	83.9	948	17	US-10-470-048B-69
16	177	83.9	961	15	US-10-282-122A-43778
17	177	83.9	1018	9	US-09-815-242-5797
18	177	83.9	1018	9	US-09-815-242-12838
19	177	83.9	1018	17	US-10-470-048B-68
20	177	83.9	1027	8	US-08-781-986A-5254
21	177	83.9	1027	15	US-10-329-624-5254
22	177	83.9	1038	15	US-10-282-122A-43827
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36	166	78.7	38	18	US-10-731-238-47
37	158	74.9	38	18	US-10-731-238-7
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ALIGNMENTS

Sequence 5899, Ap
Sequence 13140, A
Sequence 424, App
Sequence 69, Appl
Sequence 43778, A
Sequence 5797, Ap
Sequence 12838, A
Sequence 68, Appl
Sequence 5254, Ap
Sequence 5254, Ap
Sequence 43827, A
Sequence 39, Appl
Sequence 40, Appl
Sequence 41, Appl
Sequence 38, Appl
Sequence 42, Appl
Sequence 5456, Ap
Sequence 12686, A
Sequence 8, Appl
Sequence 35, Appl
Sequence 49, Appl
Sequence 56, Appl
Sequence 46, Appl
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Sequence 7, Appl
Sequence 48, Appl
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Sequence 58, Appl
Sequence 59, Appl
Sequence 1, Appl
Sequence 2, Appl
Sequence 170477, Ap
Sequence 105, Ap

RESULT 1
US-10-731-238-44
Sequence 44, Application US/10731238
Publication No. US20050123552A1
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
Patti, Joseph M.
House-Pompeo, Karen L.
Speziale, Pietro
Joh, Danny
McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/731,238
FILING DATE: 10-Dec-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE: 21-Jan-1998
APPLICATION NUMBER: US 60/036,139

FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TANK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 44:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 44:
US-10-731-238-44

Query Match 100.0%; Score 211; DB 18; Length 38;
Best Local Similarity 100.0%; Pred. No. 1.5e-19;
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QNSGNQSFPPDTEEDKPKYEOPPNIVDIDFDSVPQIHG 38
DB 1 QNSGNQSFPPDTEEDKPKYEOPPNIVDIDFDSVPQIHG 38

RESULT 2
US-10-731-238-50
Sequence 50, Application US/10731238
Publication No. US20050123552A1
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
Patti, Joseph M.
House-Pompeo, Karen L.
Speziale, Pietro
John, Danny
McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/731,238
FILING DATE: 10-Dec-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE: 21-Jan-1998
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TANK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 50:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>

TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 50:
US-10-731-238-50

Query Match 91.0%; Score 192; DB 18; Length 38;
Best Local Similarity 86.8%; Pred. No. 3.8e-17;
Matches 33; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 QNSGNQSFPPDTEEDKPKYEOPPNIVDIDFDSVPQIHG 38
DB 1 QNSGNQSFPPDTEEDKPKYEOPPNIVDIDFDSVPQIHG 38

RESULT 3
US-10-731-238-6
Sequence 6, Application US/10731238
Publication No. US20050123552A1
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
Patti, Joseph M.
House-Pompeo, Karen L.
Speziale, Pietro
John, Danny
McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/731,238
FILING DATE: 10-Dec-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE: 21-Jan-1998
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TANK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-10-731-238-6

Query Match 88.2%; Score 186; DB 18; Length 38;
Best Local Similarity 92.1%; Pred. No. 2.2e-16;
Matches 35; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 QNSGNQSFPPDTEEDKPKYEOPPNIVDIDFDSVPQIHG 38
DB 1 QNSGNQSFPPDTEEDKPKYEOPPNIVDIDFDSVPQIHG 38

RESULT 4
US-10-731-238-43
Sequence 43, Application US/10731238
Publication No. US20050123552A1
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
Patti, Joseph M.
House-Pompeo, Karen L.
Speziale, Pietro
Joh, Danny
McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Releasee #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/731,238
FILING DATE: 10-Dec-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE: 21-Jan-1998
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Habler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAMK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 43:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 43:
US-10-731-238-43
Query Match 88.2%; Score 186; DB 18; Length 38;
Best Local Similarity 92.1%; Pred. No. 2.2e-16;
Matches 35; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 QNSGNOSFPPTDEEDKPKYEQPNIIVDIDFDSVPQIHG 38
DB 1 QNSGNOSFEEDTEEDKPKYEQGNIVDIDFDSVPQIHG 38
RESULT 5
US-10-731-238-36
Sequence 36, Application US/10731238
Publication No. US20050123552A1
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
Patti, Joseph M.
House-Pompeo, Karen L.
Speziale, Pietro
Joh, Danny
McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
AND METHODS OF USE

NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Releasee #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/731,238
FILING DATE: 10-Dec-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE: 21-Jan-1998
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Habler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAMK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 36:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 36:
US-10-731-238-36
Query Match 87.7%; Score 185; DB 18; Length 38;
Best Local Similarity 92.1%; Pred. No. 3e-16;
Matches 35; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 QNSGNOSFPPTDEEDKPKYEQPNIIVDIDFDSVPQIHG 38
DB 1 QNSGNOSFEEDTEEDKPKYEQGNIVDIDFDSVPQIHG 38
RESULT 6
US-10-731-238-37
Sequence 37, Application US/10731238
Publication No. US20050123552A1
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
Patti, Joseph M.
House-Pompeo, Karen L.
Speziale, Pietro
Joh, Danny
McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Releasee #1.0, Version #1.30

1 CURRENT APPLICATION DATA:
2 APPLICATION NUMBER: US/10/731,238
3 FILING DATE: 10-Dec-2003
4 CLASSIFICATION: <Unknown>
5 PRIOR APPLICATION DATA:
6 APPLICATION NUMBER: US/09/010,317
7 FILING DATE: 21-Jan-1998
8 APPLICATION NUMBER: US 60/036,139
9 FILING DATE: 21-JAN-1997
10 ATTORNEY/AGENT INFORMATION:
11 NAME: Hibley, David W.
12 REGISTRATION NUMBER: 41,071
13 REFERENCE/DOCKET NUMBER: TAMK:189
14 TELECOMMUNICATION INFORMATION:
15 TELEPHONE: 512-418-3000
16 TELEFAX: 512-474-7577
17 INFORMATION FOR SEQ ID NO: 37:
18 SEQUENCE CHARACTERISTICS:
19 LENGTH: 38 amino acids
20 TYPE: amino acid
21 STRANDEDNESS: <Unknown>
22 TOPOLOGY: linear
23 SEQUENCE DESCRIPTION: SEQ ID NO: 37:
24 US-10-731-238-37
25
26 Query Match 87.7%; Score 185; DB 18; Length 38;
27 Best Local Similarity 92.1%; Pred. No. 3e-16; Mismatches 3; Indels 0; Gaps 0;
28 Matches 35; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
29
30 QY 1 QNSGNQSFPPTEEDKPKYEQPPNIVDIDPDSVPQIHG 38
31 1 QNSGNQSFPPTEEDKPKYEQGNIVDIDPDSVPQIHG 38
32 Db 1 QNSGNQSFPPTEEDKPKYEQGNIVDIDPDSVPQIHG 38
33
34 RESULT 7
35 US-10-731-238-5
36 Sequence 5, Application US/10731238
37 Publication No. US20050123552A1
38 GENERAL INFORMATION:
39 APPLICANT: Hook, Magnus
40 Patti, Joseph M.
41 House-Pompeo, Karen L.
42 Speziale, Pietro
43 Joh, Danny
44 McGavin, Martin J.
45 TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
46 AND METHODS OF USE
47 NUMBER OF SEQUENCES: 105
48 CORRESPONDENCE ADDRESS:
49 ADDRESSEE: Arnold, White & Durkee
50 STREET: P.O. Box 4433
51 CITY: Houston
52 STATE: TX
53 COUNTRY: USA
54 ZIP: 77210-4433
55 COMPUTER READABLE FORM:
56 MEDIUM TYPE: floppy disk
57 COMPUTER: IBM PC compatible
58 OPERATING SYSTEM: PC-DOS/MS-DOS
59 SOFTWARE: Patentin Release #1.0, Version #1.30
60 CURRENT APPLICATION DATA:
61 APPLICATION NUMBER: US/10/731,238
62 FILING DATE: 10-Dec-2003
63 CLASSIFICATION: <Unknown>
64 PRIOR APPLICATION DATA:
65 APPLICATION NUMBER: US/09/010,317
66 FILING DATE: 21-Jan-1998
67 APPLICATION NUMBER: US 60/036,139
68 FILING DATE: 21-JAN-1997
69 ATTORNEY/AGENT INFORMATION:
70 NAME: Hibley, David W.
71 REGISTRATION NUMBER: 41,071
72 REFERENCE/DOCKET NUMBER: TAMK:189

1 TELECOMMUNICATION INFORMATION:
2 TELEPHONE: 512-418-3000
3 TELEFAX: 512-474-7577
4 INFORMATION FOR SEQ ID NO: 5:
5 SEQUENCE CHARACTERISTICS:
6 LENGTH: 38 amino acids
7 TYPE: amino acid
8 STRANDEDNESS: <Unknown>
9 TOPOLOGY: linear
10 SEQUENCE DESCRIPTION: SEQ ID NO: 5:
11 US-10-731-238-5
12
13 Query Match 83.9%; Score 177; DB 18; Length 38;
14 Best Local Similarity 89.5%; Pred. No. 3.1e-15;
15 Matches 34; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
16
17 QY 1 QNSGNQSFPPTEEDKPKYEQPPNIVDIDPDSVPQIHG 38
18 1 QNSGNQSFPPTEEDKPKYEQGNIVDIDPDSVPQIHG 38
19 Db 1 QNSGNQSFPPTEEDKPKYEQGNIVDIDPDSVPQIHG 38
20
21 RESULT 8
22 US-09-813-820-8
23 Sequence 8, Application US/09813820
24 Patent No. US20020102262A1
25 GENERAL INFORMATION:
26 APPLICANT: Hook, Magnus
27 Patti, Joseph M.
28 House-Pompeo, Karen
29 Schanam, Narayana
30 Symersky, Jindrich
31 TITLE OF INVENTION: COLLAGEN BINDING PROTEIN COMPOSITIONS
32 AND METHODS OF USE
33 NUMBER OF SEQUENCES: 8
34 CORRESPONDENCE ADDRESS:
35 ADDRESSEE: Arnold, White & Durkee
36 STREET: P.O. Box 4433
37 CITY: Houston
38 STATE: Texas
39 COUNTRY: U.S.
40 ZIP: 77210
41 COMPUTER READABLE FORM:
42 MEDIUM TYPE: floppy disk
43 COMPUTER: IBM PC compatible
44 OPERATING SYSTEM: PC-DOS/MS-DOS
45 SOFTWARE: Patentin Release #1.0, Version #1.30
46 CURRENT APPLICATION DATA:
47 APPLICATION NUMBER: US/09/813,820
48 FILING DATE: 22-Mar-2001
49 CLASSIFICATION: <Unknown>
50 PRIOR APPLICATION DATA:
51 APPLICATION NUMBER: 08/856,253
52 FILING DATE: <Unknown>
53 ATTORNEY/AGENT INFORMATION:
54 NAME: Kitchell, Barbara S.
55 REGISTRATION NUMBER: 33,928
56 REFERENCE/DOCKET NUMBER: TAMK:193
57 TELECOMMUNICATION INFORMATION:
58 TELEPHONE: (512) 418-3000
59 TELEFAX: (512) 474-7577
60 INFORMATION FOR SEQ ID NO: 8:
61 SEQUENCE CHARACTERISTICS:
62 LENGTH: 139 amino acids
63 TYPE: amino acid
64 STRANDEDNESS: <Unknown>
65 TOPOLOGY: linear
66 SEQUENCE DESCRIPTION: SEQ ID NO: 8:
67 US-09-813-820-8
68
69 Query Match 83.9%; Score 177; DB 9; Length 139;
70 Best Local Similarity 89.5%; Pred. No. 1.4e-14;
71 Matches 34; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 QNSGNOSPPPTEDBKPKYEQPNIVDIDFDSVPQIHG 38
Db 16 QNSGNOSFEEDTEBDKPKYEQGNIVDIDFDSVPQIHG 53

RESULT 9
US-08-901-062-1
Sequence 1, Application US/08901062
Publication No. US20020025324A1
GENERAL INFORMATION:
APPLICANT: SEALS, JONATHAN R.
TITLE OF INVENTION: RECOMBINANT BIVALENT BACTERIAL VACCINE
TITLE OF INVENTION: FOR THE PREVENTION OF MASTITIS
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: HALE AND DORR LLP
STREET: 60 State Street
CITY: Boston
STATE: MA
COUNTRY: United States Of America
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/901,062
FILING DATE: 25-JUL-1997
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Baker, Hollie L.
REGISTRATION NUMBER: 31,321
REFERENCE/DOCKET NUMBER: 106941.153
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 526-6000
TELEFAX: (617) 526-5000
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 388 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-901-062-1

Query Match 83.9%; Score 177; DB 8; Length 388;
Best Local Similarity 89.5%; Pred. No. 4.5e-14;
Matches 34; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 QNSGNOSPPPTEDBKPKYEQPNIVDIDFDSVPQIHG 38
Db 265 QNSGNOSFEEDTEBDKPKYEQGNIVDIDFDSVPQIHG 302

RESULT 10
US-08-781-986A-5251
Sequence 5251, Application US/08781986A
Publication No. US20030054436A1
GENERAL INFORMATION:
APPLICANT: Charles Kunsch
TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
NUMBER OF SEQUENCES: 5255
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COUNTRY: USA
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/781,986A
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Benson, Bob
REGISTRATION NUMBER: 30,446
REFERENCE/DOCKET NUMBER: PB248PP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 5251:
SEQUENCE CHARACTERISTICS:
LENGTH: 559 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-781-986A-5251

Query Match 83.9%; Score 177; DB 8; Length 559;
Best Local Similarity 89.5%; Pred. No. 6.9e-14;
Matches 34; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 QNSGNOSPPPTEDBKPKYEQPNIVDIDFDSVPQIHG 38
Db 301 QNSGNOSFEEDTEBDKPKYEQGNIVDIDFDSVPQIHG 338

RESULT 11
US-10-329-624-5251
Sequence 5251, Application US/10329624
Publication No. US20040043037A1
GENERAL INFORMATION:
APPLICANT: Charles Kunsch
GIL H. Choi
Patrick S. Dillon
Craig A. Rosen
Steven C. Barash
Michael R. Fannon
TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
NUMBER OF SEQUENCES: 5256
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COUNTRY: USA
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/329,624
FILING DATE: 27-Dec-2002
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/956,171
FILING DATE: October 20, 1997
APPLICATION NUMBER: 60/003,861
FILING DATE: January 5, 1996
APPLICATION NUMBER: 08/781,986
FILING DATE: January 3, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Mark J. Hyman

MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/781,986A
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Benson, Bob
REGISTRATION NUMBER: 30,446
REFERENCE/DOCKET NUMBER: PB248PP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 5251:
SEQUENCE CHARACTERISTICS:
LENGTH: 559 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-781-986A-5251

Query Match 83.9%; Score 177; DB 8; Length 559;
Best Local Similarity 89.5%; Pred. No. 6.9e-14;
Matches 34; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 QNSGNOSPPPTEDBKPKYEQPNIVDIDFDSVPQIHG 38
Db 301 QNSGNOSFEEDTEBDKPKYEQGNIVDIDFDSVPQIHG 338

RESULT 11
US-10-329-624-5251
Sequence 5251, Application US/10329624
Publication No. US20040043037A1
GENERAL INFORMATION:
APPLICANT: Charles Kunsch
GIL H. Choi
Patrick S. Dillon
Craig A. Rosen
Steven C. Barash
Michael R. Fannon
TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
NUMBER OF SEQUENCES: 5256
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COUNTRY: USA
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/329,624
FILING DATE: 27-Dec-2002
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/956,171
FILING DATE: October 20, 1997
APPLICATION NUMBER: 60/003,861
FILING DATE: January 5, 1996
APPLICATION NUMBER: 08/781,986
FILING DATE: January 3, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Mark J. Hyman

REGISTRATION NUMBER: 46,789
REFERENCE/DOCKET NUMBER: PB248PID1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (240) 314-1224
TELEFAX: (301) 309-8439
INFORMATION FOR SEQ ID NO: 5251:
SEQUENCE CHARACTERISTICS:
LENGTH: 559 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 5251:
US-10-329-624-5251

Query Match 83.9%; Score 177; DB 15; Length 559;
Best Local Similarity 89.5%; Pred. No. 6, 9e-14;
Matches 34; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 ONSGNQSFPPTEEDKPKYEQPNIVDIDFDSVPQIHG 38
Db 301 ONSGNQSFPEETEDKPKYEQGNIVDIDFDSVPQIHG 338

RESULT 12
US-09-815-242-5899
Sequence 5899, Application US/09815242
Patent No. US20020061569A1
GENERAL INFORMATION:
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Karl L.
APPLICANT: Zykkind, Judith W.
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John D.
APPLICANT: Carr, Grant J.
APPLICANT: Yamamoto, Robert T.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 5899
LENGTH: 767
TYPE: PRT
ORGANISM: Staphylococcus aureus
US-09-815-242-5899

Query Match 83.9%; Score 177; DB 9; Length 767;
Best Local Similarity 89.5%; Pred. No. 1e-13;
Matches 34; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 ONSGNQSFPPTEEDKPKYEQPNIVDIDFDSVPQIHG 38
Db 682 ONSGNQSFPEETEDKPKYEQGNIVDIDFDSVPQIHG 719

RESULT 13
US-09-815-242-13140
Sequence 13140, Application US/09815242
Patent No. US20020061569A1
GENERAL INFORMATION:
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Karl L.
APPLICANT: Zykkind, Judith W.
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John D.
APPLICANT: Carr, Grant J.
APPLICANT: Yamamoto, Robert T.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 13140
LENGTH: 767
TYPE: PRT
ORGANISM: Staphylococcus aureus
US-09-815-242-13140

Query Match 83.9%; Score 177; DB 9; Length 767;
Best Local Similarity 89.5%; Pred. No. 1e-13;
Matches 34; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 ONSGNQSFPPTEEDKPKYEQPNIVDIDFDSVPQIHG 38
Db 682 ONSGNQSFPEETEDKPKYEQGNIVDIDFDSVPQIHG 719

RESULT 14
US-10-470-048B-424
Sequence 424, Application US/10470048B
Publication No. US20050037444A1
GENERAL INFORMATION:
APPLICANT: MEINKE ET AL.
TITLE OF INVENTION: A METHOD FOR IDENTIFICATION, ISOLATION AND PRODUCTION OF
TITLE OF INVENTION: ANTIGENS TO A SPECIFIC PATHOGEN
FILE REFERENCE: SONN.035US
CURRENT APPLICATION NUMBER: US/10/470,048B
CURRENT FILING DATE: 2003-07-25
NUMBER OF SEQ ID NOS: 603
SOFTWARE: PatentIn version 3.1
SEQ ID NO 424
LENGTH: 940
TYPE: PRT
ORGANISM: Staphylococcus aureus
US-10-470-048B-424

Query Match 83.9%; Score 177; DB 17; Length 940;
Best Local Similarity 89.5%; Pred. No. 1.3e-13;
Matches 34; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 ONSGNQSFPPTEEDKPKYEQPNIVDIDFDSVPQIHG 38

Db 682 QNSGNOSFEEDTEEDKPKYEGCGNIVDIDFDSVPQIHG 719

RESULT 15

US-10-470-048B-69
 ; Sequence 69, Application US/10470048B
 ; Publication No. US2005003744A1
 ; GENERAL INFORMATION:
 ; APPLICANT: MEINKE ET AL.
 ; TITLE OF INVENTION: A METHOD FOR IDENTIFICATION, ISOLATION AND PRODUCTION OF
 ; TITLE OF INVENTION: ANTIGENS TO A SPECIFIC PATHOGEN
 ; FILE REFERENCE: SONN:035US
 ; CURRENT APPLICATION NUMBER: US/10/470,048B
 ; CURRENT FILING DATE: 2003-07-25
 ; NUMBER OF SEQ ID NOS: 603
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 69
 ; LENGTH: 948
 ; TYPE: PR1
 ; ORGANISM: Staphylococcus aureus
 US-10-470-048B-69

Query Match 83.9%; Score 177; DB 17; Length 948;
 Best Local Similarity 89.5%; Pred. No. 1.3e-13;
 Matches 34; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 QNSGNOSFPDPTBEDKPKYEQPPNIVDIDFDSVPQIHG 38
 Db 690 QNSGNOSFEEDTEEDKPKYEGCGNIVDIDFDSVPQIHG 727

Search completed: October 22, 2005, 12:09:27
 Job time : 70.1256 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 22, 2005, 04:14:19 ; Search time 13.8905 Seconds
(without alignments)
263.219 Million cell updates/sec

Title: US-10-731-238-44

Perfect score: 211
Sequence: 1 QNSGNQSPFPDTEBDKPKYEQPNIVIDFDSVPQIHG 38

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Length	DB ID	Description
1	177	83.9	940 2 S19702	fibronectin-binding
2	177	83.9	961 2 G90053	fibronectin-prote
3	177	83.9	1018 2 A32192	fibronectin-binding
4	177	83.9	1038 2 H90053	hypothetical prote
5	60	28.4	370 2 AB2578	membrane-bound lyp
6	60	28.4	370 2 A97360	outer membrane lip
7	59	28.0	606 1 S24758	catechol oxidase (
8	59	28.0	2647 2 T218161	hypothetical prote
9	58	27.5	1613 2 S39059	protein BRG1 - hum
10	58	27.5	3433 1 S28381	utrophin - human
11	57	27.0	7403 1 A48723	replication licens
12	57	27.0	920 2 F64697	isooleucine-tRNA 11
13	57	27.0	1647 2 S45252	SNF2beta protein -
14	56	26.5	621 2 T22904	hypothetical prote
15	56	26.5	1022 2 T53078	homeotic gene regu
16	55.5	26.3	428 2 T32952	hypothetical prote
17	55	26.1	657 2 C89815	methionyl-tRNA syn
18	55	26.1	920 2 T43263	cell division prot
19	55	26.1	2500 2 G71609	hypothetical prote
20	54	25.6	264 2 B64351	hypothetical prote
21	54	25.6	275 2 T24593	hypothetical prote
22	54	25.6	669 2 T38029	matrix metalloprote
23	54	25.6	920 2 T18852	hypothetical prote
24	54	25.6	1000 2 T46521	titin - rabbit (fr
25	54	25.6	6805 2 S20901	titin - cardiac mus
26	54	25.6	26926 1 T38344	titin, cardiac mus
27	53.5	25.4	375 2 D96037	probable ABC trans
28	53.5	25.4	1273 1 TDRIT7	leukocyte common a
29	53	25.1	156 1 R3H511	ribosomal protein

30	53	25.1	459 2 T21097	hypothetical prote
31	53	25.1	501 2 T05640	histone deacetylase
32	53	25.1	582 2 T38028	matrix metalloprote
33	53	25.1	834 2 B82940	conserved hypothet
34	53	25.1	1232 2 S40766	hypothetical prote
35	52.5	24.9	474 2 A40598	glutamate-ammonia
36	52.5	24.9	624 2 T49366	myocyte-specific e
37	52.5	24.9	729 2 A29651	KEK1 protein precu
38	52.5	24.9	1291 1 A28334	protein-tyrosine-p
39	52	24.6	330 2 S22140	nodulin Emod2 - Se
40	52	24.6	497 1 WMBELM	membrane protein L
41	52	24.6	517 2 E89530	protein H28G03.2 (
42	52	24.6	1254 2 B86160	hypothetical prote
43	51.5	24.4	208 2 T02447	hypothetical prote
44	51.5	24.4	396 1 A58938	surface protein rh
45	51.5	24.4	477 2 F89689	protein F18H3.4 (l

ALIGNMENTS

RESULT 1

S19702
fibronectin-binding protein B - Staphylococcus aureus
C:Species: Staphylococcus aureus
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #ext_change 09-Jul-2004
C:Accession: S19702
R:Joensson, K.; Signaes, C.; Mueller, H.P.; Lindberg, M.
Eur. J. Biochem. 202, 1041-1048, 1991
A:Title: Two different genes encode fibronectin binding proteins in Staphylococcus aureus
A:Reference number: S19702; PMID:92111475; PMID:1837266
A:Accession: S19702
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-940 <JOB>
A:Cross-references: UNIPROT:Q53682; EMBL:X62992; NID:G49040; PIDN:CAA44726.1; PID:G58156;
C:Keywords: fibronectin binding

Query Match 83.9%; Score 177; DB 2; Length 940;
Best Local Similarity 89.5%; Pred. No. 5.2e-15;
Matches 34; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 QNSGNQSPFPDTEBDKPKYEQPNIVIDFDSVPQIHG 38
DB 682 QNSGNQSPFPDTEBDKPKYEQGNIVIDFDSVPQIHG 719

RESULT 2

G90053
hypothetical protein fmb (imported) - Staphylococcus aureus (strain N315)
C:Species: Staphylococcus aureus
C:Date: 10-May-2001 #sequence_revision 10-May-2001 #ext_change 09-Jul-2004
A:Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.
A:Reference number: A89758; PMID:11418146
A:Accession: G90053
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-961 <KUR>
A:Cross-references: UNIPROT:Q99RD3; GB:BA000018; PID:G13702452; PIDN:BA843593.1; GSPDB:G
C:Genetics:
A:Experimental source: strain N315
A:Gene: fmb

Query Match 83.9%; Score 177; DB 2; Length 961;
Best Local Similarity 89.5%; Pred. No. 5.4e-15;
Matches 34; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 QNSGNQSPFPDTEBDKPKYEQPNIVIDFDSVPQIHG 38

Db 693 QNSGNQSFEDTDEKPKYEGCGNIVDIDFDSVPQIHG 730

RESULT 3

A32192
 fibronectin-binding protein - Staphylococcus aureus
 C:Species: Staphylococcus aureus
 C:Date: 31-Jul-1989 #sequence_revision 31-Jul-1989 #text_change 16-Feb-1997
 C:Accession: A32192
 R:Signaess, C.; Rauceti, G.; Joensson, K.; Lindgren, P.E.; Anantharamaiah, G.M.; Hoeseck, M.
 Proc. Natl. Acad. Sci. U.S.A. 86, 699-703, 1989
 A:Title: Nucleotide sequence of the gene for a fibronectin-binding protein from Staphylococcus aureus
 A:Reference number: A32192; MUID:89098998; PMID:2521391
 A:Accession: A32192
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-1018 <SIG>
 A:Cross-references: GB:J04151
 C:Keywords: fibronectin binding

Query Match 83.9%; Score 177; DB 2; Length 1018;
 Best Local Similarity 89.5%; Pred. No. 5.8e-15;
 Matches 34; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Oy 1 QNSGNQSFEDTDEKPKYEGCGNIVDIDFDSVPQIHG 38
 Db 746 QNSGNQSFEDTDEKPKYEGCGNIVDIDFDSVPQIHG 783

RESULT 4

H90053
 hypochlorite protein fnb [imported] - Staphylococcus aureus (strain N315)
 C:Species: Staphylococcus aureus
 C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
 C:Accession: H90053
 R:Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguma, A.; Mizutani-U, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramoto, K.
 Lancet 357, 1225-1240, 2001
 A:Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.
 A:Reference number: A9758; MUID:21311952; PMID:11418146
 A:Accession: H90053
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-1038 <KUR>
 A:Cross-references: UNIPROT:Q95RD2; GB:BA000018; PID:g13702453; PIDN:BA043594.1; GSPDB:G
 A:Experimental source: strain N315
 C:Genetics:
 A:Gene: fnb

Query Match 83.9%; Score 177; DB 2; Length 1038;
 Best Local Similarity 89.5%; Pred. No. 5.9e-15;
 Matches 34; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Oy 1 QNSGNQSFEDTDEKPKYEGCGNIVDIDFDSVPQIHG 38
 Db 742 QNSGNQSFEDTDEKPKYEGCGNIVDIDFDSVPQIHG 779

RESULT 5

AB2578
 membrane-bound lytic murein transglycosylase mlta [imported] - Agrobacterium tumefaciens
 C:Species: Agrobacterium tumefaciens
 C:Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 09-Jul-2004
 C:Accession: AB2578
 R:Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, I.
 erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kuyavlin, T.; Levy, R.; Li, M.; McCell
 : Karp, P.; Romero, P.; Zhang, S.
 Science 294, 2317-2323, 2001
 A:Accession: AB2578
 A:Reference number: A32192; MUID:89098998; PMID:2521391
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-1018 <SIG>
 A:Cross-references: GB:J04151
 C:Keywords: fibronectin binding

A:Reference number: AB2577; MUID:21608550; PMID:11743193

A:Accession: AB2578
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-370 <KUR>
 A:Cross-references: UNIPROT:Q8UB9; GB:AE008688; PIDN:AAL1040.1; PID:g17738325; GSPDB:G
 A:Experimental source: strain C58 (Dupont)
 C:Genetics:
 A:Gene: mlta
 A:Map position: circular chromosome

Query Match 28.4%; Score 60; DB 2; Length 370;
 Best Local Similarity 46.4%; Pred. No. 4;
 Matches 13; Conservative 3; Mismatches 12; Indels 0; Gaps 0;

Oy 7 SPPDTEEDKPKYEGCGNIVDIDFDSVP 34
 Db 107 SATPDVWRYPYRPPPLVDIDNDNR 134

RESULT 6

A97360
 outer membrane lipoprotein gna33 (ecoli_mltA homolog) (AF226403) [imported] - Agrobacteri
 C:Species: Agrobacterium tumefaciens
 C:Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 09-Jul-2004
 C:Accession: A97360
 R:Goodner, B.; Hinkle, G.; Galtung, S.; Miller, N.; Blanchard, M.; Quorillo, B.; Goldman, A.; Liu, F.; Wollam, C.; Allinger, M.; Doughy, D.; Scott, C.; Lappas, C.; Markelz, B.;
 Science 294, 2323-2328, 2001
 A:Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tumefaciens
 A:Reference number: A97359; MUID:21608551; PMID:11743194
 A:Accession: A97360
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-370 <KUR>
 A:Cross-references: UNIPROT:Q8UB9; GB:AE007869; PIDN:AAK5834.1; PID:g15154867; GSPDB:G
 A:Genetics:
 A:Map position: circular chromosome

Query Match 28.4%; Score 60; DB 2; Length 370;
 Best Local Similarity 46.4%; Pred. No. 4;
 Matches 13; Conservative 3; Mismatches 12; Indels 0; Gaps 0;

Oy 7 SPPDTEEDKPKYEGCGNIVDIDFDSVP 34
 Db 107 SATPDVWRYPYRPPPLVDIDNDNR 134

RESULT 7

S24758
 catechol oxidase (EC 1.10.3.1) precursor - fava bean
 M:Alternate names: polyphenol oxidase
 C:Species: Vicia faba (fava bean)
 C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
 C:Accession: S24758; S19805
 R:Carly, J.W.; Lax, A.R.; Flurkey, W.H.
 Plant Mol. Biol. 20, 245-253, 1992
 A:Title: Cloning and characterization of cDNAs coding for Vicia faba polyphenol oxidase.
 A:Reference number: S24758; MUID:93004477; PMID:1391768
 A:Accession: S24758
 A:Molecule type: mRNA
 A:Residues: 1-606 <CAR>
 A:Cross-references: UNIPROT:Q06215; EMBL:Z11702
 R:Carly, J.
 submitted to the EMBL Data Library, February 1992
 A:Reference number: S19805
 A:Accession: S19805
 A:Molecule type: mRNA
 A:Residues: 1-247, 'T', 249-250, 'A', 252-278, 'IG', 281-283, 286, 'RW', 287-606 <CA2>
 A:Cross-references: EMBL:Z11702; NID:g22028; PIDN:CAA77764.1; PID:g22029
 C:Superfamily: catechol oxidase
 C:Keywords: chloroplast; copper; metalloprotein; oxidoreductase

F.1-92/Domain: transit peptide (chloroplast) #status predicted <TMP>
 F.93-606/Product: catechol oxidase #status predicted <MAT>
 F.202,211/Binding site: copper (His) #status predicted
 F.333,337,367/Binding site: copper (His) #status predicted

Query Match 28.0%; Score 59; DB 1; Length 606;
 Best Local Similarity 37.1%; Pred. No. 9.7;
 Matches 13; Conservative 7; Mismatches 7; Indels 8; Gaps 2;

Qy 12 TREDKPKYE-----QPNVIDPF-DSVPOIHG 38
 Db 251 TDKASPLIDELRNASHQPTLIDNFCDSDSIHG 265

RESULT 8

T28161
 Hypothetical protein FCR3-varT11-1 - malaria parasite (Plasmodium falciparum) (fragments)

C:Species: Plasmodium falciparum
 C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004

C:Accession: T28161
 R.Hernandez-Rivas, R.; Mattei, D.; Sterkers, Y.; Peterson, D.S.; Wellems, T.E.; Scherf, M.O. Cell. Biol. 17, 604-611, 1997

A:Title: Expressed var genes are found in Plasmodium falciparum subtelomeric regions.
 A:Reference number: Z20483; MUID:97154495; PMID:9001213

A:Accession: T28161
 A:Status: preliminary; translated from GB/EMBL/DBJ

A:Residues: 1-2647 <HEB>
 A:Cross-references: UNIPROT:P90580; EMBL:U67959; NID:gi1794255; PID:gi1809295; PIDN:AA0474

A:Experimental source: strain FCQ27/PNG
 C:Genetics:
 A:Introns: 2158/3

A:Note: FCR3-varT11-1

Query Match 28.0%; Score 59; DB 2; Length 2647;
 Best Local Similarity 35.5%; Pred. No. 57;
 Matches 11; Conservative 8; Mismatches 12; Indels 0; Gaps 0;

Qy 3 SGNQSPPTEDKPKYEQPNVIDIDFDSV 33
 Db 2267 SGNNTASDTQNDIPSDPTPTDDEMTL 2297

RESULT 9

S39059
 protein BRG1 - human

C:Species: Homo sapiens (man)
 C:Date: 25-Feb-1994 #sequence_revision 17-Nov-1995 #text_change 09-Jul-2004

C:Accession: S39059
 R.Khavari, P.A.; Peterson, C.L.; Tamkun, J.W.; Mendel, D.B.; Crabtree, G.R.

A:Title: BRG1 contains a conserved domain of the SM12/SMN2 family necessary for normal
 A:Reference number: S39059; MUID:94050144; PMID:8232556

A:Accession: S39059
 A:Status: preliminary

A:Molecule type: mRNA
 A:Residues: 1-1613 <KHA>

A:Cross-references: UNIPROT:Q9HBJ3
 C:Superfamily: human SMN2alpha protein; bromodomain homology

F.1451-1506/Domain: bromodomain homology <BKO>

Query Match 27.5%; Score 58; DB 2; Length 1613;
 Best Local Similarity 29.5%; Pred. No. 42;
 Matches 13; Conservative 9; Mismatches 14; Indels 8; Gaps 1;

Qy 1 QNSGNQSPPTEDKPKYEQPNVIDIDFDSV 36
 Db 657 BEGSESEEESEEBEQPOQAQPTLPVEBKXKIPDPSDVSIV 700

RESULT 10

S28381
 utrophin - human

N.Alternate names: dystrophin-related protein

C:Species: Homo sapiens (man)
 C:Date: 17-Apr-1993 #sequence_revision 03-Oct-1995 #text_change 09-Jul-2004

C:Accession: S28381; S28914; S03966
 R.Tinsley, J.M.

A:Reference number: S28381
 submitted to the EMBL Data Library, November 1992

A:Accession: S28381
 A:Molecule type: mRNA

A:Residues: 1-3433 <TIN1>
 A:Cross-references: UNIPROT:P46939; EMBL:X69086; NID:g34811; PIDN:CAA48829.1; PID:g34812

R.Tinsley, J.M.; Blake, D.J.; Roche, A.; Fairbrother, U.; Riss, J.; Byth, B.C.; Knight, J.
 Nature 360, 591-593, 1992

A:Title: Primary structure of dystrophin-related protein.
 A:Reference number: S28914; MUID:93096045; PMID:1461283

A:Accession: S28914
 A:Molecule type: mRNA

A:Residues: 27-246; 2839-3343 <TIN2>
 A:Cross-references: EMBL:X69086

R.Love, D.R.; Hill, D.F.; Dickson, G.; Spurr, N.K.; Byth, B.C.; Marsden, R.F.; Walsh, F.
 Nature 339, 55-58, 1989

A:Title: An autosomal transcript in skeletal muscle with homology to dystrophin.
 A:Reference number: S03966; MUID:89238543; PMID:2541343

A:Accession: S03966
 A:Molecule type: mRNA

A:Residues: 2944-3433 <LOV>
 A:Cross-references: EMBL:X15488; NID:g30933; PIDN:CAA33515.1; PID:g930062

C:Comment: This protein is found primarily at the neuromuscular junctions in adult muscle
 d regenerating muscle.
 C:Genetics:

A:Gene: GDB:UTRN; DMDL
 A:Map position: 6q24-q24

C:Superfamily: dystrophin; alpha-actinin actin-binding domain homology; spectrin/dystrophin
 C:Keywords: actin binding; cytoskeleton; leucine zipper; membrane-associated protein; mus

F.130-248/Domain: spectrin/actinin repeat homology <ACT>
 F.308-417/Domain: spectrin/dystrophin repeat homology <SP01>

F.418-526/Domain: spectrin/dystrophin repeat homology <SP02>
 F.528-637/Domain: spectrin/dystrophin repeat homology <SP03>

F.638-685/Region: hinge
 F.686-796/Domain: spectrin/dystrophin repeat homology <SP04>

F.804-902/Domain: spectrin/dystrophin repeat homology <SP05>
 F.906-1013/Domain: spectrin/dystrophin repeat homology <SP06>

F.1015-1122/Domain: spectrin/dystrophin repeat homology <SP07>
 F.1124-1230/Domain: spectrin/dystrophin repeat homology <SP08>

F.1232-1334/Domain: spectrin/dystrophin repeat homology <SP09>
 F.1339-1450/Domain: spectrin/dystrophin repeat homology <SP10>

F.1451-1541/Domain: spectrin/dystrophin repeat homology <SP11>
 F.1543-1649/Domain: spectrin/dystrophin repeat homology <SP12>

F.1651-1755/Domain: spectrin/dystrophin repeat homology <SP13>
 F.1856-1973/Domain: spectrin/dystrophin repeat homology <SP14>

F.1975-2081/Domain: spectrin/dystrophin repeat homology <SP15>
 F.2083-2185/Domain: spectrin/dystrophin repeat homology <SP16>

F.2227-2333/Domain: spectrin/dystrophin repeat homology <SP17>
 F.2335-2440/Domain: spectrin/dystrophin repeat homology <SP18>

F.2442-2556/Domain: spectrin/dystrophin repeat homology <SP19>
 F.2558-2668/Domain: spectrin/dystrophin repeat homology <SP20>

F.2690-2797/Domain: spectrin/dystrophin repeat homology <SP21>
 F.2798-2869/Region: hinge

F.2812-2849/Domain: WW repeat homology <WML>
 F.2837-3117/Region: cysteine-rich
 F.3263-3284/Region: leucine zipper motif
 F.3328-3349/Region: leucine zipper motif

Query Match 27.5%; Score 58; DB 1; Length 3433;
 Best Local Similarity 34.6%; Pred. No. 1e+02;
 Matches 9; Conservative 6; Mismatches 11; Indels 0; Gaps 0;

Qy 6 QSFPPDTEKPKYEQPNVIDIDFD 31
 Db 285 QSTAPSEBESHPAERTPTTEVDMD 310

RESULT 11

A48723
 replication licensing factor MCM5 - fission yeast (*Schizosaccharomyces pombe*)
 N/Alternate names: cell division control protein CDC46; cell division control protein nd
 C/Species: *Schizosaccharomyces pombe*
 C/Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 09-Jul-2004
 C/Accession: A48723; T38702
 R/Miyake, S.; Okishio, N.; Samejima, I.; Hiraoka, Y.; Toda, T.; Satoh, I.; Yanagida, M.
 Mol. Biol. Cell 4, 1003-1015, 1993
 A/Title: Fission yeast genes nda1(+) and nda4(+), mutations of which lead to S-phase bld
 A/Reference number: A48723; MUID:94129084; PMID:8298187
 A/Accession: A48723
 A/Molecule type: DNA
 A/Status: preliminary
 A/Residues: 1-720 <MT>
 A/Cross-references: UNIPROT:P41389; GB:S68467; NID:9545210; PIDN:AA60568.1; PID:9545211
 R/Murphy, L.; Harris, D.; Barrett, B.G.; Rajandream, M.A.; Walsh, S.V.
 submitted to the EMBL Data Library, February 1996
 A/Reference number: 221807
 A/Accession: T38702
 A/Molecule type: DNA
 A/Residues: 72-460, 'A', 462-584, 'R', 586-699, 'U', 701-720 <MUR>
 A/Cross-references: EMBL:Z69369; PIDN:CAA93299.1; GSPDB:GN00066; SPDB:SPAC3F10.01
 C/Comment: The complex of six MCM proteins is one of several proteins that must be bound
 phosphorylated and disassociate from the chromatin.
 C/Genetics:
 A/Gene: nda4+
 C/Complex: The predominant form is a heterohexamer of MCM2, MCM3, MCM4, MCM5, MCM6, and
 C/Function:
 A/Description: part of the replication licensing system that permits DNA replication to
 C/Superfamily: replication licensing factor MCM5; MCM homology
 C/Keywords: cell cycle control; DNA replication initiation; nucleus
 F/132-636/Domain: MCM homology <MCM>

Query Match 27.0%; Score 57; DB 1; Length 720;
 Best Local Similarity 34.1%; Pred. No. 22;
 Matches 14; Conservative 12; Mismatches 11; Indels 4; Gaps 2;

OY 2 NSGNQSFPPDTEBDKPKY---EQPNVIDFDSDV-POIHG 38
 DB 296 NDGSKSTPLFSBEEEFLEISRTNLYDITSNISIPALYG 336

RESULT 12

F64697
 Isolucine-tRNA ligase (EC 6.1.1.5) - Helicobacter pylori (strain 26695)
 C/Species: *Helicobacter pylori*
 C/Date: 09-Aug-1997 #sequence_revision 09-Aug-1997 #text_change 09-Jul-2004
 C/Accession: F64697
 R/Tomb, J.F.; White, O.; Kertavagae, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.D.
 Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khaliak, H.G.; Glodek, A.; McKenney
 son, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Wattey, L.
 Nature 388, 539-547, 1997
 A/Author: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser, C.
 A/Title: The complete genome sequence of the gastric pathogen *Helicobacter pylori*.
 A/Reference number: A64520; MUID:97394467; PMID:9252185
 A/Accession: F64697
 A/Status: preliminary; nucleic acid sequence not shown; translation not shown
 A/Molecule type: DNA
 A/Residues: 1-920 <TOM>
 A/Cross-references: UNIPROT:P56456; GB:AE000642; GB:AE000511; NID:92314587; PIDN:AAD0846
 C/Genetics:
 A/Start codon: GTG
 C/Superfamily: Isolucine-tRNA ligase
 C/Keywords: ligase

Query Match 27.0%; Score 57; DB 2; Length 920;
 Best Local Similarity 45.8%; Pred. No. 29;
 Matches 11; Conservative 5; Mismatches 8; Indels 0; Gaps 0;

OY 9 PPTTEEDKPKTEQPNVIDFDSDV 32
 DB 521 PPSYQEDAKHYEKIMHIDVWFD 544

RESULT 13

S45252
 SNF2beta protein - human
 C/Species: *Homo sapiens* (man)
 C/Date: 10-Dec-1994 #sequence_revision 17-Nov-1995 #text_change 09-Jul-2004
 C/Accession: S45252
 R/Chiba, H.; Muramatsu, M.; Nomoto, A.; Kato, H.
 Nucleic Acids Res. 22, 1815-1820, 1994
 A/Title: Two human homologues of *Saccharomyces cerevisiae* SWI2/SNF2 and *Drosophila* brahma
 A/Reference number: S45251; MUID:94268902; PMID:8208605
 A/Accession: S45252
 A/Status: preliminary
 A/Molecule type: mRNA
 A/Residues: 1-1647 <CHI>
 A/Cross-references: UNIPROT:P51532; GB:D26156; NID:9505087; PIDN:BA005143.1; PID:9505088
 C/Superfamily: human SNF2alpha protein; bromodomain homology
 F/1485-1540/Domain: bromodomain homology <BRO>

Query Match 27.0%; Score 57; DB 2; Length 1647;
 Best Local Similarity 29.5%; Pred. No. 59;
 Matches 13; Conservative 9; Mismatches 14; Indels 8; Gaps 1;

OY 1 QNSGNQSFPPDTEBDKPKYEQP-----NIVDIDFSDVPQI 36
 DB 658 EESGSEEESEEEBQPOAQPPLVPEKKKIPDPDSDDVSEV 701

RESULT 14

T22904
 hypochlorite protein F58B4.1 - *Caenorhabditis elegans*
 C/Species: *Caenorhabditis elegans*
 C/Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
 C/Accession: T22904
 R/Wilkinson, U.
 submitted to the EMBL Data Library, June 1996
 A/Reference number: Z19634
 A/Accession: T22904
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: DNA
 A/Residues: 1-621 <WIL>
 A/Cross-references: UNIPROT:Q20975; EMBL:Z74038; PIDN:CAA98497.1; GSPDB:GN00023; CESP:FSF
 A/Experimental source: clone F58B4
 C/Genetics:
 A/Gene: CESP:F58B4.1
 A/Map position: 5
 A/Introns: 47/3; 94/3; 135/2; 157/1; 185/1; 218/3; 253/3; 328/1; 366/3; 447/2; 511/2; 581

Query Match 26.5%; Score 56; DB 2; Length 621;
 Best Local Similarity 32.4%; Pred. No. 25;
 Matches 12; Conservative 10; Mismatches 15; Indels 0; Gaps 0;

OY 1 QNSGNQSFPPDTEBDKPKYEQPNVIDFDSDVPQIH 37
 DB 81 ONAGTNGCAGTEOQKPLREKPRDRVKMGDTLHQVN 117

RESULT 15

I53078
 homeotic gene regulator - mouse (fragment)
 C/Species: *Mus sp.* (mouse)
 C/Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 09-Jul-2004
 C/Accession: I53078
 R/Randazzo, F.M.; Khavari, P.; Crabtree, G.; Tankun, J.; Rosent, J.
 Dev. Biol. 161, 229-242, 1994
 A/Title: brg1, a putative murine homologue of the *Drosophila* *brachy* gene, a homeotic gene
 A/Reference number: I53078; MUID:94123856; PMID:7904967
 A/Accession: I53078
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: mRNA
 A/Residues: 1-1022 <RES>
 A/Cross-references: UNIPROT:Q63928; GB:S68108; NID:9545017; PIDN:AA60670.1; PID:9545018
 C/Genetics:

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 22, 2005, 04:10:49 ; Search time 69.6361 Seconds
(without alignments)
279.439 Million cell updates/sec

Title: US-10-731-238-44
Perfect score: 211
Sequence: 1 QNSGNQSPPTBEDPKRYEQPNIVIDIDFDSVPQIHG 38

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues
Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 200000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_03:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	177	83.9	Q53682	Q53682 staphylococ
2	177	83.9	Q8NNU8	Q8NNU8 staphylococ
3	177	83.9	Q6G6H4	Q6G6H4 staphylococ
4	177	83.9	Q99RD3	Q99RD3 staphylococ
5	177	83.9	Q7A3J8	Q7A3J8 staphylococ
6	177	83.9	Q7A3J8	Q7A3J8 staphylococ
7	177	83.9	Q99RD2	Q99RD2 staphylococ
8	177	83.9	Q7A3J7	Q7A3J7 staphylococ
9	176	83.4	Q6GDU5	Q6GDU5 staphylococ
10	169	80.1	Q8NNU7	Q8NNU7 staphylococ
11	169	80.1	Q6G6H3	Q6G6H3 staphylococ
12	166	78.7	Q9AEP9	Q9AEP9 staphylococ
13	80.5	38.2	Q69L72	Q69L72 oryza sativ
14	62	29.4	Q96VQ5	Q96VQ5 aspergillus
15	61	28.9	Q69133	Q69133 human herpe
16	61	28.9	Q66551	Q66551 human herpe
17	61	28.9	Q66556	Q66556 human herpe
18	61	28.9	Q41940	Q41940 murid herpe
19	61	28.9	Q83342	Q83342 murid herpe
20	61	28.9	Q6FRE8	Q6FRE8 candida gla
21	60.5	28.7	Q8N7Y8	Q8N7Y8 homo sapien
22	60.5	28.7	Q6P2C0	Q6P2C0 homo sapien
23	60	28.4	Q8UUB9	Q8UUB9 agrobacteri
24	60	28.4	Q6PRT9	Q6PRT9 brachydanio
25	59	28.0	Q697U9	Q697U9 thermoplaem
26	59	28.0	P90580	P90580 plasmodium
27	58.5	27.7	Q6K603	Q6K603 oryza sativ
28	58	27.5	5181	ATRI1 HUMAN
29	58	27.5	819	Q9VY48
30	58	27.5	3433	UTRO_HUMAN
31	57.5	27.3	498	Q710D7

32	57	27.0	183	2	Q69134	Q69134 human herpe
33	57	27.0	549	2	Q7TSC5	Q7TSC5 mus musculu
34	57	27.0	720	1	MCMS_SCHPO	P41389 schizosacch
35	57	27.0	745	2	Q7SAB9	Q7SAB9 neurospora
36	57	27.0	746	2	Q6FTT2	Q6FTT2 candida gla
37	57	27.0	920	1	SVI_HELPY	P56456 helicobacte
38	57	27.0	1647	1	SN24_HUMAN	P51532 h possible
39	57	27.0	1647	2	Q9HBD3	Q9HBD3 homo sapien
40	57	27.0	1679	2	Q9HBD4	Q9HBD4 homo sapien
41	56.5	26.8	261	2	Q804V5	Q804V5 xenopus lae
42	56.5	26.8	484	2	Q911I0	Q911I0 frog adenov
43	56	26.5	118	2	Q66553	Q66553 human herpe
44	56	26.5	118	2	Q66559	Q66559 human herpe
45	56	26.5	118	2	Q66563	Q66563 human herpe

ALIGNMENTS

RESULT 1	ID	Q53682	PRELIMINARY;	PRT;	940 AA.
AC	Q53682;				
DT	01-NOV-1996 (TREMBlrel. 01, Created)				
DT	01-NOV-1996 (TREMBlrel. 01, Last sequence update)				
DT	01-MAR-2004 (TREMBlrel. 26, Last annotation update)				
DE	Fibronectin binding protein B.				
GN	Name=fnbB;				
OS	Staphylococcus aureus.				
OC	Bacteria; Firmicutes; Bacillales; Staphylococcus.				
OX	NCBI_Taxid=1280;				
RN	(1)				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=8325-4;				
RC	MEDLINE=8325-4; PubMed=1837266;				
RA	Jonsson K., Signas C., Muller H.P., Lindberg M.,				
RT	"Two different genes encode fibronectin binding proteins in				
RT	Staphylococcus aureus. The complete nucleotide sequence and				
RT	characterization of the second gene."				
RL	Bur. J. Blochem. 202:1041-1048 (1991).				
CC	-1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by				
CC	an amide bond (By similarity).				
DR	EMBL: X62992; CAA44726.1; -				
DR	PIR: S19702; S19702.				
DR	HSSP: Q53653; 1N67.				
DR	GO: GO:0009986; C:cell surface; IEA.				
DR	GO: GO:0005618; C:cell wall; IEA.				
DR	GO: GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.				
DR	GO: GO:0016020; C:membrane; IEA.				
DR	GO: GO:007155; P:cell adhesion; IEA.				
DR	InterPro: IPR008966; Adhes_Bact.				
DR	InterPro: IPR004237; Fn_bind.				
DR	InterPro: IPR005877; Gpos_YSRK.				
DR	InterPro: IPR001899; Gram_pos_anchor.				
DR	Pfam: PF02986; Fn_bind; 2.				
DR	Pfam: PF00746; Gram_pos_anchor; 1.				
DR	Pfam: PF04650; YSRK_signal; 1.				
DR	TIGRPFAM: TIGR01167; LpxTG_anchor; 1.				
DR	TIGRPFAM: TIGR01168; YSRK_signal; 1.				
DR	PROSITE: PSS0847; GRAM_POS_ANCHORING; 1.				
KW	Cell wall; Peptidoglycan-anchor.				
SEQ	SEQUENCE 940 AA; 10355 MW; E35FBBCA907AB345 CRC64;				
Query Match 83.9%; Score 177; DB 2; Length 940;					
Best local Similarity 89.5%; Pred. No. 3.6e-13;					
Matches 34; Conservative 0; Mismatches 4; Indels 0; Gaps 0;					
QY	1 QNSGNQSPPTBEDPKRYEQPNIVIDIDFDSVPQIHG 38				
DB	682 QNSGNQSPPTBEDPKRYEQGNIVIDIDFDSVPQIHG 719				
RESULT 2					

```
08NUT8      PRELIMINARY;      PRT;      943 AA.
ID 08NUT8
AC 08NUT8;
DT 01-OCT-2002 (TReMBLrel. 22, Created)
DT 01-OCT-2002 (TReMBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE Fimb protein.
GN Name=fimb; OrderedLocustNames=MM2420;
OS Staphylococcus aureus (strain MM2);
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=196620;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MM2;
RX MEDLINE=22040717; PubMed=12044378; DOI=10.1016/S0140-6736(02)08713-5;
RA Baba T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Oguchi A.,
RA Yamamoto K., Hiramatsu K.;
RT "Genome and virulence determinants of high virulence community-
acquired MRSA.";
RL Lancet 359:1819-1827(2002)
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
an amide bond (By similarity).
DR EMBL; AP004830; BAB96285.1; -.
DR HSSP; Q53653; 1N67.
DR GO; GO:0009986; C:cell surface; IEA.
DR GO; GO:0005618; C:cell wall; IEA.
DR GO; GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0007155; P:cell adhesion; IEA.
DR InterPro; IPR008966; Adhes_bact.
DR InterPro; IPR004237; Fm_bind.
DR InterPro; IPR005877; Gpos_Ysirk.
DR InterPro; IPR001899; Gram_pos_anchor.
DR Pfam; PF02986; Fm_bind; 1.
DR Pfam; PF00746; Gram_pos_anchor; 1.
DR TIGRFAMs; TIGR01167; LpxTG_anchor; 1.
DR TIGRFAMs; TIGR01168; Ysirk_signal; 1.
DR PROSITE; PS50847; GRAM_POS_ANCHORING; 1.
DR Cell wall, Complete proteome; Peptidoglycan-anchor.
SQ SEQUENCE 943 AA; 104537 MW; DA8A5F31947E1B6A CRC64;

Query Match      83.9%; Score 177; DB 2; Length 943;
Best Local Similarity 89.5%; Pred. No. 3.6e-13;
Matches 34; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 1 QNSGNQSFPPTEBDKPYEQPNIVDIDFDSVPQIHG 38
DB 689 QNSGNQSFEDTEBDKPYEQGCGNIVDIDFDSVPQIHG 726

RESULT 3
O6G6H4      PRELIMINARY;      PRT;      957 AA.
ID 06G6H4
AC 06G6H4;
DT 05-JUN-2004 (TReMBLrel. 27, Created)
DT 05-JUN-2004 (TReMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TReMBLrel. 27, Last annotation update)
DE Fibronectin-binding protein.
GN Name=fnbB; OrderedLocustNames=SA52387;
OS Staphylococcus aureus (strain MSSA476).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=282459;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=M50 / ATCC 700699;
RX PubMed=15213324; DOI=10.1073/pnas.0402521101;
RA Holden M.T.G., Fell E.J., Lindsay J.A., Peacock S.J., Day N.P.J.,
RA Enright M.C., Foster T.J., Moore C.E., Hurst L., Atkin R., Barron A.,
RA Baason N., Bentley S.D., Chillingworth C., Chillingworth T.,
RA Churcher C., Clark L., Corton C., Cronin A., Doggett J., Dowd L.,
RA Feltham T., Hance Z., Harris B., Hauser H., Holtroyd S., Jagels K.,
RA James K.D., Lennard N., Line A., Mayes R., Moule S., Mungall K.,
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RA Ormond D., Quail M.A., Rabinowitsch E., Rutherford K.M., Sanders M.,
RA Sharp S., Simmonds M., Stevens K., Whitehead S., Barrell B.G.,
RA Spratt B.G., Parkhill J.;
RT "Complete genomes of two clinical Staphylococcus aureus strains:
evidence for the rapid evolution of virulence and drug resistance.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:9786-9791(2004).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
an amide bond (By similarity).
DR EMBL; BX571857; CAG4201.1; -.
DR GO; GO:0009986; C:cell surface; IEA.
DR GO; GO:0005618; C:cell wall; IEA.
DR GO; GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0007155; P:cell adhesion; IEA.
DR InterPro; IPR008966; Adhes_bact.
DR InterPro; IPR004237; Fm_bind.
DR InterPro; IPR005877; Gpos_Ysirk.
DR InterPro; IPR001899; Gram_pos_anchor.
DR Pfam; PF02986; Fm_bind; 1.
DR Pfam; PF00746; Gram_pos_anchor; 1.
DR TIGRFAMs; TIGR01167; LpxTG_anchor; 1.
DR TIGRFAMs; TIGR01168; Ysirk_signal; 1.
DR PROSITE; PS50847; GRAM_POS_ANCHORING; 1.
DR Cell wall, Complete proteome; Peptidoglycan-anchor.
SQ SEQUENCE 957 AA; 105980 MW; 28F8BA7FDFD3EAF CRC64;

Query Match      83.9%; Score 177; DB 2; Length 957;
Best Local Similarity 89.5%; Pred. No. 3.7e-13;
Matches 34; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 1 QNSGNQSFPPTEBDKPYEQPNIVDIDFDSVPQIHG 38
DB 689 QNSGNQSFEDTEBDKPYEQGCGNIVDIDFDSVPQIHG 726

RESULT 4
O99RD3      PRELIMINARY;      PRT;      961 AA.
ID 099RD3
AC 099RD3;
DT 01-JUN-2001 (TReMBLrel. 17, Created)
DT 01-JUN-2001 (TReMBLrel. 17, Last sequence update)
DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)
DE Fibronectin-binding protein homolog.
GN Name=fnbB; OrderedLocustNames=SAV2502;
OS Staphylococcus aureus (strain M50 / ATCC 700699).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=158878;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=M50 / ATCC 700699;
RX MEDLINE=21311952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2;
RA Kuroda M., Onota T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Iian J.-Q., Ito T.,
RA Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hoshoyama C.,
RA Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kato C.,
RA Sekimizu K., Hiraoka H., Kuhara S., Goto S., Yabuzaki J.,
RA Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
RA Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
RT "Whole genome sequencing of methicillin-resistant Staphylococcus
aureus.";
RL Lancet 357:1225-1240(2001).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
an amide bond (By similarity).
DR EMBL; AP003365; BAB58664.1; -.
DR PIR; G90053; G90053.
DR HSSP; Q53653; 1N67.
DR GO; GO:0009986; C:cell surface; IEA.
DR GO; GO:0005618; C:cell wall; IEA.
DR GO; GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0007155; P:cell adhesion; IEA.
DR InterPro; IPR008966; Adhes_bact.
```

DR InterPro: IPR0042377; Fn_bind.
DR InterPro: IPR005877; Gpos_YsIRK.
DR InterPro: IPR001899; Gram_pos_anchor.
DR Pfam: PF02986; Fn_bind; 1.
DR Pfam: PF00746; Gram_pos_anchor; 1.
DR Pfam: PF04650; YsIRK_signal; 1.
DR TIGRFAMs: TIGR01167; LpxTG_anchor; 1.
DR TIGRFAMs: TIGR01168; YsIRK_signal; 1.
DR PROSITE: PS00847; GRAM_POS_ANCHORING; 1.
KW Cell wall, Complete proteome; Peptidoglycan-anchor.
SQ SEQUENCE 961 AA; 106010 MW; 364940F84EA4101 CRC64;

Query Match 83.9%; Score 177; DB 2; Length 961;
Best Local Similarity 89.5%; Pred. No. 3.7e-13;
Matches 34; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

1 ONSGNQSFPPDTEEDKPKYEGQPNIVDIDFDSVPQIHG 38
Db 693 ONSGNQSFPPDTEEDKPKYEGQGNIVDIDFDSVPQIHG 730
|||||

RESULT 5
Q7A3J8 PRELIMINARY; PRT; 961 AA.
Q7A3J8
AC 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE FmbB protein.
GN Name=FmbB; OrderedLocustNames=SA2290;
OS Staphylococcus aureus (strain N315).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=158879;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21331952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2;
RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Iken U.-Q., Ito T.,
RA Kanamori M., Matsumaru H., Matuyama A., Murakami H., Hoshiyama A.,
RA Katsumata-Uji Y., Takahashi N.K., Sawano T., Inoue R.-I., Kato C.,
RA Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
RA Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
RA Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
RT "Whole genome sequencing of methicillin-resistant Staphylococcus
RT aureus.";
RL Lancet 357:1225-1240(2001).
CC -1 SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC an amide bond (By similarity).
CC EMBL: AP003137; BAB3593.1; -;
DR GO: GO:0009986; C:cell surface; IEA.
DR GO: GO:0005618; C:cell wall; IEA.
DR GO: GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO: GO:0016020; C:membrane; IEA.
DR GO: GO:0007155; P:cell adhesion; IEA.
DR InterPro: IPR008966; Adhes_bact.
DR InterPro: IPR004237; Fn_bind.
DR InterPro: IPR005877; Gpos_YsIRK.
DR InterPro: IPR001899; Gram_pos_anchor.
DR Pfam: PF02986; Fn_bind; 1.
DR Pfam: PF00746; Gram_pos_anchor; 1.
DR Pfam: PF04650; YsIRK_signal; 1.
DR TIGRFAMs: TIGR01167; LpxTG_anchor; 1.
DR TIGRFAMs: TIGR01168; YsIRK_signal; 1.
DR PROSITE: PS00847; GRAM_POS_ANCHORING; 1.
KW Cell wall, Complete proteome; Peptidoglycan-anchor.
SQ SEQUENCE 961 AA; 106010 MW; 364940F84EA4101 CRC64;

Query Match 83.9%; Score 177; DB 2; Length 961;
Best Local Similarity 89.5%; Pred. No. 3.7e-13;
Matches 34; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

1 ONSGNQSFPPDTEEDKPKYEGQPNIVDIDFDSVPQIHG 38

ID	FNBA_STAAU	STANDARD;	PRT;	1018 AA.
RESULT 6				
FNBA_STAAU				
ID	FNBA_STAAU	STANDARD;	PRT;	1018 AA.
AC	P14738;			
DT	01-APR-1990 (Rel. 14, Created)			
DT	01-APR-1990 (Rel. 14, Last sequence update)			
DT	25-OCT-2004 (Rel. 45, Last annotation update)			
DE	Fibronectin-binding protein precursor (FNBP).			
GN	Name=fnba;			
OS	Staphylococcus aureus.			
CC	Bacteria; Firmicutes; Bacillales; Staphylococcus.			
OK	NCBI_TaxId=1280;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=NTC 8325-4;			
RX	MEDLINE=89098998; PubMed=2521391;			
RA	Signase C., Raucic G., Joensen K., Lindgren P.-E.,			
RA	Amanturamiah G.M., Hoeck M., Lindberg M.;			
RT	"Nucleotide sequence of the gene for a fibronectin-binding protein			
RT	from <i>Staphylococcus aureus</i> : use of this peptide sequence in the			
RT	synthesis of biologically active peptides."			
RL	Proc. Natl. Acad. Sci. U.S.A. 86:699-703(1989).			
CC	-I- FUNCTION: The ability of bacteria to bind fibronectin has been			
CC	proposed as a virulence factor enabling bacteria to colonize wound			
CC	tissues and blood clots. Binding of plasma fibronectin to the			
CC	bacterial surface might block adhesion receptors on <i>S.aureus</i> , thus			
CC	representing an important defense mechanism against tissue			
CC	invasion.			
CC	-I- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by			
CC	an amide bond (Potential).			
CC	-----			
CC	THIS SWISS-PROT entry is copyright. It is produced through a collaboration			
CC	between the Swiss Institute of Bioinformatics and the EMBL Outstation			
CC	the European Bioinformatics Institute. There are no restrictions on its			
CC	use by non-profit institutions as long as its content is in no way			
CC	modified and this statement is not removed. Usage by and for			
CC	entities requires a license agreement (see http://www.isb-sib.ch/announce/ib-sib.ch).			
CC	or send an email to license@ib-sib.ch .			
CC	-----			
DR	EMBL, J04151: AAA26632.1; -.			
DR	InterPro; IPR004237; FN_bind.			
DR	InterPro; IPR005877; Gpos_Y5IRK.			
DR	InterPro; IPR001899; Gram_pos_anchor.			
DR	Pfam; PF02986; Fn_bind; 1.			
DR	Pfam; PF00746; Gram_pos_anchor; 1.			
DR	Pfam; PF04650; Y5IRK_signal; 1.			
DR	TIGRFAMs; TIGR01167; LPXTG_anchor; 1.			
DR	TIGRFAMs; TIGR01168; Y5IRK_signal; 1.			
DR	PROSITE; PS50847; GRAM_POS_ANCHORING; 1.			
KW	Cell adhesion; Cell wall; Peptidoglycan-anchor; Repeat; Signal;			
KW	Virulence.			
FT	SIGNAL	1	36	
FT	CHAIN	37	985	Fibronectin-binding protein.
FT	PROSEP	966	1018	Removed by sortase (Potential).
FT	REPEAT	545	574	B-1.
FT	REPEAT	575	604	B-2.
FT	DOMAIN	745	878	4 X approximate tandem repeats,
FT				fibronectin-binding domain.
FT	REPEAT	745	782	D-1.
FT	REPEAT	783	820	D-2.
FT	REPEAT	821	859	D-3.
FT	REPEAT	860	878	D-4 (incomplete).
FT	DOMAIN	879	948	5 X tandem repeats, Pro-rich (WR).
FT	REPEAT	879	892	WR 1.
FT	REPEAT	893	906	WR 2.
FT	REPEAT	907	920	WR 3.
FT	REPEAT	921	934	WR 4.
FT	REPEAT	935	948	WR 5.
FT	SITE	982	986	LPXTG sorting signal (Potential).
FT	MOD_RES	985	985	Pentaglycyl murein peptidoglycan anchored

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FT          threonine (Potential).
SQ SEQUENCE 1018 AA; 111780 MW; 58155E00208E81F CRC64;
Query Match 83.9%; Score 177; DB 1; Length 1018;
Best Local Similarity 89.5%; Pred. No. 3.9e-13;
Matches 34; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Oy 1 QNSGNQSFPPTEBEDKRYEQPNIVDIDFDSVPQIHG 38
Db 746 QNSGNQSFEEDETDKRYEQGNIVDIDFDSVPQIHG 783

RESULT 7
AC Q99RD2 PRELIMINARY; PRT; 1038 AA.
AC Q99RD2;
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Fibronectin-binding protein homolog.
GN Name=fnb; OrderedLocusNames=SAV2503;
OS Staphylococcus aureus (strain MU50 / ATCC 700639).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=158878;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MU50 / ATCC 700639;
RX MEDLINE=21311952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2;
RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Iian J.-Q., Ito T.,
RA Kanamori M., Matsumaru H., Murakami H., Hoshoyama A.,
RA Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
RA Sekimizu K., Hiraoka H., Kuhara S., Goto S., Yahuzaki J.,
RA Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
RA Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
RT "Whole genome sequencing of methicillin-resistant Staphylococcus
RT aureus.";
RL Lancer 357:1225-1240(2001).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC an amide bond (by similarity).
DR EMBL; AP003137; BAB3594.1; -.
DR PIR; H90053; H90053.
DR GO; GO:0009986; C:cell surface; IEA.
DR GO; GO:0005618; C:cell wall; IEA.
DR GO; GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR InterPro; IPR008966; Adhes_bact.
DR InterPro; IPR004237; Fn_bind.
DR InterPro; IPR005877; Gpos_YsIRK.
DR InterPro; IPR001899; Gram_pos_anchor.
DR Pfam; PF02986; Fn_bind; 1.
DR Pfam; PF00746; Gram_pos_anchor; 1.
DR Pfam; PF04650; YsIRK_signal; 1.
DR TIGRFAMs; TIGR01167; LpxTG_anchor; 1.
DR TIGRFAMs; TIGR01168; YsIRK_signal; 1.
DR PROSITE; PS50847; GRAM_POS_ANCHORING; 1.
KM Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ SEQUENCE 1038 AA; 113618 MW; 6668FBF2FBEB12 CRC64;

Query Match 83.9%; Score 177; DB 2; Length 1038;
Best Local Similarity 89.5%; Pred. No. 4e-13;
Matches 34; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Oy 1 QNSGNQSFPPTEBEDKRYEQPNIVDIDFDSVPQIHG 38
Db 742 QNSGNQSFEEDETDKRYEQGNIVDIDFDSVPQIHG 779

RESULT 8
AC Q7A3J7 PRELIMINARY; PRT; 1038 AA.
AC Q7A3J7;

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DT 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE Fnb protein.
GN Name=fnb; OrderedLocusNames=SA42291;
OS Staphylococcus aureus (strain N315).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=158879;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21311952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2;
RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Iian J.-Q., Ito T.,
RA Kanamori M., Matsumaru H., Murakami H., Hoshoyama A.,
RA Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
RA Sekimizu K., Hiraoka H., Kuhara S., Goto S., Yahuzaki J.,
RA Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
RA Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
RT "Whole genome sequencing of methicillin-resistant Staphylococcus
RT aureus.";
RL Lancer 357:1225-1240(2001).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC an amide bond (by similarity).
DR EMBL; AP003137; BAB3594.1; -.
DR GO; GO:0009986; C:cell surface; IEA.
DR GO; GO:0005618; C:cell wall; IEA.
DR GO; GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0009275; P:cell adhesion; IEA.
DR InterPro; IPR008966; Adhes_bact.
DR InterPro; IPR004237; Fn_bind.
DR InterPro; IPR005877; Gpos_YsIRK.
DR InterPro; IPR001899; Gram_pos_anchor.
DR Pfam; PF02986; Fn_bind; 1.
DR Pfam; PF00746; Gram_pos_anchor; 1.
DR Pfam; PF04650; YsIRK_signal; 1.
DR TIGRFAMs; TIGR01167; LpxTG_anchor; 1.
DR TIGRFAMs; TIGR01168; YsIRK_signal; 1.
DR PROSITE; PS50847; GRAM_POS_ANCHORING; 1.
KM Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ SEQUENCE 1038 AA; 113618 MW; 6668FBF2FBEB12 CRC64;

Query Match 83.9%; Score 177; DB 2; Length 1038;
Best Local Similarity 89.5%; Pred. No. 4e-13;
Matches 34; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Oy 1 QNSGNQSFPPTEBEDKRYEQPNIVDIDFDSVPQIHG 38
Db 742 QNSGNQSFEEDETDKRYEQGNIVDIDFDSVPQIHG 779

RESULT 9
OQGDUS PRELIMINARY; PRT; 965 AA.
ID OQGDUS;
AC OQGDUS;
DT 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE Fibronectin-binding protein.
GN Name=fnbA; OrderedLocusNames=SA2580;
OS Staphylococcus aureus (strain MRSA252).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=282458;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=15213324; DOI=10.1073/pnae.040251101;
RA Holden M.T.G., Fell E.J., Lindsay J.A., Peacock S.J., Day N.P.J.,
RA Enright M.C., Foster T.J., Moore C.E., Hurst L., Atkin R., Barton A.,
RA Baeson N., Bentley S.D., Chillingworth C., Chillingworth T.,
RA Churcher C., Clark L., Cotton C., Cronin A., Doggett J., Dowd L.,
RA Fellwell T., Hance Z., Harris B., Hauser H., Holtroyd S., Jørgels K.,
RA James K.D., Lennard N., Line A., Mayes R., Moule S., Mungall K.,
RA Ormond D., Quail M.A., Rabinowitsch E., Rutherford K.M., Sanders M.,

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AC Q9AEP9;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Fibronectin-binding protein (Fragment).
GN Name=fib;
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
CX NCBI_TaxID=1280;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CMRSA-1;
RX MEDLINE=21246681; PubMed=11349044;
RX DOI=10.1128/IAI.69.6.3791-3799.2001;
RA Rice K., Huesca M., Vaz D., McGavin M.J.;
RT "Variance in fibronectin binding and fnb locus polymorphisms in
RT Staphylococcus aureus: identification of antigenic variation in a
RT fibronectin binding protein adhesin of the epidemic CMRSA-1 strain of
RT methicillin-resistant S. aureus."
RL Infect. Immun. 69:3791-3799(2001).
DR EMBL: AY029184; AAK31588.1; -.
FT NON_TER 1
FT NON_TER 152
SQ SEQUENCE 152 AA; 17193 MW; CFA3913C2B11C025 CRC64;

Query Match 78.7%; Score 166; DB 2; Length 152;
Best Local Similarity 84.2%; Pred. No. 1e-12;
Matches 32; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Oy 1 QNSGNQSPPTEDBKPKYEQPPNIVIDPDSVPQIIG 38
Db 1 QNTGNQSFEDTDEBKPKYEQGNIVIDPDSVPQIIG 38

RESULT 13
ID Q69J72 PRELIMINARY; PRT; 923 AA.
AC Q69J72;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Putative PMS2 postmeiotic segregation increased 2.
GN Name=OSJNBa0016G10.12;
OS Oryza sativa (Japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaceae; Oryza.
CX NCBI_TaxID=39947;
RN [1]
RP SEQUENCE FROM N.A.
RA Sasaki T., Matsumoto T., Katayose Y.;
RT "Oryza sativa n1pponbare(GA3) genomic DNA, chromosome 2, BAC
RT clone:OSJNBa0016G10."
RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: AP005874; BAD34084.1; -.
DR GO: GO:0005524; F:ATP binding; IEA.
DR GO: GO:0006298; P:mismatch repair; IEA.
DR InterPro: IPR003594; ATPbind_ATPase.
DR InterPro: IPR002099; DNA_mis_repair.
DR InterPro: IPR00102; MAP1B_neuraxin.
DR Pfam: PF01119; DNA_mis_repair; 1.
DR Pfam: PF02518; HATPase_C; 1.
DR TIGRFAMs: TIGR00585; mtl1; 1.
DR PROSITE: PS00058; DNA_MISMATCH_REPAIR_1; UNKNOWN_1.
DR PROSITE: PS00230; MAP1B_NEURAXIN; UNKNOWN_1.
SQ SEQUENCE 923 AA; 101237 MW; ASFD02C047947191 CRC64;

Query Match 38.2%; Score 80.5; DB 2; Length 923;
Best Local Similarity 51.6%; Pred. No. 0.34;
Matches 16; Conservative 5; Mismatches 9; Indels 1; Gaps 1;

Oy 6 QSPPTEDBKPKYEQPPNIVIDPDSVPQI 36
Db 6 QSPPTEDBKPKYEQPPNIVIDPDSVPQI 36
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Db 551 QSFVPEPDESPQHSPEPNIVS-HRDEVPOL 580

RESULT 14
ID Q96U05 PRELIMINARY; PRT; 574 AA.
AC Q96U05;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE ATP sulphurylase (EC 2.7.7.4).
OS Aspergillus fumigatus (Sartorya fumigata).
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC Eurotiiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
CX NCBI_TaxID=5085;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC46645;
RX MEDLINE=21371694; PubMed=11479709;
RX De Lucas J.R., Dominguez A.I., Mendoza A., Higuero Y., Romero B.,
RA laborda F.;
RT "development of a homologous transformation system for the
RT opportunistic human pathogen Aspergillus fumigatus based on the sc
RT gene encoding ATP sulphurylase."
RL Arch. Microbiol. 176:106-113(2001).
DR EMBL: AJ292542; CAC82078.1; -.
DR HSSP: Q12650; IMBP.
DR GO: GO:0005524; F:ATP binding; IEA.
DR GO: GO:0016301; F:kinase activity; IEA.
DR GO: GO:0016779; F:nucleotidyltransferase activity; IEA.
DR GO: GO:0004781; F:sulfate adenylyltransferase (ATP) activity; IEA.
DR GO: GO:0000103; P:sulfate assimilation; IEA.
DR InterPro: IPR002891; APS_kinase.
DR InterPro: IPR002650; ATP-sulfonylase.
DR Pfam: PF01583; APS_kinase; 1.
DR Pfam: PF01747; ATP-sulfonylase; 1.
DR ProDom: PD002350; APS_kinase; 1.
DR ProDom: PD002381; ATP-sulfonylase; 1.
DR TIGRFAMs: TIGR00455; apsk; 1.
DR TIGRFAMs: TIGR00339; sopt; 1.
DR NucleotideTransferase.
SQ SEQUENCE 574 AA; 64345 MW; ASBE279DC9C29B9C CRC64;

Query Match 29.4%; Score 62; DB 2; Length 574;
Best Local Similarity 47.8%; Pred. No. 39;
Matches 11; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

Oy 7 SFPPTEDBKPKYEQPPNIVID 29
Db 334 TYLPDTDEYKPKDEVPPGVKTL 356

RESULT 15
ID Q69I33 PRELIMINARY; PRT; 117 AA.
AC Q69I33;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Latent membrane protein 2A (Fragment).
GN Name=LMP 2A;
OS Human herpesvirus 4 (Epstein-Barr virus).
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Gammaherpesvirinae; Lymphocryptovirus.
CX NCBI_TaxID=10376;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88283646; PubMed=2840285;
RA Laux G., Pericaudet M., Farrell P.J.;
RT "A spliced Epstein-Barr virus gene expressed in immortalized
RT lymphocytes is created by circularization of the linear viral
RT genome."
RL EMBO J. 7:769-774(1988).
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RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=89095024; PubMed=2536113;
RA Sample J., Liebowitz D., Kieff E.D.;
RT "Two related Epstein-Barr virus membrane proteins are encoded by
RL separate genes.";
RL J. Virol. 63:933-937(1989).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=92219426; PubMed=1313931;
RA Busson P., McCoy R., Sadler R., Gilligan K., Tursz T., Raab-Traub N.;
RT "Consistent transcription of the Epstein-Barr virus LMP2 gene in
RL nasopharyngeal carcinoma.";
RL J. Virol. 66:3257-3262(1992).
DR EMBL: M87778; AAA45885.1; -
DR InterPro: IPR010881; Herpes_LMP2.
DR Pfam: PF07415; Herpes_LMP2; 1.
FT NON_TER 117
SQ SEQUENCE 117 AA; 12345 MW; 2F9248A628D30784 CRC64;
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Query Match 28.9%; Score 61; DB 2; Length 117;
Best Local Similarity 41.4%; Pred. No. 8.3;
Matches 12; Conservative 5; Mismatches 12; Indels 0; Gaps 0;

QY 2 NSGNOSFPPTREDDKPKYEQPPNIVDIDF 30
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DB 30 SSGNTPTTPNDEDERESNEEPPPYEDLDW 58

Search completed: October 22, 2005, 06:06:04
Job time : 71.6361 secs

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OM protein - protein search, using sw model

Run on: October 22, 2005, 03:51:22 ; Search time 21.1723 Seconds
(without alignments)
133.980 Million cell updates/sec

Title: US-10-731-238-48

Perfect score: 213
Sequence: 1 ONKGNQSFEBPEKPKYEHGNIIDFDVPHIIG 38

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

1: Issued Patents AA.*
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16: /cgn2_6/ptodata/1/iaa/6M.COMB.pep.*
17: /cgn2_6/ptodata/1/iaa/6N.COMB.pep.*
18: /cgn2_6/ptodata/1/iaa/6O.COMB.pep.*
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27: /cgn2_6/ptodata/1/iaa/6X.COMB.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	213	100.0	38	4	US-09-010-317-48
2	205	96.2	38	1	US-08-234-622A-3
3	205	96.2	38	4	US-09-010-317-7
4	205	96.2	114	1	US-08-259-000-3
5	205	96.2	139	3	US-08-856-253-8
6	205	96.2	1027	4	US-08-956-171E-5254
7	205	96.2	1027	4	US-08-781-986A-5254
8	200	93.9	130	2	US-08-459-135A-7
9	200	93.9	130	2	US-08-459-135A-8
10	200	93.9	130	2	US-08-495-559-7
11	200	93.9	130	3	US-08-495-559-8
12	200	93.9	174	2	US-08-459-135A-10
13	200	93.9	174	3	US-08-495-559-10
14	200	93.9	176	3	US-08-495-559-6
15	200	93.9	178	2	US-08-459-135A-12
16	200	93.9	178	3	US-08-495-559-12
17	200	93.9	181	2	US-08-459-135A-6
18	199	93.4	38	1	US-08-729-767-4
19	199	93.4	38	4	US-09-010-317-46
20	199	93.4	38	4	US-09-010-317-47
21	197	92.5	38	4	US-09-010-317-8
22	197	92.5	38	4	US-09-010-317-49
23	195	91.5	38	4	US-09-010-317-45
24	192	90.1	174	2	US-08-459-135A-13
25	192	90.1	174	3	US-08-495-559-13
26	192	90.1	559	4	US-08-956-171E-5251
27	192	90.1	559	4	US-08-781-986A-5251

28	187	87.8	38	4	US-09-010-317-38	Sequence 38, Appl
29	182	85.4	36	4	US-09-010-317-58	Sequence 58, Appl
30	179	84.0	38	1	US-08-234-622A-2	Sequence 2, Appl
31	179	84.0	38	4	US-09-010-317-5	Sequence 5, Appl
32	177	83.1	38	4	US-09-010-317-41	Sequence 41, Appl
33	177	83.1	38	4	US-09-010-317-50	Sequence 50, Appl
34	174	81.7	36	4	US-09-010-317-59	Sequence 59, Appl
35	173	81.2	38	1	US-08-729-767-3	Sequence 3, Appl
36	173	81.2	38	4	US-09-010-317-36	Sequence 36, Appl
37	173	81.2	38	4	US-09-010-317-37	Sequence 37, Appl
38	173	81.2	38	4	US-09-010-317-39	Sequence 39, Appl
39	173	81.2	38	4	US-09-010-317-40	Sequence 40, Appl
40	172	80.8	38	4	US-09-010-317-42	Sequence 42, Appl
41	171	80.3	38	4	US-09-010-317-6	Sequence 6, Appl
42	171	80.3	38	4	US-09-010-317-43	Sequence 43, Appl
43	171	80.3	38	4	US-09-010-317-35	Sequence 35, Appl
44	168.5	79.1	39	4	US-09-010-317-56	Sequence 56, Appl
45	160.5	75.4	39	4	US-09-010-317-57	Sequence 57, Appl

ALIGNMENTS

RESULT 1
US-09-010-317-48
Sequence 48, Application US/09010317
Patent No. 6685943
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
APPLICANT: Patti, Joseph M.
APPLICANT: House-Pompeo, Karen L.
APPLICANT: Speziale, Pietro
APPLICANT: John, Danny
APPLICANT: McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
TITLE OF INVENTION: AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAMK:189
TELEPHONE: 512-418-5000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 48:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-09-010-317-48
Query Match 100.0%; Score 213; DB 4; Length 38;
Best Local Similarity 100.0%; Pred. No. 8.5e-24;

	Matches	38;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;																								
Qy	1	Q	N	K	G	N	S	E	E	P	T	E	K	D	K	P	K	T	E	H	G	G	N	I	I	D	F	S	V	P	I	H	G	38
Db	1	Q	N	K	G	N	S	E	E	P	T	E	K	D	K	P	K	T	E	H	G	G	N	I	I	D	F	S	V	P	I	H	G	38

RESULT 2
US-08-234-622A-3
; Sequence 3, Application US/08234622A

```

1: GENERAL INFORMATION:
2: APPLICANT: HOOK, Magnus
3: APPLICANT: MCGAVIN, Martin
4: APPLICANT: RAOCCI, Giuseppe
5: TITLE OF INVENTION: A FIBRONECTIN BINDING PEPTIDE
6: NUMBER OF SEQUENCES: 4
7: CORRESPONDENCE ADDRESS:
8: ADDRESSEE: Burns, Doane, Swecker & Mathis
9: STREET: P.O. Box 1404
10: CITY: Alexandria
11: STATE: Virginia
12: COUNTRY: United States
13: ZIP: 22113-1404
14: COMPUTER READABLE FORM:
15: MEDIUM TYPE: Floppy disk
16: COMPUTER: IBM PC compatible
17: OPERATING SYSTEM: PC-DOS/MS-DOS
18: SOFTWARE: Patent in Release #1.0, Version #1.30
19: CURRENT APPLICATION DATA:
20: APPLICATION NUMBER: US/08/234,622A
21: FILING DATE: 28-Apr-1994
22: CLASSIFICATION: 510
23: PRIOR APPLICATION DATA:
24: APPLICATION NUMBER: SE 9002617-0
25: FILING DATE: 10-AUG-1990
26: PRIOR APPLICATION DATA:
27: APPLICATION NUMBER: WO PCT/SE91/00534
28: FILING DATE: 09-AUG-1991
29: ATTORNEY/AGENT INFORMATION:
30: NAME: Meuth, Donna M
31: REGISTRATION NUMBER: 36,607
32: REFERENCE/DOCKET NUMBER: 012885-044
33: TELECOMMUNICATION INFORMATION:
34: TELEPHONE: (703) 836-6620
35: TELEFAX: (703) 836-2021
36: INFORMATION FOR SEQ ID NO: 3:
37: SEQUENCE CHARACTERISTICS:
38: LENGTH: 38 amino acids
39: TYPE: amino acid
40: STRANDEDNESS: single
41: TOPOLOGY: linear
42: MOLECULE TYPE: peptide
43: US-08-234-622A-3
44:
45: Query Match 96.2%; Score 205; DB 1; Length 38;
46: Best Local Similarity 97.4%; Pred. No. 1.2e-22;
47: Matches 37; Conservative 0; Mismatches 1; Indels
48:
49: Qy 1 QNKGNSFEEBTEKDKRKYEHGNIIDIDFDSVPPIHG 38
50: Db 1 QNKGNSFEEBTEKDKRKYEHGNIIDIDFDSVPPIHG 38
51:
52: RESULT 3
53: US-09-010-317-7
54: Sequence 7, Application US/09010317
55: Patent No. 6685943
56: GENERAL INFORMATION:
57: APPLICANT: Hook, Magnus
58: APPLICANT: Patti, Joseph M.
59: APPLICANT: House-Pompeo, Karen L.
60: APPLICANT: Speziale, Pietro

```

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1  APPLICANT: Job, Danny
2  APPLICANT: McGavin, Martin J
3  TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
4  TITLE OF INVENTION: AND METHODS OF USE
5  NUMBER OF SEQUENCES: 105
6  CORRESPONDENCE ADDRESS:
7  ADDRESSEE: Arnold, White & Durkee
8  STREET: P.O. Box 4433
9  CITY: Houston
10 STATE: TX
11 COUNTRY: USA
12 ZIP: 77210-4433
13 COMPUTER READABLE FORM:
14 MEDIUM TYPE: Floppy disk
15 COMPUTER: IBM PC compatible
16 OPERATING SYSTEM: PC-DOS/MS-DOS
17 SOFTWARE: Patentn Release #1.0, Version #1.30
18 CURRENT APPLICATION DATA:
19 APPLICATION NUMBER: US/09/010.317
20 FILING DATE:
21 CLASSIFICATION:
22 PRIOR APPLICATION DATA:
23 APPLICATION NUMBER: US 60/036,139
24 FILING DATE: 21-JAN-1997
25 ATTORNEY/AGENT INFORMATION:
26 NAME: Hibler, David W.
27 REGISTRATION NUMBER: 41,071
28 REFERENCE/DOCKET NUMBER: TAMK:189
29 TELECOMMUNICATION INFORMATION:
30 TELEPHONE: 512-418-3000
31 TELEFAX: 512-474-7577
32 INFORMATION FOR SEQ ID NO: 7:
33 SEQUENCE CHARACTERISTICS:
34 LENGTH: 38 amino acids
35 TYPE: amino acid
36 STRANDEDNESS:
37 TOPOLOGY: linear
38 US-09-010-317-7
39
40 Query Match 96.2%; Score 205; DB 4; Length 38;
41 Best Local Similarity 97.4%; Pred. No. 1.2e-22;
42 Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
43
44 Oy 1 QNKGNSFPEPTKDKPKRYEHGNIIDIDPSVPHNG 38
45 Db 1 QNKGNSFPEPTKDKPKRYEHGNIIDIDPSVPHNG 38
46
47 RESULT 4
48 US-08-259-000-3
49 Sequence 3, Application US/08259000
50 Patent No. 5571514
51 GENERAL INFORMATION:
52 APPLICANT: HOOK, Magnus
53 APPLICANT: LINDBERG, Martin Kjell
54 APPLICANT: SIGNAS, Lars Christer
55 APPLICANT: WADSTROM, Torkel Mikael
56 APPLICANT: FROWAN, Gunnar
57 TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN AS WELL AS
58 NUMBER OF SEQUENCES: 4
59 CORRESPONDENCE ADDRESS:
60 ADDRESSEE: Burns, Doane, Swecker & Mathis
61 STREET: P.O. Box 1404
62 CITY: Alexandria
63 STATE: Virginia
64 COUNTRY: United States
65 ZIP: 22313-1404
66 COMPUTER READABLE FORM:
67 MEDIUM TYPE: Floppy disk
68 COMPUTER: IBM PC compatible
69 OPERATING SYSTEM: PC-DOS/MS-DOS
70 SOFTWARE: Patentn Release #1.0 Version #1.25

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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/259,000
FILING DATE: 13-JUN-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: SE 8702272-9
FILING DATE: 01-JUN-1987
ATTORNEY/AGENT INFORMATION:
NAME: Meuth, Donna M
REGISTRATION NUMBER: 36,607
REFERENCE/DOCKET NUMBER: 012885-062
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 114 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-259-000-3

Query Match 96.2%; Score 205; DB 1; Length 114;
Best Local Similarity 97.4%; Pred. No. 4.8e-22;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QNKGNSFEPTKDKPKYEHGNIIDIDPSVPHNG 38
Db 40 QNKGNSFEPTKDKPKYEHGNIIDIDPSVPHNG 77

RESULT 5
US-08-856-253-8
Sequence 8, Application US/08856253
Patent No. 6288214
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
APPLICANT: Patti, Joseph M.
APPLICANT: House-Pompeo, Karen
APPLICANT: Sthanam, Narayana
APPLICANT: Symersky, Jindrich
TITLE OF INVENTION: COLLAGEN BINDING PROTEIN COMPOSITIONS
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: Texas
COUNTRY: U.S.
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/856,253
FILING DATE: Concurrently Herewith
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/017,678
FILING DATE: 16-MAY-1996
ATTORNEY/AGENT INFORMATION:
NAME: Kitchell, Barbara S.
REGISTRATION NUMBER: 33,928
REFERENCE/DOCKET NUMBER: TAWK:193
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
TELEFAX: (512) 474-7577
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:

LENGTH: 139 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-08-856-253-8

Query Match 96.2%; Score 205; DB 3; Length 139;
Best Local Similarity 97.4%; Pred. No. 6.1e-22;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QNKGNSFEPTKDKPKYEHGNIIDIDPSVPHNG 38
Db 54 QNKGNSFEPTKDKPKYEHGNIIDIDPSVPHNG 91

RESULT 6
US-08-956-171E-5254
Sequence 5254, Application US/08956171E
Patent No. 6593114
GENERAL INFORMATION:
APPLICANT: Charles Kunsch
Gil H. Choi
Patrick S. Dillon
Craig A. Rosen
Steven C. Barash
Michael R. Fannon

TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences

NUMBER OF SEQUENCES: 5256
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.

STREET: 9410 Key West Avenue

CITY: Rockville

STATE: Maryland

COUNTRY: USA

ZIP: 20850

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4mb storage

COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/956,171E
FILING DATE: 20-Oct-1997

CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/009,861

FILING DATE: January 5, 1996
APPLICATION NUMBER: 08/781,986
FILING DATE: January 3, 1997

ATTORNEY/AGENT INFORMATION:
NAME: Mark J. Hyman

REGISTRATION NUMBER: 46,789
REFERENCE/DOCKET NUMBER: PB248P1

TELECOMMUNICATION INFORMATION:
TELEPHONE: (240) 314-1224

TELEFAX: (301) 309-8439

INFORMATION FOR SEQ ID NO: 5254:
SEQUENCE CHARACTERISTICS:
LENGTH: 1027 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear

MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 5254:

US-08-956-171E-5254

Query Match 96.2%; Score 205; DB 4; Length 1027;
Best Local Similarity 97.4%; Pred. No. 7.3e-21;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QNKGNSFEPTKDKPKYEHGNIIDIDPSVPHNG 38
Db 793 QNKGNSFEPTKDKPKYEHGNIIDIDPSVPHNG 830

RESULT 7
US-08-781-986A-5254
Sequence 5254, Application US/08781986A
Patent No. 6737248
GENERAL INFORMATION:
APPLICANT: Charles Kunach
TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
NUMBER OF SEQUENCES: 5255
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COUNTRY: USA
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4MB storage
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/781,986A
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Benson, Bob
REGISTRATION NUMBER: 30,446
REFERENCE/DOCKET NUMBER: PB248PP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 5254:
SEQUENCE CHARACTERISTICS:
LENGTH: 1027 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-781-986A-5254

Query Match 96.2%; Score 205; DB 4; Length 1027;
Best Local Similarity 97.4%; Pred. No. 7.3e-21;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QNKGNSFEPTKDKPKYEHGNIIDIDPDSVPHIG 38
DB 793 QNKGNSFEPTKDKPKYEHGNIIDIDPDSVPHIG 830

RESULT 8
US-08-459-135A-7
Sequence 7, Application US/08459135A
Patent No. 5955078
GENERAL INFORMATION:
APPLICANT: BURNHAM, Martin Karl Russel
APPLICANT: CHOPRA, Ian
APPLICANT: CRITCHLEY, Ian Alfred
APPLICANT: KNOWLES, David Justin Charles
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN: MONOCLONAL ANTIBODY AND THEIR US
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
STATE: PA
COUNTRY: U.S.A.
ZIP: 19406-0939
COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: Fastseq, Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/459,135A
FILING DATE: 02-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB/94/00215
FILING DATE: 04-Feb-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Gimm1, Edward R
REGISTRATION NUMBER: 38,891
REFERENCE/DOCKET NUMBER: P30591C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-4478
TELEFAX: 610-270-5090
TELEX:
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 130 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-459-135A-7

Query Match 93.9%; Score 200; DB 2; Length 130;
Best Local Similarity 94.7%; Pred. No. 3e-21;
Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 QNKGNSFEPTKDKPKYEHGNIIDIDPDSVPHIG 38
DB 40 QNKGNSFEPTKDKPKYEHGNIIDIDPDSVPHIG 77

RESULT 9
US-08-459-135A-8
Sequence 8, Application US/08459135A
Patent No. 5955078
GENERAL INFORMATION:
APPLICANT: BURNHAM, Martin Karl Russel
APPLICANT: CHOPRA, Ian
APPLICANT: CRITCHLEY, Ian Alfred
APPLICANT: KNOWLES, David Justin Charles
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN: MONOCLONAL ANTIBODY AND THEIR US
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
STATE: PA
COUNTRY: U.S.A.
ZIP: 19406-0939
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: Fastseq, Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/459,135A
FILING DATE: 02-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB/94/00215
FILING DATE: 04-Feb-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Gimm1, Edward R
REGISTRATION NUMBER: 38,891
REFERENCE/DOCKET NUMBER: P30591C2
TELECOMMUNICATION INFORMATION:

TELEPHONE: 610-270-4478
TELEFAX: 610-270-5090
TELEX:
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 130 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-459-135A-8

Query Match 93.9%; Score 200; DB 2; Length 130;
Best Local Similarity 94.7%; Pred. No. 3e-21;
Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QNKGNSFEPTKDKPKYEHGNIIDIDPSVPHIH 38
Db 40 QNKGDSFEPTKDKPKYEHGNIIDIDPSVPHIH 77

RESULT 10
US-08-495-559-7
Sequence 7, Application US/08495559A
Patent No. 6034572
GENERAL INFORMATION:
APPLICANT: BURHAM, Martin Karl Russel
APPLICANT: CHOPRA, Ian
APPLICANT: CRITCHLEY, Ian Alfred
APPLICANT: KNOWLES, David Justin Charles
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN: MONOCLONAL
FILE REFERENCE: P30591
CURRENT APPLICATION NUMBER: US/08/495,559A
CURRENT FILING DATE: 1995-08-03
EARLIER FILING DATE: 1993-02-05
EARLIER APPLICATION NUMBER: GB 9302289.5
EARLIER FILING DATE: 1993-02-05
EARLIER APPLICATION NUMBER: GB 9321592.9
NUMBER OF SEQ ID NOS: 13
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 7
LENGTH: 130
TYPE: PRT
ORGANISM: Staphylococcus aureus
US-08-495-559-7

Query Match 93.9%; Score 200; DB 3; Length 130;
Best Local Similarity 94.7%; Pred. No. 3e-21;
Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QNKGNSFEPTKDKPKYEHGNIIDIDPSVPHIH 38
Db 40 QNKGDSFEPTKDKPKYEHGNIIDIDPSVPHIH 77

RESULT 11
US-08-495-559-8
Sequence 8, Application US/08495559A
Patent No. 6034572
GENERAL INFORMATION:
APPLICANT: BURHAM, Martin Karl Russel
APPLICANT: CHOPRA, Ian
APPLICANT: CRITCHLEY, Ian Alfred
APPLICANT: KNOWLES, David Justin Charles
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN: MONOCLONAL
FILE REFERENCE: P30591
CURRENT APPLICATION NUMBER: US/08/495,559A
CURRENT FILING DATE: 1995-08-03
EARLIER APPLICATION NUMBER: GB 9302289.5
EARLIER FILING DATE: 1993-02-05
EARLIER APPLICATION NUMBER: GB 9321592.9
EARLIER FILING DATE: 1993-10-20

NUMBER OF SEQ ID NOS: 13
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 8
LENGTH: 130
TYPE: PRT
ORGANISM: Staphylococcus aureus
US-08-495-559-8

Query Match 93.9%; Score 200; DB 3; Length 130;
Best Local Similarity 94.7%; Pred. No. 4.2e-21;
Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QNKGNSFEPTKDKPKYEHGNIIDIDPSVPHIH 38
Db 40 QNKGDSFEPTKDKPKYEHGNIIDIDPSVPHIH 77

RESULT 12
US-08-459-135A-10
Sequence 10, Application US/08459135A
Patent No. 595078
GENERAL INFORMATION:
APPLICANT: BURHAM, Martin Karl Russel
APPLICANT: CHOPRA, Ian
APPLICANT: CRITCHLEY, Ian Alfred
APPLICANT: KNOWLES, David Justin Charles
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN: MONOCLONAL ANTIBODY AND THEIR US
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
STATE: PA
COUNTRY: U.S.A.
ZIP: 19406-0939
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: Fastseq, Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/459,135A
FILING DATE: 02-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB/94/00215
FILING DATE: 04-Feb-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Gimmi, Edward R
REGISTRATION NUMBER: 38,891
REFERENCE/DOCKET NUMBER: P30591C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-4478
TELEFAX: 610-270-5090
TELEX:
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 174 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: Protein
US-08-459-135A-10

Query Match 93.9%; Score 200; DB 2; Length 174;
Best Local Similarity 94.7%; Pred. No. 4.2e-21;
Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QNKGNSFEPTKDKPKYEHGNIIDIDPSVPHIH 38
Db 40 QNKGDSFEPTKDKPKYEHGNIIDIDPSVPHIH 77

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RESULT 13
US-08-495-559-10
; Sequence 10, Application US/08495559A
; Patent No. 6054572
; GENERAL INFORMATION:
; APPLICANT: BURHAM, Martin Karl Russel
; APPLICANT: CHOPRA, Ian
; APPLICANT: CRITCHLEY, Ian Alfred
; APPLICANT: KNOWLES, David Justin Charles
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN: MONOCLONAL
; FILE REFERENCE: P30591
; CURRENT APPLICATION NUMBER: US/08/495,559A
; EARLIER FILING DATE: 1995-08-03
; EARLIER APPLICATION NUMBER: GB 9302289.5
; EARLIER FILING DATE: 1993-02-05
; EARLIER APPLICATION NUMBER: GB 931592.9
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 10
; LENGTH: 174
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-08-495-559-10

Query Match          93.9%; Score 200; DB 3; Length 174;
Best Local Similarity 94.7%; Pred. No. 4.2e-21;
Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1 QNKGNSFEPTKDKPKYEHGNIIDIDPDSVPHHG 38
      |||:|||||:|||||:|||||:|||||:|||||:|||||:
DB      40 QNKGDSFEPTKDKPKYEHGNIIDIDPDSVPHHG 77

RESULT 14
US-08-495-559-6
; Sequence 6, Application US/08495559A
; Patent No. 6054572
; GENERAL INFORMATION:
; APPLICANT: BURHAM, Martin Karl Russel
; APPLICANT: CHOPRA, Ian
; APPLICANT: CRITCHLEY, Ian Alfred
; APPLICANT: KNOWLES, David Justin Charles
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN: MONOCLONAL
; FILE REFERENCE: P30591
; CURRENT APPLICATION NUMBER: US/08/495,559A
; EARLIER FILING DATE: 1995-08-03
; EARLIER APPLICATION NUMBER: GB 9302289.5
; EARLIER FILING DATE: 1993-02-05
; EARLIER APPLICATION NUMBER: GB 931592.9
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 176
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-08-495-559-6

Query Match          93.9%; Score 200; DB 3; Length 176;
Best Local Similarity 94.7%; Pred. No. 4.3e-21;
Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1 QNKGNSFEPTKDKPKYEHGNIIDIDPDSVPHHG 38
      |||:|||||:|||||:|||||:|||||:|||||:|||||:
DB      40 QNKGDSFEPTKDKPKYEHGNIIDIDPDSVPHHG 77

RESULT 15
US-08-459-135A-12
; Sequence 12, Application US/08459135A
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; Patent No. 5955078
; GENERAL INFORMATION:
; APPLICANT: BURHAM, Martin Karl Russel
; APPLICANT: CHOPRA, Ian
; APPLICANT: CRITCHLEY, Ian Alfred
; APPLICANT: KNOWLES, David Justin Charles
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN: MONOCLONAL ANTIBODY AND THEIR US
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corporation
; STREET: 709 Swedeland Road
; CITY: King of Prussia
; STATE: PA
; COUNTRY: U.S.A.
; ZIP: 19406-0939
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: Fastseq, Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/459,135A
; FILING DATE: 02-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB/94/00215
; FILING DATE: 04-Feb-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Gimm1, Edward R
; REGISTRATION NUMBER: 38, 891
; REFERENCE/DOCKET NUMBER: P30591C2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-270-4478
; TELEFAX: 610-270-5090
; TELEX:
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 178 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Protein
US-08-459-135A-12

Query Match          93.9%; Score 200; DB 2; Length 178;
Best Local Similarity 94.7%; Pred. No. 4.4e-21;
Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1 QNKGNSFEPTKDKPKYEHGNIIDIDPDSVPHHG 38
      |||:|||||:|||||:|||||:|||||:|||||:|||||:
DB      40 QNKGDSFEPTKDKPKYEHGNIIDIDPDSVPHHG 77

Search completed: October 22, 2005, 05:46:47
Job time : 22.2223 secs
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OM protein - protein search, using sw model

Run on: October 22, 2005, 11:35:03 ; Search time 70.1256 Seconds
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226.232 Million cell updates/sec

Title: US-10-731-238-48

Perfect score: 213

Sequence: 1 QNKGNSFSEPTKDKPKYEHGNCNIDIPDSVPHNG 38

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1862951 seqs, 41791010 residues

Total number of hits satisfying chosen parameters: 1862951

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA.*
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2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
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16: /cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pep.*
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18: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
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21: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
22: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	205	96.2	139	9	US-10-731-238-7
3	205	96.2	139	9	US-08-813-820-8
4	205	96.2	1018	9	US-08-815-242-5797
5	205	96.2	1018	9	US-09-815-242-12838
6	205	96.2	1018	17	US-10-470-048B-68
7	205	96.2	1027	8	US-08-781-986A-5254
8	205	96.2	1027	15	US-10-329-624-5254
9	199	93.4	38	18	US-10-731-238-46
10	199	93.4	38	18	US-10-731-238-47
11	197	92.5	38	18	US-10-731-238-8

12	197	92.5	38	18	US-10-731-238-49	Sequence 49, Appl
13	195	91.5	38	18	US-10-731-238-45	Sequence 45, Appl
14	192	90.1	388	8	US-08-901-062-1	Sequence 1, Appl
15	192	90.1	559	8	US-08-781-986A-5251	Sequence 5251, Ap
16	192	90.1	559	15	US-10-329-624-5251	Sequence 5251, Ap
17	192	90.1	767	9	US-09-815-242-5899	Sequence 5899, Ap
18	192	90.1	767	9	US-09-815-242-13140	Sequence 13140, A
19	192	90.1	940	17	US-10-470-048B-424	Sequence 424, App
20	192	90.1	948	17	US-10-470-048B-69	Sequence 69, Appl
21	192	90.1	1038	15	US-10-282-122A-43827	Sequence 43827, A
22	187	87.8	38	18	US-10-731-238-38	Sequence 38, Appl
23	184	86.4	978	9	US-09-815-242-5456	Sequence 5456, Ap
24	184	86.4	1001	9	US-09-815-242-12686	Sequence 12686, A
25	182	85.4	36	18	US-10-731-238-58	Sequence 58, Appl
26	180	84.5	961	15	US-10-282-132A-43778	Sequence 43778, A
27	179	84.0	38	18	US-10-731-238-5	Sequence 5, Appl
28	177	83.1	38	18	US-10-731-238-41	Sequence 41, Appl
29	177	83.1	38	18	US-10-731-238-50	Sequence 50, Appl
30	174	81.7	36	18	US-10-731-238-59	Sequence 59, Appl
31	173	81.2	38	18	US-10-731-238-36	Sequence 36, Appl
32	173	81.2	38	18	US-10-731-238-37	Sequence 37, Appl
33	173	81.2	38	18	US-10-731-238-39	Sequence 39, Appl
34	172	80.8	38	18	US-10-731-238-40	Sequence 40, Appl
35	172	80.8	38	18	US-10-731-238-42	Sequence 42, Appl
36	171	80.3	38	18	US-10-731-238-6	Sequence 6, Appl
37	171	80.3	38	18	US-10-731-238-43	Sequence 43, Appl
38	169	79.3	38	18	US-10-731-238-35	Sequence 35, Appl
39	168.5	79.1	39	18	US-10-731-238-56	Sequence 56, Appl
40	160.5	75.4	39	18	US-10-731-238-57	Sequence 57, Appl
41	151	70.9	38	18	US-10-731-238-44	Sequence 44, Appl
42	139	65.3	30	14	US-10-287-821-1	Sequence 1, Appl
43	139	65.3	31	14	US-10-287-821-2	Sequence 2, Appl
44	84.5	39.7	37	20	US-11-066-697-1134	Sequence 1134, Ap
45	77	36.2	14	18	US-10-731-238-103	Sequence 103, Ap

ALIGNMENTS

RESULT 1
US-10-731-238-48
Sequence 48, Application US/10731238
Publication No. US20050123552A1
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
Patel, Joseph M.
House-Pompeo, Karen L.
Speziale, Pietro
Joh, Danny
McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/731.238
FILING DATE: 10-Dec-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/010.317
FILING DATE: 21-Jan-1998
APPLICATION NUMBER: US 60/036.139

FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAMK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 48:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 48:
US-10-731-238-48

Query Match 100.0%; Score 213; DB 18; Length 38;
Best Local Similarity 100.0%; Pred. No. 1.2e-21;
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ONKGNQSFEEPTKDKPKYEHGNIIDIDFDSVPHIHG 38
DB 1 ONKGNQSFEEPTKDKPKYEHGNIIDIDFDSVPHIHG 38

RESULT 2
US-10-731-238-7
Sequence 7, Application US/10731238
Publication No. US20050123552A1
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
Pattl, Joseph M.
House-Pompeo, Karen L.
Speziale, Pietro
Jon, Danny
McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/731,238
FILING DATE: 10-Dec-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE: 21-Jan-1998
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAMK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>

TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-10-731-238-7

Query Match 96.2%; Score 205; DB 18; Length 38;
Best Local Similarity 97.4%; Pred. No. 1.5e-20;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ONKGNQSFEEPTKDKPKYEHGNIIDIDFDSVPHIHG 38
DB 1 ONKGNQSFEEPTKDKPKYEHGNIIDIDFDSVPHIHG 38

RESULT 3
US-09-813-820-8
Sequence 8, Application US/09813820
Patent No. US20020102262A1
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
Pattl, Joseph M.
House-Pompeo, Karen
Stanam, Narayana
Symeraky, Jindrich
TITLE OF INVENTION: COLLAGEN BINDING PROTEIN COMPOSITIONS
AND METHODS OF USE
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: Texas
COUNTRY: U.S.
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/813,820
FILING DATE: 22-Mar-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/856,253
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Kitchell, Barbara S.
REGISTRATION NUMBER: 33,928
REFERENCE/DOCKET NUMBER: TAMK:193
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
TELEFAX: (512) 474-7577
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 139 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-09-813-820-8

Query Match 96.2%; Score 205; DB 9; Length 139;
Best Local Similarity 97.4%; Pred. No. 6.8e-20;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ONKGNQSFEEPTKDKPKYEHGNIIDIDFDSVPHIHG 38
DB 54 ONKGNQSFEEPTKDKPKYEHGNIIDIDFDSVPHIHG 91

RESULT 4
US-09-815-242-5797
Sequence 5797, Application US/09815242

Patent No. US20020061569A1
GENERAL INFORMATION:
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Karl L.
APPLICANT: Zyekind, Judith W.
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John D.
APPLICANT: Carr, Grant J.
APPLICANT: Yamamoto, Robert T.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in
FILE REFERENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 5797
LENGTH: 1018
TYPE: PRT
ORGANISM: Staphylococcus aureus
US-09-815-242-5797

Query Match 96.2%; Score 205; DB 9; Length 1018;
Best Local Similarity 97.4%; Pred. No. 7.2e-19;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QNKGNSFEPTKDKPKYEHGNIIDIDPDSVPHING 38
DB 784 QNKGNSFEPTKDKPKYEHGNIIDIDPDSVPHING 821

RESULT 5
US-09-815-242-12838
Sequence 12838, Application US/09815242
Patent No. US20020061569A1
GENERAL INFORMATION:
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Karl L.
APPLICANT: Zyekind, Judith W.
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John D.
APPLICANT: Carr, Grant J.
APPLICANT: Yamamoto, Robert T.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in
FILE REFERENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625

PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 12838
LENGTH: 1018
TYPE: PRT
ORGANISM: Staphylococcus aureus
US-09-815-242-12838

Query Match 96.2%; Score 205; DB 9; Length 1018;
Best Local Similarity 97.4%; Pred. No. 7.2e-19;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QNKGNSFEPTKDKPKYEHGNIIDIDPDSVPHING 38
DB 784 QNKGNSFEPTKDKPKYEHGNIIDIDPDSVPHING 821

RESULT 6
US-10-470-048B-68
Sequence 68, Application US/10470048B
Publication No. US2005003744A1
GENERAL INFORMATION:
APPLICANT: MEINKE ET AL.
TITLE OF INVENTION: A METHOD FOR IDENTIFICATION, ISOLATION AND PRODUCTION OF
FILE REFERENCE: SONN.035US
CURRENT APPLICATION NUMBER: US/10/470,048B
CURRENT FILING DATE: 2003-07-25
NUMBER OF SEQ ID NOS: 603
SOFTWARE: PatentIn version 3.1
SEQ ID NO 68
LENGTH: 1018
TYPE: PRT
ORGANISM: Staphylococcus aureus
US-10-470-048B-68

Query Match 96.2%; Score 205; DB 17; Length 1018;
Best Local Similarity 97.4%; Pred. No. 7.2e-19;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QNKGNSFEPTKDKPKYEHGNIIDIDPDSVPHING 38
DB 784 QNKGNSFEPTKDKPKYEHGNIIDIDPDSVPHING 821

RESULT 7
US-08-781-986A-5254
Sequence 5254, Application US/08781986A
Publication No. US2003005436A1
GENERAL INFORMATION:
APPLICANT: Charles Kunsch
TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
NUMBER OF SEQUENCES: 5255
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COUNTRY: USA
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4MB storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/781,986A
FILING DATE:

```
/ CLASSIFICATION: 435
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER:
/ FILING DATE:
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Benson, Bob
/ REGISTRATION NUMBER: 30,446
/ REFERENCE/DOCKET NUMBER: PB248PP
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (301) 309-8504
/ TELEFAX: (301) 309-8512
/ INFORMATION FOR SEQ ID NO: 5254:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 1027 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ US-08-781-986A-5254

Query Match          96.2%; Score 205; DB 8; Length 1027;
Best Local Similarity 97.4%; Pred. No. 7.3e-19;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 QNKGNSFEPTKDKPKYEHGNIIDIDFDSVPHIHG 38
DB      793 QNKGNSFEPTKDKPKYEHGNIIDIDFDSVPHIHG 830

RESULT 8
US-10-329-624-5254
/ Sequence 5254, Application US/10329624
/ Publication No. US20040043037A1
/ GENERAL INFORMATION:
/ APPLICANT: Charles Kunesh
/      Gil H. Choi
/      Patrick S. Dillon
/      Craig A. Rosen
/      Steven C. Barash
/      Michael R. Fannon
/ TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
/ NUMBER OF SEQUENCES: 5256
/ SOFTWARE: Patentin Release #1.0, Version #1.30
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Human Genome Sciences, Inc.
/ STREET: 9410 Key West Avenue
/ CITY: Rockville
/ STATE: Maryland
/ COUNTRY: USA
/ ZIP: 20850
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Diskette, 3.50 inch, 1.4mb storage
/ COMPUTER: HP Vectra 486/33
/ OPERATING SYSTEM: MSDOS version 6.2
/ SOFTWARE: ASCII Text
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/10/329,624
/ FILING DATE: 27-Dec-2002
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/956,171
/ FILING DATE: October 20, 1997
/ APPLICATION NUMBER: 60/009,861
/ FILING DATE: January 5, 1996
/ APPLICATION NUMBER: 08/781,986
/ FILING DATE: January 3, 1997
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Mark J. Hyman
/ REGISTRATION NUMBER: 46,789
/ REFERENCE/DOCKET NUMBER: PB248P1D1
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (240) 314-1224
/ TELEFAX: (301) 309-8439
/ INFORMATION FOR SEQ ID NO: 5254:
/ SEQUENCE CHARACTERISTICS:
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/ LENGTH: 1027 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ SEQUENCE DESCRIPTION: SEQ ID NO: 5254:
US-10-329-624-5254

Query Match          96.2%; Score 205; DB 15; Length 1027;
Best Local Similarity 97.4%; Pred. No. 7.3e-19;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 QNKGNSFEPTKDKPKYEHGNIIDIDFDSVPHIHG 38
DB      793 QNKGNSFEPTKDKPKYEHGNIIDIDFDSVPHIHG 830

RESULT 9
US-10-731-238-46
/ Sequence 46, Application US/10731238
/ Publication No. US20050123552A1
/ GENERAL INFORMATION:
/ APPLICANT: Hook, Magnus
/      Patil, Joseph M.
/      House-Pompeo, Karen L.
/      Speziale, Pietro
/      Job, Danny
/      McGavin, Martin J.
/ TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
/ AND METHODS OF USE
/ NUMBER OF SEQUENCES: 105
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Arnold, White & Durkee
/ STREET: P.O. Box 4433
/ CITY: Houston
/ STATE: TX
/ COUNTRY: USA
/ ZIP: 77210-4433
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patentin Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/10/731,238
/ FILING DATE: 10-Dec-2003
/ CLASSIFICATION: <Unknown>
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US/09/010,317
/ FILING DATE: 21-Jan-1998
/ APPLICATION NUMBER: US 60/036,139
/ FILING DATE: 21-Jan-1997
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Hibler, David W.
/ REGISTRATION NUMBER: 41,071
/ REFERENCE/DOCKET NUMBER: TAMK:189
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 512-418-3000
/ TELEFAX: 512-474-7577
/ INFORMATION FOR SEQ ID NO: 46:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 38 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: <Unknown>
/ TOPOLOGY: linear
/ SEQUENCE DESCRIPTION: SEQ ID NO: 46:
US-10-731-238-46

Query Match          93.4%; Score 199; DB 18; Length 38;
Best Local Similarity 94.7%; Pred. No. 9.7e-20;
Matches 36; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 QNKGNSFEPTKDKPKYEHGNIIDIDFDSVPHIHG 38
```

Db 1 QNKGNSFEPTDKPKYEHGNIIDIDPSVPHNG 38

RESULT 10

US-10-731-238-47

Sequence 47, Application US/10731238
Publication No. US20050123552A1

GENERAL INFORMATION:

APPLICANT: Hook, Magnus

Patli, Joseph M.

House-Pompeo, Karen L.

Speziale, Pietro

John, Danny

McGavin, Martin J.

TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
AND METHODS OF USE

NUMBER OF SEQUENCES: 105

CORRESPONDENCE ADDRESS: 105

ADDRESSEE: Arnold, White & Durkee

STREET: P.O. Box 4433

CITY: Houston

STATE: TX

COUNTRY: USA

ZIP: 77210-4433

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/731,238

FILING DATE: 10-Dec-2003

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/010,317

FILING DATE: 21-Jan-1998

APPLICATION NUMBER: US 60/036,139

FILING DATE: 21-JAN-1997

ATTORNEY/AGENT INFORMATION:

NAME: Hibler, David W.

REGISTRATION NUMBER: 41,071

REFERENCE/DOCKET NUMBER: TAMK:189

TELECOMMUNICATION INFORMATION:

TELEPHONE: 512-418-3000

TELEFAX: 512-474-7577

INFORMATION FOR SEQ ID NO: 47:

SEQUENCE CHARACTERISTICS:

LENGTH: 38 amino acids

TYPE: amino acid

STRANDEDNESS: <Unknown>

TOPOLOGY: linear

SEQUENCE DESCRIPTION: SEQ ID NO: 47:

US-10-731-238-47

Query Match 93.4%; Score 199; DB 18; Length 38;

Best Local Similarity 94.7%; Pred. No. 9,7e-20;

Matches 36; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 QNKGNSFEPTDKPKYEHGNIIDIDPSVPHNG 38

Db 1 QNKGNSFEPTDKPKYEHGNIIDIDPSVPHNG 38

RESULT 11

US-10-731-238-8

Sequence 8, Application US/10731238

Publication No. US20050123552A1

GENERAL INFORMATION:

APPLICANT: Hook, Magnus

Patli, Joseph M.

House-Pompeo, Karen L.

Speziale, Pietro

John, Danny
McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
AND METHODS OF USE

NUMBER OF SEQUENCES: 105

CORRESPONDENCE ADDRESS: 105

ADDRESSEE: Arnold, White & Durkee

STREET: P.O. Box 4433

CITY: Houston

STATE: TX

COUNTRY: USA

ZIP: 77210-4433

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/731,238

FILING DATE: 10-Dec-2003

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/010,317

FILING DATE: 21-Jan-1998

APPLICATION NUMBER: US 60/036,139

FILING DATE: 21-JAN-1997

ATTORNEY/AGENT INFORMATION:

NAME: Hibler, David W.

REGISTRATION NUMBER: 41,071

REFERENCE/DOCKET NUMBER: TAMK:189

TELECOMMUNICATION INFORMATION:

TELEPHONE: 512-418-3000

TELEFAX: 512-474-7577

INFORMATION FOR SEQ ID NO: 8:

SEQUENCE CHARACTERISTICS:

LENGTH: 38 amino acids

TYPE: amino acid

STRANDEDNESS: <Unknown>

TOPOLOGY: linear

SEQUENCE DESCRIPTION: SEQ ID NO: 8:

US-10-731-238-8

Query Match 92.5%; Score 197; DB 18; Length 38;

Best Local Similarity 94.7%; Pred. No. 1.8e-19;

Matches 36; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 QNKGNSFEPTDKPKYEHGNIIDIDPSVPHNG 38

Db 1 QNKGNSFEPTDKPKYEHGNIIDIDPSVPHNG 38

RESULT 12

US-10-731-238-49

Sequence 49, Application US/10731238

Publication No. US20050123552A1

GENERAL INFORMATION:

APPLICANT: Hook, Magnus

Patli, Joseph M.

House-Pompeo, Karen L.

Speziale, Pietro

John, Danny

McGavin, Martin J.

TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
AND METHODS OF USE

NUMBER OF SEQUENCES: 105

CORRESPONDENCE ADDRESS: 105

ADDRESSEE: Arnold, White & Durkee

STREET: P.O. Box 4433

CITY: Houston

STATE: TX

COUNTRY: USA

ZIP: 77210-4433

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/731,238
FILING DATE: 10-Dec-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE: 21-Jan-1998
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAMK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 49:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 49:
US-10-731-238-49

Query Match 92.5%; Score 197; DB 18; Length 38;
Best Local Similarity 94.7%; Pred. No. 1,8e-19;
Matches 36; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 QNKGNSFPEPTKDKPKYEHGNIIDIDFDSVPHIHG 38
1 QNKGNSFPEPTKDKPKYEHGNIIDIDFDSVPHIHG 38

DB 1 QNKGNSFPEPTKDKPKYEHGNIIDIDFDSVPHIHG 38

RESULT 13
US-10-731-238-45
Sequence 45, Application US/107121238
Publication No. US20050123552A1
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
Patel, Joseph M.
House-Pompeo, Karen L.
Speziale, Pietro
Joh, Danny
McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/731,238
FILING DATE: 10-Dec-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE: 21-Jan-1998
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997

ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAMK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 45:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 45:
US-10-731-238-45

Query Match 91.5%; Score 195; DB 18; Length 38;
Best Local Similarity 94.7%; Pred. No. 3,4e-19;
Matches 36; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 QNKGNSFPEPTKDKPKYEHGNIIDIDFDSVPHIHG 38
1 QNKGNSFPEPTKDKPKYEHGNIIDIDFDSVPHIHG 38

DB 1 QNKGNSFPEPTKDKPKYEHGNIIDIDFDSVPHIHG 38

RESULT 14
US-08-901-062-1
Sequence 1, Application US/08901062
Publication No. US20020025324A1
GENERAL INFORMATION:
APPLICANT: SEALS, JONATHAN R.
TITLE OF INVENTION: RECOMBINANT BIVALENT BACTERIAL VACCINE
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: HALE AND DORR LLP
STREET: 60 State Street
CITY: Boston
STATE: MA
COUNTRY: United States of America
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/901,062
FILING DATE: 25-JUL-1997
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Baker, Hollie L.
REGISTRATION NUMBER: 31,321
REFERENCE/DOCKET NUMBER: 106941.153
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 526-6000
TELEFAX: (617) 526-5000
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 388 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-901-062-1

Query Match 90.1%; Score 192; DB 8; Length 388;
Best Local Similarity 92.1%; Pred. No. 1,4e-17;
Matches 35; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 QNKGNSFPEPTKDKPKYEHGNIIDIDFDSVPHIHG 38

DB 303 QNNGNOSFEEDTEKPKRYEQQGNIIIDIDFDSVPHIHG 340

RESULT 15

US-08-781-986A-5251
 ; Sequence 5251, Application US/08781986A
 ; Publication No. US20030054436A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Charles Kunsch
 ; TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
 ; NUMBER OF SEQUENCES: 5255
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Human Genome Sciences, Inc.
 ; STREET: 9410 Key West Avenue
 ; CITY: Rockville
 ; STATE: Maryland
 ; COUNTRY: USA
 ; ZIP: 20850
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
 ; COMPUTER: HP Vectra 486/33
 ; OPERATING SYSTEM: MSDOS version 6.2
 ; SOFTWARE: ASCII Text
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/781,986A
 ; FILING DATE:
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER:
 ; FILING DATE:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Benson, Bob
 ; REGISTRATION NUMBER: 30,446
 ; REFERENCE/DOCKET NUMBER: PB248PP
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (301) 309-8504
 ; TELEFAX: (301) 309-8512
 ; INFORMATION FOR SEQ ID NO: 5251:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 559 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULAR TYPE: protein
 ; US-08-781-986A-5251

Query Match 90.1%; Score 192; DB 8; Length 559;

Best Local Similarity 92.1%; Pred. No. 2.1e-17;
 Matches 35; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 QNNGNOSFEEDTEKPKRYEQQGNIIIDIDFDSVPHIHG 38
 DB 339 QNNGNOSFEEDTEKPKRYEQQGNIIIDIDFDSVPHIHG 376

Search completed: October 22, 2005, 12:09:29
 Job time : 70.1256 secs

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GenCore version 5.1.6
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OM protein - protein search, using SW model

Run on: October 22, 2005, 04:14:19 ; Search time 13.8905 Seconds
(without alignments)
263.219 Million cell updates/sec

Title: US-10-731-238-48

Perfect score: 213

Sequence: 1 QNKGNSFEEDTEKDKPKYEHGNIIDIDPDSVPHING 38

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	205	96.2	1018	2	A32192 fibronectin-binding
2	192	90.1	940	2	S19702 fibronectin-binding
3	192	90.1	1038	2	H80053 hypothetical prote
4	180	84.5	961	2	G90053 hypothetical prote
5	67	26.8	214	2	A89895 hypothetical prote
6	57	26.8	183	2	D83840 hypothetical prote
7	57	26.8	413	2	T31663 isoleucine-tRNA li
8	56.5	26.5	788	2	T30510 viral enhancing fa
9	54.5	25.6	428	2	T32952 hypothetical prote
10	54.5	25.6	582	2	I48673 matrix metalloprot
11	54.5	25.6	582	2	I38028 matrix metalloprot
12	54	25.4	1199	2	T15826 hypothetical prote
13	53	24.9	218	2	A95232 ribulose-phosphate
14	53	24.9	218	2	C98096 ribulose-phosphate
15	53	24.9	467	2	A62390 transposase all1467
16	53	24.9	1142	2	T37455 enamein precursor
17	52.5	24.6	669	2	I38029 matrix metalloprot
18	52	24.4	427	2	S38002 hypothetical prote
19	52	24.4	442	2	H72266 asEB/chur-related
20	52	24.4	658	2	F85024 probable CIP-rich
21	51.5	24.2	240	1	R5H52L ribosomal protein
22	51.5	24.2	264	1	C87605 hypothetical prote
23	51.5	24.2	317	2	T00146 matrix metalloprot
24	51.5	24.2	582	2	I84471 serine/threonine-s
25	51.5	24.2	603	2	S34130 glycine-tRNA ligase
26	51.5	24.2	739	2	A55314 pneumolysin - Stre
27	51	23.9	471	2	A28568 pneumolysin (impor
28	51	23.9	471	2	F95224
29	51	23.9	471	2	A99089 hypothetical prote

30	51	23.9	547	2	T02274 hypothetical prote
31	51	23.9	570	1	VHXPL2 major structural n
32	51	23.9	584	2	S06696 hypothetical prote
33	51	23.9	658	2	T40107 hypothetical 57.9
34	51	23.9	713	2	H64464 hypothetical prote
35	51	23.9	790	2	T47959 hypothetical prote
36	51	23.9	1952	2	T48814 uncharacterized pr
37	50.5	23.7	105	2	D97169 triacylglycerol li
38	50.5	23.7	613	2	J50763 beta-hexosaminidas
39	50.5	23.7	841	2	B82755 B. subtilis YTHO p
40	50.5	23.7	952	2	AG1209 conserved hypochet
41	50	23.5	211	2	G83632 hypothetical prote
42	50	23.5	481	2	B75167 glycine-tRNA synth
43	50	23.5	576	2	B84386 propionyl-CoA carb
44	50	23.5	591	2	C84420
45	50	23.5	684	2	S52835 hypothetical prote

ALIGNMENTS

RESULT 1

A32192
fibronectin-binding protein - Staphylococcus aureus
C:Species: Staphylococcus aureus
C>Date: 31-Jul-1989 #sequence_revision 31-Jul-1989 #text_change 16-Feb-1997
C:Accession: A32192
R:Signaes, C.; Raucel, G.; Joensson, K.; Lindgren, P.E.; Anantharamaiah, G.M.; Hoeoek,
Proc. Natl. Acad. Sci. U.S.A. 86, 699-703, 1989
A:Title: Nucleotide sequence of the gene for a fibronectin-binding protein from Staphy]
A:Reference number: A32192; MUID:8908998; PMID:2521391
A:Accession: A32192
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1018 <SIG>
A:Cross-references: GB:J04151
C:Keywords: fibronectin binding

Query Match 96.2%; Score 205; DB 2; Length 1018;
Best Local Similarity 97.4%; Pred. No. 6.7e-15;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QNKGNSFEEDTEKDKPKYEHGNIIDIDPDSVPHING 38
Db 784 QNKGNSFEEDTEKDKPKYEHGNIIDIDPDSVPHING 821

RESULT 2

S19702
fibronectin-binding protein B - Staphylococcus aureus
C:Species: Staphylococcus aureus
C>Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
C:Accession: S19702
R:Joensson, K.; Signaes, C.; Mueller, H.P.; Lindberg, M.
Eur. J. Biochem. 202, 1041-1048, 1991
A:Title: Two different genes encode fibronectin binding proteins in Staphylococcus aure
A:Reference number: S19702; MUID:92111475; PMID:1837286
A:Accession: S19702
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-940 <JOB>
A:Cross-references: UNIPROT:Q53682; EMBL:X62992; NID:949040; PIDD:CAA44726.1; PID:95815
C:Keywords: fibronectin binding

Query Match 90.1%; Score 192; DB 2; Length 940;
Best Local Similarity 92.1%; Pred. No. 3.2e-17;
Matches 35; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 QNKGNSFEEDTEKDKPKYEHGNIIDIDPDSVPHING 38
Db 720 QNKGNSFEEDTEKDKPKYEGGNIIDIDPDSVPHING 757

RESULT 8
T30510
viral enhancing factor 2 - lymphantia dispar nuclear polyhedrosis virus
C/Species: Lymphantia dispar nuclear polyhedrosis virus, LdMNPV
C/Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
C/Accession: T30510
R/Kuzio, J.; Pearson, M.N.; Harwood, S.H.; Funk, C.J.; Evans, J.T.; Slavicek, J.M.; Roth
Virology 253, 17-34, 1999
A/Title: Sequence and analysis of the genome of a baculovirus pathogenic for Lymphantia d
A/Reference number: Z20836; MUID:99124785; PMID:9887315
A/Accession: T30510
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-788 <KUZ>
A/Cross-references: UNIPROT:Q9YMG8; EMBL:AF081810; PIDN:AAC70346.1

Query Match 26.5%; Score 56.5; DB 2; Length 788;
Best Local Similarity 54.5%; Pred. No. 25;
Matches 12; Conservative 1; Mismatches 4; Indels 5; Gaps 1;

QY 17 PTEKDKPKY-HEGNGNIDIDF-----DSV 33
DB 114 PLYEHGNAVAPADPKSMRDSV 135

RESULT 9

T32952
hypothetical protein C15E6.1 - Caenorhabditis elegans
C/Species: Caenorhabditis elegans
C/Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999
C/Accession: T32952
R/Rohlfing, T.; Biewald, T.
submitted to the EMBL Data Library, February 1998
A/Description: The sequence of C. elegans cosmid C15E6.
A/Reference number: Z21253
A/Accession: T32952
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-428 <ROH>
A/Cross-references: EMBL:AF045636; PIDN:AAC02559.1; GSPDB:GN00022; CESP:C15E6.1
A/Experimental source: strain Bristol N2; clone C15E6
C/Genetics:
A/Genes: CESP:C15E6.1
A/Map position: 4
A/Introns: 124/2; 196/3

Query Match 25.6%; Score 54.5; DB 2; Length 428;
Best Local Similarity 46.4%; Pred. No. 23;
Matches 13; Conservative 2; Mismatches 12; Indels 1; Gaps 1;

QY 11 PTEKDKPKY-HEGNGNIDIDFDSVPHTH 37
DB 244 PEKPKPAIPAFDNAYADPDNSPPLH 271

RESULT 10

I48673
matrix metalloproteinase (EC 3.4.24.-) membrane type precursor - mouse
C/Species: Mus musculus (house mouse)
C/Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 22-Jun-1999
C/Accession: I48673
R/Okada, A.; Bellocq, J.P.; Rouyer, N.; Chenard, M.P.; Rio, M.C.; Chambon, P.; Basset, F.
Proc. Natl. Acad. Sci. U.S.A. 92, 2730-2734, 1995
A/Title: Membrane-type matrix metalloproteinase (MT-MMP) gene is expressed in stromal ce
A/Reference number: I38046; MUID:95224014; PMID:7708715
A/Accession: I48673
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-582 <RES>
A/Cross-references: EMBL:X8336; NID:9804999; PIDN:CAA58520.1; PID:9805000
C/Superfamily: interstitial collagenase; hemopexin repeat homology; matrix metalloprotei
C/Keywords: hydrolase; metalloproteinase; zinc; zymogen

F/1-23/Domain: signal sequence #status predicted <SIG>
F/24-97/Domain: activation peptide #status predicted <PRO>
F/61-284/Domain: matrix metalloproteinase homology <MP>
F/313-508/Domain: hemopexin repeat homology <PAN>
F/33,229,243,249/Binding site: zinc, catalytic (Cys, His, His, His) (inhibited) #status
F/239,243,249/Binding site: zinc, catalytic (His) (active) #status predicted
F/240/Active site: Glu #status predicted

Query Match 25.6%; Score 54.5; DB 2; Length 582;
Best Local Similarity 44.8%; Pred. No. 33;
Matches 13; Conservative 5; Mismatches 10; Indels 1; Gaps 1;

QY 11 PTEKDKPKY-HEGNGNIDIDFDSVPHTH 38
DB 303 PSVPDPKPAIPAFDNAYADPDNSPPLH 331

RESULT 11

I38028
matrix metalloproteinase 14 (EC 3.4.24.-) membrane type precursor - human
N/Alternate names: matrix metalloproteinase MMP14; membrane type matrix metalloproteina
C/Species: Homo sapiens (man)
C/Date: 17-May-1996 #sequence_revision 17-May-1996 #text_change 09-Jul-2004
C/Accession: I38028; G02274; I38046; S78011; S45341; S71384
R/Mill, H.; Hinzmann, B.
Eur. J. Biochem. 231, 602-608, 1995
A/Title: cDNA sequence and mRNA tissue distribution of a novel human matrix metalloprot
A/Reference number: I38028; MUID:95377289; PMID:7649159
A/Accession: I38028
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-582 <MIL>
A/Cross-references: UNIPROT:P50281; EMBL:Z48481; NID:9963053; PIDN:CAA88372.1; PID:9963
R/Luo, G.
submitted to the EMBL Data Library, November 1995
A/Reference number: H00963
A/Accession: G02274
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-582 <LUO>
A/Cross-references: EMBL:U41078; NID:91127836; PIDN:AAA83770.1; PID:91127837
R/Okada, A.; Bellocq, J.P.; Rouyer, N.; Chenard, M.P.; Rio, M.C.; Chambon, P.; Basset, F.
Proc. Natl. Acad. Sci. U.S.A. 92, 2730-2734, 1995
A/Title: Membrane-type matrix metalloproteinase (MT-MMP) gene is expressed in stromal c
A/Reference number: I38046; MUID:95224014; PMID:7708715
A/Accession: I38046
A/Status: translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-7, 'S', '9-582 <OKA>
A/Cross-references: EMBL:X83535; NID:9804999; PIDN:CAA58519.1; PID:9804994
R/Seiki, M.
submitted to the EMBL Data Library, January 1994
A/Reference number: S78011
A/Accession: S78011
A/Molecule type: mRNA
A/Residues: 1-7, 'S', '9-337, 'K', '339-582 <SEI>
A/Cross-references: EMBL:D26512; NID:9793762; PIDN:BA05519.1; PID:9793763
R/Sato, H.; Takino, T.; Okada, Y.; Cao, J.; Shinagawa, A.; Yamamoto, E.; Seiki, M.
Nature 370, 61-65, 1994
A/Title: A matrix metalloproteinase expressed on the surface of invasive tumour cells.
A/Reference number: S45341; MUID:94286011; PMID:8015608
A/Accession: S45341
A/Molecule type: nucleic acid sequence not shown
A/Status: nucleic acid sequence not shown
A/Residues: 1-7, 'S', '9-188, 'R', '190, 'A', '192-267, 'K', '269-272, 'HY', '275, 'P', '277-285, 'KQ', '288
A/Cross-references: EMBL:D26512
R/Sato, H.; Kinoshita, T.; Takino, T.; Nakayama, K.; Seiki, M.
FEBS Lett. 393, 101-104, 1996
A/Title: Activation of a recombinant membrane type 1-matrix metalloproteinase (MT1-MMP)
A/Reference number: S71384; MUID:96397540; PMID:8804434
A/Accession: S71384
A/Molecule type: protein
A/Residues: 112-116 <SAM>

```

C:Genetics9:
A:Gene: GDB:MMP14; MTL-MMP
A:Cross-References: GDB:375731; OMIM:600754
A:Map position: 14q11-14q12
C:Superfamily: Interstitial collagenase; hemopexin repeat homology; matrix metalloproteinase
C:Keywords: glycoprotein; hydrolase; metalloproteinase; zinc; zymogen
F:1-23/Domain: signal sequence #status predicted <STG>
F:24-27/Domain: activation peptide #status predicted <PRO>
F:61-84/Domain: matrix metalloproteinase 14 membrane type #status predicted <MAT>
F:1285-1313/Domain: hinge #status predicted <HNG>
F:1314-508/Domain: hemopexin repeat homology <PXN>
F:539-562/Domain: transmembrane #status predicted <TM>
F:593-639-243-249/Binding site: zinc, catalytic (Cys, His, His) (inhibited) #status
F:130/Binding site: carboxylate (Asn) (covalent) #status predicted
F:239-243-249/Binding site: zinc, catalytic (His) (active) #status predicted
F:240/Active site: Glu #status predicted
F:319-508/Disulfide bonds: #status predicted

Query Match      25.6%; Score 54.5; DB 2; Length 582;
Best Local Similarity 44.8%; Pred. No. 33;
Matches 13; Conservative 5; Mismatches 10; Indels 1; Gaps 1;

QY      11 PTEKDKPKY-EHGNTIDIDPDSYPHTG 38
          ||||| : ||| : ||| :
Db       303 PSVPDRKPPTGYGNICDGNFTVAMLRG 331

RESULT 12
T15826
Hypothetical protein C52E12.1 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
C:Accession: T15826
R:Du Z.
Submitted to the EMBL Data Library, February 1996
A:Description: The sequence of C. elegans cosmid C52E12.
A:Reference number: Z18412
A:Accession: T15826
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-1199 <DUZ>
A:Cross-References: EMBL:U50135; NID:G1208884; PID:AAA93457.1; CESP:C52E12
C:Genetics9:
A:Gene: CESP:C52E12.1
A:Introns: 56/3; 90/2; 120/3; 159/2; 208/3; 248/1; 270/3; 291/3; 309/1; 348/3; 374/3; 46

Query Match      25.4%; Score 54; DB 2; Length 1199;
Best Local Similarity 36.7%; Pred. No. 89;
Matches 11; Conservative 5; Mismatches 14; Indels 0; Gaps 0;

QY      5 NOSFEPTEDKPYEHGNTIDIDPDSVP 34
          ||||| : ||| : ||| :
Db       326 NOSSROPTKVDMKKTERMISAAHTFSDFP 355

RESULT 13
A95232
Ribulose-phosphate 3-epimerase [imported] - Streptococcus pneumoniae (strain TIGR4)
C:Species: Streptococcus pneumoniae
C>Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 09-Jul-2004
C:Accession: A95232
R:Rettelin, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Heldson, U.J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Redune, D.; Holzapfel, neon, T.; Hickey, E.K.; Holt, I.E.
Science 293, 498-506, 2001
A:Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison, A.
Title: Complete Genome Sequence of a Virulent Isolate of Streptococcus pneumoniae.
A:Reference number: A95000; MUID:21357209; PMID:11463916
A:Accession: A95232
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-218 <KUR>
```

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A:Cross-references: UNIPROT:Q97NN7; GB:AE005672; PIDN:AAK76050.1; PID:g14973490; GSPDB:C
A:Experimental source: strain TIGR4
C:Genetics:
A:Gene: SPI983
C:Superfamily: yeast ribulose-5-phosphate-epimerase

Query Match          24.9%; Score 53; DB 2; Length 218;
Best Local Similarity 52.9%; Pred. No. 17;
Matches 9; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 22 GGNIIIDFDSVPHIHG 38
Db 84 GADIIISHVEATPHIHG 100

RESULT 14
C98096
ribulose-phosphate 3-epimerase (EC 5.1.3.1) [imported] - Streptococcus pneumoniae (strain
C:Species: Streptococcus pneumoniae
C:Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 09-Jul-2004
C:Accession: C98096
R:Hoskins, J.A.; Albom Jr., W.; Arnold, J.; Blaszcak, L.; Burgess, S.; DeHoff, B.S.; E
e, R.; LeBlanc, D.J.; Lee, L.N.; Lefkowitz, E.J.; Lu, J.; Matsuhashima, P.; McAhren, S.; M
y, P.; Sun, P.M.; Winkler, M.E.
Y. Bacteriol. 183, 5709-5717, 2001
A:Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Askunas, S.R.;
A:Title: Genome of the Bacterium Streptococcus pneumoniae Strain R6.
A:Reference number: A97872; MUID:21429245; PMID:11544234
A:Accession: C98096
A:Status: Preliminary
A:Molecule type: DNA
A:Residues: 1-218 <KUR>
A:Cross-references: UNIPROT:Q8DND5; GB:AE007317; PIDN:ALU00600.1; PID:g15459482; GSPDB:G
C:Genetics:
A:Gene: rpe
C:Superfamily: yeast ribulose-5-phosphate-epimerase
C:Keywords: isomerase

Query Match          24.9%; Score 53; DB 2; Length 218;
Best Local Similarity 52.9%; Pred. No. 17;
Matches 9; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 22 GGNIIIDFDSVPHIHG 38
Db 84 GADIIISHVEATPHIHG 100

RESULT 15
AC2390
transposase all4675 [imported] - Nostoc sp. (strain PCC 7120)
C:Species: Nostoc sp. PCC 7120
A:Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C:Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004
C:Accession: AC2390
R:Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi
Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S
DNA Res. 8, 205-213, 2001
A:Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana
A:Reference number: AB1807; MUID:21595285; PMID:11759840
A:Accession: AC2390
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-467 <KUR>
A:Cross-references: UNIPROT:Q8Y93; GB:BA000019; PIDN:BA876374.1; PID:g17133812; GSPDB:C
A:Experimental source: strain PCC 7120
C:Genetics:
A:Gene: all4675

Query Match          24.9%; Score 53; DB 2; Length 467;
Best Local Similarity 37.5%; Pred. No. 40;
Matches 15; Conservative 5; Mismatches 10; Indels 10; Gaps 2;

QY 3 KGNQSFEE-----PTKDKPKY--EHGNGNIIDFDS 32

```

DB 368 KPNFSSQECSECGYISPTNRDKEKFLCEHCGHHADADIDA 407

Search completed: October 22, 2005, 06:09:54
Job time : 13.8905 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 22, 2005, 04:10:49 ; Search time 69.6361 Seconds
(without alignments)
279.439 Million cell updates/sec

Title: US-10-731-238-48

Perfect score: 213
Sequence: 1 QNKGNSFEPEKPKYEHGNIIDFDSPVPHHG 38

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : UniProt_03.*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	205	96.2	1018	1 FNBA_STAUV	P14738 staphylococ
2	200	93.9	943	2 Q8NUU8	Q8NUU8 staphylococ
3	200	93.9	943	2 Q6G6H4	Q6G6H4 staphylococ
4	197	92.5	152	2 Q9AEP9	Q9AEP9 staphylococ
5	192	90.1	940	2 Q53682	Q53682 staphylococ
6	192	90.1	1038	2 Q99RD2	Q99RD2 staphylococ
7	192	90.1	1038	2 Q7A3J7	Q7A3J7 staphylococ
8	184	86.4	1015	2 Q8NUU7	Q8NUU7 staphylococ
9	184	86.4	1015	2 Q6G6H3	Q6G6H3 staphylococ
10	180	84.5	961	2 Q99RD3	Q99RD3 staphylococ
11	180	84.5	961	2 Q7A3J8	Q7A3J8 staphylococ
12	180	84.5	965	2 Q6GDU5	Q6GDU5 staphylococ
13	64	30.0	610	2 Q6CJN0	Q6CJN0 Kluvermyc
14	63	29.6	367	1 COBD_THETN	COBD_THETN
15	62	29.1	716	2 Q7RB60	Q7RB60 plasmodium
16	61	28.6	1246	2 Q7UKY7	Q7UKY7 rhodospirill
17	60	28.2	214	2 Q99UP6	Q99UP6 staphylococ
18	60	28.2	214	2 Q7A126	Q7A126 staphylococ
19	60	28.2	214	2 Q7A5Z7	Q7A5Z7 staphylococ
20	60	28.2	214	2 Q6G9Z1	Q6G9Z1 staphylococ
21	60	28.2	214	2 Q6GHI3	Q6GHI3 staphylococ
22	60	28.2	904	2 Q543Z4	Q543Z4 sulfolobus
23	59.5	27.9	1054	2 Q9NAZ5	Q9NAZ5 drosophila
24	59.5	27.9	1257	2 Q6BW72	Q6BW72 debaryomyce
25	59	27.7	839	2 Q6DE51	Q6DE51 xenopus lae
26	57.5	27.0	851	2 Q6MSY9	Q6MSY9 mycoplasma
27	57	26.8	183	2 Q9KCP5	Q9KCP5 bacillus ha
28	57	26.8	288	2 Q6MEU6	Q6MEU6 parachlamyd
29	57	26.8	354	2 Q7RRM0	Q7RRM0 plasmodium
30	57	26.8	413	1 S71_CIOIN	Q94425 clona intes
31	57	26.8	964	2 Q42489	Q42489 gallus gall

ALIGNMENTS

32	57	26.8	1100	2 Q9NV82	Q9NV82 homo sapien
33	57	26.8	1298	2 Q7Z312	Q7Z312 homo sapien
34	57	26.8	1299	2 Q6Y7W6	Q6Y7W6 homo sapien
35	57	26.8	1299	2 Q722Z8	Q722Z8 homo sapien
36	56.5	26.5	788	2 Q9YMG8	Q9YMG8 lymantria d
37	56.5	26.5	1858	2 Q8MSU5	Q8MSU5 drosophila
38	56.5	26.5	2145	2 Q9W003	Q9W003 drosophila
39	56.5	26.5	5922	2 Q81IN2	Q81IN2 plasmodium
40	36	26.3	1124	2 Q73154	Q73154 wolbachia p
41	56	26.3	215	2 Q8G8U1	Q8G8U1 uncultured
42	56	26.3	215	2 Q6G1A0	Q6G1A0 chinese yam
43	56	26.3	288	2 Q761A1	Q761A1 chinese yam
44	56	26.3	288	2 Q761A2	Q761A2 chinese yam
45	56	26.3	288	2 Q761A3	Q761A3 chinese yam

RESULT 1
FNBA_STAUV STANDARD; PRT; 1018 AA.
ID FNBA_STAUV
AC P14738;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Fibronectin-binding protein precursor (FNBP).
GN Name=fnba;
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1280;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NCTC 8325-4;
RX MEDLINE=89098998; Pubmed=2521391;
RA Signaes G., Raucsi G., Joensson K., Lindgren P.-E.,
RA Manantaramalah G.M., Hoeck M., Lindberg M.;
RA "Nucleotide sequence of the gene for a fibronectin-binding protein
RT from Staphylococcus aureus: use of this peptide sequence in the
RT synthesis of biologically active peptides."
RL Proc. Natl. Acad. Sci. U.S.A. 86:699-703(1989).
CC -!- FUNCTION: The ability of bacteria to bind fibronectin has been
CC proposed as a virulence factor enabling bacteria to colonize wound
CC tissues and blood clots. Binding of plasma fibronectin to the
CC bacterial surface might block adhesion receptors on S.aureus, thus
CC representing an important defense mechanism against tissue
CC invasion.
CC -!- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC an amide bond (potential).
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC The European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
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CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@sib-sib.ch).
CC -----
CC EMBL: J04151; AAA26632.1; -;
CC InterPro: IPR004237; Fn_bind.
CC InterPro: IPR005877; Gpos_XSIRK.
CC InterPro: IPR001899; Gram_pos_anchor.
CC Pfam: PF02986; Fn_bind; 1.
CC Pfam: PF00746; Gram_pos_anchor; 1.
CC Pfam: PF04650; XSIRK_signal; 1.
CC TIGRfams: TIGR01167; LPTXG_anchor; 1.
CC TIGRfams: TIGR01168; XSIRK_signal; 1.
CC TIGRfams: TIGR01169; XSIRK_signal; 1.
CC PROSITE: PS50847; GRAM_POS_ANCHORING; 1.
CC Cell adhesion; Cell wall; Peptidoglycan-anchor; Repeat; Signal;
CC Virulence.
CC SIGNAL 1 36
CC CHAIN 37 985 Fibronectin-binding protein.
CC PROPEP 986 1018 Removed by sortase (potential).
CC FT

```
FT REPEAT 545 574 B-1.
FT REPEAT 575 604 B-2.
FT DOMAIN 745 878 4 X approximate tandem repeats,
  fibronectin-binding domain.
FT REPEAT 745 782 D-1.
FT REPEAT 821 820 D-2.
FT REPEAT 821 859 D-3.
FT DOMAIN 860 878 D-4 (incomplete).
FT REPEAT 879 948 5 X tandem repeats, Pro-rich (WR).
FT REPEAT 893 906 WR 1.
FT REPEAT 907 920 WR 2.
FT REPEAT 921 934 WR 3.
FT REPEAT 935 948 WR 4.
FT SITE 982 986 WR 5.
FT MOD_RES 985 985 LpXTG sorting signal (potential).
  Pentaglycyl murein peptidoglycan amidated
  threonine (Potential).
SQ SEQUENCE 1018 AA; 111780 MW; 58175E020E81F1F CRC64;

Query Match 96.2%; Score 205; DB 1; Length 1018;
Best Local Similarity 97.4%; Pred. No. 1,le-17;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 ONKGNOSFEPEPTKDKPKYEHGNGNIIDIDPDSVPHIHG 38
Db 784 ONKGNOSFEEDTEKDKPKYEHGNGNIIDIDPDSVPHIHG 821

RESULT 2
O8NU08 PRELIMINARY; PRT; 943 AA.
AC O8NU08;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE FnBb protein.
GN Name=fnBb; OrderedlocusNames=MM2420;
OS Staphylococcus aureus (strain MM2).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=196620;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MM2;
RX MEDLINE=22040717; PubMed=12044378; DOI=10.1016/S0140-6736(02)08713-5;
  Baba T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Oguchi A.,
  Nagai Y., Iwama N., Aano K., Naimi T., Kuroda H., Cui L.,
  Yamamoto K., Hiramatsu K.;
RA "Genome and virulence determinants of high virulence community-
RT acquired MRSA.";
RL Lancet 359:1819-1827(2002).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
  an amide bond (By similarity).
EMBL: AP004830; BAB96285.1; -.
DR HSSP: O53653; IN67.
DR GO: GO:0009986; C:cell surface; IEA.
DR GO: GO:0005618; C:cell wall; IEA.
DR GO: GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO: GO:0016020; C:membrane; IEA.
DR GO: GO:0007155; P:cell adhesion; IEA.
DR InterPro: IPR008966; Adhes_bact.
DR InterPro: IPR004237; Fn_bind.
DR InterPro: IPR005877; Gpos_YsIRK.
DR InterPro: IPR001899; Gram_pos_anchor.
DR Pfam: PF02986; Fn_bind.1.
DR Pfam: PF00746; Gram_pos_anchor.1.
DR Pfam: PF04650; YsIRK_signal.1.
DR TIGRfam: TIGR01167; LpXTG_anchor.1.
DR TIGRfam: TIGR01168; YsIRK_signal.1.
DR PROSITE: PSS0847; GRAM_POS_ANCHORING.1.
DR Cell wall; Complete proteome; Peptidoglycan-anchor.
KW Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ SEQUENCE 943 AA; 104537 MW; DA8A5F31947E1B6A CRC64;

Query Match 93.9%; Score 200; DB 2; Length 943;
```

```
Best Local Similarity 94.7%; Pred. No. 4,6e-17;
Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 ONKGNOSFEPEPTKDKPKYEHGNGNIIDIDPDSVPHIHG 38
Db 727 ONKGNOSFEEDTEKDKPKYEHGNGNIIDIDPDSVPHIHG 764

RESULT 3
O6G6H4 PRELIMINARY; PRT; 957 AA.
AC O6G6H4;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Fibronectin-binding protein.
GN Name=fnBb; OrderedlocusNames=SAS2387;
OS Staphylococcus aureus (strain MSSA76).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=282459;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=1523324; DOI=10.1073/pnas.0402521101;
  Holden M.T.G., Fell E.J., Lindsay J.A., Peacock S.J., Day N.P.J.,
  Burright M.C., Foster T.J., Moore C.E., Hurst L., Acklin R., Barron A.,
  Bason N., Bentley S.D., Chillingworth C., Chillingworth T.,
  Churcher C., Clark L., Corton C., Cronin A., Doggett J., Dowd L.,
  Felwell T., Hance Z., Harris B., Hauser H., Holroyd S., Jagels K.,
  James K.D., Kennard N., Line A., Mayes R., Moule S., Mungall K.,
  Ormond D., Quail M.A., Rabinowitch E., Rutherford K.M., Sanders M.,
  Sharp S., Simmonds M., Stevens K., Whitehead S., Barrall B.G.,
  Spratt B.G., Parkhill J.;
RA "Complete genomes of two clinical Staphylococcus aureus strains:
RT evidence for the rapid evolution of virulence and drug resistance.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:9786-9791(2004).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
  an amide bond (By similarity).
EMBL: BX571857; CAG44201.1; -.
DR GO: GO:0009986; C:cell surface; IEA.
DR GO: GO:0005618; C:cell wall; IEA.
DR GO: GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO: GO:0016020; C:membrane; IEA.
DR GO: GO:0007155; P:cell adhesion; IEA.
DR InterPro: IPR008966; Adhes_bact.
DR InterPro: IPR004237; Fn_bind.
DR InterPro: IPR005877; Gpos_YsIRK.
DR InterPro: IPR001899; Gram_pos_anchor.
DR Pfam: PF02986; Fn_bind.1.
DR Pfam: PF00746; Gram_pos_anchor.1.
DR Pfam: PF04650; YsIRK_signal.1.
DR TIGRfam: TIGR01167; LpXTG_anchor.1.
DR TIGRfam: TIGR01168; YsIRK_signal.1.
DR PROSITE: PSS0847; GRAM_POS_ANCHORING.1.
DR Cell wall; Complete proteome; Peptidoglycan-anchor.
KW Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ SEQUENCE 957 AA; 105980 MW; 28F8BA7FFDFD3EAF CRC64;

Query Match 93.9%; Score 200; DB 2; Length 957;
Best Local Similarity 94.7%; Pred. No. 4,6e-17;
Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 ONKGNOSFEPEPTKDKPKYEHGNGNIIDIDPDSVPHIHG 38
Db 727 ONKGNOSFEEDTEKDKPKYEHGNGNIIDIDPDSVPHIHG 764

RESULT 4
O9AEP9 PRELIMINARY; PRT; 152 AA.
AC O9AEP9;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Fibronectin-binding protein (Fragment).
```

Query Match	92.5%;	Score 197;	DB 2;	Length 152;
Best Local Similarity	94.7%;	Pred. No. 1.5e-17;		
Matches 36;	Conservative 0;	Mismatches 2;	Indels 0;	Gaps 0;

proteins in
ence and
peptidoglycan by

acteria); IEA.

[illegible]

22 PRELIMINARY; PRT; 1038 AA.

Staphylococcus aureus (strain Mu50 / ATCC 700699).
TaxID=158878;

Rissa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T., Mori M., Ogasawara N., Hayashi H., Hiramatsu K.;
The genome sequencing of melicillin-resistant *Staphylococcus*

SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by an amide bond (By similarity).

ECO:0009986; C:cell surface; IEA.
ECO:0005618; C:cell wall; IEA.
ECO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.

```

cPro; IPR004237; Fn_bind.
cPro; IPR005877; Gpos_YSRK.
cPro; IPR001899; Gram_pos_anchor

```

```
; PF04650; YSIRK_signal; 1.  
PFAMs; TIGR01167; LPXTG_anchor; 1  
MICROB1168; YSRPV_signal; 1
```

```

wall: Complete proteome: Peptidoglycan-anchor.
FAM6; IIGK01168; ISIRK_signal; 1.
ITE; PS50847; GRAM_POS_ANCHORING; 1.

```

1038 AA; 113618 MM; 666BF6BF2BFBB12 CRC64;

Batch	Score	DB 2	Length
90.1%;	192;		
92.1%;	Pred. No. 5.6e-16;		

35; Conservative 1; Mismatches 2; Indels

1 QNKGNSFEETEKDKPYEHGNIIDIDFDSVPHIHG 38
|||:||| ||| ||| ||| ||| ||| ||| |||

780 QNKGDQSFEEDEKDKPKYEHGNIIDIDFDSVPQIHG 817

PRELIMINARY; PRT; 1038 AA.

JUL-2004 (Tremblay et al., 2004) (EMBL accession number F06789)

UL-2004 (MEMBLrel. 27, last sequence update)
UL-2004 (MEMBLrel. 27, last sequence update)
UL-2004 (MEMBLrel. 27, last sequence update)


```
DE Fnb protein.
GN Name=fnb; OrderedLocusNames=SA2291;
OS Staphylococcus aureus (strain N315).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxId=158879;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=2111992; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2;
RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Iian J.-Q., Ito T.,
RA Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoeyama A.,
RA Mizumori-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
RA Sekimizu K., Yamakawa H., Kohara S., Goto S., Yabuuchi J.,
RA Kanetsuna M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
RA Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
RA "Whole genome sequencing of methicillin-resistant Staphylococcus
RT aureus";
RL Lancet 357:1225-1240(2001).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC an amide bond (By similarity).
DR EMBL: AP003137; BAB43594.1; -.
DR GO: GO:0009986; C:cell surface; IEA.
DR GO: GO:0005618; C:cell wall; IEA.
DR GO: GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO: GO:0016020; C:membrane; IEA.
DR GO: GO:0007155; P:cell adhesion; IEA.
DR InterPro: IPR008966; Adhes_bact.
DR InterPro: IPR004237; Fn_bind.
DR InterPro: IPR005877; Gpos_YsIRK.
DR InterPro: IPR001899; Gram_pos_anchor.
DR Pfam: PF02986; Fn_bind_1.
DR Pfam: PF04650; YsIRK_signal; 1.
DR TIGRFAMs: TIGR01167; LPXTG_anchor; 1.
DR TIGRFAMs: TIGR01168; YsIRK_signal; 1.
DR PROSITE: PS50847; GRAM_POS_ANCHORING; 1.
DR Cell wall; Complete proteome; Peptidoglycan-anchor.
KM SEQUENCE 1038 AA; 113618 MW; 666BFBFB2BFB212 CRC64;
SQ
Query Match 90.1%; Score 192; DB 2; Length 1038;
Best Local Similarity 92.1%; Pred. No. 5.6e-16;
Matches 35; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 1 QNKGNSFEETPKDKPKYHGNGNIIDIDPDSVPHIHG 38
DB 780 QNKGDSFEETDKPKYHGNGNIIDIDPDSVPHIHG 817
RESULT 8
ID Q8NUU7 PRELIMINARY; PRT; 1015 AA.
AC Q8NUU7;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Fnb protein.
GN Name=fnb; OrderedLocusNames=MW2421;
OS Staphylococcus aureus (strain MW2).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxId=196620;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=MW2;
RX MEDLINE=22040717; PubMed=12044378; DOI=10.1016/S0140-6736(02)08713-5;
RA Baba T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Oguchi A.,
RA Nagai Y., Iwama N., Asano K., Naimi T., Kuroda H., Cui L.,
RA Yamanoto K., Hiramatsu K.;
RA "Genome and virulence determinants of high virulence community-
RT acquired MRSA.";
RL Lancet 359:1819-1827(2002).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC an amide bond (By similarity).
EMBL: AP004830; BAB96286.1; -;
```

```
DR GO: GO:0009986; C:cell surface; IEA.
DR GO: GO:0005618; C:cell wall; IEA.
DR GO: GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO: GO:0016020; C:membrane; IEA.
DR GO: GO:0007155; P:cell adhesion; IEA.
DR InterPro: IPR008966; Adhes_bact.
DR InterPro: IPR004237; Fn_bind.
DR InterPro: IPR005877; Gpos_YsIRK.
DR InterPro: IPR001899; Gram_pos_anchor.
DR Pfam: PF02986; Fn_bind_1.
DR Pfam: PF04650; YsIRK_signal; 1.
DR TIGRFAMs: TIGR01167; LPXTG_anchor; 1.
DR TIGRFAMs: TIGR01168; YsIRK_signal; 1.
DR PROSITE: PS50847; GRAM_POS_ANCHORING; 1.
DR Cell wall; Complete proteome; Peptidoglycan-anchor.
KM SEQUENCE 1015 AA; 111145 MW; D0F9281B864D4D2 CRC64;
SQ
Query Match 86.4%; Score 184; DB 2; Length 1015;
Best Local Similarity 89.5%; Pred. No. 6e-15;
Matches 34; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 1 QNKGNSFEETPKDKPKYHGNGNIIDIDPDSVPHIHG 38
DB 785 QNKGNSFEETDKPKYHGNGNIIDIDPDSVPHIHG 822
RESULT 9
ID Q6G6H3 PRELIMINARY; PRT; 1015 AA.
AC Q6G6H3;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Fibronectin-binding protein.
GN OrderedLocusNames=SA52388;
OS Staphylococcus aureus (strain MSSA476).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxId=282459;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=15233324; DOI=10.1073/pnas.0402521101.
RA Holden M.T.G., Fell E.J., Lindsay J.A., Peacock S.J., Day N.P.J.,
RA Burright M.C., Foster T.J., Moore C.E., Hurst L., Atkin R., Barron A.,
RA Bason N., Bentley S.D., Chillingworth C., Chillingworth T.,
RA Churcher C., Clark L., Corton C., Cronin A., Doggett J., Dowd L.,
RA Fellwell T., Hance Z., Harris B., Hauser H., Holtroyd S., Jagels K.,
RA James K.D., Lennard N., Line A., Mayes R., Moule S., Mungall K.,
RA Ormond D., Quail M.A., Rabinowitsch E., Rutherford K.M., Sanders M.,
RA Sharp S., Simmonds M., Stevens K., Whitehead S., Barrett B.G.,
RA Spratt B.G., Parkhill J.;
RA "Complete genomes of two clinical Staphylococcus aureus strains:
RT evidence for the rapid evolution of virulence and drug resistance.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:9786-9791(2004).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC an amide bond (By similarity).
EMBL: BX571857; CAG44202.1; -.
DR GO: GO:0009986; C:cell surface; IEA.
DR GO: GO:0005618; C:cell wall; IEA.
DR GO: GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO: GO:0016020; C:membrane; IEA.
DR GO: GO:0007155; P:cell adhesion; IEA.
DR InterPro: IPR008966; Adhes_bact.
DR InterPro: IPR004237; Fn_bind.
DR InterPro: IPR005877; Gpos_YsIRK.
DR InterPro: IPR001899; Gram_pos_anchor.
DR Pfam: PF02986; Fn_bind_1.
DR Pfam: PF04650; YsIRK_signal; 1.
DR TIGRFAMs: TIGR01167; LPXTG_anchor; 1.
DR TIGRFAMs: TIGR01168; YsIRK_signal; 1.
DR PROSITE: PS50847; GRAM_POS_ANCHORING; 1.
DR Cell wall; Complete proteome; Peptidoglycan-anchor.
KM
```

SQ SEQUENCE 1015 AA; 111145 MW; D0F9281BB64D4D2 CRC64;
 Query Match 86.4%; Score 184; DB 2; Length 1015;
 Best Local Similarity 89.5%; Pred. No. 6e-15;
 Matches 34; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 QNKGNSFEPTEDKPKYEHGNIIDIDPDSVPHNG 38
 DB 785 QNKGNSFEPTEDKPKYEHGNIIDIDPDSVPHNG 822

RESULT 10
 Q99RD3 PRELIMINARY; PRT; 961 AA.
 AC Q99RD3; (TRENBLREL. 17, Created)
 DT 01-JUN-2001 (TRENBLREL. 17, Last sequence update)
 DT 01-JUN-2001 (TRENBLREL. 24, Last annotation update)
 DE Fibronectin-binding protein homolog.
 GN Name=fnb3; OrderedLocustNames=SAV2502;
 OS Staphylococcus aureus (strain Mu50 / ATCC 700699).
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 NCBI_TaxID=158878;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Mu50 / ATCC 700699;
 RA MEDLINE=21311952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2;
 RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
 RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Iian J.-Q., Ito T.,
 RA Kanamori M., Matsunaru H., Maruyama A., Murakami H., Hoshoyama A.,
 RA Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
 RA Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
 RA Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
 RA Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
 RT "Whole genome sequencing of methicillin-resistant Staphylococcus
 aureus."
 RL Lancet 357:1225-1240(2001).
 CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
 an amide bond (By similarity).
 DR EMBL: AP003137; BAB43593.1; -;
 DR PIR: G90053; G90053.
 DR HSSP: Q53653; 1N67.
 DR GO: GO:0009986; C:cell surface; IEA.
 DR GO: GO:0005618; C:cell wall; IEA.
 DR GO: GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
 DR GO: GO:0016020; C:membrane; IEA.
 DR GO: GO:0007155; P:cell adhesion; IEA.
 DR InterPro: IPR008966; Adhes_bact.
 DR InterPro: IPR004237; Fn_bind.
 DR InterPro: IPR005877; Gpos_YsIRK.
 DR InterPro: IPR001899; Gram_pos_anchor.
 DR Pfam: PF02986; Fn_bind; 1.
 DR Pfam: PF00746; Gram_pos_anchor; 1.
 DR Pfam: PF04650; YsIRK_signal; 1.
 DR TIGRFAMs: TIGR01167; LPXTG_anchor; 1.
 DR TIGRFAMs: TIGR01168; YsIRK_signal; 1.
 DR PROSITE: PS50847; GRAM_POS_ANCHORING; 1.
 KW Cell wall, Complete proteome; Peptidoglycan-anchor.
 SQ SEQUENCE 961 AA; 106010 MW; 364940F884EA4101 CRC64;

Query Match 84.5%; Score 180; DB 2; Length 961;
 Best Local Similarity 86.8%; Pred. No. 1.9e-14;
 Matches 33; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 QNKGNSFEPTEDKPKYEHGNIIDIDPDSVPHNG 38
 DB 731 QNKGNSFEPTEDKPKYEHGNIIDIDPDSVPHNG 768

RESULT 11
 Q7A3J8 PRELIMINARY; PRT; 961 AA.
 AC Q7A3J8;

DT 05-JUL-2004 (TRENBLREL. 27, Created)
 DT 05-JUL-2004 (TRENBLREL. 27, Last sequence update)
 DT 05-JUL-2004 (TRENBLREL. 27, Last annotation update)
 DE FnbB protein.
 GN Name=fnb3; OrderedLocustNames=SA2290;
 OS Staphylococcus aureus (strain N315).
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 NCBI_TaxID=158879;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21311952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2;
 RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
 RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Iian J.-Q., Ito T.,
 RA Kanamori M., Matsunaru H., Maruyama A., Murakami H., Hoshoyama A.,
 RA Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
 RA Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
 RA Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
 RA Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
 RT "Whole genome sequencing of methicillin-resistant Staphylococcus
 aureus."
 RL Lancet 357:1225-1240(2001).
 CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
 an amide bond (By similarity).
 DR EMBL: AP003137; BAB43593.1; -;
 DR GO: GO:0009986; C:cell surface; IEA.
 DR GO: GO:0005618; C:cell wall; IEA.
 DR GO: GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
 DR GO: GO:0016020; C:membrane; IEA.
 DR GO: GO:0007155; P:cell adhesion; IEA.
 DR InterPro: IPR008966; Adhes_bact.
 DR InterPro: IPR004237; Fn_bind.
 DR InterPro: IPR005877; Gpos_YsIRK.
 DR InterPro: IPR001899; Gram_pos_anchor.
 DR Pfam: PF02986; Fn_bind; 1.
 DR Pfam: PF00746; Gram_pos_anchor; 1.
 DR Pfam: PF04650; YsIRK_signal; 1.
 DR TIGRFAMs: TIGR01167; LPXTG_anchor; 1.
 DR TIGRFAMs: TIGR01168; YsIRK_signal; 1.
 DR PROSITE: PS50847; GRAM_POS_ANCHORING; 1.
 KW Cell wall; Complete proteome; Peptidoglycan-anchor.
 SQ SEQUENCE 961 AA; 106010 MW; 364940F884EA4101 CRC64;

Query Match 84.5%; Score 180; DB 2; Length 961;
 Best Local Similarity 86.8%; Pred. No. 1.9e-14;
 Matches 33; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 QNKGNSFEPTEDKPKYEHGNIIDIDPDSVPHNG 38
 DB 731 QNKGNSFEPTEDKPKYEHGNIIDIDPDSVPHNG 768

RESULT 12
 Q6GDUS PRELIMINARY; PRT; 965 AA.
 AC Q6GDUS; (TRENBLREL. 27, Created)
 DT 05-JUL-2004 (TRENBLREL. 27, Last sequence update)
 DT 05-JUL-2004 (TRENBLREL. 27, Last annotation update)
 DE Fibronectin-binding protein.
 GN Name=fnbA; OrderedLocustNames=SA2580;
 OS Staphylococcus aureus (strain MRSA252).
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 NCBI_TaxID=282458;
 RN [1]
 RP SEQUENCE FROM N.A.
 RP PubMed=15213324; DOI=10.1073/pnas.0402521101;
 RA Holden M.T.G., Feil E.J., Lindsay J.A., Peacock S.J., Day N.P.J.,
 RA Baeson N., Bentley S.D., Chillingworth C., Chillingworth T.,
 RA Churcher C., Clark L., Corton C., Cronin A., Doggett J., Dowd L.,
 RA Feltwell T., Hance Z., Harris B., Hauser H., Holtroyd S., Jørgensen K.,
 RA James K.D., Lennard N., Line A., Mayes R., Moule S., Mungall K.,
 RA Ormond D., Quail M.A., Rabinowitsch E., Rutherford K.M., Sanders M.,

RA Sharp S.G., Simmonds M., Stevens K., Whitehead S., Barrell B.G.,
RT "Complete genomes of two clinical *Staphylococcus aureus* strains:
evidence for the rapid evolution of virulence and drug resistance.",
Proc. Natl. Acad. Sci. U.S.A. 101:9786-9791(2004).
RL -1 SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC an amide bond (by similarity).
CC EMBL: X571856; CACG1560.1; -.
DR GO: GO:0009986; C:cell surface; IEA.
DR GO: GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO: GO:0016020; C:membrane; IEA.
DR GO: GO:0007155; P:cell adhesion; IEA.
DR InterPro: IPR008966; Adhes_bact.
DR InterPro: IPR004237; Fn_bind.
DR InterPro: IPR005877; Gpos_XSIRK.
DR InterPro: IPR001899; Gram_pos_anchor.
DR Pfam: PF02986; Fn_bind; 1.
DR Pfam: PF00746; Gram_pos_anchor; 1.
DR Pfam: PF04650; XSIRK_signal; 1.
DR TIGRFAMs: TIGR01167; LpxTG_anchor; 1.
DR TIGRFAMs: TIGR01168; XSIRK_signal; 1.
DR PROSITE: PS50847; GRAM_POS_ANCHORING; 1.
KW Cell wall, Complete proteome, Peptidoglycan-anchor.
SQ SEQUENCE 965 AA; 105691 MW; 2982EI32164D0551 CRC64;

Query Match 84.5%; Score 180; DB 2; Length 965;
Best Local Similarity 86.8%; Pred. No. 1,9e-14;
Matches 33; Conservative 1; Mismatches 4; Indels 0; Gaps 0,

Qy 1 QNKGNSFEPEPTKDKPKYEHNGNIIDIDFDSVPVPHG 38
Db 749 QNSGNQSFEDTDEKDPKTEQGSGNIIDIDFDSVPVPHG 786

RESULT 13
OECJNO ID PRELIMINARY; PRT; 610 AA.
AC OECJNO:
DT 25-OCT-2004 (TREMBLrel. 28, Created)
DT 25-OCT-2004 (TREMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TREMBLrel. 28, Last annotation update)
DE Desulfatibacillus salinarum strain DSMZ 11536
MLM2
GN ORFNames=KLIA0F17347g;
CS Kluyveromyces lactis NRRL Y-1140.
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Kluyveromyces.
CX NCBI_TaxID=284590;
[1]
RN SEQUENCE FROM N.A.
RP STRAIN=NRRL Y-1140;
RG Genolevures;
RA Dujon B., Sherman D., Fischer G., Durrens P., Casaregola S.,
lafontaine I., de Montigny J., Marcq C., Neuvéglise C., Talla E.,
Goffard N., Frangeul L., Aigle M., Anthouard V., Babour A., Barbé V.,
Barney S., Blanchin S., Beckerich J.M., Beyne E., Bleykasten C.,
Boissarie A., Boyer J., Catalillo L., Confantolletti F., de Darvar A.,
Despons L., Fabre E., Fairhead C., Ferry-Dunazet H., Groppi A.,
Hantreay F., Hennequin C., Jaunaux N., Joyet P., Kachouri R.,
Kerret A., Koszul R., Lemaire M., Leœur I., Ma L., Müller H.,
Nicoud J.M., Nikolski M., Oztaç S., Özier-Kalogeropoulos O.,
Pellens S., Petier S., Richard G.F., Straub M.L., Suleau A.,
Swenne D., Tekela F., Wesolowski-Louvel M., Westhof E., Wirth B.,
Zenou-Meyer M., Zivanovic I., Bolotin-Fukuhara M., Thierry A.,
Bouchier C., Caudron B., Scarpelli C., Galliardin C., Weissenbach J.,
Wincker P., Souciet J.L.;
RT "Genome evolution in yeasts."
RN Nature 430:35-44(2004).
[2]
RN SEQUENCE FROM N.A.
RP STRAIN=NRRL Y-1140;
RC Genoscope;
RA Submitted (JUL-2004) to the EMBL/genBank/DDBI databases.

```

SQ EMBL; CR382126; CAG98567.1; -.
Query Match          30.0%; Score 64; DB 2; Length 610;
Best Local Similarity 31.4%; Pred. No. 13;
Matches    11; Conservative   10; Mismatches     8; Indels      6; Gaps       1;

Oy           1 ONKGNQSFEEPTKE-----DKPRYEHGNNIIDD 29
Db            |::|::|||::|::|::|::|::|::|::|::|::|::|:
              486 QTQSSEFFOEFTSKRRRLLENDEPYDHSTLLVDIE 520


RESULT 14
COBD_THETN        STANDARD;             PRT;         367 AA.

AC ORSUA;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Putative threonine-phosphate decarboxylase (EC 4.1.1.81) (l-threonine-
DE O-3-phosphate decarboxylase).
CN Name=CoBd_OrderedlocusNames-TTB380;
CS Thermocaneobacter tengcongensis.
OC Bacteria; Firmicutes; Clostridia; Thermodurales;
CX Thermocaneobacteriaceae; Thermocaneobacter.
XX NCBI_TaxID=119072;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=M8 / JCM 11007;
RX MEDLINE=21992816; PubMed=11997336; DOI=10.1101/gr.219302;
RA Bao Q., Tian Y., Li W., Xu Z., Xuan Z., Hu S., Dong W., Yang J.,
RA Chen Y., Xue Y., Xu Y., Lai X., Huang L., Dong X., Ma Y., Ling L.,
RA Tan H., Chen R., Wang J., Yu J., Yang H.;
RT "A complete genome of the T. tengcongensis genome." ;
RL Genome Res. 12:689-700(2002).
CC -1 FUNCTION: Decarboxylates l-threonine-O-3-phosphate to yield (R)-1-l-
amino-2-propanol O-2-phosphate, the precursor for the linkage
between the nucleotide loop and the corrin ring in cobalamin (By
similarity)
CC -1 CATALYTIC ACTIVITY: l-threonine O-3-phosphate = (R)-1-amino-2-propa-
nol + CO(2).
CC -1 COFACTOR: Pyridoxal phosphate (by similarity).
CC -1 PATHWAY: Adenosylcobalamín biosynthesis; conversion of
adenosylcobyrinic acid to adenosylcobamidate.
CC CC SIMILARITY: Belongs to the class-II pyridoxal-phosphate-dependent
amino-transferase family.
---
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL Outstation - ite
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@lsb.sib.ch).
---
DR EMBL; AE013011; AAM23667.1; -.
DR HSBB; P97084; ILC5.
DR InterPro; IPRO01176; ACC_synthase.
DR InterPro; IPRO04839; Aminotrans_I/I.
DR InterPro; IPRO01917; Aminotrans_II.
DR InterPro; IPRO05860; CoBd.
DR Pfam; PF00155; Aminotran_1_2; 1.
DR PRINTS; PRO0753; ACCSYNTASE.
DR TRIGNAMS; TIGR01140; CoBd; 1.
DR POSITE; PS00599; AA TRANSFER CLASS 2; FALSE NEG.
FW Cobalamin biosynthesis; Complete proteome; Lyase; Pyridoxal phosphat-.
KT BINDING 213 213 Pyridoxal phosphate (by similarity).
SQ SEQUENCE 367 AA; 42396 MW; 222512FBEIF8435 CRC64;
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QY 13 EKDKPKYHGGNIID-----IDFDS 32
 DB 5 EKMKP-YEHGNIYDYQGNIIDFSS 28

RESULT 15

Q7RB60 PRELIMINARY; PRT; 716 AA.
 ID Q7RB60
 AC Q7RB60;
 DT 01-MAR-2004 (TrEMBLrel. 26, Created)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Hypothetical protein.
 GN Name=PY06288;
 OS Plasmodium yoelii yoelii.
 OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
 OX NCBI_TaxID=73239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=17XNL;
 RX PubMed=1366865; DOI=10.1038/nature01099;
 RA Carlson J.M., Angiuoli S.V., Suh B.B., Koof J.T.W., Pertea M.,
 RA Silva J.C., Ermolaeva M.D., Allen J.E., Selengut J.D., Koo H.L.,
 RA Peterson J.D., Pop M., Kosack D.S., Shumway M.F., Bidwell S.L.,
 RA Shalom S.J., van Aken S.E., Riedmuller S.B., Feldblyum T.V.,
 RA Cho J.K., Quackenbush J., Sedegah M., Shoabdi A., Cummings L.M.,
 RA Florens L., Yates F.R. III, Raine J.D., Sinden R.E., Harris M.A.,
 RA Cunningham D.A., Preiser P.R., Bergman L.W., Valdivia A.B.,
 RA van Lin L.H., Janse C.J., Waters A.P., Smith H.O., White O.R.,
 RA Salzberg S.L., Venter J.C., Fraser C.M., Hoffman S.L., Gardner M.J.,
 RA Carucci D.J.;
 RT "Genome sequence and comparative analysis of the model rodent malaria
 parasite Plasmodium yoelii yoelii.";
 RL Nature 419:512-519(2002).
 CC -!- CAUTION: The sequence shown here is derived from an
 EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 preliminary data.
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 DR EMBL; AABL01002106; EAA18479.1; -.
 DR InterPro; IPR008941; TPR-like.
 KM Hypothetical protein.
 SQ SEQUENCE 716 AA; 86559 MW; E11BE234A397B6F7 CRC64;

Query Match 29.1%; Score 62; DB 2; Length 716;
 Best Local Similarity 34.3%; Pred. No. 29;
 Matches 12; Conservative 6; Mismatches 17; Indels 0; Gaps 0;

QY 2 NKGNSFEPTPEKDKPKYHGGNIIDIDFDSVPHI 36
 DB 109 NNYNHTWEKKKQSKFPNNNIFDVSYEQVRKI 143

Search completed: October 22, 2005, 06:06:10
 Job time : 70.6361 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 25, 2005, 19:38:38 ; Search time 83.8325 Seconds
(without alignments)
175.313 Million cell updates/sec

Title: US-10-731-238-49

Perfect score: 213

Sequence: 1 QNKGNSFEDTEKDKPKYEHGPNIDIDFDSVPHIHG 38

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :
1: geneseq_16Dec04:*
2: geneseqp1980s:*
3: geneseqp1990s:*
4: geneseqp2000s:*
5: geneseqp2001s:*
6: geneseqp2002s:*
7: geneseqp2003as:*
8: geneseqp2003bs:*
9: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	213	100.0	38	2	AAW65705
2	204	95.8	38	2	AAW65663
3	204	95.8	134	2	AAW29087
4	204	95.8	139	2	AAW31556
5	204	95.8	1018	1	AAW82115
6	204	95.8	1018	4	AAU37245
7	204	95.8	1018	4	AAU34301
8	204	95.8	1018	6	ABW18922
9	204	95.8	1018	6	ABW18922
10	204	95.8	1027	2	AAW89806
11	199	93.4	77	2	AAW88749
12	199	93.4	113	2	AAW90937
13	199	93.4	130	2	AAW58807
14	199	93.4	130	2	AAW58807
15	199	93.4	130	2	AAW91202
16	199	93.4	130	2	AAW91201
17	199	93.4	162	2	AAW90942
18	199	93.4	164	2	AAW90938
19	199	93.4	174	2	AAW58808
20	199	93.4	174	2	AAW91203
21	199	93.4	181	2	AAW58805
22	199	93.4	181	2	AAW91200
23	198	93.0	38	1	AAW80661
24	198	93.0	38	1	AAW82117
25	198	93.0	38	2	AAW65703

26	198	93.0	38	2	AAW65702	AAW65702 Fibronect
27	197	92.5	38	2	AAW65704	AAW65704 Fibronect
28	196	92.0	38	2	AAW65664	AAW65664 Fibronect
29	194	91.1	38	2	AAW65701	AAW65701 Fibronect
30	193	90.6	38	2	AAW65706	AAW65706 Fibronect
31	191	89.7	134	2	AAW29088	AAW29088 S. aureus
32	191	89.7	559	2	AAW69803	AAW69803 Staphyloc
33	191	89.7	767	4	AAW34403	AAW34403 Staphyloc
34	191	89.7	767	4	AAU37547	AAU37547 Staphyloc
35	191	89.7	940	2	AAW07070	AAW07070 Fibronect
36	191	89.7	940	6	ABU19111	ABU19111 Pathogen
37	191	89.7	948	6	ADA89470	ADA89470 Staphyloc
38	191	89.7	948	6	ABU18923	ABU18923 Pathogen
39	191	89.7	948	6	ABW72536	ABW72536 Staphyloc
40	191	89.7	1038	6	ABU15903	ABU15903 Protein e
41	187	87.8	38	2	AAW65699	AAW65699 Fibronect
42	183	85.9	978	4	AAU33960	AAU33960 Staphyloc
43	183	85.9	1001	4	AAU37093	AAU37093 Staphyloc
44	182	85.4	134	2	AAW29089	AAW29089 Cloned fi
45	181	85.0	36	2	AAW65714	AAW65714 Fibronect

ALIGNMENTS

RESULT 1
AAW65705
ID AAW65705 standard; peptide; 38 AA.

AC AAW65705;

DT 16-OCT-1998 (first entry)

DE Fibronectin binding protein-derived peptide #49.

XX microbial surface components recognising adhesive matrix molecule;

KW MCGRAMM; fibronectin; fibronectin-binding protein; antibody; epitope;

KM antibiotic; bacterial infection; antibiotic-resistant strain.

OS Synthetic.

OS Staphylococcus aureus.

PN MO9831389-A2.

XX 23-JUL-1998.

PF 21-JAN-1998; 98WO-US001222.

PR 21-JAN-1997; 97US-0036139P.

XX (TEXA) UNIV TEXAS A & M SYSTEM.

PI Hooeok M, Patti JM, House-Pompeo KL, Speziale P, Joh D;

PI Mcgavin MJ;

XX WPI; 1998-413816/35.

PT Antibody that binds to fibronectin-binding protein, preventing its

PT binding to fibronectin - used to treat or prevent bacterial infection,

PT especially by Staphylococci and Streptococci.

XX Example 8; Page 102; 201p; English.

The invention relates to antibodies that bind to a fibronectin-binding domain of a fibronectin-binding protein, and inhibit binding of the protein to a fibronectin. Also claimed are: (1) isolated peptides of a fibronectin-binding protein that do not bind to fibronectin; (2) fusion protein containing at least one peptide of a fibronectin-binding protein linked to a second amino acid sequence; (3) nucleic acid encoding the isolated peptide of (1). Antibodies, the isolated peptides of (1) and the nucleic acids are all useful for immunisation (active or passive) and (by inhibiting binding of bacteria to fibronectin) for preventing or creating infection in humans or other animals, particularly by staphylococci or

CC streptococci, e.g. meningitis, otitis media, pneumonia, endocarditis,
 CC mastitis in cattle, abortion in horses and many others. Since the
 CC antibodies block binding of bacteria, they should be effective against
 CC antibiotic-resistant strains, and may replace antibiotic therapy or
 CC increase its effectiveness. Sequences AAW65701-706 represent a series of
 CC synthetic peptides based on the D2 region of *S. aureus* fibronectin
 CC binding protein A. They were synthesised to contain mutations

XX Sequence 38 AA;

Query Match 100.0%; Score 213; DB 2; Length 38;
 Best Local Similarity 100.0%; Pred. No. 6, 8e-23;
 Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QNKGNSFEEDTEKDKPKYEHGPNIIIDFDSVPHIHG 38
 DB 1 QNKGNSFEEDTEKDKPKYEHGPNIIIDFDSVPHIHG 38

RESULT 2
 ID AAW65663 standard; peptide; 38 AA.
 XX AAW65663;

DT 16-OCT-1998 (first entry)
 XX Fibronectin binding protein-derived peptide #7.

XX microbial surface components recognising adhesive matrix molecule;
 KM MSCRAMM; fibronectin; fibronectin-binding protein; antibody; epitope;
 KM antibiotic; bacterial infection; antibiotic-resistant strain.

XX Synthetic.
 OS *Staphylococcus aureus*.

XX WO9831389-A2.

XX 23-JUL-1998.

XX 21-JAN-1998; 98WO-US001222.

XX 21-JAN-1997; 97US-0036139P.

XX (TEXA) UNIV TEXAS A & M SYSTEM.

XX Hoeoek M, Paci JM, House-Pompeo KL, Speziale P, Joh D;
 PI McGavin MJ;

XX WPI, 1998-413816/35.

PT Antibody that binds to fibronectin-binding protein, preventing its
 binding to fibronectin - used to treat or prevent bacterial infection,
 PT especially by *Staphylococci* and *Streptococci*.

XX Example 2; Page 92; 201pp; English.

XX The invention relates to antibodies that bind to a fibronectin-binding
 CC domain of a fibronectin-binding protein, and inhibit binding of the
 CC protein to fibronectin. Also claimed are: (1) isolated peptides of a
 CC fibronectin-binding protein that do not bind to fibronectin; (2) fusion
 CC protein containing at least one peptide of a fibronectin-binding protein
 CC linked to a second amino acid sequence; (3) nucleic acid encoding the
 CC isolated peptide of (1). Antibodies, the isolated peptides of (1) and the
 CC nucleic acids are all useful for immunisation (active or passive) and (by
 CC inhibiting binding of bacteria to fibronectin) for preventing or treating
 CC infection in humans or other animals, particularly by *Staphylococci* or
 CC streptococci, e.g. meningitis, otitis media, pneumonia, endocarditis,
 CC mastitis in cattle, abortion in horses and many others. Since the
 CC antibodies block binding of bacteria, they should be effective against
 CC antibiotic-resistant strains, and may replace antibiotic therapy or
 CC increase its effectiveness. Sequences AAW65659-68 represent synthetic
 CC epitopes from the fibronectin binding domains DU and DI-D4 of the *S.*

CC aureus fnbA gene
 XX Sequence 38 AA;

Query Match 95.8%; Score 204; DB 2; Length 38;
 Best Local Similarity 97.4%; Pred. No. 1, 3e-21;
 Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QNKGNSFEEDTEKDKPKYEHGPNIIIDFDSVPHIHG 38
 DB 1 QNKGNSFEEDTEKDKPKYEHGPNIIIDFDSVPHIHG 38

RESULT 3
 ID AAY29087 standard; protein; 134 AA.
 XX AAY29087;

DT 28-SEP-1999 (first entry)

XX *S. aureus* fibronectin binding protein A (FnBA) binding domain.

XX Bovine herpes virus-2; BHV-2; cytokine; immune response; immunogen; IL;
 KM interleukin; colony stimulating factor; CSF; interferon; IFN; TNF;
 KM tumour necrosis factor; recombinant virus; vaccine; mucosal disease;
 KM mastitis; breast cancer; stress-induced disease; binding domain; FnBA;
 KM fibronectin binding protein.

XX *Staphylococcus aureus*.

XX WO916892-A1.

XX 08-APR-1999.

XX 29-SEP-1998; 98WO-GB002927.

XX 29-SEP-1997; 97GB-00020633.

XX (UYBR-) UNIV BRISTOL.

XX Bradley AJ, Duffas WPH;

XX WPI, 1999-255101/21.

XX N-PSDB; AAX91504.

XX New bovine herpes virus-2 vectors.
 PT Example 2; Fig 8A-B; 130pp; English.

XX The invention provides bovine herpes virus-2 (BHV-2) based vectors that
 CC comprise at least one cytokine-encoding DNA sequence. The expression of
 CC cytokines in mammals can up-regulate immune responses to the immunogens.
 CC The cytokine is selected from interleukin (IL), colony stimulating
 CC factors (CSF), interferons (IFN) and tumour necrosis factors (TNF). The
 CC BHV-2 based vector or recombinant virus can be used as vaccines. They can
 CC be used for preventing or treating a mucosal disease in a subject, e.g.
 CC ruminants, cattle, sheep, goats, dogs, cats, horses, or man, particularly
 CC mastitis in cows or breast cancers in humans. They can also be used for
 CC preventing or treating a stress-induced disease. The present sequence
 CC represents the binding domain of a previously published *S. aureus*
 CC fibronectin binding protein A (FnBA) sequence. The FnB binding domain
 CC gene sequence FnBAB, cloned for use in this invention, has 97.8 percent
 CC identity when compared to the previously published FnBA and FnBB gene
 CC sequences

XX Sequence 134 AA;

Query Match 95.8%; Score 204; DB 2; Length 134;
 Best Local Similarity 97.4%; Pred. No. 6, 2e-21;
 Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QNKGNSFEEDTEKDKPKYEHGPNIIIDFDSVPHIHG 38

DB 40 QNKGNSFEEDTEKDKPKYEHGNIIDIDFDSVPHING 77

RESULT 4

AAW31556 standard; protein; 139 AA.

AAW31556;

27-AUG-2003 (revised)

25-MAR-2003 (revised)

21-MAY-1998 (first entry)

Fibronectin-binding MSCRAMM derivative PQD.

Fibronectin; PQD; collagen binding protein; sepsis; infection;

microbial surface component recognising adhesive matrix molecule; MSCRAMM;

adhesin; vaccine; immunisation; diagnosis; therapy; mastitis.

Staphylococcus aureus.

Key Location/Qualifiers

Peptide 1..12 /note= "vector POE30-derived peptide"

MO9743314-A2.

20-NOV-1997.

14-MAY-1997; 97MO-US008210.

16-MAY-1996; 96US-0017678P.

(TEXA) UNIV TEXAS A & M SYSTEM.

(UABR-) UAB RES FOUND.

Hoeek M, Patil JM, House-Pompeo K, Sthanam N, Symersky J;

WPI; 1998-006801/01.

Antibody that interacts with collagen binding domain of Staphylococcal

cna gene product - useful to prevent bacterial sepsis in animal infected

with Staphylococcus aureus.

PS Disclosure; Page 91; 143pp; English.

CC This protein comprises Staphylococcus aureus fibronectin-binding

CC microbial surface component regionising adhesive matrix molecule (MSCRAMM)

CC derivative PQD, plus a vector-derived N-terminal peptide. The invention

CC relates to claimed nucleic acid sequences (see AA793436-38) encoding S.

CC aureus collagen binding protein (CBP) epitopes M17, M31 and M55 (see

CC AA793436-38) that confer protection against S. aureus infection. CBP

CC protein and antigenic epitopes are contemplated for use in the treatment

CC of pathological infections, especially to prevent bacterial adhesion to

CC collagen. The epitopes are also contemplated for use in the preparation

CC of vaccines and as carrier proteins in vaccine formulations, as well as

CC in the formulation of compositions for the prevention of S. aureus

CC infection. PCR33 and PQD (see AA793436) were used to raise anti-MSCRAMM

CC polyclonal antibodies used in passive immunisation against bovine

CC mastitis. (Updated on 25-MAR-2003 to correct PI field.) (Updated on 27-

CC AUG-2003 to correct OS field.)

XX Sequence 139 AA;

SO Query Match 95.8%; Score 204; DB 2; Length 139;

Best Local Similarity 97.4%; Pred. No. 6.4e-21;

Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QNKGNSFEEDTEKDKPKYEHGNIIDIDFDSVPHING 38

DB 54 QNKGNSFEEDTEKDKPKYEHGNIIDIDFDSVPHING 91

RESULT 5
AAP82115 standard; protein; 1018 AA.

AAP82115;

25-MAR-2003 (revised)

05-JUN-1990 (first entry)

Fibronectin binding protein.

Fibronectin binding protein; S. aureus; immunisation; mastitis; ruminants;

wound infection; diagnosis.

Staphylococcus aureus.

EP294349-A.

07-DEC-1988.

30-MAY-1988; 88EP-00850188.

01-JUN-1987; 87SE-00002272.

(ALFA) ALFA LAVAL AGRIC INT AB.

Lindberg MK, Signas LC, Wadstrom TM, Froman G;

WPI; 1988-347978/49.

P-PADB; AAP82115.

Hybrid DNA encoding Staphylococcus aureus fibronectin binding protein -

useful for immunisation and topical application to prevent staphylococcal

infections.

PS Disclosure; Fig. 8A:1-8A:2; 23pp; English.

CC The S. aureus fibronectin binding protein may be included in a hybrid

CC protein. The protein may be used to immunise ruminants against

CC staphylococcal mastitis, pref. when given at 0.5-5 microg/kg, using 3

CC doses at 1-3 week intervals; and for topical applicn. to prevent wound

CC infection, pref. using isotonic saline soln. of concn. 25-250 microg/mg.

CC The DNA encoding the binding protein and the hybrid protein may be

CC immobilised on a carrier and used to diagnose staphylococcal infections.

CC (Updated on 25-MAR-2003 to correct PA field.)

XX Sequence 1018 AA;

SO Query Match 95.8%; Score 204; DB 1; Length 1018;

Best Local Similarity 97.4%; Pred. No. 7.4e-20;

Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QNKGNSFEEDTEKDKPKYEHGNIIDIDFDSVPHING 38

DB 784 QNKGNSFEEDTEKDKPKYEHGNIIDIDFDSVPHING 821

RESULT 6

AAU37245 standard; protein; 1018 AA.

AAU37245;

14-FEB-2002 (first entry)

Staphylococcus aureus cellular proliferation protein #1415.

Antisense; prokaryotic cellular proliferation protein; antibiotic;

antibacterial; drug design.

Staphylococcus aureus.


```
PN WO200170955-A2.
XX
XX
PD 27-SEP-2001.
XX
PF 21-MAR-2001; 2001WO-US009180.
XX
PR 21-MAR-2000; 2000US-0191078P.
PR 23-MAY-2000; 2000US-0206848P.
PR 26-MAY-2000; 2000US-0207127P.
PR 23-OCT-2000; 2000US-0242578P.
PR 27-NOV-2000; 2000US-0253625P.
PR 22-DEC-2000; 2000US-0257931P.
PR 16-FEB-2001; 2001US-0269308P.
XX
XX
PA (ELIT-) ELITRA PHARM INC.
XX
PI Haselbeck R, Ohlsen KL, Zyskind JW, Wall D, Trawick JD, Carr GJ,
PI Yamamoto RT, Xu HH;
XX
DR WPI; 2001-611495/70.
DR N-PSDB; AAS55104.
XX
XX
PT New polynucleotides for the identification and development of
PT antibiotics, comprise sequences of antisense nucleic acids.
XX
XX
PS Example 3; SEQ ID NO 12838; 511pp; English.
XX
XX
CC The invention relates to antisense inhibitors of genes essential to
CC prokaryotic cellular proliferation, their use in identifying the genes,
CC their use in the discovery of novel antibiotics, the essential genes
CC themselves and the encoded proteins. The prokaryotes used are Escherichia
CC coli, Staphylococcus aureus, Salmonella typhi, Klebsiella pneumoniae,
CC Pseudomonas aeruginosa and Enterococcus faecalis. The invention is also
CC useful for the identification of potential new targets for antibiotic
CC development. The antisense nucleic acids can also be used to identify
CC proteins used in proliferation, to express these proteins, and to obtain
CC antibodies capable of binding to the expressed proteins. The proteins can
CC be used to screen compounds in rational drug discovery programmes. The
CC antisense nucleic acid sequence is also useful to screen for homologous
CC nucleic acids which are required for cell proliferation in a wide variety
CC of organisms. The present sequence represents an essential prokaryotic
CC cellular proliferation protein. Note: The sequence data for this patent
CC did not form part of the printed specification, but was obtained in
CC electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX
SQ Sequence 1018 AA;
XX
XX
Query Match 95.8%; Score 204; DB 4; Length 1018;
Best Local Similarity 97.4%; Pred. No. 7.4e-20;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
QY 1 QNKGNSFEEDTEKDKPKYEHGPNIIIDIPDSVPHHG 38
XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
Db 784 QNKGNSFEEDTEKDKPKYEHGPNIIIDIPDSVPHHG 821
XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
XX
XX
RESULT 7
AAU34301
ID AAU34301 standard; protein; 1018 AA.
XX
XX
AC AAU34301;
XX
XX
DT 14-FEB-2002 (first entry)
XX
DE Staphylococcus aureus cellular proliferation protein #577.
XX
XX
KM Antisense; prokaryotic cellular proliferation protein; antibiotic;
KM antibacterial; drug design.
XX
XX
OS Staphylococcus aureus.
XX
XX
PN WO200170955-A2.
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XX
XX
PD 27-SEP-2001.
XX
PF 21-MAR-2001; 2001WO-US009180.
XX
PR 21-MAR-2000; 2000US-0191078P.
PR 23-MAY-2000; 2000US-0206848P.
PR 26-MAY-2000; 2000US-0207127P.
PR 23-OCT-2000; 2000US-0242578P.
PR 27-NOV-2000; 2000US-0253625P.
PR 22-DEC-2000; 2000US-0257931P.
PR 16-FEB-2001; 2001US-0269308P.
XX
XX
PA (ELIT-) ELITRA PHARM INC.
XX
PI Haselbeck R, Ohlsen KL, Zyskind JW, Wall D, Trawick JD, Carr GJ,
PI Yamamoto RT, Xu HH;
XX
DR WPI; 2001-611495/70.
DR N-PSDB; AAS52160.
XX
XX
PT New polynucleotides for the identification and development of
PT antibiotics, comprise sequences of antisense nucleic acids.
XX
XX
PS Example 3; SEQ ID NO 5797; 511pp; English.
XX
XX
CC The invention relates to antisense inhibitors of genes essential to
CC prokaryotic cellular proliferation, their use in identifying the genes,
CC their use in the discovery of novel antibiotics, the essential genes
CC themselves and the encoded proteins. The prokaryotes used are Escherichia
CC coli, Staphylococcus aureus, Salmonella typhi, Klebsiella pneumoniae,
CC Pseudomonas aeruginosa and Enterococcus faecalis. The invention is also
CC useful for the identification of potential new targets for antibiotic
CC development. The antisense nucleic acids can also be used to identify
CC proteins used in proliferation, to express these proteins, and to obtain
CC antibodies capable of binding to the expressed proteins. The proteins can
CC be used to screen compounds in rational drug discovery programmes. The
CC antisense nucleic acid sequence is also useful to screen for homologous
CC nucleic acids which are required for cell proliferation in a wide variety
CC of organisms. The present sequence represents an essential prokaryotic
CC cellular proliferation protein. Note: The sequence data for this patent
CC did not form part of the printed specification, but was obtained in
CC electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX
SQ Sequence 1018 AA;
XX
XX
Query Match 95.8%; Score 204; DB 4; Length 1018;
Best Local Similarity 97.4%; Pred. No. 7.4e-20;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
QY 1 QNKGNSFEEDTEKDKPKYEHGPNIIIDIPDSVPHHG 38
XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
Db 784 QNKGNSFEEDTEKDKPKYEHGPNIIIDIPDSVPHHG 821
XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
XX
XX
RESULT 8
ABJ18922
ID ABJ18922 standard; protein; 1018 AA.
XX
XX
AC ABJ18922;
XX
XX
DT 06-MAR-2003 (first entry)
XX
DE Pathogen specific antigen related staphylococcal protein SEQ ID No 60.
XX
XX
KM Antibacterial; virucide; fungicide; protozoacide; cytostatic; anti-HIV;
KM hyperimmune; serum-reactive; antigen; pathogen; tumour; allergen;
KM auto-immunity; vaccine; staphylococcal infection; antibody; cancer;
KM autoimmune disease; HIV; hepatitis.
XX
XX
OS Staphylococcus sp.
XX
XX
```

PN W0200259148-A2.
 XX 01-AUG-2002.
 XX 21-JAN-2002; 2002MO-EP000546.
 PF 26-JAN-2001; 2001AT-00000130.
 XX (CISTEM) BIOTECHNOLOGIES GMBH.
 XX
 PI Meinke A, Nagy E, Von Ahnen U, Klade C, Henics T, Zauner W;
 PI Minh DB, Vytvytska O, Etz H, Dryla A, Weichert T, Hafner M;
 PI Tempelmeier B;
 XX WPI; 2003-075410/07.
 DR
 PT Identifying, isolating and producing hyperimmune serum-reactive antigens
 PT from a pathogen, for preparing vaccine or medicament for treating or
 PT preventing e.g. staphylococcal infections, comprises providing antibody
 PT preparation.
 XX
 PS Example 7; Page 157; 252pp; English.
 XX
 CC The invention relates to a novel method for identifying, isolating and
 CC producing hyperimmune serum-reactive antigens from a pathogen, tumour,
 CC allergen, a tissue or host prone to auto-immunity, where the antigens are
 CC used in a vaccine, comprises providing antibody preparation from a plasma
 CC pool of a type of animal, or individual sera with antibodies against the
 CC specific pathogen, tumour, allergen, tissue or host prone to auto-
 CC immunity. The hyperimmune serum-reactive antigens comprising any of the
 CC 62 sequences of 53-2261 amino acids fully defined in the specification,
 CC or their hyperimmune fragments are useful for the manufacture of a
 CC pharmaceutical preparation, particularly a vaccine against staphylococcal
 CC infections or colonisation against *S. aureus* or *S. epidermidis*. The
 CC preparation of antibodies is useful for the manufacture of a medicament
 CC for treating or preventing staphylococcal infections or colonisation
 CC against *S. aureus* or *S. epidermidis*. The antibody preparations may also
 CC be used for diagnostic and imaging purposes. Other conditions that can be
 CC treated include cancer, autoimmune diseases or infections caused by viral
 CC (e.g. HIV, hepatitis A, B or C), fungal or protozoan pathogens. This
 CC sequence represents a staphylococcal protein relating to the method for
 CC identifying and producing pathogen specific antigens of the invention
 CC
 XX
 SQ Sequence 1018 AA;
 CC
 Query Match 95.8%; Score 204; DB 6; Length 1018;
 Best Local Similarity 97.4%; Pred. No. 7.4e-20;
 Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 OY 1 QNKGNSFEEDTEKDKPKYEHGPNIIIDPDSVPHNG 38
 |||||
 DB 784 QNKGNSFEEDTEKDKPKYEHGPNIIIDPDSVPHNG 821

PF 27-MAR-2002; 2002MO-IB002637.
 XX 27-MAR-2001; 2001GB-00007661.
 XX (CHIR-) CHIRON SPA.
 XX
 PI Maignani V, Mora M, Scarselli M;
 PI WPI; 2003-120786/11.
 DR N-PADB; ACF74097.
 DR
 PT New Staphylococcus aureus protein, useful as a vaccine for treating or
 PT preventing Staphylococcal infection, specifically an infection caused by
 PT *S. aureus*, e.g. sepsis.
 XX
 PS Claim 1; SEQ ID NO 3554; 49pp; English.
 XX
 CC The invention relates to novel genes and encoded proteins from
 CC Staphylococcus aureus. A composition comprising the *S. aureus* protein, a
 CC nucleic acid encoding the protein, or an antibody to the protein, is
 CC useful as a pharmaceutical, particularly as a vaccine for treating or
 CC preventing infection due to Staphylococcus bacteria, specifically an
 CC infection caused by *S. aureus*. The composition is particularly useful for
 CC treating or preventing sepsis in a patient. The composition can also be
 CC used for diagnostics. The protein is also used in an assay for enzymatic
 CC studies and as a target for antibiotics. This sequence represents one of
 CC the novel *S. aureus* proteins of the invention
 CC
 XX
 SQ Sequence 1018 AA;
 CC
 Query Match 95.8%; Score 204; DB 6; Length 1018;
 Best Local Similarity 97.4%; Pred. No. 7.4e-20;
 Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 OY 1 QNKGNSFEEDTEKDKPKYEHGPNIIIDPDSVPHNG 38
 |||||
 DB 784 QNKGNSFEEDTEKDKPKYEHGPNIIIDPDSVPHNG 821

RESULT 10
 AAM89806
 ID AAM89806 standard; protein; 1027 AA.
 XX
 AC AAM89806;
 XX
 DT 16-MAR-1999 (first entry)
 XX
 DE Staphylococcus aureus protein SEQ ID #5254.
 XX
 KW Computer readable medium; vaccine; *S. aureus* infection; immunodetection;
 KW cellulitis; eyelid infection; food poisoning; osteomyelitis; therapy;
 KW skin infection; surgical wound infection; scalded skin syndrome;
 KW toxic shock syndrome.
 XX
 OS Staphylococcus aureus.
 XX
 PN EP786519-A2.
 XX
 PD 30-JUL-1997.
 XX
 PF 07-JAN-1997; 97EP-00100117.
 XX
 PR 05-JAN-1996; 96US-0009861P.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 XX
 PI Kunsch CA, Choi GH, Barash SC, Dillon RJ, Fannon MR, Rosen CA;
 PI WPI; 1997-374922/35.
 DR
 XX Polynucleotide(s) and proteins derived from Staphylococcus aureus -
 PT stored on computer readable medium and used in the production of anti-
 PT *S. aureus* vaccines.

XX Claim 23; Page 3263-3267; 3271pp; English.
XX
PS This sequence represents a Staphylococcus aureus protein sequence of the
XX invention. The DNA sequences encoding the S.aureus proteins are recorded
CC on a computer readable medium, preferably selected from a floppy or hard
CC disk, random access memory (RAM), read-only memory (ROM) or CD-ROM.
CC Homology searches using the S.aureus DNA sequences allows putative
CC functions to be assigned so that protein-encoding or regulatory regions
CC of commercial, therapeutic or industrial importance can be obtained.
CC Specifically, sequences which are likely to encode antigens have been
CC identified and these polypeptides can be used in a vaccine composition
CC against S.aureus infection. The polypeptides can also be used in a kit
CC for the immunodetection of S.aureus in a sample. S.aureus is implicated
CC in numerous human diseases, including cellulitis, eyelid infections, food
CC poisoning, osteomyelitis, skin and surgical wound infections, scalded
CC skin syndrome, toxic shock syndrome, etc. Organisms transformed with the
CC DNA sequences can be used for recombinant production of the polypeptides.
CC The new DNA sequences (and their fragments) are useful as primers or
CC probes for isolating homologues of any of the 5191 S.aureus DNA sequences
CC contained on the computer readable medium
CC
XX
SQ Sequence 1027 AA;

Query Match 95.8%; Score 204; DB 2; Length 1027;
Best Local Similarity 97.4%; Pred. No. 7.5e-20;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ONKGNQSFEDTEKDKPKYEHGPNIIIDIDFDSVPHING 38
Db 793 ONKGNQSFEDTEKDKPKYEHGPNIIIDIDFDSVPHING 830

RESULT 11
AAR8749
ID AAR8749 standard; protein; 77 AA.
XX
AC AAR8749;
XX
DT 24-SEP-1996 (first entry)
XX
DE S. aureus fibronectin binding protein D2D3 polypeptide.
XX
KW Fibronectin binding protein; D2D3; prevention; adhesion; bacteria;
KM gram positive; extra-cellular matrix protein; in-dwelling device;
KM catheter; wound; D2D3; oral pathogen; oral cavity; J2385; NCIMB 40532.
XX
OS Staphylococcus aureus.
XX
PN MO9604380-A1.
XX
PD 15-FEB-1996.
XX
PF 28-JUL-1995; 95MO-EP003039.
XX
PR 05-AUG-1994; 94GB-00015901.
XX
PA (SMIK) SMITHKLINE BEECHAM PLC.
XX
PI Crichtley IA, Dodd I, Barnett P, Mossakowska DEI;
XX
DR WPI; 1996-129397/13.
DR N-PSDB; AAT12582.
XX
XX
PT Staphylococcus aureus fibronectin binding protein D2D3 polypeptide -
PT useful for combating infection at wound sites, surgical implants, etc.
PT and as antiladherent agent in oral hygiene.
XX
PS Claim 5; Page 26; 38pp; English.
XX
XX The present sequence is the S. aureus fibronectin binding protein
CC polypeptide D2D3, which can be used to prevent adhesion of (e.g. gram
CC positive) bacteria, to extra-cellular matrix proteins on in-dwelling

CC devices, e.g. catheters or in wounds. D2D3 can also be used to prevent
CC oral pathogens from binding to extra-cellular matrix proteins, in the
CC oral cavity. D2D3 was found to be effective at inhibiting S. aureus 8325-
CC 4, and 120 adhesion to fibronectin coated PMMA coverslips, at a min.
CC adhesion inhibitor concn. of 10 microg/mL. D2D3 was derived from the D2
CC and D3 regions of the S. aureus J2385 (NCIMB 40532) fibronectin binding
CC protein
XX
SQ Sequence 77 AA;

Query Match 93.4%; Score 199; DB 2; Length 77;
Best Local Similarity 94.7%; Pred. No. 1.6e-20;
Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 ONKGNQSFEDTEKDKPKYEHGPNIIIDIDFDSVPHING 38
Db 2 ONKGNQSFEDTEKDKPKYEHGPNIIIDIDFDSVPHING 39

RESULT 12
AAR90937
ID AAR90937 standard; peptide; 113 AA.
XX
AC AAR90937;
XX
DT 23-SEP-1996 (first entry)
XX
DE D3D4 polypeptide #1.
XX
KW Fibronectin binding protein; Fbp; S.aureus J2385; monoclonal antibody;
KM infection; surgical implant; antiladherent agent; hygiene; adhesion;
KM extracellular matrix protein; oral pathogen; oral cavity.
XX
OS Staphylococcus aureus.
XX
FH Key Location/Qualifiers
FT Region 1..21
FT /note= "D1 region fragment"
FT Region 22..59
FT /note= "D2 region"
FT Region 60..98
FT /note= "D3 region"
FT Region 99..113
FT /note= "D4 region"
FT Misc-difference 113
FT /note= "P113T"
XX
PN MO9604381-A1.
XX
PD 15-FEB-1996.
XX
PF 28-JUL-1995; 95MO-EP003040.
XX
PR 05-AUG-1994; 94GB-00015900.
XX
PA (SMIK) SMITHKLINE BEECHAM PLC.
XX
PI Crichtley IA, Dodd I, Barnett P, Mcbay DL;
XX
DR WPI; 1996-129397/13.
XX
XX
PT Polypeptide(s) derived from Staphylococcus aureus fibronectin binding
PT protein - inhibit binding of bacteria to extracellular matrix proteins,
PT for combating infection at the site of wounds and surgical implants, and
PT in oral hygiene.
XX
PS Claim 6; Page 24; 35pp; English.
XX
XX AAR90937-R90942 represent D3D4 polypeptides. These sequences correspond
CC to fragments of the Staphylococcus aureus fibronectin binding protein
CC (Fbp). This sequence corresponds to residues 18-130 of S.aureus J2385
CC Fbp, and also contains the D2 region, and a portion of the D1 region.
CC These sequences, and monoclonal antibodies against them can be used to


```

XX 15-FEB-1996.
PD
XX
XX 18-JUL-1995; 95WO-EP02825.
PF
XX
XX 05-AUG-1994; 94GB-00015902.
PR
XX
XX (SMIR ) SMITHKLINE BEECHAM PLC.
PA
XX
XX Barnett P, Critchley IA, Dodd I;
PI
XX
XX WPI; 1996-129122/13.
DR
XX
XX
XX Prevention of adherence of oral pathogens in the oral cavity, partic.
PT tooth surfaces - by application of a fibronectin binding protein or
PT polypeptide or a monoclonal antibody or fragment against it.
XX
XX
XX Claim 5; Page 32; 41pp; English.
PS
XX
XX Adherence of oral pathogens, particularly to tooth surfaces, can be
CC prevented by application of a fibronectin binding protein or polypeptide.
CC The fibronectin binding protein or polypeptide is useful in the
CC manufacture of oral hygiene compositions, eg. toothpaste, liquid
CC dentifrice, mouthwash or lozenge. They are useful to prevent the plaque-
CC related development of carious lesions, gingivitis, calculus or
CC periodontal disease and to combat oral cavity infections, eg.
CC candidiasis. They may also be useful in oral surgery e.g. in guided
CC tissue regeneration procedures to prevent subsequent bacterial infection,
CC and for irrigation of periodontal pockets. This sequence corresponds to
CC amino acids 709-838 of the D1-D4 fibronectin binding domain of
CC Staphylococcus aureus
XX
XX Sequence 130 AA;
SQ

```

```

Query Match          93.4%; Score 199; DB 2; Length 130;
Best Local Similarity 94.7%; Pred. No. 3.1e-20;
Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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```

QY 1 QNKGNSFEEDTEKDKPKYEHGPNIIDIDFDSVPHIHG 38
   |||:|||||
DB 40 QNKGDSFEEDTEKDKPKYEHGNIIDIDFDSVPHIHG 77

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Search completed: October 25, 2005, 20:21:06
 Job time : 83.8825 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 22, 2005, 03:51:22 ; Search time 21.1723 Seconds
(without alignments)
133.980 Million cell updates/sec

Title: US-10-731-238-49

Perfect score: 213
Sequence: 1 QNKGNSFEEDTEKDKPYEHGPNIDIDFDSVPHIHG 38

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA: *
1: /cgn2_6/ptodata/1/iaa/5A.COMB.pep: *
2: /cgn2_6/ptodata/1/iaa/5B.COMB.pep: *
3: /cgn2_6/ptodata/1/iaa/6A.COMB.pep: *
4: /cgn2_6/ptodata/1/iaa/6B.COMB.pep: *
5: /cgn2_6/ptodata/1/iaa/PCUS.COMB.pep: *
6: /cgn2_6/ptodata/1/iaa/backfilee1.pep: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	213	100.0	38	4	US-09-010-317-49 Sequence 49, Appl
2	204	95.8	38	1	US-08-234-622A-3 Sequence 3, Appl
3	204	95.8	38	4	US-09-010-317-7 Sequence 3, Appl
4	204	95.8	114	1	US-08-259-000-3 Sequence 7, Appl
5	204	95.8	139	3	US-08-856-253-8 Sequence 8, Appl
6	204	95.8	1027	4	US-08-956-171E-5254 Sequence 5254, Ap
7	204	95.8	1027	4	US-08-781-986A-5254 Sequence 5254, Ap
8	199	93.4	130	2	US-08-459-135A-7 Sequence 7, Appl
9	199	93.4	130	2	US-08-459-135A-8 Sequence 8, Appl
10	199	93.4	130	3	US-08-495-559-7 Sequence 7, Appl
11	199	93.4	130	3	US-08-495-559-8 Sequence 8, Appl
12	199	93.4	174	2	US-08-459-135A-10 Sequence 10, Appl
13	199	93.4	174	3	US-08-495-559-6 Sequence 6, Appl
14	199	93.4	176	3	US-08-495-559-10 Sequence 10, Appl
15	199	93.4	178	2	US-08-459-135A-12 Sequence 12, Appl
16	199	93.4	178	2	US-08-495-559-12 Sequence 12, Appl
17	199	93.4	181	1	US-08-459-135A-6 Sequence 6, Appl
18	199	93.4	38	1	US-08-729-767-4 Sequence 4, Appl
19	198	93.0	38	4	US-09-010-317-46 Sequence 46, Appl
20	198	93.0	38	4	US-09-010-317-47 Sequence 47, Appl
21	197	92.5	38	4	US-09-010-317-48 Sequence 48, Appl
22	196	92.0	38	4	US-09-010-317-8 Sequence 8, Appl
23	194	91.1	38	4	US-09-010-317-45 Sequence 45, Appl
24	193	90.6	38	4	US-09-010-317-50 Sequence 50, Appl
25	191	89.7	174	2	US-08-459-135A-13 Sequence 13, Appl
26	191	89.7	174	3	US-08-495-559-13 Sequence 13, Appl
27	191	89.7	559	4	US-08-956-171E-5251 Sequence 5251, Ap

28	191	89.7	559	4	US-08-781-986A-5251	Sequence 5251, Ap
29	187	87.8	38	4	US-09-010-317-43	Sequence 43, Appl
30	181	85.0	38	4	US-09-010-317-58	Sequence 58, Appl
31	178	83.6	38	1	US-08-234-622A-2	Sequence 2, Appl
32	178	83.6	38	4	US-09-010-317-5	Sequence 5, Appl
33	176	82.6	38	4	US-09-010-317-41	Sequence 41, Appl
34	173	81.2	38	4	US-09-010-317-59	Sequence 59, Appl
35	172	80.8	38	1	US-08-729-767-3	Sequence 3, Appl
36	172	80.8	38	4	US-09-010-317-36	Sequence 36, Appl
37	172	80.8	38	4	US-09-010-317-37	Sequence 37, Appl
38	172	80.8	38	4	US-09-010-317-39	Sequence 39, Appl
39	172	80.8	38	4	US-09-010-317-40	Sequence 40, Appl
40	171	80.3	38	4	US-09-010-317-38	Sequence 38, Appl
41	171	80.3	38	4	US-09-010-317-42	Sequence 42, Appl
42	170	79.8	38	4	US-09-010-317-6	Sequence 6, Appl
43	168	78.9	38	4	US-09-010-317-35	Sequence 35, Appl
44	167.5	78.6	39	4	US-09-010-317-56	Sequence 56, Appl
45	167	78.4	38	4	US-09-010-317-44	Sequence 44, Appl

ALIGNMENTS

RESULT 1
US-09-010-317-49
Sequence 49, Application US/09010317
Patent No. 6685943
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
APPLICANT: Patti, Joseph M.
APPLICANT: House-Pompeo, Karen L.
APPLICANT: Speziale, Pietro
APPLICANT: Jon, Danny
APPLICANT: McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
TITLE OF INVENTION: AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/010.317
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/036.139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAMK.189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-5000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 49:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-09-010-317-49
Query Match 100.0%; Score 213; DB 4; Length 38;
Best Local Similarity 100.0%; Pred. No. 2.8e-23;

Matches	38;	Conservative	0;	Mismatches	0;	Indels
Qy	1	QNKGNSFEDDEKDKPKYEHGNIIDIDFDSPVPHHG	38			
Dd	1	QNKGNSFEDDEKDKPKYEHGNIIDIDFDSPVPHHG	38			

RESULT 2
US-08-234-622A-3
Sequence 3, Application US/08234622A

1 GENERAL INFORMATION: 2
3 APPLICANT: HOOK, Magnus 4
5 APPLICANT: MCCAVIN, Martin 6
7 APPLICANT: MCGAVIN, Giuseppe 8
9 TITLE OF INVENTION: A FIBRONECTIN BINDING PEPTIDE 10
11
12 NUMBER OF SEQUENCES: 4 13
14
15 CORRESPONDENCE ADDRESS: 16
17 ADDRESSEE: Burns, Doane, Swecker & Mathis 18
19 STREET: P.O. Box 1404 20
21 CITY: Alexandria 22
23 STATE: Virginia 24
25
26 COUNTRY: United States 27
28
29 ZIP: 22313-1404 30
31
32 COMPUTER READABLE FORM: 33
34
35 MEDIUM TYPE: Floppy disk 36
37 COMPUTER: IBM PC compatible 38
39 OPERATING SYSTEM: PC-DOS/MS-DOS 40
41 SOFTWARE: Patent in Release #1.0, Version #1.30 42
43
44 CURRENT APPLICATION DATA: 45
46
47 APPLICATION NUMBER: US/08/234,622A 48
49
50 FILING DATE: 28-APR-1994 51

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1  APPLICATION NUMBER: SE 9002617-0
2  FILING DATE: 10-AUG-1990
3  PRIOR APPLICATION DATA:
4  APPLICATION NUMBER: WO PCT/SE91/00534
5  FILING DATE: 09-AUG-1991
6  ATTORNEY/AGENT INFORMATION:
7  NAME: Meuth, Donna M
8  REGISTRATION NUMBER: 36,607
9  REFERENCE/DOCKET NUMBER: 012885-044
10 TELECOMMUNICATION INFORMATION:
11 TELEPHONE: (703) 836-6620
12 TELEFAX: (703) 836-4021
13 INFORMATION FOR SEQ ID NO: 3:
14     SEQUENCE CHARACTERISTICS:
15         LENGTH: 38 amino acids
16         TYPE: amino acid
17         STRANDEDNESS: single
18         TOPOLOGY: linear
19     MOLECULE TYPE: peptide
20     US-08-234-622A-3

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Qy      1 QNKGNSGFEDTDEKDKRYEKGNIIDIDPSVPHNG 38
        |||
Db      1 QNKGNSGFEDTDEKDKRYEKGNIIDIDPSVPHNG 38
        |||
Query Match          95.88; Score 204; DB 1; Length 38
Best Local Similarity 97.48; Pred. No. 5.3e-22;
Matches 37; Conservative 0; Mismatches 1; Indels

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RESULT 3
US-09-010-317-7
; Sequence 7, Application US/09010317
; Patent No. 6685993
; GENERAL INFORMATION:
; APPLICANT: Hook, Magnus
; APPLICANT: Patti, Joseph M.
; APPLICANT: House-Pompeo, Karen L.
; APPLICANT: Speciale, Pietro

```

1 APPLICANT: Joh, Danny
2 APPLICANT: McGavin, Martin J.
3 TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
4 TITLE OF INVENTION: AND METHODS OF USE
5 NUMBER OF SEQUENCES: 105
6 CORRESPONDENCE ADDRESS:
7 ADDRESSEE: Arnold, White & Durkee
8 STREET: P.O. Box 4433
9 CITY: Houston
10 STATE: TX
11 COUNTRY: USA
12 ZIP: 77210-4433
13 COMPUTER READABLE FORM:
14 MEDIUM TYPE: Floppy disk
15 COMPUTER: IBM PC compatible
16 OPERATING SYSTEM: PC-DOS/MS-DOS
17 SOFTWARE: Patentln Release #1.0, Version #1.30
18 CURRENT APPLICATION DATA:
19 APPLICATION NUMBER: US/09/010,317
20 FILING DATE:
21 CLASSIFICATION:
22 PRIOR APPLICATION DATA:
23 APPLICATION NUMBER: US 60/036,139
24 FILING DATE: 21-JAN-1997
25 ATTORNEY/AGENT INFORMATION:
26 NAME: Hibler, David W.
27 REGISTRATION NUMBER: 41,071
28 REFERENCE/DOCKET NUMBER: TAMK:189
29 TELECOMMUNICATION INFORMATION:
30 TELEPHONE: 512-418-3000
31 TELEFAX: 512-474-7577
32 INFORMATION FOR SEQ ID NO: 7:
33 SEQUENCE CHARACTERISTICS:
34 LENGTH: 38 amino acids
35 TYPE: amino acid
36 STRANDEDNESS:
37 TOPOLOGY: linear
38 US-09-010-317-7
39
40 Query Match 95.8%; Score 204; DB 4; Length 38;
41 Best Local Similarity 97.4%; Pred. No. 5.3e-22;
42 Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
43
44 QY 1 ONKGNOSFEEDTEKDKPKYREHPNIIIDPDSVPHNG 38
45 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
46 Db 1 ONKGNOSFEEDTEKDKPKYREHGNIIIDPDSVPHNG 38
47
48 RESULT 4
49 US-08-259-000-3
50 Sequence 3, Application US/08259000
51 Patent No. 5571514
52 GENERAL INFORMATION:
53 APPLICANT: HOOK, Magnus
54 APPLICANT: LINDBERG, Martin Kjell
55 APPLICANT: SIGNAS, Lars Christer
56 APPLICANT: WADSTROM, Torkei Mikael
57 TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN AS WELL AS
58 TITLE OF INVENTION: ITS PREPARATION
59 NUMBER OF SEQUENCES: 4
60 CORRESPONDENCE ADDRESS:
61 ADDRESSEE: Burns, Doane, Swecker & Mathis
62 STREET: P.O. Box 1404
63 CITY: Alexandria
64 STATE: Virginia
65 COUNTRY: United States
66 ZIP: 22313-1404
67 COMPUTER READABLE FORM:
68 MEDIUM TYPE: Floppy disk
69 COMPUTER: IBM PC compatible
70 OPERATING SYSTEM: PC-DOS/MS-DOS
71 SOFTWARE: Patentln Release #1.0, Version #1.25
72

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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/259,000
FILING DATE: 13-JUN-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: SE 8702272-9
FILING DATE: 01-JUN-1987
ATTORNEY/AGENT INFORMATION:
NAME: Meuth, Donna M
REGISTRATION NUMBER: 36,607
REFERENCE/DOCKET NUMBER: 012885-062
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 114 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-259-000-3

Query Match 95.8%; Score 204; DB 1; Length 114;
Best Local Similarity 97.4%; Pred. No. 2e-21;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QNKGNSFEEDTEKDKPKYEHGPNIIIDPDSVPHHG 38
DB 40 QNKGNSFEEDTEKDKPKYEHGNIIDPDSVPHHG 77

RESULT 5
US-08-856-253-8
Sequence 8, Application US/08856253
Patent No. 6288214
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
APPLICANT: Patti, Joseph M.
APPLICANT: House-Pompeo, Karen
APPLICANT: Stanham, Narayana
APPLICANT: Symersky, Jindrich
TITLE OF INVENTION: COLLAGEN BINDING PROTEIN COMPOSITIONS
TITLE OF INVENTION: AND METHODS OF USE
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: Texas
COUNTRY: U.S.
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/856,253
FILING DATE: Concurrently Herewith
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/017,678
FILING DATE: 16-MAY-1996
ATTORNEY/AGENT INFORMATION:
NAME: Kitchell, Barbara S.
REGISTRATION NUMBER: 33,928
REFERENCE/DOCKET NUMBER: TANK:193
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
TELEFAX: (512) 474-7577
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:

LENGTH: 139 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-08-856-253-8

Query Match 95.8%; Score 204; DB 3; Length 139;
Best Local Similarity 97.4%; Pred. No. 2.6e-21;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QNKGNSFEEDTEKDKPKYEHGPNIIIDPDSVPHHG 38
DB 54 QNKGNSFEEDTEKDKPKYEHGNIIDPDSVPHHG 91

RESULT 6
US-08-956-171E-5254
Sequence 5254, Application US/08956171E
Patent No. 6593114
GENERAL INFORMATION:
APPLICANT: Charles Kunsch
Gil H. Choi
Patrick S. Dillon
Craig A. Rosen
Steven C. Barash
Michael R. Fannon
TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
NUMBER OF SEQUENCES: 5256
CORRESPONDENCE ADDRESS:
ADDRESSSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COUNTRY: USA
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/956,171E
FILING DATE: 20-Oct-1997
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/009,861
FILING DATE: January 5, 1996
APPLICATION NUMBER: 08/781,986
FILING DATE: January 3, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Mark J. Hyman
REGISTRATION NUMBER: 46,789
REFERENCE/DOCKET NUMBER: PB248P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (240) 314-1224
TELEFAX: (301) 309-8439
INFORMATION FOR SEQ ID NO: 5254:
SEQUENCE CHARACTERISTICS:
LENGTH: 1027 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 5254:
US-08-956-171E-5254

Query Match 95.8%; Score 204; DB 4; Length 1027;
Best Local Similarity 97.4%; Pred. No. 3e-20;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QNKGNSFEEDTEKDKPKYEHGPNIIIDPDSVPHHG 38
DB 793 QNKGNSFEEDTEKDKPKYEHGNIIDPDSVPHHG 830


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RESULT 7
US-08-781-986A-5254
; Sequence 5254, Application US/08781986A
; Patent No. 6737248
; GENERAL INFORMATION:
; APPLICANT: Charles Kunsch
; TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
; NUMBER OF SEQUENCES: 5255
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4MB storage
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/781,986A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Benson, Bob
; REGISTRATION NUMBER: 30,446
; REFERENCE/DOCKET NUMBER: PB248PP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 5254:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1027 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-781-986A-5254

Query Match          95.8%; Score 204; DB 4; Length 1027;
Best Local Similarity 97.4%; Pred. No. 3e-20;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 QNKGNSFEEDTEKDKPKYEHGNIIDIDPDSVPHHG 38
DB      793 QNKGNSFEEDTEKDKPKYEHGNIIDIDPDSVPHHG 830

RESULT 8
US-08-459-135A-7
; Sequence 7, Application US/08459135A
; Patent No. 5955078
; GENERAL INFORMATION:
; APPLICANT: BURHAM, Martin Karl Russel
; APPLICANT: CRITCHLEY, Ian Alfred
; APPLICANT: KNOWLES, David Justin Charles
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN: MONOCLONAL ANTIBODY AND THEIR US
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corporation
; STREET: 709 Swedeland Road
; CITY: King of Prussia
; STATE: PA
; COUNTRY: U.S.A.
; ZIP: 19406-0939
; COMPUTER READABLE FORM:
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; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: Fastseq, Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/459,135A
; FILING DATE: 02-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB/94/00215
; FILING DATE: 04-Feb-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Glimmi, Edward R
; REGISTRATION NUMBER: 38,891
; REFERENCE/DOCKET NUMBER: P30591C2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-270-4478
; TELEFAX: 610-270-5090
; TELEX:
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 130 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-459-135A-7

Query Match          93.4%; Score 199; DB 2; Length 130;
Best Local Similarity 94.7%; Pred. No. 1.2e-20;
Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1 QNKGNSFEEDTEKDKPKYEHGNIIDIDPDSVPHHG 38
DB      40 QNKGNSFEEDTEKDKPKYEHGNIIDIDPDSVPHHG 77

RESULT 9
US-08-459-135A-8
; Sequence 8, Application US/08459135A
; Patent No. 5955078
; GENERAL INFORMATION:
; APPLICANT: BURHAM, Martin Karl Russel
; APPLICANT: CRITCHLEY, Ian Alfred
; APPLICANT: KNOWLES, David Justin Charles
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN: MONOCLONAL ANTIBODY AND THEIR US
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corporation
; STREET: 709 Swedeland Road
; CITY: King of Prussia
; STATE: PA
; COUNTRY: U.S.A.
; ZIP: 19406-0939
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: Fastseq, Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/459,135A
; FILING DATE: 02-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB/94/00215
; FILING DATE: 04-Feb-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Glimmi, Edward R
; REGISTRATION NUMBER: 38,891
; REFERENCE/DOCKET NUMBER: P30591C2
; TELECOMMUNICATION INFORMATION:
```

TELEPHONE: 610-270-4478
TELEFAX: 610-270-5090
TELEX:
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 130 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-459-135A-8

Query Match 93.4%; Score 199; DB 2; Length 130;
Best Local Similarity 94.7%; Pred. No. 1.2e-20;
Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 QNKGNSFEEDTEKDKPKYEHGPNIIIDPDSVPHNG 38
DB 40 QNKGDSFEEDTEKDKPKYEHGNIIDIDPDSVPHNG 77

RESULT 10
US-08-495-559-7
Sequence 7, Application US/08495559A
Patent No. 6054572

GENERAL INFORMATION:
APPLICANT: BURHAM, Martin Karl Russel
APPLICANT: CHOPRA, Ian
APPLICANT: CRITCHLEY, Ian Alfred
APPLICANT: KNOWLES, David Justin Charles
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN: MONOCLONAL
TITLE OF INVENTION: ANTIBODY AND THEIR USE IN PREVENTING BACTERIAL ADHESION
FILE REFERENCE: P30591
CURRENT APPLICATION NUMBER: US/08/495,559A
CURRENT FILING DATE: 1995-08-03
EARLIER APPLICATION NUMBER: GB 9302289.5
EARLIER FILING DATE: 1993-02-05
EARLIER APPLICATION NUMBER: GB 9321592.9
EARLIER FILING DATE: 1993-10-20
NUMBER OF SEQ ID NOS: 13
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 7
LENGTH: 130
TYPE: PRT
ORGANISM: Staphylococcus aureus
US-08-495-559-7

Query Match 93.4%; Score 199; DB 3; Length 130;
Best Local Similarity 94.7%; Pred. No. 1.2e-20;
Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 QNKGNSFEEDTEKDKPKYEHGPNIIIDPDSVPHNG 38
DB 40 QNKGDSFEEDTEKDKPKYEHGNIIDIDPDSVPHNG 77

RESULT 11
US-08-495-559-8
Sequence 8, Application US/08495559A
Patent No. 6054572

GENERAL INFORMATION:
APPLICANT: BURHAM, Martin Karl Russel
APPLICANT: CHOPRA, Ian
APPLICANT: CRITCHLEY, Ian Alfred
APPLICANT: KNOWLES, David Justin Charles
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN: MONOCLONAL
TITLE OF INVENTION: ANTIBODY AND THEIR USE IN PREVENTING BACTERIAL ADHESION
FILE REFERENCE: P30591
CURRENT APPLICATION NUMBER: US/08/495,559A
CURRENT FILING DATE: 1995-08-03
EARLIER APPLICATION NUMBER: GB 9302289.5
EARLIER FILING DATE: 1993-02-05
EARLIER APPLICATION NUMBER: GB 9321592.9
EARLIER FILING DATE: 1993-10-20

NUMBER OF SEQ ID NOS: 13
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 8
LENGTH: 130
TYPE: PRT
ORGANISM: Staphylococcus aureus
US-08-495-559-8

Query Match 93.4%; Score 199; DB 3; Length 130;
Best Local Similarity 94.7%; Pred. No. 1.2e-20;
Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 QNKGNSFEEDTEKDKPKYEHGPNIIIDPDSVPHNG 38
DB 40 QNKGDSFEEDTEKDKPKYEHGNIIDIDPDSVPHNG 77

RESULT 12
US-08-459-135A-10

Sequence 10, Application US/08459135A
Patent No. 5955078
GENERAL INFORMATION:
APPLICANT: BURHAM, Martin Karl Russel
APPLICANT: CHOPRA, Ian
APPLICANT: CRITCHLEY, Ian Alfred
APPLICANT: KNOWLES, David Justin Charles
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN: MONOCLONAL ANTIBODY AND THEIR USE
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
STATE: PA
COUNTRY: U.S.A.
ZIP: 19406-0939
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: Fastseq, Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/459,135A
FILING DATE: 02-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB/94/00215
FILING DATE: 04-Feb-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Gilmml, Edward R
REGISTRATION NUMBER: 38,891
REFERENCE/DOCKET NUMBER: P30591C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-4478
TELEFAX: 610-270-5090
TELEX:
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 174 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: Protein
US-08-459-135A-10

Query Match 93.4%; Score 199; DB 2; Length 174;
Best Local Similarity 94.7%; Pred. No. 1.7e-20;
Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 QNKGNSFEEDTEKDKPKYEHGPNIIIDPDSVPHNG 38
DB 40 QNKGDSFEEDTEKDKPKYEHGNIIDIDPDSVPHNG 77

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RESULT 13
US-08-495-559-10
; Sequence 10, Application US/08495559A
; Patent No. 6054572
; GENERAL INFORMATION:
; APPLICANT: BURHAM, Martin Karl Russel
; APPLICANT: CHOPRA, Ian
; APPLICANT: CRITCHLEY, Ian Alfred
; APPLICANT: KNOWLES, David Justin Charles
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN: MONOCLONAL
; FILE REFERENCE: P30591
; CURRENT APPLICATION NUMBER: US/08/495,559A
; EARLIER FILING DATE: 1995-08-03
; EARLIER APPLICATION NUMBER: GB 9302289.5
; EARLIER FILING DATE: 1993-02-05
; EARLIER APPLICATION NUMBER: GB 931592.9
; EARLIER FILING DATE: 1993-10-20
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 10
; LENGTH: 174
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-08-495-559-10

Query Match          93.4%; Score 199; DB 3; Length 174;
Best Local Similarity 94.7%; Pred. No. 1.7e-20;
Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1 QNKGNSFEEDTEKDKPKYEHGPNIIDIDFDSVPHING 38
DB      40 QNKGDSFEEDTEKDKPKYEHGNIIDIDFDSVPHING 77

RESULT 14
US-08-495-559-6
; Sequence 6, Application US/08495559A
; Patent No. 6054572
; GENERAL INFORMATION:
; APPLICANT: BURHAM, Martin Karl Russel
; APPLICANT: CHOPRA, Ian
; APPLICANT: CRITCHLEY, Ian Alfred
; APPLICANT: KNOWLES, David Justin Charles
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN: MONOCLONAL
; FILE REFERENCE: P30591
; CURRENT APPLICATION NUMBER: US/08/495,559A
; EARLIER FILING DATE: 1995-08-03
; EARLIER APPLICATION NUMBER: GB 9302289.5
; EARLIER FILING DATE: 1993-02-05
; EARLIER APPLICATION NUMBER: GB 931592.9
; EARLIER FILING DATE: 1993-10-20
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 176
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-08-495-559-6

Query Match          93.4%; Score 199; DB 3; Length 176;
Best Local Similarity 94.7%; Pred. No. 1.8e-20;
Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1 QNKGNSFEEDTEKDKPKYEHGPNIIDIDFDSVPHING 38
DB      40 QNKGDSFEEDTEKDKPKYEHGNIIDIDFDSVPHING 77

RESULT 15
US-08-459-135A-12
; Sequence 12, Application US/08459135A
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; Patent No. 5955078
; GENERAL INFORMATION:
; APPLICANT: BURHAM, Martin Karl Russel
; APPLICANT: CHOPRA, Ian
; APPLICANT: CRITCHLEY, Ian Alfred
; APPLICANT: KNOWLES, David Justin Charles
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN: MONOCLONAL ANTIBODY AND THEIR US
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corporation
; STREET: 709 Swedeland Road
; CITY: King of Prussia
; STATE: PA
; COUNTRY: U.S.A.
; ZIP: 19406-0939
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: Fastseq, Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/459,135A
; FILING DATE: 02-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB/94/00215
; FILING DATE: 04-Feb-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Gimm1, Edward R
; REGISTRATION NUMBER: 38, 891
; REFERENCE/DOCKET NUMBER: P30591C2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-270-4478
; TELEFAX: 610-270-5090
; TELEX:
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 178 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Protein
US-08-459-135A-12

Query Match          93.4%; Score 199; DB 2; Length 178;
Best Local Similarity 94.7%; Pred. No. 1.8e-20;
Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1 QNKGNSFEEDTEKDKPKYEHGPNIIDIDFDSVPHING 38
DB      40 QNKGDSFEEDTEKDKPKYEHGNIIDIDFDSVPHING 77
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Search completed: October 22, 2005, 05:46:47
Job time : 21.2223 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 22, 2005, 11:35:03 ; Search time 70.1256 Seconds
(without alignments)
226.232 Million cell updates/sec

Title: US-10-731-238-49

Perfect score: 213

Sequence: 1 QNKGNSFEEDTEKDKRYEHGNIIDIDPDSVPHIHG 38

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1862951 seqs, 417491010 residues

Total number of hits satisfying chosen parameters: 1862951

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :
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3: /cgn2_6/prodata/2/pubpaa/US06_NEW_PUB.pep.*
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5: /cgn2_6/prodata/2/pubpaa/US07_NEW_PUB.pep.*
6: /cgn2_6/prodata/2/pubpaa/PCTUS_PUBCOMB.pep.*
7: /cgn2_6/prodata/2/pubpaa/US08_NEW_PUB.pep.*
8: /cgn2_6/prodata/2/pubpaa/US08_PUBCOMB.pep.*
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11: /cgn2_6/prodata/2/pubpaa/US09C_PUBCOMB.pep.*
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19: /cgn2_6/prodata/2/pubpaa/US11A_PUBCOMB.pep.*
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22: /cgn2_6/prodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	213	100.0	38	18	US-10-731-238-49
2	204	95.8	38	18	US-10-731-238-7
3	204	95.8	139	9	US-09-813-820-8
4	204	95.8	1018	9	US-09-815-242-5797
5	204	95.8	1018	9	US-09-815-242-12838
6	204	95.8	1018	17	US-10-470-0488-68
7	204	95.8	1027	8	US-08-781-986A-5254
8	204	95.8	1027	15	US-10-329-624-5254
9	198	93.0	38	18	US-10-731-238-46
10	198	93.0	38	18	US-10-731-238-47
11	197	92.5	38	18	US-10-731-238-48

12	196	92.0	38	18	US-10-731-238-8	Sequence 8, Appl1
13	194	91.1	38	18	US-10-731-238-45	Sequence 45, Appl1
14	193	90.6	38	18	US-10-731-238-50	Sequence 50, Appl1
15	191	89.7	388	8	US-08-901-062-1	Sequence 1, Appl1
16	191	89.7	559	8	US-08-781-986A-5251	Sequence 5251, Ap
17	191	89.7	559	15	US-10-329-624-5251	Sequence 5251, Ap
18	191	89.7	767	9	US-09-815-242-5899	Sequence 5899, Ap
19	191	89.7	767	9	US-09-815-242-13140	Sequence 13140, A
20	191	89.7	940	17	US-10-470-048B-424	Sequence 424, App
21	191	89.7	948	17	US-10-470-048B-69	Sequence 69, Appl
22	191	89.7	1038	15	US-10-282-122A-43827	Sequence 43827, A
23	187	87.8	38	18	US-10-731-238-43	Sequence 43, Appl
24	183	85.9	978	9	US-09-815-242-5456	Sequence 5456, Ap
25	183	85.9	1001	9	US-09-815-242-12686	Sequence 12686, A
26	181	85.0	36	18	US-10-731-238-58	Sequence 58, Appl
27	179	84.0	961	15	US-10-282-122A-43778	Sequence 43778, A
28	178	83.6	38	18	US-10-731-238-5	Sequence 5, Appl1
29	176	82.6	38	18	US-10-731-238-41	Sequence 41, Appl1
30	173	81.2	36	18	US-10-731-238-59	Sequence 59, Appl1
31	172	80.8	38	18	US-10-731-238-36	Sequence 36, Appl1
32	172	80.8	38	18	US-10-731-238-37	Sequence 37, Appl1
33	172	80.8	38	18	US-10-731-238-39	Sequence 39, Appl1
34	172	80.8	38	18	US-10-731-238-40	Sequence 40, Appl1
35	171	80.3	38	18	US-10-731-238-34	Sequence 34, Appl1
36	171	80.3	38	18	US-10-731-238-42	Sequence 42, Appl1
37	170	79.8	38	18	US-10-731-238-35	Sequence 35, Appl1
38	168	78.9	38	18	US-10-731-238-3	Sequence 3, Appl1
39	167.5	78.6	39	18	US-10-731-238-56	Sequence 56, Appl1
40	167	78.4	38	18	US-10-731-238-44	Sequence 44, Appl1
41	159.5	74.9	39	18	US-10-731-238-57	Sequence 57, Appl1
42	138	64.8	30	14	US-10-287-821-1	Sequence 1, Appl1
43	138	64.8	31	14	US-10-287-821-2	Sequence 2, Appl1
44	83.5	39.2	37	20	US-11-066-697-1134	Sequence 1134, Ap
45	72	33.8	14	18	US-10-731-238-105	Sequence 105, App

ALIGNMENTS

RESULT 1
US-10-731-238-49
Sequence 49, Application US/10731238
Publication No. US20050123552A1
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
Pattl, Joseph M.
House-Pompeo, Karen L.
Speziale, Pietro
John, Danny
McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/731,238
FILING DATE: 10-Dec-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE: 21-Jan-1998
APPLICATION NUMBER: US 60/036,139

FILED DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAMK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 49:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 49:
US-10-731-238-49

Query Match 100.0%; Score 213; DB 18; Length 38;
Best Local Similarity 100.0%; Pred. No. 9, 7e-21;
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QNKGNSFEEDTEKDKPKYEHGPNIIIDIDFDSVPHIHG 38
Db 1 QNKGNSFEEDTEKDKPKYEHGPNIIIDIDFDSVPHIHG 38

RESULT 2
US-10-731-238-7
Sequence 7, Application US/10731238
Publication No. US20050123552A1
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
Patti, Joseph M.
House-Pompeo, Karen L.
Speziale, Pietro
John, Danny
McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/731,238
FILING DATE: 10-Dec-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE: 21-Jan-1998
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAMK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>

TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-10-731-238-7

Query Match 95.8%; Score 204; DB 18; Length 38;
Best Local Similarity 97.4%; Pred. No. 1, 5e-19;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QNKGNSFEEDTEKDKPKYEHGPNIIIDIDFDSVPHIHG 38
Db 1 QNKGNSFEEDTEKDKPKYEHGPNIIIDIDFDSVPHIHG 38

RESULT 3
US-09-813-820-8
Sequence 8, Application US/09813820
Patent No. US20020102262A1
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
Patti, Joseph M.
House-Pompeo, Karen
Stanam, Narayana
Symersky, Jindrich
TITLE OF INVENTION: COLLAGEN BINDING PROTEIN COMPOSITIONS
AND METHODS OF USE
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: Texas
COUNTRY: U.S.
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/813,820
FILING DATE: 22-Mar-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/856,253
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Kitchell, Barbara S.
REGISTRATION NUMBER: 33,928
REFERENCE/DOCKET NUMBER: TAMK:193
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-1000
TELEFAX: (512) 474-7577
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 139 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-09-813-820-8

Query Match 95.8%; Score 204; DB 9; Length 139;
Best Local Similarity 97.4%; Pred. No. 6, 8e-19;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QNKGNSFEEDTEKDKPKYEHGPNIIIDIDFDSVPHIHG 38
Db 54 QNKGNSFEEDTEKDKPKYEHGPNIIIDIDFDSVPHIHG 91

RESULT 4
US-09-815-242-5797
Sequence 5797, Application US/09815242

```
Patent No. US20020061569A1
GENERAL INFORMATION:
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Karl L.
APPLICANT: Zyskind, Judith W.
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John D.
APPLICANT: Carr, Grant J.
APPLICANT: Yamamoto, Robert T.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in
FILE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 5797
LENGTH: 1018
TYPE: PRT
ORGANISM: Staphylococcus aureus
US-09-815-242-5797
```

```
Query Match          95.8%; Score 204; DB 9; Length 1018;
Best Local Similarity 97.4%; Pred. No. 6,9e-18;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      1 QNKGNSFEEDTEKDKPKYEHGPNIIIDFDSVPHHG 38
DB      784 QNKGNSFEEDTEKDKPKYEHGPNIIIDFDSVPHHG 821
```

```
RESULT 5
US-09-815-242-12838
Sequence 12838, Application US/09815242
```

```
GENERAL INFORMATION:
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Karl L.
APPLICANT: Zyskind, Judith W.
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John D.
APPLICANT: Carr, Grant J.
APPLICANT: Yamamoto, Robert T.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in
FILE REFERENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
```

```
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 12838
LENGTH: 1018
TYPE: PRT
ORGANISM: Staphylococcus aureus
US-09-815-242-12838
```

```
Query Match          95.8%; Score 204; DB 9; Length 1018;
Best Local Similarity 97.4%; Pred. No. 6,9e-18;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      1 QNKGNSFEEDTEKDKPKYEHGPNIIIDFDSVPHHG 38
DB      784 QNKGNSFEEDTEKDKPKYEHGPNIIIDFDSVPHHG 821
```

```
RESULT 6
US-10-470-048B-68
Sequence 68, Application US/10470048B
Publication No. US2005003744A1
GENERAL INFORMATION:
APPLICANT: MEINKE ET AL.
TITLE OF INVENTION: A METHOD FOR IDENTIFICATION, ISOLATION AND PRODUCTION OF
FILE REFERENCE: SONN.035US
CURRENT APPLICATION NUMBER: US/10/470,048B
CURRENT FILING DATE: 2003-07-25
NUMBER OF SEQ ID NOS: 603
SOFTWARE: PatentIn version 3.1
SEQ ID NO 68
LENGTH: 1018
TYPE: PRT
ORGANISM: Staphylococcus aureus
US-10-470-048B-68
```

```
Query Match          95.8%; Score 204; DB 17; Length 1018;
Best Local Similarity 97.4%; Pred. No. 6,9e-18;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      1 QNKGNSFEEDTEKDKPKYEHGPNIIIDFDSVPHHG 38
DB      784 QNKGNSFEEDTEKDKPKYEHGPNIIIDFDSVPHHG 821
```

```
RESULT 7
US-08-781-986A-5254
Sequence 5254, Application US/08781986A
Publication No. US20030054436A1
GENERAL INFORMATION:
APPLICANT: Charles Kunsch
TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
NUMBER OF SEQUENCES: 5255
CORRESPONDENCE ADDRESS:
ADDRESSER: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COUNTRY: USA
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/781,986A
FILING DATE:
```

CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Benson, Bob
REGISTRATION NUMBER: 30,446
REFERENCE/DOCKET NUMBER: PB248PP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 5254:
SEQUENCE CHARACTERISTICS:
LENGTH: 1027 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-781-986A-5254

Query Match 95.8%; Score 204; DB 8; Length 1027;
Best Local Similarity 97.4%; Pred. No. 7e-18;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QNKGNSFEEDTEKDKPKYEHGPNIIDIDFDSVPHIHG 38
DB 793 QNKGNSFEEDTEKDKPKYEHGPNIIDIDFDSVPHIHG 830

RESULT 8
US-10-329-624-5254
Sequence 5254, Application US/10329624
Publication No. US20040043037A1
GENERAL INFORMATION:
APPLICANT: Charles Kunsch
Gil H. Choi
Patrick S. Dillon
Craig A. Rosen
Steven C. Barash
Michael R. Fannon
TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
NUMBER OF SEQUENCES: 5256
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COUNTRY: USA
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/329,624
FILING DATE: 27-Dec-2002
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/956,171
FILING DATE: October 20, 1997
APPLICATION NUMBER: 60/009,861
FILING DATE: January 5, 1996
APPLICATION NUMBER: 08/781,986
FILING DATE: January 3, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Mark J. Hyman
REGISTRATION NUMBER: 46,789
REFERENCE/DOCKET NUMBER: PB248P1D1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (240) 314-1224
TELEFAX: (301) 309-8439
INFORMATION FOR SEQ ID NO: 5254:
SEQUENCE CHARACTERISTICS:

LENGTH: 1027 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 5254:
US-10-329-624-5254

Query Match 95.8%; Score 204; DB 15; Length 1027;
Best Local Similarity 97.4%; Pred. No. 7e-18; 1; Indels 0; Gaps 0;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QNKGNSFEEDTEKDKPKYEHGPNIIDIDFDSVPHIHG 38
DB 793 QNKGNSFEEDTEKDKPKYEHGPNIIDIDFDSVPHIHG 830

RESULT 9
US-10-731-238-46
Sequence 46, Application US/10731238
Publication No. US20050123552A1
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
Pacifi, Joseph M.
House-Pompeo, Karen L.
Speziale, Pietro
Job, Danny
McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/731,238
FILING DATE: 10-Dec-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE: 21-Jan-1998
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-Jan-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAMK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 46:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 46:
US-10-731-238-46

Query Match 93.0%; Score 198; DB 18; Length 38;
Best Local Similarity 94.7%; Pred. No. 9.3e-19;
Matches 36; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 QNKGNSFEEDTEKDKPKYEHGPNIIDIDFDSVPHIHG 38

Db 1 QNKGNSFPEDTEKDKPKYEHGNIIDIDFDSVPHIHG 38

RESULT 10
US-10-731-238-47
Sequence 47, Application US/10731238
Publication No. US20050123552A1

GENERAL INFORMATION:

APPLICANT: Hook, Magnus

Patl, Joseph M.

House-Pompeo, Karen L.

Speziale, Pietro

John, Danny

McGavin, Martin J.

TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
AND METHODS OF USE

NUMBER OF SEQUENCES: 105

CORRESPONDENCE ADDRESSES:

ADDRESSEE: Arnold, White & Durkee

STREET: P.O. Box 4433

CITY: Houston

STATE: TX

COUNTRY: USA

ZIP: 77210-4433

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/731.238

FILING DATE: 10-Dec-2003

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/010.317

FILING DATE: 21-Jan-1998

APPLICATION NUMBER: US 60/036.139

FILING DATE: 21-JAN-1997

ATTORNEY/AGENT INFORMATION:

NAME: Hblier, David W.

REGISTRATION NUMBER: 41,071

REFERENCE/DOCKET NUMBER: TANK:189

TELECOMMUNICATION INFORMATION:

TELEPHONE: 512-418-3000

TELEFAX: 512-474-7577

INFORMATION FOR SEQ ID NO: 47:

SEQUENCE CHARACTERISTICS:

LENGTH: 38 amino acids

TYPE: amino acid

STRANDEDNESS: <Unknown>

TOPOLOGY: linear

SEQUENCE DESCRIPTION: SEQ ID NO: 47:

US-10-731-238-47

Query Match 93.0%; Score 198; DB 18; Length 38;

Best Local Similarity 94.7%; Pred. No. 9.3e-19;

Matches 36; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Db 1 QNKGNSFPEDTEKDKPKYEHGNIIDIDFDSVPHIHG 38

RESULT 11
US-10-731-238-48
Sequence 48, Application US/10731238
Publication No. US20050123552A1

GENERAL INFORMATION:

APPLICANT: Hook, Magnus

Patl, Joseph M.

House-Pompeo, Karen L.

Speziale, Pietro

John, Danny
McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
AND METHODS OF USE

NUMBER OF SEQUENCES: 105

CORRESPONDENCE ADDRESSES:

ADDRESSEE: Arnold, White & Durkee

STREET: P.O. Box 4433

CITY: Houston

STATE: TX

COUNTRY: USA

ZIP: 77210-4433

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/731.238

FILING DATE: 10-Dec-2003

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/010.317

FILING DATE: 21-Jan-1998

APPLICATION NUMBER: US 60/036.139

FILING DATE: 21-JAN-1997

ATTORNEY/AGENT INFORMATION:

NAME: Hblier, David W.

REGISTRATION NUMBER: 41,071

REFERENCE/DOCKET NUMBER: TANK:189

TELECOMMUNICATION INFORMATION:

TELEPHONE: 512-418-3000

TELEFAX: 512-474-7577

INFORMATION FOR SEQ ID NO: 48:

SEQUENCE CHARACTERISTICS:

LENGTH: 38 amino acids

TYPE: amino acid

STRANDEDNESS: <Unknown>

TOPOLOGY: linear

SEQUENCE DESCRIPTION: SEQ ID NO: 48:

US-10-731-238-48

Query Match 92.5%; Score 197; DB 18; Length 38;

Best Local Similarity 94.7%; Pred. No. 1.3e-18;

Matches 36; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Db 1 QNKGNSFPEDTEKDKPKYEHGNIIDIDFDSVPHIHG 38

RESULT 12
US-10-731-238-8
Sequence 8, Application US/10731238
Publication No. US20050123552A1

GENERAL INFORMATION:

APPLICANT: Hook, Magnus

Patl, Joseph M.

House-Pompeo, Karen L.

Speziale, Pietro

John, Danny

McGavin, Martin J.

TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
AND METHODS OF USE

NUMBER OF SEQUENCES: 105

CORRESPONDENCE ADDRESSES:

ADDRESSEE: Arnold, White & Durkee

STREET: P.O. Box 4433

CITY: Houston

STATE: TX

COUNTRY: USA

ZIP: 77210-4433

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/731,238
FILING DATE: 10-Dec-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE: 21-Jan-1998
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAMK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-10-731-238-8
Query Match 92.0%; Score 196; DB 18; Length 38;
Best Local Similarity 94.7%; Pred. No. 1,7e-18;
Matches 36; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 ONKGNQFEEDTEKDKPKYEHGPNIIDIDPDSVPHNG 38
1 ONKGNQFEEDTEKDKPKYEHGPNIIDIDPDSVPHNG 38
DB 1 ONKGNQFEEDTEKDKPKYEHGPNIIDIDPDSVPHNG 38
RESULT 13
US-10-731-238-45
Sequence 45, Application US/10731238
Publication No. US20050123552A1
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
Patti, Joseph M.
House-Pompeo, Karen L.
Speziale, Pietro
McGavin, Martin J.
John, Danny
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/731,238
FILING DATE: 10-Dec-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE: 21-Jan-1998
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997

ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAMK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 45:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 45:
US-10-731-238-45
Query Match 91.1%; Score 194; DB 18; Length 38;
Best Local Similarity 94.7%; Pred. No. 3.1e-18;
Matches 36; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 ONKGNQFEEDTEKDKPKYEHGPNIIDIDPDSVPHNG 38
1 ONKGNQFEEDTEKDKPKYEHGPNIIDIDPDSVPHNG 38
DB 1 ONKGNQFEEDTEKDKPKYEHGPNIIDIDPDSVPHNG 38
RESULT 14
US-10-731-238-50
Sequence 50, Application US/10731238
Publication No. US20050123552A1
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
Patti, Joseph M.
House-Pompeo, Karen L.
Speziale, Pietro
McGavin, Martin J.
John, Danny
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/731,238
FILING DATE: 10-Dec-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE: 21-Jan-1998
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAMK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 50:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear

SEQUENCE DESCRIPTION: SEQ ID NO: 50:
US-10-731-238-50

Query Match 90.6%; Score 193; DB 18; Length 38;
Best Local Similarity 92.1%; Pred. No. 4.2e-18;
Matches 35; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 QNKGNSFEEDTEKDKPKYEHGPNIIIDIDPDSVPHIHG 38
Db 1 QNKGNSFPPTDEKDKPKYEHGPNIIIDIDPDSVPHIHG 38

RESULT 15
US-08-901-062-1
Sequence 1, Application US/08901062
Publication No. US20020025324A1
GENERAL INFORMATION:
APPLICANT: SEALS, JONATHAN R.
TITLE OF INVENTION: RECOMBINANT BIVALENT BACTERIAL VACCINE
TITLE OF INVENTION: FOR THE PREVENTION OF MASTITIS
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: HALE AND DORR LLP
STREET: 60 State Street
CITY: Boston
STATE: MA
COUNTRY: United States Of America
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/901,062
FILING DATE: 25-JUL-1997
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Baker, Hollie L.
REGISTRATION NUMBER: 31,321
REFERENCE/DOCKET NUMBER: 106941.153
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 526-6000
TELEFAX: (617) 526-5000
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 388 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-901-062-1

Query Match 89.7%; Score 191; DB 8; Length 388;
Best Local Similarity 92.1%; Pred. No. 1.2e-16;
Matches 35; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 QNKGNSFEEDTEKDKPKYEHGPNIIIDIDPDSVPHIHG 38
Db 303 QNKGNSFEEDTEKDKPKYEHGPNIIIDIDPDSVPHIHG 340

Search completed: October 22, 2005, 12:09:29
Job time : 70.1256 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 22, 2005, 04:14:19 ; Search time 13.8905 Seconds
(without alignments)
263.219 Million cell updates/sec

Title: US-10-731-238-49

Perfect score: 213

Sequence: 1 QNKGNSFEEDTEKDKPKYEHGPNIIDIDFDSVPHIHG 38

Scoring table: BLOSUM62

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database: PIR_79:*

1: p1r1:*

2: p1r2:*

3: p1r3:*

4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Length	DB ID	Description
1	204	95.8	1018 2 A32192	fibronectin-binding
2	191	89.7	940 2 S19702	fibronectin-binding
3	191	89.7	1038 2 H90053	hypothetical prote
4	179	84.0	961 2 G90053	hypothetical prote
5	63	29.6	511 1 S31308	aldehyde dehydroge
6	59.5	27.9	214 2 A69895	hypothetical prote
7	58.5	27.5	582 2 I48673	matrix metalloprot
8	58.5	27.5	582 2 I38028	matrix metalloprot
9	57	26.8	591 2 C84220	propionyl-CoA carb
10	57	26.8	821 2 T16412	hypothetical prote
11	56	26.3	669 2 I18029	matrix metalloprot
12	55.5	26.1	582 2 I84471	probable coiled-co
13	55.5	26.1	1115 2 T41342	hypothetical prote
14	55	25.8	345 2 T33906	hypothetical prote
15	55	25.8	1185 2 I18009	gene BRCC5 protein
16	55	25.8	1186 2 S35993	DNA repair protein
17	54	25.4	264 2 C87605	hypothetical prote
18	54	25.4	284 2 S67062	hypothetical prote
19	54	25.4	427 2 S38002	hypothetical prote
20	54	25.4	811 1 A40083	transcription fact
21	52.5	24.6	571 2 H69704	protein-export mem
22	52.5	24.6	1169 2 H70178	exodeoxyribonuclea
23	52	24.4	175 2 A84323	50S ribosomal prot
24	52	24.4	218 2 A35232	ribulose-phosphate
25	52	24.4	218 2 C98096	ribulose-phosphate
26	52	24.4	391 1 S15617	E2 protein - human
27	52	24.4	790 2 T47959	hypothetical prote
28	52	24.4	920 2 T18852	hypothetical prote
29	52	24.4	2647 2 T28161	hypothetical prote

30	51.5	24.2	155 1 RNBR6	DNA-directed RNA p
31	51.5	24.2	309 2 H72626	probable 2-oxoacid
32	51.5	24.2	2013 2 A11489	probable peptidogl
33	51	23.9	426 2 T51670	myb-related transc
34	51	23.9	294 2 D81434	probable 4-hydroxy
35	51	23.9	470 2 D86848	hypothetical prote
36	51	23.9	533 2 A39410	aldehyde dehydroge
37	51	23.9	658 2 F85024	probable CHP-rich
38	51	23.9	720 1 A48723	replication licens
39	51	23.9	979 2 S62469	probable transcrip
40	50.5	23.7	208 2 S34238	leukotoxin A - Pae
41	50.5	23.7	305 2 D97169	uncharacterized pr
42	50.5	23.7	384 2 A10556	conserved hypotet
43	50.5	23.7	754 2 A11627	protein-export mem
44	50.5	23.7	955 1 A35254	leukotoxin A - Pae
45	50.5	23.7	1226 2 S44824	F5472.1 protein -

ALIGNMENTS

RESULT 1

A32192
fibronectin-binding protein - Staphylococcus aureus

C/Species: Staphylococcus aureus

C/Date: 31-Jul-1989 #sequence_revision 31-Jul-1989 #text_change 16-Feb-1997

C/Accession: A32192

R/Signaes, C.; Raucet, G.; Joensson, K.; Lindgren, P.E.; Anantharamaiah, G.M.; Hoeoek, Proc. Natl. Acad. Sci. U.S.A. 86, 699-703, 1989

A/Title: Nucleotide sequence of the gene for a fibronectin-binding protein from Staphy1

A/Reference number: A32192; PMID:8908998; PMID:2521391

A/Accession: A32192

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-1018 <SIG>

A/Cross-references: GB:J04151

C/Keywords: fibronectin binding

Query Match 95.8%; Score 204; DB 2; Length 1018;

Best Local Similarity 97.4%; Pred. No. 1,4e-18;

Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QNKGNSFEEDTEKDKPKYEHGPNIIDIDFDSVPHIHG 38

DB 784 QNKGNSFEEDTEKDKPKYEHGPNIIDIDFDSVPHIHG 821

RESULT 2

S19702
fibronectin-binding protein B - Staphylococcus aureus

C/Species: Staphylococcus aureus

C/Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004

C/Accession: S19702

R/Joensson, K.; Signaes, C.; Mueller, H.P.; Lindberg, M. Eur. J. Biochem. 202, 1041-1048, 1991

A/Title: Two different genes encode fibronectin binding proteins in Staphylococcus aure

A/Reference number: S19702; PMID:9211475; PMID:1857286

A/Accession: S19702

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-940 <JOB>

A/Cross-references: UNIPROT:Q53682; EMBL:X62992; NID:949040; PIDD:CAA44726.1; PID:95815

C/Keywords: fibronectin binding

Query Match 89.7%; Score 191; DB 2; Length 940;

Best Local Similarity 92.1%; Pred. No. 6.3e-17;

Matches 35; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 QNKGNSFEEDTEKDKPKYEHGPNIIDIDFDSVPHIHG 38

DB 720 QNKGNSFEEDTEKDKPKYEGGNIIDIDFDSVPHIHG 757

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RESULT 3
H90053
hypothetical protein fmb [imported] - Staphylococcus aureus (strain N315)
C:Species: Staphylococcus aureus
C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C:Accession: H90053
R:Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguc
ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.;
C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiratake, K.
Lancet 357, 1225-1240, 2001
A:Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.
A:Reference number: AB9758; MUID:21311952; PMID:11418146
A:Accession: H90053
A:Status: Preliminary
A:Molecule type: DNA
A:Cross-references: UNIPROT:Q99RD2; GB:BA000018; PID:g13702453; PIDN:BA843594.1; GSPDB:G
A:Experimental source: strain N315
A:Genetics: fmb

Query Match      89.7%; Score 191; DB 2; Length 1038;
Best Local Similarity 92.1%; Pred. No. 7,18-17;
Matches 35; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Oy      1 QNKGNSFEEDTEKDKPKYEHGPNIIIDIDPDSVPHIHG 38
||||:||||:||||:||||:||||:||||:||||:||||:
Db      780 QNKGDSFEEDTEKDKPKYEHGNNIIDIDPDSVPQIHG 817

RESULT 4
G90053
hypothetical protein fmb [imported] - Staphylococcus aureus (strain N315)
C:Species: Staphylococcus aureus
C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C:Accession: G90053
R:Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguc
ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.;
C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiratake, K.
Lancet 357, 1225-1240, 2001
A:Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.
A:Reference number: AB9758; MUID:21311952; PMID:11418146
A:Accession: G90053
A:Status: Preliminary
A:Molecule type: DNA
A:Residues: 1-961 <KUR>
A:Cross-references: UNIPROT:Q99RD3; GB:BA000018; PID:g13702452; PIDN:BA843593.1; GSPDB:G
A:Experimental source: strain N315
A:Genetics: fmb

Query Match      84.0%; Score 179; DB 2; Length 961;
Best Local Similarity 86.8%; Pred. No. 2,56-15;
Matches 33; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Oy      1 QNKGNSFEEDTEKDKPKYEHGPNIIIDIDPDSVPHIHG 38
||||:||||:||||:||||:||||:||||:||||:||||:
Db      731 QNKGNSFEEDTEKDKPKYEGNNIIDIDPDSVPQIHG 768

RESULT 5
S31308
aldenup dehydrogenase (NAD) (BC 1.2.1.3) 2 precursor, mitochondrial - Yeast (Saccharomy
C:Species: Saccharomyces cerevisiae
C:Date: 28-May-1993 #sequence_revision 31-Jan-1997 #text_change 09-Jul-2004
C:Accession: S31308
R:Thielen, J.
submitted to the EMBL Data Library, October 1992
A:Reference number: S31308
A:Accession: S31308
A:Molecule type: DNA
A:Residues: 1-511 <THI>
A:Cross-references: UNIPROT:P32872; EMBL:Z17214; NID:g3361; PIDN:CAA78962.1; PID:g3362

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C:Comment: This form is probably mitochondrial.
C:Genetics:
A:Gene: ALD2
A:Description: catalyzes the oxidation of an aldehyde to an acid using NAD+ and water
A:Function:
A:Note: enzymes with this activity are involved in diverse metabolic pathways in various
C:Superfamily: NAD-dependent aldehyde dehydrogenase; aldehyde dehydrogenase homology
C:Keywords: alcohol metabolism; mitochondrion; NAD: oxidoreductase
F:1-21/Domain: transit peptide (mitochondrion) #status predicted <TNP>
F:12-511/Product: aldehyde dehydrogenase (NAD+) 2 #status predicted <MAR>
F:80-351/Domain: aldehyde dehydrogenase homology <ALD2>
F:297-331/Active site: Glu, Cys #status predicted
F:483/Binding site: NAD (Cys) #status predicted

Query Match      29.6%; Score 63; DB 1; Length 511;
Best Local Similarity 42.4%; Pred. No. 2.2;
Matches 14; Conservative 5; Mismatches 6; Indels 8; Gaps 2;

Oy      4 GNQSFEDTEKDKPKYEHGPNIIIDPDSVPHI 36
Db      361 GN-PFESDT-----RVSQILKIEFDSIRPL 365

RESULT 6
A89895
hypothetical protein cfxe (imported) - Staphylococcus aureus (strain N315)
C:Species: Staphylococcus aureus
C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C:Accession: A89895
A:Reference: 1-214 <KUR>
A:Reference number: A89895; MUID:21311952; PMID:11418146
A:Accession: A89895
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-214 <KUR>
A:Cross-references: UNIPROT:Q99UP6; GB:BA000018; PID:G13701022; PIDN:BAB42317.1; GSPDB:G
A:Experimental source: strain N315
C:Genetics:
A:Gene: cfxe
C:Superfamily: yeast ribulose-5-phosphate-epimerase

Query Match      27.9%; Score 59.5; DB 2; Length 214;
Best Local Similarity 44.8%; Pred. No. 2.3;
Matches 13; Conservative 5; Mismatches 10; Indels 1; Gaps 1;

Oy      10 EDTEDKPKY-EHGPNIIDPDSVPHI 37
Db      69 ENPEKYIASFAEHGADMISIHVESTPHIH 97

RESULT 7
I48673
matrix metalloproteinase (EC 3.4.24.-) membrane type precursor - mouse
C:Species: Mus musculus (house mouse)
C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 22-Jun-1999
C:Accession: I48673
R:Okada, A.; Belluco, J.P.; Rouyer, N.; Chenard, M.P.; Rio, M.C.; Chambon, P.; Basset, F.
Proc. Natl. Acad. Sci. U.S.A. 92, 2730-2734, 1995
A>Title: Membrane-type matrix metalloproteinase (MT-MMP) gene is expressed in stromal cells
A:Reference number: I38046; MUID:95224014; PMID:7708715
A:Accession: I48673
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-582 <RES>
A:Cross-references: EMBL:X83316; NID:G804999; PIDN:CA58520.1; PID:G805000
C:Superfamily: interstitial collagenase; hemopexin repeat homology; matrix metalloproteinase
C:Keywords: hydrolase; metalloproteinase; zinc; zymogen
F:1-33/Domain: signal sequence #status predicted <SIG>
F:24-97/Domain: activation peptide #status predicted <PRO>

```

F.61-284/Domain: matrix metalloproteinase homology <MMP>
F.313-508/Domain: hemopexin repeat homology <EPN>
F.239,239,243,249/Binding site: zinc, catalytic (Cys, His, His, His) (inhibited) #status
F.239,243,249/Binding site: zinc, catalytic (His) (active) #status predicted
F.240/Active site: Glu #status predicted

Query Match 27.5%; Score 58.5; DB 2; Length 582;
Best Local Similarity 52.0%; Pred. No. 10;
Matches 13; Conservative 4; Mismatches 7; Indels 1; Gaps 1;

QY 15 DKPKY-EHGPNIIDFDSVPHIHG 38
DB 307 DKPKNPATGPNICDGNFTVAMLRG 331

RESULT 8
138028
Matrix metalloproteinase 14 (EC 3.4.24.-) membrane type precursor - human
N:Alternate names: matrix metalloproteinase MMP14; membrane type matrix metalloproteinase
C:Species: Homo sapiens (man)
C>Date: 17-May-1996 #sequence_revision 17-May-1996 #text_change 09-Jul-2004
C:Accession: 138028; G02274; I38046; S78011; S45341; S71384
R:Will, H.; Hinzmann, B.
Eur. J. Biochem. 231, 602-608, 1995
A:Title: cDNA sequence and mRNA tissue distribution of a novel human matrix metalloproc
A:Reference number: I38028; MUID:95377289; PMID:7649159
A:Accession: 138028
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1582 <WILL>
A:Cross-references: UNIPROT:P50281; EMBL:Z48481; NID:G963053; PIDN:CAA88372.1; PID:G9630
R: Luo, G.
submitted to the EMBL Data Library, November 1995
A:Reference number: H00963
A:Accession: G02274
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1582 <LUO>
A:Cross-references: EMBL:U41078; NID:G1127836; PIDN:AAA83770.1; PID:G1127837
R: Okada, A.; Bellocq, J.P.; Rouyer, N.; Chenard, M.P.; Rlo, M.C.; Chambon, P.; Bassec, F
Proc. Natl. Acad. Sci. U.S.A. 92, 2730-2734, 1995
A:Title: Membrane-type matrix metalloproteinase (MT-MMP) gene is expressed in stromal ce
A:Reference number: I38046; MUID:95224014; PMID:7708715
A:Accession: 138046
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 17, 'S', '9-582 <OKA>
A:Cross-references: EMBL:X83535; NID:G804993; PIDN:CAA58519.1; PID:G804994
R: Seiki, M.
submitted to the EMBL Data Library, January 1994
A:Reference number: S78011
A:Accession: S78011
A:Molecule type: mRNA
A:Residues: 1-7, 'S', '9-337, 'K', '339-582 <SEI>
A:Cross-references: EMBL:D6512; NID:G9793762; PIDN:BA05519.1; PID:G9793763
R: Sato, H.; Takino, T.; Okada, Y.; Cao, J.; Shinagawa, A.; Yamamoto, E.; Seiki, M.
Nature 370, 61-65, 1994
A:Title: A matrix metalloproteinase expressed on the surface of invasive tumour cells.
A:Reference number: S45341; MUID:94286011; PMID:8015608
A:Accession: S45341
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-7, 'S', '9-188, 'R', '190, 'A', '192-267, 'K', '269-272, 'HY', '275, 'P', '277-285, 'KQ', '288,
R: Sato, H.; Kinoshita, T.; Takino, T.; Nakayama, K.; Seiki, M.
FEBS Lett. 393, 101-104, 1996
A:Title: Activation of a recombinant membrane type 1-matrix metalloproteinase (MT1-MMP)
A:Reference number: S71384; MUID:96397540; PMID:8804434
A:Accession: S71384
A:Molecule type: protein
A:Residues: 112-116 <SAW>
C:Genetics:
A:Gene: GDB:MMP14; MT1-MMP

A:Cross-references: GDB:375731; OMIM:600754
A:Map position: 14q11-14q12
C:Superfamily: interstitial collagenase; hemopexin repeat homology: matrix metalloprotei
C:Keywords: glycoprotein; hydrolase; metalloproteinase; zinc; zymogen
F.1-23/Domain: signal sequence #status predicted <SIG>
F.1-24-97/Domain: activation peptide #status predicted <PRO>
F.61-284/Domain: matrix metalloproteinase homology <MMP>
F.61-582/Product: matrix metalloproteinase 14 membrane type #status predicted <MAT>
F.285-313/Domain: hinge #status predicted <HNC>
F.314-508/Domain: hemopexin repeat homology <EPN>
F.539-562/Domain: transmembrane #status predicted <TM>
F.239,239,243,249/Binding site: zinc, catalytic (Cys, His, His, His) (inhibited) #status
F.239,243,249/Binding site: carbonyl (Asn) (covalent) #status predicted
F.239,243,249/Binding site: zinc, catalytic (His) (active) #status predicted
F.240/Active site: Glu #status predicted
F.319-508/Disulfide bonds: #status predicted

Query Match 27.5%; Score 58.5; DB 2; Length 582;
Best Local Similarity 52.0%; Pred. No. 10;
Matches 13; Conservative 4; Mismatches 7; Indels 1; Gaps 1;

QY 15 DKPKY-EHGPNIIDFDSVPHIHG 38
DB 307 DKPKNPATGPNICDGNFTVAMLRG 331

RESULT 9
C84220
propionyl-CoA carboxylase homology [imported] - Halobacterium sp. NRC-1
C:Species: Halobacterium sp. NRC-1
C>Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
C:Accession: C84220
R:Ng, W.V.; Kennedy, S.P.; Mahataas, G.G.; Berquiat, B.; Pan, M.; Shukla, H.D.; Lasky,
J.; Leitbauer, B.; Keller, K.; Cruz, R.; Dawson, M.J.; Hough, D.W.; Maddocks, D.G.; Jabl
Jung, K.H.; Alam, M.; Fretz, T.
Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000
A:Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ebhardt, H.; Lowe, T.M.; L
A:Title: Genome sequence of Halobacterium species NRC-1.
A:Reference number: A84160; MUID:20504483; PMID:11016950
A:Accession: C84220
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1591 <STO>
A:Cross-references: UNIPROT:Q9HRN1; GB:AE004437; NID:G10580213; PIDN:AA619127.1; GSPDB:
C:Genetics:
A:Gene: yngE
C:Superfamily: propionyl-CoA carboxylase beta chain

Query Match 26.8%; Score 57; DB 2; Length 591;
Best Local Similarity 62.5%; Pred. No. 16;
Matches 10; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 7 SPEEDTEKDKPKYEHG 22
DB 573 SPEEDTEKDKPKYEHG 588

RESULT 10
T16412
hypothetical protein F48B.4 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C:Accession: T16412
R: Kirsten, J.
submitted to the EMBL Data Library, March 1995
A:Description: The sequence of C. elegans cosmid F48B.
A:Reference number: S59413
A:Accession: T16412
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-821 <KIR>
A:Cross-references: UNIPROT:Q09396; EMBL:U23514; NID:G746484; PID:G746491; PIDN:AA64654
A:Experimental source: strain Bristol N2

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C:Genetics:
A:Gene: CESP:F4EB8.4
A:Introns: 98/3; 150/1; 207/3; 342/1; 377/3; 406/2; 493/2; 589/3; 647/2; 680/3; 776/1

Query Match          26.8%; Score 57; DB 2; Length 821;
Best Local Similarity 43.3%; Pred. No. 23;
Matches 13; Conservative 2; Mismatches 9; Indels 6; Gaps 1;

OY      2 NKGNQSFE-----EDTEKDKPKYEKGPNIT 25
       : ||| | | | | | | | | | | | | | |
DB      81 SKGGQKFACSLPVEDVVKDCKPKSKKNPKI 110

RESULT 11
138029
matrix metalloproteinase 15 (EC 3.4.24.-) membrane type precursor - human
N/Alternate names: membrane-type matrix metalloproteinase 2 (MT2MMP); MMP15
C/Species: Homo sapiens (man)
C/Date: 17-May-1996 #sequence_revision 17-May-1996 #text_change 09-Jul-2004
C/Acession: I38029; GI00041
R/Will, H.; Hinzmann, B.
Eur. J. Biochem. 231, 602-608, 1995
A>Title: CDNA sequence and mRNA tissue distribution of a novel human matrix metalloprote
A:Reference number: I38028; MUID:95377289; PMID:7649159
C/Acession: I38029
A>Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: mRNA
A:Residues: 1-669 <WIL>
A:Cross-references: UNIPROT:P51511; EMBL:Z48482; NID:g963055; PIDN:CAA8373.1; PID:g96310
R/Setkl, M.
Submitted to GenBank, July 1996
A:Reference number: H00041
C/Acession: G00041
A>Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: mRNA
A:Residues: 106-608, 'R', 610-669 <SEI>
A:Cross-references: GB:D86331; NID:g1418214; PIDN:BAA13071.1; PID:g1418215
C:Genetics:
A:Gene: GDB:MMP15; MT2-MMP
A:Cross-references: GDB:642246
C:Superfamily: intersitial collagenase; hemopexin repeat homology; matrix metalloprotein
C:Keywords: glycoprotein; hydrolase; metalloproteinase; zinc; zymogen
F:1-41/Domain: signal sequence #status predicted <SIG>
F:42-125/Domain: activation peptide #status predicted <ACT>
F:179-304/Domain: matrix metalloproteinase homology <MMP>
F:133-669/Product: matrix metalloproteinase 15 #status predicted <MAT>
F:364-559/Domain: hemopexin repeat homology <PXN>
F:624-644/Domain: transmembrane #status predicted <TRM>
F:111,259,263,269/Binding site: zinc, catalytic (Cys, His, His, His) (inhibited) #status
F:150/Binding site: carbohydrate (Asn) (covalent) #status predicted
F:259,263,269/Binding site: zinc, catalytic (His) (active) #status predicted
F:260/Active site: Glu #status predicted

Query Match          26.3%; Score 56; DB 2; Length 669;
Best Local Similarity 52.6%; Pred. No. 25;
Matches 10; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

OY      20 EHGPNIIDPDSPVHIHG 38
       ::||| | | | | | | | | | |
DB     364 QYGPNICDGDPTVAMLRG 382

RESULT 12
184471
matrix metalloproteinase (EC 3.4.24.-) membrane type precursor - rat
N/Alternate names: membrane-type metalloproteinase
C/Species: Rattus norvegicus (Norway rat)
C/Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C/Acession: I84471; I61946
R/Okada, A.; Bellocq, J.P.; Rouyer, N.; Chenard, M.P.; Rio, M.C.; Chambon, P.; Bassett, F.
Proc. Natl. Acad. Sci. U.S.A. 92, 2730-2734, 1995
A>Title: Membrane-type matrix metalloproteinase (MT-MMP) gene is expressed in stromal ce
A:Reference number: I38046; MUID:95224014; PMID:7708715
```

```

A.Accession: I84471
A.Status: preliminary; translated from GB/EMBL/DDBJ
A.Molecule type: mRNA
A.Residues: 1-562 <RES>
A.Cross-references: UNIPROT:Q10739, EMBL:X83537, NID:g805012, PIDN:CAA58521.1; PID:g8050
A.Accession: I61946
A.Status: preliminary; translated from GB/EMBL/DDBJ
A.Molecule type: mRNA
A.Residues: 1-67,'M','69'-254,'A','256'-582 <RE2>
A.Cross-references: EMBL:X91785, NID:g1001926; PIDN:CAA62897.1; PID:g1001927
C.Genetics:
A.Gene: mt-mmp
C.Superfamily: interstitial collagenase, hemopexin repeat homology; matrix metalloprotein
C.Keywords: hydrolase; metalloprotease; zinc; zymogen
P.1-33/Dominant: signal sequence #status predicted <SIG>
F.124-97/Dominant: activation peptide #status predicted <PRO>
F.61-284/Dominant: matrix metalloproteinase homology <mmp>
F.313-508/Dominant: hemopexin repeat homology <PNX>
F.93_239_243_249/Binding site: zinc, catalytic (CyE, His, His, His) (Inhibited) #status
F.239_243_249/Binding site: zinc, catalytic (His) (active) #status predicted
F.240/Active site: Glu #status predicted

Query Match          26.1%; Score 55.5; DB 2; Length 582;
Best Local Similarity 48.0%; Pred. No. 25;
Matches      12; Conservative     5; Mismatches    7; Indels       1; Gaps        1;

CY         15 DKPKY-EHGPNITDIDFDVSYPHIIG 38
           ||||| :|||| |::| ::| 
Db          307 DKRNPVTPGPNICDGNFDTVMALRG 331

RESULT 13
T11342
probable coiled-coil protein - fission yeast (Schizosaccharomyces pombe)
C.Species: Schizosaccharomyces pombe
C.Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C.Accession: T41342
R.Lytle, M., Rajandream, M.A.; Barrell, B.G.; Vojtkoert, G.
submitted to the EMBL Data Library, January 1999
A.Reference number: Z21970
A.Accession: T41342
A.Status: preliminary; translated from GB/EMBL/DDBJ
A.Molecule type: DNA
A.Residues: 1-115 <LYN>
A.Cross-references: UNIPROT:O94486; EMBL:AL035076; PIDN:CAA22653.1; GSPPDB:GN00066; SPDB
A.Experimental source: strain 972n-; cosmid c417
C.Genetics:
A.Gene: SPD:BSPCC417.07c
A.Map position: 1

Query Match          26.1%; Score 55.5; DB 2; Length 115;
Best Local Similarity 32.5%; Pred. No. 53;
Matches      13; Conservative     6; Mismatches   16; Indels       5; Gaps        1;

CY         2 NKGNQSFEEDTEKDKPRKH-----GPNIIDIDPDVPPI 36
           |:|:|||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db          144 NGFSOSQEYEDSYNNVDYTSDPSSENYISSLDQLPHL 183

RESULT 14
T33906
hypothetical protein Y25CIA.8 - Caenorhabditis elegans
C.Species: Caenorhabditis elegans
C.Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
C.Accession: T33906
R.Kalicki, J., Smith, A.; Gibson, A.
submitted to the EMBL Data Library, February 1999
A.Description: The sequence of C. elegans comid Y25CIA.
A.Reference number: Z21437
A.Accession: T33906
A.Status: preliminary; translated from GB/EMBL/DDBJ
A.Molecule type: DNA
A.Residues: 1-345 <PAL>
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Comugen Ltd.

OM protein - protein search, using sw model

Run on: October 22, 2005, 04:10:49 ; Search time 69.6361 Seconds
(without alignments)
279.439 Million cell updates/sec

Title: US-10-731-238-49

Perfect score: 213
Sequence: 1 QNKGNSFEEDTEKDKPKYEHGPNITIDIPDSVPHIIG 38

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: UniProt_03:*
1: uniProt_sprot:*
2: uniProt_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	204	95.8	1018	1 FNBA_STNAU	P14738 staphylococ
2	199	93.4	943	2 Q8NUU8	Q8NUU8 staphylococ
3	199	93.4	957	2 Q6G6H4	Q6G6H4 staphylococ
4	196	92.0	152	2 Q9AEP9	Q9AEP9 staphylococ
5	191	89.7	940	2 Q53682	Q53682 staphylococ
6	191	89.7	1038	2 Q99RP2	Q99RP2 staphylococ
7	191	89.7	1038	2 Q7A3J7	Q7A3J7 staphylococ
8	183	85.9	1015	2 Q8NUU7	Q8NUU7 staphylococ
9	183	85.9	1015	2 Q6G6H3	Q6G6H3 staphylococ
10	179	84.0	961	2 Q99RD3	Q99RD3 staphylococ
11	179	84.0	961	2 Q7A3J8	Q7A3J8 staphylococ
12	179	84.0	965	2 Q6GDU5	Q6GDU5 staphylococ
13	179	84.0	965	2 Q6GDU5	Q6GDU5 staphylococ
14	179	84.0	965	2 Q6GDU5	Q6GDU5 staphylococ
15	179	84.0	965	2 Q6GDU5	Q6GDU5 staphylococ
16	179	84.0	965	2 Q6GDU5	Q6GDU5 staphylococ
17	179	84.0	965	2 Q6GDU5	Q6GDU5 staphylococ
18	179	84.0	965	2 Q6GDU5	Q6GDU5 staphylococ
19	179	84.0	965	2 Q6GDU5	Q6GDU5 staphylococ
20	179	84.0	965	2 Q6GDU5	Q6GDU5 staphylococ
21	179	84.0	965	2 Q6GDU5	Q6GDU5 staphylococ
22	179	84.0	965	2 Q6GDU5	Q6GDU5 staphylococ
23	179	84.0	965	2 Q6GDU5	Q6GDU5 staphylococ
24	179	84.0	965	2 Q6GDU5	Q6GDU5 staphylococ
25	179	84.0	965	2 Q6GDU5	Q6GDU5 staphylococ
26	179	84.0	965	2 Q6GDU5	Q6GDU5 staphylococ
27	179	84.0	965	2 Q6GDU5	Q6GDU5 staphylococ
28	179	84.0	965	2 Q6GDU5	Q6GDU5 staphylococ
29	179	84.0	965	2 Q6GDU5	Q6GDU5 staphylococ
30	179	84.0	965	2 Q6GDU5	Q6GDU5 staphylococ
31	179	84.0	965	2 Q6GDU5	Q6GDU5 staphylococ

32	58.5	27.5	582	1 MM14 MOUSE	P53690 mus musculu
33	58.5	27.5	582	2 Q9GUE4	Q9GUE4 bos taurus
34	58.5	27.5	582	2 Q9XEP0	Q9XEP0 capra hircu
35	58.5	27.5	582	2 Q6DRU5	Q6DRU5 mus musculu
36	58.5	27.5	582	2 Q6BRTX2	Q6BRTX2 mus musculu
37	58.5	27.5	582	2 CC48 CAPAN	Q6BRTX2 mus musculu
38	57.5	27.0	307	2 Q7RE71	Q7RE71 plasmodium
39	57.5	27.0	307	2 Q6BWH6	Q6BWH6 debaryomyc
40	57.5	27.0	307	2 Q6DDJ3	Q6DDJ3 xenopus lae
41	57.5	27.0	307	2 Q6BWH6	Q6BWH6 debaryomyc
42	57.5	27.0	307	2 Q6BWH6	Q6BWH6 debaryomyc
43	57.5	27.0	307	2 Q6BWH6	Q6BWH6 debaryomyc
44	57.5	27.0	307	2 Q6BWH6	Q6BWH6 debaryomyc
45	57.5	27.0	307	2 Q6BWH6	Q6BWH6 debaryomyc

ALIGNMENTS

RESULT 1
FNBA_STNAU STANDARD; PRT; 1018 AA.
ID FNBA_STNAU
AC P14738;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Fibronectin-binding protein precursor (FNBP).
GN Name=fnba;
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1280;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NCTC 8325-4;
RX MEDLINE=8909898; PubMed=2521391;
RA Signaes C., Raucsi G., Joensen K., Lindgren P.-E.,
RA Anantharamiah G.M., Hoeck M., Lindberg M.;
RT "Nucleotide sequence of the gene for a fibronectin-binding protein
from Staphylococcus aureus: use of this peptide sequence in the
synthesis of biologically active peptides."
Proc. Natl. Acad. Sci. U.S.A. 86:699-703(1989).
CC -!- FUNCTION: The ability of bacteria to bind fibronectin has been
proposed as a virulence factor enabling bacteria to colonize wound
tissues and blood clots. Binding of plasma fibronectin to the
bacterial surface might block adhesion receptors on S.aureus, thus
representing an important defense mechanism against tissue
invasion.
CC -!- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
an amide bond (Potential).
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See <http://www.ebi.ac.uk/announcements>)
or send an email to license@ebi.ac.uk.
CC EMBL: J04151; AAA26632.1; -!
DR InterPro: IPR004237; Fn_bind.
DR InterPro: IPR005877; Gpos_XSIRK.
DR InterPro: IPR001893; Gram_pos_anchor.
DR Pfam: PF00746; Gram_pos_anchor; 1.
DR Pfam: PF04650; XSIRK_signal; 1.
DR TIGRPFAMs: TIGR01167; LPXTG_anchor; 1.
DR TIGRPFAMs: TIGR01168; XSIRK_signal; 1.
DR PROSITE: PS00847; GRAM_POS_ANCHORING; 1.
KW Cell adhesion; Cell wall; Peptidoglycan-anchor; Repeat; Signal;
KW Virulence.
FT CHAIN 37 985 Fibronectin-binding protein.
FT PROPEP 986 1018 Removed by sortase (Potential).
FT

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FT REPEAT 545 574 B-1.
FT REPEAT 575 604 B-2.
FT DOMAIN 745 878 4 X approximate tandem repeats,
  fibronectin-binding domain.
FT REPEAT 745 782 D-1.
FT REPEAT 783 820 D-2.
FT REPEAT 821 859 D-3.
FT REPEAT 860 878 D-4 (incomplete).
FT DOMAIN 879 948 5 X tandem repeats, Pro-rich (WR).
FT REPEAT 879 892 WR 1.
FT REPEAT 893 905 WR 2.
FT REPEAT 907 920 WR 3.
FT REPEAT 921 934 WR 4.
FT REPEAT 935 948 WR 5.
FT SITE 982 986 LPTXG sorting signal (potential).
FT MOT_RES 985 985 Pentaglycyl murein peptidoglycan amidated
  threonine (Potential).
SQ SEQUENCE 1018 AA; 111780 MW; 58175E020E81F1F CRC64;

Query Match 95.8%; Score 204; DB 1; Length 1018;
Best Local Similarity 97.4%; Pred. No. 6.5e-17;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 ONKGNOSFEEDTEKDKPKYEHGPNIIIDIDFDSVPHIHG 38
DB 784 ONKGNOSFEEDTEKDKPKYEHGNIIDIDFDSVPHIHG 821

RESULT 2
O8NU08 PRELIMINARY; PRT; 943 AA.
AC O8NU08;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE FnBb protein.
GN Name=fnbB; OrderedLocustNames=MW2420;
OS Staphylococcus aureus (strain MW2).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
NC NCB1_TaxID=196620;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=MW2;
RA MEDLINE=22040717; PubMed=12044378; DOI=10.1016/S0140-6736(02)08713-5;
RA Baba T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Oguchi A.,
RA Nagai Y., Iwama N., Amano K., Naito T., Kuroda H., Cui L.,
RA Yamamoto K., Hiramatsu K.;
RT "Genome and virulence determinants of high virulence community-
  acquired MRSA";
RL Lancet 359:1819-1827(2002).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
  an amide bond (By similarity).
DR EMBL; AP004830; BAB96285.1; -;
DR HSSP; O53653; 1N67.
DR GO; GO:0009886; C:cell surface; IEA.
DR GO; GO:0005618; C:cell wall; IEA.
DR GO; GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0007155; P:cell adhesion; IEA.
DR InterPro; IPR008966; Adhes bact.
DR InterPro; IPR004237; Fn_bind.
DR InterPro; IPR005877; Gpos_YsIRK.
DR InterPro; IPR001899; Gram_pos_anchor.
DR Pfam; PF02986; Fn_bind.1.
DR Pfam; PF00746; Gram_pos_anchor.1.
DR TIGRfam; TIGR01167; LPTXG_anchor.1.
DR TIGRfam; TIGR01168; YsIRK_signal.1.
DR PROSITE; PS50847; GRAM_POS_ANCHORING; 1.
DR Cell wall; Complete proteome; Peptidoglycan-anchor.
KW SEQUENCE 943 AA; 104537 MW; DA8A5F31947E1B6A CRC64;

Query Match 93.4%; Score 199; DB 2; Length 943;

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Best Local Similarity 94.7%; Pred. No. 2.6e-16;
Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 ONKGNOSFEEDTEKDKPKYEHGPNIIIDIDFDSVPHIHG 38
DB 727 ONKGNOSFEEDTEKDKPKYEHGNIIDIDFDSVPHIHG 764

RESULT 3
O6G6H4 PRELIMINARY; PRT; 957 AA.
AC O6G6H4;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Fibronectin-binding protein.
GN Name=fnbB; OrderedLocustNames=SAS2387;
OS Staphylococcus aureus (strain MSSA476).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
NC NCB1_TaxID=282459;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=15213324; DOI=10.1073/pnas.0402521101;
RA Holden M.T.G., Fell B.J., Lindsay J.A., Peacock S.J., Day N.P.J.,
RA Enright M.C., Foster T.J., Moore C.E., Hurst L., Atkin R., Barron A.,
RA Bason N., Bentley S.D., Chillingworth C., Chillingworth T.,
RA Churcher C., Clark L., Corton C., Cronin A., Doggett J., Dowd L.,
RA Felwell T., Hance Z., Harris B., Hauser H., Holtroyd S., Jagels K.,
RA James K.D., Lennard N., Line A., Mayes R., Moule S., Mungall K.,
RA Ormond D., Quail M.A., Rabinowitch E., Rutherford K.M., Sanders M.,
RA Sharp S., Simmonds M., Stevens K., Whitehead S., Barrell B.G.,
RA Spratt B.G., Parkhill J.;
RT "Complete genomes of two clinical Staphylococcus aureus strains:
  evidence for the rapid evolution of virulence and drug resistance.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:9786-9791(2004).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
  an amide bond (By similarity).
DR EMBL; BX571857; CAG44201.1; -;
DR GO; GO:0009886; C:cell surface; IEA.
DR GO; GO:0005618; C:cell wall; IEA.
DR GO; GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0007155; P:cell adhesion; IEA.
DR InterPro; IPR008966; Adhes bact.
DR InterPro; IPR004237; Fn_bind.
DR InterPro; IPR005877; Gpos_YsIRK.
DR InterPro; IPR001899; Gram_pos_anchor.
DR Pfam; PF02986; Fn_bind.1.
DR Pfam; PF00746; Gram_pos_anchor.1.
DR TIGRfam; TIGR01167; LPTXG_anchor.1.
DR TIGRfam; TIGR01168; YsIRK_signal.1.
DR PROSITE; PS50847; GRAM_POS_ANCHORING; 1.
DR Cell wall; Complete proteome; Peptidoglycan-anchor.
KW SEQUENCE 957 AA; 105980 MW; 28F8BA7FFDFD3EAF CRC64;

Query Match 93.4%; Score 199; DB 2; Length 957;
Best Local Similarity 94.7%; Pred. No. 2.6e-16;
Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 ONKGNOSFEEDTEKDKPKYEHGPNIIIDIDFDSVPHIHG 38
DB 727 ONKGNOSFEEDTEKDKPKYEHGNIIDIDFDSVPHIHG 764

RESULT 4
O9AEP9 PRELIMINARY; PRT; 152 AA.
AC O9AEP9;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Fibronectin-binding protein (Fragment).

```

GN Name=fnb;
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1280;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CMRSA-1;
RX MEDLINE=21246681; PubMed=11349044;
RA DOI=10.1128/IAI.69.6.3791-3799.2001;
RT "Rice K., Huesca M., Vaz D., McGavin M.J.;
RT "variance in fibronectin binding and fnb locus polymorphisms in
RT Staphylococcus aureus: identification of antigenic variation in a
RT methicillin-resistant S. aureus.";
DR Infect. Immun. 69:3791-3799(2001).
EMBL; AY029184; AAK31588.1; -.
FT NON_TER 1 152
SQ SEQUENCE 152 AA; 17193 MW; CFA3913C2B11C025 CRC64;

Query Match 92.0%; Score 196; DB 2; Length 152;
Best Local Similarity 94.7%; Pred. No. 8.2e-17;
Matches 36; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 QNKGNSFEEDTEKDKPKYEHGPNIIIDPDSVPHNG 38
Db 77 QNKGNSFEEDTEKDKPKYEHGPNIIIDPDSVPHNG 114

RESULT 5
O53682
ID O53682 PRELIMINARY; PRT; 940 AA.
AC O53682;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE Fibronectin binding protein B.
GN Name=fnbB;
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1280;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=8325-4;
RX MEDLINE=92111475; PubMed=1837266;
RA "Joneson K., Sigmas C., Muller H.P., Lindberg M.;
RT "Two different genes encode fibronectin binding proteins in
RT Staphylococcus aureus. The complete nucleotide sequence and
RT characterization of the second gene.";
RL Eur. J. Biochem. 202:1041-1048(1991).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC an amide bond (By similarity).
EMBL; X62992; CAA44726.1; -.
DR PIR; S19702; S19702.
DR HSP; O53653; IN67.
DR GO; GO:0009986; C:cell surface; IEA.
DR GO; GO:0005618; C:cell wall; IEA.
DR GO; GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0007155; P:cell adhesion; IEA.
DR InterPro; IPR008966; Adhes_bact.
DR InterPro; IPR004237; Fn_bind.
DR InterPro; IPR005877; Gpos_YsIRK.
DR InterPro; IPR001899; Gram_pos_anchor.
DR Pfam; PF02986; Fn_bind; 2.
DR Pfam; PF00746; Gram_pos_anchor; 1.
DR Pfam; PF04650; YsIRK_signal; 1.
DR TIGRfams; TIGR01167; LPXTG_anchor; 1.
DR TIGRfams; TIGR01168; YsIRK_signal; 1.
DR PROSITE; PS50847; GRAM_POS_ANCHORING; 1.
KW Cell wall; peptidoglycan-anchor.
SQ SEQUENCE 940 AA; 10355 MW; E35FBBCA907AE345 CRC64;

Query Match 89.7%; Score 191; DB 2; Length 940;
Best Local Similarity 92.1%; Pred. No. 2.6e-15;
Matches 35; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 QNKGNSFEEDTEKDKPKYEHGPNIIIDPDSVPHNG 38
Db 720 QNKGNSFEEDTEKDKPKYEQGNNIIIDPDSVPHNG 757

RESULT 6
O99RD2
ID O99RD2 PRELIMINARY; PRT; 1038 AA.
AC O99RD2;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE Fibronectin-binding protein homolog.
GN Name=fnb; OrderedLocName=SAV2503;
OS Staphylococcus aureus (strain Mu50 / ATCC 700699).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=158878;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Mu50 / ATCC 700699;
RX MEDLINE=21311952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2;
RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
RA Cul L., Oguchi A., Aoki K.-I., Nagai Y., Iian J.-Q., Ito T.,
RA Kanamori M., Matsunaru H., Maruyama A., Marukami H., Hoshoyama A.,
RA Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
RA Sekimizu K., Hirakawa H., Kubara S., Goto S., Yabuzaki J.,
RA Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
RA Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
RT "Whole genome sequencing of methicillin-resistant Staphylococcus
RT aureus.";
RL Lancet 357:1225-1240(2001).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC an amide bond (By similarity).
EMBL; AP003365; BAB58665.1; -.
DR PIR; H90053; H90053.
DR GO; GO:0009986; C:cell surface; IEA.
DR GO; GO:0005618; C:cell wall; IEA.
DR GO; GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0007155; P:cell adhesion; IEA.
DR InterPro; IPR008966; Adhes_bact.
DR InterPro; IPR004237; Fn_bind.
DR InterPro; IPR005877; Gpos_YsIRK.
DR InterPro; IPR001899; Gram_pos_anchor.
DR Pfam; PF02986; Fn_bind; 1.
DR Pfam; PF00746; Gram_pos_anchor; 1.
DR Pfam; PF04650; YsIRK_signal; 1.
DR TIGRfams; TIGR01167; LPXTG_anchor; 1.
DR TIGRfams; TIGR01168; YsIRK_signal; 1.
DR PROSITE; PS50847; GRAM_POS_ANCHORING; 1.
KW Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ SEQUENCE 1038 AA; 113618 MW; 666BFB28FBEB12 CRC64;

Query Match 89.7%; Score 191; DB 2; Length 1038;
Best Local Similarity 92.1%; Pred. No. 2.9e-15;
Matches 35; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 QNKGNSFEEDTEKDKPKYEHGPNIIIDPDSVPHNG 38
Db 780 QNKGNSFEEDTEKDKPKYEHGNNIIIDPDSVPHNG 817

RESULT 7
O7A3J7
ID O7A3J7 PRELIMINARY; PRT; 1038 AA.
AC O7A3J7;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)

```
DE Fnb protein.
GN Name=fnb; OrderedlocusNames=SA2291;
OS Staphylococcus aureus (strain N315).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=158879;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=2111952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2;
RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Lian J.-Q., Ito T.,
RA Kanmori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,
RA Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
RA Sekimizu K., Hirakawa H., Kohara S., Goto S., Yabuzaki J.,
RA Kanehisa K., Yamashita A., Ohshima K., Furuya K., Yoshino C., Shiba T.,
RA Hattori M., Ogasawara N., Hayaishi H., Hiramatsu K.,
RT "Whole genome sequencing of methicillin-resistant Staphylococcus
RT aureus ";
RL Lancet 357.1225-1240(2001).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC an amide bond (By similarity).
CC EMBL; AP003137; BAB43594.1; -.
DR GO; GO:0009986; C:cell surface; IEA.
DR GO; GO:0005618; C:cell wall; IEA.
DR GO; GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:007155; P:cell adhesion; IEA.
DR InterPro; IPR008966; Adhes_Dact.
DR InterPro; IPR004237; Fn_bind.
DR InterPro; IPR005877; Gpos_YsIRK.
DR InterPro; IPR001899; Gram_pos_anchor.
DR Pfam; PF02986; Fn_bind; 1.
DR Pfam; PF00746; Gram_pos_anchor; 1.
DR Pfam; PF04650; YsIRK_signal; 1.
DR TIGRPFAM; TIGR01167; LPXTG_anchor; 1.
DR TIGRPFAM; TIGR01168; YsIRK_signal; 1.
DR PROSITE; PS50847; GRAM_POS_ANCHORING; 1.
KW Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ SEQUENCE 1038 AA; 113618 MW; 666BF6B2BFEB12 CRC64;

Query Match 89.7%; Score 191; DB 2; Length 1038;
Best Local Similarity 92.1%; Pred. No. 2.9e-15;
Matches 35; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 QNKGNSFEEDTEKDKPKYEHGNIIDIDFDSVPHIH 38
DB 780 QNKGNSFEEDTEKDKPKYEHGNIIDIDFDSVPHIH 817

RESULT 8
Q8NUU7 PRELIMINARY; PRT; 1015 AA.
AC Q8NUU7;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Fnb protein.
GN Name=fnb; OrderedlocusNames=WM2421;
OS Staphylococcus aureus (strain WM2).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=196620;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=WM2;
RX MEDLINE=22040717; PubMed=12044378; DOI=10.1016/S0140-6736(02)08713-5;
RA Baba T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Oguchi A.,
RA Nagai Y., Trama N., Asano K., Naimi T., Kuroda H., Cui L.,
RA Yamamoto K., Hiramatsu K.,
RT "Genome and virulence determinants of high virulence community-
RT acquired MRSA ";
RL Lancet 359.1819-1827(2002).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC an amide bond (By similarity).
EMBL; AF004630; BAB96286.1; -.
```

```
DR GO; GO:0009986; C:cell surface; IEA.
DR GO; GO:0005618; C:cell wall; IEA.
DR GO; GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:007155; P:cell adhesion; IEA.
DR InterPro; IPR008966; Adhes_Dact.
DR InterPro; IPR004237; Fn_bind.
DR InterPro; IPR005877; Gpos_YsIRK.
DR InterPro; IPR001899; Gram_pos_anchor.
DR Pfam; PF02986; Fn_bind; 1.
DR Pfam; PF00746; Gram_pos_anchor; 1.
DR Pfam; PF04650; YsIRK_signal; 1.
DR TIGRPFAM; TIGR01167; LPXTG_anchor; 1.
DR TIGRPFAM; TIGR01168; YsIRK_signal; 1.
DR PROSITE; PS50847; GRAM_POS_ANCHORING; 1.
KW Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ SEQUENCE 1015 AA; 111145 MW; D0F9281BB64D44D2 CRC64;

Query Match 85.9%; Score 183; DB 2; Length 1015;
Best Local Similarity 89.5%; Pred. No. 2.9e-14;
Matches 34; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 QNKGNSFEEDTEKDKPKYEHGNIIDIDFDSVPHIH 38
DB 785 QNKGNSFEEDTEKDKPKYEHGNIIDIDFDSVPHIH 822

RESULT 9
Q6G6H3 PRELIMINARY; PRT; 1015 AA.
AC Q6G6H3;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Fibronectin-binding protein.
GN OrderedlocusNames=SA8238;
OS Staphylococcus aureus (strain MSSA476).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=282459;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=15213324; DOI=10.1073/pnas.0402521101;
RA Holden M.T.G., Fell E.J., Lindsey J.A., Peacock S.J., Day N.P.J.,
RA Enright M.C., Foster T.J., Moore C.E., Hurst L., Atkin R., Barron A.,
RA Bason N., Bentley S.D., Chillingworth C., Chillingworth T.,
RA Churcher C., Clark L., Corton C., Cronin A., Doggett J., Dowd L.,
RA Felwell T., Hance Z., Harris B., Hauser H., Holtroyd S., Jagsels K.,
RA James K.D., Lennard N., Line A., Mayes R., Moulis S., Mungall K.,
RA Ormond D., Quail M.A., Rabinowitch B., Rutherford K.M., Sanders M.,
RA Sharp S., Simmonds M., Stevens K., Whitehead S., Barrett B.G.,
RA Spratt B.G., Parkhill J.,
RT "Complete genomes of two clinical Staphylococcus aureus strains:
RT evidence for the rapid evolution of virulence and drug resistance.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:9786-9791(2004).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC an amide bond (By similarity).
EMBL; BX571857; CNG44202.1; -.
DR GO; GO:0009986; C:cell surface; IEA.
DR GO; GO:0005618; C:cell wall; IEA.
DR GO; GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:007155; P:cell adhesion; IEA.
DR InterPro; IPR008966; Adhes_Dact.
DR InterPro; IPR004237; Fn_bind.
DR InterPro; IPR005877; Gpos_YsIRK.
DR InterPro; IPR001899; Gram_pos_anchor.
DR Pfam; PF02986; Fn_bind; 1.
DR Pfam; PF00746; Gram_pos_anchor; 1.
DR Pfam; PF04650; YsIRK_signal; 1.
DR TIGRPFAM; TIGR01167; LPXTG_anchor; 1.
DR TIGRPFAM; TIGR01168; YsIRK_signal; 1.
DR PROSITE; PS50847; GRAM_POS_ANCHORING; 1.
KW Cell wall; Complete proteome; Peptidoglycan-anchor.
```

SQ SEQUENCE 1015 AA; 111145 MW; D0F9281BB64D4D2 CRC64;
 Query Match 85.9%; Score 183; DB 2; Length 1015;
 Best Local Similarity 89.5%; Pred. No. 2.9e-14;
 Matches 34; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 QY 1 QNKGNSFEEDTEKDKRYEGHPNIIDIDPDSVPHNG 38
 DB 785 QNKGNSFEEDTEKDKRYEGHPNIIDIDPDSVPHNG 822
 RESULT 10
 QY99RD3 PRELIMINARY; PRT; 961 AA.
 AC Q99RD3; 01-JUN-2001 (TrEMBLrel. 17, Created)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
 DE 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Fibronectin-binding protein homolog.
 GN Name=fnbB; OrderedLocustNames=SAV2502;
 OS Staphylococcus aureus (strain Mu50 / ATCC 700699).
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 OX NCBI_TaxID=158878;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=M50 / ATCC 700699;
 RA MEDLINE=21311952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2;
 RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
 RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Iano J.-O., Ito T.,
 RA Kanamori M., Matsunaru H., Maruyama A., Murakami H., Hoshoyama A.,
 RA Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
 RA Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
 RA Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
 RA Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
 RT "Whole genome sequencing of methicillin-resistant Staphylococcus
 aureus.";
 RL Lancet 357:1225-1240(2001).
 CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
 an amide bond (By similarity).
 DR EMBL: AP003365; BAB58664.1; -.
 DR PIR: G90053; G90053.
 DR HSBP; Q53653; IN67.
 DR GO: GO:0009986; C:cell surface; IEA.
 DR GO: GO:0005618; C:cell wall; IEA.
 DR GO: GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
 DR GO: GO:0016020; C:membrane; IEA.
 DR GO: GO:0007155; P:cell adhesion; IEA.
 DR InterPro: IPR008966; Adhes_bact.
 DR InterPro: IPR004237; Fn_bind.
 DR InterPro: IPR005877; Gpos_YsIRK.
 DR InterPro: IPR001899; Gram_pos_anchor.
 DR Pfam: PF02986; Fn_bind; 1.
 DR Pfam: PF00746; Gram_pos_anchor; 1.
 DR Pfam: PF04650; YsIRK_signal; 1.
 DR TIGRFAMs: TIGR01167; LPXTG_anchor; 1.
 DR TIGRFAMs: TIGR01168; YsIRK_signal; 1.
 DR PROSITE: PS50847; GRAM_POS_ANCHORING; 1.
 KW Cell wall; Complete proteome; Peptidoglycan-anchor.
 SQ SEQUENCE 961 AA; 106010 MW; 364940F884EA4101 CRC64;
 Query Match 84.0%; Score 179; DB 2; Length 961;
 Best Local Similarity 86.8%; Pred. No. 8.8e-14;
 Matches 33; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
 QY 1 QNKGNSFEEDTEKDKRYEGHPNIIDIDPDSVPHNG 38
 DB 731 QNKGNSFEEDTEKDKRYEGHPNIIDIDPDSVPHNG 768
 RESULT 11
 ID Q7A3J8 PRELIMINARY; PRT; 961 AA.
 AC Q7A3J8;

DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DE fnbB protein.
 GN Name=fnbB; OrderedLocustNames=SA2290;
 OS Staphylococcus aureus (strain N315).
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 OX NCBI_TaxID=158879;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21311952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2;
 RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
 RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Iano J.-O., Ito T.,
 RA Kanamori M., Matsunaru H., Maruyama A., Murakami H., Hoshoyama A.,
 RA Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
 RA Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
 RA Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
 RA Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
 RT "Whole genome sequencing of methicillin-resistant Staphylococcus
 aureus.";
 RL Lancet 357:1225-1240(2001).
 CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
 an amide bond (By similarity).
 DR EMBL: AP003337; BAB43593.1; -.
 DR GO: GO:0009986; C:cell surface; IEA.
 DR GO: GO:0005618; C:cell wall; IEA.
 DR GO: GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
 DR GO: GO:0016020; C:membrane; IEA.
 DR GO: GO:0007155; P:cell adhesion; IEA.
 DR InterPro: IPR008966; Adhes_bact.
 DR InterPro: IPR004237; Fn_bind.
 DR InterPro: IPR005877; Gpos_YsIRK.
 DR InterPro: IPR001899; Gram_pos_anchor.
 DR Pfam: PF02986; Fn_bind; 1.
 DR Pfam: PF00746; Gram_pos_anchor; 1.
 DR Pfam: PF04650; YsIRK_signal; 1.
 DR TIGRFAMs: TIGR01167; LPXTG_anchor; 1.
 DR TIGRFAMs: TIGR01168; YsIRK_signal; 1.
 DR PROSITE: PS50847; GRAM_POS_ANCHORING; 1.
 KW Cell wall; Complete proteome; Peptidoglycan-anchor.
 SQ SEQUENCE 961 AA; 106010 MW; 364940F884EA4101 CRC64;
 Query Match 84.0%; Score 179; DB 2; Length 961;
 Best Local Similarity 86.8%; Pred. No. 8.8e-14;
 Matches 33; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
 QY 1 QNKGNSFEEDTEKDKRYEGHPNIIDIDPDSVPHNG 38
 DB 731 QNKGNSFEEDTEKDKRYEGHPNIIDIDPDSVPHNG 768
 RESULT 12
 ID Q6GDUS PRELIMINARY; PRT; 965 AA.
 AC Q6GDUS; 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DE 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Fibronectin-binding protein.
 GN Name=fnbA; OrderedLocustNames=SA2580;
 OS Staphylococcus aureus (strain MRSA252).
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 OX NCBI_TaxID=282458;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX PubMed=15213324; DOI=10.1073/pnas.040251101;
 RA Holden M.T.G., Feil E.J., Lindsay J.A., Peacock S.J., Day N.P.J.,
 RA Enright M.C., Foster T.J., Moore C.E., Hurst L., Atkin R., Barron A.,
 RA Baeson N., Bentley S.D., Chillingworth C., Chillingworth T.,
 RA Churcher C., Clark L., Corton C., Cronin A., Doggett J., Dowd L.,
 RA Feltwell T., Hance Z., Harris B., Hauser H., Holtroyd S., Jasele K.,
 RA James K.D., Lennard N., Line A., Mayes R., Mungall K.,
 RA Ormond D., Quail M.A., Rabinowitch E., Rutherford K.M., Sanders M.,

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RA Sharp S., Simmonds M., Stevens K., Whitehead S., Barrett B.G.,
RA Spratt B.G., Parkhill J.,
RT "Complete genomes of two clinical Staphylococcus aureus strains:
RT evidence for the rapid evolution of virulence and drug resistance."
RT Proc. Natl. Acad. Sci. U.S.A. 101:9786-9791(2004).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC an amide bond (By similarity).
DR EMBL: BX571856; C:CG41560.1; -.
DR GO: GO:0009986; C:cell surface; IEA.
DR GO: GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO: GO:0016020; C:membrane; IEA.
DR GO: GO:0007155; P:cell adhesion; IEA.
DR InterPro: IPR008966; Adhes_bact.
DR InterPro: IPR004237; Fn_bind.
DR InterPro: IPR005877; Gpos_YSTRK.
DR InterPro: IPR01899; Gram_pos_anchor.
DR Pfam: PF02986; Fn_bind_1.
DR Pfam: PF00746; Gram_pos_anchor; 1.
DR Pfam: PF04650; YSTRK_signal; 1.
DR TIGRfam: TIGR01167; LPXG_anchor; 1.
DR TIGRfam: TIGR01168; YSTRK_signal; 1.
DR PROSITE: PS00847; GRAM_POS_ANCHORING; 1.
DR Cell wall; Complete proteome; Peptidoglycan-anchor.
SO SEQUENCE 965 AA; 105691 MW; 2982E132164D0551 CRC64;

Query Match 84.0%; Score 179; DB 2; Length 965;
Best Local Similarity 86.8%; Pred. No. 8; 9e-14;
Matches 33; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 ONKGNQSFEDTEKDKPKYEHGPNIIIDIPDSVPPIHG 38
DB 749 QNSGNQSFEDTEKDKPKYEGNIIIDIPDSVPPIHG 786

RESULT 13
DHAY YEAST STANDARD; PRT; 511 AA.
AC P32872;
DT 01-OCT-1993 (Rel. 27, Created)
DT 01-OCT-1993 (Rel. 27, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Aldehyde dehydrogenase 2, mitochondrial precursor (EC 1.2.1.3).
GN Name:ALD2; Synonyms:ALDH2;
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RA Thieleen J.;
RA Theiss (1993), Heinrich-Heine University / Duesseldorf, Germany.
CC -1- CATALYTIC ACTIVITY: An aldehyde + NAD(+) + H(2)O = an acid + NADH.
CC -1- PATHWAY: Ethanol utilization; second step.
CC -1- SUBCELLULAR LOCATION: Mitochondrial matrix (potentially).
CC -1- SIMILARITY: Belongs to the aldehyde dehydrogenase family.
CC -1- CAUTION: Is not present in yeast genome.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC
CC EMBL: Z17314; CAAT8962.1; -.
CC PIR: S31308; S31308.
DR HSSP: P05091; 1004.
DR InterPro: IPR002086; Aldehyde_dehydr.
DR Pfam: PF00171; Aldehyd_1.
DR TIGRfam: TIGR01804; BADH_1.
DR TIGRfam: TIGR01780; SSADH_1.
DR PROSITE: PS00070; ALDEHYDE_DEHYDR_CYS; 1.

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DR PROSITE: PS00687; ALDEHYDE_DEHYDR_GLU; 1.
KW Mitochondrion; NAD; Oxidoreductase; Transit peptide.
FT TRANSIT 1 21 Mitochondrion.
FT CHAIN 22 511 Aldehyde dehydrogenase 2.
FT NP BIND 274 279 NAD (ADP part) (By similarity).
FT ACT SITE 297 297 By similarity.
FT ACT SITE 331 331 By similarity.
SO SEQUENCE 511 AA; 56466 MW; 70EDA951B84EE4A CRC64;

Query Match 29.6%; Score 63; DB 1; Length 511;
Best Local Similarity 42.4%; Pred. No. 20;
Matches 14; Conservative 5; Mismatches 6; Indels 8; Gaps 2;

QY 4 GNQSFEDTEKDKPKYEHGPNIIIDIPDSVPPI 36
DB 361 GN-PFESDT-----RYGQPLKIEFDSIRPL 365

RESULT 14
Q7RB60 PRELIMINARY; PRT; 716 AA.
AC Q7RB60;
DT 01-MAR-2004 (TReMBLrel. 26, Created)
DT 01-MAR-2004 (TReMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)
DE Hypothetical protein.
GN Name=PY06288;
OS Plasmodium yoelii yoelii.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=73339;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=17XNL;
RC PubMed=1236865; DOI=10.1038/nature01099;
RA Carlton J.W., Anguioni S.V., Sun B.B., Kocif T.W., Pertea M.,
RA Silva J.C., Ermolaeva M.D., Allen J.E., Selengut J.D., Koo H.L.,
RA Peterson J.D., Pop M., Kosack D.S., Shumway M.F., Bidwell S.L.,
RA Shallom S.J., van Aken S.B., Riedmiller S.B., Feldblum T.V.,
RA Cho J.K., Quackenbush J., Sedegah M., Shoaihi A., Cummings L.M.,
RA Florens L., Yates F.R. III, Raine J.D., Sinden R.E., Harris M.A.,
RA Cunningham D.A., Preiser P.R., Bergman L.W., Valdivia A.B.,
RA van Lin L.H., Janse C.J., Waters A.P., Smith H.O., White O.R.,
RA Salzberg S.L., Venter J.C., Fraser C.M., Hoffman S.L., Gardner M.J.,
RA Carucci D.J.;
RA "Genome sequence and comparative analysis of the model rodent malaria
RT parasite Plasmodium yoelii yoelii."
RL Nature 419:512-519(2002).
CC -1- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL: AAB101002106; EAA18479.1; -.
DR InterPro: IPR008941; TPR-like.
DR Hypothetical protein.
SQ SEQUENCE 716 AA; 86599 MW; E11BE234A397B6F7 CRC64;

Query Match 29.6%; Score 63; DB 2; Length 716;
Best Local Similarity 34.3%; Pred. No. 30;
Matches 12; Conservative 7; Mismatches 16; Indels 0; Gaps 0;

QY 2 NKGNSFEDTEKDKPKYEHGPNIIIDIPDSVPHI 36
DB 109 NMYNHTWEKKKQKSPHNNNIFDVSYEQVRI 143

RESULT 15
Q54324 PRELIMINARY; PRT; 904 AA.
ID Q54324;
AC Q54324;
DT 01-NOV-1996 (TReMBLrel. 01, Created)
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)
DE ORF904; Method: conceptual translation supplied by author.
OS Sulfolobus islandicus.

```

OG plasmid pRN1.
 OC Archaea; Crenarchaeota; Thermoprotei; Sulfolobales; Sulfolobaceae;
 OC Sulfolobus.
 OX NCBI_TaxID=43080;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=REN1H1;
 RX MEDLINE=96271189; PubMed=8700967; DOI=10.1006/plas.1996.0016;
 RA Keeling P.J., Klenk H.P., Singh R.K., Feeley O., Schleper C.,
 RA Zillig W., Doolittle W.F., Senses C.W.;
 RT "Complete nucleotide sequence of the Sulfolobus islandicus multicopy
 RT plasmid pRN1."
 RL Plasmid 35:141-144(1996).
 DR EMBL; U36383; AAC411.1.1; .
 DR PDB; 1RN1; X-ray; A=40-255.
 DR PDB; 1RO0; X-ray; A=40-255.
 DR PDB; 1RO2; X-ray; A=40-255.
 DR InterPro; IPR004968; Pox_D5.
 DR InterPro; IPR006500; Primase_C.
 DR InterPro; IPR009058; Wing_hlx_DNA_bnd.
 DR Pfam; PF03288; Pox_D5; 1.
 DR TIGRFAMs; TIGR01613; primase_Cterm; 1.
 KM plasmid.
 SQ SEQUENCE 904 AA; 105816 MW; 3726C107EC6E57F CRC64;

Query Match 28.9%; Score 61.5; DB 2; Length 904;
 Best Local Similarity 38.9%; Pred. No. 59;
 Matches 14; Conservative 6; Mismatches 11; Indels 5; Gaps 1;

OY 2 NKGNSFEEDTEKDKPKY-----EHGPNIIDIDPDS 32
 | | | | | : : : | | | | | : |
 DB 29 NSGNKDFSSNFSERIRYAKWFLHGFNIIPIDPS 64

Search completed: October 22, 2005, 06:06:11
 Job time : 70.6361 secs

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CC streptococci, e.g. meningitis, otitis media, pneumonia, endocarditis,
CC mastitis in cattle, abortion in horses and many others. Since the
CC antibodies block binding of bacteria, they should be effective against
CC antibiotic-resistant strains, and may replace antibiotic therapy or
CC increase its effectiveness. Sequences AAW65701-706 represent a series of
CC synthetic peptides based on the D2 region of *S. aureus* fibronectin
CC binding protein A. They were synthesised to contain mutations
XX
SQ Sequence 38 AA;
XX
Query Match 100.0%; Score 218; DB 2; Length 38;
Best Local Similarity 100.0%; Pred. No. 8.4e-22;
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1 QNKGNSPPDTEKDKPKYEHHPNIIDIDFDSVPHIHG 38
DB 1 QNKGNSPPDTEKDKPKYEHHPNIIDIDFDSVPHIHG 38
XX
RESULT 2
AAW65664
ID AAW65664 standard; peptide; 38 AA.
XX
AC AAW65664;
XX
DT 16-OCT-1998 (first entry)
XX
DE Fibronectin binding protein-derived peptide #8.
XX
OS microbial surface components recognising adhesive matrix molecule;
KM MSCRAMM; fibronectin; fibronectin-binding protein; antibody; epitope;
KW antibiotic; bacterial infection; antibiotic-resistant strain.
XX
OS Synthetic.
OS Staphylococcus aureus.
XX
PN WO9813389-A2.
XX
PD 23-JUL-1998.
XX
PF 21-JAN-1998; 98WO-US001222.
XX
PR 21-JAN-1997; 97US-0036139P.
XX
PA (TEXA) UNIV TEXAS A & M SYSTEM.
XX
PI Hoeoek M, Patti JM, House-Pompeo KL, Speciale P, Joh D;
PI McGavin MJ;
XX
DR WPI; 1998-413816/35.
XX
PT Antibody that binds to fibronectin-binding protein, preventing its
PT binding to fibronectin - used to treat or prevent bacterial infection,
PT especially by Staphylococci and Streptococci.
XX
PS Example 2; Page 92; 201pp; English.
XX
CC The invention relates to antibodies that bind to a fibronectin-binding
CC domain of a fibronectin-binding protein, and inhibit binding of the
CC protein to fibronectin. Also claimed are: (1) isolated peptides of a
CC fibronectin-binding protein that do not bind to fibronectin; (2) fusion
CC protein containing at least one peptide of a fibronectin-binding protein
CC linked to a second amino acid sequence; (3) nucleic acid encoding the
CC isolated peptide of (1). Antibodies, the isolated peptides of (1) and the
CC nucleic acids are all useful for immunisation (active or passive) and (by
CC inhibiting binding of bacteria to fibronectin) for preventing or treating
CC infection in humans or other animals, particularly by staphylococci or
CC streptococci, e.g. meningitis, otitis media, pneumonia, endocarditis,
CC mastitis in cattle, abortion in horses and many others. Since the
CC antibodies block binding of bacteria, they should be effective against
CC antibiotic-resistant strains, and may replace antibiotic therapy or
CC increase its effectiveness. Sequences AAW65659-68 represent synthetic
CC epitopes from the fibronectin binding domains DU and DI-D4 of the *S.*

CC aureus *fnbA* gene
XX
SQ Sequence 38 AA;
XX
Query Match 88.5%; Score 193; DB 2; Length 38;
Best Local Similarity 92.1%; Pred. No. 1.9e-18;
Matches 35; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
XX
QY 1 QNKGNSPPDTEKDKPKYEHHPNIIDIDFDSVPHIHG 38
DB 1 QNKGNSFEDTEKDKPKYEHHPNIIDIDFDSVPHIHG 38
XX
RESULT 3
AAW65705
ID AAW65705 standard; peptide; 38 AA.
XX
AC AAW65705;
XX
DT 16-OCT-1998 (first entry)
XX
DE Fibronectin binding protein-derived peptide #49.
XX
OS microbial surface components recognising adhesive matrix molecule;
KM MSCRAMM; fibronectin; fibronectin-binding protein; antibody; epitope;
KW antibiotic; bacterial infection; antibiotic-resistant strain.
XX
OS Synthetic.
OS Staphylococcus aureus.
XX
PN WO9813389-A2.
XX
PD 23-JUL-1998.
XX
PF 21-JAN-1998; 98WO-US001222.
XX
PR 21-JAN-1997; 97US-0036139P.
XX
PA (TEXA) UNIV TEXAS A & M SYSTEM.
XX
PI Hoeoek M, Patti JM, House-Pompeo KL, Speciale P, Joh D;
PI McGavin MJ;
XX
DR WPI; 1998-413816/35.
XX
PT Antibody that binds to fibronectin-binding protein, preventing its
PT binding to fibronectin - used to treat or prevent bacterial infection,
PT especially by Staphylococci and Streptococci.
XX
PS Example 8; Page 102; 201pp; English.
XX
CC The invention relates to antibodies that bind to a fibronectin-binding
CC domain of a fibronectin-binding protein, and inhibit binding of the
CC protein to fibronectin. Also claimed are: (1) isolated peptides of a
CC fibronectin-binding protein that do not bind to fibronectin; (2) fusion
CC protein containing at least one peptide of a fibronectin-binding protein
CC linked to a second amino acid sequence; (3) nucleic acid encoding the
CC isolated peptide of (1). Antibodies, the isolated peptides of (1) and the
CC nucleic acids are all useful for immunisation (active or passive) and (by
CC inhibiting binding of bacteria to fibronectin) for preventing or treating
CC infection in humans or other animals, particularly by staphylococci or
CC streptococci, e.g. meningitis, otitis media, pneumonia, endocarditis,
CC mastitis in cattle, abortion in horses and many others. Since the
CC antibodies block binding of bacteria, they should be effective against
CC antibiotic-resistant strains, and may replace antibiotic therapy or
CC increase its effectiveness. Sequences AAW65701-706 represent a series of
CC synthetic peptides based on the D2 region of *S. aureus* fibronectin
CC binding protein A. They were synthesised to contain mutations
XX
SQ Sequence 38 AA;
XX
Query Match 88.5%; Score 193; DB 2; Length 38;
Best Local Similarity 92.1%; Pred. No. 1.9e-18;

Matches 35; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 ONKGNOSFPPTDEKDKRKYEHPPNIIDIDFDSVPHIHG 38
 ID |||||
 DB 1 ONKGNOSFPEDETKDKRKYEHGPNIIDIDFDSVPHIHG 38

RESULT 4

AAW65703 standard; peptide; 38 AA.

AAW65703;

16-OCT-1998 (first entry)

Fibronectin binding protein-derived peptide #47.

microbial surface components recognising adhesive matrix molecule;

MSCRAMM; fibronectin; fibronectin-binding protein; antibody; epitope;

antibiotic; bacterial infection; antibiotic-resistant strain.

Synthetic.

Staphylococcus aureus.

WO9831389-A2.

23-JUL-1998.

21-JAN-1998; 98WO-US001222.

21-JAN-1997; 97US-0036139P.

(TEXA) UNIV TEXAS A & M SYSTEM.

Heoek M, Patl JM, House-Pompeo KL, Speziale P, Joh D;

Megavln MJ;

WPI; 1998-413816/35.

Antibody that binds to fibronectin-binding protein, preventing its

binding to fibronectin - used to treat or prevent bacterial infection,

especially by Staphylococci and Streptococci.

Example 8; Page 102; 201p; English.

The invention relates to antibodies that bind to a fibronectin-binding

domain of a fibronectin-binding protein, and inhibit binding of the

protein to fibronectin. Also claimed are: (1) isolated peptides of a

fibronectin-binding protein that do not bind to fibronectin; (2) fusion

protein containing at least one peptide of a fibronectin-binding protein

linked to a second amino acid sequence; (3) nucleic acid encoding the

isolated peptide of (1). Antibodies, the isolated peptides of (1) and the

nucleic acids are all useful for immunisation (active or passive) and (by

inhibiting binding of bacteria to fibronectin) for preventing or treating

infection in humans or other animals, particularly by staphylococci or

streptococci, e.g. meningitis, otitis media, pneumonia, endocarditis,

mastitis in cattle, abortion in horses and many others. Since the

antibodies block binding of bacteria, they should be effective against

antibiotic-resistant strains, and may replace antibiotic therapy or

increase its effectiveness. Sequences AAW65701-706 represent a series of

synthetic peptides based on the D2 region of S. aureus fibronectin

binding protein A. They were synthesised to contain mutations

Sequence 38 AA;

Query Match 88.1%; Score 192; DB 2; Length 38;

Best Local Similarity 92.1%; Pred. No. 2.6e-18;

Matches 35; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 ONKGNOSFPPTDEKDKRKYEHPPNIIDIDFDSVPHIHG 38
 ID |||||
 DB 1 ONKGNOSFPEDETKDKRKYEHGPNIIDIDFDSVPHIHG 38

RESULT 5

AAW65700 standard; peptide; 38 AA.

AAW65700;

16-OCT-1998 (first entry)

Fibronectin binding protein-derived peptide #44.

microbial surface components recognising adhesive matrix molecule;

MSCRAMM; fibronectin; fibronectin-binding protein; antibody; epitope;

antibiotic; bacterial infection; antibiotic-resistant strain.

Synthetic.

Staphylococcus aureus.

WO9831389-A2.

23-JUL-1998.

21-JAN-1998; 98WO-US001222.

21-JAN-1997; 97US-0036139P.

(TEXA) UNIV TEXAS A & M SYSTEM.

Heoek M, Patl JM, House-Pompeo KL, Speziale P, Joh D;

Megavln MJ;

WPI; 1998-413816/35.

Antibody that binds to fibronectin-binding protein, preventing its

binding to fibronectin - used to treat or prevent bacterial infection,

especially by Staphylococci and Streptococci.

Example 8; Page 102; 201p; English.

The invention relates to antibodies that bind to a fibronectin-binding

domain of a fibronectin-binding protein, and inhibit binding of the

protein to fibronectin. Also claimed are: (1) isolated peptides of a

fibronectin-binding protein that do not bind to fibronectin; (2) fusion

protein containing at least one peptide of a fibronectin-binding protein

linked to a second amino acid sequence; (3) nucleic acid encoding the

isolated peptide of (1). Antibodies, the isolated peptides of (1) and the

nucleic acids are all useful for immunisation (active or passive) and (by

inhibiting binding of bacteria to fibronectin) for preventing or treating

infection in humans or other animals, particularly by staphylococci or

streptococci, e.g. meningitis, otitis media, pneumonia, endocarditis,

mastitis in cattle, abortion in horses and many others. Since the

antibodies block binding of bacteria, they should be effective against

antibiotic-resistant strains, and may replace antibiotic therapy or

increase its effectiveness. Sequences AAW6591-700 represent a series of

synthetic peptides based on the D1 region of S. aureus fibronectin

binding protein A. They were synthesised to contain mutations

Sequence 38 AA;

Query Match 88.1%; Score 192; DB 2; Length 38;

Best Local Similarity 86.8%; Pred. No. 2.6e-18;

Matches 33; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 ONKGNOSFPPTDEKDKRKYEHPPNIIDIDFDSVPHIHG 38
 ID |||||
 DB 1 QNSGNOSFPPTDEKDKRKYEQPNIVIDIDFDSVPHIHG 38

RESULT 6

AAW65702 standard; peptide; 38 AA.

AAW65702;

```

XX 16-OCT-1998 (first entry)
XX Fibronectin binding protein-derived peptide #46.
XX
XX Microbial surface components recognising adhesive matrix molecule;
XX MSCRAMM; fibronectin; fibronectin-binding protein; antibody; epitope;
XX antibiotic; bacterial infection; antibiotic-resistant strain.
XX
XX Synthetic.
XX Staphylococcus aureus.
XX
XX WO961389-A2.
XX
XX 23-JUL-1998.
XX
XX 21-JAN-1998; 98WO-US001222.
XX
XX 21-JAN-1997; 97US-0036139P.
XX
XX (TEXA ) UNIV TEXAS A & M SYSTEM.
XX
XX Hoeoek M, Patti JM, House-Pompeo KL, Speziale P, Joh D;
XX McGavin MJ;
XX
XX WPI; 1998-413816/35.
XX
XX Antibody that binds to fibronectin-binding protein, preventing its
XX binding to fibronectin - used to treat or prevent bacterial infection,
XX especially by Staphylococci and Streptococci.
XX
XX Example 8; Page 102; 201pp; English.
XX
XX The invention relates to antibodies that bind to a fibronectin-binding
XX domain of a fibronectin-binding protein, and inhibit binding of the
XX protein to fibronectin. Also claimed are: (1) isolated peptides of a
XX fibronectin-binding protein that do not bind to fibronectin; (2) fusion
XX protein containing at least one peptide of a fibronectin-binding protein
XX linked to a second amino acid sequence; (3) nucleic acid encoding the
XX isolated peptide of (1). Antibodies, the isolated peptides of (1) and the
XX nucleic acids are all useful for immunisation (active or passive) and (by
XX inhibiting binding of bacteria to fibronectin) for preventing or treating
XX infection in humans or other animals, particularly by staphylococci or
XX streptococci, e.g. meningitis, otitis media, pneumonia, endocarditis,
XX mastitis in cattle, abortion in horses and many others. Since the
XX antibodies block binding of bacteria, they should be effective against
XX antibiotic-resistant strains, and may replace antibiotic therapy or
XX increase its effectiveness. Sequences AAW65701-706 represent a series of
XX synthetic peptides based on the D2 region of S. aureus fibronectin
XX binding protein A. They were synthesised to contain mutations
XX
XX Sequence 38 AA:
XX
XX Query Match 88.1%; Score 192; DB 2; Length 38;
XX Best Local Similarity 92.1%; Pred. No. 2, 6e-18;
XX Matches 35; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
XX
XX QY 1 QNKGNSFPEDTEKDKPKYEHPPNIIDIDFDSVPHHG 38
XX ID 1 QNKGNSFPEDTEKDKPKYEHGNIIDIDFDSVPHHG 38
XX DB
XX
XX RESULT 7
XX AAW65663
XX ID AAW65663 standard; peptide; 38 AA.
XX
XX AAW65663;
XX
XX 16-OCT-1998 (first entry)
XX Fibronectin binding protein-derived peptide #7.
XX
XX microbial surface components recognising adhesive matrix molecule;

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XX MSCRAMM; fibronectin; fibronectin-binding protein; antibody; epitope;
XX antibiotic; bacterial infection; antibiotic-resistant strain.
XX
XX Synthetic.
XX Staphylococcus aureus.
XX
XX WO961389-A2.
XX
XX 23-JUL-1998.
XX
XX 21-JAN-1998; 98WO-US001222.
XX
XX 21-JAN-1997; 97US-0036139P.
XX
XX (TEXA ) UNIV TEXAS A & M SYSTEM.
XX
XX Hoeoek M, Patti JM, House-Pompeo KL, Speziale P, Joh D;
XX McGavin MJ;
XX
XX WPI; 1998-413816/35.
XX
XX Antibody that binds to fibronectin-binding protein, preventing its
XX binding to fibronectin - used to treat or prevent bacterial infection,
XX especially by Staphylococci and Streptococci.
XX
XX Example 2; Page 92; 201pp; English.
XX
XX The invention relates to antibodies that bind to a fibronectin-binding
XX domain of a fibronectin-binding protein, and inhibit binding of the
XX protein to fibronectin. Also claimed are: (1) isolated peptides of a
XX fibronectin-binding protein that do not bind to fibronectin; (2) fusion
XX protein containing at least one peptide of a fibronectin-binding protein
XX linked to a second amino acid sequence; (3) nucleic acid encoding the
XX isolated peptide of (1). Antibodies, the isolated peptides of (1) and the
XX nucleic acids are all useful for immunisation (active or passive) and (by
XX inhibiting binding of bacteria to fibronectin) for preventing or treating
XX infection in humans or other animals, particularly by staphylococci or
XX streptococci, e.g. meningitis, otitis media, pneumonia, endocarditis,
XX mastitis in cattle, abortion in horses and many others. Since the
XX antibodies block binding of bacteria, they should be effective against
XX antibiotic-resistant strains, and may replace antibiotic therapy or
XX increase its effectiveness. Sequences AAW6559-68 represent synthetic
XX epitopes from the fibronectin binding domains DV and D1-D4 of the S.
XX aureus fnba gene
XX
XX Sequence 38 AA:
XX
XX Query Match 84.4%; Score 184; DB 2; Length 38;
XX Best Local Similarity 89.5%; Pred. No. 3, 1e-17;
XX Matches 34; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
XX
XX QY 1 QNKGNSFPEDTEKDKPKYEHPPNIIDIDFDSVPHHG 38
XX ID 1 QNKGNSFPEDTEKDKPKYEHGNIIDIDFDSVPHHG 38
XX DB
XX
XX RESULT 8
XX AAY29087
XX ID AAY29087 standard; protein; 134 AA.
XX
XX AAY29087;
XX
XX 28-SEP-1999 (first entry)
XX
XX S. aureus fibronectin binding protein A (FnBA) binding domain.
XX
XX Bovine herpes virus-2; BHV-2; cytokine; immune response; immunogen; IL;
XX interleukin; colony stimulating factor; CSF; interferon; IFN; TNF;
XX tumour necrosis factor; recombinant virus; vaccine; mucosal disease;
XX mastitis; breast cancer; stress-induced disease; binding domain; Fnba;
XX fibronectin binding protein.
XX
XX Staphylococcus aureus.

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XX WO916892-A1.
 PN 08-APR-1999.
 XX 29-SEP-1998; 98WO-GB002927.
 PF 29-SEP-1997; 97GB-00020633.
 PR (UYBR-) UNIV BRISTOL.
 XX
 PA Bradley AJ, Duffas WPJ;
 PI WPI; 1995-255101/21.
 DR N-PSDB; AAX91504.
 XX
 PT New bovine herpes virus-2 vectors.
 PS Example 2; Fig 8A-B; 130pp; English.
 XX
 CC The invention provides bovine herpes virus-2 (BHV-2) based vectors that
 CC comprise at least one cytokine-encoding DNA sequence. The expression of
 CC cytokines in mammals can up-regulate immune responses to the immunogens.
 CC The cytokine is selected from interleukins (IL), colony stimulating
 CC factors (CSF), interferons (IFN) and tumour necrosis factors (TNF). The
 CC BHV-2 based vector or recombinant virus can be used as vaccines. They can
 CC be used for preventing or treating a mucosal disease in a subject, e.g.
 CC ruminants, cattle, sheep, goats, dogs, cats, horses, or man, particularly
 CC mastitis in cows or breast cancers in humans. They can also be used for
 CC preventing or treating a stress-induced disease. The present sequence
 CC represents the binding domain of a previously published S. aureus
 CC fibronectin binding protein A (FnBA) sequence. The FnB binding domain
 CC gene sequence FNBA, cloned for use in this invention has 97.8 percent
 CC identity when compared to the previously published FNBA and FNBB gene
 CC sequences
 CC
 XX Sequence 134 AA;
 SQ
 Query Match 84.4%; Score 184; DB 2; Length 134;
 Best Local Similarity 89.5%; Pred. No. 1.3e-16;
 Matches 34; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 QY 1 QNKGNSFPPTDEKDKPYEHHPNIIDIDPSVPHING 38
 Db 40 QNKGNSFPEDTEKDKPYEHGNIIDIDPSVPHING 77
 RESULT 9
 AAW31556
 ID AAW31556 standard; protein; 139 AA.
 XX
 AC AAW31556;
 XX
 DT 27-AUG-2003 (revised)
 DT 25-MAR-2003 (revised)
 DT 21-MAY-1998 (first entry)
 XX
 DE Fibronectin-binding MSCRAMM derivative pOD.
 KW Fibronectin; pOD; collagen binding protein; sepsis; infection;
 KW microbial surface component responsible adhesive matrix molecule; MSCRAMM;
 KW adhesin; vaccine; immunisation; diagnosis; therapy; mastitis.
 XX
 OS Staphylococcus aureus.
 XX
 FT Key Location/Qualifiers
 FT Peptide 1..12
 FT /note= "vector pOE30-derived peptide"
 XX
 PN WO9743314-A2.
 PD 20-NOV-1997.
 XX

PF 14-MAY-1997; 97WO-US008210.
 XX 16-MAY-1996; 96US-0017678P.
 XX (TEXA) UNIV TEXAS A & M SYSTEM.
 PA (UABR-) UAB RES FOUND.
 XX
 PI Hoeoek M, Patti JM, House-Pompeo K, Sthanam N, Symersky J;
 DR WPI; 1998-008801/01.
 XX
 PT Antibody that interacts with collagen binding domain of Staphylococcal
 PT cna gene product - useful to prevent bacterial sepsis in animal infected
 PT with Staphylococcus aureus.
 XX
 PS Disclosure; Page 91; 143pp; English.
 XX
 CC This protein comprises Staphylococcus aureus fibronectin-binding
 CC microbial surface component regioning adhesive matrix molecule (MSCRAMM)
 CC derivative pOD, plus a vector-derived N-terminal peptide. The invention
 CC relates to claimed nucleic acid sequences (see AAT93436-38) encoding S.
 CC aureus collagen binding protein (CBP) epitopes M17, M31 and M55 (see
 CC AAW31552-54) that confer protection against S. aureus infection. CBP
 CC protein and antigenic epitopes are contemplated for use in the treatment
 CC of pathological infections, especially to prevent bacterial adhesion to
 CC collagen. The epitopes are also contemplated for use in the preparation
 CC of vaccines and as carrier proteins in vaccine formulations, as well as
 CC in the formulation of compositions for the prevention of S. aureus
 CC infection. pCPf3 and pOD (see AAW31556) were used to raise anti-MSCRAMM
 CC polyclonal antibodies used in passive immunisation against bovine
 CC mastitis (updated on 25-MAR-2003 to correct PI field.) (Updated on 27-
 CC AUG-2003 to correct OS field.)
 CC
 XX Sequence 139 AA;
 SQ
 Query Match 84.4%; Score 184; DB 2; Length 139;
 Best Local Similarity 89.5%; Pred. No. 1.4e-16;
 Matches 34; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 QY 1 QNKGNSFPPTDEKDKPYEHHPNIIDIDPSVPHING 38
 Db 54 QNKGNSFPEDTEKDKPYEHGNIIDIDPSVPHING 91
 RESULT 10
 AAP82115
 ID AAP82115 standard; protein; 1018 AA.
 XX
 AC AAP82115;
 XX
 DT 25-MAR-2003 (revised)
 DT 05-JAN-1990 (first entry)
 XX
 DE Fibronectin binding protein.
 KW Fibronectin binding protein; S. aureus; immunisation; mastitis; ruminants;
 KW wound infection; diagnosis.
 XX
 OS Staphylococcus aureus.
 XX
 PN EP294349-A.
 PD 07-DEC-1988.
 XX
 PF 30-MAY-1988; 88EP-00850188.
 XX
 PR 01-JUN-1987; 87SE-00002272.
 XX
 PA (ALFA) ALFA LAVAL AGRIC INT AB.
 XX
 PI Lindberg MK, Signae LC, Wadstrom TM, Froman G;
 DR WPI; 1988-347976/49.
 XX

DR P-PSDB; AA082115.
XX Hybrid DNA encoding Staphylococcus aureus fibronectin binding protein -
PT useful for immunisation and topical application to prevent staphylococcal
PT infections.
XX
PS Disclosure; Fig. 8A:1-8A:2; 23pp; English.
XX
CC The S.aureus fibronectin binding protein may be included in a hybrid
CC protein. The protein may be used to immunise runnants against
CC staphylococcal mastitis, pref. when given at 0.5-5 microg/kg, using 3
CC doses at 1-3 week intervals; and for topical applic. to prevent wound
CC infection, pref. using isotonic saline soln. of concn. 25-250 microg/mg.
CC The DNA encoding the binding protein and the hybrid protein may be
CC immobilised on a carrier and used to diagnose staphylococcal infections.
CC (Updated on 25-MAR-2003 to correct PA field.)
XX
SQ Sequence 1018 AA;
XX
Query Match 84.4%; Score 184; DB 1; Length 1018;
Best Local Similarity 89.5%; Pred. No. 1.3e-15;
Matches 34; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 1 QNKGNSFPDTEKDKPKYEHPPNIIDIDFDSVPHIHG 38
DB 784 QNKGNSFEDTEKDKPKYEHGNIIDIDFDSVPHIHG 821
RESULT 11
AAU37245
ID AAU37245 standard; protein; 1018 AA.
XX
AC AAU37245;
XX
DT 14-FEB-2002 (first entry)
XX
DE Staphylococcus aureus cellular proliferation protein #1415.
XX
KW Antisense; prokaryotic cellular proliferation protein; antibiotic;
KM antibacterial; drug design.
XX
OS Staphylococcus aureus.
XX
PN MO200170955-A2.
XX
PD 27-SEP-2001.
XX
PF 21-MAR-2001; 2001MO-US009180.
XX
PR 21-MAR-2000; 2000US-0191078P.
PR 23-MAY-2000; 2000US-0206848P.
PR 26-MAY-2000; 2000US-0207727P.
PR 23-OCT-2000; 2000US-0242578P.
PR 27-NOV-2000; 2000US-0253625P.
PR 22-DEC-2000; 2000US-0257931P.
PR 16-FEB-2001; 2001US-0269308P.
XX
PA (ELIT-) ELITRA PHARM INC.
XX
PI Haselbeck R, Ohlsen KL, Zyskind JW, Wall D, Trawick JD, Carr GJ;
PI Yamamoto RT, Xu HH;
XX
DR WPI; 2001-611495/70.
DR N-PSDB; AAS55104.
XX
PT New polynucleotides for the identification and development of
PT antibiotics, comprise sequences of antisense nucleic acids.
XX
PS Example 3; SEQ ID NO 12838; 51pp; English.
XX
CC The invention relates to antisense inhibitors of genes essential to
CC prokaryotic cellular proliferation, their use in identifying the genes,
CC their use in the discovery of novel antibiotics, the essential genes

CC themselves and the encoded proteins. The prokaryotes used are Escherichia
CC coli, Staphylococcus aureus, Salmonella typhi, Klebsiella pneumoniae,
CC Pseudomonas aeruginosa and Enterococcus faecalis. The invention is also
CC useful for the identification of potential new targets for antibiotic
CC development. The antisense nucleic acids can also be used to identify
CC proteins used in proliferation, to express these proteins, and to obtain
CC antibodies capable of binding to the expressed proteins. The proteins can
CC be used to screen compounds in rational drug discovery programmes. The
CC antisense nucleic acid sequence is also useful to screen for homologous
CC nucleic acids which are required for cell proliferation in a wide variety
CC of organisms. The present sequence represents an essential prokaryotic
CC cellular proliferation protein. Note: The sequence data for this patent
CC did not form part of the printed specification, but was obtained in
CC electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 1018 AA;
XX
Query Match 84.4%; Score 184; DB 4; Length 1018;
Best Local Similarity 89.5%; Pred. No. 1.3e-15;
Matches 34; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 1 QNKGNSFPDTEKDKPKYEHPPNIIDIDFDSVPHIHG 38
DB 784 QNKGNSFEDTEKDKPKYEHGNIIDIDFDSVPHIHG 821
RESULT 12
AAU34301
ID AAU34301 standard; protein; 1018 AA.
XX
AC AAU34301;
XX
DT 14-FEB-2002 (first entry)
XX
DE Staphylococcus aureus cellular proliferation protein #577.
XX
KW Antisense; prokaryotic cellular proliferation protein; antibiotic;
KM antibacterial; drug design.
XX
OS Staphylococcus aureus.
XX
PN MO200170955-A2.
XX
PD 27-SEP-2001.
XX
PF 21-MAR-2001; 2001MO-US009180.
XX
PR 21-MAR-2000; 2000US-0191078P.
PR 23-MAY-2000; 2000US-0206848P.
PR 26-MAY-2000; 2000US-0207727P.
PR 23-OCT-2000; 2000US-0242578P.
PR 27-NOV-2000; 2000US-0253625P.
PR 22-DEC-2000; 2000US-0257931P.
PR 16-FEB-2001; 2001US-0269308P.
XX
PA (ELIT-) ELITRA PHARM INC.
XX
PI Haselbeck R, Ohlsen KL, Zyskind JW, Wall D, Trawick JD, Carr GJ;
PI Yamamoto RT, Xu HH;
XX
DR WPI; 2001-611495/70.
DR N-PSDB; AAS52160.
XX
PT New polynucleotides for the identification and development of
PT antibiotics, comprise sequences of antisense nucleic acids.
XX
PS Example 3; SEQ ID NO 5797; 51pp; English.
XX
CC The invention relates to antisense inhibitors of genes essential to
CC prokaryotic cellular proliferation, their use in identifying the genes,
CC their use in the discovery of novel antibiotics, the essential genes
CC themselves and the encoded proteins. The prokaryotes used are Escherichia

CC coli, *Staphylococcus aureus*, *Salmonella typhi*, *Klebsiella pneumoniae*,
 CC *Pseudomonas aeruginosa* and *Enterococcus faecalis*. The invention is also
 CC useful for the identification of potential new targets for antibiotic
 CC development. The antisense nucleic acids can also be used to identify
 CC proteins used in proliferation, to express these proteins, and to obtain
 CC antidiodes capable of binding to the expressed proteins. The proteins can
 CC be used to screen compounds in rational drug discovery programmes. The
 CC antisense nucleic acid sequence is also useful to screen for homologous
 CC nucleic acids which are required for cell proliferation in a wide variety
 CC of organisms. The present sequence represents an essential prokaryotic
 CC cellular proliferation protein. Note: The sequence data for this patent
 CC did not form part of the printed specification, but was obtained in
 CC electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences

XX Sequence 1018 AA;

Query Match 84.4%; Score 184; DB 4; Length 1018;
 Best Local Similarity 89.5%; Pred. No. 1.3e-15;
 Matches 34; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 QNKGNSFPDPTEKDKPKYEHHPNIIDIDPDSVPHNG 38
 DB 784 QNKGNSFPDPTEKDKPKYEHGNIIDIDPDSVPHNG 821

RESULT 13

ABJ18922
 ID ABJ18922 standard; protein; 1018 AA.

XX ABJ18922;

DT 06-MAR-2003 (first entry)

XX Pathogen specific antigen related staphylococcal protein SEQ ID No 68.

XX Antibacterial; virucide; fungicide; protozoacide; cytostatic; anti-HIV;

XX hyperimmune; serum-reactive; antigen; pathogen; tumour; allergen;

KW auto-immunity; vaccine; staphylococcal infection; antibody; cancer;

KW autoimmune disease; HIV; hepatitis.

XX *Staphylococcus* sp.

OS WO200259148-A2.

XX 01-AUG-2002.

PF 21-JAN-2002; 2002WO-EP000546.

XX 26-JAN-2001; 2001AT-00000130.

XX (CIST-) CISTEM BIOTECHNOLOGIES GMBH.

XX Meinke A, Nagy E, Von Ahsen U, Klade C, Henics T, Zauner W,

PI Mih DB, Vytvetecka O, Elz H, Dryla A, Weichart T, Hahner M,

PI Tempelmeier B;

XX WPI; 2003-075410/07.

XX Identifying, isolating and producing hyperimmune serum-reactive antigens
 PT from a pathogen, for preparing vaccine or medicament for treating or
 PT preventing e.g. staphylococcal infections, comprises providing antibody
 PT preparation.

XX Example 7; Page 157; 252pp; English.

XX The invention relates to a novel method for identifying, isolating and
 CC producing hyperimmune serum-reactive antigens from a pathogen, tumour,
 CC allergen, a tissue or host prone to auto-immunity, where the antigens are
 CC used in a vaccine, comprises providing antibody preparation from a plasma
 CC pool of a type of animal, or individual sera with antibodies against the
 CC specific pathogen, tumour, allergen, tissue or host prone to auto-
 CC immunity. The hyperimmune serum-reactive antigens comprising any of the

CC 62 sequences of 53-2261 amino acids fully defined in the specification,
 CC or their hyperimmune fragments are useful for the manufacture of a
 CC pharmaceutical preparation, particularly a vaccine against staphylococcal
 CC infections or colonisation against *S. aureus* or *S. epidermidis*. The
 CC preparation of antibodies is useful for the manufacture of a medicament
 CC for treating or preventing staphylococcal infections or colonisation
 CC against *S. aureus* or *S. epidermidis*. The antibody preparations may also
 CC be used for diagnostic and imaging purposes. Other conditions that can be
 CC treated include cancer, autoimmune diseases or infections caused by viral
 CC (e.g. HIV, hepatitis A, B or C), fungal or protozoan pathogens. This
 CC sequence represents a staphylococcal protein relating to the method for
 CC identifying and producing pathogen specific antigens of the invention

XX Sequence 1018 AA;

Query Match 84.4%; Score 184; DB 6; Length 1018;
 Best Local Similarity 89.5%; Pred. No. 1.3e-15;
 Matches 34; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 QNKGNSFPDPTEKDKPKYEHHPNIIDIDPDSVPHNG 38
 DB 784 QNKGNSFPDPTEKDKPKYEHGNIIDIDPDSVPHNG 821

RESULT 14

ABM72537
 ID ABM72537 standard; protein; 1018 AA.

XX ABM72537;

DT 20-NOV-2003 (first entry)

XX *Staphylococcus aureus* protein #1777.

XX Antibacterial; vaccine; gene therapy; infection; sepsis; diagnosis;

KW enzymatic assay; antibiotic target.

XX *Staphylococcus aureus*.

PN WO200294868-A2.

XX 28-NOV-2002.

PF 27-MAR-2002; 2002WO-IB002637.

XX 27-MAR-2001; 2001GB-00007661.

XX (CHIR-) CHIRON SPA.

XX Maignani V, Mora M, Scarselli M;

XX WPI; 2003-120786/11.

DR N-PSDB; ACF74097.

XX New *Staphylococcus aureus* protein, useful as a vaccine for treating or
 PT preventing *Staphylococcal* infection, specifically an infection caused by
 PT *S. aureus*, e.g. sepsis.

XX Claim 1; SEQ ID NO 3554; 49pp; English.

XX The invention relates to novel genes and encoded proteins from

CC *Staphylococcus aureus*. A composition comprising the *S. aureus* protein, a

CC nucleic acid encoding the protein, or an antibody to the protein, is

CC useful as a pharmaceutical, particularly as a vaccine for treating or

CC preventing infection due to *Staphylococcus* bacteria, specifically an

CC infection caused by *S. aureus*. The composition is particularly useful for

CC treating or preventing sepsis in a patient. The composition can also be

CC used for diagnostics. The protein is also used in an assay for enzymatic

CC studies and as a target for antibodies. This sequence represents one of

RESULT 4
US-10-731-238-36
; Sequence 36, Application US/10731238
; Publication No. US20050123552A1
; GENERAL INFORMATION:
; APPLICANT: Hook, Magnus
; Patti, Joseph M.
; House-Pompeo, Karen L.
; Speciale, Pietro
; Joh, Danny
; McGavin, Martin J.
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
; AND METHODS OF USE
; NUMBER OF SEQUENCES: 105
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: TX
; COUNTRY: USA
; ZIP: 77210-4433
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/731,238
; FILING DATE: 10-Dec-2003
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/010,317
; FILING DATE: 21-Jan-1998
; APPLICATION NUMBER: US 60/036,139
; FILING DATE: 21-JAN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Hibler, David W.
; REGISTRATION NUMBER: 41,071
; REFERENCE/DOCKET NUMBER: TAMK:189
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 512-418-3000
; TELEFAX: 512-474-7577
; INFORMATION FOR SEQ ID NO: 36:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 38 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 36:
US-10-731-238-36
Query Match 100.0%; Score 53; DB 18; Length 38;
Best Local Similarity 100.0%; Pred. No. 0.035;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 YE0GGNIVDI 10
| | | | | | | | | |
| | | | | | | | | |
DB 19 YE0GGNIVDI 28
RESULT 5
US-10-731-238-37
; Sequence 37, Application US/10731238
; Publication No. US20050123552A1
; GENERAL INFORMATION:
; APPLICANT: Hook, Magnus
; Patti, Joseph M.
; House-Pompeo, Karen L.
; Speciale, Pietro
; Joh, Danny
; McGavin, Martin J.
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
; AND METHODS OF USE

NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/731,238
FILING DATE: 10-Dec-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE: 21-Jan-1998
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAMK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 37:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 37:
US-10-731-238-37
Query Match 100.0%; Score 53; DB 18; Length 38;
Best Local Similarity 100.0%; Pred. No. 0.035;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 YE0GGNIVDI 10
| | | | | | | | | |
| | | | | | | | | |
DB 19 YE0GGNIVDI 28
RESULT 6
US-10-731-238-38
; Sequence 38, Application US/10731238
; Publication No. US20050123552A1
; GENERAL INFORMATION:
; APPLICANT: Hook, Magnus
; Patti, Joseph M.
; House-Pompeo, Karen L.
; Speciale, Pietro
; Joh, Danny
; McGavin, Martin J.
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
; AND METHODS OF USE
; NUMBER OF SEQUENCES: 105
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: TX
; COUNTRY: USA
; ZIP: 77210-4433
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30

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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/731,238
FILING DATE: 10-Dec-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE: 21-Jan-1998
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAMK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-478-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 38:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 38:
US-10-731-238-38

Query Match      100.0%; Score 53; DB 18; Length 38;
Best Local Similarity 100.0%; Pred. No. 0.035;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 YE0GGNIVDI 10
        |||||
        19 YE0GGNIVDI 28

RESULT 7
US-10-731-238-39
Sequence 39, Application US/10731238
Publication No. US20050123552A1
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
          Patti, Joseph M.
          House-Pompeo, Karen L.
          Speziale, Pietro
          Joh, Danny
          McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/731,238
FILING DATE: 10-Dec-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE: 21-Jan-1998
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAMK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-478-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 40:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 40:
US-10-731-238-40

Query Match      100.0%; Score 53; DB 18; Length 38;
Best Local Similarity 100.0%; Pred. No. 0.035;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 YE0GGNIVDI 10
        |||||
        19 YE0GGNIVDI 28

Db      19 YE0GGNIVDI 28
```

```

TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 39:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 39:
US-10-731-238-39

Query Match      100.0%; Score 53; DB 18; Length 38;
Best Local Similarity 100.0%; Pred. No. 0.035;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 YE0GGNIVDI 10
        |||||
        19 YE0GGNIVDI 28

Db      19 YE0GGNIVDI 28

RESULT 8
US-10-731-238-40
Sequence 40, Application US/10731238
Publication No. US20050123552A1
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
          Patti, Joseph M.
          House-Pompeo, Karen L.
          Speziale, Pietro
          Joh, Danny
          McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/731,238
FILING DATE: 10-Dec-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE: 21-Jan-1998
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAMK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 40:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 40:
US-10-731-238-40

Query Match      100.0%; Score 53; DB 18; Length 38;
Best Local Similarity 100.0%; Pred. No. 0.035;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

Best Local Similarity 100.0%; Pred. No. 0.035;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YEOGNIYDI 10
| | | | | | | |
Db 19 YEOGNIYDI 28

RESULT 9

US-10-731-238-41
; Sequence 41, Application US/10731238
; Publication No. US20050123552A1
; GENERAL INFORMATION:
; APPLICANT: Hook, Magnus
; Patti, Joseph M.
; House-Pompeo, Karen L.
; Speziale, Pietro
; John, Danny
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
; AND METHODS OF USE
; NUMBER OF SEQUENCES: 105
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: TX
; COUNTRY: USA
; ZIP: 77210-4433
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/731,238
; FILING DATE: 10-Dec-2003
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/010,317
; FILING DATE: 21-Jan-1998
; APPLICATION NUMBER: US 60/036,139
; FILING DATE: 21-JAN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Hibler, David W.
; REGISTRATION NUMBER: 41,071
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 512-418-3000
; TELEFAX: 512-474-7577
; INFORMATION FOR SEQ ID NO: 41:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 38 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 41:
US-10-731-238-41

Query Match 100.0%; Score 53; DB 18; Length 38;
Best Local Similarity 100.0%; Pred. No. 0.035;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YEOGNIYDI 10
| | | | | | | |
Db 19 YEOGNIYDI 28

RESULT 10
US-10-731-238-42
; Sequence 42, Application US/10731238
; Publication No. US20050123552A1
; GENERAL INFORMATION:
; APPLICANT: Hook, Magnus
; Patti, Joseph M.
; House-Pompeo, Karen L.
; Speziale, Pietro
; John, Danny
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
; AND METHODS OF USE
; NUMBER OF SEQUENCES: 105
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston

APPLICANT: Hook, Magnus
Patti, Joseph M.
House-Pompeo, Karen L.
Speziale, Pietro
John, Danny

TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
AND METHODS OF USE

NUMBER OF SEQUENCES: 105

CORRESPONDENCE ADDRESS:

ADDRESSEE: Arnold, White & Durkee

STREET: P.O. Box 4433

CITY: Houston

STATE: TX

COUNTRY: USA

ZIP: 77210-4433

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/731,238

FILING DATE: 10-Dec-2003

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/010,317

FILING DATE: 21-Jan-1998

APPLICATION NUMBER: US 60/036,139

FILING DATE: 21-JAN-1997

ATTORNEY/AGENT INFORMATION:

NAME: Hibler, David W.

REGISTRATION NUMBER: 41,071

REFERENCE/DOCKET NUMBER: TAMK:189

TELECOMMUNICATION INFORMATION:

TELEPHONE: 512-418-3000

TELEFAX: 512-474-7577

INFORMATION FOR SEQ ID NO: 42:

SEQUENCE CHARACTERISTICS:

LENGTH: 38 amino acids

TYPE: amino acid

STRANDEDNESS: <Unknown>

TOPOLOGY: linear

SEQUENCE DESCRIPTION: SEQ ID NO: 42:

US-10-731-238-42

Query Match 100.0%; Score 53; DB 18; Length 38;
Best Local Similarity 100.0%; Pred. No. 0.035;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YEOGNIYDI 10
| | | | | | | |
Db 19 YEOGNIYDI 28

RESULT 11

US-10-731-238-56
; Sequence 56, Application US/10731238
; Publication No. US20050123552A1
; GENERAL INFORMATION:
; APPLICANT: Hook, Magnus
; Patti, Joseph M.
; House-Pompeo, Karen L.
; Speziale, Pietro
; John, Danny
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
; AND METHODS OF USE
; NUMBER OF SEQUENCES: 105
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston

STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/731,238
FILING DATE: 10-Dec-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE: 21-Jan-1998
APPLICATION NUMBER: US 60/036,139
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAMK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 56:
SEQUENCE CHARACTERISTICS:
LENGTH: 39 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 56:
US-10-731-238-56

Query Match 100.0%; Score 53; DB 18; Length 39;
Best Local Similarity 100.0%; Pred. No. 0.035;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YE0GGNIVDI 10
DB 19 YE0GGNIVDI 28

RESULT 12
US-09-813-820-8
Sequence 8, Application US/09813820
Patent No. US20020102262A1
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
Pactl, Joseph M.
House-Pompeo, Karen
Schanam, Narayana
Symersky, Jindrich
TITLE OF INVENTION: COLLAGEN BINDING PROTEIN COMPOSITIONS
AND METHODS OF USE
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: Texas
COUNTRY: U.S.
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/813,820
FILING DATE: 22-Mar-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/856,253

FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Kitchell, Barbara S.
REGISTRATION NUMBER: 33,928
REFERENCE/DOCKET NUMBER: TAMK:193
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
TELEFAX: (512) 474-7577
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 139 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-09-813-820-8

Query Match 100.0%; Score 53; DB 9; Length 139;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YE0GGNIVDI 10
DB 34 YE0GGNIVDI 43

RESULT 13
US-08-901-062-1
Sequence 1, Application US/08901062
Publication No. US20020025124A1
GENERAL INFORMATION:
APPLICANT: SEALS, JONATHAN R.
TITLE OF INVENTION: RECOMBINANT BIVALENT BACTERIAL VACCINE
FOR THE PREVENTION OF MASTITIS
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: HALE AND DORR LLP
STREET: 60 State Street
CITY: Boston
STATE: MA
COUNTRY: United States Of America
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/901,062
FILING DATE: 25-JUL-1997
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Baker, Hollie L.
REGISTRATION NUMBER: 31,321
REFERENCE/DOCKET NUMBER: 106941.153
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 526-6000
TELEFAX: (617) 526-5000
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 388 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-901-062-1

Query Match 100.0%; Score 53; DB 8; Length 388;
Best Local Similarity 100.0%; Pred. No. 0.39;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YEOGGINVIDI 10
DB 283 YEOGGINVIDI 292

RESULT 14

US-08-781-986A-5251
Sequence 5251, Application US/08781986A
Publication No. US20030054436A1
GENERAL INFORMATION:
APPLICANT: Charles Kunsch
TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
NUMBER OF SEQUENCES: 5255
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COUNTRY: USA
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4MB storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/781,986A
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Benson, Bob
REGISTRATION NUMBER: 30,446
REFERENCE/DOCKET NUMBER: PB248PP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 5251:
SEQUENCE CHARACTERISTICS:
LENGTH: 559 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-781-986A-5251

Query Match 100.0%; Score 53; DB 8; Length 559;
Best Local Similarity 100.0%; Pred. No. 0.57;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 YEOGGINVIDI 10
DB 319 YEOGGINVIDI 328

RESULT 15

US-10-329-624-5251
Sequence 5251, Application US/10329624
Publication No. US20040043037A1
GENERAL INFORMATION:
APPLICANT: Charles Kunsch
TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
NUMBER OF SEQUENCES: 5256
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue

CITY: Rockville
STATE: Maryland
COUNTRY: USA
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4MB storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/329,624
FILING DATE: 27-Dec-2002
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/956,171
FILING DATE: October 20, 1997
APPLICATION NUMBER: 60/009,861
FILING DATE: January 5, 1996
APPLICATION NUMBER: 08/781,986
FILING DATE: January 3, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Mark J. Hyman
REGISTRATION NUMBER: 46,789
REFERENCE/DOCKET NUMBER: PB248P1D1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (240) 314-1224
TELEFAX: (301) 309-8439
INFORMATION FOR SEQ ID NO: 5251:
SEQUENCE CHARACTERISTICS:
LENGTH: 559 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 5251:
US-10-329-624-5251

Query Match 100.0%; Score 53; DB 15; Length 559;
Best Local Similarity 100.0%; Pred. No. 0.57;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 YEOGGINVIDI 10
DB 319 YEOGGINVIDI 328

Search completed: October 22, 2005, 12:39:44
Job time : 57.25 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 22, 2005, 06:10:10 ; Search time 11.45 Seconds
(without alignments)
84.032 Million cell updates/sec

Title: US-10-731-238-72
Perfect score: 53
Sequence: 1 YEOGNNIVDI 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 segs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	53	100.0	940	2	S19702 fibronectin-binding
2	53	100.0	961	2	G90053 hypothetical prote
3	53	100.0	1018	2	A32192 fibronectin-binding
4	53	100.0	1038	2	H90053 hypothetical prote
5	41	77.4	208	2	D83318 periplasmic chap
6	40	75.5	215	2	H72290 conserved hypochet
7	39	73.6	599	1	A64235 cytochrome-acces
8	38	71.7	62	2	H89941 hypothetical prote
9	38	71.7	212	2	S56199 hypothetical prote
10	38	71.7	363	2	S19419 hypothetical prote
11	38	71.7	672	1	S73715 cytochrome acces
12	37	69.8	222	2	AD2454 two-component resp
13	37	69.8	329	2	S67807 hypothetical prote
14	37	69.8	376	2	S51335 probable aryl-alco
15	37	69.8	412	2	H90244 pre mRNA splicing
16	37	69.8	420	2	H22718 hypothetical prote
17	37	69.8	677	2	E95417 probable oxidoredu
18	36	67.9	109	2	G87206 hypothetical prote
19	36	67.9	129	2	JG0019 flagellar basal-bo
20	36	67.9	311	2	S72967 hypothetical prote
21	36	67.9	326	2	A41732 heterogeneous ribo
22	36	67.9	326	2	H72472 hypothetical prote
23	36	67.9	365	2	A26459 helix-desstabilizin
24	36	67.9	366	1	S22315 snRNP-associated
25	36	67.9	667	2	AE2943 oxidoreductase Atu
26	36	67.9	667	2	E98339 probable oxidoredu
27	35	66.0	145	2	E70168 flagellar protein
28	35	66.0	216	2	D89827 conserved hypochet
29	35	66.0	317	2	T49591 probable 35 kDa ri

10	35	66.0	317	2	AD1542 oxidoreductases ho
31	35	66.0	317	2	AP1184 oxidoreductases ho
32	35	66.0	344	2	T03499 integrase/recombin
33	35	66.0	370	2	AB3175 hypothetical prote
34	35	66.0	377	2	T26958 hypothetical prote
35	35	66.0	378	2	T26684 hypothetical prote
36	35	66.0	470	2	A87298 hypothetical prote
37	35	66.0	489	2	F97118 levanase (limpo
38	35	66.0	606	2	JM0054 amiloride-sensitiv
39	35	66.0	809	2	E90016 hyaluronate lyase
40	35	66.0	1447	1	VG1HE3 E2 glycoprotein pr
41	35	66.0	1447	1	VG1HE2 E2 glycoprotein pr
42	35	66.0	1449	1	AA3573 E2 glycoprotein pr
43	35	66.0	1449	1	VG1HES E2 glycoprotein pr
44	35	66.0	1449	2	S47423 E2 glycoprotein pr
45	35	66.0	1451	1	Q01719 E2 glycoprotein pr

ALIGNMENTS

RESULT 1

S19702
fibronectin-binding protein B - Staphylococcus aureus
C:Species: Staphylococcus aureus
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
C:Accession: S19702
R:Joensson, K.; Signaess, C.; Mueller, H.P.; Lindberg, M.
Eur. J. Biochem. 202, 1041-1048, 1991
A:Title: Two different genes encode fibronectin binding proteins in Staphylococcus aureus
A:Reference number: S19702; MUID:92111475; PMID:1837266
A:Accession: S19702
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-940 <JOB>
A:Cross-references: UNIPROT:Q53682; EMBL:X62992; NID:949040; PIDN:CAA44726.1; PID:G58156
C:Keywords: fibronectin binding

Query Match 100.0%; Score 53; DB 2; Length 940;
Best Local Similarity 100.0%; Pred. No. 0.11;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YEOGNNIVDI 10
DB 700 YEOGNNIVDI 709

RESULT 2

hypothetical protein fmbB (imported) - Staphylococcus aureus (strain N315)
C:Species: Staphylococcus aureus
C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C:Accession: G90053
R:Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Ogura, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
A:Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.
A:Reference number: AB9758; MUID:21111952; PMID:11418146
A:Accession: G90053
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-961 <KUR>
A:Cross-references: UNIPROT:Q99RD3; GB:BA000018; PID:G13702452; PIDN:BAR43593.1; GSPD:
A:Experimental source: strain N315
C:Genetics:
A:Gene: fmbB

Query Match 100.0%; Score 53; DB 2; Length 961;
Best Local Similarity 100.0%; Pred. No. 0.12;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YEOGNNIVDI 10

Db 711 YE0GGNIVDI 720

RESULT 3

A32192
fibronectin-binding protein - Staphylococcus aureus
C:Species: Staphylococcus aureus
C:Date: 31-Jul-1989 #sequence_revision 31-Jul-1989 #text_change 16-Feb-1997
C:Accession: A32192
R:Stinson, C.; Raucci, G.; Joenson, K.; Lindgren, P.E.; Anantharamiah, G.M.; Hoeck, M.
Proc. Natl. Acad. Sci. U.S.A. 86, 659-703, 1989
A:Title: Nucleotide sequence of the gene for a fibronectin-binding protein from Staphylo-
A:Reference number: A32192; MUID:89098998; PMID:2521391
A:Accession: A32192
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1018 <SIG>
A:Cross-references: GB:J04151
C:Keywords: fibronectin binding

Query Match 100.0%; Score 53; DB 2; Length 1018;
Best Local Similarity 100.0%; Pred. No. 0.12;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 YE0GGNIVDI 10
Db 764 YE0GGNIVDI 773

RESULT 4

H90053
hypothetical protein fnb [imported] - Staphylococcus aureus (strain N315)
C:Species: Staphylococcus aureus
C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C:Accession: H90053
R:Kuroda, M.; Ohba, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguc
ma, A.; Mizutani-Uji, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.;
C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiratsugu, K.
Lancet 357, 1225-1240, 2001
A:Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.
A:Reference number: A89758; MUID:21311952; PMID:11418146
A:Accession: H90053
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1038 <KUR>
A:Cross-references: UNIPROT:Q99RD2; GB:BA000018; PID:g13702453; PIDN:BA843594.1; GSPDB:G
A:Experimental source: strain N315
C:Genetics:
A:Gene: fnb

Query Match 100.0%; Score 53; DB 2; Length 1038;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 YE0GGNIVDI 10
Db 760 YE0GGNIVDI 769

RESULT 5

DB3318
periplasmic chaperone lola PA2614 [imported] - Pseudomonas aeruginosa (strain PA01)
C:Species: Pseudomonas aeruginosa
C:Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004
C:Accession: DB3318
R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.; B
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kae, A.; Lapid, K.; Lam,
.; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patho-
A:Reference number: A82950; MUID:20437337; PMID:10984043
A:Accession: DB3318

A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-208 <STO>
A:Cross-references: UNIPROT:Q910M4; GB:AE004690; GB:AE004091; NID:g9948678; PIDN:AA06
A:Experimental source: strain PA01
C:Genetics:
A:Gene: lola; PA2614
C:Superfamily: outer membrane lipoprotein carrier protein precursor

Query Match 77.4%; Score 41; DB 2; Length 208;
Best Local Similarity 66.7%; Pred. No. 3.9;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

OY 1 YE0GGNIVD 9
Db 132 YE0GGNIVD 140

RESULT 6

H72290
conserved hypothetical protein - Thermotoga maritima (strain MSB8)
C:Species: Thermotoga maritima
C:Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
C:Accession: H72290
R:Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwin, M.L.; Dodson, R.J.; Haft, D.H.; Hickey
Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.
C.M.
Nature 399, 323-329, 1999
A:Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome seq
A:Reference number: A72200; MUID:99287316; PMID:10360571
A:Accession: H72290
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-215 <ARN>
A:Cross-references: UNIPROT:Q9X0M4; GB:AE001771; GB:AE000512; NID:g4981678; PIDN:AA03621
A:Experimental source: strain MSB8
C:Genetics:
A:Gene: TM1140

Query Match 75.5%; Score 40; DB 2; Length 215;
Best Local Similarity 70.0%; Pred. No. 6.3;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 YE0GGNIVDI 10
Db 164 YE0GGNIVDI 173

RESULT 7

A64235
cytadherence-accessory protein (hmv3) homolog MG317 - Mycoplasma genitalium
C:Species: Mycoplasma genitalium
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: A64235
R:Fraser, C.M.; Gocayne, J.D.; White, O.; Adams, M.D.; Clayton, R.A.; Fleischmann, R.D.
M.; Fuhrmann, J.; Nguyen, D.; Uitterback, T.R.; Saudek, D.M.; Phillips, C.A.; Merrick, J.
C.A.; Venter, J.C.
Science 270, 397-403, 1995
A:Title: The minimal gene complement of Mycoplasma genitalium.
A:Reference number: A64200; MUID:96026346; PMID:7569993
A:Accession: A64235
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-599 <TIG>
A:Cross-references: UNIPROT:Q57081; GB:U39713; GB:L43967; NID:g1046014; PID:g1046018; TI
A:Experimental source: strain G-37
C:Genetics:
A:Genetic code: SGC3
C:Superfamily: cytadherence-accessory protein hmv3

Query Match 73.6%; Score 39; DB 1; Length 599;
Best Local Similarity 50.0%; Pred. No. 28;
Matches 5; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 1 YE0GNNIVD 10
 |||||:
 Db 106 YDONGNVLDD 115

RESULT 8

H89941
 hypothetical protein SA1429 [imported] - Staphylococcus aureus (strain N315)
 C/Species: Staphylococcus aureus
 C/Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
 C/Accession: H89941
 R/Kutoda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguc
 ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.;
 C./ Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
 Lancet 357, 1225-1240, 2001
 A/Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.
 A/Reference number: A89758; PMID:11418146
 A/Accession: H89941
 A/Status: Preliminary
 A/Molecule type: DNA
 A/Residues: 1-62 <KUR>
 A/Cross-references: UNIPROT:Q99TP8; GB:BA000018; PID:g13701399; PIDN:BA842693.1; GSPDB:G
 A/Experimental source: strain N315
 C/Genetics:
 A/Gene: SA1429

Query Match 71.7%; Score 38; DB 2; Length 62;
 Best Local Similarity 87.5%; Pred. No. 4;
 Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YE0GNNIVD 8
 |||||:
 Db 2 YE0GNNIVD 9

RESULT 9
 S56199
 hypothetical protein YF056c - yeast (Saccharomyces cerevisiae)
 N/Alternate names: hypothetical protein R015
 C/Species: Saccharomyces cerevisiae
 C/Date: 02-Sep-1995 #sequence_revision 19-Oct-1995 #text_change 09-Jul-2004
 C/Accession: S56199; S62281
 R/Murkanti, Y.; Naitou, M.; Hagiwara, H.; Shibata, T.; Ozawa, M.; Sasamura, S.I.; Sasanu
 submitted to the EMBL Data Library, May 1995
 A/Description: Analysis of the nucleotide sequence of chromosome VI from Saccharomyces ce
 A/Reference number: S56186
 A/Accession: S56199
 A/Molecule type: DNA
 A/Residues: 1-212 <MUR>
 A/Cross-references: UNIPROT:P43547; EMBL:DS0617; NID:g836685; PIDN:BA09185.1; PID:g8366
 R/Murkanti, Y.
 submitted to the EMBL Data Library, December 1994
 A/Reference number: S62230
 A/Accession: S62281
 A/Molecule type: DNA
 A/Residues: 1-212 <WUM>
 A/Cross-references: EMBL:DA4603; NID:g871957; PIDN:BA08063.1; PID:g871970
 C/Genetics:
 A/Gene: SGD:AAD6
 A/Cross-references: SGD:S0001838
 A/Map position: 6L
 C/Superfamily: fission yeast pyridoxine 4-dehydrogenase

Query Match 71.7%; Score 38; DB 2; Length 212;
 Best Local Similarity 66.7%; Pred. No. 15;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 YE0GNNIVD 9
 |||||:
 Db 63 YE0GNNIVD 71

RESULT 10

S19419
 hypothetical protein YCR107w - yeast (Saccharomyces cerevisiae)
 C/Species: Saccharomyces cerevisiae
 C/Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 09-Jul-2004
 C/Accession: S19419
 R/Grenson, M.; Jauniaux, J.C.; Urrestarazu, L.A.
 submitted to the Protein Sequence Database, March 1992
 A/Reference number: S19376
 A/Accession: S19419
 A/Molecule type: DNA
 A/Residues: 1-363 <GRS>
 A/Cross-references: UNIPROT:P25612; EMBL:X59720; NID:g1907116; PID:g1907245; GSPDB:GN000
 A/Gene: SGD:AAD3; MIPS:YCR107w
 A/Cross-references: SGD:S0000704
 A/Map position: 3R
 C/Superfamily: fission yeast pyridoxine 4-dehydrogenase

Query Match 71.7%; Score 38; DB 2; Length 363;
 Best Local Similarity 66.7%; Pred. No. 26;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 YE0GNNIVD 9
 |||||:
 Db 60 YE0GNNIVD 68

RESULT 11

S73715
 cytochrome accessory protein HMW3 - Mycoplasma pneumoniae
 N/Alternate names: hypothetical protein H08_orf672
 C/Species: Mycoplasma pneumoniae
 A/Variety: ATCC 29342
 C/Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
 C/Accession: S73715; A43851; PH0112
 R/Himmelsreich, R.; Hilbert, H.; Plagens, H.; Pirl, E.; Li, B.C.; Herrmann, R.
 Nucleic Acids Res. 24, 4420-4449, 1996
 A/Title: Complete sequence analysis of the genome of the bacterium Mycoplasma pneumonia
 A/Reference number: S73327; PMID:97105885; PMID:8948633
 A/Accession: S73715
 A/Status: nucleic acid sequence not shown; translation not shown
 A/Molecule type: DNA
 A/Residues: 1-672 <HIM>
 A/Cross-references: UNIPROT:Q50360; EMBL:AE000037; GB:U00089; NID:g1674065; PIDN:AA8960
 A/Experimental source: ATCC 29342
 A/Note: the nucleotide sequence was submitted to the EMBL Data Library, November 1996
 R/Ogle, K.F.; Lee, K.K.; Krause, D.C.
 Infect. Immun. 60, 1631-1641, 1992
 A/Title: Nucleotide sequence analysis reveals novel features of the phase-variable cyto
 A/Reference number: A43851; PMID:92192840; PMID:1548085
 A/Accession: A43851
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-672 <OGU1>
 A/Cross-references: GB:U38997; GB:M82965; GB:S89246; GB:U11381; NID:g6339784; PIDN:AAA61
 A/Note: sequence extracted from NCBI backbone (NCBI:89246, NCBI:P:89247)
 R/Ogle, K.F.; Lee, K.K.; Krause, D.C.
 Gene 97, 69-75, 1991
 A/Title: Cloning and analysis of the gene encoding the cytochrome phase-variable prot
 A/Reference number: PH0112; PMID:9113898; PMID:1899847
 A/Accession: PH0112
 A/Molecule type: protein
 A/Residues: 279-287, 'R', 289-290 <OGU2>
 A/Note: the amino end of the mature protein is blocked
 C/Genetics:
 A/Gene: hmw3
 A/genetic code: SGC3
 C/Superfamily: cytochrome-accessory protein hmw3
 C/Keywords: blocked amino end

Query Match 71.7%; Score 38; DB 1; Length 672;
 Best Local Similarity 50.0%; Pred. No. 49;

Matches 5; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 1 YE0GGINVDI 10
|||:::
Db 106 YD0GGINVDI 115

RESULT 12
AD2454
Two-component response regulator alr5188 [imported] - Nostoc sp. (strain PCC 7120)
C/Species: Nostoc sp. PCC 7120
A/Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C/Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004
C/Accession: AD2454
R/Kaneko, T.; Nakamura, Y.; Molk, C.P.; Kuritz, T.; Saeguchi, S.; Watanabe, A.; Iriiguchi, N.; Nakazaki, N.; Shimo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S.
DNA Res. 8, 205-213, 2001
A/Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Anabaena PCC 7120
A/Reference number: AB1807; MUID:21595285; PMID:11759840
A/Accession: AD2454
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-222 <KUR>
A/Residues: 1-222 <KUR>
A/Cross-references: UNIPROT:O8YLV8; GB:BA000019; PIDN:BA076887.1; PID:g17134327; GSPDB:G
A/Experimental source: strain PCC 7120
C/Genetics:
A/Gene: alr5188
C/Superfamily: ompR protein; response regulator homology

Query Match 69.8%; Score 37; DB 2; Length 222;
Best Local Similarity 60.0%; Pred. No. 23;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 YE0GGINVDI 10
|||:::
Db 187 YD0GGINVDI 196

RESULT 13
S67807
Hypothetical protein YDL243C - yeast (Saccharomyces cerevisiae)
N/Alternate names: hypothetical protein D0752
C/Species: Saccharomyces cerevisiae
C/Date: 12-Jul-1996 #sequence_revision 12-Jul-1996 #text_change 09-Jul-2004
C/Accession: S67807
R/Alt-Moerbe, J.; Schneider, C.; Moro, M.
submitted to the Protein Sequence Database, July 1996
A/Reference number: S67798
A/Accession: S67807
A/Molecule type: DNA
A/Residues: 1-329 <ALT>
A/Cross-references: UNIPROT:O07747; EMBL:Z74291; NID:g1431413; PID:g1431414; GSPDB:GN000
A/Experimental source: strain S288C
C/Genetics:
A/Gene: SGD:AD4; MIPS:YDL243C
A/Cross-references: SGD:S0002402
A/Map position: 4L
C/Superfamily: fission yeast pyridoxine 4-dehydrogenase

Query Match 69.8%; Score 37; DB 2; Length 329;
Best Local Similarity 66.7%; Pred. No. 36;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 YE0GGINVDI 9
|||:::
Db 17 YE0GGINVDI 25

RESULT 14
S51335
probable aryl-alcohol dehydrogenase (NADP) (EC 1.1.1.91) YNL331c - yeast (Saccharomyces
N/Alternate names: protein N0300
C/Species: Saccharomyces cerevisiae

C/Date: 23-Feb-1995 #sequence_revision 12-May-1995 #text_change 09-Jul-2004
C/Accession: S51335; S57392; S63314; S63317
R/van Dyck, L.; Pascual-Palmer, A.; Goffeau, A.
submitted to the EMBL Data Library, December 1994
A/Description: A 8.2 kb DNA segment from chromosome XIV carries the RPD3 and PAS8 genes
located gene for a putative aryl-alcohol dehydrogenase.
A/Reference number: S51334
A/Accession: S51335
A/Molecule type: DNA
A/Residues: 1-376 <VAN>
A/Cross-references: UNIPROT:P42884; EMBL:X83226; NID:G642335; PID:G642337
R/van Dyck, L.; Pascual-Palmer, A.; Purnelle, B.; Goffeau, A.
Yeast 11, 987-991, 1995
A/Title: An 8.2 kb DNA segment from chromosome XIV carries the RPD3 and PAS8 genes as we
d gene for a putative aryl-alcohol dehydrogenase.
A/Reference number: S57391; MUID:96021610; PMID:8533474
A/Accession: S57392
A/Status: nucleic acid sequence not shown
A/Molecule type: DNA
A/Residues: 1-223, 'K', 225-277, 'G', 279-376 <VAN>
A/Cross-references: EMBL:X83226
A/Note: the authors did not display the tryptophanes at positions 43, 84, 88, 144, 152,
R/Coster, F.; Jomiaux, J.L.; Goffeau, A.; Purnelle, B.; Van Dyck, L.
submitted to the Protein Sequence Database, April 1996
A/Reference number: S63151
A/Accession: S63314
A/Molecule type: DNA
A/Residues: 1-376 <COS>
A/Cross-references: EMBL:Z71607; NID:g1302452; PID:g1302453; MIPS:YNL331c
A/Experimental source: strain S288C
R/Obermayer, B.; Piravandi, E.; Rinke, M.
submitted to the Protein Sequence Database, April 1996
A/Reference number: S63317
A/Accession: S63317
A/Molecule type: DNA
A/Residues: 1-376 <OBR>
A/Cross-references: EMBL:Z71607; NID:g1302452; PID:g1302453; MIPS:YNL331c
A/Experimental source: strain S288C
C/Genetics:
A/Gene: SGD:AD14
A/Cross-references: SGD:S0005275
A/Map position: 14L
C/Superfamily: fission yeast pyridoxine 4-dehydrogenase
C/Keywords: alcohol metabolism; NADP; oxidoreductase

Query Match 69.8%; Score 37; DB 2; Length 376;
Best Local Similarity 66.7%; Pred. No. 41;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 YE0GGINVDI 9
|||:::
Db 63 YE0GGINVDI 71

RESULT 15
H90244
pre mRNA splicing protein [imported] - Sulfolobus solfataricus
C/Species: Sulfolobus solfataricus
C/Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 09-Jul-2004
C/Accession: H90244
R/She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Chan-
Jong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thl-Ngoc, H.P.; Redder, P.
submitted to GenBank, April 2001
A/Description: Sulfolobus solfataricus complete genome.
A/Reference number: A99139
A/Accession: H90244
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-412 <KUR>
A/Cross-references: UNIPROT:O97ZH3; GB:AE006641; NID:g13814119; PIDN:AAK41215.1; GSPDB:G
C/Genetics:
A/Gene: SSO0939

C:Superfamily: garden pea SAR DNA-binding protein

Query Match 69.8%; Score 37; DB 2; Length 412;

Best Local Similarity 66.7%; Pred. No. 45;

Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 YEOGNIVD 9

||: |||||

Db 16 YDENGIVD 24

Search completed: October 22, 2005, 08:04:27
Job time : 12.45 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 22, 2005, 06:06:36 ; Search time 55.85 Seconds
(without alignments)
91.688 Million cell updates/sec

Title: US-10-731-238-72

Perfect score: 53

Sequence: 1 YEOGGNIVDI 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database: UniProt_03:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	53	100.0	152	2	Q9AEP9
2	53	100.0	940	2	Q53682
3	53	100.0	943	2	Q8NUH8
4	53	100.0	957	2	Q6G6H4
5	53	100.0	961	2	Q99RD3
6	53	100.0	961	2	Q7A3J8
7	53	100.0	1015	2	Q8NDU7
8	53	100.0	1015	2	Q6G6H3
9	53	100.0	1018	1	FNBA_STAAU
10	53	100.0	1038	2	Q99RD2
11	53	100.0	1038	2	Q7A3J7
12	52	98.1	965	2	Q6GDU5
13	44	83.0	289	2	Q8KBG2
14	42	79.2	315	2	Q8J2U7
15	42	79.2	388	1	NORA_ASPFL
16	42	79.2	388	1	NORA_ASPPA
17	41	77.4	208	1	LOLA_PSEAE
18	41	77.4	382	2	Q6UEH5
19	41	77.4	591	2	Q8KVV4
20	40	75.5	215	2	Q9XOM4
21	40	75.5	287	2	Q7N3W7
22	39	73.6	129	2	Q9ONQ0
23	39	73.6	363	2	Q7S8R6
24	39	73.6	367	1	COBD_THETN
25	39	73.6	599	1	HMW3_MYCCE
26	39	73.6	699	2	Q7NN53
27	39	73.6	1566	2	Q9LJL0
28	38	71.7	62	2	Q99TP8
29	38	71.7	62	2	Q7A5A8
30	38	71.7	212	1	AAD6_YEAST
31	38	71.7	212	2	Q6BIB9

32	38	71.7	224	2	Q8ING7	Q8ING7 bacillus an
33	38	71.7	229	2	Q8NW97	Q8NW97 staphylococ
34	38	71.7	229	2	Q6G8W7	Q6G8W7 staphylococ
35	38	71.7	232	2	Q68YA7	Q68YA7 rhodococcus
36	38	71.7	234	2	Q59893	Q59893 penicillium
37	38	71.7	253	2	Q6N965	Q6N965 rhodopseudo
38	38	71.7	363	1	AD3_YEAST	P25612 saccharomyc
39	38	71.7	387	1	STCV_EMENT	Q00727 emericeila
40	38	71.7	672	1	HMW3_MYCPN	Q50360 mycoplasma
41	38	71.7	949	2	Q8GFA5	Q8GFA5 photorhabdu
42	38	71.7	985	2	Q982Q7	Q982Q7 rhizobium 1
43	38	71.7	1043	2	Q85157	Q85157 photorhabdu
44	38	71.7	1043	2	Q7M2V7	Q7M2V7 photorhabdu
45	38	71.7	1258	2	Q81EB3	Q81EB3 plasmodium

ALIGNMENTS

RESULT 1					
Q9AEP9	PRELIMINARY;	PRT;	152 AA.		
AC Q9AEP9;					
DT 01-JUN-2001 (TrEMBLrel. 17, Created)					
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)					
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)					
DE Fibronectin-binding protein (Fragment).					
GN Name=fnb;					
OS Staphylococcus aureus.					
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.					
OX NCBI_TaxID=1280;					
RN [1]					
RP SEQUENCE FROM N.A.					
RC STRAIN=CMRSA-1;					
RX MEDLINE=21246681; PubMed=11349044;					
RA DOI=10.1128/IAI.69.6.3791-3799.2001;					
RZ Rice K., Huesca M., Vaz D., McGavin M.J.;					
RT "variance in fibronectin binding and fnb locus polymorphisms in					
RT Staphylococcus aureus: identification of antigenic variation in a					
RT fibronectin binding protein adhesin of the epidemic CMRSA-1 strain of					
RT methicillin-resistant S. aureus."					
RL Infect. Immun. 69:3791-3799(2001).					
DR EMBL: AY029184; AAK31588.1; -					
FT NON_TER					
FT NON_TER					
FT NON_TER					
SQ SEQUENCE	152 AA;	17193 MW;	CFA3913C2B1C025 CRC64;		
Query Match					
Best Local Similarity 100.0%; Score 53; DB 2; Length 152;					
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;					
QY	1	YEOGGNIVDI	10		
Db	19	YEOGGNIVDI	28		
RESULT 2					
Q53682	PRELIMINARY;	PRT;	940 AA.		
AC Q53682;					
DT 01-NOV-1996 (TrEMBLrel. 01, Created)					
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)					
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)					
DE Fibronectin binding protein B.					
GN Name=fnbB;					
OS Staphylococcus aureus.					
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.					
OX NCBI_TaxID=1280;					
RN [1]					
RP SEQUENCE FROM N.A.					
RC STRAIN=8325-4;					
RX MEDLINE=92111475; PubMed=1837266;					
RA Jonsson K., Signas C., Muller H.P., Lindberg M.;					

```

RT      "Two different genes encode fibronectin binding proteins in
RT      Staphylococcus aureus. The complete nucleotide sequence and
RT      characterization of the second gene."
RL      Eur. J. Biochem. 202;1041-1048 (1991).
CC      -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC      an amide bond (By similarity).
DR      EMBL: X62992; CAA44726.1; -.
DR      PIR: S19702; S19702.
DR      HSSP: Q53653; 1N67.
DR      GO: GO:0009986; C:cell surface; IEA.
DR      GO: GO:0005618; C:cell wall; IEA.
DR      GO: GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR      GO: GO:0016020; C:membrane; IEA.
DR      GO: GO:0007155; P:cell adhesion; IEA.
DR      InterPro: IPR008966; Adhes_bact.
DR      InterPro: IPR004237; Fn_bind.
DR      InterPro: IPR005877; Gpos_YsIRK.
DR      pfam: PF02986; Fn_bind_2.
DR      pfam: PF04650; YsIRK_signal; 1.
DR      TIGRFAMs: TIGR01167; LpXTG_anchor; 1.
DR      TIGRFAMs: TIGR01168; YsIRK_signal; 1.
DR      PROSITE: PS50847; GRAM_POS_ANCHORING; 1.
KW      Cell wall; Peptidoglycan-anchor.
SQ      SEQUENCE 940 AA; 103555 MW; E35FBBCA907AE345 CRC64;

Query Match          100.0%; Score 53; DB 2; Length 940;
Best Local Similarity 100.0%; Pred. No. 0.53;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      1 YE0GGNIVDI 10
DB      700 YE0GGNIVDI 709

RESULT 3
O8NU08      PRELIMINARY;      PRT;      943 AA.
ID      O8NU08
AC      O8NU08;
DT      01-OCT-2002 (TrEMBLrel. 22, Created)
DT      01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT      01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE      FnbB protein.
GN      Name=fnbB; OrderedLocustNames=MM2420;
OS      Staphylococcus aureus (strain MM2).
OC      Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX      NCBI_TaxID=196620;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN=MM2.
RX      MEDLINE=22040717; PubMed=12044378; DOI=10.1016/S0140-6736(02)08713-5;
RA      Baba T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Oguchi A.,
RA      Nagai Y., Iwama N., Asano K., Naito T., Kuroda H., Cui L.,
RA      Yamamoto K., Hiramatsu K.;
RT      "Genome and virulence determinants of high virulence community-
RT      acquired MRSA.";
RL      Lancet 359;1819-1827(2002).
CC      -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC      an amide bond (By similarity).
DR      EMBL: AP004830; BAB96285.1; -.
DR      HSSP: Q53653; 1N67.
DR      GO: GO:0009986; C:cell surface; IEA.
DR      GO: GO:0005618; C:cell wall; IEA.
DR      GO: GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR      GO: GO:0016020; C:membrane; IEA.
DR      GO: GO:0007155; P:cell adhesion; IEA.
DR      InterPro: IPR008966; Adhes_bact.
DR      InterPro: IPR004237; Fn_bind.
DR      InterPro: IPR005877; Gpos_YsIRK.
DR      InterPro: IPR001899; Gram_pos_anchor.
DR      pfam: PF02986; Fn_bind_1.
DR      pfam: PF00746; Gram_pos_anchor; 1.

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DR      pfam: PF04650; YsIRK_signal; 1.
DR      TIGRFAMs: TIGR01167; LpXTG_anchor; 1.
DR      TIGRFAMs: TIGR01168; YsIRK_signal; 1.
DR      PROSITE: PS50847; GRAM_POS_ANCHORING; 1.
KW      Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ      SEQUENCE 943 AA; 104537 MW; DA8A5FF31947B1B6A CRC64;

Query Match          100.0%; Score 53; DB 2; Length 943;
Best Local Similarity 100.0%; Pred. No. 0.53;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      1 YE0GGNIVDI 10
DB      707 YE0GGNIVDI 716

RESULT 4
O6G6H4      PRELIMINARY;      PRT;      957 AA.
ID      O6G6H4
AC      O6G6H4;
DT      05-JUL-2004 (TrEMBLrel. 27, Created)
DT      05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT      05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE      Fibronectin-binding protein.
GN      Name=fnbB; OrderedLocustNames=SN52387;
OS      Staphylococcus aureus (strain MSSA476).
OC      Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX      NCBI_TaxID=282459;
RN      [1]
RP      SEQUENCE FROM N.A.
RX      PubMed=15213324; DOI=10.1073/pnas.0402521101;
RA      Holden M.T.G., Fell E.J., Lindsey J.A., Peacock S.J., Day N.P.J.,
RA      Enright M.C., Foster T.J., Moore C.E., Hurst L., Atkin R., Barron A.,
RA      Baeson N., Bentley S.D., Chillingworth C., Chillingworth T.,
RA      Churcher C., Clark L., Cotton C., Cronin A., Doggett U., Dowd L.,
RA      Feltham T., Hance Z., Harris B., Hauser H., Holtroyd S., Jagels K.,
RA      James K.D., Leonard N., Line A., Mayes R., Moule S., Mungall K.,
RA      Ormond D., Quail M.A., Rabinowitch E., Rutherford K.M., Sanders M.,
RA      Sharp S., Simmonds M., Stevens K., Whitehead S., Barrall B.G.,
RA      Spratt B.G., Parkhill J.;
RT      "Complete genomes of two clinical Staphylococcus aureus strains:
RT      evidence for the rapid evolution of virulence and drug resistance.";
RL      Proc. Natl. Acad. Sci. U.S.A. 101:9786-9791(2004).
CC      -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC      an amide bond (By similarity).
DR      EMBL: BX571857; CAG44201.1; -.
DR      GO: GO:0009986; C:cell surface; IEA.
DR      GO: GO:0005618; C:cell wall; IEA.
DR      GO: GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR      GO: GO:0016020; C:membrane; IEA.
DR      GO: GO:0007155; P:cell adhesion; IEA.
DR      InterPro: IPR008966; Adhes_bact.
DR      InterPro: IPR004237; Fn_bind.
DR      InterPro: IPR005877; Gpos_YsIRK.
DR      InterPro: IPR001899; Gram_pos_anchor.
DR      pfam: PF02986; Fn_bind_1.
DR      pfam: PF00746; Gram_pos_anchor; 1.
DR      pfam: PF04650; YsIRK_signal; 1.
DR      TIGRFAMs: TIGR01167; LpXTG_anchor; 1.
DR      TIGRFAMs: TIGR01168; YsIRK_signal; 1.
DR      PROSITE: PS50847; GRAM_POS_ANCHORING; 1.
KW      Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ      SEQUENCE 957 AA; 105980 MW; 28F8BA7FFDFP3EAF CRC64;

Query Match          100.0%; Score 53; DB 2; Length 957;
Best Local Similarity 100.0%; Pred. No. 0.54;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      1 YE0GGNIVDI 10
DB      707 YE0GGNIVDI 716

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RESULT 5
Q99RD3 PRELIMINARY; PRT; 961 AA.
ID 099RD3;
AC 099RD3;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Fibronectin-binding protein homolog.
GN Name=fnbB; OrderedLocuNames=SAV2502;
OS Staphylococcus aureus (strain Mu50 / ATCC 700699).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=158878;
RN 11)
RP SEQUENCE FROM N.A.
RC STRAIN=MU50 / ATCC 700699;
RX MEDLINE=21311952; PubMed=1418146; DOI=10.1016/S0140-6736(00)04403-2;
RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Lian J.-Q., Ito T.,
RA Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,
RA Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
RA Sekitizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
RA Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
RA Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.,
RT "Whole genome sequencing of methicillin-resistant Staphylococcus
RT aureus."
RT Lancet 357:1225-1240(2001).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC an amide bond (By similarity).
EMBL: AP003365; BAB58664.1; -.
DR PIR; G90053; G90053.
DR HSSP; Q53653; IN67.
DR GO; GO:0009986; C:cell surface; IEA.
DR GO; GO:0005618; C:cell wall; IEA.
DR GO; GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0007155; P:cell adhesion; IEA.
DR InterPro; IPR008966; Adhes_bact.
DR InterPro; IPR004237; Fn_bind.
DR InterPro; IPR005877; Gpos_YsIRK.
DR InterPro; IPR001899; Gram_pos_anchor.
DR Pfam; PF02986; Fn_bind_1.
DR Pfam; PF00746; Gram_pos_anchor_1.
DR Pfam; PF04650; YsIRK_signal; 1.
DR TIGRFAMs; TIGR01167; LPXTG_anchor; 1.
DR TIGRFAMs; TIGR01168; YsIRK_signal; 1.
DR PROSITE; PS50847; GRAM_POS_ANCHORING; 1.
KW Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ SEQUENCE 961 AA; 106010 MW; 364940F884EA4101 CRC64;

Query Match 100.0%; Score 53; DB 2; Length 961;
Best Local Similarity 100.0%; Pred. No. 0.54;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YEOGGINVDI 10
DB 711 YEOGGINVDI 720

RESULT 6
Q7A3J8 PRELIMINARY; PRT; 961 AA.
ID 07A3J8;
AC 07A3J8;
DT 05-JUN-2004 (TrEMBLrel. 27, Created)
DT 05-JUN-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUN-2004 (TrEMBLrel. 27, Last annotation update)
DE FnbB protein.
GN Name=fnbB; OrderedLocuNames=SA2290;
OS Staphylococcus aureus (strain N315).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=158879;
RN 11)
RP SEQUENCE FROM N.A.
RX MEDLINE=21311952; PubMed=1418146; DOI=10.1016/S0140-6736(00)04403-2;

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RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Lian J.-Q., Ito T.,
RA Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,
RA Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
RA Sekitizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
RA Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
RA Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.,
RT "Whole genome sequencing of methicillin-resistant Staphylococcus
RT aureus."
RT Lancet 357:1225-1240(2001).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC an amide bond (By similarity).
EMBL: AP003337; BAB43593.1; -.
DR GO; GO:0009986; C:cell surface; IEA.
DR GO; GO:0005618; C:cell wall; IEA.
DR GO; GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0007155; P:cell adhesion; IEA.
DR InterPro; IPR008966; Adhes_bact.
DR InterPro; IPR004237; Fn_bind.
DR InterPro; IPR005877; Gpos_YsIRK.
DR InterPro; IPR001899; Gram_pos_anchor.
DR Pfam; PF02986; Fn_bind_1.
DR Pfam; PF00746; Gram_pos_anchor_1.
DR Pfam; PF04650; YsIRK_signal; 1.
DR TIGRFAMs; TIGR01167; LPXTG_anchor; 1.
DR TIGRFAMs; TIGR01168; YsIRK_signal; 1.
DR PROSITE; PS50847; GRAM_POS_ANCHORING; 1.
KW Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ SEQUENCE 961 AA; 106010 MW; 364940F884EA4101 CRC64;

Query Match 100.0%; Score 53; DB 2; Length 961;
Best Local Similarity 100.0%; Pred. No. 0.54;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YEOGGINVDI 10
DB 711 YEOGGINVDI 720

RESULT 7
Q8NU7 PRELIMINARY; PRT; 1015 AA.
ID 08NU7;
AC 08NU7;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE FnbB protein.
GN Name=fnbB; OrderedLocuNames=MM2421;
OS Staphylococcus aureus (strain MM2).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=196620;
RN 11)
RP SEQUENCE FROM N.A.
RC STRAIN=MM2;
RX MEDLINE=22040717; PubMed=12044378; DOI=10.1016/S0140-6736(02)08713-5;
RA Baba T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Oguchi A.,
RA Nagai Y., Iwama N., Asano K., Naimi T., Kuroda H., Cui L.,
RA Yamamoto K., Hiramatsu K.,
RT "genome and virulence determinants of high virulence community-
RT acquired MRSA."
RT Lancet 359:1819-1827(2002).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC an amide bond (By similarity).
EMBL: AP004830; BAB96286.1; -.
DR GO; GO:0009986; C:cell surface; IEA.
DR GO; GO:0005618; C:cell wall; IEA.
DR GO; GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0007155; P:cell adhesion; IEA.
DR InterPro; IPR008966; Adhes_bact.
DR InterPro; IPR004237; Fn_bind.
DR InterPro; IPR005877; Gpos_YsIRK.

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DR InterPro: IPR001899; Gram_pos_anchor.
DR Pfam: PF02986; Fn_bind; 1.
DR Pfam: PF00746; Gram_pos_anchor; 1.
DR Pfam: PF04650; YSIRK_signal; 1.
DR TIGRFAMs: TIGR01167; LPXTG_anchor; 1.
DR TIGRFAMs: TIGR01168; YSIRK_signal; 1.
DR PROSITE: PS50847; GRAM_POS_ANCHORING; 1.
DR Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ SEQUENCE 1015 AA; 111145 MW; DDF9281BB64D44D2 CRC64;

Query Match          100.0%; Score 53; DB 2; Length 1015;
Best Local Similarity 100.0%; Pred. No. 0.57;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YE0GGNIVDI 10
Db 765 YE0GGNIVDI 774

RESULT 8
ID Q6G6H3 PRELIMINARY; PRT; 1015 AA.
AC Q6G6H3;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE Fibronectin-binding protein.
GN OrderedLocustNames=SA52388;
OS Staphylococcus aureus (strain MSSA476).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=282459;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=15213324; DOI=10.1073/pnas.0402521101;
RA Holden M.T.G., Fell E.J., Lindsey J.A., Peacock S.J., Day N.P.J.,
RA Enright M.C., Foster T.J., Moore C.E., Hurst L., Atkin R., Barton A.,
RA Bason N., Bentley S.D., Chillingworth C., Chillingworth T.,
RA Churcher C., Clark L., Corton C., Cronin A., Doggett J., Dowd L.,
RA Felwell T., Hance Z., Harris B., Hauser H., Holtroyd S., Jagels K.,
RA James K.D., Leonard N., Line A., Mayes R., Moule S., Mungall K.,
RA Ormond D., Quail M.A., Rabinowitsch E., Rutherford K.M., Sanders M.,
RA Sharp S., Simmonds M., Stevens K., Whitehead S., Barrett B.G.,
RA Spratt B.G., Parkhill J.;
RT "Complete genomes of two clinical Staphylococcus aureus strains:
RT evidence for the rapid evolution of virulence and drug resistance.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:9786-9791 (2004).
CC -!- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC an amide bond (By similarity).
DR EMBL: BX571857; CAG44202.1; -.
DR GO: GO:0009986; C:cell surface; IEA.
DR GO: GO:0006181; C:cell wall; IEA.
DR GO: GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO: GO:0016020; C:membrane; IEA.
DR GO: GO:0007155; P:cell adhesion; IEA.
DR InterPro: IPR008966; Adhes_bact.
DR InterPro: IPR004237; Fn_bind.
DR InterPro: IPR005877; Gpos_YSIRK.
DR InterPro: IPR001899; Gram_pos_anchor.
DR Pfam: PF02986; Fn_bind; 1.
DR Pfam: PF00746; Gram_pos_anchor; 1.
DR Pfam: PF04650; YSIRK_signal; 1.
DR TIGRFAMs: TIGR01167; LPXTG_anchor; 1.
DR TIGRFAMs: TIGR01168; YSIRK_signal; 1.
DR PROSITE: PS50847; GRAM_POS_ANCHORING; 1.
DR Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ SEQUENCE 1015 AA; 111145 MW; DDF9281BB64D44D2 CRC64;

Query Match          100.0%; Score 53; DB 2; Length 1015;
Best Local Similarity 100.0%; Pred. No. 0.57;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YE0GGNIVDI 10

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```

Db 765 YE0GGNIVDI 774

RESULT 9
ID FNBA_STAUV STANDARD; PRT; 1018 AA.
FNBA_STAUV
AC P14738;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Fibronectin-binding protein precursor (FNBP).
GN Name=fnbp;
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1280;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NTC 8325-4; PubMed=2521391;
RX MEDLINE=89098998; PubMed=2521391;
RA Signaes C., Raucel G., Joensson K., Lindgren P.-E.,
RA Anantharamaiah G.M., Hoocek M., Lindberg M.;
RT "Nucleotide sequence of the gene for a fibronectin-binding protein
RT from Staphylococcus aureus: use of this peptide sequence in the
RT synthesis of biologically active peptides.";
RL Proc. Natl. Acad. Sci. U.S.A. 86:699-703 (1989).
CC -!- FUNCTION: The ability of bacteria to bind fibronectin has been
CC proposed as a virulence factor enabling bacteria to colonize wound
CC tissues and blood clots. Binding of plasma fibronectin to the
CC bacterial surface might block adhesion receptors on S.aureus, thus
CC representing an important defense mechanism against tissue
CC invasion.
CC -!- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC an amide bond (potential).
CC
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CC
DR EMBL: J04151; AAA26632.1; -.
DR InterPro: IPR004237; Fn_bind.
DR InterPro: IPR005877; Gpos_YSIRK.
DR InterPro: IPR001899; Gram_pos_anchor.
DR Pfam: PF02986; Fn_bind; 1.
DR Pfam: PF00746; Gram_pos_anchor; 1.
DR Pfam: PF04650; YSIRK_signal; 1.
DR TIGRFAMs: TIGR01167; LPXTG_anchor; 1.
DR TIGRFAMs: TIGR01168; YSIRK_signal; 1.
DR PROSITE: PS50847; GRAM_POS_ANCHORING; 1.
DR Cell adhesion; Cell wall; Peptidoglycan-anchor; Repeat; Signal;
KW Virulence.
FT SIGNAL 1 36
FT CHAIN 37 985
FT PROPEP 986 1018
FT REPEAT 545 574
FT REPEAT 575 604
FT DOMAIN 745 878
FT REPEAT 745 782
FT REPEAT 783 820
FT REPEAT 821 859
FT REPEAT 860 878
FT DOMAIN 879 948
FT REPEAT 879 892
FT REPEAT 893 906
FT REPEAT 907 920
FT REPEAT 921 934
FT REPEAT 935 948
FT SITE 982 986
FT MOD_RES 985 985

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FT SEQUENCE 1018 AA; 111780 MW; 58175E0020E81F1P CRC64;
 SQ Query Match 100.0%; Score 53; DB 1; Length 1018;
 Best Local Similarity 100.0%; Pred. No. 0.57;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YEOGGINVIDI 10
 DB 764 YEOGGINVIDI 773

RESULT 10
 Q99RD2 PRELIMINARY; PRT; 1038 AA.
 AC Q99RD2; 01-JUN-2001 (TrEMBLrel. 17, Created)
 DT 01-JUN-2001 (TrEMBLrel. 26, Last sequence update)
 DE 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 GN Name=fnb; OrderedlocusNames=SAV2503;
 DE Fibronectin-binding protein homolog.
 OS Staphylococcus aureus (strain Mu50 / ATCC 700699).
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 NC NCB1_TaxID=158878;
 RX MEDLINE=11311952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2;
 RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
 RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Iino J.-O., Ito T.,
 RA Kanamori M., Matsunari H., Maruyama A., Murakami H., Hoshiyama A.,
 RA Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
 RA Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuuchi J.,
 RA Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
 RA Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
 RT "Whole genome sequencing of methicillin-resistant Staphylococcus
 aureus.";
 RL Lancet 357:1225-1240(2001).
 CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
 an amide bond (By similarity).
 DR EMBL: AP003365; BAB58665.1; -.
 DR PIR: H90053; H90053.
 DR GO: GO:0009986; C:cell surface; IEA.
 DR GO: GO:0005618; C:cell wall; IEA.
 DR GO: GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
 DR GO: GO:0016020; C:membrane; IEA.
 DR GO: GO:0007155; P:cell adhesion; IEA.
 DR InterPro: IPR008966; Adhes_bact.
 DR InterPro: IPR004237; Fn_bind.
 DR InterPro: IPR005877; Gpos_YsIRK.
 DR InterPro: IPR001899; Gram_pos_anchor.
 DR Pfam: PF02986; Fn_bind_1.
 DR Pfam: PF00746; Gram_pos_anchor; 1.
 DR Pfam: PF04650; YsIRK_signal; 1.
 DR TIGRFAMs: TIGR01167; LEXTG_anchor; 1.
 DR TIGRFAMs: TIGR01168; YsIRK_signal; 1.
 DR PROSITE: PS50847; GRAM_POS_ANCHORING; 1.
 KW Cell wall; Complete proteome; Peptidoglycan-anchor.
 SQ SEQUENCE 1038 AA; 113618 MW; 666BF6F2FBEB12 CRC64;

Query Match 100.0%; Score 53; DB 2; Length 1038;
 Best Local Similarity 100.0%; Pred. No. 0.58;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YEOGGINVIDI 10
 DB 760 YEOGGINVIDI 769

RESULT 11
 Q7A3J7 PRELIMINARY; PRT; 1038 AA.
 AC Q7A3J7;

DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DE 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 GN Fnb protein.
 OS Staphylococcus aureus (strain N315).
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 NC NCB1_TaxID=158879;
 RX MEDLINE=21311952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2;
 RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
 RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Iino J.-O., Ito T.,
 RA Kanamori M., Matsunari H., Maruyama A., Murakami H., Hoshiyama A.,
 RA Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
 RA Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuuchi J.,
 RA Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
 RA Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
 RT "Whole genome sequencing of methicillin-resistant Staphylococcus
 aureus.";
 RL Lancet 357:1225-1240(2001).
 CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
 an amide bond (By similarity).
 DR EMBL: AP003337; BAB43594.1; -.
 DR GO: GO:0009986; C:cell surface; IEA.
 DR GO: GO:0005618; C:cell wall; IEA.
 DR GO: GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
 DR GO: GO:0016020; C:membrane; IEA.
 DR GO: GO:0007155; P:cell adhesion; IEA.
 DR InterPro: IPR008966; Adhes_bact.
 DR InterPro: IPR004237; Fn_bind.
 DR InterPro: IPR005877; Gpos_YsIRK.
 DR InterPro: IPR001899; Gram_pos_anchor.
 DR Pfam: PF02986; Fn_bind_1.
 DR Pfam: PF00746; Gram_pos_anchor; 1.
 DR Pfam: PF04650; YsIRK_signal; 1.
 DR TIGRFAMs: TIGR01167; LEXTG_anchor; 1.
 DR TIGRFAMs: TIGR01168; YsIRK_signal; 1.
 DR PROSITE: PS50847; GRAM_POS_ANCHORING; 1.
 KW Cell wall; Complete proteome; Peptidoglycan-anchor.
 SQ SEQUENCE 1038 AA; 113618 MW; 666BF6F2FBEB12 CRC64;

Query Match 100.0%; Score 53; DB 2; Length 1038;
 Best Local Similarity 100.0%; Pred. No. 0.58;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YEOGGINVIDI 10
 DB 760 YEOGGINVIDI 769

RESULT 12
 Q6GDUS PRELIMINARY; PRT; 965 AA.
 AC Q6GDUS; 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DE 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 GN Fibronectin-binding protein.
 OS Name=fnbA; OrderedlocusNames=SA2580;
 OS Staphylococcus aureus (strain MRSA252).
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 NC NCB1_TaxID=282458;
 RX MEDLINE=1521324; DOI=10.1073/pnas.0402521101;
 RA Holden M.T.G., Fell E.J., Lindsey J.A., Peacock S.J., Day N.P.J.,
 RA Enright M.C., Foster T.J., Moore C.E., Hurst L., Actin R., Barron A.,
 RA Bason N., Bentley S.D., Chillingworth C., Chillingworth T.,
 RA Churcher C., Clark L., Corton C., Cronin A., Doggett J., Dowd L.,
 RA Felwell T., Hance Z., Harris B., Hauser H., Holtroyd S., Jagsels K.,
 RA James K.D., Lennard N., Line A., Mayes R., Mungall K.,
 RA Ormond D., Quail M.A., Rabinowitz E., Rutherford K.M., Sanders M.,

RA Sharp S., Simmonds M., Stevens K., Whitehead S., Barrell B.G.,
 RA Spratt B.G., Parkhill J.;
 RT "Complete genomes of two clinical *Staphylococcus aureus* strains:
 CC evidence for the rapid evolution of virulence and drug resistance";
 RT Proc. Natl. Acad. Sci. U.S.A. 101:9786-9791(2004).
 CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
 an amide bond (By similarity).
 CC EMBL: BX571856; CAG41560.1; -.
 DR GO: GO:0009986; C:cell surface; IEA.
 DR GO: GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
 DR GO: GO:0016020; C:membrane; IEA.
 DR GO: GO:0071155; P:cell adhesion; IEA.
 DR InterPro: IPR008966; Adhes_bact.
 DR InterPro: IPR004237; Fn_bind.
 DR InterPro: IPR005877; Gpoc_Ysirk.
 DR InterPro: IPR001899; Gram_pos_anchor.
 DR Pfam: PF02986; Fn_bind; 1.
 DR Pfam: PF00746; Gram_pos_anchor; 1.
 DR TIGRPFAM: TIGR01167; Lpxng_anchor; 1.
 DR TIGRPFAM: TIGR01168; Ysirk_signal; 1.
 DR PROSITE: PS50847; GRAM_POS_ANCHORING; 1.
 DR Cell wall; Complete proteome; Peptidoglycan-anchor.
 KW SEQUENCE 965 AA; 105691 MW; 2982E132164D0551 CRC64;
 SQ

Query Match 98.1%; Score 52; DB 2; Length 965;
 Best Local Similarity 90.0%; Pred. No. 0.83;
 Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YEOGGINVIDI 10
 Db 767 YEOGGINVIDI 776

RESULT 13
 O8KBG2 PRELIMINARY; PRT; 289 AA.
 ID O8KBG2
 AC O8KBG2;
 DT 01-OCT-2002 (TREMblrel. 22, Created)
 DT 01-OCT-2002 (TREMblrel. 22, Last sequence update)
 DT 01-MAR-2004 (TREMblrel. 26, Last annotation update)
 DE Formyletetrahydrofolate deformylase.
 GN Name: purI; Ordered locus names: CT1825;
 OS *Chlorobium tepidum*.
 OC Bacteria; Chlorobi; Chlorobia; Chlorobiales; Chlorobiaceae;
 CC Chlorobaculum.
 OX NCBI_TaxID=1097;
 RX SEQUENCE FROM N.A.
 RP STRAIN=TLS / ATCC 49652 / DSM 12025;
 RC MEDLINE=22103685; PubMed=12093901; DOI=10.1073/pnas.132181499;
 RA Eisen J.A., Neilson K.E., Paulsen I.T., Heidelberg J.F., Wu M.,
 RA Dodson R.J., DeBoy R.T., Gwinn M.L., Nelson W.C., Haft D.H.,
 RA Hickey E.K., Peterson J.D., Durkin A.S., Kolonay J.F., Yang F.,
 RA Holt I.E., Umayam L.A., Mason T.M., Brenner M., Shea T.P.,
 RA Parisey D.S., Niemeyer W.C., Feldblyum T.V., Hansen C.T., Craven M.B.,
 RA Radune D., Vamathevan J.J., Khouri H.M., White O., Gruber T.M.,
 RA Ketchum K.A., Venter J.C., Tettelin H., Bryant D.A., Fraser C.M.;
 RT "The complete genome sequence of *Chlorobium tepidum* TLS, a
 RT photoreducative, anaerobic, green-sulfur bacterium";
 RT Proc. Natl. Acad. Sci. U.S.A. 99:9509-9514(2002).
 DR EMBL: AE012935; AAM73046.1; -.
 DR HSSP: P22102; IMEO.
 DR TIGR: CT1825; -.
 DR GO: GO:0016597; P:amino acid binding; IEA.
 DR GO: GO:0008864; P:formyletetrahydrofolate deformylase activity; IEA.
 DR GO: GO:0016742; P:hydroxymethyl-, formyl- and related transfe. .; IEA.
 DR GO: GO:0006189; P:de novo IMP biosynthesis; IEA.
 DR GO: GO:0009058; P:biosynthesis; IEA.
 DR InterPro: IPR002912; ACT.
 DR InterPro: IPR002376; Formyl_transf_N.
 DR InterPro: IPR004810; PurI.
 DR Pfam: PF01842; ACT; 1.

DR Pfam: PF00551; Formyl_transf_N; 1.
 DR PRINTS: PR01575; PF04HYDRASE.
 DR TIGRPFAM: TIGR00655; PurI; 1.
 KW Complete proteome.
 SQ SEQUENCE 289 AA; 32964 MW; 2D1F2898BC5C07E CRC64;
 Query Match 83.0%; Score 44; DB 2; Length 289;
 Best Local Similarity 70.0%; Pred. No. 7.4;
 Matches 7; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YEOGGINVIDI 10
 Db 31 YEOGGINVIDI 40

RESULT 14
 O8J2U7 PRELIMINARY; PRT; 315 AA.
 ID O8J2U7
 AC O8J2U7;
 DT 01-MAR-2003 (TREMblrel. 23, Created)
 DT 01-MAR-2003 (TREMblrel. 23, Last sequence update)
 DT 01-MAR-2004 (TREMblrel. 26, Last annotation update)
 DE Putative norsolorinic acid reductase.
 GN Name: norA;
 OS *Aspergillus oryzae*.
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
 OC Eurotiiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
 OX NCBI_TaxID=5062;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=RIB40;
 RA Yamada O.;
 RL Submitted (SEP-2001) to the EMBL/Genbank/DBJ databases.
 DR EMBL: AB071288; BAC15569.1; -.
 DR HSSP: Q46933; ILQA.
 DR InterPro: IPR001395; Aldo/ket_red.
 DR Pfam: PF00248; Aldo_ket_red; 1.
 DR PRINTS: PR00069; ALDKETREDTASE.
 DR ProDom: PD000288; Aldo/ket_red; 1.
 SQ SEQUENCE 315 AA; 35601 MW; D99419FD58D5D2B CRC64;
 Query Match 79.2%; Score 42; DB 2; Length 315;
 Best Local Similarity 60.0%; Pred. No. 19;
 Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 YEOGGINVIDI 10
 Db 61 YEOGGINVIDI 70

RESULT 15
 NCRA_ASPFL
 ID NCRA_ASPFL STANDARD; PRT; 388 AA.
 AC Q00049;
 DT 15-JUL-1999 (Rel. 38, Created)
 DT 15-JUL-1999 (Rel. 38, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Norsolorinic acid reductase (EC 1.1.1.-).
 GN Name: NCRA; Synonym: ADH-2;
 OS *Aspergillus flavus*.
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
 OC Eurotiiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
 OX NCBI_TaxID=5059;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=NRRL 3357;
 RX MEDLINE=96156784; PubMed=8593042;
 RA Cary J.W., Wright M., Bhatnagar D., Lee R., Chu F.;
 RT "Molecular characterization of an *Aspergillus parasiticus*
 RT dehydrogenase gene, norA, located on the aflatoxin biosynthesis gene
 RT cluster";
 RT Appl. Environ. Microbiol. 62:360-366(1996).
 CC -1- PATHWAY: Aflatoxin biosynthesis.

```

CC -1- SIMILARITY: Belongs to the aldo/keto reductase 2 family.
CC -----
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CC -----
DR EMBL: U32377; AAC49167.1; -.
DR HSSP: Q46933; ILQA.
DR InterPro: IPR001395; Aldo/ket_red.
DR Pfam: PF00248; Aldo_ket_red; 1.
DR PRINTS: PR00069; ALDKETRDASE.
DR ProDom: PD000288; Aldo/ket_red; 1.
KW NADP: Oxidoreductase.
FT NP_BIND 233 243 NADP (By similarity).
FT ACT_SITE 74 74 Proton donor (By similarity).
SQ SEQUENCE 388 AA; 43751 MW; 758B8187187BFSB0 CRC64;
Query Match 79.2%; Score 42; DB 1; Length 388;
Best Local Similarity 60.0%; Pred. No. 24;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
QY 1 YEOGGINVDI 10
Db 61 YEOGGINPIDV 70

```

Search completed: October 22, 2005, 08:00:37
 Job time : 57.85 secs

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OM protein - protein search, using sw model

Run on: October 25, 2005, 20:21:18 ; Search time 63.2 Seconds
(without alignments)
61.196 Million cell updates/sec

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Title: US-10-731-238-73
Perfect score: 53
Sequence: 1 QGGNIVDIDF 10
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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

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Minimum DB seq length: 0
Maximum DB seq length: 20000000000
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Post-processing:	Minimum Match	0%
	Maximum Match	100%
	Listing first	45 summaries

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Database :
1: A_GeneSeqp_16Dec04.*
2: GeneSeqp1980s.*
3: GeneSeqp1990s.*
4: GeneSeqp2000s.*
5: GeneSeqp2003s.*
6: GeneSeqp2003as.*
7: GeneSeqp2003bs.*
8: GeneSeqp2004as.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	53	100.0	10	AAM65729 Fibronect
2	53	100.0	14	AAM65716 Fibronect
3	53	100.0	38	AAM65692 Fibronect
4	53	100.0	38	AAM65695 Fibronect
5	53	100.0	38	AAM65696 Fibronect
6	53	100.0	38	AAM65697 Fibronect
7	53	100.0	38	AAM65694 Fibronect
8	53	100.0	38	AAM65691 Fibronect
9	53	100.0	38	AAM65661 Fibronect
10	53	100.0	38	AAM65693 Fibronect
11	53	100.0	38	AAM65698 Fibronect
12	53	100.0	39	AAM65712 Fibronect
13	53	100.0	113	AAR90937 DfD4 poly
14	53	100.0	130	AAR58806 Fibronect
15	53	100.0	130	AAR58807 Fibronect
16	53	100.0	130	AAR91202 DI-D4 fibr
17	53	100.0	130	AAR91201 DI-D4 fibr
18	53	100.0	134	AAIY28089 Cloned fi
19	53	100.0	134	AAY28088 S. aureus
20	53	100.0	134	AAV29087 S. aureus
21	53	100.0	139	AAIM31556 Fibronect
22	53	100.0	162	AAR90942 DfD4 poly
23	53	100.0	164	AAR90938 DfD4 poly
24	53	100.0	174	AAR58808 Fbp fibr
25	53	100.0	174	AAR91203 DI-D4 fibr

26	53	100.0	181	2	AAr58805	AAr58805	Fibronect
27	53	100.0	181	2	AAr91200	AAr91200	D1-D4 fib
28	53	100.0	559	2	AAw89603	AAw89603	Staphyloc
29	53	100.0	767	4	AAU34403	AAU34403	Staphyloc
30	53	100.0	767	4	AAU37547	AAU37547	Staphyloc
31	53	100.0	940	2	AAr07070	AAr07070	Fibronect
32	53	100.0	940	6	ABJ19111	ABJ19111	Pathogen
33	53	100.0	948	6	ADw89470	ADw89470	Staphyloc
34	53	100.0	948	6	ABJ18923	ABJ18923	Pathogen
35	53	100.0	948	6	AAw72536	AAw72536	Staphyloc
36	53	100.0	961	6	ABU15854	ABU15854	Protein e
37	53	100.0	978	4	AAU33960	AAU33960	Staphyloc
38	53	100.0	1001	4	AAU37093	AAU37093	Staphyloc
39	53	100.0	1018	1	AAw82115	AAw82115	Fibronect
40	53	100.0	1018	4	AAU37745	AAU37745	Staphyloc
41	53	100.0	1018	4	AAU34501	AAU34501	Pathogen
42	53	100.0	1018	6	ABU18922	ABU18922	Staphyloc
43	53	100.0	1018	6	AAw72537	AAw72537	Staphyloc
44	53	100.0	1027	2	AAw89806	AAw89806	Staphyloc
45	53	100.0	1038	6	ABU15903	ABU15903	Protein e

ALIGNMENTS

RESULT 1
AAW65729
ID AAW65729 standard; peptide; 10 AA.

AC AAW65729 ;

DT 16-OCT-1998 (first entry)

Fibronectin binding protein-derived peptide #73.

KW microbial surface components recognising adhesive matrix molecule;
KW MSCRAMM; fibronectin; fibronectin-binding protein; antibody; epitope
KW antibiotic; bacterial infection; antibiotic-resistant strain.

OS	Synthetic.
OS	<i>Staphylococcus aureus</i> .

PN W09831389-A2

PD 23-JUL-1998

PF 21-JAN-1998; 98WO-US001222.

PR 21-JAN-1997; 97US-0036139P.

PA (TEXA) UNIV TEXAS A & M SYSTEM.

PI Hoeek M, patci JM, House-Pompeo KL, speciale P, von D
PI McCann MT.

DR WPI; 1998-413816/35.

PT Antibody that binds to fibrinogen-binding protein, preventing its binding to fibrinogen - used to treat or prevent bacterial infection, especially by *Staphylococci* and *Streptococci*.

PS Example 9; Page 110; 201pp; English

The invention relates to antibodies that bind to a fibronectin-binding domain of a fibronectin-binding protein, and inhibit binding of the protein to fibronectin. Also claimed are: (1) isolated peptides of a fibronectin-binding protein that do not bind to fibronectin; (2) fusion protein containing at least one peptide of a fibronectin-binding protein linked to a second amino acid sequence; (3) nucleic acid encoding the isolated peptide of (1). Antibodies; the isolated peptides of (1) and the nucleic acids are all useful for immunisation (active or passive) and (b) inhibiting binding of bacteria to fibronectin) for preventing or treating infection in humans or other animals, particularly by staphylococci or

CC streptococci, e.g. meningitis, otitis media, pneumonia, endocarditis,
 CC mastitis in cattle, abortion in horses and many others. Since the
 CC antibodies block binding of bacteria, they should be effective against
 CC antibiotic-resistant strains, and may replace antibiotic therapy or
 CC increase its effectiveness. Sequences AAW65719-41 and AAW65658 represent
 CC peptides which were synthesised to span the D1 motif and the N-terminal
 CC 18 amino acids of D2, with each peptide overlapping by eight amino acids
 CC with the previous sequence

XX
 SQ Sequence 10 AA;

Query Match 100.0%; Score 53; DB 2; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.0029;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 OGGNIVDIDF 10
 |||||
 DB 1 OGGNIVDIDF 10

RESULT 2
 AAW65716 .
 ID AAW65716 standard; peptide; 14 AA.

XX
 AC AAW65716;
 XX
 DT 16-OCT-1998 (first entry)

XX Fibronectin binding protein fragment (residues 21-34 of D1 motif).

XX
 DE
 XX
 KM microbial surface components recognising adhesive matrix molecule;
 KM MSCRAMM; fibronectin; fibronectin-binding protein; antibody; epitope;
 KM antibiotic; bacterial infection; antibiotic-resistant strain.

XX Synthetic.
 OS Staphylococcus aureus.

XX WO9831389-A2.

XX 23-JUL-1998.

XX 21-JAN-1998; 98WO-US001222.

XX 21-JAN-1997; 97US-0036139P.

XX (TEXA) UNIV TEXAS A & M SYSTEM.

XX Hoecek M, Patti JM, House-Pompeo KL, Speziale P, Joh D;
 PI Mcgavin MJ;

XX WPI; 1998-413816/35.

XX Antibody that binds to fibronectin-binding protein, preventing its
 PT binding to fibronectin - used to treat or prevent bacterial infection,
 PT especially by Staphylococci and Streptococci.

PS Claim 42; Page 105; 201pp; English.

XX The invention relates to antibodies that bind to a fibronectin-binding
 CC domain of a fibronectin-binding protein, and inhibit binding of the
 CC protein to fibronectin. Also claimed are: (1) isolated peptides of a
 CC fibronectin-binding protein that do not bind to fibronectin; (2) fusion
 CC protein containing at least one peptide of a fibronectin-binding protein
 CC linked to a second amino acid sequence; (3) nucleic acid encoding the
 CC isolated peptide of (1). Antibodies, the isolated peptides of (1) and the
 CC nucleic acids are all useful for immunisation (active or passive) and (by
 CC inhibiting binding of bacteria to fibronectin) for preventing or treating
 CC infection in humans or other animals, particularly by staphylococci or
 CC streptococci, e.g. meningitis, otitis media, pneumonia, endocarditis,
 CC mastitis in cattle, abortion in horses and many others. Since the
 CC antibodies block binding of bacteria, they should be effective against
 CC antibiotic-resistant strains, and may replace antibiotic therapy or
 CC increase its effectiveness. The present sequence represents a

CC specifically claimed peptide
 XX
 SQ Sequence 14 AA;

Query Match 100.0%; Score 53; DB 2; Length 14;
 Best Local Similarity 100.0%; Pred. No. 0.0042;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 OGGNIVDIDF 10
 |||||
 DB 1 OGGNIVDIDF 10

RESULT 3
 AAW65692
 ID AAW65692 standard; peptide; 38 AA.

XX
 AC AAW65692;
 XX
 DT 16-OCT-1998 (first entry)

XX Fibronectin binding protein-derived peptide #36.

XX
 DE
 XX
 KM microbial surface components recognising adhesive matrix molecule;
 KM MSCRAMM; fibronectin; fibronectin-binding protein; antibody; epitope;
 KM antibiotic; bacterial infection; antibiotic-resistant strain.

XX Synthetic.
 OS Staphylococcus aureus.

XX WO9831389-A2.

XX 23-JUL-1998.

XX 21-JAN-1998; 98WO-US001222.

XX 21-JAN-1997; 97US-0036139P.

XX (TEXA) UNIV TEXAS A & M SYSTEM.

XX Hoecek M, Patti JM, House-Pompeo KL, Speziale P, Joh D;
 PI Mcgavin MJ;

XX WPI; 1998-413816/35.

XX Antibody that binds to fibronectin-binding protein, preventing its
 PT binding to fibronectin - used to treat or prevent bacterial infection,
 PT especially by Staphylococci and Streptococci.

PS Example 8; Page 101; 201pp; English.

XX The invention relates to antibodies that bind to a fibronectin-binding
 CC domain of a fibronectin-binding protein, and inhibit binding of the
 CC protein to fibronectin. Also claimed are: (1) isolated peptides of a
 CC fibronectin-binding protein that do not bind to fibronectin; (2) fusion
 CC protein containing at least one peptide of a fibronectin-binding protein
 CC linked to a second amino acid sequence; (3) nucleic acid encoding the
 CC isolated peptide of (1). Antibodies, the isolated peptides of (1) and the
 CC nucleic acids are all useful for immunisation (active or passive) and (by
 CC inhibiting binding of bacteria to fibronectin) for preventing or treating
 CC infection in humans or other animals, particularly by staphylococci or
 CC streptococci, e.g. meningitis, otitis media, pneumonia, endocarditis,
 CC mastitis in cattle, abortion in horses and many others. Since the
 CC antibodies block binding of bacteria, they should be effective against
 CC antibiotic-resistant strains, and may replace antibiotic therapy or
 CC increase its effectiveness. Sequences AAW65691-700 represent a series of
 CC synthetic peptides based on the D1 region of S. aureus fibronectin
 CC binding protein A. They were synthesised to contain mutations

XX Sequence 38 AA;

Query Match 100.0%; Score 53; DB 2; Length 38;
 Best Local Similarity 100.0%; Pred. No. 0.013;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 OGGNIVDIDF 10
 |||||
 DB 21 OGGNIVDIDF 30

RESULT 4

AAW65695 standard; peptide; 38 AA.

AAW65695;

16-OCT-1998 (first entry)

Fibronectin binding protein-derived peptide #39.

microbial surface components recognising adhesive matrix molecule;
 MSCRAMM; fibronectin; fibronectin-binding protein; antibody; epitope;
 antibiotic; bacterial infection; antibiotic-resistant strain.

Synthetic.

Staphylococcus aureus.

WO9831389-A2.

23-JUL-1998.

21-JAN-1998; 98WO-US001222.

21-JAN-1997; 97US-0036139P.

(TEXA) UNIV TEXAS A & M SYSTEM.

Hoecek M, Patti JM, House-Pompeo KL, Speciale P, Joh D;
 McGavin MJ;

WPI; 1998-413816/35.

Antibody that binds to fibronectin-binding protein, preventing its
 binding to fibronectin - used to treat or prevent bacterial infection,
 especially by Staphylococci and Streptococci.

Example 8; Page 102; 201pp; English.

The invention relates to antibodies that bind to a fibronectin-binding
 domain of a fibronectin-binding protein, and inhibit binding of the
 protein to fibronectin. Also claimed are: (1) isolated peptides of a
 fibronectin-binding protein that do not bind to fibronectin; (2) fusion
 protein containing at least one peptide of a fibronectin-binding protein
 linked to a second amino acid sequence; (3) nucleic acid encoding the
 isolated peptide of (1). Antibodies, the isolated peptides of (1) and the
 nucleic acids are all useful for immunisation (active or passive) and (by
 inhibiting binding of bacteria to fibronectin) for preventing or treating
 infection in humans or other animals, particularly by staphylococci or
 streptococci, e.g. meningitis, otitis media, pneumonia, endocarditis,
 mastitis in cattle, abortion in horses and many others. Since the
 antibodies block binding of bacteria, they should be effective against
 antibiotic-resistant strains, and may replace antibiotic therapy or
 increase its effectiveness. Sequences AAW65691-700 represent a series of
 synthetic peptides based on the DI region of S. aureus fibronectin
 binding protein A. They were synthesised to contain mutations

Sequence 38 AA;

Query Match 100.0%; Score 53; DB 2; Length 38;

Best Local Similarity 100.0%; Pred. No. 0.013;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 5
 AAW65696 standard; peptide; 38 AA.

AAW65696;

16-OCT-1998 (first entry)

Fibronectin binding protein-derived peptide #40.

microbial surface components recognising adhesive matrix molecule;
 MSCRAMM; fibronectin; fibronectin-binding protein; antibody; epitope;
 antibiotic; bacterial infection; antibiotic-resistant strain.

Synthetic.

Staphylococcus aureus.

WO9831389-A2.

23-JUL-1998.

21-JAN-1998; 98WO-US001222.

21-JAN-1997; 97US-0036139P.

(TEXA) UNIV TEXAS A & M SYSTEM.

Hoecek M, Patti JM, House-Pompeo KL, Speciale P, Joh D;
 McGavin MJ;

WPI; 1998-413816/35.

Antibody that binds to fibronectin-binding protein, preventing its
 binding to fibronectin - used to treat or prevent bacterial infection,
 especially by Staphylococci and Streptococci.

Example 8; Page 102; 201pp; English.

The invention relates to antibodies that bind to a fibronectin-binding
 domain of a fibronectin-binding protein, and inhibit binding of the
 protein to fibronectin. Also claimed are: (1) isolated peptides of a
 fibronectin-binding protein that do not bind to fibronectin; (2) fusion
 protein containing at least one peptide of a fibronectin-binding protein
 linked to a second amino acid sequence; (3) nucleic acid encoding the
 isolated peptide of (1). Antibodies, the isolated peptides of (1) and the
 nucleic acids are all useful for immunisation (active or passive) and (by
 inhibiting binding of bacteria to fibronectin) for preventing or treating
 infection in humans or other animals, particularly by staphylococci or
 streptococci, e.g. meningitis, otitis media, pneumonia, endocarditis,
 mastitis in cattle, abortion in horses and many others. Since the
 antibodies block binding of bacteria, they should be effective against
 antibiotic-resistant strains, and may replace antibiotic therapy or
 increase its effectiveness. Sequences AAW65691-700 represent a series of
 synthetic peptides based on the DI region of S. aureus fibronectin
 binding protein A. They were synthesised to contain mutations

Sequence 38 AA;

Query Match 100.0%; Score 53; DB 2; Length 38;

Best Local Similarity 100.0%; Pred. No. 0.013;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 6
 AAW65697 standard; peptide; 38 AA.

AAW65697;


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XX 16-OCT-1998 (first entry)
DE Fibronectin binding protein-derived peptide #41.
XX
XX microbial surface components recognising adhesive matrix molecule;
KM MSCRAMM; fibronectin-binding protein; antibody; epitope;
XX antibiotic; bacterial infection; antibiotic-resistant strain.
XX
XX Synthetic.
OS Staphylococcus aureus.
XX
XX MO98J1389-A2.
XX
XX 23-JUL-1998.
XX
XX 21-JAN-1998; 98WO-US001222.
XX
XX 21-JAN-1997; 97US-0036139P.
XX
XX (TEXA ) UNIV TEXAS A & M SYSTEM.
XX
XX Hoeoek M, Patti JM, House-Pompeo KU, Speziale P, Joh D;
XX Mcgavin MJ;
XX
XX WPI; 1998-413816/35.
XX
XX Antibody that binds to fibronectin-binding protein, preventing its
XX binding to fibronectin - used to treat or prevent bacterial infection,
XX especially by Staphylococci and Streptococci.
XX
XX Example 8; Page 102; 201pp; English.
XX
XX The invention relates to antibodies that bind to a fibronectin-binding
XX domain of a fibronectin-binding protein, and inhibit binding of the
XX protein to fibronectin. Also claimed are: (1) isolated peptides of a
XX fibronectin-binding protein that do not bind to fibronectin; (2) fusion
XX protein containing at least one peptide of a fibronectin-binding protein
XX linked to a second amino acid sequence; (3) nucleic acid encoding the
XX isolated peptide of (1). Antibodies, the isolated peptides of (1) and the
XX nucleic acids are all useful for immunisation (active or passive) and (by
XX inhibiting binding of bacteria to fibronectin) for preventing or treating
XX infection in humans or other animals, particularly by staphylococci or
XX streptococci, e.g. meningitis, otitis media, pneumonia, endocarditis,
XX mastitis in cattle, abortion in horses and many others. Since the
XX antibodies block binding of bacteria, they should be effective against
XX antibiotic-resistant strains, and may replace antibiotic therapy or
XX increase its effectiveness. Sequences AAW65691-700 represent a series of
XX synthetic peptides based on the D1 region of S. aureus fibronectin
XX binding protein A. They were synthesised to contain mutations
XX
XX Sequence 38 AA;
XX
XX Query Match 100.0%; Score 53; DB 2; Length 38;
XX Best Local Similarity 100.0%; Pred. No. 0.013;
XX Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 OGGNIVDIDF 10
XX |||||
XX 21 OGGNIVDIDF 30
XX
XX RESULT 7
XX AAW65694
XX ID AAW65694 standard; peptide; 38 AA.
XX
XX AC AAW65694;
XX
XX DT 16-OCT-1998 (first entry)
XX
XX DE Fibronectin binding protein-derived peptide #38.
XX
XX microbial surface components recognising adhesive matrix molecule;
XX

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KM MSCRAMM; fibronectin-binding protein; antibody; epitope;
XX antibiotic; bacterial infection; antibiotic-resistant strain.
XX
XX Synthetic.
OS Staphylococcus aureus.
XX
XX MO98J1389-A2.
XX
XX 23-JUL-1998.
XX
XX 21-JAN-1998; 98WO-US001222.
XX
XX 21-JAN-1997; 97US-0036139P.
XX
XX (TEXA ) UNIV TEXAS A & M SYSTEM.
XX
XX Hoeoek M, Patti JM, House-Pompeo KU, Speziale P, Joh D;
XX Mcgavin MJ;
XX
XX WPI; 1998-413816/35.
XX
XX Antibody that binds to fibronectin-binding protein, preventing its
XX binding to fibronectin - used to treat or prevent bacterial infection,
XX especially by Staphylococci and Streptococci.
XX
XX Example 8; Page 102; 201pp; English.
XX
XX The invention relates to antibodies that bind to a fibronectin-binding
XX domain of a fibronectin-binding protein, and inhibit binding of the
XX protein to fibronectin. Also claimed are: (1) isolated peptides of a
XX fibronectin-binding protein that do not bind to fibronectin; (2) fusion
XX protein containing at least one peptide of a fibronectin-binding protein
XX linked to a second amino acid sequence; (3) nucleic acid encoding the
XX isolated peptide of (1). Antibodies, the isolated peptides of (1) and the
XX nucleic acids are all useful for immunisation (active or passive) and (by
XX inhibiting binding of bacteria to fibronectin) for preventing or treating
XX infection in humans or other animals, particularly by staphylococci or
XX streptococci, e.g. meningitis, otitis media, pneumonia, endocarditis,
XX mastitis in cattle, abortion in horses and many others. Since the
XX antibodies block binding of bacteria, they should be effective against
XX antibiotic-resistant strains, and may replace antibiotic therapy or
XX increase its effectiveness. Sequences AAW65691-700 represent a series of
XX synthetic peptides based on the D1 region of S. aureus fibronectin
XX binding protein A. They were synthesised to contain mutations
XX
XX Sequence 38 AA;
XX
XX Query Match 100.0%; Score 53; DB 2; Length 38;
XX Best Local Similarity 100.0%; Pred. No. 0.013;
XX Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 OGGNIVDIDF 10
XX |||||
XX 21 OGGNIVDIDF 30
XX
XX RESULT 8
XX AAW65691
XX ID AAW65691 standard; peptide; 38 AA.
XX
XX AC AAW65691;
XX
XX DT 16-OCT-1998 (first entry)
XX
XX DE Fibronectin binding protein-derived peptide #35.
XX
XX microbial surface components recognising adhesive matrix molecule;
XX MSCRAMM; fibronectin-binding protein; antibody; epitope;
XX antibiotic; bacterial infection; antibiotic-resistant strain.
XX
XX Synthetic.
OS Staphylococcus aureus.
XX

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PN WO981389-A2.
 XX 23-JUL-1998.
 PD 21-JAN-1998; 98WO-US001222.
 XX 21-JAN-1997; 97US-0036139P.
 PR (TEXA) UNIV TEXAS A & M SYSTEM.
 XX Hoeoek M, Patti JM, House-Pompeo KL, Speziale P, Joh D;
 PI Mcgavin MJ;
 DR WPI; 1998-413816/35.
 XX Antibody that binds to fibronectin-binding protein, preventing its
 PT binding to fibronectin - used to treat or prevent bacterial infection,
 PT especially by Staphylococci and Streptococci.
 XX Example 8; Page 101; 201pp; English.
 PS The invention relates to antibodies that bind to a fibronectin-binding
 CC domain of a fibronectin-binding protein, and inhibit binding of the
 CC protein to fibronectin. Also claimed are: (1) isolated peptides of a
 CC fibronectin-binding protein that do not bind to fibronectin; (2) fusion
 CC protein containing at least one peptide of a fibronectin-binding protein
 CC linked to a second amino acid sequence; (3) nucleic acid encoding the
 CC isolated peptide of (1). Antibodies, the isolated peptides of (1) and the
 CC nucleic acids are all useful for immunisation (active or passive) and (by
 CC inhibiting binding of bacteria to fibronectin) for preventing or treating
 CC infection in humans or other animals, particularly by staphylococci or
 CC streptococci, e.g. meningitis, otitis media, pneumonia, endocarditis,
 CC mastitis in cattle, abortion in horses and many others. Since the
 CC antibodies block binding of bacteria, they should be effective against
 CC antibiotic-resistant strains, and may replace antibiotic therapy or
 CC increase its effectiveness. Sequences AAW65691-700 represent a series of
 CC synthetic peptides based on the D1 region of S. aureus fibronectin
 CC binding protein A. They were synthesised to contain mutations
 XX
 SQ Sequence 38 AA:
 Query Match 100.0%; Score 53; DB 2; Length 38;
 Best Local Similarity 100.0%; Pred. No. 0.013;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 OGGNIVDIDF 10
 DB 21 OGGNIVDIDF 30
 RESULT 9
 AAW65661
 ID AAW65661 standard; peptide; 38 AA.
 XX
 AC AAW65661;
 XX
 DT 16-OCT-1998 (first entry)
 XX
 DE Fibronectin binding protein-derived peptide #5.
 XX
 XX microbial surface components recognising adhesive matrix molecule;
 KM MSCRAMM; fibronectin; fibronectin-binding protein; antibody; epitope;
 KM antibiotic; bacterial infection; antibiotic-resistant strain.
 XX
 OS Synthetic.
 OS Staphylococcus aureus.
 XX
 XX WO981389-A2.
 XX
 PD 23-JUL-1998.
 XX
 PF 21-JAN-1998; 98WO-US001222.
 XX

PR 21-JAN-1997; 97US-0036139P.
 XX (TEXA) UNIV TEXAS A & M SYSTEM.
 XX Hoeoek M, Patti JM, House-Pompeo KL, Speziale P, Joh D;
 PI Mcgavin MJ;
 DR WPI; 1998-413816/35.
 XX Antibody that binds to fibronectin-binding protein, preventing its
 PT binding to fibronectin - used to treat or prevent bacterial infection,
 PT especially by Staphylococci and Streptococci.
 XX Example 2; Page 92; 201pp; English.
 PS The invention relates to antibodies that bind to a fibronectin-binding
 CC domain of a fibronectin-binding protein, and inhibit binding of the
 CC protein to fibronectin. Also claimed are: (1) isolated peptides of a
 CC fibronectin-binding protein that do not bind to fibronectin; (2) fusion
 CC protein containing at least one peptide of a fibronectin-binding protein
 CC linked to a second amino acid sequence; (3) nucleic acid encoding the
 CC isolated peptide of (1). Antibodies, the isolated peptides of (1) and the
 CC nucleic acids are all useful for immunisation (active or passive) and (by
 CC inhibiting binding of bacteria to fibronectin) for preventing or treating
 CC infection in humans or other animals, particularly by staphylococci or
 CC streptococci, e.g. meningitis, otitis media, pneumonia, endocarditis,
 CC mastitis in cattle, abortion in horses and many others. Since the
 CC antibodies block binding of bacteria, they should be effective against
 CC antibiotic-resistant strains, and may replace antibiotic therapy or
 CC increase its effectiveness. Sequences AAW65659-68 represent synthetic
 CC epitopes from the fibronectin binding domains DV and D1-D4 of the S.
 CC aureus fnbA gene
 XX
 SQ Sequence 38 AA:
 Query Match 100.0%; Score 53; DB 2; Length 38;
 Best Local Similarity 100.0%; Pred. No. 0.013;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 OGGNIVDIDF 10
 DB 21 OGGNIVDIDF 30
 RESULT 10
 AAW65693
 ID AAW65693 standard; peptide; 38 AA.
 XX
 AC AAW65693;
 XX
 DT 16-OCT-1998 (first entry)
 XX
 DE Fibronectin binding protein-derived peptide #37.
 XX
 XX microbial surface components recognising adhesive matrix molecule;
 KM MSCRAMM; fibronectin; fibronectin-binding protein; antibody; epitope;
 KM antibiotic; bacterial infection; antibiotic-resistant strain.
 XX
 OS Synthetic.
 OS Staphylococcus aureus.
 XX
 XX WO981389-A2.
 XX
 PD 23-JUL-1998.
 XX
 PF 21-JAN-1998; 98WO-US001222.
 XX
 XX 21-JAN-1997; 97US-0036139P.
 XX
 PR (TEXA) UNIV TEXAS A & M SYSTEM.
 XX
 XX Hoeoek M, Patti JM, House-Pompeo KL, Speziale P, Joh D;
 PI Mcgavin MJ;

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XX DR WPI, 1998-413816/35.
XX PS
XX PT Antibody that binds to fibronectin-binding protein, preventing its
XX PT binding to fibronectin - used to treat or prevent bacterial infection,
XX PT especially by Staphylococci and Streptococci.
XX PS
XX PS Example 8; Page 102; 201pp; English.
XX CC The invention relates to antibodies that bind to a fibronectin-binding
XX CC domain of a fibronectin-binding protein, and inhibit binding of the
XX CC protein to fibronectin. Also claimed are: (1) isolated peptides of a
XX CC fibronectin-binding protein that do not bind to fibronectin; (2) fusion
XX CC protein containing at least one peptide of a fibronectin-binding protein
XX CC linked to a second amino acid sequence; (3) nucleic acid encoding the
XX CC isolated peptide of (1). Antibodies, the isolated peptides of (1) and the
XX CC nucleic acids are all useful for immunisation (active or passive) and (by
XX CC inhibiting binding of bacteria to fibronectin) for preventing or treating
XX CC infection in humans or other animals, particularly by staphylococci or
XX CC streptococci, e.g. meningitis, otitis media, pneumonia, endocarditis,
XX CC mastitis in cattle, abortion in horses and many others. Since the
XX CC antibodies block binding of bacteria, they should be effective against
XX CC antibiotic-resistant strains, and may replace antibiotic therapy or
XX CC increase its effectiveness. Sequences AAM65691-700 represent a series of
XX CC synthetic peptides based on the D1 region of S. aureus fibronectin
XX CC binding protein A. They were synthesised to contain mutations
XX SQ
XX Sequence 38 AA:
XX
XX Query Match          100.0%; Score 53; DB 2; Length 38;
XX Best Local Similarity 100.0%; Pred. No. 0.013;
XX Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY      1 OGGNIVDIDF 10
XX          |||||
XX          21 OGGNIVDIDF 30
XX DB
XX
XX RESULT 11
XX AAM65698 standard; peptide; 38 AA.
XX ID
XX AC AAM65698;
XX XX
XX DT 16-OCT-1998 (first entry)
XX DE Fibronectin binding protein-derived peptide #42.
XX XX
XX KW microbial surface components recognising adhesive matrix molecule;
XX MSCRAMM; fibronectin; fibronectin-binding protein; antibody; epitope;
XX KW antibiotic; bacterial infection; antibiotic-resistant strain.
XX XX
XX OS Synthetic.
XX OS Staphylococcus aureus.
XX OS
XX PN WO9831389-A2.
XX XX
XX PD 23-JUL-1998.
XX XX
XX PF 21-JAN-1998; 98WO-US001222.
XX XX
XX PR 21-JAN-1997; 97US-0036139P.
XX XX
XX PA (TEXA ) UNIV TEXAS A & M SYSTEM.
XX XX
XX PI Hoeoek M, Patti JM, House-Pompeo KL, Speziale P, Joh D;
XX PI McGavin MJ;
XX XX
XX DR WPI, 1998-413816/35.
XX XX
XX PT Antibody that binds to fibronectin-binding protein, preventing its
XX PT binding to fibronectin - used to treat or prevent bacterial infection,
XX PT especially by Staphylococci and Streptococci.

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XX XX Example 8; Page 102; 201pp; English.
XX PS
XX CC The invention relates to antibodies that bind to a fibronectin-binding
XX CC domain of a fibronectin-binding protein, and inhibit binding of the
XX CC protein to fibronectin. Also claimed are: (1) isolated peptides of a
XX CC fibronectin-binding protein that do not bind to fibronectin; (2) fusion
XX CC protein containing at least one peptide of a fibronectin-binding protein
XX CC linked to a second amino acid sequence; (3) nucleic acid encoding the
XX CC isolated peptide of (1). Antibodies, the isolated peptides of (1) and the
XX CC nucleic acids are all useful for immunisation (active or passive) and (by
XX CC inhibiting binding of bacteria to fibronectin) for preventing or treating
XX CC infection in humans or other animals, particularly by staphylococci or
XX CC streptococci, e.g. meningitis, otitis media, pneumonia, endocarditis,
XX CC mastitis in cattle, abortion in horses and many others. Since the
XX CC antibodies block binding of bacteria, they should be effective against
XX CC antibiotic-resistant strains, and may replace antibiotic therapy or
XX CC increase its effectiveness. Sequences AAM65691-700 represent a series of
XX CC synthetic peptides based on the D1 region of S. aureus fibronectin
XX CC binding protein A. They were synthesised to contain mutations
XX SQ
XX Sequence 38 AA:
XX
XX Query Match          100.0%; Score 53; DB 2; Length 38;
XX Best Local Similarity 100.0%; Pred. No. 0.013;
XX Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY      1 OGGNIVDIDF 10
XX          |||||
XX          21 OGGNIVDIDF 30
XX DB
XX
XX RESULT 12
XX AAM65712 standard; peptide; 39 AA.
XX ID
XX AC AAM65712;
XX XX
XX DT 16-OCT-1998 (first entry)
XX DE Fibronectin binding protein-derived peptide #56.
XX XX
XX KW microbial surface components recognising adhesive matrix molecule;
XX MSCRAMM; fibronectin; fibronectin-binding protein; antibody; epitope;
XX KW antibiotic; bacterial infection; antibiotic-resistant strain.
XX XX
XX OS Synthetic.
XX OS Staphylococcus aureus.
XX OS
XX PN WO9831389-A2.
XX XX
XX PD 23-JUL-1998.
XX XX
XX PF 21-JAN-1998; 98WO-US001222.
XX XX
XX PR 21-JAN-1997; 97US-0036139P.
XX XX
XX PA (TEXA ) UNIV TEXAS A & M SYSTEM.
XX XX
XX PI Hoeoek M, Patti JM, House-Pompeo KL, Speziale P, Joh D;
XX PI McGavin MJ;
XX XX
XX DR WPI, 1998-413816/35.
XX XX
XX PT Antibody that binds to fibronectin-binding protein, preventing its
XX PT binding to fibronectin - used to treat or prevent bacterial infection,
XX PT especially by Staphylococci and Streptococci.
XX PS
XX PS Example 8; Page 104; 201pp; English.
XX XX
XX CC The invention relates to antibodies that bind to a fibronectin-binding
XX CC domain of a fibronectin-binding protein, and inhibit binding of the
XX CC protein to fibronectin. Also claimed are: (1) isolated peptides of a

```

CC fibronectin-binding protein that do not bind to fibronectin; (2) fusion
 CC protein containing at least one peptide of a fibronectin-binding protein
 CC linked to a second amino acid sequence; (3) nucleic acid encoding the
 CC isolated peptide of (1). Antibodies, the isolated peptides of (1) and the
 CC nucleic acids are all useful for immunisation (active or passive) and (by
 CC inhibiting binding of bacteria to fibronectin) for preventing or treating
 CC infection in humans or other animals, particularly by staphylococci or
 CC streptococci, e.g. meningitis, otitis media, pneumonia, endocarditis,
 CC mastitis in cattle, abortion in horses and many others. Since the
 CC antibodies block binding of bacteria, they should be effective against
 CC antibiotic-resistant strains, and may replace antibiotic therapy or
 CC increase its effectiveness. The present sequence is shown in the
 CC specification
 XX

Sequence 39 AA;

Query Match 100.0%; Score 53; DB 2; Length 39;
 Best Local Similarity 100.0%; Pred. No. 0.013; Mismatches 0; Indels 0; Gaps 0;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 OGGNIYDIDF 10
 |||||
 DB 21 OGGNIYDIDF 30

RESULT 13

AAR90937 standard; peptide; 113 AA.

AC AAR90937;
 DT 23-SBP-1996 (first entry)
 XX
 DE D3D4 polypeptide #1.

XX Fibronectin binding protein; Fbp; S. aureus J2385; monoclonal antibody;
 KW infection; surgical implant; antidiabetic agent; hygiene; adhesion;
 KW extracellular matrix protein; oral pathogen; oral cavity.

OS Staphylococcus aureus.

XX Key Location/Qualifiers
 FT Region 1..21
 FT /note="D1 region fragment"
 FT Region 22..59
 FT /note="D2 region"
 FT Region 60..98
 FT /note="D3 region"
 FT Region 99..113
 FT /note="D4 region"
 FT Misc-difference 113
 FT /note="P113r"

XX WO9604381-A1.

XX 15-FEB-1996.

XX 28-JUL-1995; 95WO-EP003040.

XX 05-AUG-1994; 94GB-00015900.

XX (SMIK) SMITHKLINE BEECHAM PLC.

XX C-itchley IA, Dodd I, Barnett P, Mcbay DL;

XX WPI; 1996-129397/13.

XX Polypeptide(s) derived from Staphylococcus aureus fibronectin binding
 PT protein - inhibit binding of bacteria to extracellular matrix proteins,
 PT for combating infection at the site of wounds and surgical implants, and
 PT in oral hygiene.

XX Claim 6; Page 24; 35pp; English.

XX AAR90937-R90942 represent D3D4 polypeptides. These sequences correspond
 CC to fragments of the Staphylococcus aureus fibronectin binding protein
 CC (Fbp). This sequence corresponds to residues 18-130 of S. aureus J2385
 CC Fbp, and also contains the D2 region, and a portion of the D1 region.
 CC These sequences, and monoclonal antibodies against them can be used to
 CC combat infection at the site of wound, surgical implants and other in-
 CC dwelling devices (such as catheters), and as adherent agents in oral
 CC hygiene. They can also be used in the manufacture of a medicament for the
 CC prevention of adhesion of bacteria to extracellular matrix proteins
 CC present on in-dwelling devices or in wounds, or of oral pathogens to
 CC similar proteins on surfaces in the oral cavity
 XX

Sequence 113 AA;

Query Match 100.0%; Score 53; DB 2; Length 113;
 Best Local Similarity 100.0%; Pred. No. 0.044; Mismatches 0; Indels 0; Gaps 0;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 OGGNIYDIDF 10
 |||||
 DB 5 OGGNIYDIDF 14

RESULT 14

AAR58806 standard; protein; 130 AA.

AC AAR58806;

DT 25-MAR-2003 (revised)
 DT 30-MAR-1995 (first entry)

XX Fibronectin binding domain D1-D4 (709-838 (P838T)).

XX Fibronectin binding protein; Fbp; fibronectin binding domain;
 KW monoclonal antibody; Mab; adhesion; Gram-positive bacterium; bacteraemia;
 KW Escherichia coli.

OS Staphylococcus aureus.

XX WO9418327-A1.

XX 18-AUG-1994.

XX 04-FEB-1994; 94WO-GB000215.

XX 05-FEB-1993; 93GB-00002289.

XX 20-OCT-1993; 93GB-00021592.

XX (SMIK) SMITHKLINE BEECHAM PLC.

XX Burnham MKR, Chopra I, Citchley IA, Knowles DJC;

XX WPI; 1994-279748/34.

XX Fibronectin binding protein and monoclonal antibodies specific for Fbp -
 PT useful to prevent adherence of Gram-positive bacteria to indwelling
 PT devices or wounds.

XX Disclosure; Page 30; 40pp; English.

XX Polypeptides corresponding to residues 7709-7886 plus PPIVPT, 7709-
 CC P838(P838T) and 7709-P838 (AAR58805-07, respectively) of S. aureus J2385
 CC (NCIMB 40532) Fbp type A fibronectin binding domain D1-D4 region
 CC (AAR58808) were expressed in E. coli BL21 (DE4) and used to raise MAbs
 CC specific for Fbp. (Updated on 25-MAR-2003 to correct PN field.)
 XX

Sequence 130 AA;

Query Match 100.0%; Score 53; DB 2; Length 130;
 Best Local Similarity 100.0%; Pred. No. 0.052; Mismatches 0; Indels 0; Gaps 0;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 OGGNIVDIDF 10
 |||||
 Db 22 OGGNIVDIDF 31

RESULT 15

AA858807
 ID AA858807 standard; protein; 130 AA.

XX
 AC AA858807;

XX
 DT 25-MAR-2003 (revised)
 DT 30-MAR-1995 (first entry)

DE Fibronectin binding domain D1-D4(709-838).

XX Fibronectin binding protein; FBP; fibronectin binding domain;
 KW monoclonal antibody; Mab; adhesion; Gram-positive bacterium; bacteraemia;
 KM Escherichia coli.
 XX

OS Staphylococcus aureus.

PN WO9418327-A1.

PD 18-AUG-1994.

PF 04-FEB-1994; 94WO-GB000215.

PR 05-FEB-1993; 93GB-00002289.

PR 20-OCT-1993; 93GB-00021592.

XX (SMK) SMITHKLINE BEECHAM PLC.

XX Burnham MKR, Chopra I, Critchley IA, Knowles DJC;

DR WPI; 1994-279748/34.

XX
 PT Fibronectin binding protein and monoclonal antibodies specific for Fbp -
 PT useful to prevent adherence of Gram-positive bacteria to indwelling
 PT devices or wounds.

PS Disclosure; Page 30; 40pp; English.

XX Polypeptides corresponding to residues G709-P886 plus PIVVPT, G709-
 CC P838(P838T) and G709-P838 (AA858805-07, respectively) of S. aureus J2385
 CC (NCIMB 40532) Fbp type A fibronectin binding domain D1-D4 region
 CC (AA858808) were expressed in E. coli BL21(DE4) and used to raise Mabs
 CC specific for Fbp. (Updated on 25-MAR-2003 to correct PN field.)
 XX

SQ Sequence 130 AA;

Query Match 100.0%; Score 53; DB 2; Length 130;

Best Local Similarity 100.0%; Pred. No. 0.052;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 OGGNIVDIDF 10
 |||||
 Db 22 OGGNIVDIDF 31

Search completed: October 25, 2005, 20:58:43
 Job time : 63.2 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 22, 2005, 05:46:56 ; Search time 17.3 Seconds
(without alignments)
43.150 Million cell updates/sec

Title: US-10-731-238-73

Perfect score: 53

Sequence: 1 OCGNIVDIDF 10

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*

- 1: /cgn2_6/prodata/1/iaa/5A_COMB.pep:*
- 2: /cgn2_6/prodata/1/iaa/5B_COMB.pep:*
- 3: /cgn2_6/prodata/1/iaa/6A_COMB.pep:*
- 4: /cgn2_6/prodata/1/iaa/6B_COMB.pep:*
- 5: /cgn2_6/prodata/1/iaa/6C_COMB.pep:*
- 6: /cgn2_6/prodata/1/iaa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	53	100.0	10	4	US-09-010-317-73
2	53	100.0	14	4	US-09-010-317-60
3	53	100.0	38	1	US-08-234-622A-2
4	53	100.0	38	1	US-08-729-767-3
5	53	100.0	38	4	US-09-010-317-5
6	53	100.0	38	4	US-09-010-317-35
7	53	100.0	38	4	US-09-010-317-36
8	53	100.0	38	4	US-09-010-317-37
9	53	100.0	38	4	US-09-010-317-38
10	53	100.0	38	4	US-09-010-317-39
11	53	100.0	38	4	US-09-010-317-40
12	53	100.0	38	4	US-09-010-317-41
13	53	100.0	38	4	US-09-010-317-42
14	53	100.0	39	4	US-09-010-317-56
15	53	100.0	114	1	US-08-259-000-3
16	53	100.0	130	2	US-08-459-135A-7
17	53	100.0	130	2	US-08-459-135A-8
18	53	100.0	130	3	US-08-495-559-7
19	53	100.0	130	3	US-08-495-559-8
20	53	100.0	139	3	US-08-856-253-8
21	53	100.0	174	2	US-08-459-135A-10
22	53	100.0	174	2	US-08-459-135A-13
23	53	100.0	174	3	US-08-495-559-10
24	53	100.0	174	3	US-08-495-559-13
25	53	100.0	176	3	US-08-495-559-6
26	53	100.0	178	2	US-08-459-135A-12
27	53	100.0	178	3	US-08-495-559-12

ALIGNMENTS

28	53	100.0	181	2	US-08-459-135A-6	Sequence 6, Appl1
29	53	100.0	559	4	US-08-956-171E-5251	Sequence 5251, Ap
30	53	100.0	559	4	US-08-781-986A-5251	Sequence 5251, Ap
31	53	100.0	1027	4	US-08-956-171E-5254	Sequence 5254, Ap
32	53	100.0	1027	4	US-08-781-986A-5254	Sequence 5254, Ap
33	47	88.7	14	4	US-09-010-317-103	Sequence 58, Appl
34	47	88.7	36	1	US-09-010-317-58	Sequence 58, Appl
35	47	88.7	38	1	US-08-234-622A-3	Sequence 7, Appl1
36	47	88.7	38	1	US-08-729-767-4	Sequence 7, Appl1
37	47	88.7	38	4	US-09-010-317-7	Sequence 45, Appl
38	47	88.7	38	4	US-09-010-317-45	Sequence 46, Appl
39	47	88.7	38	4	US-09-010-317-46	Sequence 47, Appl
40	47	88.7	38	4	US-09-010-317-47	Sequence 48, Appl
41	47	88.7	38	4	US-09-010-317-48	Sequence 6, Appl1
42	45	84.9	38	4	US-09-010-317-6	Sequence 43, Appl
43	45	84.9	38	4	US-09-010-317-43	Sequence 57, Appl
44	45	84.9	39	4	US-09-010-317-57	Sequence 74, Appl
45	42	79.2	10	4	US-09-010-317-74	

RESULT 1
US-09-010-317-73
Sequence 73, Application US/09010317
Patent No. 6685943
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
APPLICANT: Patti, Joseph M.
APPLICANT: House-Pompeo, Karen L.
APPLICANT: Speziale, Pietro
APPLICANT: Jon, Danny
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
TITLE OF INVENTION: AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAMK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 73:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-09-010-317-73
Query Match 100.0%; Score 53; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0012;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 OGGNIVDIDF 10
|||||

Db 1 OGGNIVDIDF 10

RESULT 2

US-09-010-317-60

; Sequence 60, Application US/09010317
; Patent No. 6685943

; GENERAL INFORMATION:

; APPLICANT: Hook, Magnus

; APPLICANT: Patti, Joseph M.

; APPLICANT: House-Pompeo, Karen L.

; APPLICANT: Speziale, Pietro

; APPLICANT: McGavin, Martin J.

; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS

; NUMBER OF SEQUENCES: 105

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Arnold, White & Durkee

; STREET: P.O. Box 4433

; CITY: Houston

; STATE: TX

; COUNTRY: USA

; ZIP: 77210-4433

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/010,317

; FILING DATE:

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 60/036,139

; FILING DATE: 21-JAN-1997

; ATTORNEY/AGENT INFORMATION:

; NAME: Hibler, David W.

; REGISTRATION NUMBER: 41,071

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 512-418-3000

; TELEFAX: 512-474-7577

; INFORMATION FOR SEQ ID NO: 60:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 14 amino acids

; TYPE: amino acid

; STRANDEDNESS:

; TOPOLOGY: linear

US-09-010-317-60

Query Match 100.0%; Score 53; DB 4; Length 14;

Best Local Similarity 100.0%; Pred. No. 0.0017; Mismatches 0; Indels 0; Gaps 0;

QY 1 OGGNIVDIDF 10
|||||

Db 1 OGGNIVDIDF 10

RESULT 3

US-08-234-622A-2

; Sequence 2, Application US/08234622A

; Patent No. 5440014

; GENERAL INFORMATION:

; APPLICANT: HOOK, Magnus

; APPLICANT: MCGAVIN, Martin

; APPLICANT: RAUCCI, Giuseppe

; TITLE OF INVENTION: A FIBRONECTIN BINDING PEPTIDE

; NUMBER OF SEQUENCES: 4

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Burns, Doane, Swecker & Mathis

; STREET: P.O. Box 1404

; CITY: Alexandria

; STATE: Virginia

; COUNTRY: United States

; ZIP: 22313-1404

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/234,622A

; FILING DATE: 28-APR-1994

; CLASSIFICATION: 530

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: SE 9002617-0

; FILING DATE: 10-AUG-1990

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: WO PCT/SE91/00534

; FILING DATE: 09-AUG-1991

; ATTORNEY/AGENT INFORMATION:

; NAME: Neuth, Donna M

; REGISTRATION NUMBER: 36,607

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (703) 836-6620

; INFORMATION FOR SEQ ID NO: 2:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 38 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

US-08-234-622A-2

Query Match 100.0%; Score 53; DB 1; Length 38;

Best Local Similarity 100.0%; Pred. No. 0.0051; Mismatches 0; Indels 0; Gaps 0;

QY 1 OGGNIVDIDF 10
|||||

Db 21 OGGNIVDIDF 30

RESULT 4

US-08-729-767-3

; Sequence 3, Application US/08729767

; Patent No. 5770702

; GENERAL INFORMATION:

; APPLICANT: HOOK, Magnus

; APPLICANT: LINDBERG, Martin Kjell

; APPLICANT: SIGNAS, Lars Christer

; APPLICANT: WADSTROM, Torkel Mikael

; APPLICANT: FROMAN, Gunnar

; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN AS WELL AS

; NUMBER OF SEQUENCES: 6

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Burns, Doane, Swecker & Mathis, L.L.P.

; STREET: P.O. Box 1404

; CITY: Alexandria

; STATE: Virginia

; COUNTRY: United States

; ZIP: 22313-1404

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/729,767
FILING DATE: 07-OCT-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/259,000
FILING DATE: 13-JUN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/007,817
FILING DATE: 22-JAN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/201,028
FILING DATE: 01-JUN-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: SE 8702272-9
FILING DATE: 01-JUN-1987
ATTORNEY/AGENT INFORMATION:
NAME: McGowan, Malcolm K.
REGISTRATION NUMBER: 39,300
REFERENCE/DOCKET NUMBER: 012889-036
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-729-767-3

Query Match 100.0%; Score 53; DB 1; Length 38;
Best Local Similarity 100.0%; Pred. No. 0.0051;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 OGNNIVDIDF 10
Db 22 OGNNIVDIDF 31

RESULT 5
US-09-010-317-5
Sequence 5, Application US/09010317
Patent No. 6685943
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
APPLICANT: Patti, Joseph M.
APPLICANT: House-Pompeo, Karen L.
APPLICANT: Speziale, Pietro
APPLICANT: Joh, Danny
APPLICANT: McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
TITLE OF INVENTION: AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/036,139

FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TANK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-09-010-317-5

Query Match 100.0%; Score 53; DB 4; Length 38;
Best Local Similarity 100.0%; Pred. No. 0.0051;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 OGNNIVDIDF 10
Db 21 OGNNIVDIDF 30

RESULT 6
US-09-010-317-35
Sequence 35, Application US/09010317
Patent No. 6685943
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
APPLICANT: Patti, Joseph M.
APPLICANT: House-Pompeo, Karen L.
APPLICANT: Speziale, Pietro
APPLICANT: Joh, Danny
APPLICANT: McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
TITLE OF INVENTION: AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TANK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 35:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-09-010-317-35

Query Match 100.0%; Score 53; DB 4; Length 38;
Best Local Similarity 100.0%; Pred. No. 0.0051;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 OGGNIVDIDF 10
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DB 21 OGGNIVDIDF 30

RESULT 7

US-09-010-317-36
; Sequence 36, Application US/09010317
; Patent No. 6685943
; GENERAL INFORMATION:
; APPLICANT: Hook, Magnus
; APPLICANT: Patti, Joseph M.
; APPLICANT: House-Pompeo, Karen L.
; APPLICANT: Speziale, Pietro
; APPLICANT: Joh, Danny
; APPLICANT: McGavin, Martin J.
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
; NUMBER OF SEQUENCES: 105
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: TX
; COUNTRY: USA
; ZIP: 77210-4433
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/010,317
; FILING DATE:
; STRANDEDNESS:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/036,139
; FILING DATE: 21-JAN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Hibler, David W.
; REGISTRATION NUMBER: 41,071
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 512-418-3000
; TELEFAX: 512-474-7577
; INFORMATION FOR SEQ ID NO: 36:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 38 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
US-09-010-317-36

Query Match 100.0%; Score 53; DB 4; Length 38;
Best Local Similarity 100.0%; Pred. No. 0.0051;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 OGGNIVDIDF 10
| | | | | | | |
DB 21 OGGNIVDIDF 30

RESULT 8

US-09-010-317-37
; Sequence 37, Application US/09010317
; Patent No. 6685943
; GENERAL INFORMATION:
; APPLICANT: Hook, Magnus
; APPLICANT: Patti, Joseph M.

; APPLICANT: House-Pompeo, Karen L.
; APPLICANT: Speziale, Pietro
; APPLICANT: Joh, Danny
; APPLICANT: McGavin, Martin J.
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
; NUMBER OF SEQUENCES: 105
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: TX
; COUNTRY: USA
; ZIP: 77210-4433
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/010,317
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/036,139
; FILING DATE: 21-JAN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Hibler, David W.
; REGISTRATION NUMBER: 41,071
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 512-418-3000
; TELEFAX: 512-474-7577
; INFORMATION FOR SEQ ID NO: 37:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 38 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
US-09-010-317-37

Query Match 100.0%; Score 53; DB 4; Length 38;
Best Local Similarity 100.0%; Pred. No. 0.0051;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 OGGNIVDIDF 10
| | | | | | | |
DB 21 OGGNIVDIDF 30

RESULT 9

US-09-010-317-38
; Sequence 38, Application US/09010317
; Patent No. 6685943
; GENERAL INFORMATION:
; APPLICANT: Hook, Magnus
; APPLICANT: Patti, Joseph M.
; APPLICANT: House-Pompeo, Karen L.
; APPLICANT: Speziale, Pietro
; APPLICANT: Joh, Danny
; APPLICANT: McGavin, Martin J.
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
; NUMBER OF SEQUENCES: 105
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: TX
; COUNTRY: USA
; ZIP: 77210-4433
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TANK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 38:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-09-010-317-38

Query Match 100.0%; Score 53; DB 4; Length 38;
Best Local Similarity 100.0%; Pred. No. 0.0051;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 OGGNIVDIF 10
| | | | | | | | | |
Db 21 OGGNIVDIF 30

RESULT 10
US-09-010-317-39
Sequence 39, Application US/09010317
Patent No. 6685943
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
APPLICANT: Patti, Joseph M.
APPLICANT: House-Pompeo, Karen L.
APPLICANT: Speziale, Pietro
APPLICANT: Joh, Danny
APPLICANT: McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
TITLE OF INVENTION: AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TANK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 40:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-09-010-317-40

Query Match 100.0%; Score 53; DB 4; Length 38;
Best Local Similarity 100.0%; Pred. No. 0.0051;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 OGGNIVDIF 10
| | | | | | | | | |
Db 21 OGGNIVDIF 30

RESULT 11
US-09-010-317-40
Sequence 40, Application US/09010317
Patent No. 6685943
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
APPLICANT: Patti, Joseph M.
APPLICANT: House-Pompeo, Karen L.
APPLICANT: Speziale, Pietro
APPLICANT: Joh, Danny
APPLICANT: McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
TITLE OF INVENTION: AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TANK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 40:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-09-010-317-40

Query Match 100.0%; Score 53; DB 4; Length 38;
Best Local Similarity 100.0%; Pred. No. 0.0051;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 OGGNIVDIF 10
| | | | | | | | | |
Db 21 OGGNIVDIF 30

TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 39:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-09-010-317-39

Query Match 100.0%; Score 53; DB 4; Length 38;
Best Local Similarity 100.0%; Pred. No. 0.0051;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 OGGNIVDIF 10
| | | | | | | | | |
Db 21 OGGNIVDIF 30

RESULT 11
US-09-010-317-40
Sequence 40, Application US/09010317
Patent No. 6685943
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
APPLICANT: Patti, Joseph M.
APPLICANT: House-Pompeo, Karen L.
APPLICANT: Speziale, Pietro
APPLICANT: Joh, Danny
APPLICANT: McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
TITLE OF INVENTION: AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TANK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 40:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-09-010-317-40

Query Match 100.0%; Score 53; DB 4; Length 38;
Best Local Similarity 100.0%; Pred. No. 0.0051;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 OGGNIVDIF 10
| | | | | | | | | |
Db 21 OGGNIVDIF 30

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RESULT 12
US-09-010-317-41
; Sequence 41, Application US/09010317
; Patent No. 6685943
; GENERAL INFORMATION:
; APPLICANT: Hook, Magnus
; APPLICANT: Patti, Joseph M.
; APPLICANT: House-Pompeo, Karen L.
; APPLICANT: Speziale, Pietro
; APPLICANT: Joh, Danny
; APPLICANT: McGavin, Martin J.
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
; NUMBER OF SEQUENCES: 105
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P. O. Box 4433
; CITY: Houston
; STATE: TX
; COUNTRY: USA
; ZIP: 77210-4433
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/010,317
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/036,139
; FILING DATE: 21-JAN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Hibler, David W.
; REGISTRATION NUMBER: 41,071
; REFERENCE/DOCKET NUMBER: TANK:189
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 512-418-3000
; TELEFAX: 512-474-7577
; INFORMATION FOR SEQ ID NO: 41:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 38 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; US-09-010-317-41

Query Match      100.0%; Score 53; DB 4; Length 38;
Best Local Similarity 100.0%; Pred. No. 0.0051;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  OGGNIVDIDF 10
Db      21  OGGNIVDIDF 30

RESULT 13
US-09-010-317-42
; Sequence 42, Application US/09010317
; Patent No. 6685943
; GENERAL INFORMATION:
; APPLICANT: Hook, Magnus
; APPLICANT: Patti, Joseph M.
; APPLICANT: House-Pompeo, Karen L.
; APPLICANT: Speziale, Pietro
; APPLICANT: Joh, Danny
; APPLICANT: McGavin, Martin J.
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
; NUMBER OF SEQUENCES: 105
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; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P. O. Box 4433
; CITY: Houston
; STATE: TX
; COUNTRY: USA
; ZIP: 77210-4433
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/010,317
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/036,139
; FILING DATE: 21-JAN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Hibler, David W.
; REGISTRATION NUMBER: 41,071
; REFERENCE/DOCKET NUMBER: TANK:189
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 512-418-3000
; TELEFAX: 512-474-7577
; INFORMATION FOR SEQ ID NO: 42:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 38 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; US-09-010-317-42

Query Match      100.0%; Score 53; DB 4; Length 38;
Best Local Similarity 100.0%; Pred. No. 0.0051;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  OGGNIVDIDF 10
Db      21  OGGNIVDIDF 30

RESULT 14
US-09-010-317-56
; Sequence 56, Application US/09010317
; Patent No. 6685943
; GENERAL INFORMATION:
; APPLICANT: Hook, Magnus
; APPLICANT: Patti, Joseph M.
; APPLICANT: House-Pompeo, Karen L.
; APPLICANT: Speziale, Pietro
; APPLICANT: Joh, Danny
; APPLICANT: McGavin, Martin J.
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
; NUMBER OF SEQUENCES: 105
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P. O. Box 4433
; CITY: Houston
; STATE: TX
; COUNTRY: USA
; ZIP: 77210-4433
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/010,317
; FILING DATE:
; CLASSIFICATION:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Habler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAMK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 56:
SEQUENCE CHARACTERISTICS:
LENGTH: 39 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-09-010-317-56

Query Match 100.0%; Score 53; DB 4; Length 39;
Best Local Similarity 100.0%; Pred. No. 0.0053;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QGNIVIDIF 10
|||
Db 21 QGNIVIDIF 30

RESULT 15
US-08-259-000-3
Sequence 3, Application US/08259000
Patent No. 5571514
GENERAL INFORMATION:
APPLICANT: HOOK, Magnus
APPLICANT: LINDBERG, Martin Kjell
APPLICANT: SIGNAS, Lars Christer
APPLICANT: MADSTROM, Torkel Mikael
APPLICANT: FROMAN, Gunnar
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN AS WELL AS
NUMBER OF SEQUENCES: 4
TITLE OF INVENTION: ITS PREPARATION
CORRESPONDENCE ADDRESS:
ADDRESSER: Burns, Doane, Swecker & Mathis
STREET: P.O. Box 1404
CITY: Alexandria
STATE: Virginia
COUNTRY: United States
ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/259,000
FILING DATE: 13-JUN-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: SE 8702272-9
FILING DATE: 01-JUN-1987
ATTORNEY/AGENT INFORMATION:
NAME: Meuth, Donna M
REGISTRATION NUMBER: 36,607
REFERENCE/DOCKET NUMBER: 012885-062
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 114 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein

US-08-259-000-3

Query Match 100.0%; Score 53; DB 1; Length 114;
Best Local Similarity 100.0%; Pred. No. 0.017;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QGNIVIDIF 10
|||
Db 22 QGNIVIDIF 31

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Job time: 18.35 secs

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OM protein - protein search, using sw model

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Title: US-10-731-238-73

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Gapop 10.0 , Gapext 0.5

Searched: 1862951 seqs, 417491010 residues

Total number of hits satisfying chosen parameters: 1862951

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Published Applications_AA:*
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22: /cgn2_6/ptodata/2/pubppa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	53	100.0	10	US-10-731-238-73	Sequence 73, Appl
2	53	100.0	14	US-10-731-238-60	Sequence 60, Appl
3	53	100.0	38	US-10-731-238-5	Sequence 5, Appl
4	53	100.0	38	US-10-731-238-35	Sequence 35, Appl
5	53	100.0	38	US-10-731-238-36	Sequence 36, Appl
6	53	100.0	38	US-10-731-238-37	Sequence 37, Appl
7	53	100.0	38	US-10-731-238-38	Sequence 38, Appl
8	53	100.0	38	US-10-731-238-39	Sequence 39, Appl
9	53	100.0	38	US-10-731-238-40	Sequence 40, Appl
10	53	100.0	38	US-10-731-238-41	Sequence 41, Appl
11	53	100.0	38	US-10-731-238-42	Sequence 42, Appl

12	53	100.0	39	US-10-731-238-56	Sequence 56, Appl
13	53	100.0	139	US-09-813-820-8	Sequence 8, Appl
14	53	100.0	388	US-08-901-062-1	Sequence 1, Appl
15	53	100.0	559	US-08-781-986A-5251	Sequence 5251, Ap
16	53	100.0	559	US-10-329-624-5251	Sequence 5251, Ap
17	53	100.0	767	US-09-815-242-5899	Sequence 5899, Ap
18	53	100.0	767	US-09-815-242-13140	Sequence 13140, A
19	53	100.0	940	US-10-470-048B-624	Sequence 424, App
20	53	100.0	948	US-10-470-048B-69	Sequence 69, App
21	53	100.0	961	US-10-282-122A-43778	Sequence 43778, A
22	53	100.0	978	US-09-815-242-5456	Sequence 5456, Ap
23	53	100.0	1001	US-09-815-242-12686	Sequence 12686, A
24	53	100.0	1018	US-09-815-242-5797	Sequence 5797, Ap
25	53	100.0	1018	US-09-815-242-12838	Sequence 12838, A
26	53	100.0	1018	US-10-470-048B-68	Sequence 68, Appl
27	53	100.0	1027	US-08-781-986A-5254	Sequence 5254, Ap
28	53	100.0	1027	US-10-329-624-5254	Sequence 5254, Ap
29	53	100.0	1038	US-10-282-122A-43827	Sequence 43827, A
30	47	88.7	14	US-10-731-238-103	Sequence 103, App
31	47	88.7	36	US-10-731-238-58	Sequence 58, Appl
32	47	88.7	38	US-10-731-238-7	Sequence 7, Appl
33	47	88.7	38	US-10-731-238-45	Sequence 45, Appl
34	47	88.7	38	US-10-731-238-46	Sequence 46, Appl
35	47	88.7	38	US-10-731-238-47	Sequence 47, Appl
36	47	88.7	38	US-10-731-238-48	Sequence 48, Appl
37	46	86.6	30	US-10-287-821-1	Sequence 1, Appl
38	46	86.6	31	US-10-287-821-2	Sequence 2, Appl
39	45	84.9	38	US-10-731-238-6	Sequence 6, Appl
40	45	84.9	38	US-10-731-238-43	Sequence 43, Appl
41	45	84.9	39	US-10-731-238-57	Sequence 57, Appl
42	43	81.1	1240	US-10-840-512-211	Sequence 211, Appl
43	42	79.2	10	US-10-731-238-74	Sequence 74, Appl
44	42	79.2	318	US-10-425-115-322904	Sequence 322904, A
45	42	79.2	339	US-10-425-114-68576	Sequence 68576, A

ALIGNMENTS

RESULT 1

US-10-731-238-73

Sequence 73, Application US/10731238

Publication No. US20050123552A1

GENERAL INFORMATION:

APPLICANT: Hook, Magnus

Patel, Joseph M.

Houee-Pompeo, Karen L.

Speziale, Pietro

Job, Danny

McGavin, Martin J.

TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS

AND METHODS OF USE

NUMBER OF SEQUENCES: 105

CORRESPONDENCE ADDRESSES:

ADDRESSER: Arnold, White & Durkee

STREET: P.O. Box 4433

CITY: Houston

STATE: TX

COUNTRY: USA

ZIP: 77210-4433

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/731.238

FILING DATE: 10-Dec-2003

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/010.317

FILING DATE: 21-Jan-1998

APPLICATION NUMBER: US 60/036.139

```

;
; FILING DATE: 21-JAN-1997
; ATTORNEY/AGENT INFORMATION:
;   NAME: Hibler, David W.
;   REGISTRATION NUMBER: 41,071
;   REFERENCE/DOCKET NUMBER: TAMK:189
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE: 512-418-3000
;     TELEFAX: 512-474-7577
; INFORMATION FOR SEQ ID NO: 73:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH: 10 amino acids
;     TYPE: amino acid
;     STRANDEDNESS: <Unknown>
;     TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 73:
US-10-731-238-73

Query Match      100.0%; Score 53; DB 18; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0094;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 OGGNTVIDIF 10
        |||||
Db      1 OGGNTVIDIF 10

RESULT 2
US-10-731-238-60
; Sequence 60, Application US/10731238
; Publication No. US20050123552A1
; GENERAL INFORMATION:
;   APPLICANT: Hook, Magnus
;             Patti, Joseph M.
;             House-Pompeo, Karen L.
;             Speziale, Pietro
;             Joh, Danny
;             McGavin, Martin J.
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
;
; NUMBER OF SEQUENCES: 105
; CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Arnold, White & Durkee
;   STREET: P.O. Box 4433
;   CITY: Houston
;   STATE: TX
;   COUNTRY: USA
;   ZIP: 77210-4433
; COMPUTER READABLE FORM:
;   MEDIUM TYPE: floppy disk
;   OPERATING SYSTEM: IBM PC compatible
;   SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/10/731,238
;   FILING DATE: 10-Dec-2003
;   CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US/09/010,317
;   FILING DATE: 21-Jan-1998
;   APPLICATION NUMBER: US 60/036,139
;   FILING DATE: 21-JAN-1997
; ATTORNEY/AGENT INFORMATION:
;   NAME: Hibler, David W.
;   REGISTRATION NUMBER: 41,071
;   REFERENCE/DOCKET NUMBER: TAMK:189
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE: 512-418-3000
;     TELEFAX: 512-474-7577
; INFORMATION FOR SEQ ID NO: 60:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH: 14 amino acids
;     TYPE: amino acid
;     STRANDEDNESS: <Unknown>

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;
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 60:
US-10-731-238-60

Query Match      100.0%; Score 53; DB 18; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.013;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 OGGNTVIDIF 10
        |||||
Db      1 OGGNTVIDIF 10

RESULT 3
US-10-731-238-5
; Sequence 5, Application US/10731238
; Publication No. US20050123552A1
; GENERAL INFORMATION:
;   APPLICANT: Hook, Magnus
;             Patti, Joseph M.
;             House-Pompeo, Karen L.
;             Speziale, Pietro
;             Joh, Danny
;             McGavin, Martin J.
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
;
; NUMBER OF SEQUENCES: 105
; CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Arnold, White & Durkee
;   STREET: P.O. Box 4433
;   CITY: Houston
;   STATE: TX
;   COUNTRY: USA
;   ZIP: 77210-4433
; COMPUTER READABLE FORM:
;   MEDIUM TYPE: floppy disk
;   OPERATING SYSTEM: IBM PC compatible
;   SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/10/731,238
;   FILING DATE: 10-Dec-2003
;   CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US/09/010,317
;   FILING DATE: 21-Jan-1998
;   APPLICATION NUMBER: US 60/036,139
;   FILING DATE: 21-JAN-1997
; ATTORNEY/AGENT INFORMATION:
;   NAME: Hibler, David W.
;   REGISTRATION NUMBER: 41,071
;   REFERENCE/DOCKET NUMBER: TAMK:189
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE: 512-418-3000
;     TELEFAX: 512-474-7577
; INFORMATION FOR SEQ ID NO: 5:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH: 38 amino acids
;     TYPE: amino acid
;     STRANDEDNESS: <Unknown>
;     TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-10-731-238-5

Query Match      100.0%; Score 53; DB 18; Length 38;
Best Local Similarity 100.0%; Pred. No. 0.019;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 OGGNTVIDIF 10
        |||||
Db      21 OGGNTVIDIF 30

```

RESULT 4
US-10-731-238-35
; Sequence 35, Application US/10731238
; Publication No. US20050123552A1
; GENERAL INFORMATION:
; APPLICANT: Hook, Magnus
; Patti, Joseph M.
; House-Pompeo, Karen L.
; Speciale, Pietro
; Joh, Danny
; McGavin, Martin J.
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
; AND METHODS OF USE
; NUMBER OF SEQUENCES: 105
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: TX
; COUNTRY: USA
; ZIP: 77210-4433
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentln Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/731,238
; FILING DATE: 10-Dec-2003
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/010,317
; FILING DATE: 21-Jan-1998
; APPLICATION NUMBER: US 60/036,139
; FILING DATE: 21-JAN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Hibler, David W.
; REGISTRATION NUMBER: 41,071
; REFERENCE/DOCKET NUMBER: TAMK:189
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 512-418-3000
; TELEFAX: 512-474-7577
; INFORMATION FOR SEQ ID NO: 35:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 38 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 35:
US-10-731-238-35
Query Match 100.0%; Score 53; DB 18; Length 38;
Best Local Similarity 100.0%; Pred. No. 0.039;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 OGGNIVDIDF 10
Db 21 OGGNIVDIDF 30
RESULT 5
US-10-731-238-36
; Sequence 36, Application US/10731238
; Publication No. US20050123552A1
; GENERAL INFORMATION:
; APPLICANT: Hook, Magnus
; Patti, Joseph M.
; House-Pompeo, Karen L.
; Speciale, Pietro
; Joh, Danny
; McGavin, Martin J.
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
; AND METHODS OF USE

NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/731,238
FILING DATE: 10-Dec-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE: 21-Jan-1998
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAMK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 36:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 36:
US-10-731-238-36
Query Match 100.0%; Score 53; DB 18; Length 38;
Best Local Similarity 100.0%; Pred. No. 0.039;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 OGGNIVDIDF 10
Db 21 OGGNIVDIDF 30
RESULT 6
US-10-731-238-37
; Sequence 37, Application US/10731238
; Publication No. US20050123552A1
; GENERAL INFORMATION:
; APPLICANT: Hook, Magnus
; Patti, Joseph M.
; House-Pompeo, Karen L.
; Speciale, Pietro
; Joh, Danny
; McGavin, Martin J.
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
; AND METHODS OF USE
; NUMBER OF SEQUENCES: 105
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: TX
; COUNTRY: USA
; ZIP: 77210-4433
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentln Release #1.0, Version #1.30


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;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/731,238
; FILING DATE: 10-Dec-2003
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/010,317
; FILING DATE: 21-Jan-1998
; APPLICATION NUMBER: US 60/036,139
; FILING DATE: 21-JAN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Hibler, David W.
; REGISTRATION NUMBER: 41,071
; REFERENCE/DOCKET NUMBER: TAMK:189
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 512-418-3000
; TELEFAX: 512-474-7577
; INFORMATION FOR SEQ ID NO: 37:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 38 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
;
; SEQUENCE DESCRIPTION: SEQ ID NO: 37:
US-10-731-238-37

Query Match      100.0%; Score 53; DB 18; Length 38;
Best Local Similarity 100.0%; Pred. No. 0.039;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 0GGNIVDIDF 10
        |||||
Db      21 0GGNIVDIDF 30

RESULT 7
US-10-731-238-38
; Sequence 38, Application US/10731238
; Publication No. US20050123552A1
; GENERAL INFORMATION:
; APPLICANT: Hook, Magnus
;          Patti, Joseph M.
;          House-Pompeo, Karen L.
;          Speziale, Pietro
;          Joh, Danny
;          McGavin, Martin J.
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
; AND METHODS OF USE
; NUMBER OF SEQUENCES: 105
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: TX
; COUNTRY: USA
; ZIP: 77210-4433
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/731,238
; FILING DATE: 10-Dec-2003
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/010,317
; FILING DATE: 21-Jan-1998
; APPLICATION NUMBER: US 60/036,139
; FILING DATE: 21-JAN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Hibler, David W.
; REGISTRATION NUMBER: 41,071
; REFERENCE/DOCKET NUMBER: TAMK:189
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 512-418-3000
; TELEFAX: 512-474-7577
; INFORMATION FOR SEQ ID NO: 39:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 38 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
;
; SEQUENCE DESCRIPTION: SEQ ID NO: 39:
US-10-731-238-39

Query Match      100.0%; Score 53; DB 18; Length 38;
Best Local Similarity 100.0%; Pred. No. 0.039;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 0GGNIVDIDF 10
        |||||
Db      21 0GGNIVDIDF 30
```

```

;
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 512-418-3000
; TELEFAX: 512-474-7577
; INFORMATION FOR SEQ ID NO: 38:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 38 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
;
; SEQUENCE DESCRIPTION: SEQ ID NO: 38:
US-10-731-238-38

Query Match      100.0%; Score 53; DB 18; Length 38;
Best Local Similarity 100.0%; Pred. No. 0.039;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 0GGNIVDIDF 10
        |||||
Db      21 0GGNIVDIDF 30

RESULT 8
US-10-731-238-39
; Sequence 39, Application US/10731238
; Publication No. US20050123552A1
; GENERAL INFORMATION:
; APPLICANT: Hook, Magnus
;          Patti, Joseph M.
;          House-Pompeo, Karen L.
;          Speziale, Pietro
;          Joh, Danny
;          McGavin, Martin J.
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
; AND METHODS OF USE
; NUMBER OF SEQUENCES: 105
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: TX
; COUNTRY: USA
; ZIP: 77210-4433
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/731,238
; FILING DATE: 10-Dec-2003
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/010,317
; FILING DATE: 21-Jan-1998
; APPLICATION NUMBER: US 60/036,139
; FILING DATE: 21-JAN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Hibler, David W.
; REGISTRATION NUMBER: 41,071
; REFERENCE/DOCKET NUMBER: TAMK:189
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 512-418-3000
; TELEFAX: 512-474-7577
; INFORMATION FOR SEQ ID NO: 39:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 38 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
;
; SEQUENCE DESCRIPTION: SEQ ID NO: 39:
US-10-731-238-39

Query Match      100.0%; Score 53; DB 18; Length 38;
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Best Local Similarity 100.0%; Pred. No. 0.039;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 OGGNVIDIF 10
|||||
Db 21 OGGNVIDIF 30

RESULT 9

US-10-731-238-40
; Sequence 40, Application US/10731238
; Publication No. US20050123552A1
; GENERAL INFORMATION:

APPLICANT: Hook, Magnus
Patti, Joseph M.
House-Pompeo, Karen L.
Speziale, Pietro
John, Danny

TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
AND METHODS OF USE

NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:

ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX

COUNTRY: USA
ZIP: 77210-4433

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/731,238
FILING DATE: 10-Dec-2003
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE: 21-Jan-1998

APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997

ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071

REFERENCE/DOCKET NUMBER: TMMK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577

INFORMATION FOR SEQ ID NO: 40:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear

SEQUENCE DESCRIPTION: SEQ ID NO: 40:
US-10-731-238-40

Query Match 100.0%; Score 53; DB 18; Length 38;
Best Local Similarity 100.0%; Pred. No. 0.039;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 OGGNVIDIF 10
|||||
Db 21 OGGNVIDIF 30

US-10-731-238-41
; Sequence 41, Application US/10731238
; Publication No. US20050123552A1
; GENERAL INFORMATION:

APPLICANT: Hook, Magnus
Patti, Joseph M.
House-Pompeo, Karen L.
Speziale, Pietro
John, Danny

TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
AND METHODS OF USE

NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:

ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston

APPLICANT: Hook, Magnus
Patti, Joseph M.
House-Pompeo, Karen L.
Speziale, Pietro
John, Danny

TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
AND METHODS OF USE

NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:

ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX

COUNTRY: USA
ZIP: 77210-4433

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/731,238
FILING DATE: 10-Dec-2003
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE: 21-Jan-1998

APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997

ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071

REFERENCE/DOCKET NUMBER: TMMK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577

INFORMATION FOR SEQ ID NO: 41:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear

SEQUENCE DESCRIPTION: SEQ ID NO: 41:
US-10-731-238-41

Query Match 100.0%; Score 53; DB 18; Length 38;
Best Local Similarity 100.0%; Pred. No. 0.039;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 OGGNVIDIF 10
|||||
Db 21 OGGNVIDIF 30

US-10-731-238-42
; Sequence 42, Application US/10731238
; Publication No. US20050123552A1
; GENERAL INFORMATION:

APPLICANT: Hook, Magnus
Patti, Joseph M.
House-Pompeo, Karen L.
Speziale, Pietro
John, Danny

TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
AND METHODS OF USE

NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:

ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston

STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/731,238
FILING DATE: 10-Dec-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE: 21-Jan-1998
APPLICATION NUMBER: US 60/036,139
ATTORNEY/AGENT INFORMATION:
NAME: Habler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAMK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 42:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 42:
US-10-731-238-42

Query Match 100.0%; Score 53; DB 18; Length 38;
Best Local Similarity 100.0%; Pred. No. 0.039;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 OGGINVIDIDF 10
DB 21 OGGINVIDIDF 30
RESULT 12
US-10-731-238-56
Sequence 56, Application US/10731238
Publication No. US20050123552A1
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
Patti, Joseph M.
House-Pompeo, Karen L.
Speziale, Pietro
Jon, Danny
McGavin, Martin J.
TITLE OF INVENTION: FIBROCONNECTIN BINDING PROTEIN COMPOSITIONS
AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/731,238
FILING DATE: 10-Dec-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/010,317
FILING DATE: 21-Jan-1998
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-Jan-1997
ATTORNEY/AGENT INFORMATION:
NAME: Habler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAMK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 56:
SEQUENCE CHARACTERISTICS:
LENGTH: 39 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 56:
US-10-731-238-56

Query Match 100.0%; Score 53; DB 18; Length 39;
Best Local Similarity 100.0%; Pred. No. 0.04; Indels 0; Gaps 0;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 OGGINVIDIDF 10
DB 21 OGGINVIDIDF 30
RESULT 13
US-09-813-820-8
Sequence 8, Application US/09813820
Patent No. US20020102262A1
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
Patti, Joseph M.
House-Pompeo, Karen
Schanam, Narayana
Symeraky, Jindrich
TITLE OF INVENTION: COLLAGEN BINDING PROTEIN COMPOSITIONS
AND METHODS OF USE
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: Texas
COUNTRY: U.S.
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/813,820
FILING DATE: 22-Mar-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/856,253
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Kitchell, Barbara S.
REGISTRATION NUMBER: 33,928
REFERENCE/DOCKET NUMBER: TAMK:193
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
TELEFAX: (512) 474-7577
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 139 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>

TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-09-813-820-8

Query Match 100.0%; Score 53; DB 9; Length 139;
Best Local Similarity 100.0%; Pred. No. 0.15;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 OGGNIVDIDF 10
|||||
Db 36 OGGNIVDIDF 45

RESULT 14
US-08-901-062-1
Sequence 1, Application US/08901062
Publication No. US2002002534A1
GENERAL INFORMATION:
APPLICANT: SEALS, JONATHAN R.
TITLE OF INVENTION: RECOMBINANT BIVALENT BACTERIAL VACCINE
TITLE OF INVENTION: FOR THE PREVENTION OF MASTITIS
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: HALE AND DORR LLP
STREET: 60 State Street
CITY: Boston
STATE: MA
COUNTRY: United States Of America
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/901,062
FILING DATE: 25-JUL-1997
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Baker, Hollie L.
REGISTRATION NUMBER: 31,321
REFERENCE/DOCKET NUMBER: 106941.153
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 526-6000
TELEFAX: (617) 526-5000
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 388 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-901-062-1

Query Match 100.0%; Score 53; DB 8; Length 388;
Best Local Similarity 100.0%; Pred. No. 0.46;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 OGGNIVDIDF 10
|||||
Db 285 OGGNIVDIDF 294

RESULT 15
US-08-781-986A-5251
Sequence 5251, Application US/08781986A
Publication No. US20030054436A1
GENERAL INFORMATION:
APPLICANT: Charles Kunsch
TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
NUMBER OF SEQUENCES: 5255

CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COUNTRY: USA
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/781,986A
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Benson, Bob
REGISTRATION NUMBER: 30,446
REFERENCE/DOCKET NUMBER: PB248PP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 5251:
SEQUENCE CHARACTERISTICS:
LENGTH: 559 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-781-986A-5251

Query Match 100.0%; Score 53; DB 8; Length 559;
Best Local Similarity 100.0%; Pred. No. 0.67;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 OGGNIVDIDF 10
|||||
Db 321 OGGNIVDIDF 330

Search completed: October 22, 2005, 12:39:45
Job time : 58.25 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 22, 2005, 06:10:10 ; Search time 11.45 Seconds
(without alignments)
84.032 Million cell updates/sec

Title: US-10-731-238-73

Performance: 53 OGGNIVDIDF 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-Processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79:***
1: pir1:***
2: pir2:***
3: pir3:***
4: pir4:***

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	53	100.0	940	2	S19702	fibronectin-binding
2	53	100.0	961	2	G90053	hypothetical prote
3	53	100.0	1018	2	A32192	fibronectin-binding
4	53	100.0	1038	2	H90053	hypothetical prote
5	39	73.6	158	2	E95396	protein [imported
6	39	73.6	357	2	AG1072	conserved hypotet
7	39	73.6	357	2	S56601	hypothetical 39.8K
8	39	73.6	357	2	B86137	hypothetical prote
9	39	73.6	357	2	G91295	hypothetical prote
10	39	73.6	423	2	AH0053	conserved hypotet
11	37	69.8	222	2	A56276	carbon monoxide ox
12	37	69.8	264	2	B90535	hypothetical prote
13	37	69.8	526	2	A86097	hypothetical prote
14	37	69.8	526	2	E91256	hypothetical prote
15	37	69.8	540	2	A71610	HSP60 fold T-compl
16	36	67.9	109	2	G87206	hypothetical prote
17	36	67.9	311	2	S72967	hypothetical prote
18	36	67.9	470	2	S39733	amino acid permeas
19	36	67.9	474	1	T05239	acid phosphatase (
20	36	67.9	651	2	A96781	unknown protein P9
21	36	67.9	802	2	C90326	hypothetical prote
22	36	67.9	933	2	T43201	MutS protein homol
23	36	67.9	1139	2	T20660	hypothetical prote
24	36	67.9	1835	2	S46082	urea carboxylase (
25	36	67.9	2028	2	T08025	DNA-directed RNA p
26	35	66.0	315	1	S63990	thioredoxin-disulf
27	35	66.0	370	2	AB3175	hypothetical prote
28	35	66.0	612	2	T40481	hypothetical prote
29	35	66.0	809	2	E90016	hyaluronate lyase

30	35	66.0	833	2	A84513	hypothetical prote
31	35	66.0	1067	2	T18196	pol protein - silk
32	34	64.2	155	2	H75075	hypothetical prote
33	34	64.2	169	2	C63394	hypothetical prote
34	34	64.2	262	2	D71685	cyas protein (cyasQ
35	34	64.2	300	2	T00274	outer membrane pro
36	34	64.2	315	2	A36944	outer membrane pro
37	34	64.2	317	2	A31387	omptin (EC 3.4.21.
38	34	64.2	317	2	H85694	outer membrane pro
39	34	64.2	317	2	G90836	outer membrane pro
40	34	64.2	319	2	E82760	conserved hypotet
41	34	64.2	345	2	T41355	Surt homolog - fib
42	34	64.2	346	1	B64176	hypothetical prote
43	34	64.2	354	2	E82850	fimbrin adhesin p
44	34	64.2	357	2	S21209	4-hydroxyphenylpyr
45	34	64.2	367	2	F87293	deoxyhypusine synt

ALIGNMENTS

RESULT 1
S19702
fibronectin-binding protein B - Staphylococcus aureus
C:Species: Staphylococcus aureus
C>Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
C:Accession: S19702
R:Jenssen, K.; Signaes, C.; Mueller, H.P.; Lindberg, M.
Eur. J. Biochem. 202, 1041-1048, 1991
A>Title: Two different genes encode fibronectin binding proteins in Staphylococcus aure
A:Reference number: S19702; PMID:92111475; PMID:1837266
A:Accession: S19702
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-940 <JOB>
A:Cross-references: UNIPROT:Q53682; EMBL:X62992; NID:G49040; PIDN:CAA44726.1; PID:G5815
C:Keywords: fibronectin binding

Query Match 100.0%; Score 53; DB 2; Length 940;
Best Local Similarity 100.0%; Pred. No. 0.082;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 OGGNIVDIDF 10
DB 702 OGGNIVDIDF 711

RESULT 2
G90053
hypothetical protein fnbB [imported] - Staphylococcus aureus (strain N315)
C:Species: Staphylococcus aureus
C>Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
R:Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Ogura, A.; Mizutani, U.; Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kato, C.; Sekimizu, K.; Ma, A.; Shibata, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
A>Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.
A:Reference number: A89758; PMID:21311952; PMID:11418146
A:Accession: G90053
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-961 <KUR>
A:Cross-references: UNIPROT:Q99RD3; GB:BA000018; PID:G13702452; PIDN:BA843593.1; GSPDB:
C:Experimental source: strain N315
C:Genetics:
A:Gene: fnbB

Query Match 100.0%; Score 53; DB 2; Length 961;
Best Local Similarity 100.0%; Pred. No. 0.084;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 OGGNIVDIDF 10

Db 713 OCGNIVDIDF 722

RESULT 3

A32192

fibronectin-binding protein - Staphylococcus aureus

C:Species: Staphylococcus aureus
C>Date: 31-Jul-1989 #sequence_revision 31-Jul-1989 #text_change 16-Feb-1997
C:Accession: A32192
R:Signaee, C.; Rautci, G.; Joenson, K.; Lindgren, P.E.; Anantharamaiah, G.M.; Hoecek, W
Proc. Natl. Acad. Sci. U.S.A. 86, 699-703, 1989
A>Title: Nucleotide sequence of the gene for a fibronectin-binding protein from Staphylo
A:Reference number: A32192; MUID:89098998; PMID:2521391
A:Accession: A32192
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1018 <SIG>
A:Cross-references: GB:J04151
C:Keywords: fibronectin binding

Query Match 100.0%; Score 53; DB 2; Length 1018;
Best Local Similarity 100.0%; Pred. No. 0.09;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 OCGNIVDIDF 10

Db 766 OCGNIVDIDF 775

RESULT 4

H90053

hypothetical protein fmb [imported] - Staphylococcus aureus (strain N315)

C:Species: Staphylococcus aureus
C>Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C:Accession: H90053
R:Kurdo, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguc
ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.;
C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
A>Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.
A:Reference number: A89758; MUID:21311952; PMID:11418146
A:Accession: H90053
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1038 <KUR>
A:Cross-references: UNIPROT:Q99RD2; GB:BA000018; PID:G13702453; PIDN:BA843594.1; GSPDB:G
A:Experimental source: strain N315
C:Genetics:
A:Gene: fmb

Query Match 100.0%; Score 53; DB 2; Length 1038;
Best Local Similarity 100.0%; Pred. No. 0.091;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 OCGNIVDIDF 10

Db 762 OCGNIVDIDF 771

RESULT 5

E95396

protein [imported] - Sinorhizobium meliloti (strain 1021) magaplasmid pSymA

C:Species: Sinorhizobium meliloti
C>Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 16-Aug-2004
C:Accession: E95396
R:Barnett, M.J.; Fisher, R.F.; Jones, T.; Komp, C.; Abola, A.P.; Barloy-Hubler, F.; Bows
.; Kalman, S.; Keating, D.H.; Palm, C.; Peck, M.C.; Surzycki, R.; Wells, D.H.; Yeh, K.C.
Proc. Natl. Acad. Sci. U.S.A. 98, 9883-9888, 2001
A>Title: Nucleotide sequence and predicted functions of the entire Sinorhizobium melilot
A:Reference number: A95262; MUID:21396509; PMID:11481432
A:Accession: E95396
A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-158 <KUR>

A:Cross-references: UNIPROT:Q92Y11; GB:AE006469; PIDN:AAK65735.1; PID:G14524231; GSPDB:G
A:Experimental source: strain 1021, megaplasmid pSymA
R:Galibert, F.; Finan, T.M.; Long, S.R.; Fuhrer, A.; Abola, P.; Ampe, F.; Barloy-Hubler,
pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.;
L.; Hyman, R.W.; Jones, T.
Science 293, 668-672, 2001

A:Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; LeLaure,
heault, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K.
A>Title: The composite genome of the legume symbiont Sinorhizobium meliloti.
A:Reference number: A56039; MUID:21368234; PMID:11474104
A:Contents: annotation
C:Genetics:
A:Gene: Sma1965

A:Genome: plasmid
C:Superfamily: Uncharacterized protein with CYTH and CHAD domains, YgIF type

Query Match 73.6%; Score 39; DB 2; Length 158;
Best Local Similarity 66.7%; Pred. No. 5.5;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 OCGNIVDID 9

Db 66 RGNLVDLD 74

RESULT 6

AG1072

conserved hypothetical protein STY4914 [imported] - Salmonella enterica subsp. enterica

C:Species: Salmonella enterica subsp. enterica serovar Typh
A>Note: this species has also been called Salmonella typhi
C>Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
C:Accession: AG1072
R:Parthill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Main, J.; Churcher,
th, T.; Connerton, P.; Cronin, A.; Davies, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar,
S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001

A:Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.;
A>Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov
A:Reference number: AB0502; MUID:21534947; PMID:11677608
A:Accession: AG1072
A:Status: preliminary
A:Molecule type: DNA

A:Residues: 1-357 <PAR>
A:Cross-references: GB:AU513382; PIDN:CAD03398.1; PID:G16505667; GSPDB:GN00176
C:Genetics:
A:Gene: STY4914

Query Match 73.6%; Score 39; DB 2; Length 357;
Best Local Similarity 50.0%; Pred. No. 13;
Matches 5; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 1 OCGNIVDIDF 10

Db 99 RGNLVDLDW 108

RESULT 7

S56601

hypothetical 39.8K protein (osmX-deoc intergenic region) - Escherichia coli (strain K-12

N:Alternate names: hypothetical protein o357
C:Species: Escherichia coli
C>Date: 28-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 09-Jul-2004
C:Accession: S56601; H65252
R:Burland, V.; Plunkett III, G.; Sofia, H.J.; Daniels, D.L.; Blattner, F.R.
Nucleic Acids Res. 23, 2105-2119, 1995
A>Title: Analysis of the Escherichia coli genome VI: DNA sequence of the region from 92.
A:Reference number: S56314; MUID:95334362; PMID:7610040
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA

A:Residues: 1-357 <BUR>

A:Cross-references: UNIPROT:P39407; EMBL:U14003; NID:G1263172; PIDD:AAA97273.1; PID:9537
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, August 1994
R:Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Co
A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A:Title: The complete genome sequence of *Escherichia coli* K-12.
A:Reference number: A64720; MUID:97426617; PMID:9278503
A:Accession: H65252
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-357 <BLAT>
A:Cross-references: GB:AE000508; GB:U00096; NID:G2367382; PIDD:AACT7330.1; PID:G1790837;
A:Experimental source: strain K-12, substrain MG1655
C:Genetics:
A:Gene: yjju
A:start codon: GTG

Query Match 73.6%; Score 39; DB 2; Length 357;
Best Local Similarity 50.0%; Pred. No. 13;
Matches 5; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 1 OGGNVDIDF 10
:||||:|:
Db 99 RCGNLIDLDW 108

RESULT 8
B66137
hypothetical protein yjju [imported] - *Escherichia coli* (strain O157:H7, substrain EDL93
C:Species: *Escherichia coli*
C>Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
C:Accession: B66137
R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew
Miller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca,
Nature 409, 529-533, 2001
A:Title: Genome sequence of enterohemorrhagic *Escherichia coli* O157:H7.
A:Reference number: A85480; MUID:21074935; PMID:11206551
A:Accession: B66137
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-357 <STO>
A:Cross-references: UNIPROT:Q8XB45; GB:AE005174; NID:G12519404; PIDD:AA659558.1; GSPDB:C
A:Experimental source: strain O157:H7, substrain EDL933
C:Genetics:
A:Gene: yjju

Query Match 73.6%; Score 39; DB 2; Length 357;
Best Local Similarity 50.0%; Pred. No. 13;
Matches 5; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 1 OGGNVDIDF 10
:||||:|:
Db 99 RCGNLIDLDW 108

RESULT 9
G91295
hypothetical protein ECs5335 [imported] - *Escherichia coli* (strain O157:H7, substrain R1
C:Species: *Escherichia coli*
C>Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 09-Jul-2004
C:Accession: G91295
R:Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.;
gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001
A:Title: Complete genome sequence of enterohemorrhagic *Escherichia coli* O157:H7 and genc
A:Reference number: A9629; MUID:21156231; PMID:11258796
A:Accession: G91295
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-357 <HAY>
A:Cross-references: UNIPROT:Q8XB45; GB:BA000007; PIDD:BA838758.1; PID:G13364813; GSPDB:C
A:Experimental source: strain O157:H7, substrain R1MD 0509552
C:Genetics:

A:Gene: ECs5335

Query Match 73.6%; Score 39; DB 2; Length 357;
Best Local Similarity 50.0%; Pred. No. 13;
Matches 5; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 1 OGGNVDIDF 10
:||||:|:
Db 99 RCGNLIDLDW 108

RESULT 10
AH0053
conserved hypothetical protein YP00433 [imported] - *Yersinia pestis* (strain CO92)
C:Species: *Yersinia pestis*
C>Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Jul-2004
C:Accession: AH0053
R:Parkhill, J.; Wren, B.W.; Thomson, N.R.; Tibball, R.W.; Holden, M.T.G.; Prentice, M.B
deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.;
il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrall,
Nature 413, 523-527, 2001
A:Title: Genome sequence of *Yersinia pestis*, the causative agent of plague.
A:Reference number: AB0001; MUID:21470413; PMID:11586360
A:Accession: AH0053
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-423 <KUR>
A:Cross-references: UNIPROT:Q8Z107; GB:AL590842; PIDD:CA089291.1; PID:G15978529; GSPDB:C
C:Genetics:
A:Gene: YP00433

Query Match 73.6%; Score 39; DB 2; Length 423;
Best Local Similarity 50.0%; Pred. No. 16;
Matches 5; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 1 OGGNVDIDF 10
:||||:|:
Db 100 RCGNLIDLDW 109

RESULT 11
A56276
Carbon monoxide oxidation system transcription regulator CooA [similarity] - *Rhodospirillum*
C:Species: *Rhodospirillum rubrum*
C>Date: 03-Oct-1995 #sequence_revision 03-Oct-1995 #text_change 09-Jul-2004
C:Accession: A56276; T51325
R:Shelver, D.; Kerby, R.L.; He, Y.; Roberts, G.P.
J. Bacteriol. 177, 2157-2163, 1995
A:Title: Carbon monoxide-induced activation of gene expression in *Rhodospirillum rubrum*
A:Reference number: A56276; MUID:95238289; PMID:7721706
A:Accession: A56276
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-222 <SHL>
A:Cross-references: UNIPROT:P72322; GB:U65510; GB:U20508; NID:G1515463; PIDD:AA045127.1
A:Experimental source: strain URI
C:Genetics:
A:Gene: cooA
C:Superfamily: regulatory protein fur; cAMP receptor protein cyclic nucleotide-binding

Query Match 69.8%; Score 37; DB 2; Length 222;
Best Local Similarity 70.0%; Pred. No. 19;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 OGGNVDIDF 10
:||||:|:
Db 155 OGGVIVSDP 164

RESULT 12
B90535
hypothetical protein MYPU_1860 [imported] - *Mycoplasma pulmonis* (strain UAB CTIP)

C.Species: Mycoplasma pulmonis
C.Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 16-Aug-2004
C.Accession: B90535
R.Chenabaud, I.; Heilig, R.; Ferris, S.; Barbe, V.; Samson, D.; Galisson, F.; Moszer, I.;
Nucleic Acids Res. 29, 2145-2153, 2001
A.Title: The complete genome sequence of the murine respiratory pathogen Mycoplasma pulm
A.Reference number: A99512; MUID:21267165; PMID:11353084
A.Accession: B90535
A.Status: preliminary
A.Molecule type: DNA
A.Residues: 1-264 <KUR>
A.Cross-references: UNIPROT:Q9BR24; GB:AL445566; PID:G14089599; PIDN:CAC13359.1; GSPDB:G
A.Experimental source: strain UAB CTIP
C.Genetics:
A.Gene: MPPU_1860
A.Genetic code: SGC3
C.Superfamily: Modification methylase (cytosine-specific)

Query Match 69.8%; Score 37; DB 2; Length 264;
Best Local Similarity 77.8%; Pred. No. 23;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 QGNIVDID 9
DB 96 QGNIVDID 104

RESULT 13
A86097
hypothetical protein yjbi [imported] - Escherichia coli (strain O157:H7, substrain EDL93
C.Species: Escherichia coli
C.Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
C.Accession: A86097
R.Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew
iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; DiMantata, E.; Potamoudis, K.; Apodaca,
Nature 409, 529-533, 2001
A.Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A.Reference number: A85480; MUID:21074935; PMID:11206551
A.Accession: A86097
A.Status: preliminary
A.Molecule type: DNA
A.Residues: 1-526 <STO>
A.Cross-references: UNIPROT:Q8X5W5; GB:AE005174; NID:G12518987; PIDN:AAG59237.1; GSPDB:G
C.Genetics:
A.Gene: yjbi
C.Superfamily: Escherichia coli chorismate lyase ubic

Query Match 69.8%; Score 37; DB 2; Length 526;
Best Local Similarity 77.8%; Pred. No. 48;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 QGNIVDID 9
DB 21 QGNIVDID 29

RESULT 14
E91256
hypothetical protein ECs5021 [imported] - Escherichia coli (strain O157:H7, substrain R
C.Species: Escherichia coli
C.Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 09-Jul-2004
C.Accession: E91256
R.Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.
gasawara, N.; Yasunaga, T.; Kohara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001
A.Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and genc
A.Reference number: A99629; MUID:21156231; PMID:11258796
A.Accession: E91256
A.Status: preliminary
A.Molecule type: DNA
A.Residues: 1-526 <HAV>
A.Cross-references: UNIPROT:Q8X5W5; GB:BA000007; PIDN:BA8444.1; PID:G13364498; GSPDB:G

A.Experimental source: strain O157:H7, substrain RIMD 0509952
C.Genetics:
A.Gene: ECs5021
C.Superfamily: Escherichia coli chorismate lyase ubic

Query Match 69.8%; Score 37; DB 2; Length 526;
Best Local Similarity 77.8%; Pred. No. 48;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 QGNIVDID 9
DB 21 QGNIVDID 29

RESULT 15
A71610
Hsp60 fold T-complex protein 1 PFB0635w - malaria parasite (Plasmodium falciparum)
C.Species: Plasmodium falciparum
C.Date: 13-Nov-1998 #sequence_revision 13-Nov-1998 #text_change 09-Jul-2004
C.Accession: A71610
R.Gardner, M.J.; Tetteilin, H.; Carucci, D.J.; Cummings, L.M.; Aravind, L.; Koonin, E.V.;
.; Pettes, M.; Salzberg, S.; Zhou, L.; Sutton, G.G.; Clayton, R.; White, O.; Smith, H.O.
Science 282, 1126-1132, 1998
A.Title: Chromosome 2 sequence of the human malaria parasite Plasmodium falciparum.
A.Reference number: A71600; MUID:99021743; PMID:9804551
A.Accession: A71610
A.Status: preliminary; nucleic acid sequence not shown; translation not shown
A.Molecule type: DNA
A.Residues: 1-540 <GAR>
A.Cross-references: UNIPROT:O96220; GB:AE001407; GB:AE001362; NID:G3845234; PIDN:AACT191
A.Experimental source: clone 3D7
C.Genetics:
A.Gene: PFB0635w
C.Superfamily: molecular chaperone t-complex-type

Query Match 69.8%; Score 37; DB 2; Length 540;
Best Local Similarity 66.7%; Pred. No. 49;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 GGNIVDID 10
DB 206 GGNIVDID 214

Search completed: October 22, 2005, 08:04:28
Job time : 12.45 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 22, 2005, 06:06:36 ; Search time 55.85 Seconds
(without alignments)
91.688 Million cell updates/sec

Title: US-10-731-238-73
Perfect score: 53
Sequence: 1 OGGNIVDIDF 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues
Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : uniprot_03: *
1: uniprot_sprot: *
2: uniprot_trembl: *

Prod. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	53	100.0	152	2	Q9AEP9
2	53	100.0	940	2	Q53682
3	53	100.0	943	2	Q8NUH8
4	53	100.0	957	2	Q6G6H4
5	53	100.0	961	2	Q99RD3
6	53	100.0	961	2	Q7A3J8
7	53	100.0	1015	2	Q8NUV7
8	53	100.0	1015	2	Q6G6H3
9	53	100.0	1018	1	FNBA_STNAU
10	53	100.0	1038	2	Q99RD2
11	53	100.0	1038	2	Q7A3J7
12	52	98.1	965	2	Q6GDU5
13	40	75.5	540	2	Q975V2
14	40	75.5	711	2	Q830D1
15	40	75.5	742	2	Q7QYB1
16	39	73.6	158	2	Q92Y11
17	39	73.6	357	1	YJUT_ECOLI
18	39	73.6	357	2	Q8Z0U7
19	39	73.6	357	2	Q8Z0U2
20	39	73.6	357	2	Q7UJAO
21	39	73.6	357	2	Q8XB45
22	39	73.6	359	2	Q83IH2
23	39	73.6	369	2	Q8FA57
24	39	73.6	423	2	Q66EW3
25	39	73.6	423	2	Q8Z1Q7
26	38	71.7	1132	2	Q61EP0
27	38	71.7	2009	2	Q7QAB8
28	37	69.8	222	2	P723J2
29	37	69.8	264	2	Q98R24
30	37	69.8	524	2	Q96220
31	37	69.8	526	2	Q8X5W5

32	37	69.8	591	2	Q8KRV4	Q8KRV4 clostridium
33	37	69.8	738	2	Q6NAX1	Q6NAX1 rhodospseudo
34	37	69.8	783	1	TRR2_THEVO	Q97B03 thermoplasma
35	37	69.8	874	2	Q861Z1	Q861Z1 dictyosteli
36	37	67.9	109	2	Q9CB69	Q9CB69 mycobacteri
37	36	67.9	154	2	Q611B6	Q611B6 picrophilus
38	36	67.9	232	2	Q68YA7	Q68YA7 rhodococcus
39	36	67.9	239	1	ECR1_METKA	Q8CYC0 methanopyru
40	36	67.9	244	2	Q81GM1	Q81GM1 hordeum vul
41	36	67.9	253	2	Q6N965	Q6N965 rhodospendo
42	36	67.9	294	2	Q7XET0	Q7XET0 oryza sativ
43	36	67.9	296	2	Q6FQJ3	Q6FQJ3 candida gla
44	36	67.9	311	1	PPNR_MYCLE	Q49897 mycobacteri
45	36	67.9	342	2	Q6CFG1	Q6CFG1 yarrowia 11

ALIGNMENTS

RESULT 1					
ID	Q9AEP9	PRELIMINARY;	PRT;	152 AA.	
AC	Q9AEP9;				
DT	01-JUN-2001 (TREMBLrel. 17, Created)				
DT	01-JUN-2001 (TREMBLrel. 17, Last sequence update)				
DT	01-DEC-2001 (TREMBLrel. 19, Last annotation update)				
DE	Fibronectin-binding protein (Fragment).				
GN	Name=fnb;				
OS	Staphylococcus aureus.				
OC	Bacteria; Firmicutes; Bacillales; Staphylococcus.				
OX	NCBI_TaxID=1280;				
RN	(1)				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=CMRSA-1;				
RX	MEDLINE=21246681; PubMed=11349044;				
RX	DOI=10.1128/IAI.69.6.3791-3799.2001;				
RA	Rice K., Huesca M., Vaz D., McGavin M.J.;				
RT	"Variance in fibronectin binding and fnb locus polymorphisms in				
RT	Staphylococcus aureus: identification of antigenic variation in a				
RT	fibronectin binding protein adhesin of the epidemic CMRSA-1 strain of				
RT	methicillin-resistant S. aureus.";				
RL	Infect. Immun. 69:3791-3799(2001).				
DR	EMBL: AY029184; MAK31588.1; -.				
FT	NON_TER				
FT	NON_TER				
FT	SEQUENCE	152 AA;	17193 MW;	CFA3913CB11C025 CRC64;	
Query Match					
Best Local Similarity 100.0%; Score 53; DB 2; Length 152;					
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;					
Qy	1 OGGNIVDIDF 10				
Db	21 OGGNIVDIDF 30				
RESULT 2					
ID	Q53682	PRELIMINARY;	PRT;	940 AA.	
AC	Q53682;				
DT	01-NOV-1996 (TREMBLrel. 01, Created)				
DT	01-NOV-1996 (TREMBLrel. 01, Last sequence update)				
DT	01-MAR-2004 (TREMBLrel. 26, Last annotation update)				
DE	Fibronectin binding protein B.				
GN	Name=fnbB;				
OS	Staphylococcus aureus.				
OC	Bacteria; Firmicutes; Bacillales; Staphylococcus.				
OX	NCBI_TaxID=1280;				
RN	(1)				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=8325-4;				
RX	MEDLINE=92111475; PubMed=1837266;				
RA	Jonsson K., Sigmas C., Muller H.P., Lindberg M.;				

```
RT "Two different genes encode fibronectin binding proteins in
RT Staphylococcus aureus. The complete nucleotide sequence and
RT characterization of the second gene."
RL Eur. J. Biochem. 202;1041-1048 (1991).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC an amide bond (By similarity).
DR EMBL: X62992; CAA44726.1; -.
DR PIR: S19702; S19702.
DR HSRF: Q53653; IN67.
DR GO: GO:0009986; C:cell surface; IEA.
DR GO: GO:0005618; C:cell wall; IEA.
DR GO: GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO: GO:0016020; C:membrane; IEA.
DR GO: GO:007155; P:cell adhesion; IEA.
DR InterPro: IPR008966; Adhes_bact.
DR InterPro: IPR004237; Fn_bind.
DR InterPro: IPR005877; Gpos_YsIRK.
DR Pfam: PF02986; Fn_bind_2.
DR Pfam: PF00746; Gram_pos_anchor_1.
DR Pfam: PF04650; YsIRK_signal; 1.
DR TIGRFAMs: TIGR01167; LpXTG_anchor; 1.
DR TIGRFAMs: TIGR01168; YsIRK_signal; 1.
DR PROSITE: PS50847; GRAM_POS_ANCHORING; 1.
KW Cell wall; Peptidoglycan-anchor.
SQ SEQUENCE 940 AA; 103555 MW; E35FBBCA907AE345 CRC64;

Query Match 100.0%; Score 53; DB 2; Length 940;
Best Local Similarity 100.0%; Pred. No. 0.65;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QCGNIVDIDF 10
DB 702 QCGNIVDIDF 711

RESULT 3
Q8NU08 PRELIMINARY; PRT; 943 AA.
AC Q8NU08;
DT 01-OCT-2002 (TReMBLrel. 22, Created)
DT 01-OCT-2002 (TReMBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE Pnub protein.
GN Name=fnub; OrderedLocustNames=MM2420;
OS Staphylococcus aureus (strain MM2).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxId=196620;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MM2;
RX MEDLINE=2040717; PubMed=12044378; DOI=10.1016/S0140-6736(02)08713-5;
RA Baba T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Oguchi A.,
RA Nagai Y., Iwano N., Amano K., Naito T., Kuroda H., Cui L.,
RA Yamamoto K., Hiramoto K.;
RA "Genome and virulence determinants of high virulence community-
RT acquired MRSA."
RT Lancet 359;1819-1827(2002).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC an amide bond (By similarity).
DR EMBL: AP004830; BAB95285.1; -.
DR HSSP: Q53653; IN67.
DR GO: GO:0009986; C:cell surface; IEA.
DR GO: GO:0005618; C:cell wall; IEA.
DR GO: GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO: GO:0016020; C:membrane; IEA.
DR GO: GO:007155; P:cell adhesion; IEA.
DR InterPro: IPR008966; Adhes_bact.
DR InterPro: IPR004237; Fn_bind.
DR InterPro: IPR005877; Gpos_YsIRK.
DR Pfam: PF02986; Fn_bind_1.
DR Pfam: PF00746; Gram_pos_anchor; 1.
DR TIGRFAMs: TIGR01167; LpXTG_anchor; 1.
DR TIGRFAMs: TIGR01168; YsIRK_signal; 1.
DR PROSITE: PS50847; GRAM_POS_ANCHORING; 1.
KW Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ SEQUENCE 957 AA; 105980 MW; 28F8BA7FDFD3EAF CRC64;
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DR Pfam: PF04650; YsIRK_signal; 1.
DR TIGRFAMs: TIGR01167; LpXTG_anchor; 1.
DR TIGRFAMs: TIGR01168; YsIRK_signal; 1.
DR PROSITE: PS50847; GRAM_POS_ANCHORING; 1.
KW Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ SEQUENCE 943 AA; 104537 MW; DA8A5FF3194E1B6A CRC64;

Query Match 100.0%; Score 53; DB 2; Length 943;
Best Local Similarity 100.0%; Pred. No. 0.65;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 QCGNIVDIDF 10
DB 709 QCGNIVDIDF 718
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RESULT 4
O6G6H4 PRELIMINARY; PRT; 957 AA.
ID O6G6H4;
AC O6G6H4;
DT 05-JUL-2004 (TReMBLrel. 27, Created)
DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TReMBLrel. 27, Last annotation update)
DE Fibronectin-binding protein.
GN Name=fnub; OrderedLocustNames=SAS2387;
OS Staphylococcus aureus (strain MSSA476).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxId=282459;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=15213324; DOI=10.1073/pnas.0402521101;
RA Holden M.T.G., Fell B.J., Linday J.A., Peacock S.J., Day N.P.J.,
RA Enright M.C., Foster T.J., Moore C.E., Hurst L., Atkin R., Barron A.,
RA Baeson N., Bentley S.D., Chillingworth C., Chillingworth T.,
RA Churcher C., Clark L., Cotton C., Cronin A., Doggett J., Dowd L.,
RA Felwell T., Hance Z., Harris B., Hauser H., Holroyd S., Jagsels K.,
RA James K.D., Leonard N., Line A., Mayes R., Moule S., Mungall K.,
RA Ormond D., Quail M.A., Rabinowitch E., Rutherford K.M., Sanders M.,
RA Sharp S., Simmonds M., Stevens K., Whitehead S., Barrett B.G.,
RA Spratt B.G., Parkhill J.;
RT "Complete genomes of two clinical Staphylococcus aureus strains:
RT evidence for the rapid evolution of virulence and drug resistance."
RT Proc. Natl. Acad. Sci. U.S.A. 101:9786-9791(2004).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC an amide bond (By similarity).
DR EMBL: BX571857; CAG44201.1; -.
DR GO: GO:0009986; C:cell surface; IEA.
DR GO: GO:0005618; C:cell wall; IEA.
DR GO: GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO: GO:0016020; C:membrane; IEA.
DR GO: GO:007155; P:cell adhesion; IEA.
DR InterPro: IPR008966; Adhes_bact.
DR InterPro: IPR004237; Fn_bind.
DR InterPro: IPR005877; Gpos_YsIRK.
DR InterPro: IPR01899; Gram_pos_anchor.
DR Pfam: PF02986; Fn_bind_1.
DR Pfam: PF00746; Gram_pos_anchor; 1.
DR Pfam: PF04650; YsIRK_signal; 1.
DR TIGRFAMs: TIGR01167; LpXTG_anchor; 1.
DR TIGRFAMs: TIGR01168; YsIRK_signal; 1.
DR PROSITE: PS50847; GRAM_POS_ANCHORING; 1.
KW Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ SEQUENCE 957 AA; 105980 MW; 28F8BA7FDFD3EAF CRC64;
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Query Match 100.0%; Score 53; DB 2; Length 957;
Best Local Similarity 100.0%; Pred. No. 0.66;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QCGNIVDIDF 10
DB 709 QCGNIVDIDF 718
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RESULT 5
099RD3 PRELIMINARY; PRT; 961 AA.
ID 099RD3;
AC 099RD3;
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DE 01-JUN-2001 (TREMBLrel. 24, Last annotation update)
DE Fibronectin-binding protein homolog.
GN Name=fnbB; OrderedLocuNames=SAV2502;
OS Staphylococcus aureus (strain M50 / ATCC 700699).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=158678;
RN 11
RP SEQUENCE FROM N.A.
RC MEDLINE=M50 / ATCC 700699;
RX MEDLINE=21311952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2;
RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Iino J.-O., Ito T.,
RA Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,
RA Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
RA Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
RA Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
RA Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
RT "Whole genome sequencing of methicillin-resistant Staphylococcus
RT aureus."
RL Lancet 357:1225-1240(2001).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC an amide bond (By similarity).
DR EMBL: AP003365; BAB58664.1; -.
DR PIR: G90053; G90053.
DR HSSP: Q53653; 1N67.
DR GO: GO:0009986; C:cell surface; IEA.
DR GO: GO:0005618; C:cell wall; IEA.
DR GO: GO:0009725; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO: GO:0016020; C:membrane; IEA.
DR GO: GO:0007155; P:cell adhesion; IEA.
DR InterPro: IPR008966; Adhes_bact.
DR InterPro: IPR004237; Fn_bind.
DR InterPro: IPR005877; Gpos_YsIRK.
DR InterPro: IPR001899; Gram_pos_anchor.
DR Pfam: PF02986; Fn_bind_1.
DR Pfam: PF00746; Gram_pos_anchor_1.
DR Pfam: PF04650; YsIRK_signal_1.
DR TIGRfams: TIGR01167; LPTXG_anchor_1.
DR TIGRfams: TIGR01168; YsIRK_signal_1.
DR PROSITE: PS50847; GRAM_POS_ANCHORING; 1.
KW Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ SEQUENCE 961 AA; 106010 MW; 364940F884EA4101 CRC64;

Query Match 100.0%; Score 53; DB 2; Length 961;
Best Local Similarity 100.0%; Pred. No. 0.66;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 OGGNVIDIF 10
Db 713 OGGNVIDIF 722

RESULT 6
07A3J8 PRELIMINARY; PRT; 961 AA.
ID 07A3J8;
AC 07A3J8;
DT 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DE 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE Fnb protein.
GN Name=fnbB; OrderedLocuNames=SA2290;
OS Staphylococcus aureus (strain N315).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=158679;
RN 11
RP SEQUENCE FROM N.A.
RC MEDLINE=21311952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2;

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RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Iino J.-O., Ito T.,
RA Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,
RA Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
RA Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
RA Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
RA Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
RT "Whole genome sequencing of methicillin-resistant Staphylococcus
RT aureus."
RL Lancet 357:1225-1240(2001).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC an amide bond (By similarity).
DR EMBL: AP003373; BAB45993.1; -.
DR GO: GO:0009986; C:cell surface; IEA.
DR GO: GO:0005618; C:cell wall; IEA.
DR GO: GO:0009725; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO: GO:0016020; C:membrane; IEA.
DR GO: GO:0007155; P:cell adhesion; IEA.
DR InterPro: IPR008966; Adhes_bact.
DR InterPro: IPR004237; Fn_bind.
DR InterPro: IPR005877; Gpos_YsIRK.
DR InterPro: IPR001899; Gram_pos_anchor.
DR Pfam: PF02986; Fn_bind_1.
DR Pfam: PF00746; Gram_pos_anchor_1.
DR Pfam: PF04650; YsIRK_signal_1.
DR TIGRfams: TIGR01167; LPTXG_anchor_1.
DR TIGRfams: TIGR01168; YsIRK_signal_1.
DR PROSITE: PS50847; GRAM_POS_ANCHORING; 1.
KW Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ SEQUENCE 961 AA; 106010 MW; 364940F884EA4101 CRC64;

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Query Match 100.0%; Score 53; DB 2; Length 961;
Best Local Similarity 100.0%; Pred. No. 0.66;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 OGGNVIDIF 10
Db 713 OGGNVIDIF 722

RESULT 7
08NU7 PRELIMINARY; PRT; 1015 AA.
ID 08NU7;
AC 08NU7;
DT 01-OCT-2002 (TREMBLrel. 22, Created)
DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update)
DE 01-OCT-2002 (TREMBLrel. 25, Last annotation update)
DE Fnb protein.
GN Name=fnb; OrderedLocuNames=MW2421;
OS Staphylococcus aureus (strain MW2).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=196620;
RN 11
RP SEQUENCE FROM N.A.
RC STRAIN=MW2;
RX MEDLINE=22040717; PubMed=12044378; DOI=10.1016/S0140-6736(02)08713-5;
RA Baba T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Oguchi A.,
RA Nagai Y., Iwama N., Amano K., Naimi T., Kuroda H., Cui L.,
RA Yamamoto K., Hiramatsu K.;
RT "Genome and virulence determinants of high virulence community-
RT acquired MRSA."
RL Lancet 359:1819-1827(2002).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC an amide bond (By similarity).
DR EMBL: AP004830; BAB96286.1; -.
DR GO: GO:0009986; C:cell surface; IEA.
DR GO: GO:0005618; C:cell wall; IEA.
DR GO: GO:0009725; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO: GO:0016020; C:membrane; IEA.
DR GO: GO:0007155; P:cell adhesion; IEA.
DR InterPro: IPR008966; Adhes_bact.
DR InterPro: IPR004237; Fn_bind.
DR InterPro: IPR005877; Gpos_YsIRK.

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DR InterPro: IPR001899; Gram_pos_anchor.
 DR Pfam: PF02986; Fm_bind; 1.
 DR Pfam: PF00746; Gram_pos_anchor; 1.
 DR Pfam: PF04650; YSIRK_signal; 1.
 DR TIGRPFAM: TIGR01167; LPTXG_anchor; 1.
 DR TIGRPFAM: TIGR01167; YSIRK_signal; 1.
 DR TIGRPFAM: TIGR01168; YSIRK_signal; 1.
 DR PROSITE: PS50847; GRAM_POS_ANCHORING; 1.
 DR Cell wall; Complete proteome; Peptidoglycan-anchor.
 DR SEQUENCE 1015 AA; 111145 MW; D0F9281BB64D44D2 CRC64;
 SO

Query Match 100.0%; Score 53; DB 2; Length 1015;
 Best Local Similarity 100.0%; Pred. No. 0.7;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 OGGINVIDIDF 10
 |||||
 DB 767 OGGINVIDIDF 776

RESULT 8
 OG6G6H3 PRELIMINARY; PRT; 1015 AA.
 ID OG6G6H3
 AC OG6G6H3
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Fibronectin-binding protein.
 GN OrderedLocustNames=SAS2388;
 OS Staphylococcus aureus (Strain MSSA476).
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 OX NCBI_TaxID=282459;
 OX [1]
 RN

RP SEQUENCE FROM N.A.
 RA PubMed=15213324; DOI=10.1073/pnas.0402521101;
 RA Holden M.T.G., Fell E.J., Lindsey J.A., Peacock S.J., Day N.P.J.,
 RA Enright M.C., Foster T.J., Moore C.E., Hurst L., Atkin R., Barron A.,
 RA Baeson N., Bentley S.D., Chillingworth C., Chillingworth T.,
 RA Churcher C., Clark L., Corton C., Cronin A., Doggett J., Dowd L.,
 RA Felwell T., Hance Z., Harris B., Hauser H., Holtroyd S., Jagels K.,
 RA James K.D., Lennard N., Line A., Mayes R., Moule S., Mungall K.,
 RA Ormond D., Quail M.A., Rabinowitch E., Rutherford K.M., Sanders M.,
 RA Sharp S., Simmonds M., Stevens K., Whitehead S., Barrett B.G.,
 RA Spratt B.G., Parkhill J.;
 RT "Complete genomes of two clinical Staphylococcus aureus strains:
 evidence for the rapid evolution of virulence and drug resistance.";
 RL Proc. Natl. Acad. Sci. U.S.A. 101:9786-9791(2004).
 CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
 CC an amide bond (By similarity).
 CC EMBL: BX571857; CAG44202.1; -;
 CC DR GO: GO:0009986; C:cell surface; IEA.
 CC DR GO: GO:0005618; C:cell wall; IEA.
 CC DR GO: GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
 CC DR GO: GO:0016020; C:membrane; IEA.
 CC DR GO: GO:0007155; P:cell adhesion; IEA.
 CC DR InterPro: IPR008966; Adhes_bact.
 CC DR InterPro: IPR004237; Fm_bind.
 CC DR InterPro: IPR005877; Gpos_YSIRK.
 CC DR InterPro: IPR001899; Gram_pos_anchor.
 CC DR Pfam: PF02986; Fm_bind; 1.
 CC DR Pfam: PF00746; Gram_pos_anchor; 1.
 CC DR Pfam: PF04650; YSIRK_signal; 1.
 CC DR TIGRPFAM: TIGR01167; LPTXG_anchor; 1.
 CC DR TIGRPFAM: TIGR01167; YSIRK_signal; 1.
 CC DR PROSITE: PS50847; GRAM_POS_ANCHORING; 1.
 CC DR Cell wall; Complete proteome; Peptidoglycan-anchor.
 CC SEQUENCE 1015 AA; 111145 MW; D0F9281BB64D44D2 CRC64;
 SO

Query Match 100.0%; Score 53; DB 2; Length 1015;
 Best Local Similarity 100.0%; Pred. No. 0.7;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 OGGINVIDIDF 10
 |||||
 DB 767 OGGINVIDIDF 776

DB 767 OGGINVIDIDF 776

RESULT 9
 FNA_STAAU STANDARD; PRT; 1018 AA.
 ID FNA_STAAU
 AC 014738;
 DT 01-APR-1990 (Rel. 14, Created)
 DT 01-APR-1990 (Rel. 14, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Fibronectin-binding protein precursor (FNBP).
 GN Name=FNA;
 OS Staphylococcus aureus.
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 OX NCBI_TaxID=1280;
 OX [1]
 RN

RP SEQUENCE FROM N.A.
 RA STRAIN=NCTC 8325-4;
 RA MEDLINE=89098998; PubMed=2521391;
 RA Signaes C., Raucel G., Joensson K., Lindgren P.-E.,
 RA Anantharamiah G.M., Hoesek M., Lindberg M.;
 RT "Nucleotide sequence of the gene for a fibronectin-binding protein
 from Staphylococcus aureus: use of this peptide sequence in the
 synthesis of biologically active peptides.";
 RL Proc. Natl. Acad. Sci. U.S.A. 86:699-703(1989).
 CC -1- FUNCTION: The ability of bacteria to bind fibronectin has been
 CC proposed as a virulence factor enabling bacteria to colonize wound
 CC tissues and blood clots. Binding of plasma fibronectin to the
 CC bacterial surface might block adhesion receptors on S.aureus, thus
 CC representing an important defense mechanism against tissue
 CC invasion.
 CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
 CC an amide bond (potential).
 CC

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 CC or send an email to license@ebi.ac.uk).
 CC -----
 CC DR EMBL: J04151; AAA26632.1; -;
 CC DR InterPro: IPR004237; Fm_bind.
 CC DR InterPro: IPR005877; Gpos_YSIRK.
 CC DR InterPro: IPR001899; Gram_pos_anchor.
 CC DR Pfam: PF02986; Fm_bind; 1.
 CC DR Pfam: PF00746; Gram_pos_anchor; 1.
 CC DR Pfam: PF04650; YSIRK_signal; 1.
 CC DR TIGRPFAM: TIGR01167; LPTXG_anchor; 1.
 CC DR TIGRPFAM: TIGR01168; YSIRK_signal; 1.
 CC DR PROSITE: PS50847; GRAM_POS_ANCHORING; 1.
 CC DR Cell adhesion; Cell wall; Peptidoglycan-anchor; Repeat; Signal;
 CC KW
 CC FT SIGNAL 1 36
 CC FT CHAIN 37 985
 CC FT PROPEP 986 1018
 CC FT REPEAT 545 574
 CC FT REPEAT 575 604
 CC FT DOMAIN 745 878
 CC FT REPEAT 745 782
 CC FT REPEAT 783 820
 CC FT REPEAT 821 859
 CC FT REPEAT 860 878
 CC FT DOMAIN 879 948
 CC FT REPEAT 879 892
 CC FT REPEAT 893 906
 CC FT REPEAT 907 920
 CC FT REPEAT 921 934
 CC FT REPEAT 935 948
 CC FT SITE 982 986
 CC FT MOD_RES 985 985

Fibronectin-binding protein.
 Removed by sortase (potential).
 B-1.
 B-2.
 4 X approximate tandem repeats,
 fibronectin-binding domain.
 D-1.
 D-2.
 D-3.
 D-4 (incomplete).
 5 X tandem repeats, Pro-rich (WR).
 WR 1.
 WR 2.
 WR 3.
 WR 4.
 WR 5.
 LPTXG sorting signal (potential).
 Pentaglycyl muurin peptidoglycan amidated

FT SEQUENCE 1018 AA; 111780 MW; 58175E020E81F1F CRC64;
 SQ
 Query Match 100.0%; Score 53; DB 1; Length 1018;
 Best Local Similarity 100.0%; Pred. No. 0.7;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QCGNIVDIDF 10
 DB 766 QCGNIVDIDF 775

RESULT 10
 Q99RD2 PRELIMINARY; PRT; 1038 AA.
 ID 099RD2
 AC 099RD2
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)
 DT 01-JUN-2001 (TrEMBLrel. 26, Last sequence update)
 DE 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 GN Name=fnd; OrderedlocusNames=SAV2503;
 OS Fibronectin-binding protein homolog.
 OS Staphylococcus aureus (strain Mu50 / ATCC 700699).
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 OX NCBI_TaxId=158878;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Mu50 / ATCC 700699;
 RX MEDLINE=21311952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2;
 RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
 RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Iino J.-O., Ito T.,
 RA Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hoshiyama A.,
 RA Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
 RA Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
 RA Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
 RA Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
 RA "Whole genome sequencing of methicillin-resistant Staphylococcus
 RT aureus.";
 RL Lancet 357:1225-1240(2001).
 CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
 an amide bond (By similarity).
 EMBL: AF003365; BAB58665.1; -.
 DR PIR; H90053; H90053.
 DR GO; GO:0009986; C:cell surface; IEA.
 DR GO; GO:0005618; C:cell wall; IEA.
 DR GO; GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0007155; P:cell adhesion; IEA.
 DR InterPro; IPR008966; Adhes_bact.
 DR InterPro; IPR004237; Fn_bind.
 DR InterPro; IPR005877; Gpos_YsIRK.
 DR InterPro; IPR001899; Gram_pos_anchor.
 DR Pfam; PF02986; Fn_bind_1.
 DR Pfam; PF00746; Gram_pos_anchor; 1.
 DR Pfam; PF04650; YsIRK_signal; 1.
 DR TIGRFAMs; TIGR01167; LpxTG_anchor; 1.
 DR TIGRFAMs; TIGR01168; YsIRK_signal; 1.
 DR PROSITE; PS50847; GRAM_POS_ANCHORING; 1.
 KW Cell wall; Complete proteome; Peptidoglycan-anchor.
 SQ SEQUENCE 1038 AA; 113618 MW; 666BF6BF2FBEB12 CRC64;

Query Match 100.0%; Score 53; DB 2; Length 1038;
 Best Local Similarity 100.0%; Pred. No. 0.72;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QCGNIVDIDF 10
 DB 762 QCGNIVDIDF 771

RESULT 11
 Q7A3J7 PRELIMINARY; PRT; 1038 AA.
 ID Q7A3J7
 AC Q7A3J7;

DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DE 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 GN Fnb protein.
 GN Name=fnd; OrderedlocusNames=SA2291;
 OS Staphylococcus aureus (strain N315).
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 OX NCBI_TaxId=158879;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21311952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2;
 RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
 RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Iino J.-O., Ito T.,
 RA Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hoshiyama A.,
 RA Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
 RA Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
 RA Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
 RA Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
 RA "Whole genome sequencing of methicillin-resistant Staphylococcus
 RT aureus.";
 RL Lancet 357:1225-1240(2001).
 CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
 an amide bond (By similarity).
 EMBL: AF003337; BAB43594.1; -.
 DR GO; GO:0009986; C:cell surface; IEA.
 DR GO; GO:0005618; C:cell wall; IEA.
 DR GO; GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0007155; P:cell adhesion; IEA.
 DR InterPro; IPR008966; Adhes_bact.
 DR InterPro; IPR004237; Fn_bind.
 DR InterPro; IPR005877; Gpos_YsIRK.
 DR InterPro; IPR001899; Gram_pos_anchor.
 DR Pfam; PF02986; Fnb_bind; 1.
 DR Pfam; PF00746; Gram_pos_anchor; 1.
 DR Pfam; PF04650; YsIRK_signal; 1.
 DR TIGRFAMs; TIGR01167; LpxTG_anchor; 1.
 DR TIGRFAMs; TIGR01168; YsIRK_signal; 1.
 DR PROSITE; PS50847; GRAM_POS_ANCHORING; 1.
 KW Cell wall; Complete proteome; Peptidoglycan-anchor.
 SQ SEQUENCE 1038 AA; 113618 MW; 666BF6BF2FBEB12 CRC64;

Query Match 100.0%; Score 53; DB 2; Length 1038;
 Best Local Similarity 100.0%; Pred. No. 0.72;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QCGNIVDIDF 10
 DB 762 QCGNIVDIDF 771

RESULT 12
 Q6GDUS PRELIMINARY; PRT; 965 AA.
 ID Q6GDUS
 AC Q6GDUS
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DE 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 GN Name=fnd; OrderedlocusNames=SA2580;
 OS Staphylococcus aureus (strain MRS252).
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 OX NCBI_TaxId=282458;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX PubMed=15213324; DOI=10.1073/pnas.0402521101;
 RA Holden M.T.G., Fell E.J., Lindsay J.A., Peacock S.J., Day N.P.J.,
 RA Enright M.C., Foster T.J., Moore C.E., Hurst L., Atkin R., Barron A.,
 RA Bason N., Bentley S.D., Chillingworth C., Chillingworth T.,
 RA Churcher C., Clark L., Corton C., Cronin A., Doggett J., Dowd L.,
 RA Felwell T., Hance Z., Hauser B., Hauser H., Holtroyd S., Jørgensen K.,
 RA James K.D., Leonard N., Line A., Mayes R., Moule S., Mungall K.,
 RA Ormond D., Quail M.A., Rabinowitch E., Rutherford K.M., Sanders M.,

RA Sharp S., Simmonds M., Stevens K., Whitehead S., Barrell B.G.,
 RA Spratt B.G., Parkhill J.;
 RT "Complete genomes of two clinical *Staphylococcus aureus* strains:
 RT evidence for the rapid evolution of virulence and drug resistance";
 CC Proc. Natl. Acad. Sci. U.S.A. 101:9786-9791(2004).
 RL -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
 CC an amide bond (By similarity).
 DR EMBL: BX571856; CAG41560.1; -;
 DR GO: GO:0009986; C:cell surface; IEA.
 DR GO: GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
 DR GO: GO:0016020; C:membrane; IEA.
 DR GO: GO:007155; P:cell adhesion; IEA.
 DR InterPro: IPR008966; Adhes_bact.
 DR InterPro: IPR004237; P:bind.
 DR InterPro: IPR005877; GPos_Ysirk.
 DR InterPro: IPR001899; Gram_pos_anchor.
 DR Pfam: PF02986; Fn_bind; 1.
 DR Pfam: PF00746; Gram_pos_anchor; 1.
 DR Pfam: PF04650; Ysirk_signal; 1.
 DR TIGRPFAM: TIGR01167; Lpxg anchor; 1.
 DR TIGRPFAM: TIGR01168; Ysirk_signal; 1.
 DR PROSITE: PS00847; GRAM_POS_ANCHORING; 1.
 DR Cell wall; Complete proteome; Peptidoglycan-anchor.
 KW SEQUENCE 965 AA; 105691 MW; 2982E132164D0551 CRC64;

Query Match 98.1%; Score 52; DB 2; Length 965;
 Best Local Similarity 90.0%; Pred. No. 1;
 Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 OGGNIVDIDF 10
 Db 769 OGGNIVDIDF 778

RESULT 13
 Q975V2 PRELIMINARY; PRT; 540 AA.
 AC Q975V2;
 DT 01-DEC-2001 (TREMblrel. 19, Created)
 DT 01-DEC-2001 (TREMblrel. 19, Last sequence update)
 DT 01-JUN-2003 (TREMblrel. 24, Last annotation update)
 DE Hypothetical protein ST0320.
 GN OrderedLocustNames=ST0320;
 OS Sulfolobus tokodaii.
 CC Archaea; Crenarchaeota; Thermoprotei; Sulfolobales; Sulfolobaceae;
 CC Sulfolobus.
 OK NCBI_TaxID=11955;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC STRAIN=JCM 10545 / 7;
 RX MEDLINE=21456156; PubMed=11572479;
 RA Kawarabayashi Y., Hino Y., Horikawa H., Jin-no K., Takahashi M.,
 RA Sekine M., Baba S.-I., Aikai A., Kosugi H., Hosoyama A., Fukui S.,
 RA Nagai Y., Nishijima K., Otsuka R., Nakazawa H., Takamiya M., Kato Y.,
 RA Yoshizawa T., Tanaka T., Kudo Y., Yamazaki J., Kuehida N., Oguchi A.,
 RA Aoki K.-I., Masuda S., Yanagii M., Nishimura M., Yamagishi A.,
 RA Oshima T., Kikuchi H.;
 RT "Complete genome sequence of an aerobic thermophilic
 RT Crenarchaeon, *Sulfolobus tokodaii* strain7.";
 RL DNA Res. 8:123-140(2001).
 DR EMBL: AP000982; BAB65296.1; -;
 DR InterPro: IPR002789; DUF87.
 DR Pfam: PF01935; DUF87; 1.
 KW Complete proteome; Hypothetical protein.
 SQ SEQUENCE 540 AA; 61823 MW; 46D136D8FCEDE047 CRC64;

Query Match 75.5%; Score 40; DB 2; Length 540;
 Best Local Similarity 60.0%; Pred. No. 95;
 Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 1 OGGNIVDIDF 10
 Db 391 OGGNIVDIDF 400

RESULT 14
 Q830D1 PRELIMINARY; PRT; 711 AA.
 ID Q830D1;
 AC Q830D1;
 DT 01-JUN-2003 (TREMblrel. 24, Created)
 DT 01-JUN-2003 (TREMblrel. 24, Last sequence update)
 DT 01-OCT-2003 (TREMblrel. 25, Last annotation update)
 DE Penicillin-binding protein 2B.
 GN OrderedLocustNames=EF2857;
 OS Enterococcus faecalis (Streptococcus faecalis).
 CC Bacteria; Firmicutes; Lactobacillales; Enterococcaceae; Enterococcus.
 OK NCBI_TaxID=1351;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC STRAIN=V583 / ATCC 700802;
 RX MEDLINE=22550857; PubMed=12663927; DOI=10.1126/science.1080613;
 RA Paulsen I.T., Banerjee L., Myers G.S.A., Nelson K.E., Seehadi R.,
 RA Read T.D., Fouts D.E., Eisen J.A., Gill S.R., Heidelberg J.F.,
 RA Tettelin H., Dodson R.J., Umayam L.A., Brinkac L.M., Beanan M.J.,
 RA Daugherty S.C., Deboy R.T., Durkin S.A., Kolonay J.F., Madupu R.,
 RA Nelson W.C., Vamathevan J.V., Tran B., Upton J., Hansen T., Shetty J.,
 RA Khouri H.M., Utterback T.R., Radune D., Ketchum K.A., Dougherty B.A.,
 RA Fraser C.M.;
 RT "Role of mobile DNA in the evolution of vancomycin-resistant
 RT Enterococcus faecalis";
 RL Science 299:2071-2074(2003).
 DR EMBL: AE018936; NA082549.1; -;
 DR HSP: Q931C2; IMWT.
 DR TIGR: EF2857; -;
 DR GO: GO:000658; F:penicillin binding; IEA.
 DR GO: GO:0009273; P:cell wall biosynthesis (sensu Bacteria); IEA.
 DR InterPro: IPR005311; PBP_dimer.
 DR InterPro: IPR001460; Pencil_bind_tpept.
 DR Pfam: PF03717; PBP_dimer; 1.
 DR Pfam: PF00905; Transpeptidase; 1.
 KW Complete proteome.
 SQ SEQUENCE 711 AA; 77858 MW; A27C7168DDCF542 CRC64;

Query Match 75.5%; Score 40; DB 2; Length 711;
 Best Local Similarity 60.0%; Pred. No. 1.3e+02;
 Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 1 OGGNIVDIDF 10
 Db 537 OGGNIVDIDF 546

RESULT 15
 Q70YB1 PRELIMINARY; PRT; 742 AA.
 ID Q70YB1;
 AC Q70YB1;
 DT 01-MAR-2004 (TREMblrel. 26, Created)
 DT 01-MAR-2004 (TREMblrel. 26, Last sequence update)
 DT 01-MAR-2004 (TREMblrel. 26, Last annotation update)
 DE GLP 387 40176 37948.
 OS Giardia lamblia ATCC 50803.
 CC Eukaryota; Diplomonadida; Hexamitidae; Giardinae; Giardia.
 OK NCBI_TaxID=184922;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC STRAIN=WB C6;
 RA Morrison H.G., McArthur A.G., Adam R.D., Alek S.B., Gillin F.D.,
 RA Olsen G.J., Sogin M.L.;
 RT "Draft sequence of the *Giardia lamblia* genome.";
 RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
 CC -!- CAUTION: The sequence shown here is derived from an
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.
 DR EMBL: AACB0100052; EAA40044.1; -;
 DR GO: GO:0000214; C:RNA-intron endonuclease complex; IEA.
 DR GO: GO:0000213; F:RNA-intron endonuclease activity; IEA.

DR GO:0006388: P:trna splicing; IEA.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR006677; tRNA_int_endo_C.
DR Pfam; PF01974; tRNA_int_endo; 1.
DR PROSITE; PS00290; IG_MHC; UNKNOWN 1.
SQ SEQUENCE 742 AA; 83364 MW; 93C5AC1FF0D4F46 CRC64;

Query Match 75.5%; Score 40; DB 2; Length 742;
Best Local Similarity 60.0%; Pred. No. 1.3e+02;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 OGGNIVDIDE 10
:|:|:|:|:
Db 618 KGGQLVDVDF 627

Search completed: October 22, 2005, 08:00:39
Job time : 57.85 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 25, 2005, 20:21:18 ; Search time 63.2 Seconds
(without alignments)
61.196 Million cell updates/sec

Title: US-10-731-238-74

Perfect score: 52
Sequence: 1 GNIVDIDFDS 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-Processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:.*
1: geneseqp1808:.*
2: geneseqp1908:.*
3: geneseqp2008:.*
4: geneseqp2018:.*
5: geneseqp20028:.*
6: geneseqp20038:.*
7: geneseqp20038:.*
8: geneseqp20048:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	52	100.0	10	2 AAW65730	AAW65730 Fibrinect
2	52	100.0	14	2 AAW65716	AAW65716 Fibrinect
3	52	100.0	38	2 AAW65692	AAW65692 Fibrinect
4	52	100.0	38	2 AAW65695	AAW65695 Fibrinect
5	52	100.0	38	2 AAW65662	AAW65662 Fibrinect
6	52	100.0	38	2 AAW65696	AAW65696 Fibrinect
7	52	100.0	38	2 AAW65697	AAW65697 Fibrinect
8	52	100.0	38	2 AAW65694	AAW65694 Fibrinect
9	52	100.0	38	2 AAW65691	AAW65691 Fibrinect
10	52	100.0	38	2 AAW65661	AAW65661 Fibrinect
11	52	100.0	38	2 AAW65693	AAW65693 Fibrinect
12	52	100.0	38	2 AAW65698	AAW65698 Fibrinect
13	52	100.0	113	2 AAR90937	AAR90937 D3D4 poly
14	52	100.0	130	2 AAR58806	AAR58806 Fibrinect
15	52	100.0	130	2 AAR58807	AAR58807 Fibrinect
16	52	100.0	130	2 AAR91202	AAR91202 D1-D4 fib
17	52	100.0	130	2 AAR91201	AAR91201 D1-D4 fib
18	52	100.0	134	2 AAY28089	AAY28089 Cloned fi
19	52	100.0	134	2 AAY28088	AAY28088 S. aureus
20	52	100.0	134	2 AAY28087	AAY28087 S. aureus
21	52	100.0	139	2 AAW31556	AAW31556 Fibrinect
22	52	100.0	162	2 AAR90942	AAR90942 D3D4 poly
23	52	100.0	164	2 AAR90938	AAR90938 D3D4 poly
24	52	100.0	174	2 AAR58808	AAR58808 Fdp fibro
25	52	100.0	174	2 AAR91203	AAR91203 D1-D4 fib

26	52	100.0	181	2 AAR58805	AAR58805 Fibrinect
27	52	100.0	181	2 AAR91200	AAR91200 D1-D4 fib
28	52	100.0	559	2 AAW89803	AAW89803 Staphyloc
29	52	100.0	767	4 AAU34403	AAU34403 Staphyloc
30	52	100.0	767	4 AAU37547	AAU37547 Staphyloc
31	52	100.0	940	2 AAR07070	AAR07070 Fibrinect
32	52	100.0	940	6 ABJ19111	ABJ19111 Pathogen
33	52	100.0	948	6 ADA89470	ADA89470 Staphyloc
34	52	100.0	948	6 ABJ18923	ABJ18923 Pathogen
35	52	100.0	948	6 ABM72536	ABM72536 Staphyloc
36	52	100.0	961	6 ABU15854	ABU15854 Protein e
37	52	100.0	978	4 AAU33960	AAU33960 Staphyloc
38	52	100.0	1001	4 AAU37093	AAU37093 Staphyloc
39	52	100.0	1018	1 AAR82115	AAR82115 Fibrinect
40	52	100.0	1018	4 AAU37245	AAU37245 Staphyloc
41	52	100.0	1018	4 AAU34301	AAU34301 Staphyloc
42	52	100.0	1018	6 ABJ18922	ABJ18922 Pathogen
43	52	100.0	1018	6 ABM72537	ABM72537 Staphyloc
44	52	100.0	1027	2 AAW89806	AAW89806 Staphyloc
45	52	100.0	1038	6 ABU15903	ABU15903 Protein e

ALIGNMENTS

RESULT 1
AAW65730
ID AAW65730 standard; peptide, 10 AA.

XX AAW65730;

DT 16-OCT-1998 (first entry)

XX Fibrinectin binding protein-derived peptide #74.

XX microbial surface components recognising adhesive matrix molecule;

KW MSCRAMM; fibrinectin; fibrinectin-binding protein; antibody; epitope;

KW antibiotic; bacterial infection; antibiotic-resistant strain.

XX Synthetic.

OS Staphylococcus aureus.

XX W09831369-A2.

XX 23-JUL-1998.

XX 21-JAN-1998; 98WO-US001222.

XX 21-JAN-1997; 97US-0036139P.

XX (TEXA) UNIV TEXAS A & M SYSTEM.

XX Hoeoek M, Patti JM, House-Pompeo KL, Speziale P, Joh D;

XX Mcgavin MJ;

XX WPI; 1998-413816/35.

XX Antibody that binds to fibrinectin-binding protein, preventing its

XX binding to fibrinectin - used to treat or prevent bacterial infection,

XX especially by Staphylococci and Streptococci.

XX Example 9; Page 110; 20pp; English.

The invention relates to antibodies that bind to a fibrinectin-binding domain of a fibrinectin-binding protein, and inhibit binding of the protein to fibrinectin. Also claimed are: (1) isolated peptides of a fibrinectin-binding protein that do not bind to fibrinectin; (2) fusion protein containing at least one peptide of a fibrinectin-binding protein linked to a second amino acid sequence; (3) nucleic acid encoding the isolated peptide of (1). Antibodies, the isolated peptides of (1) and the nucleic acids are all useful for immunisation (active or passive) and (by inhibiting binding of bacteria to fibrinectin) for preventing or treating infection in humans or other animals, particularly by staphylococci or

CC streptococci, e.g. meningitis, otitis media, pneumonia, endocarditis,
 CC mastitis in cattle, abortion in horses and many others. Since the
 CC antibodies block binding of bacteria, they should be effective against
 CC antibiotic-resistant strains, and may replace antibiotic therapy or
 CC increase its effectiveness. Sequences AAW65719-41 and AAW65658 represent
 CC peptides which were synthesised to span the D1 motif and the N-terminal
 CC 18 amino acids of D2, with each peptide overlapping by eight amino acids
 CC with the previous sequence
 XX
 SQ Sequence 10 AA;

Query Match 100.0%; Score 52; DB 2; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.0015;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GNVIDIDPDS 10
 |||||
 DB 1 GNVIDIDPDS 10

RESULT 2
 AAW65716 standard; peptide; 14 AA.
 XX
 AC AAW65716;
 XX

DT 16-OCT-1998 (first entry)
 XX

DE Fibronectin binding protein fragment (residues 21-34 of D1 motif).
 XX

KW microbial surface components recognising adhesive matrix molecule;
 KM MSCRAMM; fibronectin; fibronectin-binding protein; antibody; epitope;
 KM antibiotic; bacterial infection; antibiotic-resistant strain.
 XX

XX Synthetic.
 OS

OS Staphylococcus aureus.
 XX

PN WO9831389-A2.
 XX

PD 23-JUL-1998.
 XX

PF 21-JAN-1998; 98WO-US001222.
 XX

PR 21-JAN-1997; 97US-0036139P.
 XX

PA (TEXA) UNIV TEXAS A & M SYSTEM.
 XX

PI Hoecek M, Patti JM, House-Pompeo KL, Speziale P, Joh D;
 PI McGavin MJ;
 XX

DR WPI; 1998-413816/35.
 XX

PT Antibody that binds to fibronectin-binding protein, preventing its
 PT binding to fibronectin - used to treat or prevent bacterial infection,
 PT especially by Staphylococci and Streptococci.
 XX

PS Claim 42; Page 105; 201pp; English.
 XX

CC The invention relates to antibodies that bind to a fibronectin-binding
 CC domain of a fibronectin-binding protein, and inhibit binding of the
 CC protein to fibronectin. Also claimed are: (1) isolated peptides of a
 CC fibronectin-binding protein that do not bind to fibronectin; (2) fusion
 CC protein containing at least one peptide of a fibronectin-binding protein
 CC linked to a second amino acid sequence; (3) nucleic acid encoding the
 CC isolated peptide of (1). Antibodies, the isolated peptides of (1) and the
 CC nucleic acids are all useful for immunisation (active or passive) and (by
 CC inhibiting binding of bacteria to fibronectin) for preventing or treating
 CC infection in humans or other animals, particularly by staphylococci or
 CC streptococci, e.g. meningitis, otitis media, pneumonia, endocarditis,
 CC mastitis in cattle, abortion in horses and many others. Since the
 CC antibodies block binding of bacteria, they should be effective against
 CC antibiotic-resistant strains, and may replace antibiotic therapy or
 CC increase its effectiveness. The present sequence represents a

CC specifically claimed peptide
 XX
 SQ Sequence 14 AA;

Query Match 100.0%; Score 52; DB 2; Length 14;
 Best Local Similarity 100.0%; Pred. No. 0.0022;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GNVIDIDPDS 10
 |||||
 DB 3 GNVIDIDPDS 12

RESULT 3
 AAW65692 standard; peptide; 38 AA.
 XX
 AC AAW65692;
 XX

DT 16-OCT-1998 (first entry)
 XX

DE Fibronectin binding protein-derived peptide #36.
 XX

KW microbial surface components recognising adhesive matrix molecule;
 KM MSCRAMM; fibronectin; fibronectin-binding protein; antibody; epitope;
 KM antibiotic; bacterial infection; antibiotic-resistant strain.
 XX

XX Synthetic.
 OS

OS Staphylococcus aureus.
 XX

PN WO9831389-A2.
 XX

PD 23-JUL-1998.
 XX

PF 21-JAN-1998; 98WO-US001222.
 XX

PR 21-JAN-1997; 97US-0036139P.
 XX

PA (TEXA) UNIV TEXAS A & M SYSTEM.
 XX

PI Hoecek M, Patti JM, House-Pompeo KL, Speziale P, Joh D;
 PI McGavin MJ;
 XX

DR WPI; 1998-413816/35.
 XX

PT Antibody that binds to fibronectin-binding protein, preventing its
 PT binding to fibronectin - used to treat or prevent bacterial infection,
 PT especially by Staphylococci and Streptococci.
 XX

PS Example 8; Page 101; 201pp; English.
 XX

CC The invention relates to antibodies that bind to a fibronectin-binding
 CC domain of a fibronectin-binding protein, and inhibit binding of the
 CC protein to fibronectin. Also claimed are: (1) isolated peptides of a
 CC fibronectin-binding protein that do not bind to fibronectin; (2) fusion
 CC protein containing at least one peptide of a fibronectin-binding protein
 CC linked to a second amino acid sequence; (3) nucleic acid encoding the
 CC isolated peptide of (1). Antibodies, the isolated peptides of (1) and the
 CC nucleic acids are all useful for immunisation (active or passive) and (by
 CC inhibiting binding of bacteria to fibronectin) for preventing or treating
 CC infection in humans or other animals, particularly by staphylococci or
 CC streptococci, e.g. meningitis, otitis media, pneumonia, endocarditis,
 CC mastitis in cattle, abortion in horses and many others. Since the
 CC antibodies block binding of bacteria, they should be effective against
 CC antibiotic-resistant strains, and may replace antibiotic therapy or
 CC increase its effectiveness. Sequences AAW65691-700 represent a series of
 CC synthetic peptides based on the D1 region of S. aureus fibronectin
 CC binding protein A. They were synthesised to contain mutations
 XX

SQ Sequence 38 AA;

Query Match 100.0%; Score 52; DB 2; Length 38;
 Best Local Similarity 100.0%; Pred. No. 0.0069;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GNVVDIDFDS 10
 |||||
 DB 23 GNVVDIDFDS 32

RESULT 4

AAW65695
 ID AAW65695 standard; peptide; 38 AA.

AC AAW65695;
 DT 16-OCT-1998 (first entry)

DE Fibronectin binding protein-derived peptide #39.

XX microbial surface components recognising adhesive matrix molecule;
 KM MSCRAMM; fibronectin; fibronectin-binding protein; antibody; epitope;
 KW antibiotic; bacterial infection; antibiotic-resistant strain.

XX Synthetic.

OS Staphylococcus aureus.

XX WO9831389-A2.

XX 23-JUL-1998.

PF 21-JAN-1998; 98WO-US001222.

XX 21-JAN-1997; 97US-0036139P.

XX (TEXA) UNIV TEXAS A & M SYSTEM.

PI Hoeck M, Patel JM, House-Pompeo KL, Speziale P, Joh D;
 PI McGavin MJ;

DR WPI; 1998-413816/35.

XX Antibody that binds to fibronectin-binding protein, preventing its
 PT binding to fibronectin - used to treat or prevent bacterial infection,
 PT especially by Staphylococci and Streptococci.

XX Example 8; Page 102; 201pp; English.

CC The invention relates to antibodies that bind to a fibronectin-binding
 CC domain of a fibronectin-binding protein, and inhibit binding of the
 CC protein to fibronectin. Also claimed are: (1) isolated peptides of a
 CC fibronectin-binding protein that do not bind to fibronectin; (2) fusion
 CC protein containing at least one peptide of a fibronectin-binding protein
 CC linked to a second amino acid sequence; (3) nucleic acid encoding the
 CC isolated peptide of (1). Antibodies, the isolated peptides of (1) and the
 CC nucleic acids are all useful for immunisation (active or passive) and (by
 CC inhibiting binding of bacteria to fibronectin) for preventing or treating
 CC infection in humans or other animals, particularly by Staphylococci or
 CC streptococci, e.g. meningitis, otitis media, pneumonia, endocarditis,
 CC mastitis in cattle, abortion in horses and many others. Since the
 CC antibodies block binding of bacteria, they should be effective against
 CC antibiotic-resistant strains, and may replace antibiotic therapy or
 CC increase its effectiveness. Sequences AAW65691-700 represent a series of
 CC synthetic peptides based on the DI region of S. aureus fibronectin
 CC binding protein A. They were synthesised to contain mutations

XX Sequence 38 AA:

Query Match 100.0%; Score 52; DB 2; Length 38;
 Best Local Similarity 100.0%; Pred. No. 0.0069;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GNVVDIDFDS 10
 |||||
 DB 23 GNVVDIDFDS 32

RESULT 5
 ID AAW65662
 XX AAW65662 standard; peptide; 38 AA.
 XX

AC AAW65662;
 DT 16-OCT-1998 (first entry)

DE Fibronectin binding protein-derived peptide #6.

XX microbial surface components recognising adhesive matrix molecule;
 KM MSCRAMM; fibronectin; fibronectin-binding protein; antibody; epitope;
 KW antibiotic; bacterial infection; antibiotic-resistant strain.

XX Synthetic.

OS Staphylococcus aureus.

XX WO9831389-A2.

XX 23-JUL-1998.

PF 21-JAN-1998; 98WO-US001222.

XX 21-JAN-1997; 97US-0036139P.

XX (TEXA) UNIV TEXAS A & M SYSTEM.

PI Hoeck M, Patel JM, House-Pompeo KL, Speziale P, Joh D;
 PI McGavin MJ;

DR WPI; 1998-413816/35.

XX Antibody that binds to fibronectin-binding protein, preventing its
 PT binding to fibronectin - used to treat or prevent bacterial infection,
 PT especially by Staphylococci and Streptococci.

XX Example 2; Page 92; 201pp; English.

CC The invention relates to antibodies that bind to a fibronectin-binding
 CC domain of a fibronectin-binding protein, and inhibit binding of the
 CC protein to fibronectin. Also claimed are: (1) isolated peptides of a
 CC fibronectin-binding protein that do not bind to fibronectin; (2) fusion
 CC protein containing at least one peptide of a fibronectin-binding protein
 CC linked to a second amino acid sequence; (3) nucleic acid encoding the
 CC isolated peptide of (1). Antibodies, the isolated peptides of (1) and the
 CC nucleic acids are all useful for immunisation (active or passive) and (by
 CC inhibiting binding of bacteria to fibronectin) for preventing or treating
 CC infection in humans or other animals, particularly by Staphylococci or
 CC streptococci, e.g. meningitis, otitis media, pneumonia, endocarditis,
 CC mastitis in cattle, abortion in horses and many others. Since the
 CC antibodies block binding of bacteria, they should be effective against
 CC antibiotic-resistant strains, and may replace antibiotic therapy or
 CC increase its effectiveness. Sequences AAW6569-68 represent synthetic
 CC epitopes from the fibronectin binding domains DU and DI-D4 of the S.
 CC aureus fnbA gene

XX Sequence 38 AA:

Query Match 100.0%; Score 52; DB 2; Length 38;
 Best Local Similarity 100.0%; Pred. No. 0.0069;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GNVVDIDFDS 10
 |||||
 DB 23 GNVVDIDFDS 32

RESULT 6

AAW65696
 ID AAW65696 standard; peptide; 38 AA.
 XX

AC AAW65696;

```

XX 16-OCT-1998 (first entry)
DT
XX Fibronectin binding protein-derived peptide #40.
DE
XX Microbial surface components recognising adhesive matrix molecule;
XX MSCRAMM; fibronectin; fibronectin-binding protein; antibody; epitope;
XX antibiotic; bacterial infection; antibiotic-resistant strain.
XX
XX Synthetic.
OS Staphylococcus aureus.
XX
XX WO9831389-A2.
XX
XX 23-JUL-1998.
XX
XX 21-JAN-1998; 98WO-US001222.
XX
XX 21-JAN-1997; 97US-0036139P.
XX
XX (TEXA ) UNIV TEXAS A & M SYSTEM.
XX
XX Hoecek M, Patti JM, House-Pompeo KL, Speziale P, Joh D;
XX McGavin MJ;
XX
XX WPI; 1998-413816/35.
XX
XX Antibody that binds to fibronectin-binding protein, preventing its
XX binding to fibronectin - used to treat or prevent bacterial infection,
XX especially by Staphylococci and Streptococci.
XX
XX Example 8; Page 102; 201pp; English.
XX
XX The invention relates to antibodies that bind to a fibronectin-binding
XX domain of a fibronectin-binding protein, and inhibit binding of the
XX protein to fibronectin. Also claimed are: (1) isolated peptides of a
XX fibronectin-binding protein that do not bind to fibronectin; (2) fusion
XX protein containing at least one peptide of a fibronectin-binding protein
XX linked to a second amino acid sequence; (3) nucleic acid encoding the
XX isolated peptide of (1). Antibodies, the isolated peptides of (1) and the
XX nucleic acids are all useful for immunisation (active or passive) and (by
XX inhibiting binding of bacteria to fibronectin) for preventing or treating
XX infection in humans or other animals, particularly by staphylococci or
XX streptococci, e.g. meningitis, otitis media, pneumonia, endocarditis,
XX mastitis in cattle, abortion in horses and many others. Since the
XX antibodies block binding of bacteria, they should be effective against
XX antibiotic-resistant strains, and may replace antibiotic therapy or
XX increase its effectiveness. Sequences AAW65691-700 represent a series of
XX synthetic peptides based on the DI region of S. aureus fibronectin
XX binding protein A. They were synthesised to contain mutations
XX
XX Sequence 38 AA;
SQ
XX
XX Query Match 100.0%; Score 52; DB 2; Length 38;
XX Best Local Similarity 100.0%; Pred. No. 0.0069;
XX Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 GNIVDIDFDS 10
XX |||||
XX 23 GNIVDIDFDS 32
XX
XX Db
XX
XX RESULT 7
XX AAW65697
XX ID AAW65697 standard; peptide; 38 AA.
XX
XX AC AAW65697;
XX
XX DT 16-OCT-1998 (first entry)
XX
XX DE Fibronectin binding protein-derived peptide #41.
XX
XX microbial surface components recognising adhesive matrix molecule;
XX
XX

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XX MSCRAMM; fibronectin; fibronectin-binding protein; antibody; epitope;
XX antibiotic; bacterial infection; antibiotic-resistant strain.
XX
XX Synthetic.
OS Staphylococcus aureus.
XX
XX WO9831389-A2.
XX
XX 23-JUL-1998.
XX
XX 21-JAN-1998; 98WO-US001222.
XX
XX 21-JAN-1997; 97US-0036139P.
XX
XX (TEXA ) UNIV TEXAS A & M SYSTEM.
XX
XX Hoecek M, Patti JM, House-Pompeo KL, Speziale P, Joh D;
XX McGavin MJ;
XX
XX WPI; 1998-413816/35.
XX
XX Antibody that binds to fibronectin-binding protein, preventing its
XX binding to fibronectin - used to treat or prevent bacterial infection,
XX especially by Staphylococci and Streptococci.
XX
XX Example 8; Page 102; 201pp; English.
XX
XX The invention relates to antibodies that bind to a fibronectin-binding
XX domain of a fibronectin-binding protein, and inhibit binding of the
XX protein to fibronectin. Also claimed are: (1) isolated peptides of a
XX fibronectin-binding protein that do not bind to fibronectin; (2) fusion
XX protein containing at least one peptide of a fibronectin-binding protein
XX linked to a second amino acid sequence; (3) nucleic acid encoding the
XX isolated peptide of (1). Antibodies, the isolated peptides of (1) and the
XX nucleic acids are all useful for immunisation (active or passive) and (by
XX inhibiting binding of bacteria to fibronectin) for preventing or treating
XX infection in humans or other animals, particularly by staphylococci or
XX streptococci, e.g. meningitis, otitis media, pneumonia, endocarditis,
XX mastitis in cattle, abortion in horses and many others. Since the
XX antibodies block binding of bacteria, they should be effective against
XX antibiotic-resistant strains, and may replace antibiotic therapy or
XX increase its effectiveness. Sequences AAW65691-700 represent a series of
XX synthetic peptides based on the DI region of S. aureus fibronectin
XX binding protein A. They were synthesised to contain mutations
XX
XX Sequence 38 AA;
SQ
XX
XX Query Match 100.0%; Score 52; DB 2; Length 38;
XX Best Local Similarity 100.0%; Pred. No. 0.0069;
XX Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 GNIVDIDFDS 10
XX |||||
XX 23 GNIVDIDFDS 32
XX
XX Db
XX
XX RESULT 8
XX AAW65694
XX ID AAW65694 standard; peptide; 38 AA.
XX
XX AC AAW65694;
XX
XX DT 16-OCT-1998 (first entry)
XX
XX DE Fibronectin binding protein-derived peptide #38.
XX
XX microbial surface components recognising adhesive matrix molecule;
XX MSCRAMM; fibronectin; fibronectin-binding protein; antibody; epitope;
XX antibiotic; bacterial infection; antibiotic-resistant strain.
XX
XX Synthetic.
OS Staphylococcus aureus.
XX

```

PN WO9831389-A2.
 XX
 PD 23-JUL-1998.
 XX
 XX
 PR 21-JAN-1998; 98WO-US001222.
 XX
 XX
 PR 21-JAN-1997; 97US-0036139P.
 XX
 XX
 PA (TEXA) UNIV TEXAS A & M SYSTEM.
 XX
 PI Hoeek M, Patti JM, House-Pompeo KL, Speziale P, Joh D;
 PI Mcgavin MJ;
 DR WPI; 1998-413816/35.
 XX
 XX
 PT Antibody that binds to fibronectin-binding protein, preventing its
 PT binding to fibronectin - used to treat or prevent bacterial infection,
 PT especially by Staphylococci and Streptococci.
 XX
 XX
 PS Example 8; Page 102; 201pp; English.
 CC The invention relates to antibodies that bind to a fibronectin-binding
 CC domain of a fibronectin-binding protein, and inhibit binding of the
 CC protein to fibronectin. Also claimed are: (1) isolated peptides of a
 CC fibronectin-binding protein that do not bind to fibronectin; (2) fusion
 CC protein containing at least one peptide of a fibronectin-binding protein
 CC linked to a second amino acid sequence; (3) nucleic acid encoding the
 CC isolated peptide of (1). Antibodies, the isolated peptides of (1) and the
 CC nucleic acids are all useful for immunisation (active or passive) and (by
 CC inhibiting binding of bacteria to fibronectin) for preventing or treating
 CC infection in humans or other animals, particularly by staphylococci or
 CC streptococci, e.g. meningitis, otitis media, pneumonia, endocarditis,
 CC mastitis in cattle, abortion in horses and many others. Since the
 CC antibodies block binding of bacteria, they should be effective against
 CC antibiotic-resistant strains, and may replace antibiotic therapy or
 CC increase its effectiveness. Sequences AAW65691-700 represent a series of
 CC synthetic peptides based on the D1 region of S. aureus fibronectin
 CC binding protein A. They were synthesised to contain mutations
 XX
 XX
 SQ Sequence 38 AA:
 Query Match 100.0%; Score 52; DB 2; Length 38;
 Best Local Similarity 100.0%; Pred. No. 0.0069;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GNVVIDIDFDS 10
 DB 23 GNVVIDIDFDS 32
 RESULT 9
 ID AAW65691 standard; peptide; 38 AA.
 XX
 AC AAW65691;
 XX
 DT 16-OCT-1998 (first entry)
 XX
 DE Fibronectin binding protein-derived peptide #35.
 XX
 XX microbial surface components recognising adhesive matrix molecule;
 KM MSCRAMM; fibronectin; fibronectin-binding protein; antibody; epitope;
 KM antibiotic; bacterial infection; antibiotic-resistant strain.
 XX
 OS Synthetic.
 OS Staphylococcus aureus.
 XX
 XX WO9831389-A2.
 XX
 PD 23-JUL-1998.
 XX
 PF 21-JAN-1998; 98WO-US001222.
 XX

PR 21-JAN-1997; 97US-0036139P.
 XX
 XX
 PA (TEXA) UNIV TEXAS A & M SYSTEM.
 XX
 XX
 PI Hoeek M, Patti JM, House-Pompeo KL, Speziale P, Joh D;
 PI Mcgavin MJ;
 DR WPI; 1998-413816/35.
 XX
 XX
 PT Antibody that binds to fibronectin-binding protein, preventing its
 PT binding to fibronectin - used to treat or prevent bacterial infection,
 PT especially by Staphylococci and Streptococci.
 XX
 XX
 PS Example 8; Page 101; 201pp; English.
 CC The invention relates to antibodies that bind to a fibronectin-binding
 CC domain of a fibronectin-binding protein, and inhibit binding of the
 CC protein to fibronectin. Also claimed are: (1) isolated peptides of a
 CC fibronectin-binding protein that do not bind to fibronectin; (2) fusion
 CC protein containing at least one peptide of a fibronectin-binding protein
 CC linked to a second amino acid sequence; (3) nucleic acid encoding the
 CC isolated peptide of (1). Antibodies, the isolated peptides of (1) and the
 CC nucleic acids are all useful for immunisation (active or passive) and (by
 CC inhibiting binding of bacteria to fibronectin) for preventing or treating
 CC infection in humans or other animals, particularly by staphylococci or
 CC streptococci, e.g. meningitis, otitis media, pneumonia, endocarditis,
 CC mastitis in cattle, abortion in horses and many others. Since the
 CC antibodies block binding of bacteria, they should be effective against
 CC antibiotic-resistant strains, and may replace antibiotic therapy or
 CC increase its effectiveness. Sequences AAW65691-700 represent a series of
 CC synthetic peptides based on the D1 region of S. aureus fibronectin
 CC binding protein A. They were synthesised to contain mutations
 XX
 XX
 SQ Sequence 38 AA:
 Query Match 100.0%; Score 52; DB 2; Length 38;
 Best Local Similarity 100.0%; Pred. No. 0.0069;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GNVVIDIDFDS 10
 DB 23 GNVVIDIDFDS 32
 RESULT 10
 ID AAW65661 standard; peptide; 38 AA.
 XX
 AC AAW65661;
 XX
 DT 16-OCT-1998 (first entry)
 XX
 DE Fibronectin binding protein-derived peptide #5.
 XX
 XX microbial surface components recognising adhesive matrix molecule;
 KM MSCRAMM; fibronectin; fibronectin-binding protein; antibody; epitope;
 KM antibiotic; bacterial infection; antibiotic-resistant strain.
 XX
 OS Synthetic.
 OS Staphylococcus aureus.
 XX
 XX WO9831389-A2.
 XX
 PD 23-JUL-1998.
 XX
 PF 21-JAN-1998; 98WO-US001222.
 XX
 XX
 PR 21-JAN-1997; 97US-0036139P.
 XX
 XX
 PA (TEXA) UNIV TEXAS A & M SYSTEM.
 XX
 XX
 PI Hoeek M, Patti JM, House-Pompeo KL, Speziale P, Joh D;
 PI Mcgavin MJ;

```

XX DR MPI; 1998-413816/35.
XX PT Antibody that binds to fibronectin-binding protein, preventing its
XX binding to fibronectin - used to treat or prevent bacterial infection,
XX especially by Staphylococci and Streptococci.
XX PS Example 2; Page 92; 201pp; English.
XX CC The invention relates to antibodies that bind to a fibronectin-binding
XX domain of a fibronectin-binding protein, and inhibit binding of the
XX protein to fibronectin. Also claimed are: (1) isolated peptides of a
XX fibronectin-binding protein that do not bind to fibronectin; (2) fusion
XX protein containing at least one peptide of a fibronectin-binding protein
XX linked to a second amino acid sequence; (3) nucleic acid encoding the
XX isolated peptide of (1). Antibodies, the isolated peptides of (1) and the
XX nucleic acids are all useful for immunisation (active or passive) and (by
XX inhibiting binding of bacteria to fibronectin) for preventing or treating
XX infection in humans or other animals, particularly by staphylococci or
XX streptococci, e.g. meningitis, otitis media, pneumonia, endocarditis,
XX mastitis in cattle, abortion in horses and many others. Since the
XX antibodies block binding of bacteria, they should be effective against
XX antibiotic-resistant strains, and may replace antibiotic therapy or
XX increase its effectiveness. Sequences AAW65659-68 represent synthetic
XX epitopes from the fibronectin binding domains DU and DI-D4 of the S.
XX aureus fnbA gene
XX SQ Sequence 38 AA;
XX
XX Query Match          100.0%; Score 52; DB 2; Length 38;
XX Best Local Similarity 100.0%; Pred. No. 0.0069;
XX Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 GNVIDIDFDS 10
XX      |||||
XX DB 23 GNVIDIDFDS 32
XX
XX RESULT 11
XX AAW65693
XX ID AAW65693 standard; peptide; 38 AA.
XX AC AAW65693;
XX XX
XX DT 16-OCT-1998 (first entry)
XX DE Fibronectin binding protein-derived peptide #37.
XX XX
XX KM microbial surface components recognising adhesive matrix molecule;
XX MSCRAMM; fibronectin; fibronectin-binding protein; antibody; epitope;
XX antibiotic; bacterial infection; antibiotic-resistant strain.
XX XX
XX OS Synthetic.
XX OS Staphylococcus aureus.
XX XX
XX PN WO9831389-A2.
XX PD 23-JUL-1998.
XX PF 21-JAN-1998; 98WO-US001222.
XX PR 21-JAN-1997; 97US-0036139P.
XX PA (TEXA ) UNIV TEXAS A & M SYSTEM.
XX PI Hoeoek M, Patci JM, House-Pompeo KL, Speziale P, Joh D;
XX PI McGavin MJ;
XX XX
XX DR MPI; 1998-413816/35.
XX PT Antibody that binds to fibronectin-binding protein, preventing its
XX binding to fibronectin - used to treat or prevent bacterial infection,
XX especially by Staphylococci and Streptococci.

```

```

XX PS Example 8; Page 102; 201pp; English.
XX CC The invention relates to antibodies that bind to a fibronectin-binding
XX domain of a fibronectin-binding protein, and inhibit binding of the
XX protein to fibronectin. Also claimed are: (1) isolated peptides of a
XX fibronectin-binding protein that do not bind to fibronectin; (2) fusion
XX protein containing at least one peptide of a fibronectin-binding protein
XX linked to a second amino acid sequence; (3) nucleic acid encoding the
XX isolated peptide of (1). Antibodies, the isolated peptides of (1) and the
XX nucleic acids are all useful for immunisation (active or passive) and (by
XX inhibiting binding of bacteria to fibronectin) for preventing or treating
XX infection in humans or other animals, particularly by staphylococci or
XX streptococci, e.g. meningitis, otitis media, pneumonia, endocarditis,
XX mastitis in cattle, abortion in horses and many others. Since the
XX antibodies block binding of bacteria, they should be effective against
XX antibiotic-resistant strains, and may replace antibiotic therapy or
XX increase its effectiveness. Sequences AAW65691-700 represent a series of
XX synthetic peptides based on the DI region of S. aureus fibronectin
XX binding protein A. They were synthesised to contain mutations
XX
XX SQ Sequence 38 AA;
XX
XX Query Match          100.0%; Score 52; DB 2; Length 38;
XX Best Local Similarity 100.0%; Pred. No. 0.0069;
XX Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 GNVIDIDFDS 10
XX      |||||
XX DB 23 GNVIDIDFDS 32
XX
XX RESULT 12
XX AAW65698
XX ID AAW65698 standard; peptide; 38 AA.
XX AC AAW65698;
XX XX
XX DT 16-OCT-1998 (first entry)
XX DE Fibronectin binding protein-derived peptide #42.
XX XX
XX KM microbial surface components recognising adhesive matrix molecule;
XX MSCRAMM; fibronectin; fibronectin-binding protein; antibody; epitope;
XX antibiotic; bacterial infection; antibiotic-resistant strain.
XX XX
XX OS Synthetic.
XX OS Staphylococcus aureus.
XX XX
XX PN WO9831389-A2.
XX PD 23-JUL-1998.
XX PF 21-JAN-1998; 98WO-US001222.
XX PR 21-JAN-1997; 97US-0036139P.
XX PA (TEXA ) UNIV TEXAS A & M SYSTEM.
XX PI Hoeoek M, Patci JM, House-Pompeo KL, Speziale P, Joh D;
XX PI McGavin MJ;
XX XX
XX DR MPI; 1998-413816/35.
XX PT Antibody that binds to fibronectin-binding protein, preventing its
XX binding to fibronectin - used to treat or prevent bacterial infection,
XX especially by Staphylococci and Streptococci.
XX PS Example 8; Page 102; 201pp; English.
XX CC The invention relates to antibodies that bind to a fibronectin-binding
XX domain of a fibronectin-binding protein, and inhibit binding of the
XX protein to fibronectin. Also claimed are: (1) isolated peptides of a

```

CC fibronectin-binding protein that do not bind to fibronectin; (2) fusion
 CC protein containing at least one peptide of a fibronectin-binding protein
 CC linked to a second amino acid sequence; (3) nucleic acid encoding the
 CC isolated peptide of (1). Antibodies, the isolated peptides of (1) and the
 CC nucleic acids are all useful for immunisation (active or passive) and (by
 CC inhibiting binding of bacteria to fibronectin) for preventing or treating
 CC infection in humans or other animals, particularly by staphylococci or
 CC streptococci, e.g. meningitis, otitis media, pneumonia, endocarditis,
 CC mastitis in cattle, abortion in horses and many others. Since the
 CC antibodies block binding of bacteria, they should be effective against
 CC antibiotic-resistant strains, and may replace antibiotic therapy or
 CC increase its effectiveness. Sequences AAm65691-700 represent a series of
 CC synthetic peptides based on the D1 region of *S. aureus* fibronectin
 CC binding protein A. They were synthesised to contain mutations

XX Sequence 38 AA;

Query Match 100.0%; Score 52; DB 2; Length 38;
 Best Local Similarity 100.0%; Pred. No. 0.0069; Mismatches 0; Indels 0; Gaps 0;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GNIVDIDFDS 10
 |||||
 DB 23 GNIVDIDFDS 32

RESULT 13

AAR90937 AAR90937 standard; peptide; 113 AA.

AC AAR90937;

DT 23-SEP-1996 (first entry)

DE D3D4 polypeptide #1.

XX Fibronectin binding protein; Fbp; *S. aureus* J3385; monoclonal antibody;
 KM infection; surgical implant; antiaherent agent; hygiene; adhesion;
 KM extracellular matrix protein; oral pathogen; oral cavity.

XX Staphylococcus aureus.

XX Key Location/Qualifiers

FT Region 1..21 /note= "D1 region fragment"

FT Region 22..59 /note= "D2 region"

FT Region 60..98 /note= "D3 region"

FT Region 99..113 /note= "D4 region"

FT Misc-difference 113 /note= "P113"

XX WO9604381-A1.

XX 15-FEB-1996.

XX 28-JUL-1995; 95WO-EP003040.

XX 05-AUG-1994; 94GB-00015900.

XX (SMIK) SMITHKLINE BEECHAM PLC.

XX Critchley IA, Dodd I, Barnett P, Mcday DL;

XX WPI; 1996-129397/13.

PT Polypeptide(s) derived from *Staphylococcus aureus* fibronectin binding
 PT protein - inhibit binding of bacteria to extracellular matrix proteins,
 PT for combating infection at the site of wounds and surgical implants, and
 PT in oral hygiene.

PS Claim 6; Page 24; 35pp; English.

XX AAR90937-R30942 represent D3D4 polypeptides. These sequences correspond
 CC to fragments of the *Staphylococcus aureus* fibronectin binding protein
 CC (Fbp). This sequence corresponds to residues 18-130 of *S. aureus* J3385
 CC Fbp, and also contains the D2 region, and a portion of the D1 region.
 CC These sequences, and monoclonal antibodies against them can be used to
 CC combat infection at the site of wounds, surgical implants and other in-
 CC dwelling devices (such as catheters), and as antiaherent agents in oral
 CC hygiene. They can also be used in the manufacture of a medicament for the
 CC prevention of adhesion of bacteria to extracellular matrix proteins
 CC present on in-dwelling devices or in wounds, or of oral pathogens to
 CC similar proteins on surfaces in the oral cavity

XX Sequence 113 AA;

Query Match 100.0%; Score 52; DB 2; Length 113;
 Best Local Similarity 100.0%; Pred. No. 0.025; Mismatches 0; Indels 0; Gaps 0;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GNIVDIDFDS 10
 |||||
 DB 7 GNIVDIDFDS 16

RESULT 14

AAR58806 AAR58806 standard; protein; 130 AA.

AC AAR58806;

DT 25-MAR-2003 (revised)

DT 30-MAR-1995 (first entry)

DE Fibronectin binding domain D1-D4 (709-838 (P838T)).

XX Fibronectin binding protein; Fbp; fibronectin binding domain;

KM monoclonal antibody; MAb; adhesion; Gram-positive bacterium; bacteremia;

XX *Escherichia coli*.

XX Staphylococcus aureus.

XX WO9418327-A1.

XX 18-AUG-1994.

XX 04-FEB-1994; 94WO-GB000215.

XX 05-FEB-1993; 93GB-00002289.

XX 20-OCT-1993; 93GB-00021592.

XX (SMIK) SMITHKLINE BEECHAM PLC.

XX Burnham MKR, Chopra I, Critchley IA, Knowles DJC;

XX WPI; 1994-279748/34.

XX Fibronectin binding protein and monoclonal antibodies specific for Fbp -

XX devices or wounds.

XX Disclosure; Page 30; 40pp; English.

XX Polypeptides corresponding to residues G709-T886 plus PPIVPT, G709-

CC P838(P838T) and G709-P838 (AAR58805-07, respectively) of *S. aureus* J3385

CC (NCIMB 40532) Fbp type A fibronectin binding domain D1-D4 region

CC (AAR58808) were expressed in *E. coli* BL21 (DE3) and used to raise MAbs

CC specific for Fbp. (Updated on 25-MAR-2003 to correct PN field.)

XX Sequence 130 AA;

Query Match 100.0%; Score 52; DB 2; Length 130;
 Best Local Similarity 100.0%; Pred. No. 0.025;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GNIVDIDFDS 10
 |||||
 Db 24 GNIVDIDFDS 33

RESULT 15

AAR58807
 ID AAR58807 standard; protein; 130 AA.

AC AAR58807;

DT 25-MAR-2003 (revised)
 DT 30-MAR-1995 (first entry)

DE Fibronectin binding domain D1-D4 (709-838) .

XX Fibronectin binding protein; FBP; fibronectin binding domain;
 KM monoclonal antibody; MAb; adhesion; Gram-positive bacterium; bacteraemia;
 KM Escherichia coli.

OS Staphylococcus aureus.

PN WO9418327-A1.

PD 18-AUG-1994.

PF 04-FEB-1994; 94WO-G8000215.

PR 05-FEB-1993; 93GB-00002289.

PR 20-OCT-1993; 93GB-00021592.

XX (SMK) SMITHKLINE BEECHAM PLC.

XX Burnham MKR, Chopra I, Critchley IA, Knowles DJC;

XX WPI; 1994-279748/34.

XX Fibronectin binding protein and monoclonal antibodies specific for Fbp -
 PT useful to prevent adherence of Gram-positive bacteria to indwelling
 PT devices or wounds.

XX Disclosure; Page 30; 40pp; English.

XX Polypeptides corresponding to residues G709-T886 plus PPIVPT, G709-
 CC P838 (P838T) and G709-P838 (AAR58805-07, respectively) of S. aureus J2385
 CC (NCIMB 40532) Fbp type A fibronectin binding domain D1-D4 region
 CC (AAR58808) were expressed in E. coli BL21(DE4) and used to raise MAbs
 CC specific for Fbp. (Updated on 25-MAR-2003 to correct PN field.)
 XX

SQ Sequence 130 AA;

Query Match 100.0%; Score 52; DB 2; Length 130;
 Best Local Similarity 100.0%; Pred. No. 0.029;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GNIVDIDFDS 10
 |||||
 Db 24 GNIVDIDFDS 33

Search completed: October 25, 2005, 20:58:43
 Job time : 63.2 secs

GenCore version 5.1.6
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OM protein - protein search, using SW model

Run on: October 22, 2005, 05:46:56 (Search time 17.3 Seconds
(without alignments)
43.150 Million cell updates/sec

Title: US-10-731-238-74

Perfect score: 52

Sequence: 1 GNVIDIDPDS 10

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database:

Issued Patents AA:*

- 1: /cgn2_6/prodata/1/iaa/5A_COMB.pep:*
- 2: /cgn2_6/prodata/1/iaa/5B_COMB.pep:*
- 3: /cgn2_6/prodata/1/iaa/5A_COMB.pep:*
- 4: /cgn2_6/prodata/1/iaa/5B_COMB.pep:*
- 5: /cgn2_6/prodata/1/iaa/PCUTUS_COMB.pep:*
- 6: /cgn2_6/prodata/1/iaa/backfillset.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	52	100.0	10	4	US-09-010-317-74
2	52	100.0	14	4	US-09-010-317-60
3	52	100.0	38	1	US-08-234-622A-2
4	52	100.0	38	1	US-08-729-767-3
5	52	100.0	38	4	US-09-010-317-5
6	52	100.0	38	4	US-09-010-317-6
7	52	100.0	38	4	US-09-010-317-35
8	52	100.0	38	4	US-09-010-317-36
9	52	100.0	38	4	US-09-010-317-37
10	52	100.0	38	4	US-09-010-317-38
11	52	100.0	38	4	US-09-010-317-39
12	52	100.0	38	4	US-09-010-317-40
13	52	100.0	38	4	US-09-010-317-41
14	52	100.0	38	4	US-09-010-317-42
15	52	100.0	114	1	US-08-259-000-3
16	52	100.0	130	2	US-08-459-135A-7
17	52	100.0	130	2	US-08-459-135A-8
18	52	100.0	130	3	US-08-495-559-7
19	52	100.0	130	3	US-08-495-559-8
20	52	100.0	139	3	US-08-856-253-8
21	52	100.0	174	2	US-08-459-135A-10
22	52	100.0	174	2	US-08-459-135A-13
23	52	100.0	174	3	US-08-495-559-10
24	52	100.0	174	3	US-08-495-559-13
25	52	100.0	176	2	US-08-495-559-6
26	52	100.0	178	2	US-08-459-135A-12
27	52	100.0	178	3	US-08-495-559-12

28	52	100.0	181	2	US-08-459-135A-6	Sequence 6, Appl1
29	52	100.0	559	4	US-08-956-171E-5251	Sequence 5251, Ap
30	52	100.0	559	4	US-08-781-986A-5251	Sequence 5251, Ap
31	52	100.0	1027	4	US-08-956-171E-5251	Sequence 5251, Ap
32	52	100.0	1027	4	US-08-781-986A-5254	Sequence 5254, Ap
33	51	98.1	14	4	US-09-010-317-103	Sequence 103, Appl
34	51	98.1	36	4	US-09-010-317-58	Sequence 58, Appl
35	51	98.1	36	4	US-09-010-317-59	Sequence 59, Appl
36	51	98.1	36	1	US-08-234-622A-3	Sequence 3, Appl1
37	51	98.1	38	1	US-08-729-767-4	Sequence 4, Appl1
38	51	98.1	38	4	US-09-010-317-7	Sequence 7, Appl1
39	51	98.1	38	4	US-09-010-317-8	Sequence 8, Appl1
40	51	98.1	38	4	US-09-010-317-45	Sequence 45, Appl1
41	51	98.1	38	4	US-09-010-317-46	Sequence 46, Appl1
42	51	98.1	38	4	US-09-010-317-47	Sequence 47, Appl1
43	51	98.1	38	4	US-09-010-317-48	Sequence 48, Appl1
44	46	88.5	38	4	US-09-010-317-43	Sequence 43, Appl1
45	46	88.5	38	4	US-09-010-317-44	Sequence 44, Appl1

ALIGNMENTS

RESULT 1
US-09-010-317-74
Sequence 74, Application US/09010317
Patent No. 6685943
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
APPLICANT: Patti, Joseph M.
APPLICANT: House-Pompeo, Karen L.
APPLICANT: Speziale, Pietro
APPLICANT: John, Danny
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
TITLE OF INVENTION: AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TANK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 74:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-09-010-317-74
Query Match 100.0%; Score 52; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.00048;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GNVIDIDFDS 10
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Db 1 GNVIDIDFDS 10

RESULT 2

US-09-010-317-60
; Sequence 60, Application US/09010317
; Patent No. 6685943
; GENERAL INFORMATION:
; APPLICANT: Hook, Magnus
; APPLICANT: Patti, Joseph M.
; APPLICANT: House-Pompeo, Karen L.
; APPLICANT: Speziale, Pietro
; APPLICANT: Joh, Danny
; APPLICANT: McGavin, Martin J.
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
; TITLE OF INVENTION: AND METHODS OF USE
; NUMBER OF SEQUENCES: 105
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: TX
; COUNTRY: USA
; ZIP: 77210-4433
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/010.317
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/036,139
; FILING DATE: 21-JAN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Hibler, David W.
; REGISTRATION NUMBER: 41, 071
; REFERENCE/DOCKET NUMBER: TANK:189
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 512-418-3000
; TELEFAX: 512-474-7577
; INFORMATION FOR SEQ ID NO: 60:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; US-09-010-317-60

Query Match 100.0%; Score 52; DB 4; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.00071;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GNVIDIDFDS 10
| | | | | | | | | |
Db 3 GNVIDIDFDS 12

RESULT 3

US-08-234-622A-2
; Sequence 2, Application US/08234622A
; Patent No. 5440014
; GENERAL INFORMATION:
; APPLICANT: Hook, Magnus
; APPLICANT: MCGAVIN, Martin
; APPLICANT: RAUCCI, Giuseppe
; TITLE OF INVENTION: A FIBRONECTIN BINDING PEPTIDE

NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Doane, Swecker & Mathis
; STREET: P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/234.622A
; FILING DATE: 28-APR-1994
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: SE 9002617-0
; FILING DATE: 10-AUG-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/SE91/00534
; FILING DATE: 09-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Meuth, Donna M
; REGISTRATION NUMBER: 36, 607
; REFERENCE/DOCKET NUMBER: 012885-044
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 38 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-234-622A-2

Query Match 100.0%; Score 52; DB 1; Length 38;
Best Local Similarity 100.0%; Pred. No. 0.0023;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GNVIDIDFDS 10
| | | | | | | | | |
Db 23 GNVIDIDFDS 32

RESULT 4

US-08-729-767-3
; Sequence 3, Application US/08729767
; Patent No. 5770702
; GENERAL INFORMATION:
; APPLICANT: Hook, Magnus
; APPLICANT: LINDBERG, Martin Kjell
; APPLICANT: SIGNAS, Lars Christer
; APPLICANT: WANDSTROM, Torkel Mikael
; APPLICANT: FROMAN, Gunnar
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN AS WELL AS
; NUMBER OF SEQUENCES: 6
; TITLE OF INVENTION: ITS PREPARATION
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Doane, Swecker & Mathis, L.L.P.
; STREET: P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/729,767
FILING DATE: 07-OCT-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/259,000
FILING DATE: 13-JUN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/007,817
FILING DATE: 22-JAN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/201,028
FILING DATE: 01-JUN-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: SE 8702272-9
FILING DATE: 01-JUN-1987
ATTORNEY/AGENT INFORMATION:
NAME: McGowan, Malcolm K.
REGISTRATION NUMBER: 39,300
REFERENCE/DOCKET NUMBER: 012889-036
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-729-767-3

Query Match 100.0%; Score 52; DB 1; Length 38;
Best Local Similarity 100.0%; Pred. No. 0.0023;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GNVIDIDFDS 10
Db 24 GNVIDIDFDS 33

RESULT 5
US-09-010-317-5
Sequence 5, Application US/09010317
Patent No. 6685943
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
APPLICANT: Patti, Joseph M.
APPLICANT: House-Pompeo, Karen L.
APPLICANT: Speziale, Pietro
APPLICANT: Joh, Danny
APPLICANT: McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
TITLE OF INVENTION: AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESSES:
ADDRESSER: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/036,139

FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TANK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-09-010-317-5

Query Match 100.0%; Score 52; DB 4; Length 38;
Best Local Similarity 100.0%; Pred. No. 0.0023;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GNVIDIDFDS 10
Db 23 GNVIDIDFDS 32

RESULT 6
US-09-010-317-6
Sequence 6, Application US/09010317
Patent No. 6685943
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
APPLICANT: Patti, Joseph M.
APPLICANT: House-Pompeo, Karen L.
APPLICANT: Speziale, Pietro
APPLICANT: Joh, Danny
APPLICANT: McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
TITLE OF INVENTION: AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESSES:
ADDRESSER: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TANK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-09-010-317-6

Query Match 100.0%; Score 52; DB 4; Length 38;
Best Local Similarity 100.0%; Pred. No. 0.0023;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GNVVIDPDS 10
DB 23 GNVVIDPDS 32

RESULT 7

US-09-010-317-35
; Sequence 35, Application US/09010317
; Patent No. 6685943
; GENERAL INFORMATION:
; APPLICANT: Hook, Magnus
; APPLICANT: Patti, Joseph M.
; APPLICANT: House-Pompeo, Karen L.
; APPLICANT: Speziale, Pietro
; APPLICANT: Joh, Danny
; APPLICANT: McGavin, Martin J.
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
; NUMBER OF SEQUENCES: 105
; CLASSIFICATION:
; TITLE OF INVENTION: AND METHODS OF USE
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: TX
; COUNTRY: USA
; ZIP: 77210-4433
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/010,317
; FILING DATE:
; STRANDEDNESS:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/036,139
; FILING DATE: 21-JAN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Hibler, David W.
; REGISTRATION NUMBER: 41,071
; REFERENCE/DOCKET NUMBER: TANK:189
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 512-418-3000
; TELEFAX: 512-474-7577
; INFORMATION FOR SEQ ID NO: 35:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 38 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
US-09-010-317-35

Query Match 100.0%; Score 52; DB 4; Length 38;
Best Local Similarity 100.0%; Pred. No. 0.0023;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GNVVIDPDS 10
DB 23 GNVVIDPDS 32

RESULT 8

US-09-010-317-36
; Sequence 36, Application US/09010317
; Patent No. 6685943
; GENERAL INFORMATION:
; APPLICANT: Hook, Magnus
; APPLICANT: Patti, Joseph M.

; APPLICANT: House-Pompeo, Karen L.

; APPLICANT: Speziale, Pietro

; APPLICANT: Joh, Danny

; APPLICANT: McGavin, Martin J.

; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS

; NUMBER OF SEQUENCES: 105

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Arnold, White & Durkee

; STREET: P.O. Box 4433

; CITY: Houston

; STATE: TX

; COUNTRY: USA

; ZIP: 77210-4433

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; OPERATING SYSTEM: IBM PC compatible

; SOFTWARE: Patentin Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/010,317

; FILING DATE:

; CLASSIFICATION:

; TITLE OF INVENTION: AND METHODS OF USE

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Arnold, White & Durkee

; STREET: P.O. Box 4433

; CITY: Houston

; STATE: TX

; COUNTRY: USA

; ZIP: 77210-4433

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; OPERATING SYSTEM: IBM PC compatible

; SOFTWARE: Patentin Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/010,317

; FILING DATE:

; CLASSIFICATION:

; TITLE OF INVENTION: AND METHODS OF USE

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Arnold, White & Durkee

; STREET: P.O. Box 4433

; CITY: Houston

; STATE: TX

; COUNTRY: USA

; ZIP: 77210-4433

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; OPERATING SYSTEM: IBM PC compatible

; SOFTWARE: Patentin Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/010,317

; FILING DATE:

; CLASSIFICATION:

; TITLE OF INVENTION: AND METHODS OF USE

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Arnold, White & Durkee

; STREET: P.O. Box 4433

; CITY: Houston

; STATE: TX

; COUNTRY: USA

; ZIP: 77210-4433

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAMK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 37:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-09-010-317-37

Query Match 100.0%; Score 52; DB 4; Length 38;
Best Local Similarity 100.0%; Pred. No. 0.0023;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GNVIDIDFDS 10
Db 23 GNVIDIDFDS 32

RESULT 10
US-09-010-317-38
Sequence 38, Application US/09010317
Patent No. 6685943
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
APPLICANT: Patti, Joseph M.
APPLICANT: House-Pompeo, Karen L.
APPLICANT: Speziale, Pietro
APPLICANT: Joh, Danny
APPLICANT: McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
TITLE OF INVENTION: AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAMK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000

TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 38:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-09-010-317-38

Query Match 100.0%; Score 52; DB 4; Length 38;
Best Local Similarity 100.0%; Pred. No. 0.0023;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GNVIDIDFDS 10
Db 23 GNVIDIDFDS 32

RESULT 11
US-09-010-317-39
Sequence 39, Application US/09010317
Patent No. 6685943
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
APPLICANT: Patti, Joseph M.
APPLICANT: House-Pompeo, Karen L.
APPLICANT: Speziale, Pietro
APPLICANT: Joh, Danny
APPLICANT: McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
TITLE OF INVENTION: AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAMK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 39:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-09-010-317-39

Query Match 100.0%; Score 52; DB 4; Length 38;
Best Local Similarity 100.0%; Pred. No. 0.0023;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GNVIDIDFDS 10
Db 23 GNVIDIDFDS 32

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RESULT 12
US-09-010-317-40
; Sequence 40, Application US/09010317
; Patent No. 6685943
; GENERAL INFORMATION:
; APPLICANT: Hook, Magnus
; APPLICANT: Patti, Joseph M.
; APPLICANT: House-Pompeo, Karen L.
; APPLICANT: Speziale, Pietro
; APPLICANT: Joh, Danny
; APPLICANT: McGavin, Martin J.
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
; TITLE OF INVENTION: AND METHODS OF USE
; NUMBER OF SEQUENCES: 105
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: TX
; COUNTRY: USA
; ZIP: 77210-4433
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/010,317
; FILING DATE:
; STRANDEDNESS:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/036,139
; FILING DATE: 21-JAN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Hibler, David W.
; REGISTRATION NUMBER: 41,071
; REFERENCE/DOCKET NUMBER: TANK:189
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 512-418-3000
; TELEFAX: 512-474-7577
; INFORMATION FOR SEQ ID NO: 40:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 38 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
;
US-09-010-317-40

Query Match      100.0%; Score 52; DB 4; Length 38;
Best Local Similarity 100.0%; Pred. No. 0.0023;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GNVIDIDFDS 10
DB      23 GNVIDIDFDS 32

RESULT 13
US-09-010-317-41
; Sequence 41, Application US/09010317
; Patent No. 6685943
; GENERAL INFORMATION:
; APPLICANT: Hook, Magnus
; APPLICANT: Patti, Joseph M.
; APPLICANT: House-Pompeo, Karen L.
; APPLICANT: Speziale, Pietro
; APPLICANT: Ubi, Danny
; APPLICANT: McGavin, Martin J.
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
; TITLE OF INVENTION: AND METHODS OF USE
; NUMBER OF SEQUENCES: 105
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; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: TX
; COUNTRY: USA
; ZIP: 77210-4433
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/010,317
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/036,139
; FILING DATE: 21-JAN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Hibler, David W.
; REGISTRATION NUMBER: 41,071
; REFERENCE/DOCKET NUMBER: TANK:189
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 512-418-3000
; TELEFAX: 512-474-7577
; INFORMATION FOR SEQ ID NO: 41:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 38 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
;
US-09-010-317-41

Query Match      100.0%; Score 52; DB 4; Length 38;
Best Local Similarity 100.0%; Pred. No. 0.0023;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GNVIDIDFDS 10
DB      23 GNVIDIDFDS 32

RESULT 14
US-09-010-317-42
; Sequence 42, Application US/09010317
; Patent No. 6685943
; GENERAL INFORMATION:
; APPLICANT: Hook, Magnus
; APPLICANT: Patti, Joseph M.
; APPLICANT: House-Pompeo, Karen L.
; APPLICANT: Speziale, Pietro
; APPLICANT: Joh, Danny
; APPLICANT: McGavin, Martin J.
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
; TITLE OF INVENTION: AND METHODS OF USE
; NUMBER OF SEQUENCES: 105
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: TX
; COUNTRY: USA
; ZIP: 77210-4433
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/010,317
; FILING DATE:
; CLASSIFICATION:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hübler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TANK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 42:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-09-010-317-42

Query Match 100.0%; Score 52; DB 4; Length 38;
Best Local Similarity 100.0%; Pred. No. 0.0023;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GNTVIDIDFDS 10
DB 23 GNTVIDIDFDS 32

RESULT 15
US-08-259-000-3
Sequence 3, Application US/08259000
Patent No. 5571514
GENERAL INFORMATION:
APPLICANT: HOOK, Magnus
APPLICANT: LINDBERG, Martin Kjell
APPLICANT: SIGMAS, Lars Christer
APPLICANT: MADSTROM, Torkel Mikael
APPLICANT: FROMAN, Gunnar
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN AS WELL AS
TITLE OF INVENTION: ITS PREPARATION
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Burns, Doane, Swecker & Mathis
STREET: P.O. Box 1404
CITY: Alexandria
STATE: Virginia
COUNTRY: United States
ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/259,000
FILING DATE: 13-JUN-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: SE 8702272-9
FILING DATE: 01-JUN-1987
ATTORNEY/AGENT INFORMATION:
NAME: Meuth, Donna M
REGISTRATION NUMBER: 36,607
REFERENCE/DOCKET NUMBER: 012885-062
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 114 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein

US-08-259-000-3

Query Match 100.0%; Score 52; DB 1; Length 114;
Best Local Similarity 100.0%; Pred. No. 0.0085;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GNTVIDIDFDS 10
DB 24 GNTVIDIDFDS 33

Search completed: October 22, 2005, 07:41:42
Job time : 17.35 secs

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OM protein - protein search, using sw model

Run on: October 22, 2005, 12:09:40 ; Search time 57.25 Seconds
(without alignments)
72.924 Million cell updates/sec

Title: US-10-731-238-74

Perfect score: 52

Sequence: 1 GN1VIDPDS 10

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Gapop 10.0, Gapext 0.5

Searched: 1862951 seqs, 417491010 residues

Total number of hits satisfying chosen parameters: 1862951

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

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2: /cgn2_6/prodata/2/pubppa/PCT_NEW_PUB.pep.*
3: /cgn2_6/prodata/2/pubppa/US06_NEW_PUB.pep.*
4: /cgn2_6/prodata/2/pubppa/US06_PUBCOMB.pep.*
5: /cgn2_6/prodata/2/pubppa/US07_NEW_PUB.pep.*
6: /cgn2_6/prodata/2/pubppa/PCTUS_PUBCOMB.pep.*
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22: /cgn2_6/prodata/2/pubppa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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2	52	100.0	14	US-10-731-238-60	Sequence 60, Appl
3	52	100.0	38	US-10-731-238-5	Sequence 5, Appl
4	52	100.0	38	US-10-731-238-6	Sequence 6, Appl
5	52	100.0	38	US-10-731-238-35	Sequence 35, Appl
6	52	100.0	38	US-10-731-238-36	Sequence 36, Appl
7	52	100.0	38	US-10-731-238-37	Sequence 37, Appl
8	52	100.0	38	US-10-731-238-38	Sequence 38, Appl
9	52	100.0	38	US-10-731-238-39	Sequence 39, Appl
10	52	100.0	38	US-10-731-238-40	Sequence 40, Appl
11	52	100.0	38	US-10-731-238-41	Sequence 41, Appl

12	52	100.0	38	US-10-731-238-42	Sequence 42, Appl
13	52	100.0	139	US-09-813-820-8	Sequence 8, Appl
14	52	100.0	388	US-08-901-052-1	Sequence 1, Appl
15	52	100.0	559	US-08-781-986A-5251	Sequence 5251, Ap
16	52	100.0	559	US-10-329-624-5251	Sequence 5251, Ap
17	52	100.0	767	US-09-815-242-5899	Sequence 5899, Ap
18	52	100.0	767	US-09-815-242-13140	Sequence 13140, A
19	52	100.0	940	US-10-470-048B-424	Sequence 424, Ap
20	52	100.0	948	US-10-470-048B-69	Sequence 69, Appl
21	52	100.0	961	US-10-282-122A-43778	Sequence 43778, A
22	52	100.0	978	US-09-815-242-5456	Sequence 5456, Ap
23	52	100.0	1001	US-09-815-242-13686	Sequence 12686, A
24	52	100.0	1018	US-09-815-242-5797	Sequence 5797, Ap
25	52	100.0	1018	US-09-815-242-12838	Sequence 12838, A
26	52	100.0	1018	US-10-470-048B-68	Sequence 68, Appl
27	52	100.0	1027	US-08-781-986A-5254	Sequence 5254, Ap
28	52	100.0	1027	US-10-329-624-5254	Sequence 43827, A
29	52	100.0	1038	US-10-282-122A-43827	Sequence 103, App
30	51	98.1	14	US-10-731-238-103	Sequence 59, Appl
31	51	98.1	36	US-10-731-238-58	Sequence 58, Appl
32	51	98.1	36	US-10-731-238-59	Sequence 59, Appl
33	51	98.1	38	US-10-731-238-7	Sequence 7, Appl
34	51	98.1	38	US-10-731-238-8	Sequence 8, Appl
35	51	98.1	38	US-10-731-238-45	Sequence 45, Appl
36	51	98.1	38	US-10-731-238-46	Sequence 46, Appl
37	51	98.1	38	US-10-731-238-47	Sequence 47, Appl
38	51	98.1	38	US-10-731-238-48	Sequence 48, Appl
39	51	98.1	38	US-10-731-238-49	Sequence 49, Appl
40	45	86.5	38	US-10-731-238-44	Sequence 44, Appl
41	45	86.5	38	US-10-731-238-44	Sequence 49, Appl
42	45	86.5	38	US-10-731-238-45	Sequence 50, Appl
43	42	80.8	39	US-10-731-238-73	Sequence 73, Appl
44	42	80.8	39	US-10-731-238-56	Sequence 56, Appl
45	42	80.8	39	US-10-731-238-57	Sequence 57, Appl

ALIGNMENTS

RESULT 1
US-10-731-238-74
Sequence 74, Application US/10731238
Publication No. US20050123552A1
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
Pacti, Joseph M.
House-Pompeo, Karen L.
Speziale, Pietro
Job, Danny
McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.10
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/731,238
FILING DATE: 10-Dec-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE: 21-Jan-1998
APPLICATION NUMBER: US 60/036,139

FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAMK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 74:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 74:
US-10-731-238-74

Query Match 100.0%; Score 52; DB 18; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0097;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GNVIDDFDS 10
DB 1 GNVIDDFDS 10

RESULT 2
US-10-731-238-60
Sequence 60, Application US/10731238
Publication No. US20050123552A1
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
Patti, Joseph M.
House-Pompeo, Karen L.
Speziale, Pietro
John, Danny
McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/731,238
FILING DATE: 10-Dec-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE: 21-Jan-1998
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAMK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 60:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>

TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 60:
US-10-731-238-60

Query Match 100.0%; Score 52; DB 18; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.014;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GNVIDDFDS 10
DB 3 GNVIDDFDS 12

RESULT 3
US-10-731-238-5
Sequence 5, Application US/10731238
Publication No. US20050123552A1
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
Patti, Joseph M.
House-Pompeo, Karen L.
Speziale, Pietro
John, Danny
McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/731,238
FILING DATE: 10-Dec-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE: 21-Jan-1998
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAMK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-10-731-238-5

Query Match 100.0%; Score 52; DB 18; Length 38;
Best Local Similarity 100.0%; Pred. No. 0.041;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GNVIDDFDS 10
DB 23 GNVIDDFDS 32

RESULT 4
US-10-731-238-6
; Sequence 6, Application US/10731238
; Publication No. US20050123552A1
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
Pattl, Joseph M.
House-Pompeo, Karen L.
Speziale, Pietro
Joh, Danny
McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/731,238
FILING DATE: 10-Dec-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE: 21-Jan-1998
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAMK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-10-731-238-6
Query Match 100.0%; Score 52; DB 18; Length 38;
Best Local Similarity 100.0%; Pred. No. 0.041;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GNTVIDIDFDS 10
Db 23 GNTVIDIDFDS 32
RESULT 5
US-10-731-238-35
; Sequence 35, Application US/10731238
; Publication No. US20050123552A1
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
Pattl, Joseph M.
House-Pompeo, Karen L.
Speziale, Pietro
Joh, Danny
McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
AND METHODS OF USE

NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/731,238
FILING DATE: 10-Dec-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE: 21-Jan-1998
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAMK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 35:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 35:
US-10-731-238-35
Query Match 100.0%; Score 52; DB 18; Length 38;
Best Local Similarity 100.0%; Pred. No. 0.041;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GNTVIDIDFDS 10
Db 23 GNTVIDIDFDS 32
RESULT 6
US-10-731-238-36
; Sequence 36, Application US/10731238
; Publication No. US20050123552A1
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
Pattl, Joseph M.
House-Pompeo, Karen L.
Speziale, Pietro
Joh, Danny
McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30

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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/731,238
FILING DATE: 10-Dec-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE: 21-Jan-1998
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TANK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 36:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 36:
US-10-731-238-36

Query Match      100.0%; Score 52; DB 18; Length 38;
Best Local Similarity 100.0%; Pred. No. 0.041;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0,

QY      1 GNVIDIDFDS 10
        |||||||
Db       23 GNVIDIDFDS 32

RESULT 7
US-10-731-238-37
Sequence 37, Application US/10731238
Publication No. US2005012352A1
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
          Patti, Joseph M.
          House-Pompeo, Karen L.
          Speziale, Pietro
          Joh, Danny
          McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESS: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/731,238
FILING DATE: 10-Dec-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE: 21-Jan-1998
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TANK:189

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Query Match      100.0%; Score 52; DB 18; Length 38;
US-10-731-238-38
SEQUENCE DESCRIPTION: SEQ ID NO: 38;
TOPOLOGY: linear
STRANDEDNESS: <Unknown>
LENGTH: 38 amino acids
TYPE: amino acid
SEQUENCE CHARACTERISTICS:
INFORMATION FOR SEQ ID NO: 37:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
TELECOMMUNICATION INFORMATION:
US-10-731-238-37
SEQUENCE DESCRIPTION: SEQ ID NO: 37;
TOPOLOGY: linear
STRANDEDNESS: <Unknown>
LENGTH: 38 amino acids
TYPE: amino acid
SEQUENCE CHARACTERISTICS:
INFORMATION FOR SEQ ID NO: 37:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
TELECOMMUNICATION INFORMATION:
Query Match      100.0%; Score 52; DB 18; Length 38;
Best Local Similarity 100.0%; Pred. No. 0.041;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY          1 GNTVIDIDPDS 10
              |||||
Db           23 GNTVIDIDPDS 32

RESULT 8
US-10-731-238--38
Sequence 38, Application US/10731238
Publication No. US20050123552A1
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
Patil, Joseph M.
House-Pompeo, Karen L.
Speziale, Pietro
Joh, Danny
McGavin, Martin J
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/731,238
FILING DATE: 10-Dec-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE: 21-Jan-1998
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TMW:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 38:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 38:
US-10-731-238-38

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Best Local Similarity 100.0%; Pred. No. 0.041;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GNTVIDIDFDS 10
|||
Db 23 GNTVIDIDFDS 32

RESULT 9
US-10-731-238-39
; Sequence 39, Application US/10731238
; Publication No. US20050123552A1
; GENERAL INFORMATION:
; APPLICANT: Hook, Magnus
; Patti, Joseph M.
; House-Pompeo, Karen L.
; Speziale, Pietro
; Joh, Danny
; McGavin, Martin J.
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
; AND METHODS OF USE
; NUMBER OF SEQUENCES: 105
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: TX
; COUNTRY: USA
; ZIP: 77210-4433
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/731,238
; FILING DATE: 10-Dec-2003
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/010,317
; FILING DATE: 21-Jan-1998
; APPLICATION NUMBER: US 60/036,139
; FILING DATE: 21-JAN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Hibler, David W.
; REGISTRATION NUMBER: 41,071
; REFERENCE/DOCKET NUMBER: TAMK:189
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 512-418-3000
; TELEFAX: 512-474-7577
; INFORMATION FOR SEQ ID NO: 39:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 38 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 39:
US-10-731-238-39
Query Match 100.0%; Score 52; DB 18; Length 38;
Best Local Similarity 100.0%; Pred. No. 0.041;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GNTVIDIDFDS 10
|||
Db 23 GNTVIDIDFDS 32

RESULT 10
US-10-731-238-40
; Sequence 40, Application US/10731238
; Publication No. US20050123552A1
; GENERAL INFORMATION:
; APPLICANT: Hook, Magnus
; Patti, Joseph M.
; House-Pompeo, Karen L.
; Speziale, Pietro
; Joh, Danny
; McGavin, Martin J.
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
; AND METHODS OF USE
; NUMBER OF SEQUENCES: 105
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: TX
; COUNTRY: USA
; ZIP: 77210-4433
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/731,238
; FILING DATE: 10-Dec-2003
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/010,317
; FILING DATE: 21-Jan-1998
; APPLICATION NUMBER: US 60/036,139
; FILING DATE: 21-JAN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Hibler, David W.
; REGISTRATION NUMBER: 41,071
; REFERENCE/DOCKET NUMBER: TAMK:189
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 512-418-3000
; TELEFAX: 512-474-7577
; INFORMATION FOR SEQ ID NO: 40:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 38 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 40:
US-10-731-238-40
Query Match 100.0%; Score 52; DB 18; Length 38;
Best Local Similarity 100.0%; Pred. No. 0.041;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GNTVIDIDFDS 10
|||
Db 23 GNTVIDIDFDS 32

APPLICANT: Hook, Magnus
Patti, Joseph M.
House-Pompeo, Karen L.
Speziale, Pietro
Joh, Danny
McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/731,238
FILING DATE: 10-Dec-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE: 21-Jan-1998
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAMK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 40:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 40:
US-10-731-238-40
Query Match 100.0%; Score 52; DB 18; Length 38;
Best Local Similarity 100.0%; Pred. No. 0.041;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GNTVIDIDFDS 10
|||
Db 23 GNTVIDIDFDS 32

RESULT 11
US-10-731-238-41
; Sequence 41, Application US/10731238
; Publication No. US20050123552A1
; GENERAL INFORMATION:
; APPLICANT: Hook, Magnus
; Patti, Joseph M.
; House-Pompeo, Karen L.
; Speziale, Pietro
; Joh, Danny
; McGavin, Martin J.
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
; AND METHODS OF USE
; NUMBER OF SEQUENCES: 105
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: TX
; COUNTRY: USA
; ZIP: 77210-4433
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/731,238
; FILING DATE: 10-Dec-2003
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/010,317
; FILING DATE: 21-Jan-1998
; APPLICATION NUMBER: US 60/036,139
; FILING DATE: 21-JAN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Hibler, David W.
; REGISTRATION NUMBER: 41,071
; REFERENCE/DOCKET NUMBER: TAMK:189
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 512-418-3000
; TELEFAX: 512-474-7577
; INFORMATION FOR SEQ ID NO: 41:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 38 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 41:
US-10-731-238-41
Query Match 100.0%; Score 52; DB 18; Length 38;
Best Local Similarity 100.0%; Pred. No. 0.041;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GNTVIDIDFDS 10
|||
Db 23 GNTVIDIDFDS 32

STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Releasee #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/731,238
FILING DATE: 10-Dec-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE: 21-Jan-1998
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-Jan-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TANK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 41:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 41:
US-10-731-238-41

Query Match 100.0%; Score 52; DB 18; Length 38;
Best Local Similarity 100.0%; Pred. No. 0.041;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GNVIDIDFDS 10
DB 23 GNVIDIDFDS 32

RESULT 12
US-10-731-238-42
Sequence 42, Application US/10731238
Publication No. US20050123552A1
GENERAL INFORMATION:
APPLICANT: Hook, Magnus M.
Patel, Joseph M.
House-Pompeo, Karen L.
Speziale, Pietro
Joh, Danny
McGavin, Martin J.
TITLE OF INVENTION: FIBROBLAST BINDING PROTEIN COMPOSITIONS
AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Releasee #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/731,238
FILING DATE: 10-Dec-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/010,317
FILING DATE: 21-Jan-1998
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-Jan-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TANK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 42:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 42:
US-10-731-238-42

Query Match 100.0%; Score 52; DB 18; Length 38;
Best Local Similarity 100.0%; Pred. No. 0.041;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GNVIDIDFDS 10
DB 23 GNVIDIDFDS 32

RESULT 13
US-09-813-820-8
Sequence 8, Application US/09813820
Patent No. US20020102262A1
GENERAL INFORMATION:
APPLICANT: Hook, Magnus M.
Patel, Joseph M.
House-Pompeo, Karen L.
Schanam, Narayana
Symerky, Jindrich
TITLE OF INVENTION: COLLAGEN BINDING PROTEIN COMPOSITIONS
AND METHODS OF USE
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: Texas
COUNTRY: U.S.
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Releasee #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/813,820
FILING DATE: 22-Mar-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/856,253
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Kitchell, Barbara S.
REGISTRATION NUMBER: 33,928
REFERENCE/DOCKET NUMBER: TANK:193
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
TELEFAX: (512) 474-7577
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 139 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>

TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-09-813-820-8

Query Match 100.0%; Score 52; DB 9; Length 139;
Best Local Similarity 100.0%; Pred. No. 0.16;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GNIVDIDFDS 10
DB 38 GNIVDIDFDS 47

RESULT 14
US-08-901-062-1
Sequence 1, Application US/08901062
Publication No. US20020025324A1
GENERAL INFORMATION:
APPLICANT: SEALS, JONATHAN R.
TITLE OF INVENTION: RECOMBINANT BIVALENT BACTERIAL VACCINE
TITLE OF INVENTION: FOR THE PREVENTION OF MASTITIS
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSER: HALE AND DORR LLP
STREET: 60 State Street
CITY: Boston
STATE: MA
COUNTRY: United States Of America
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/901,062
FILING DATE: 25-JUL-1997
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Baker, Hollie L.
REGISTRATION NUMBER: 31,321
REFERENCE/DOCKET NUMBER: 106941.153
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 526-5000
TELEFAX: (617) 526-5000
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 388 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-901-062-1

Query Match 100.0%; Score 52; DB 8; Length 388;
Best Local Similarity 100.0%; Pred. No. 0.49;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GNIVDIDFDS 10
DB 287 GNIVDIDFDS 296

RESULT 15
US-08-781-986A-5251
Sequence 5251, Application US/08781986A
Publication No. US20030054436A1
GENERAL INFORMATION:
APPLICANT: Charles Kunsch
TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
NUMBER OF SEQUENCES: 5255

CORRESPONDENCE ADDRESS:
ADDRESSER: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COUNTRY: USA
ZIP: 20850

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.50 inch, 1.4mb storage

COMPUTER: HP Vectra 486/33

OPERATING SYSTEM: MSDOS version 6.2

SOFTWARE: ASCII Text

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/781,986A

FILING DATE:

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Benson, Bob

REGISTRATION NUMBER: 30,446

REFERENCE/DOCKET NUMBER: PB248PP

TELECOMMUNICATION INFORMATION:

TELEPHONE: (301) 309-8504

TELEFAX: (301) 309-8512

INFORMATION FOR SEQ ID NO: 5251:

SEQUENCE CHARACTERISTICS:

LENGTH: 559 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-781-986A-5251

Query Match 100.0%; Score 52; DB 8; Length 559;
Best Local Similarity 100.0%; Pred. No. 0.72;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GNIVDIDFDS 10
DB 323 GNIVDIDFDS 332

Search completed: October 22, 2005, 12:39:45
Job time : 57.25 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 22, 2005, 06:10:10 ; Search time 11.45 Seconds
(without alignments)
84.032 Million cell updates/sec

Title: US-10-731-238-74
Perfect score: 52
Sequence: 1 GNIVDIDFDS 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Length	DB	ID	Description
1	52	100.0	940	2	S19702	fibronectin-binding
2	52	100.0	961	2	G90053	hypothetical prote
3	52	100.0	1018	2	A32192	fibronectin-binding
4	52	100.0	1038	2	H90053	hypothetical prote
5	38	73.1	471	2	A28568	pneumolysin - Stre
6	38	73.1	471	2	F95224	pneumolysin (impor
7	38	73.1	471	2	A99089	hypothetical prote
8	38	73.1	933	2	T43201	MutS protein homol
9	38	73.1	957	2	E86489	protein T32E20.19
10	38	73.1	1139	2	T20660	hypothetical prote
11	38	73.1	1375	2	T42586	major capsid prote
12	37	71.2	976	2	C71248	hypothetical prote
13	37	71.2	1465	2	A70199	hypothetical prote
14	37	71.2	1650	2	SS1457	dominant autoantig
15	37	71.2	1750	2	G84649	hypothetical prote
16	37	71.2	4660	2	T42737	gp330 protein prec
17	36	69.2	124	2	A84313	glycine decarboxyl
18	36	69.2	226	2	T27843	hypothetical prote
19	36	69.2	237	2	B64502	bifunctional prote
20	36	69.2	268	2	S74772	hypothetical prote
21	36	69.2	478	2	T12818	hypothetical prote
22	36	69.2	687	2	SS1398	hypothetical prote
23	36	69.2	853	2	T07036	lipoygenase (EC 1
24	36	69.2	875	2	C81209	capa protein NMB03
25	36	69.2	880	2	G81786	Neisseria-specific
26	36	69.2	976	2	E75212	oligosaccharyl tra
27	36	69.2	1376	1	VCBBD6	major capsid prote
28	36	69.2	2028	2	T08025	DNA-directed RNA p
29	35	67.3	155	2	H75075	hypothetical prote

30	35	67.3	239	2	G64236	hypothetical prote
31	35	67.3	249	2	E90391	conserved hypothet
32	35	67.3	284	2	E84616	probable BH1 tran
33	35	67.3	287	2	T01758	hypothetical prote
34	35	67.3	308	2	D30315	methyl viologen-re
35	35	67.3	303	1	C30315	coenzyme-M-7-merca
36	35	67.3	315	1	S63990	thioredoxin-disulf
37	35	67.3	539	2	E87676	ATP synthase F1, b
38	35	67.3	662	2	T13900	hypothetical prote
39	35	67.3	675	2	A75627	H+/K+-exchanging A
40	35	67.3	686	2	G87446	potassium-transpor
41	35	67.3	694	2	A13022	potassium-transpor
42	35	67.3	709	2	A70624	H+/K+-exchanging A
43	35	67.3	718	2	A98262	H+/K+-exchanging A
44	35	67.3	986	2	AB2209	two-component sens
45	35	67.3	1014	2	T39743	U4/U6 splicing fac

ALIGNMENTS

RESULT 1
S19702
fibronectin-binding protein B - Staphylococcus aureus
C/Species: Staphylococcus aureus
C/Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #ext_change 09-Jul-2004
R/Accession: S19702
R/Accession: S19702
Euz. J. Biochem. 202, 1041-1048, 1991
A/Title: Two different genes encode fibronectin binding proteins in Staphylococcus aure
A/Reference number: S19702; PMID:92111475; PMID:1837266
A/Accession: S19702
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-940 <JOE>
A/Cross-references: UNIPROT:Q53682; EMBL:X62992; NID:G49040; PIDN:CAA44726.1; PID:G5815
C/Keywords: fibronectin binding

Query Match 100.0%; Score 52; DB 2; Length 940;
Best Local Similarity 100.0%; Pred. No. 0.15;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GNIVDIDFDS 10
DB 704 GNIVDIDFDS 713

RESULT 2

hypothetical protein fmb (imported) - Staphylococcus aureus (strain N315)
C/Species: Staphylococcus aureus
C/Date: 10-May-2001 #sequence_revision 10-May-2001 #ext_change 09-Jul-2004
C. Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
A/Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.
A/Reference number: AB9758; PMID:21311952; PMID:11418146
A/Accession: G90053
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-961 <KUR>
A/Cross-references: UNIPROT:Q99RD3; GB:BA000018; PTD:G13702452; PIDN:BA843593.1; GSPDB:
A/Experimental source: strain N315
C/Genetics:
A/Genes: fmb

Query Match 100.0%; Score 52; DB 2; Length 961;
Best Local Similarity 100.0%; Pred. No. 0.16;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GNIVDIDFDS 10

Db 715 GNIVDIDFDS 724

RESULT 3

A32192

C:Species: Staphylococcus aureus

C>Date: 31-Jul-1989 #sequence_revision 31-Jul-1989 #text_change 16-Feb-1997

C:Accession: A32192

R:Signaee, C.; Raucel, G.; Joansson, K.; Lindgren, P.E.; Anantharamiah, G.M.; Hoecek, W

Proc. Natl. Acad. Sci. U.S.A. 86, 699-703, 1989

A:Title: Nucleotide sequence of the gene for a fibronectin-binding protein from Staphylo

C:Reference number: A32192; PMID:89088998; PMID:2521391

A:Accession: A32192

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-1018 <SIG>

A:Cross-references: GB:J04151

C:Keywords: fibronectin binding

Query Match 100.0%; Score 52; DB 2; Length 1018;
Best Local Similarity 100.0%; Pred. No. 0.17;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GNIVDIDFDS 10
|||:|||||:
Db 768 GNIVDIDFDS 777

RESULT 4

H90053

C:Species: Staphylococcus aureus

C>Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004

C:Accession: H90053

R:Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Ogu

me, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.;

C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.

Lancet 357, 1225-1240, 2001

A:Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.

A:Reference number: A89758; PMID:11418146

A:Accession: H90053

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-1038 <KUR>

A:Cross-references: UNIPROT:Q99RD2; GB:BA000018; PID:G13702453; PIDN:BA843594.1; GSPDB:G

A:Experimental source: strain N315

C:Genetics:

A:Gene: fnb

Query Match 100.0%; Score 52; DB 2; Length 1038;
Best Local Similarity 100.0%; Pred. No. 0.17;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GNIVDIDFDS 10
|||:|||||:
Db 764 GNIVDIDFDS 773

RESULT 5

A28568

C:Species: Streptococcus pneumoniae

C>Date: 19-Nov-1988 #sequence_revision 19-Nov-1988 #text_change 20-Aug-1999

C:Accession: A28568; S12829

R:Walker, J.A.; Allen, R.L.; Palmagne, P.; Johnson, M.K.; Boulnois, G.J.

Infect. Immun. 55, 1184-1189, 1987

A:Title: Molecular cloning, characterization, and complete nucleotide sequence of the ge

A:Reference number: A28568; PMID:87193109; PMID:3552992

A:Accession: A28568

A:Molecule type: DNA

A:Residues: 1-471 <WAL>

R.Mitchell, T.J.; Mendez, F.; Paton, J.C.; Andrew, P.W.; Boulnois, G.J.

Molec. Acids Res. 18, 4010, 1990

A:Title: Comparison of pneumolysin genes and proteins from Streptococcus pneumoniae type

A:Reference number: S12829; PMID:90326546; PMID:2374733

A:Accession: S12829

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-471 <MT>

A:Cross-references: EMBL:X52474; NID:947403; PIDN:CAA36714.1; PID:947404

C:Superfamily: dipeptide transport protein

F.2.471/Product: pneumolysin #status predicted <MAT>

Query Match 73.1%; Score 38; DB 2; Length 471;
Best Local Similarity 70.0%; Pred. No. 29;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 GNIVDIDFDS 10
|||:|||||:
Db 173 GNSLDIDFDS 182

RESULT 6

F95224

C:Species: Streptococcus pneumoniae (strain TIGR4)

C>Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 09-Jul-2004

C:Accession: F95224

R:Retzelin, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Held

on, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapfle,

nson, T.; Hickey, E.K.; Holt, I.E.

Science 293, 498-506, 2001

A:Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison,

A:Title: Complete Genome Sequence of a virulent isolate of Streptococcus pneumoniae.

A:Reference number: A85000; PMID:21357209; PMID:11463916

A:Accession: F95224

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-471 <KUR>

A:Cross-references: UNIPROT:P11990; GB:AE005672; PIDN:AAK75991.1; PID:G14973427; GSPDB:G

A:Experimental source: strain TIGR4

C:Genetics:

A:Gene: SPI923

Query Match 73.1%; Score 38; DB 2; Length 471;
Best Local Similarity 70.0%; Pred. No. 29;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 GNIVDIDFDS 10
|||:|||||:
Db 173 GNSLDIDFDS 182

RESULT 7

A99089

C:Species: Streptococcus pneumoniae (strain R6)

C>Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 09-Jul-2004

C:Accession: A99089

R:Hoskins, J.A.; Alborn Jr., W.; Arnold, J.; Blaszcak, L.; Burgett, S.; Dehoff, B.S.; E

e, R.; LeBlanc, D.J.; Lee, L.N.; Lefkowitz, E.J.; Lu, J.; Matsushima, P.; McAhren, S.; M

Y, P.; Sun, P.M.; Winkler, M.E.

J. Bacteriol. 183, 5709-5717, 2001

A:Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaekunas, S.R.;

A:Title: Genome of the Bacterium Streptococcus pneumoniae Strain R6.

A:Reference number: A97872; PMID:21429245; PMID:11544234

A:Accession: A99089

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-471 <KUR>

A:Cross-references: UNIPROT:P11990; GB:AE007317; PIDN:AAL00542.1; PID:G15459419; GSPDB:G

C:Genetics:

A:Gene: ply

C:Superfamily: dipeptide transport protein

Query Match 73.1%; Score 38; DB 2; Length 471;
Best Local Similarity 70.0%; Pred. No. 29;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 GNVIDIDFDS 10
DB 173 GNLVIDIDFDS 182

RESULT 8

T43201 Muts protein homolog - Caenorhabditis elegans (fragment)

C:Species: Caenorhabditis elegans

C:Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 09-Jul-2004

C:Accession: T43201

R:Minand, N.J.; Panzer, J.A.; Kolodner, R.D.

Genomics 53, 69-80, 1998

A:Title: Cloning and characterization of the human and Caenorhabditis elegans homologs

A:Reference number: Z23333; PMID:99005534; PMID:9787078

A:Accession: T43201

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-933 <MIN>

A:Cross-references: UNIPROT:Q19272; EMBL:AF070070; NID:93831700; PIDN:AACT0065.1; PID:93

C:Genetics:

A:Gene: meh-5

Query Match 73.1%; Score 38; DB 2; Length 933;
Best Local Similarity 60.0%; Pred. No. 62;
Matches 6; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 GNVIDIDFDS 10
DB 275 GNLVIDIDFDS 284

RESULT 9

E86489 Protein T32E20.19 [imported] - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)

C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004

C:Accession: E86489

R:Theologis, A.; Eckert, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, J.

Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;

ansen, N.F.; Hughes, B.; Huizart, L.

Nature 408, 816-820, 2000

A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.

C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luross, J.S.; Maitl, R.; Marziani,

Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shim, P.; Southwick, A.M.; Sun, H.; Tallon,

Ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.; Sun, H.; Tallon,

A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.

A:Reference number: A86141; PMID:21016719; PMID:11130712

A:Accession: E86489

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-957 <STO>

A:Cross-references: UNIPROT:Q9LPA1; GB:AE005172; NID:98778796; PIDN:AAF79804.1; GSPDB:GN

C:Genetics:

A:Gene: T32E20.19

A:Map position: 1

Query Match 73.1%; Score 38; DB 2; Length 957;
Best Local Similarity 66.7%; Pred. No. 64;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 GNVIDIDFDS 9
DB 81 GYVVDVDFD 89

RESULT 10

T20660 Hypothetical protein F09E8.3 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999

C:Accession: T20660

R:Percy, C.

submitted to the EMBL Data Library, May 1996

A:Reference number: Z19307

A:Accession: T20660

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-1139 <WIL>

A:Cross-references: EMBL:Z73896; PIDN:CA98059.1; GSPDB:GN00022; CESP:F09E8.3

A:Experimental source: Clone F09E8

C:Genetics:

A:Gene: CESP:F09E8.3

A:Map position: 4

A:Introns: 52/1; 105/1; 132/1; 198/1; 237/3; 274/2; 444/3; 471/3; 508/3; 533/3; 558/1; 6

Query Match 73.1%; Score 38; DB 2; Length 1139;
Best Local Similarity 60.0%; Pred. No. 78;
Matches 6; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 GNVIDIDFDS 10
DB 275 GNLVIDIDFDS 284

RESULT 11

T42586 Major capsid protein 42 - equine herpesvirus 4 (strain NS80567)

C:Species: equine herpesvirus 4

A:Variety: strain NS80567

C:Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 09-Jul-2004

C:Accession: T42586

R:Telford, E.A.; Watson, M.S.; Perry, J.; Gullinane, A.A.; Davison, A.J.

J. Gen. Virol. 79, 1197-1203, 1998

A:Title: The DNA sequence of equine herpesvirus-4.

A:Reference number: Z22173; PMID:98264497; PMID:9603335

A:Accession: T42586

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-1375 <TEH>

A:Cross-references: UNIPROT:Q39283; EMBL:AF030027; NID:92605950; PIDN:AACT59560.1; PID:9

A:Experimental source: strain NS80567

C:Genetics:

A:Gene: 42

C:Superfamily: varicella-zoster virus major capsid protein

Query Match 73.1%; Score 38; DB 2; Length 1375;
Best Local Similarity 70.0%; Pred. No. 96;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 GNVIDIDFDS 10
DB 446 GNLVIDIDFDS 455

RESULT 12

C71248 Hypothetical protein PH0242 - Pyrococcus horikoshii

C:Species: Pyrococcus horikoshii

C:Date: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 09-Jul-2004

C:Accession: C71248

R:Kawarabayashi, Y.; Sawada, M.; Horikawa, H.; Halkawa, Y.; Hino, Y.; Yamamoto, S.; Seki,

M.; Ohfuku, Y.; Funahashi, T.; Tanaka, T.; Kudo, Y.; Yamazaki, J.; Kushida, N.; Oguchi

DNA Res. 5, 55-76, 1998

A:Title: Complete sequence and gene organization of the genome of a hyper-thermophilic

A:Reference number: A71000; PMID:98344137; PMID:9679194

A:Accession: C71248

A:Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-976 <KAW>
 A:Cross-references: UNIPROT:Q74088; GB:AP000001; NID:g3236128; PIDN:BA29314.1; PID:g325
 A:Experimental source: strain OT3
 A>Note: This accession replaces an interim accession for a sequence replaced by GenBank
 C:Genetics: PH0242
 A:Gene: PH0242

Query Match 71.2% Score 37; DB 2; Length 976;
 Best Local Similarity 60.0%; Pred. No. 1e+02;
 Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GNVIDIDPDS 10
 Db 552 GNISEVDPEFS 561

RESULT 13
 A:0199
 hypochlorite protein BB0794 - Lyme disease spirochete
 C:Species: Borrelia burgdorferi (Lyme disease spirochete)
 C>Date: 13-Feb-1998 #sequence_revision 13-Feb-1998 #text_change 09-Jul-2004
 C:Accession: A70199
 R:Fraser, C.M.; Caajens, S.; Huang, W.M.; Sutton, G.G.; Clayton, R.; Lathigra, R.; White
 son, D.; Peterson, J.; Kexlavage, A.R.; Quackenbush, J.; Salzberg, S.; Hanson, M.; Vugt,
 ; Bowman, C.; Garland, S.; Fujii, C.; Cotton, M.D.; Horst, K.; Roberts, K.; Hatch, B.
 Nature 390, 580-586, 1997
 A:Authors: Smith, H.O.; Venter, J.C.
 A>Title: Genomic sequence of a Lyme disease spirochete, Borrelia burgdorferi.
 A:Reference number: A70199; MUID:98065943; PMID:9403685
 A:Accession: A70199
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-1465 <KLB>
 A:Cross-references: UNIPROT:Q51734; GB:AE001178; GB:AE000783; NID:g2668731; PIDN:AAC6714
 A:Experimental source: strain B31

Query Match 71.2% Score 37; DB 2; Length 1465;
 Best Local Similarity 70.0%; Pred. No. 1.6e+02;
 Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GNVIDIDPDS 10
 Db 962 GNVVDIKFDS 971

RESULT 14
 S53457
 dominant autoantigen gp 330 - rat (fragment)
 C:Species: Rattus norvegicus (Norway rat)
 C>Date: 01-Aug-1995 #sequence_revision 01-Sep-1995 #text_change 18-Aug-2000
 C:Accession: S53457
 R:Jokhadde, G.G.; Oleinikov, A.V.; Kanala, J.J.; Makker, S.P.
 Biochem. J. 305, 711-713, 1995
 A>Title: Different molecular forms of rat kidney gp330, the dominant autoantigen of acti
 A:Reference number: S53457; MUID:95151000; PMID:7848267
 A:Accession: S53457
 A:Status: preliminary; nucleic acid sequence not shown
 A:Molecule type: mRNA
 A:Residues: 1-1650 <JOK>
 C:Superfamily: alpha-2-macroglobulin receptor; EGF homology; LDL receptor ligand-binding
 F:29-65/Domain: LDL receptor ligand-binding repeat homology <LDL1>
 F:72-106/Domain: LDL receptor ligand-binding repeat homology <LDL2>
 F:111-147/Domain: EGF homology <EG1>
 F:153-188/Domain: EGF homology <EG2>
 F:196-235/Domain: LDL receptor WYTD-containing repeat homology <YW01>
 F:236-278/Domain: LDL receptor WYTD-containing repeat homology <YW02>
 F:279-329/Domain: LDL receptor WYTD-containing repeat homology <YW03>
 F:330-373/Domain: LDL receptor WYTD-containing repeat homology <YW04>
 F:374-414/Domain: LDL receptor WYTD-containing repeat homology <YW05>
 F:415-457/Domain: LDL receptor WYTD-containing repeat homology <YW06>
 F:466-505/Domain: EGF homology <EG3>
 F:509-545/Domain: LDL receptor ligand-binding repeat homology <LDL2>
 F:550-586/Domain: LDL receptor ligand-binding repeat homology <LDL4>

F:595-631/Domain: LDL receptor ligand-binding repeat homology <LDL3>
 F:636-672/Domain: LDL receptor ligand-binding repeat homology <LDL4>
 F:679-715/Domain: LDL receptor ligand-binding repeat homology <LDL5>
 F:720-755/Domain: LDL receptor ligand-binding repeat homology <LDL6>
 F:760-794/Domain: LDL receptor ligand-binding repeat homology <LDL7>
 F:799-833/Domain: LDL receptor ligand-binding repeat homology <LDL8>
 F:843-879/Domain: LDL receptor ligand-binding repeat homology <LDL9>
 F:884-921/Domain: LDL receptor ligand-binding repeat homology <LDL10>
 F:929-963/Domain: LDL receptor ligand-binding repeat homology <LDL11>
 F:971-1006/Domain: EGF homology <EG4>
 F:1012-1048/Domain: EGF homology <EG5>
 F:1055-1099/Domain: LDL receptor WYTD-containing repeat homology #status atypical <YW07>
 F:1100-1154/Domain: LDL receptor WYTD-containing repeat homology #status atypical <YW08>
 F:1155-1188/Domain: LDL receptor WYTD-containing repeat homology #status atypical <YW09>
 F:1189-1232/Domain: LDL receptor WYTD-containing repeat homology <YW10>
 F:1234-1273/Domain: LDL receptor WYTD-containing repeat homology <YW11>
 F:1274-1316/Domain: LDL receptor WYTD-containing repeat homology <YW12>
 F:1326-1359/Domain: EGF homology <EG6>

Query Match 71.2% Score 37; DB 2; Length 1650;
 Best Local Similarity 66.7%; Pred. No. 1.8e+02;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GNVIDIDPD 9
 Db 224 GNVVALDPD 232

RESULT 15
 G84649
 hypochlorite protein At2g25550 (imported) - Arabidopsis thaliana
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C>Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
 C:Accession: G84649
 R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Beilto, M.I.; Town, C.D.; Fujii, C.Y.;
 M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanKen, S.E.; Umayam, L.; Tallon, L.;
 euss, D.; Nielsen, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.
 Nature 402, 761-768, 1999
 A>Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
 A:Reference number: A84420; MUID:20083487; PMID:10617157
 A:Accession: G84649
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-1750 <STO>
 A:Cross-references: UNIPROT:Q9SKJ4; GB:AE002093; NID:g4432866; PIDN:AAD20714.1; GSPDB:GN
 A:Gene: At2g25550
 A:Map position: 2

Query Match 71.2% Score 37; DB 2; Length 1750;
 Best Local Similarity 55.6%; Pred. No. 1.9e+02;
 Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GNVIDIDPD 9
 Db 148 GNVADVPD 156

Search completed: October 22, 2005, 08:04:30
 Job time : 13.45 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 22, 2005, 06:06:36 ; Search time 55.85 Seconds
(without alignments)
91.688 Million cell updates/sec

Title: US-10-731-238-74
Perfect score: 52
Sequence: 1 GNIVDIDPDS 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues
Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	52	100.0	152	2	Q9AEP9
2	52	100.0	940	2	Q53682
3	52	100.0	943	2	Q8NUT8
4	52	100.0	957	2	Q6G6H4
5	52	100.0	961	2	Q99RD3
6	52	100.0	961	2	Q7A3U8
7	52	100.0	1015	2	Q8NTU7
8	52	100.0	1015	2	Q6G6H3
9	52	100.0	1018	1	FNBA STRAU
10	52	100.0	1038	2	Q99RD2
11	52	100.0	1038	2	Q7A3U7
12	51	98.1	965	2	Q6GDU5
13	43	82.7	402	2	Q83629
14	42	80.8	467	1	ATPB WOLSU
15	40	76.9	105	1	CYAY CHRVO
16	40	76.9	287	2	Q82QG3
17	39	75.0	259	2	Q63SU6
18	39	75.0	915	2	Q6PN91
19	38	73.1	201	2	O54301
20	38	73.1	266	2	Q62A58
21	38	73.1	266	2	Q63NV1
22	38	73.1	470	1	TACY STRPN
23	38	73.1	471	2	Q7ZAK5
24	38	73.1	605	2	Q7RGV2
25	38	73.1	618	2	Q61T90
26	38	73.1	874	2	Q861Z1
27	38	73.1	957	2	Q91PA1
28	38	73.1	1115	2	Q9HGE0
29	38	73.1	1369	1	MSHS CAEEL
30	38	73.1	1375	2	Q39283
31	37	71.2	142	2	Q62GR8

32	37	71.2	142	2	Q63Q18	Q63q18 burkholderi
33	37	71.2	156	2	Q8U280	Q8u280 pyrococcus
34	37	71.2	314	2	Q6BYV5	Q6byv5 debaryomyce
35	37	71.2	346	2	Q6TNR3	Q6tnr3 brachydanio
36	37	71.2	346	2	Q6BDH7	Q6bdh7 brachydanio
37	37	71.2	347	2	Q6BHC3	Q6bhc3 debaryomyce
38	37	71.2	421	2	Q8R9F6	Q8r9f6 thermocanaer
39	37	71.2	461	2	Q8ERD5	Q8edk5 shewanella
40	37	71.2	749	2	Q7S2Q5	Q7s2q5 neurospora
41	37	71.2	782	2	Q6C0U1	Q6c0u1 yarrowia 11
42	37	71.2	864	2	Q6YWA4	Q6ywa4 oryza sativ
43	37	71.2	892	2	Q7ME87	Q7me87 vibrio vuln
44	37	71.2	892	2	Q8D783	Q8d783 vibrio vuln
45	37	71.2	967	2	Q8U4D2	Q8u4d2 pyrococcus

ALIGNMENTS

```
RESULT 1
Q9AEP9; PRELIMINARY; PRT; 152 AA.
AC Q9AEP9;
DT 01-JUN-2001 (Tremblrel. 17, Created)
DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE Fibronectin-binding protein (Fragment).
GN Name=fnb;
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1280;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CMRSA-1;
RX MEDLINE=21246681; PubMed=11349044;
RX DOI=10.1128/IAI.69.6.3791-3799.2001;
RA Rice K., Huesca M., Vaz D., McGavin M.J.;
RT "Variance in fibronectin binding and fnb locus polymorphisms in
RT Staphylococcus aureus: identification of antigenic variation in a
RT fibronectin binding protein adhesin of the epidemic CMRSA-1 strain of
RT methicillin-resistant S. aureus."
RL Infect. Immun. 69:3791-3799(2001).
DR EMBL: AY029184; AK31588.1; -.
FT NON_TER
FT 152
SQ SEQUENCE 152 AA; 17193 MW; CFA3913C2B11C025 CRC64;

Query Match 100.0%; Score 52; DB 2; Length 152;
Best Local Similarity 100.0%; Pred. No. 0.17;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GNIVDIDPDS 10
Db 23 GNIVDIDPDS 32

RESULT 2
Q53682; PRELIMINARY; PRT; 940 AA.
AC Q53682;
DT 01-NOV-1996 (Tremblrel. 01, Created)
DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)
DE Fibronectin binding protein B.
GN Name=fnb;
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1280;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=8325-4;
RX MEDLINE=92111475; PubMed=1837266;
RX Jonsson K., Sigmas C., Muller H.P., Lindberg M.;
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RT "Two different genes encode fibronectin binding proteins in
RT Staphylococcus aureus. The complete nucleotide sequence and
RT characterization of the second gene."
RL Eur. J. Biochem. 202;1041-1048(1991).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC an amide bond (By similarity).
DR EMBL: X62992; CAA4726.1; -.
DR PIR: S19702; S19702.
DR HSSP: Q53653; 1N67.
DR GO: GO:0009986; C:cell surface; IEA.
DR GO: GO:0005618; C:cell wall; IEA.
DR GO: GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO: GO:0016020; C:membrane; IEA.
DR GO: GO:0007155; P:cell adhesion; IEA.
DR InterPro: IPR008966; Adhes_bact.
DR InterPro: IPR004237; Fn_bind.
DR InterPro: IPR005877; Gpos_YsIRK.
DR Pfam: PF02986; Fn_bind; 2.
DR Pfam: PF04650; YsIRK_signal; 1.
DR TIGRFAMs: TIGR01167; LpxTG_anchor; 1.
DR TIGRFAMs: TIGR01168; YsIRK_signal; 1.
DR PROSITE: PS50847; GRAM_POS_ANCHORING; 1.
KW Cell wall; Peptidoglycan-anchor.
SQ SEQUENCE 940 AA; 103555 MW; E35FBBCA907AE345 CRC64;

Query Match 100.0%; Score 52; DB 2; Length 940;
Best Local Similarity 100.0%; Pred. No. 1.1;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GNIVDIDPDS 10
Db 704 GNIVDIDPDS 713

RESULT 3
Q8NU8 PRELIMINARY; PRT; 943 AA.
ID Q8NU8
AC Q8NU8;
DT 01-OCT-2002 (TRENBLrel. 22, Created)
DT 01-OCT-2002 (TRENBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
DE Pnb protein.
GN Name=fnb; OrderedlocusNames=MM2420;
OS Staphylococcus aureus (strain MM2).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=196620;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MM2.
RX MEDLINE=22040717; PubMed=12044378; DOI=10.1016/S0140-6736(02)08713-5;
RA Baba T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Oguchi A.,
RA Nagai Y., Iwama N., Asano K., Naimi T., Kuroda H., Cui L.,
RA Yamamoto K., Hiramatsu K.;
RT "Genome and virulence determinants of high virulence community-
RT acquired MRSA."
RL Lancet 359;1819-1827(2002).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC an amide bond (By similarity).
DR EMBL: AP004830; BAB96285.1; -.
DR HSSP: Q53653; 1N67.
DR GO: GO:0009986; C:cell surface; IEA.
DR GO: GO:0005618; C:cell wall; IEA.
DR GO: GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO: GO:0016020; C:membrane; IEA.
DR GO: GO:0007155; P:cell adhesion; IEA.
DR InterPro: IPR008966; Adhes_bact.
DR InterPro: IPR004237; Fn_bind.
DR InterPro: IPR005877; Gpos_YsIRK.
DR Pfam: PF02986; Fn_bind; 1.
DR Pfam: PF00746; Gram_pos_anchor; 1.

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DR Pfam: PF04650; YsIRK_signal; 1.
DR TIGRFAMs: TIGR01167; LpxTG_anchor; 1.
DR TIGRFAMs: TIGR01168; YsIRK_signal; 1.
DR PROSITE: PS50847; GRAM_POS_ANCHORING; 1.
KW Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ SEQUENCE 943 AA; 104537 MW; DA8A5F3194E1B6A CRC64;

Query Match 100.0%; Score 52; DB 2; Length 943;
Best Local Similarity 100.0%; Pred. No. 1.1;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GNIVDIDPDS 10
Db 711 GNIVDIDPDS 720

RESULT 4
Q6G6H4 PRELIMINARY; PRT; 957 AA.
ID Q6G6H4
AC Q6G6H4;
DT 05-JUL-2004 (TRENBLrel. 27, Created)
DT 05-JUL-2004 (TRENBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TRENBLrel. 27, Last annotation update)
DE Fibronectin-binding protein.
GN Name=fnb; OrderedlocusNames=SAS2387;
OS Staphylococcus aureus (strain MSSA476).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=282459;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=15213324; DOI=10.1073/pnas.0402521101;
RA Holden M.T.G., Fell E.J., Lindsay J.A., Peacock S.J., Day N.P.J.,
RA Enright M.C., Foster T.J., Moore C.E., Hurst L., Atkin R., Barron A.,
RA Bacon N., Bentley S.D., Chillingworth C., Chillingworth T.,
RA Churcher C., Clark L., Cotton C., Cronin A., Doggett U., Dowd L.,
RA Felwell T., Leonard N., Line A., Mayes R., Moule S., Jagsle K.,
RA James K.D., Lennard N., Line A., Mayes R., Moule S., Jagsle K.,
RA Ormond D., Quail M.A., Rabinowitch E., Rutherford K.M., Sanders M.,
RA Sharp S., Simmonds M., Stevens K., Whitehead S., Barrett B.G.,
RA Spratt B.G., Parkhill J.;
RT "Complete genomes of two clinical Staphylococcus aureus strains:
RT evidence for the rapid evolution of virulence and drug resistance."
RL Proc. Natl. Acad. Sci. U.S.A. 101:9786-9791(2004).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC an amide bond (By similarity).
DR EMBL: BX571857; CAG44201.1; -.
DR GO: GO:0009986; C:cell surface; IEA.
DR GO: GO:0005618; C:cell wall; IEA.
DR GO: GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO: GO:0016020; C:membrane; IEA.
DR GO: GO:0007155; P:cell adhesion; IEA.
DR InterPro: IPR008966; Adhes_bact.
DR InterPro: IPR004237; Fn_bind.
DR InterPro: IPR005877; Gpos_YsIRK.
DR InterPro: IPR001899; Gram_pos_anchor.
DR Pfam: PF02986; Fn_bind; 1.
DR Pfam: PF00746; Gram_pos_anchor; 1.
DR TIGRFAMs: TIGR01167; LpxTG_anchor; 1.
DR TIGRFAMs: TIGR01168; YsIRK_signal; 1.
DR PROSITE: PS50847; GRAM_POS_ANCHORING; 1.
KW Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ SEQUENCE 957 AA; 105980 MW; 28F8BA7FFDF3EAF CRC64;

Query Match 100.0%; Score 52; DB 2; Length 957;
Best Local Similarity 100.0%; Pred. No. 1.2;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GNIVDIDPDS 10
Db 711 GNIVDIDPDS 720

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RESULT 5
099RD3 PRELIMINARY; PRT; 961 AA.
ID 099RD3;
AC 099RD3;
DT 01-JUN-2001 (TReMBLrel. 17, Created)
DT 01-JUN-2001 (TReMBLrel. 17, Last sequence update)
DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)
DE Name=fndb; OrderedlocusNames=SAV2502;
GN Staphylococcus aureus (strain Mu50 / ATCC 700699).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxId=158878;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MU50 / ATCC 700699;
RX MEDLINE=21311952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2;
RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Iino J.-O., Ito T.,
RA Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,
RA Mizutani-Ul Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
RA Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
RA Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
RA Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
RT "Whole genome sequencing of methicillin-resistant Staphylococcus
RT aureus."
RT Lancet 357:1225-1240(2001).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC an amide bond (By similarity).
DR EMBL: AP003137; BAB593.1; -.
DR PIR: G90053; G90053.
DR HSSP: Q53653; IN67.
DR DR GO: 0009986; C:cell surface; IEA.
DR GO: 0005618; C:cell wall; IEA.
DR GO: 0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO: 0016020; C:membrane; IEA.
DR GO: 0007155; P:cell adhesion; IEA.
DR InterPro: IPR008966; Adhes_bact.
DR InterPro: IPR004237; Fn_bind.
DR InterPro: IPR005877; Gpos_YsIRK.
DR InterPro: IPR001899; Gram_pos_anchor.
DR Pfam: PF02986; Fn_bind; 1.
DR Pfam: PF00746; Gram_pos_anchor; 1.
DR Pfam: PF04650; YsIRK_signal; 1.
DR TIGRfams: TIGR01167; LpxTG_anchor; 1.
DR TIGRfams: TIGR01168; YsIRK_signal; 1.
DR PROSITE: PS50847; GRAM_POS_ANCHORING; 1.
KW Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ SEQUENCE 961 AA; 106010 MW; 364940F884EA4101 CRC64;

Query Match 100.0%; Score 52; DB 2; Length 961;
Best Local Similarity 100.0%; Pred. No. 1.2;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GNIVDIDFDS 10
Db 715 GNIVDIDFDS 724

RESULT 6
07A3J8 PRELIMINARY; PRT; 961 AA.
ID 07A3J8;
AC 07A3J8;
DT 05-JUL-2004 (TReMBLrel. 27, Created)
DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TReMBLrel. 27, Last annotation update)
DE Fndb protein.
GN Name=fndb; OrderedlocusNames=SA2290;
OC Staphylococcus aureus (strain N315).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxId=158879;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21311952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2;

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RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Iino J.-O., Ito T.,
RA Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,
RA Mizutani-Ul Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
RA Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
RA Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
RA Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
RT "Whole genome sequencing of methicillin-resistant Staphylococcus
RT aureus."
RT Lancet 357:1225-1240(2001).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC an amide bond (By similarity).
DR EMBL: AP003137; BAB4593.1; -.
DR GO: 0009986; C:cell surface; IEA.
DR GO: 0005618; C:cell wall; IEA.
DR GO: 0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO: 0016020; C:membrane; IEA.
DR GO: 0007155; P:cell adhesion; IEA.
DR InterPro: IPR008966; Adhes_bact.
DR InterPro: IPR004237; Fn_bind.
DR InterPro: IPR005877; Gpos_YsIRK.
DR InterPro: IPR001899; Gram_pos_anchor.
DR Pfam: PF02986; Fn_bind; 1.
DR Pfam: PF00746; Gram_pos_anchor; 1.
DR Pfam: PF04650; YsIRK_signal; 1.
DR TIGRfams: TIGR01167; LpxTG_anchor; 1.
DR TIGRfams: TIGR01168; YsIRK_signal; 1.
DR PROSITE: PS50847; GRAM_POS_ANCHORING; 1.
KW Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ SEQUENCE 961 AA; 106010 MW; 364940F884EA4101 CRC64;

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Query Match 100.0%; Score 52; DB 2; Length 961;
Best Local Similarity 100.0%; Pred. No. 1.2;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GNIVDIDFDS 10
Db 715 GNIVDIDFDS 724

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RESULT 7
08NUU7 PRELIMINARY; PRT; 1015 AA.
ID 08NUU7;
AC 08NUU7;
DT 01-OCT-2002 (TReMBLrel. 22, Created)
DT 01-OCT-2002 (TReMBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE Fndb protein.
GN Name=fndb; OrderedlocusNames=MW2421;
OC Staphylococcus aureus (strain MW2).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxId=196620;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MW2;
RX MEDLINE=22040717; PubMed=12044378; DOI=10.1016/S0140-6736(02)08713-5;
RA Baba T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Oguchi A.,
RA Nagai Y., Iwama N., Amano K., Naimi T., Kuroda H., Cui L.,
RA Yamamoto K., Hiramatsu K.;
RT "Genome and virulence determinants of high virulence community-
RT acquired MRSA."
RT Lancet 359:1819-1827(2002).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC an amide bond (By similarity).
DR EMBL: AP004830; BAB96286.1; -.
DR GO: 0009986; C:cell surface; IEA.
DR GO: 0005618; C:cell wall; IEA.
DR GO: 0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO: 0016020; C:membrane; IEA.
DR GO: 0007155; P:cell adhesion; IEA.
DR InterPro: IPR008966; Adhes_bact.
DR InterPro: IPR004237; Fn_bind.
DR InterPro: IPR005877; Gpos_YsIRK.

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DR InterPro; IPR001899; Gram_pos_anchor.
DR Pfam; PF02986; Fn_bind; 1.
DR Pfam; PF00746; Gram_pos_anchor; 1.
DR Pfam; PF04650; YSIRK_signal; 1.
DR TIGRFAMs; TIGR01167; LpXTG_anchor; 1.
DR TIGRFAMs; TIGR01168; YSIRK_signal; 1.
DR PROSITE; PS50847; GRAM_POS_ANCHORING; 1.
DR Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ SEQUENCE 1015 AA; 111145 MW; D0F9281BB64D44D2 CRC64;

Query Match 100.0%; Score 52; DB 2; Length 1015;
Best Local Similarity 100.0%; Pred. No. 1.2;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GNVIDIDFDS 10
Db 769 GNVIDIDFDS 778

RESULT 8
O6G6H3 PRELIMINARY; PRT; 1015 AA.
ID O6G6H3;
AC O6G6H3;
DT 05-JUL-2004 (TRENBLrel. 27, Created)
DT 05-JUL-2004 (TRENBLrel. 27, Last sequence update)
DE Fibronectin-binding protein.
GN OrderedLocustNames=SA82388;
OS Staphylococcus aureus (strain MSSA476).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxId=282459;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=15213324; DOI=10.1073/pnas.0402521101;
RA Holden M.T.G., Fell E.J., Lindsey J.A., Peacock S.J., Day N.P.J.,
RA Enright M.C., Foster T.J., Moore C.E., Hurst L., Atkin R., Barron A.,
RA Baeson N., Bentley S.D., Chillingworth C., Chillingworth T.,
RA Churcher C., Clark L., Cotton C., Cronin A., Doggett V., Dowd L.,
RA Fellwell T., Harris Z., Harris B., Haubert H., Holroyd S., Jagels K.,
RA James K.D., Leonard N., Line A., Mayes R., Moule S., Mungall K.,
RA Ormond D., Quail M.A., Rabinowitch E., Rutherford K.M., Sanders M.,
RA Sharp S., Simmonds M., Stevens K., Whitehead S., Barrett B.G.,
RA Spratt B.G., Parkhill J.;
RT "Complete genomes of two clinical Staphylococcus aureus strains:
RT evidence for the rapid evolution of virulence and drug resistance.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:9786-9791(2004).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC an amide bond (By similarity).
DR EMBL; BX571857; CAG44202.1; -;
DR GO; GO:000986; C:cell surface; IEA.
DR GO; GO:0005618; C:cell wall; IEA.
DR GO; GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0007155; P:cell adhesion; IEA.
DR InterPro; IPR008966; Adhes_bact.
DR InterPro; IPR004237; Fn_bind.
DR InterPro; IPR005877; Gpos_YSIRK.
DR InterPro; IPR001899; Gram_pos_anchor.
DR Pfam; PF02986; Fn_bind; 1.
DR Pfam; PF00746; Gram_pos_anchor; 1.
DR Pfam; PF04650; YSIRK_signal; 1.
DR TIGRFAMs; TIGR01167; LpXTG_anchor; 1.
DR TIGRFAMs; TIGR01168; YSIRK_signal; 1.
DR PROSITE; PS50847; GRAM_POS_ANCHORING; 1.
DR Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ SEQUENCE 1015 AA; 111145 MW; D0F9281BB64D44D2 CRC64;

Query Match 100.0%; Score 52; DB 2; Length 1015;
Best Local Similarity 100.0%; Pred. No. 1.2;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GNVIDIDFDS 10
Db 769 GNVIDIDFDS 778

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Db 769 GNVIDIDFDS 778

RESULT 9
FNBA STAAU STANDARD; PRT; 1018 AA.
ID FNBA STAAU STANDARD; PRT; 1018 AA.
AC P14738;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Fibronectin-binding protein precursor (FNBP).
GN Name=fnbp;
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxId=1280;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NCCTC 8325-4;
RX MEDLINE=89098998; PubMed=2521391;
RA Signaes C., Raucchi G., Joensson K., Lindgren P.-E.,
RA Anantharamaiah G.M., Hoeoek M., Lindberg M.;
RT "Nucleotide sequence of the gene for a fibronectin-binding protein
RT from Staphylococcus aureus: use of this peptide sequence in the
RT synthesis of biologically active peptides.";
RL Proc. Natl. Acad. Sci. U.S.A. 86:699-703(1989).
CC -1- FUNCTION: The ability of bacteria to bind fibronectin has been
CC proposed as a virulence factor enabling bacteria to colonize wound
CC tissues and blood clots. Binding of plasma fibronectin to the
CC bacterial surface might block adhesion receptors on S.aureus, thus
CC representing an important defense mechanism against tissue
CC invasion.
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC an amide bond (Potential).
CC CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by, and for commercial/
CC entities requires a license agreement (see http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; J04151; AAA26632.1; -;
DR InterPro; IPR004237; Fn_bind.
DR InterPro; IPR005877; Gpos_YSIRK.
DR InterPro; IPR001899; Gram_pos_anchor.
DR Pfam; PF02986; Fn_bind; 1.
DR Pfam; PF00746; Gram_pos_anchor; 1.
DR Pfam; PF04650; YSIRK_signal; 1.
DR TIGRFAMs; TIGR01167; LpXTG_anchor; 1.
DR TIGRFAMs; TIGR01168; YSIRK_signal; 1.
DR PROSITE; PS50847; GRAM_POS_ANCHORING; 1.
DR Cell adhesion; Cell wall; Peptidoglycan-anchor; Repeat; Signal;
KW Virulence.
FT SIGNAL 1 36
FT CHAIN 37 985
FT PROPE 986 1018
FT REPEAT 545 574
FT REPEAT 575 604
FT DOMAIN 745 878
FT REPEAT 745 782
FT REPEAT 783 820
FT REPEAT 821 859
FT REPEAT 860 878
FT DOMAIN 879 948
FT REPEAT 879 892
FT REPEAT 893 906
FT REPEAT 907 920
FT REPEAT 921 934
FT REPEAT 935 948
FT SITE 982 986
FT MOD_RES 985 985

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FT      theonine (Potential).
SQ      SEQUENCE      1018 AA; 111780 MW; 58175E020B81F1F CRC64;
Query Match      100.0%; Score 52; DB 1; Length 1018;
Best Local Similarity 100.0%; Pred. No. 1.2;
Matches      10; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

QY      1 GNVIDIDFDS 10
DB      768 GNVIDIDFDS 777

RESULT 10
Q99RD2      PRELIMINARY; PRT; 1038 AA.
ID          099RD2;
AC          099RD2;
DT          01-JUN-2001 (TrEMBLrel. 17, Created)
DT          01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DE          01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE          Fibronectin-binding protein homolog.
GN          Name=fnb; OrderedlocusNames=SAV2503;
OS          Staphylococcus aureus (strain Mu50 / ATCC 700699).
OC          Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX          NCBI_TaxID=158878;
RN          [1]
RP          SEQUENCE FROM N.A.
RC          MEDLINE=21311952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2;
RX          MEDLINE=21311952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2;
RA          Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
RA          Cui L., Oguchi A., Aoki K.-I., Nagai Y., Iian J.-Q., Ito T.,
RA          Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,
RA          Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
RA          Sekimizu K., Hirakawa H., Kihara S., Goto S., Yabuzaki J.,
RA          Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
RA          Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
RT          "Whole genome sequencing of methicillin-resistant Staphylococcus
RT          aureus."
RL          Lancet 357:1225-1240(2001).
CC          -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC          an amide bond (By similarity).
EMBL: AP003137; BAB43594.1; -.
DR          PIR; H90053; H90053.
DR          GO; GO:0009986; C:cell surface; IEA.
DR          GO; GO:0005618; C:cell wall; IEA.
DR          GO; GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR          GO; GO:0016020; C:membrane; IEA.
DR          GO; GO:0007155; P:cell adhesion; IEA.
DR          InterPro; IPR008986; Adhes_bact.
DR          InterPro; IPR004237; Fp_bind.
DR          InterPro; IPR005877; Gpos_YsIRK.
DR          InterPro; IPR001899; Gram_pos_anchor.
DR          Pfam; PF02986; Fp_bind_1.
DR          Pfam; PF00746; Gram_pos_anchor; 1.
DR          Pfam; PF04650; YsIRK_signal; 1.
DR          TIGRfams; TIGR01167; LpxTG_anchor; 1.
DR          TIGRfams; TIGR01168; YsIRK_signal; 1.
DR          PROSITE; PS50847; GRAM_POS_ANCHORING; 1.
KW          Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ      SEQUENCE      1038 AA; 113618 MW; 666BF6BF2FBEB12 CRC64;

Query Match      100.0%; Score 52; DB 2; Length 1038;
Best Local Similarity 100.0%; Pred. No. 1.3;
Matches      10; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

QY      1 GNVIDIDFDS 10
DB      764 GNVIDIDFDS 773

RESULT 11
Q7A3J7      PRELIMINARY; PRT; 1038 AA.
ID          Q7A3J7;
AC          Q7A3J7;

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DT          05-JUL-2004 (TrEMBLrel. 27, Created)
DT          05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT          05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE          Fnb protein.
GN          Name=fnb; OrderedlocusNames=SA2291;
OS          Staphylococcus aureus (strain N315).
OC          Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX          NCBI_TaxID=158879;
RN          [1]
RP          SEQUENCE FROM N.A.
RC          MEDLINE=21311952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2;
RX          Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
RA          Cui L., Oguchi A., Aoki K.-I., Nagai Y., Iian J.-Q., Ito T.,
RA          Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,
RA          Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
RA          Sekimizu K., Hirakawa H., Kihara S., Goto S., Yabuzaki J.,
RA          Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
RA          Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
RT          "Whole genome sequencing of methicillin-resistant Staphylococcus
RT          aureus."
RL          Lancet 357:1225-1240(2001).
CC          -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC          an amide bond (By similarity).
EMBL: AP003137; BAB43594.1; -.
DR          GO; GO:0009986; C:cell surface; IEA.
DR          GO; GO:0005618; C:cell wall; IEA.
DR          GO; GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR          GO; GO:0016020; C:membrane; IEA.
DR          GO; GO:0007155; P:cell adhesion; IEA.
DR          InterPro; IPR008986; Adhes_bact.
DR          InterPro; IPR004237; Fp_bind.
DR          InterPro; IPR005877; Gpos_YsIRK.
DR          InterPro; IPR001899; Gram_pos_anchor.
DR          Pfam; PF02986; Fp_bind_1.
DR          Pfam; PF00746; Gram_pos_anchor; 1.
DR          Pfam; PF04650; YsIRK_signal; 1.
DR          TIGRfams; TIGR01167; LpxTG_anchor; 1.
DR          TIGRfams; TIGR01168; YsIRK_signal; 1.
DR          PROSITE; PS50847; GRAM_POS_ANCHORING; 1.
KW          Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ      SEQUENCE      1038 AA; 113618 MW; 666BF6BF2FBEB12 CRC64;

Query Match      100.0%; Score 52; DB 2; Length 1038;
Best Local Similarity 100.0%; Pred. No. 1.3;
Matches      10; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

QY      1 GNVIDIDFDS 10
DB      764 GNVIDIDFDS 773

RESULT 12
Q6GDUS      PRELIMINARY; PRT; 965 AA.
ID          Q6GDUS;
AC          Q6GDUS;
DT          05-JUL-2004 (TrEMBLrel. 27, Created)
DT          05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT          05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE          Fibronectin-binding protein.
GN          Name=fnbA; OrderedlocusNames=SA2580;
OS          Staphylococcus aureus (strain MRS4252).
OC          Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX          NCBI_TaxID=282458;
RN          [1]
RP          SEQUENCE FROM N.A.
RC          PubMed=1521324; DOI=10.1073/pnas.0402521101;
RX          Holden M.T.G., Fell E.J., Lindsey J.A., Peacock S.J., Day N.P.J.,
RA          Enright M.C., Foster T.J., Moore C.B., Hurst L., Atkin R., Barron A.,
RA          Bason N., Bentley S.D., Chillingworth C., Chillingworth T.,
RA          Churcher C., Clark L., Corton C., Cronin A., Doggett J., Dowd L.,
RA          Felwell T., Hance Z., Harris B., Hauser H., Holtroyd S., Jørgensen K.,
RA          James K.D., Lennard N., Line A., Mayes R., Moule S., Mungall K.,
RA          Ormond D., Quail M.A., Rabinowitch E., Rutherford K.M., Sanders M.,

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RA Sharp S., Simmonds M., Stevens K., Whitehead S., Barrell B.G.,
RA Spratt B.G., Parkhill J.:
RT "Complete genomes of two clinical Staphylococcus aureus strains:
RT evidence for the rapid evolution of virulence and drug resistance.";
CC Proc. Natl. Acad. Sci. U.S.A. 101:9786-9791(2004).
RL -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC an amide bond (By similarity).
DR EMBL: BX571856; CAC41560.1; -.
DR GO: GO:0009986; C:cell surface; IEA.
DR GO: GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO: GO:0006220; C:membrane; IEA.
DR GO: GO:0007155; P:cell adhesion; IEA.
DR InterPro: IPR008966; Adhes_bact.
DR InterPro: IPR004237; Gp_bind.
DR InterPro: IPR005877; Gpos_Ysirk.
DR InterPro: IPR001899; Gram_pos_anchor.
DR Pfam: PF02986; Fn_bind; 1.
DR Pfam: PF00746; Gram_pos_anchor; 1.
DR Pfam: PF04650; Ysirk_signal; 1.
DR TIGRFAMs: TIGR01167; LpXTG_anchor; 1.
DR TIGRFAMs: TIGR01168; Ysirk_signal; 1.
DR PROSITE: PS50847; GRAM_POS_ANCHORING; 1.
KW Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ SEQUENCE 965 AA; 105691 MW; 2982E132164D0551 CRC64;

Query Match 98.1%; Score 51; DB 2; Length 965;
Beet Local Similarity 90.0%; Pred. No. 18;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GNIVDIDFDS 10
DB 771 GNIDIDFDS 780

RESULT 13
ID Q83629 PRELIMINARY; PRT; 402 AA.
AC Q83629;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DE Extracellular protein, putative.
DE Extracellular protein, putative.
OS Enterococcus faecalis (Streptococcus faecalis).
OC Bacteria; Firmicutes; Lactobacillales; Enterococcaceae; Enterococcus.
CX NCBI_TaxId=1351;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=V583 / ATCC 700802;
RX MEDLINE=2250857; PubMed=1263927; DOI=10.1126/science.1080613;
RA Paulsen I.T., Banerjee L., Myers G.S.A., Nelson K.E., Seshadri R.,
RA Read T.D., Fouts D.E., Eisen J.A., Gill S.R., Heidelberg J.F.,
RA Tettelin H., Dodson R.J., Umayam L.A., Brinkac L.M., Beaman M.J.,
RA Daugherty S.C., DeBoy R.T., Durkin S.A., Kolonay J.F., Madupu R.,
RA Nelson W.C., Vamathevan J.J., Tran B., Upton J., Hansen T., Shetty J.,
RA Khouri H.M., Uetzelback T.R., Radune D., Ketchum K.A., Dougherty B.A.,
RA Fraser C.M.;
RT "Role of mobile DNA in the evolution of vancomycin-resistant
RT Enterococcus faecalis.";
RL Science 299:2071-2074(2003).
DR EMBL: AB016949; AAO80752.1; -.
DR TIGR: EF0944; -.
DR InterPro: IPR010611; 3D.
DR Pfam: PF06725; 3D; 1.
KW Complete proteome.
SQ SEQUENCE 402 AA; 43481 MW; 769702P5633FC7AD CRC64;

Query Match 82.7%; Score 43; DB 2; Length 402;
Beet Local Similarity 70.0%; Pred. No. 20;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 GNIVDIDFDS 10
DB 771 GNIDIDFDS 780

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DB 376 GNIDVHFDPS 385

RESULT 14
ID ATPB_WOLSU STANDARD; PRT; 467 AA.
AC P42470;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE ATP synthase beta chain (EC 3.6.3.14).
GN Name=atpD; OrderedLocNames=WS0516;
OS Molnella succinogenes.
OC Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacteriales;
OC Helicobacteraceae; Molnella.
CX NCBI_TaxId=844;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=DSM2 1740;
RX MEDLINE=94368062; PubMed=8085791;
RA Ludwig W., Neumaier J., Klugbauer N., Brockmann E., Röllner C.,
RA Klugbauer S., Reetz K., Schachtner I., Ludwigsen A., Bachleitner M.,
RA Fischer U., Schaefer K.H.;
RT "Phylogenetic relationships of Bacteria based on comparative sequence
RT analysis of elongation factor Tu and ATP-synthase beta-subunit
RT genes.";
RL Antonie Van Leeuwenhoek 64:285-305(1993).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=DSM2 1740;
RX MEDLINE=22882897; PubMed=14500908; DOI=10.1073/pnas.1932838100;
RA Baar C., Eppinger M., Radatz G., Simon J., Lanz C., Klimmek O.,
RA Nandakumar R., Grosse R., Rosins A., Keller H., Jagtap P., Linke B.,
RA Meyer F., Lederer H., Schuster S.C.;
RT "Complete genome sequence and analysis of Molnella succinogenes";
RT Proc. Natl. Acad. Sci. U.S.A. 100:11690-11695(2003).
CC -1- FUNCTION: Produces ATP from ADP in the presence of a proton
CC gradient across the membrane. The beta chain is the catalytic
CC subunit.
CC -1- CATALYTIC ACTIVITY: ATP + H(2)O + H(+) (In) = ADP + phosphate +
CC H(+) (Out).
CC -1- SUBUNIT: F-type ATPases have 2 components, CF(1) - the catalytic
CC core - and CF(0) - the membrane proton channel. CF(1) has five
CC subunits: alpha(3), beta(3), gamma(1), delta(1), epsilon(1). CF(0)
CC has three main subunits: a, b and c.
CC -1- SIMILARITY: Belongs to the ATPase alpha/beta chains family.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation
CC the European Bioinformatics Institute. There are no restrictions on its
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: X76880; CAA54207.1; -.
DR EMBL: BX571658; CAB09653.1; -.
DR HSRP: P00829; 1H8E.
DR InterPro: IPR005722; ATP_synthF1_beta.
DR InterPro: IPR000793; ATPase_a/b_C.
DR InterPro: IPR004100; ATPase_a/b_N.
DR InterPro: IPR000194; ATPase_a/b_centre.
DR InterPro: IPR009005; F1_ATPase_a/b_N.
DR Pfam: PF00006; ATP_synth_ab; 1.
DR Pfam: PF00306; ATP_synth_ab_C; 1.
DR Pfam: PF02874; ATP_synth_ab_N; 1.
DR TIGRFAMs: TIGR01039; atpD; 1.
DR PROSITE: PS00152; ATPASE_ALPHA_BETA; 1.
KW ATP synthase; ATP-binding; CF(1); Complete proteome;
KW Hydrogen ion transport; Hydrolyase.
FT NP_BIND 152 159 ATP (By similarity).
SQ SEQUENCE 467 AA; 51176 MW; 09326A046ADF0627 CRC64;

```

Query Match 80.8%; Score 42; DB 1; Length 467;
 Best Local Similarity 70.0%; Pred. No. 36;
 Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 GNVIDIDFDS 10
 |:::|
 Db 10 GPVVDVDFDS 19

RESULT 15

CYAY CHRVO STANDARD; PRT; 105 AA.
 ID CYAY CHRVO
 AC Q7P221;
 DT 25-OCT-2004 (Rel. 45, Created)
 DT 25-OCT-2004 (Rel. 45, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Cyay protein.
 GN Name=Cyay; OrderedLocustNames=CV0040;
 OS Chromobacterium violaceum.
 OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
 OC Neisseriaceae; Chromobacterium.
 OX NCBI_TaxId=536;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 12472 / DSM 30191;
 RC MEDLINE=22882880; PubMed=14500782; DOI=10.1073/pnas.1832124100;
 RA Vasconcelos A.T.R., de Almeida D.F., Hungria M., Guimaraes C.T.,
 RA Antonio R.V., Almeida F.C., de Almeida L.G.P., de Almeida R.,
 RA Alves-Gomes J.A., Andrade E.M., Araripe J., de Araujo M.F.F.,
 RA Astolfi-Filho S., Azevedo V., Baptista A.J., Bataus L.A.M.,
 RA Batista J.S., Belo A., van den Berg C., Bogo M., Bonatto S.,
 RA Bordignon J., Britido M.M., Brito C.A., Brocchi M., Burity H.A.,
 RA Camargo A.A., Cardoso D.D.P., Carneiro N.P., Carraro D.M.,
 RA Carvalho C.M.B., Cascardo J.C.M., Cavada B.S., Chueire L.M.O.,
 RA Creczynski-Pasa T.B., Cunha-Junior N.C., Fagundes N., Falcao C.L.,
 RA Fautinatti F., Farias I.P., Felipe M.S.S., Ferrari L.P., Ferro J.A.,
 RA Ferro M.I.T., Franco G.R., Goncalves P.R., Grangelro T.B.,
 RA Gazzinelli R.T., Gomes E.A., Goncalves P.R., Grangelro T.B.,
 RA Gracaspaglia D., Grizard E.C., Hanna E.S., Jardim S.N., Laurino J.,
 RA Leol L.C.T., Lima L.F.A., Loureiro M.F., Lyra M.C.C.P.,
 RA Madeira H.M.F., Manfio G.P., Maranhao A.O., Martins W.S.,
 RA di Mauro S.M.Z., de Medeiros S.R.B., Meisner R.V., Moreira M.A.M.,
 RA Nascimento F.F., Nicolas M.F., Oliveira J.G., Oliveira S.C.,
 RA Paixao R.F.C., Parente J.A., Pedrosa F.O., Pena S.D.J., Pereira J.O.,
 RA Pereira M., Pinto L.S.R.C., Pinto L.S., Porto J.I.R., Potrich D.P.,
 RA Ramalho-Neto C.E., Reis A.M.M., Rigo L.U., Rondinelli E.,
 RA Santos E.B.P., Santos F.R., Schneider M.P.C., Senanez H.N.,
 RA Silva A.M.R., da Silva A.L.C., Silva D.W., Silva R., Simoes I.C.,
 RA Simon D., Soares C.M.A., Soares R.B.A., Souza E.M., Souza K.R.L.,
 RA Souza R.C., Steffens M.B.R., Steindel M., Teixeira S.R., Umenyi T.,
 RA Vettore A., Wassen R., Zaha A., Simpson A.J.G.;
 RT "The complete genome sequence of Chromobacterium violaceum reveals
 remarkable and exploitable bacterial adaptability.";
 RL Proc. Natl. Acad. Sci. U.S.A. 100:11660-11665(2003).
 CC -1- SIMILARITY: Belongs to the frataxin family.
 CC
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
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 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC
 CC EMBL, AE016910; AAC57720.1; -
 DR HAMAP; MF_00142; -; 1.
 DR InterPro; IPR002908; Frataxin like.
 DR Pfam; PF01491; Frataxin_Cyay; 1.
 DR ProDom; PD238818; Frataxin like; 1.
 DR PROSITE; PS01344; FRATAXIN_1; FALSE_NEG.
 DR PROSITE; PSS0810; FRATAXIN_2; 1.
 KW Complete proteome.
 SQ SEQUENCE 105 AA; 11656 MW; 9908P86E90707AE9 CRC64;

Query Match 76.9%; Score 40; DB 1; Length 105;
 Best Local Similarity 60.0%; Pred. No. 17;
 Matches 6; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 GNVIDIDFDS 10
 |:::|
 Db 34 GNVLEIEFDS 43

Search completed: October 22, 2005, 08:00:41
 Job time : 57.85 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 25, 2005, 20:21:18 ; Search time 63.2 Seconds
(without alignments)
61.196 Million cell updates/sec

Title: US-10-731-238-75

Perfect score: 51

Sequence: 1 IVDIDFDSVP 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-Processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

1: A_Geneseq_16Dec04:.*
2: geneseqp19808:.*
3: geneseqp19908:.*
4: geneseqp20008:.*
5: geneseqp20018:.*
6: geneseqp20028:.*
7: geneseqp20038:.*
8: geneseqp20048:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	51	100.0	10	2	AAW65731
2	51	100.0	14	2	AAW65716
3	51	100.0	38	2	AAW65692
4	51	100.0	38	2	AAW65695
5	51	100.0	38	2	AAW65662
6	51	100.0	38	2	AAW65696
7	51	100.0	38	2	AAW65697
8	51	100.0	38	2	AAW65694
9	51	100.0	38	2	AAW65700
10	51	100.0	38	2	AAW65691
11	51	100.0	38	2	AAW65699
12	51	100.0	38	2	AAW65661
13	51	100.0	38	2	AAW65693
14	51	100.0	38	2	AAW65698
15	51	100.0	113	2	AAW65698
16	51	100.0	113	2	AAW65698
17	51	100.0	130	2	AAW65698
18	51	100.0	130	2	AAW65698
19	51	100.0	130	2	AAW65698
20	51	100.0	134	2	AAW65698
21	51	100.0	134	2	AAW65698
22	51	100.0	134	2	AAW65698
23	51	100.0	139	2	AAW65698
24	51	100.0	162	2	AAW65698
25	51	100.0	164	2	AAW65698

26	51	100.0	174	2	AAW65731	AAW65731
27	51	100.0	174	2	AAW65731	AAW65731
28	51	100.0	181	2	AAW65731	AAW65731
29	51	100.0	181	2	AAW65731	AAW65731
30	51	100.0	559	2	AAW65731	AAW65731
31	51	100.0	767	4	AAW65731	AAW65731
32	51	100.0	767	4	AAW65731	AAW65731
33	51	100.0	940	2	AAW65731	AAW65731
34	51	100.0	940	2	AAW65731	AAW65731
35	51	100.0	948	6	AAW65731	AAW65731
36	51	100.0	948	6	AAW65731	AAW65731
37	51	100.0	948	6	AAW65731	AAW65731
38	51	100.0	961	6	AAW65731	AAW65731
39	51	100.0	978	4	AAW65731	AAW65731
40	51	100.0	1001	4	AAW65731	AAW65731
41	51	100.0	1018	1	AAW65731	AAW65731
42	51	100.0	1018	4	AAW65731	AAW65731
43	51	100.0	1018	4	AAW65731	AAW65731
44	51	100.0	1018	6	AAW65731	AAW65731
45	51	100.0	1018	6	AAW65731	AAW65731

ALIGNMENTS

RESULT 1
ID AAW65731 standard; peptide; 10 AA.

AC AAW65731;

DT 16-OCT-1998 (first entry)

DE Fibronectin binding protein-derived peptide #75.

KW microbial surface components recognising adhesive matrix molecule;

KW MSCRAMM; fibronectin; fibronectin-binding protein; antibody; epitope;

KW antibiotic; bacterial infection; antibiotic-resistant strain.

OS Synthetic.

PN Staphylococcus aureus.

PD WO981389-A2.

PF 23-JUL-1998.

PI 21-JAN-1996; 98WO-US001222.

PR 21-JAN-1997; 97US-0036139P.

PS (TEXA) UNITV TEXAS A & M SYSTEM.

PT Hoeck M, Patti JM, House-Pompeo KL, Speziale P, Joh D;

PT Megavirin MJ;

PT WPI; 1998-413816/35.

PS Example 9; Page 110; 20BP; English.

XX The invention relates to antibodies that bind to a fibronectin-binding

XX domain of a fibronectin-binding protein, and inhibit binding of the

XX protein to a fibronectin. Also claimed are: (1) isolated peptides of a

XX fibronectin-binding protein that do not bind to fibronectin; (2) fusion

XX protein containing at least one peptide of a fibronectin-binding protein

XX linked to a second amino acid sequence; (3) nucleic acid encoding the

XX isolated peptide of (1). Antibodies, the isolated peptides of (1) and the

XX nucleic acids are all useful for immunisation (active or passive) and (by

XX inhibiting binding of bacteria to fibronectin) for preventing or treating

XX infection in humans or other animals, particularly by staphylococci or

CC streptococci, e.g., meningitis, otitis media, pneumonia, endocarditis,
 CC mastitis in cattle, abortion in horses and many others. Since the
 CC antibodies block binding of bacteria, they should be effective against
 CC antibiotic-resistant strains, and may replace antibiotic therapy or
 CC increase its effectiveness. Sequences AAW65719-41 and AAW65658 represent
 CC peptides which were synthesised to span the D1 motif and the N-terminal
 CC 18 amino acids of D2, with each peptide overlapping by eight amino acids
 CC with the previous sequence
 XX
 SQ Sequence 10 AA;
 Query Match 100.0%; Score 51; DB 2; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.0077;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 IVDIDFDSVP 10
 DB 1 IVDIDFDSVP 10
 RESULT 2
 ID AAW65716 standard; peptide; 14 AA.
 XX
 AC AAW65716;
 XX
 DT 16-OCT-1998 (first entry)
 XX
 DE Fibronectin binding protein fragment (residues 21-34 of D1 motif).
 XX
 KW microbial surface components recognising adhesive matrix molecule;
 KM MSCRAMM; fibronectin; fibronectin-binding protein; antibody; epitope;
 KM antibiotic; bacterial infection; antibiotic-resistant strain.
 XX
 OS Synthetic.
 OS Staphylococcus aureus.
 XX
 PN WO9831389-A2.
 XX
 PD 23-JUL-1998.
 XX
 PF 21-JAN-1998; 98WO-US001222.
 XX
 PR 21-JAN-1997; 97US-0036139P.
 XX
 PA (TEXA) UNIV TEXAS A & M SYSTEM.
 XX
 PI Hoecek M, Patti JM, House-Pompeo KL, Speziale P, Joh D;
 PI McGavin MJ;
 XX
 DR WPI; 1998-413816/35.
 XX
 PT Antibody that binds to fibronectin-binding protein, preventing its
 PT binding to fibronectin - used to treat or prevent bacterial infection,
 PT especially by Staphylococci and Streptococci.
 XX
 PS Claim 42; Page 105; 201pp; English.
 CC The invention relates to antibodies that bind to a fibronectin-binding
 CC domain of a fibronectin-binding protein, and inhibit binding of the
 CC protein to fibronectin. Also claimed are: (1) isolated peptides of a
 CC fibronectin-binding protein that do not bind to fibronectin; (2) fusion
 CC protein containing at least one peptide of a fibronectin-binding protein
 CC linked to a second amino acid sequence; (3) nucleic acid encoding the
 CC isolated peptide of (1). Antibodies, the isolated peptides of (1) and the
 CC nucleic acids are all useful for immunisation (active or passive) and (by
 CC inhibiting binding of bacteria to fibronectin) for preventing or treating
 CC infection in humans or other animals, particularly by staphylococci or
 CC streptococci, e.g., meningitis, otitis media, pneumonia, endocarditis,
 CC mastitis in cattle, abortion in horses and many others. Since the
 CC antibodies block binding of bacteria, they should be effective against
 CC antibiotic-resistant strains, and may replace antibiotic therapy or
 CC increase its effectiveness. The present sequence represents a

CC specifically claimed peptide
 XX
 SQ Sequence 14 AA;
 Query Match 100.0%; Score 51; DB 2; Length 14;
 Best Local Similarity 100.0%; Pred. No. 0.011;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 IVDIDFDSVP 10
 DB 5 IVDIDFDSVP 14
 RESULT 3
 ID AAW65692 standard; peptide; 38 AA.
 XX
 AC AAW65692;
 XX
 DT 16-OCT-1998 (first entry)
 XX
 DE Fibronectin binding protein-derived peptide #36.
 XX
 KW microbial surface components recognising adhesive matrix molecule;
 KM MSCRAMM; fibronectin; fibronectin-binding protein; antibody; epitope;
 KM antibiotic; bacterial infection; antibiotic-resistant strain.
 XX
 OS Synthetic.
 OS Staphylococcus aureus.
 XX
 PN WO9831389-A2.
 XX
 PD 23-JUL-1998.
 XX
 PF 21-JAN-1998; 98WO-US001222.
 XX
 PR 21-JAN-1997; 97US-0036139P.
 XX
 PA (TEXA) UNIV TEXAS A & M SYSTEM.
 XX
 PI Hoecek M, Patti JM, House-Pompeo KL, Speziale P, Joh D;
 PI McGavin MJ;
 XX
 DR WPI; 1998-413816/35.
 XX
 PT Antibody that binds to fibronectin-binding protein, preventing its
 PT binding to fibronectin - used to treat or prevent bacterial infection,
 PT especially by Staphylococci and Streptococci.
 XX
 PS Example 8; Page 101; 201pp; English.
 CC The invention relates to antibodies that bind to a fibronectin-binding
 CC domain of a fibronectin-binding protein, and inhibit binding of the
 CC protein to fibronectin. Also claimed are: (1) isolated peptides of a
 CC fibronectin-binding protein that do not bind to fibronectin; (2) fusion
 CC protein containing at least one peptide of a fibronectin-binding protein
 CC linked to a second amino acid sequence; (3) nucleic acid encoding the
 CC isolated peptide of (1). Antibodies, the isolated peptides of (1) and the
 CC nucleic acids are all useful for immunisation (active or passive) and (by
 CC inhibiting binding of bacteria to fibronectin) for preventing or treating
 CC infection in humans or other animals, particularly by staphylococci or
 CC streptococci, e.g., meningitis, otitis media, pneumonia, endocarditis,
 CC mastitis in cattle, abortion in horses and many others. Since the
 CC antibodies block binding of bacteria, they should be effective against
 CC antibiotic-resistant strains, and may replace antibiotic therapy or
 CC increase its effectiveness. Sequences AAW65691-700 represent a series of
 CC synthetic peptides based on the D1 region of S. aureus fibronectin
 CC binding protein A. They were synthesised to contain mutations
 XX
 SQ Sequence 38 AA;
 Query Match 100.0%; Score 51; DB 2; Length 38;
 Best Local Similarity 100.0%; Pred. No. 0.033;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IVDIDFDSVP 10
 |||||
 DB 25 IVDIDFDSVP 34

RESULT 4
 AAW65695
 ID AAW65695 standard; peptide; 38 AA.

AC AAW65695;

DT 16-OCT-1998 (first entry)

DE Fibronectin binding protein-derived peptide #39.

XX microbial surface components recognising adhesive matrix molecule;
 KM MSCRAMM; fibronectin; fibronectin-binding protein; antibody; epitope;
 KM antibiotic; bacterial infection; antibiotic-resistant strain.

OS Synthetic.

XX Staphylococcus aureus.

PN WO9831389-A2.

PD 23-JUL-1998.

PP 21-JAN-1998; 98WO-US001222.

PR 21-JAN-1997; 97US-0036139P.

PA (TEXA) UNIV TEXAS A & M SYSTEM.

PI Hoeek M, Patti JM, House-Pompeo KL, Speziale P, Joh D;

PI Mcgavin MJ;

DR WPI; 1998-413816/35.

XX Antibody that binds to fibronectin-binding protein, preventing its
 PT binding to fibronectin - used to treat or prevent bacterial infection,
 PT especially by Staphylococci and Streptococci.

XX Example 8; Page 102; 201pp; English.

CC The invention relates to antibodies that bind to a fibronectin-binding
 CC domain of a fibronectin-binding protein, and inhibit binding of the
 CC protein to fibronectin. Also claimed are: (1) isolated peptides of a
 CC fibronectin-binding protein that do not bind to fibronectin; (2) fusion
 CC protein containing at least one peptide of a fibronectin-binding protein
 CC linked to a second amino acid sequence; (3) nucleic acid encoding the
 CC isolated peptide of (1). Antibodies, the isolated peptides of (1) and the
 CC nucleic acids are all useful for immunisation (active or passive) and (by
 CC inhibiting binding of bacteria to fibronectin) for preventing or treating
 CC infection in humans or other animals, particularly by staphylococci or
 CC streptococci, e.g. meningitis, otitis media, pneumonia, endocarditis,
 CC mastitis in cattle, abortion in horses and many others. Since the
 CC antibodies block binding of bacteria, they should be effective against
 CC antibiotic-resistant strains, and may replace antibiotic therapy or
 CC increase its effectiveness. Sequences AAW65691-700 represent a series of
 CC synthetic peptides based on the D1 region of S. aureus fibronectin
 CC binding protein A. They were synthesised to contain mutations
 CC XX

SO Sequence 38 AA;

Query Match 100.0%; Score 51; DB 2; Length 38;

Best Local Similarity 100.0%; Pred. No. 0.033;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IVDIDFDSVP 10
 |||||
 DB 25 IVDIDFDSVP 34

RESULT 5
 AAW65662
 ID AAW65662 standard; peptide; 38 AA.

AC AAW65662;

DT 16-OCT-1998 (first entry)

DE Fibronectin binding protein-derived peptide #6.

XX microbial surface components recognising adhesive matrix molecule;
 KM MSCRAMM; fibronectin; fibronectin-binding protein; antibody; epitope;
 KM antibiotic; bacterial infection; antibiotic-resistant strain.

OS Synthetic.

XX Staphylococcus aureus.

PN WO9831389-A2.

PD 23-JUL-1998.

PP 21-JAN-1998; 98WO-US001222.

PR 21-JAN-1997; 97US-0036139P.

PA (TEXA) UNIV TEXAS A & M SYSTEM.

PI Hoeek M, Patti JM, House-Pompeo KL, Speziale P, Joh D;

PI Mcgavin MJ;

DR WPI; 1998-413816/35.

XX Antibody that binds to fibronectin-binding protein, preventing its
 PT binding to fibronectin - used to treat or prevent bacterial infection,
 PT especially by Staphylococci and Streptococci.

XX Example 2; Page 92; 201pp; English.

CC The invention relates to antibodies that bind to a fibronectin-binding
 CC domain of a fibronectin-binding protein, and inhibit binding of the
 CC protein to fibronectin. Also claimed are: (1) isolated peptides of a
 CC fibronectin-binding protein that do not bind to fibronectin; (2) fusion
 CC protein containing at least one peptide of a fibronectin-binding protein
 CC linked to a second amino acid sequence; (3) nucleic acid encoding the
 CC isolated peptide of (1). Antibodies, the isolated peptides of (1) and the
 CC nucleic acids are all useful for immunisation (active or passive) and (by
 CC inhibiting binding of bacteria to fibronectin) for preventing or treating
 CC infection in humans or other animals, particularly by staphylococci or
 CC streptococci, e.g. meningitis, otitis media, pneumonia, endocarditis,
 CC mastitis in cattle, abortion in horses and many others. Since the
 CC antibodies block binding of bacteria, they should be effective against
 CC antibiotic-resistant strains, and may replace antibiotic therapy or
 CC increase its effectiveness. Sequences AAW65659-68 represent synthetic
 CC epitopes from the fibronectin binding domains DU and DI-D4 of the S.
 CC aureus fnbA gene
 CC XX

SO Sequence 38 AA;

Query Match 100.0%; Score 51; DB 2; Length 38;

Best Local Similarity 100.0%; Pred. No. 0.033; Mismatches 0; Indels 0; Gaps 0;

QY 1 IVDIDFDSVP 10
 |||||
 DB 25 IVDIDFDSVP 34

RESULT 6

AAW65696

AC AAW65696;


```

XX 16-OCT-1998 (first entry)
XX Fibronectin binding protein-derived peptide #40.
DE microbial surface components recognising adhesive matrix molecule;
XX MSCRAMM; fibronectin; fibronectin-binding protein; antibody; epitope;
XX antibiotic; bacterial infection; antibiotic-resistant strain.
XX Synthetic.
OS Staphylococcus aureus.
XX WO9831389-A2.
XX 23-JUL-1998.
XX 21-JAN-1998; 98WO-US001222.
XX 21-JAN-1997; 97US-0036139P.
XX (TEXA ) UNIV TEXAS A & M SYSTEM.
XX Hoecek M, Patti JM, House-Pompeo KL, Speziale P, Joh D;
XX Mcgavin MJ;
XX WPI, 1998-413816/35.
XX Antibody that binds to fibronectin-binding protein, preventing its
XX binding to fibronectin - used to treat or prevent bacterial infection,
XX especially by Staphylococci and Streptococci.
XX Example 8; Page 102; 201pp; English.
XX The invention relates to antibodies that bind to a fibronectin-binding
XX domain of a fibronectin-binding protein, and inhibit binding of the
XX protein to fibronectin. Also claimed are: (1) isolated peptides of a
XX fibronectin-binding protein that do not bind to fibronectin; (2) fusion
XX protein containing at least one peptide of a fibronectin-binding protein
XX linked to a second amino acid sequence; (3) nucleic acid encoding the
XX isolated peptide of (1). Antibodies, the isolated peptides of (1) and the
XX nucleic acids are all useful for immunisation (active or passive) and (by
XX inhibiting binding of bacteria to fibronectin) for preventing or treating
XX infection in humans or other animals, particularly by staphylococci or
XX streptococci, e.g. meningitis, otitis media, pneumonia, endocarditis,
XX mastitis in cattle, abortion in horses and many others. Since the
XX antibodies block binding of bacteria, they should be effective against
XX antibiotic-resistant strains, and may replace antibiotic therapy or
XX increase its effectiveness. Sequences AAW65691-700 represent a series of
XX synthetic peptides based on the D1 region of S. aureus fibronectin
XX binding protein A. They were synthesised to contain mutations
XX
SQ Sequence 38 AA:
Query Match 100.0%; Score 51; DB 2; Length 38;
Best Local Similarity 100.0%; Pred. No. 0.033;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 IVDIDFDSVP 10
DB 25 IVDIDFDSVP 34
RESULT 7
AAW65697
ID AAW65697 standard; peptide; 38 AA.
XX
XX AAW65697;
AC 16-OCT-1998 (first entry)
XX
XX Fibronectin binding protein-derived peptide #41.
DE microbial surface components recognising adhesive matrix molecule;
XX MSCRAMM; fibronectin; fibronectin-binding protein; antibody; epitope;
XX antibiotic; bacterial infection; antibiotic-resistant strain.
XX Synthetic.
OS Staphylococcus aureus.
XX

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```

XX MSCRAMM; fibronectin; fibronectin-binding protein; antibody; epitope;
XX antibiotic; bacterial infection; antibiotic-resistant strain.
XX Synthetic.
OS Staphylococcus aureus.
XX WO9831389-A2.
XX 23-JUL-1998.
XX 21-JAN-1998; 98WO-US001222.
XX 21-JAN-1997; 97US-0036139P.
XX (TEXA ) UNIV TEXAS A & M SYSTEM.
XX Hoecek M, Patti JM, House-Pompeo KL, Speziale P, Joh D;
XX Mcgavin MJ;
XX WPI, 1998-413816/35.
XX Antibody that binds to fibronectin-binding protein, preventing its
XX binding to fibronectin - used to treat or prevent bacterial infection,
XX especially by Staphylococci and Streptococci.
XX Example 8; Page 102; 201pp; English.
XX The invention relates to antibodies that bind to a fibronectin-binding
XX domain of a fibronectin-binding protein, and inhibit binding of the
XX protein to fibronectin. Also claimed are: (1) isolated peptides of a
XX fibronectin-binding protein that do not bind to fibronectin; (2) fusion
XX protein containing at least one peptide of a fibronectin-binding protein
XX linked to a second amino acid sequence; (3) nucleic acid encoding the
XX isolated peptide of (1). Antibodies, the isolated peptides of (1) and the
XX nucleic acids are all useful for immunisation (active or passive) and (by
XX inhibiting binding of bacteria to fibronectin) for preventing or treating
XX infection in humans or other animals, particularly by staphylococci or
XX streptococci, e.g. meningitis, otitis media, pneumonia, endocarditis,
XX mastitis in cattle, abortion in horses and many others. Since the
XX antibodies block binding of bacteria, they should be effective against
XX antibiotic-resistant strains, and may replace antibiotic therapy or
XX increase its effectiveness. Sequences AAW65691-700 represent a series of
XX synthetic peptides based on the D1 region of S. aureus fibronectin
XX binding protein A. They were synthesised to contain mutations
XX
SQ Sequence 38 AA:
Query Match 100.0%; Score 51; DB 2; Length 38;
Best Local Similarity 100.0%; Pred. No. 0.033;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 IVDIDFDSVP 10
DB 25 IVDIDFDSVP 34
RESULT 8
AAW65694
ID AAW65694 standard; peptide; 38 AA.
XX
XX AAW65694;
AC 16-OCT-1998 (first entry)
XX
XX Fibronectin binding protein-derived peptide #38.
DE microbial surface components recognising adhesive matrix molecule;
XX MSCRAMM; fibronectin; fibronectin-binding protein; antibody; epitope;
XX antibiotic; bacterial infection; antibiotic-resistant strain.
XX Synthetic.
OS Staphylococcus aureus.
XX

```

PN W09831389-A2.
 XX 23-JUL-1998.
 XX
 XX 21-JAN-1998; 98WO-US001222.
 PF
 XX 21-JAN-1997; 97US-0036139P.
 PR
 XX (TEXA) UNIV TEXAS A & M SYSTEM.
 PA
 XX Hoeek M, Patti JM, House-Pompeo KL, Speciale P, Joh D;
 PI Mcgavin MJ;
 PS WPI, 1998-413816/35.
 DR
 XX Antibody that binds to fibronectin-binding protein, preventing its
 PT binding to fibronectin - used to treat or prevent bacterial infection,
 PR especially by Staphylococci and Streptococci.
 XX
 XX Example 8; Page 102; 201pp; English.
 XX
 XX The invention relates to antibodies that bind to a fibronectin-binding
 CC domain of a fibronectin-binding protein, and inhibit binding of the
 CC protein to fibronectin. Also claimed are: (1) isolated peptides of a
 CC fibronectin-binding protein that do not bind to fibronectin; (2) fusion
 CC protein containing at least one peptide of a fibronectin-binding protein
 CC linked to a second amino acid sequence; (3) nucleic acid encoding the
 CC isolated peptide of (1). Antibodies, the isolated peptides of (1) and the
 CC nucleic acids are all useful for immunisation (active or passive) and (by
 CC inhibiting binding of bacteria to fibronectin) for preventing or treating
 CC infection in humans or other animals, particularly by staphylococci or
 CC streptococci, e.g. meningitis, otitis media, pneumonia, endocarditis,
 CC mastitis in cattle, abortion in horses and many others. Since the
 CC antibodies block binding of bacteria, they should be effective against
 CC antibiotic-resistant strains, and may replace antibiotic therapy or
 CC increase its effectiveness. Sequences AAW65691-700 represent a series of
 CC synthetic peptides based on the D1 region of S. aureus fibronectin
 CC binding protein A. They were synthesised to contain mutations
 XX
 XX Sequence 38 AA:
 SQ
 Query Match 100.0%; Score 51; DB 2; Length 38;
 Best Local Similarity 100.0%; Pred. No. 0.033;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 IVDIDFDSVP 10
 |||||
 DB 25 IVDIDFDSVP 34
 RESULT 9
 AAW65700
 ID AAW65700 standard; peptide; 38 AA.
 XX
 XX AAW65700;
 AC
 XX 16-OCT-1998 (first entry)
 DT
 XX Fibronectin binding protein-derived peptide #44.
 DE
 XX microbial surface components recognising adhesive matrix molecule;
 KM MSCRAMM; fibronectin; fibronectin-binding protein; antibody; epitope;
 KW antibiotic; bacterial infection; antibiotic-resistant strain.
 OS Synthetic.
 OS Staphylococcus aureus.
 XX
 XX W09831389-A2.
 PN
 XX 23-JUL-1998.
 PD
 XX 21-JAN-1998; 98WO-US001222.
 PF
 XX

PR 21-JAN-1997; 97US-0036139P.
 XX
 XX (TEXA) UNIV TEXAS A & M SYSTEM.
 XX
 XX Hoeek M, Patti JM, House-Pompeo KL, Speciale P, Joh D;
 PI Mcgavin MJ;
 PS WPI, 1998-413816/35.
 DR
 XX Antibody that binds to fibronectin-binding protein, preventing its
 PT binding to fibronectin - used to treat or prevent bacterial infection,
 PR especially by Staphylococci and Streptococci.
 XX
 XX Example 8; Page 102; 201pp; English.
 XX
 XX The invention relates to antibodies that bind to a fibronectin-binding
 CC domain of a fibronectin-binding protein, and inhibit binding of the
 CC protein to fibronectin. Also claimed are: (1) isolated peptides of a
 CC fibronectin-binding protein that do not bind to fibronectin; (2) fusion
 CC protein containing at least one peptide of a fibronectin-binding protein
 CC linked to a second amino acid sequence; (3) nucleic acid encoding the
 CC isolated peptide of (1). Antibodies, the isolated peptides of (1) and the
 CC nucleic acids are all useful for immunisation (active or passive) and (by
 CC inhibiting binding of bacteria to fibronectin) for preventing or treating
 CC infection in humans or other animals, particularly by staphylococci or
 CC streptococci, e.g. meningitis, otitis media, pneumonia, endocarditis,
 CC mastitis in cattle, abortion in horses and many others. Since the
 CC antibodies block binding of bacteria, they should be effective against
 CC antibiotic-resistant strains, and may replace antibiotic therapy or
 CC increase its effectiveness. Sequences AAW65691-700 represent a series of
 CC synthetic peptides based on the D1 region of S. aureus fibronectin
 CC binding protein A. They were synthesised to contain mutations
 XX
 XX Sequence 38 AA:
 SQ
 Query Match 100.0%; Score 51; DB 2; Length 38;
 Best Local Similarity 100.0%; Pred. No. 0.033;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 IVDIDFDSVP 10
 |||||
 DB 25 IVDIDFDSVP 34
 RESULT 10
 AAW65691
 ID AAW65691 standard; peptide; 38 AA.
 XX
 XX AAW65691;
 AC
 XX 16-OCT-1998 (first entry)
 DT
 XX Fibronectin binding protein-derived peptide #35.
 DE
 XX microbial surface components recognising adhesive matrix molecule;
 KM MSCRAMM; fibronectin; fibronectin-binding protein; antibody; epitope;
 KW antibiotic; bacterial infection; antibiotic-resistant strain.
 OS Synthetic.
 OS Staphylococcus aureus.
 XX
 XX W09831389-A2.
 PN
 XX 23-JUL-1998.
 PD
 XX 21-JAN-1998; 98WO-US001222.
 PF
 XX 21-JAN-1997; 97US-0036139P.
 PR
 XX (TEXA) UNIV TEXAS A & M SYSTEM.
 PA
 XX Hoeek M, Patti JM, House-Pompeo KL, Speciale P, Joh D;
 PI Mcgavin MJ;
 PS

```

XX DR WPI: 1998-413816/35.
XX
XX PT Antibody that binds to fibronectin-binding protein, preventing its
XX PT binding to fibronectin - used to treat or prevent bacterial infection,
XX PT especially by Staphylococci and Streptococci.
XX
XX PS Example 8; Page 101; 201pp; English.
XX
XX CC The invention relates to antibodies that bind to a fibronectin-binding
XX CC domain of a fibronectin-binding protein, and inhibit binding of the
XX CC protein to fibronectin. Also claimed are: (1) isolated peptides of a
XX CC fibronectin-binding protein that do not bind to fibronectin; (2) fusion
XX CC protein containing at least one peptide of a fibronectin-binding protein
XX CC linked to a second amino acid sequence; (3) nucleic acid encoding the
XX CC isolated peptide of (1). Antibodies, the isolated peptides of (1) and the
XX CC nucleic acids are all useful for immunisation (active or passive) and (by
XX CC inhibiting binding of bacteria to fibronectin) for preventing or treating
XX CC infection in humans or other animals, particularly by staphylococci or
XX CC streptococci, e.g. meningitis, otitis media, pneumonia, endocarditis,
XX CC mastitis in cattle, abortion in horses and many others. Since the
XX CC antibodies block binding of bacteria, they should be effective against
XX CC antibiotic-resistant strains, and may replace antibiotic therapy or
XX CC increase its effectiveness. Sequences AAW65691-700 represent a series of
XX CC synthetic peptides based on the D1 region of S. aureus fibronectin
XX CC binding protein A. They were synthesised to contain mutations
XX
SQ Sequence 38 AA:
Query Match 100.0%; Score 51; DB 2; Length 38;
Best Local Similarity 100.0%; Pred. No. 0.033;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IVDIDFDSVP 10
   |||||
   25 IVDIDFDSVP 34

DB 25 IVDIDFDSVP 34

RESULT 11
AAW65699
ID AAW65699 standard; peptide; 38 AA.
AC AAW65699;
XX
XX DT 16-OCT-1998 (first entry)
XX
XX DE Fibronectin binding protein-derived peptide #43.
XX
XX KW microbial surface components recognising adhesive matrix molecule;
XX KW MSCRAMM; fibronectin; fibronectin-binding protein; antibody; epitope;
XX KW antibiotic; bacterial infection; antibiotic-resistant strain.
XX
XX OS Synthetic.
XX OS Staphylococcus aureus.
XX
XX PN WO9831389-A2.
XX
XX PD 23-JUL-1998.
XX
XX PF 21-JAN-1998; 98WO-US001222.
XX
XX PR 21-JAN-1997; 97US-0036139P.
XX
XX PA (TEXA ) UNIV TEXAS A & M SYSTEM.
XX
XX PI Hoeoek M, Patci JM, House-Pompeo KL, Speciale P, Joh D;
XX PI McGavin MJ;
XX
XX DR WPI: 1998-413816/35.
XX
XX PT Antibody that binds to fibronectin-binding protein, preventing its
XX PT binding to fibronectin - used to treat or prevent bacterial infection,
XX PT especially by Staphylococci and Streptococci.

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XX PS Example 8; Page 102; 201pp; English.
XX
XX CC The invention relates to antibodies that bind to a fibronectin-binding
XX CC domain of a fibronectin-binding protein, and inhibit binding of the
XX CC protein to fibronectin. Also claimed are: (1) isolated peptides of a
XX CC fibronectin-binding protein that do not bind to fibronectin; (2) fusion
XX CC protein containing at least one peptide of a fibronectin-binding protein
XX CC linked to a second amino acid sequence; (3) nucleic acid encoding the
XX CC isolated peptide of (1). Antibodies, the isolated peptides of (1) and the
XX CC nucleic acids are all useful for immunisation (active or passive) and (by
XX CC inhibiting binding of bacteria to fibronectin) for preventing or treating
XX CC infection in humans or other animals, particularly by staphylococci or
XX CC streptococci, e.g. meningitis, otitis media, pneumonia, endocarditis,
XX CC mastitis in cattle, abortion in horses and many others. Since the
XX CC antibodies block binding of bacteria, they should be effective against
XX CC antibiotic-resistant strains, and may replace antibiotic therapy or
XX CC increase its effectiveness. Sequences AAW65691-700 represent a series of
XX CC synthetic peptides based on the D1 region of S. aureus fibronectin
XX CC binding protein A. They were synthesised to contain mutations
XX
SQ Sequence 38 AA:
Query Match 100.0%; Score 51; DB 2; Length 38;
Best Local Similarity 100.0%; Pred. No. 0.033;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IVDIDFDSVP 10
   |||||
   25 IVDIDFDSVP 34

DB 25 IVDIDFDSVP 34

RESULT 12
AAW65661
ID AAW65661 standard; peptide; 38 AA.
AC AAW65661;
XX
XX DT 16-OCT-1998 (first entry)
XX
XX DE Fibronectin binding protein-derived peptide #5.
XX
XX KW microbial surface components recognising adhesive matrix molecule;
XX KW MSCRAMM; fibronectin; fibronectin-binding protein; antibody; epitope;
XX KW antibiotic; bacterial infection; antibiotic-resistant strain.
XX
XX OS Synthetic.
XX OS Staphylococcus aureus.
XX
XX PN WO9831389-A2.
XX
XX PD 23-JUL-1998.
XX
XX PF 21-JAN-1998; 98WO-US001222.
XX
XX PR 21-JAN-1997; 97US-0036139P.
XX
XX PA (TEXA ) UNIV TEXAS A & M SYSTEM.
XX
XX PI Hoeoek M, Patci JM, House-Pompeo KL, Speciale P, Joh D;
XX PI McGavin MJ;
XX
XX DR WPI: 1998-413816/35.
XX
XX PT Antibody that binds to fibronectin-binding protein, preventing its
XX PT binding to fibronectin - used to treat or prevent bacterial infection,
XX PT especially by Staphylococci and Streptococci.
XX
XX PS Example 2; Page 92; 201pp; English.
XX
XX CC The invention relates to antibodies that bind to a fibronectin-binding
XX CC domain of a fibronectin-binding protein, and inhibit binding of the
XX CC protein to fibronectin. Also claimed are: (1) isolated peptides of a

```

CC fibronectin-binding protein that do not bind to fibronectin; (2) fusion
 CC protein containing at least one peptide of a fibronectin-binding protein
 CC linked to a second amino acid sequence; (3) nucleic acid encoding the
 CC isolated peptide of (1). Antibodies, the isolated peptides of (1) and the
 CC nucleic acids are all useful for immunisation (active or passive) and (by
 CC inhibiting binding of bacteria to fibronectin) for preventing or treating
 CC infection in humans or other animals, particularly by staphylococci or
 CC streptococci, e.g. meningitis, otitis media, pneumonia, endocarditis,
 CC mastitis in cattle, abortion in horses and many others. Since the
 CC antibodies block binding of bacteria, they should be effective against
 CC antibiotic-resistant strains, and may replace antibiotic therapy or
 CC increase its effectiveness. Sequences AAW65691-700 represent a series of
 CC epitopes from the fibronectin binding domains DU and DI-D4 of the S.
 CC aureus fmbA gene

CC Sequence 38 AA:

Query Match 100.0%; Score 51; DB 2; Length 38;
 Best Local Similarity 100.0%; Pred. No. 0.033;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IVDIDPDSVP 10
 |||||
 DB 25 IVDIDPDSVP 34

RESULT 13

AAW65693
 ID AAW65693 standard; peptide; 38 AA.

AC AAW65693;

DT 16-OCT-1998 (first entry)

DE Fibronectin binding protein-derived peptide #37.

KW microbial surface components recognising adhesive matrix molecule;

KW MSCRAMM; fibronectin; fibronectin-binding protein; antibody; epitope;

KW antibiotic; bacterial infection; antibiotic-resistant strain.

OS Synthetic.

PN WO9831389-A2.

PD 23-JUL-1998.

PF 21-JAN-1998; 98WO-US001222.

PR 21-JAN-1997; 97US-0036139P.

PA (TEXA) UNIV TEXAS A & M SYSTEM.

PI Hoeoek M, Patti JM, House-Pompeo KL, Speziale P, Joh D;

PI McGavin MJ;

DR WPI; 1998-413816/35.

PT Antibody that binds to fibronectin-binding protein, preventing its

PT binding to fibronectin - used to treat or prevent bacterial infection,

PT especially by Staphylococci and Streptococci.

PS Example 8; Page 102; 201pp; English.

CC The invention relates to antibodies that bind to a fibronectin-binding
 CC domain of a fibronectin-binding protein, and inhibit binding of the
 CC protein to fibronectin. Also claimed are: (1) isolated peptides of a
 CC fibronectin-binding protein that do not bind to fibronectin; (2) fusion
 CC protein containing at least one peptide of a fibronectin-binding protein
 CC linked to a second amino acid sequence; (3) nucleic acid encoding the
 CC isolated peptide of (1). Antibodies, the isolated peptides of (1) and the
 CC nucleic acids are all useful for immunisation (active or passive) and (by
 CC inhibiting binding of bacteria to fibronectin) for preventing or treating

CC infection in humans or other animals, particularly by staphylococci or
 CC streptococci, e.g. meningitis, otitis media, pneumonia, endocarditis,
 CC mastitis in cattle, abortion in horses and many others. Since the
 CC antibodies block binding of bacteria, they should be effective against
 CC antibiotic-resistant strains, and may replace antibiotic therapy or
 CC increase its effectiveness. Sequences AAW65691-700 represent a series of
 CC synthetic peptides based on the DI region of S. aureus fibronectin
 CC binding protein A. They were synthesised to contain mutations

CC Sequence 38 AA:

Query Match 100.0%; Score 51; DB 2; Length 38;
 Best Local Similarity 100.0%; Pred. No. 0.033;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IVDIDPDSVP 10
 |||||
 DB 25 IVDIDPDSVP 34

RESULT 14

AAW65698
 ID AAW65698 standard; peptide; 38 AA.

AC AAW65698;

DT 16-OCT-1998 (first entry)

DE Fibronectin binding protein-derived peptide #42.

KW microbial surface components recognising adhesive matrix molecule;

KW MSCRAMM; fibronectin; fibronectin-binding protein; antibody; epitope;

KW antibiotic; bacterial infection; antibiotic-resistant strain.

OS Synthetic.

PN WO9831389-A2.

PD 23-JUL-1998.

PF 21-JAN-1998; 98WO-US001222.

PR 21-JAN-1997; 97US-0036139P.

PA (TEXA) UNIV TEXAS A & M SYSTEM.

PI Hoeoek M, Patti JM, House-Pompeo KL, Speziale P, Joh D;

PI McGavin MJ;

DR WPI; 1998-413816/35.

PT Antibody that binds to fibronectin-binding protein, preventing its

PT binding to fibronectin - used to treat or prevent bacterial infection,

PT especially by Staphylococci and Streptococci.

PS Example 8; Page 102; 201pp; English.

CC The invention relates to antibodies that bind to a fibronectin-binding
 CC domain of a fibronectin-binding protein, and inhibit binding of the
 CC protein to fibronectin. Also claimed are: (1) isolated peptides of a
 CC fibronectin-binding protein that do not bind to fibronectin; (2) fusion
 CC protein containing at least one peptide of a fibronectin-binding protein
 CC linked to a second amino acid sequence; (3) nucleic acid encoding the
 CC isolated peptide of (1). Antibodies, the isolated peptides of (1) and the
 CC nucleic acids are all useful for immunisation (active or passive) and (by
 CC inhibiting binding of bacteria to fibronectin) for preventing or treating
 CC infection in humans or other animals, particularly by staphylococci or
 CC streptococci, e.g. meningitis, otitis media, pneumonia, endocarditis,
 CC mastitis in cattle, abortion in horses and many others. Since the
 CC antibodies block binding of bacteria, they should be effective against
 CC antibiotic-resistant strains, and may replace antibiotic therapy or
 CC increase its effectiveness. Sequences AAW65691-700 represent a series of

CC similar proteins on surfaces in the oral cavity
XX
SQ Sequence 113 AA;
Query: Match 100.0%. Score 51. DB 2.

Query Match	100.0%;	Score 51;	DB 2;	Length 113;
Best Local Similarity	100.0%;	Pred. No. 0.11;		
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			Indels	Gaps 0;

QY	1	I	V	D	I	D	F	D	S	V	P	10
Db	9	I	V	D	I	D	F	D	S	V	P	18

Search completed: October 25, 2005, 20:58:44
Job time : 64.2 secs

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OM protein - protein search, using sw model

Run on: October 22, 2005, 05:46:56 ; Search time 17.3 Seconds
(without alignments)
43.150 Million cell updates/sec

Title: US-10-731-238-75

Perfect score: 51

Sequence: 1 IVDIDFDSVP 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

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- 2: /cgn2_6/prodata/1/iaa/5B_COMB.pep:*
- 3: /cgn2_6/prodata/1/iaa/6A_COMB.pep:*
- 4: /cgn2_6/prodata/1/iaa/6B_COMB.pep:*
- 5: /cgn2_6/prodata/1/iaa/PCBUS_COMB.pep:*
- 6: /cgn2_6/prodata/1/iaa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	51	100.0	10	4	US-09-010-317-75 Sequence 75, Appl
2	51	100.0	14	4	US-09-010-317-60 Sequence 60, Appl
3	51	100.0	38	1	US-08-234-622A-2 Sequence 2, Appl
4	51	100.0	38	1	US-08-729-767-3 Sequence 3, Appl
5	51	100.0	38	4	US-09-010-317-5 Sequence 5, Appl
6	51	100.0	38	4	US-09-010-317-6 Sequence 6, Appl
7	51	100.0	38	4	US-09-010-317-35 Sequence 35, Appl
8	51	100.0	38	4	US-09-010-317-36 Sequence 36, Appl
9	51	100.0	38	4	US-09-010-317-37 Sequence 37, Appl
10	51	100.0	38	4	US-09-010-317-38 Sequence 38, Appl
11	51	100.0	38	4	US-09-010-317-39 Sequence 39, Appl
12	51	100.0	38	4	US-09-010-317-40 Sequence 40, Appl
13	51	100.0	38	4	US-09-010-317-41 Sequence 41, Appl
14	51	100.0	38	4	US-09-010-317-42 Sequence 42, Appl
15	51	100.0	38	4	US-09-010-317-43 Sequence 43, Appl
16	51	100.0	38	4	US-09-010-317-44 Sequence 44, Appl
17	51	100.0	114	1	US-08-259-000-3 Sequence 3, Appl
18	51	100.0	114	1	US-08-459-135A-7 Sequence 7, Appl
19	51	100.0	130	2	US-08-459-135A-8 Sequence 8, Appl
20	51	100.0	130	2	US-08-459-135A-7 Sequence 7, Appl
21	51	100.0	130	3	US-08-495-559-7 Sequence 8, Appl
22	51	100.0	139	3	US-08-856-253-8 Sequence 8, Appl
23	51	100.0	139	3	US-08-856-253-8 Sequence 8, Appl
24	51	100.0	174	2	US-08-459-135A-10 Sequence 10, Appl
25	51	100.0	174	2	US-08-459-135A-13 Sequence 13, Appl
26	51	100.0	174	3	US-08-495-559-10 Sequence 10, Appl
27	51	100.0	176	3	US-08-495-559-6 Sequence 6, Appl

28	51	100.0	178	2	US-08-459-135A-12 Sequence 12, Appl
29	51	100.0	178	3	US-08-495-559-12 Sequence 12, Appl
30	51	100.0	181	2	US-08-459-135A-6 Sequence 6, Appl
31	51	100.0	559	4	US-08-956-171E-5251 Sequence 5251, Ap
32	51	100.0	559	4	US-08-781-986A-5251 Sequence 5251, Ap
33	51	100.0	1027	4	US-08-956-171E-5254 Sequence 5254, Ap
34	51	100.0	1027	4	US-08-781-986A-5254 Sequence 5254, Ap
35	50	98.0	14	4	US-09-010-317-103 Sequence 58, Appl
36	50	98.0	36	4	US-09-010-317-58 Sequence 59, Appl
37	50	98.0	36	4	US-09-010-317-59 Sequence 3, Appl
38	50	98.0	38	1	US-08-234-622A-3 Sequence 4, Appl
39	50	98.0	38	1	US-08-729-767-4 Sequence 7, Appl
40	50	98.0	38	4	US-09-010-317-7 Sequence 45, Appl
41	50	98.0	38	4	US-09-010-317-8 Sequence 46, Appl
42	50	98.0	38	4	US-09-010-317-45 Sequence 47, Appl
43	50	98.0	38	4	US-09-010-317-46 Sequence 48, Appl
44	50	98.0	38	4	US-09-010-317-47 Sequence 48, Appl
45	50	98.0	38	4	US-09-010-317-48 Sequence 48, Appl

ALIGNMENTS

RESULT 1
US-09-010-317-75
Sequence 75, Application US/09010317
Patent No. 6685943
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
APPLICANT: Patti, Joseph M.
APPLICANT: House-Pompeo, Karen L.
APPLICANT: Speziale, Pietro
APPLICANT: Jon, Danny
APPLICANT: McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
TITLE OF INVENTION: AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAMK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 75:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-09-010-317-75
Query Match 100.0%; Score 51; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0031;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 IVDIDPDSVP 10
| | | | | | | | | |
Db 1 IVDIDPDSVP 10

RESULT 2
US-09-010-317-60
; Sequence 60, Application US/09010317
; Patent No. 6685943
; GENERAL INFORMATION:
; APPLICANT: Hook, Magnus
; APPLICANT: Patti, Joseph M.
; APPLICANT: House-Pompeo, Karen L.
; APPLICANT: Speziale, Pietro
; APPLICANT: McGavin, Martin J.
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
; TITLE OF INVENTION: AND METHODS OF USE
; NUMBER OF SEQUENCES: 105
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: TX
; COUNTRY: USA
; ZIP: 77210-4433
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/010,317
; FILING DATE:
; CLASSIFICATION:
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: US 60/036,139
; FILING DATE: 21-JAN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Hibler, David W.
; REGISTRATION NUMBER: 41,071
; REFERENCE/DOCKET NUMBER: TANK:189
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 512-418-3000
; TELEFAX: 512-474-7577
; INFORMATION FOR SEQ ID NO: 60:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
US-09-010-317-60

Query Match 100.0%; Score 51; DB 4; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.0044;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 IVDIDPDSVP 10
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Db 5 IVDIDPDSVP 14

RESULT 3
US-08-234-622A-2
; Sequence 2, Application US/08234622A
; Patent No. 5440014
; GENERAL INFORMATION:
; APPLICANT: HOOK, Magnus
; APPLICANT: MCGAVIN, Martin
; APPLICANT: RAUCCI, Giuseppe
; TITLE OF INVENTION: A FIBRONECTIN BINDING PEPTIDE

NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Doane, Swecker & Mathis
; STREET: P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/234,622A
; FILING DATE: 28-APR-1994
; CLASSIFICATION: 530
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: SE 9002617-0
; FILING DATE: 10-AUG-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/SE91/00534
; FILING DATE: 09-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Meuth, Donna M
; REGISTRATION NUMBER: 36,607
; REFERENCE/DOCKET NUMBER: 012885-044
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 38 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-234-622A-2

Query Match 100.0%; Score 51; DB 1; Length 38;
Best Local Similarity 100.0%; Pred. No. 0.013;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 IVDIDPDSVP 10
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Db 25 IVDIDPDSVP 34

RESULT 4
US-08-729-767-3
; Sequence 3, Application US/08729767
; Patent No. 5770702
; GENERAL INFORMATION:
; APPLICANT: HOOK, Magnus
; APPLICANT: LINDBERG, Martin Kjeil
; APPLICANT: SIGNS, Lars Christer
; APPLICANT: MADSTROM, Torkel Mikael
; APPLICANT: FROWAN, Gunnar
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN AS WELL AS
; TITLE OF INVENTION: ITS PREPARATION
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Doane, Swecker & Mathis, L.L.P.
; STREET: P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/729,767
FILING DATE: 07-OCT-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/259,000
FILING DATE: 13-JUN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/007,817
FILING DATE: 22-JAN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/201,028
FILING DATE: 01-JUN-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: SE 8702272-9
FILING DATE: 01-JUN-1987
ATTORNEY/AGENT INFORMATION:
NAME: McGowan, Malcolm K.
REGISTRATION NUMBER: 39,300
REFERENCE/DOCKET NUMBER: 012889-036
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-729-767-3

Query Match 100.0%; Score 51; DB 1; Length 38;
Best local Similarity 100.0%; Pred. No. 0.013;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IVDIDFDSVP 10
Db 26 IVDIDFDSVP 35

RESULT 5
US-09-010-317-5
Sequence 5, Application US/09010317
Patent No. 6685943
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
APPLICANT: Patti, Joseph M.
APPLICANT: House-Pompeo, Karen L.
APPLICANT: Speziale, Pietro
APPLICANT: Joh, Danny
APPLICANT: McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
TITLE OF INVENTION: AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/036,139

FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TANK:189
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-09-010-317-5

Query Match 100.0%; Score 51; DB 4; Length 38;
Best local Similarity 100.0%; Pred. No. 0.013;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IVDIDFDSVP 10
Db 25 IVDIDFDSVP 34

RESULT 6
US-09-010-317-6
Sequence 6, Application US/09010317
Patent No. 6685943
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
APPLICANT: Patti, Joseph M.
APPLICANT: House-Pompeo, Karen L.
APPLICANT: Speziale, Pietro
APPLICANT: Joh, Danny
APPLICANT: McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
TITLE OF INVENTION: AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TANK:189
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-09-010-317-6

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAMK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 37:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-09-010-317-37

Query Match 100.0%; Score 51; DB 4; Length 38;
Best Local Similarity 100.0%; Pred. No. 0.013;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IVDIDPDSVP 10
DB 25 IVDIDPDSVP 34

RESULT 10
US-09-010-317-38
Sequence 38, Application US/09010317
Patent No. 6685943
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
APPLICANT: Patti, Joseph M.
APPLICANT: House-Pompeo, Karen L.
APPLICANT: Speziale, Pietro
APPLICANT: John, Danny
APPLICANT: McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
TITLE OF INVENTION: AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAMK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000

TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 38:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-09-010-317-38

Query Match 100.0%; Score 51; DB 4; Length 38;
Best Local Similarity 100.0%; Pred. No. 0.013;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IVDIDPDSVP 10
DB 25 IVDIDPDSVP 34

RESULT 11
US-09-010-317-39
Sequence 39, Application US/09010317
Patent No. 6685943
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
APPLICANT: Patti, Joseph M.
APPLICANT: House-Pompeo, Karen L.
APPLICANT: Speziale, Pietro
APPLICANT: John, Danny
APPLICANT: McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
TITLE OF INVENTION: AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAMK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 39:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-09-010-317-39

Query Match 100.0%; Score 51; DB 4; Length 38;
Best Local Similarity 100.0%; Pred. No. 0.013;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IVDIDPDSVP 10
DB 25 IVDIDPDSVP 34

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RESULT 12
US-09-010-317-40
; Sequence 40, Application US/09010317
; Patent No. 6685943
; GENERAL INFORMATION:
; APPLICANT: Hook, Magnus
; APPLICANT: Patti, Joseph M.
; APPLICANT: House-Pompeo, Karen L.
; APPLICANT: Speziale, Pietro
; APPLICANT: McGavin, Martin J.
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
; TITLE OF INVENTION: AND METHODS OF USE
; NUMBER OF SEQUENCES: 105
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: TX
; COUNTRY: USA
; ZIP: 77210-4433
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/010,317
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/036,139
; FILING DATE: 21-JAN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Hibler, David W.
; REGISTRATION NUMBER: 41,071
; REFERENCE/DOCKET NUMBER: TANK:189
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 512-418-3000
; TELEFAX: 512-474-7577
; INFORMATION FOR SEQ ID NO: 40:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 38 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
US-09-010-317-40

Query Match      100.0%; Score 51; DB 4; Length 38;
Best Local Similarity 100.0%; Pred. No. 0.013;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 IVDIDFDSVP 10
Db      25 IVDIDFDSVP 34

RESULT 13
US-09-010-317-41
; Sequence 41, Application US/09010317
; Patent No. 6685943
; GENERAL INFORMATION:
; APPLICANT: Hook, Magnus
; APPLICANT: Patti, Joseph M.
; APPLICANT: House-Pompeo, Karen L.
; APPLICANT: Speziale, Pietro
; APPLICANT: Joh, Danny
; APPLICANT: McGavin, Martin J.
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
; TITLE OF INVENTION: AND METHODS OF USE
; NUMBER OF SEQUENCES: 105
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; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: TX
; COUNTRY: USA
; ZIP: 77210-4433
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/010,317
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/036,139
; FILING DATE: 21-JAN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Hibler, David W.
; REGISTRATION NUMBER: 41,071
; REFERENCE/DOCKET NUMBER: TANK:189
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 512-418-3000
; TELEFAX: 512-474-7577
; INFORMATION FOR SEQ ID NO: 41:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 38 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
US-09-010-317-41

Query Match      100.0%; Score 51; DB 4; Length 38;
Best Local Similarity 100.0%; Pred. No. 0.013;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 IVDIDFDSVP 10
Db      25 IVDIDFDSVP 34

RESULT 14
US-09-010-317-42
; Sequence 42, Application US/09010317
; Patent No. 6685943
; GENERAL INFORMATION:
; APPLICANT: Hook, Magnus
; APPLICANT: Patti, Joseph M.
; APPLICANT: House-Pompeo, Karen L.
; APPLICANT: Speziale, Pietro
; APPLICANT: Joh, Danny
; APPLICANT: McGavin, Martin J.
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
; TITLE OF INVENTION: AND METHODS OF USE
; NUMBER OF SEQUENCES: 105
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: TX
; COUNTRY: USA
; ZIP: 77210-4433
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/010,317
; FILING DATE:
; CLASSIFICATION:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAMK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 42:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-09-010-317-42

Query Match 100.0%; Score 51; DB 4; Length 38;
Best Local Similarity 100.0%; Pred. No. 0.013;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IVDIDFDSVP 10
|||
Db 25 IVDIDFDSVP 34

RESULT 15
US-09-010-317-43
Sequence 43, Application US/09010317
Patent No. 6685943
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
APPLICANT: Patti, Joseph M.
APPLICANT: House-Pompeo, Karen L.
APPLICANT: Speziale, Pietro
APPLICANT: Jon, Danny
APPLICANT: McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
TITLE OF INVENTION: AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAMK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 43:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear

US-09-010-317-43

Query Match 100.0%; Score 51; DB 4; Length 38;
Best Local Similarity 100.0%; Pred. No. 0.013;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IVDIDFDSVP 10
|||
Db 25 IVDIDFDSVP 34

Search completed: October 22, 2005, 07:41:42
Job time : 17.35 secs

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OM protein - protein search, using sw model

Run on: October 22, 2005, 12:09:40 ; Search time 57.25 Seconds
(without alignments)
72.924 Million cell updates/sec

Title: US-10-731-238-75

Perfect score: 51

Sequence: 1 IVDIDFDSVP 10

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Gapop 10.0 , Gapext 0.5

Searched: 1862951 seqs, 417491010 residues

Total number of hits satisfying chosen parameters: 1862951

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Published Applications_AA:*

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18: /cgn2_6/prodata/2/pubppaa/US10C_PUBCOMB.pep:*

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20: /cgn2_6/prodata/2/pubppaa/US11_PUBCOMB.pep:*

21: /cgn2_6/prodata/2/pubppaa/US60_NEW_PUB.pep:*

22: /cgn2_6/prodata/2/pubppaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	51	100.0	14	US-10-731-238-60	Sequence 75, Appl
3	51	100.0	38	US-10-731-238-5	Sequence 5, Appl
4	51	100.0	38	US-10-731-238-6	Sequence 6, Appl
5	51	100.0	38	US-10-731-238-35	Sequence 35, Appl
6	51	100.0	38	US-10-731-238-36	Sequence 36, Appl
7	51	100.0	38	US-10-731-238-37	Sequence 37, Appl
8	51	100.0	38	US-10-731-238-38	Sequence 38, Appl
9	51	100.0	38	US-10-731-238-39	Sequence 39, Appl
10	51	100.0	38	US-10-731-238-40	Sequence 40, Appl
11	51	100.0	38	US-10-731-238-41	Sequence 41, Appl

Result No.	Score	Query Match	Length	ID	Description
12	51	100.0	38	US-10-731-238-42	Sequence 42, Appl
13	51	100.0	38	US-10-731-238-43	Sequence 43, Appl
14	51	100.0	38	US-10-731-238-44	Sequence 44, Appl
15	51	100.0	139	US-09-813-820-8	Sequence 1, Appl
16	51	100.0	388	US-08-901-062-1	Sequence 5251, Ap
17	51	100.0	559	US-08-781-986A-5251	Sequence 5251, Ap
18	51	100.0	559	US-10-329-624-5251	Sequence 5899, Ap
19	51	100.0	767	US-09-815-242-5899	Sequence 13140, A
20	51	100.0	767	US-09-815-242-13140	Sequence 424, Ap
21	51	100.0	940	US-10-470-048B-424	Sequence 69, Appl
22	51	100.0	948	US-10-470-048B-69	Sequence 43778, A
23	51	100.0	961	US-10-282-122A-43778	Sequence 5456, Ap
24	51	100.0	978	US-09-815-242-5456	Sequence 12686, A
25	51	100.0	1001	US-09-815-242-12686	Sequence 5797, Ap
26	51	100.0	1018	US-09-815-242-5797	Sequence 12838, A
27	51	100.0	1018	US-09-815-242-12838	Sequence 68, Appl
28	51	100.0	1018	US-10-470-048B-68	Sequence 5254, Ap
29	51	100.0	1027	US-08-781-986A-5254	Sequence 5254, Ap
30	51	100.0	1027	US-10-329-624-5254	Sequence 43827, A
31	51	100.0	1038	US-10-282-122A-43827	Sequence 103, App
32	50	98.0	14	US-10-731-238-103	Sequence 58, Appl
33	50	98.0	36	US-10-731-238-58	Sequence 59, Appl
34	50	98.0	36	US-10-731-238-59	Sequence 7, Appl
35	50	98.0	38	US-10-731-238-7	Sequence 8, Appl
36	50	98.0	38	US-10-731-238-8	Sequence 45, Appl
37	50	98.0	38	US-10-731-238-45	Sequence 46, Appl
38	50	98.0	38	US-10-731-238-46	Sequence 47, Appl
39	50	98.0	38	US-10-731-238-47	Sequence 48, Appl
40	50	98.0	38	US-10-731-238-48	Sequence 49, Appl
41	50	98.0	38	US-10-731-238-49	Sequence 50, Appl
42	50	98.0	38	US-10-731-238-50	Sequence 56, Appl
43	43	84.3	39	US-10-731-238-76	Sequence 57, Appl
44	40.5	79.4	39	US-10-731-238-56	
45	40.5	79.4	39	US-10-731-238-57	

ALIGNMENTS

RESULT 1

US-10-731-238-75

Sequence 75, Application US/10731238

Publication No. US20050123552A1

GENERAL INFORMATION:

APPLICANT: Hook, Magnus

Patel, Joseph M.

House-Pompeo, Karen L.

Speziale, Pietro

Joh, Danny

McGavin, Martin J.

TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS

AND METHODS OF USE

NUMBER OF SEQUENCES: 105

CORRESPONDENCE ADDRESS:

ADDRESSEE: Arnold, White & Durkee

STREET: P.O. Box 4433

CITY: Houston

STATE: TX

COUNTRY: USA

ZIP: 77210-4433

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/731.238

FILING DATE: 10-Dec-2003

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/010.317

FILING DATE: 21-Jan-1998

APPLICATION NUMBER: US 60/036.139

```
/ FILING DATE: 21-JAN-1997
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Hibler, David W.
/ REGISTRATION NUMBER: 41,071
/ REFERENCE/DOCKET NUMBER: TAMK:189
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 512-418-3000
/ TELEFAX: 512-474-7577
/ INFORMATION FOR SEQ ID NO: 75:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 10 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: <Unknown>
/ TOPOLOGY: linear
/ SEQUENCE DESCRIPTION: SEQ ID NO: 75:
US-10-731-238-75

Query Match      100.0%; Score 51; DB 18; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.01;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 IVDIDFDSVP 10
        |||||||
Db       1 IVDIDFDSVP 10

RESULT 2
US-10-731-238-60
/ Sequence 60, Application US/10731238
/ Publication No. US20050123552A1
/ GENERAL INFORMATION:
/ APPLICANT: Hook, Magnus
/      Patti, Joseph M.
/      House-Pompeo, Karen L.
/      Speziale, Pietro
/      Joh, Danny
/      McGavin, Martin J.
/ TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
/ AND METHODS OF USE
/ NUMBER OF SEQUENCES: 105
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Arnold, White & Durkee
/ STREET: P.O. Box 4433
/ CITY: Houston
/ STATE: TX
/ COUNTRY: USA
/ ZIP: 77210-4433
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patentin Releasee #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/10/731,238
/ FILING DATE: 10-Dec-2003
/ CLASSIFICATION: <Unknown>
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US/09/010,317
/ FILING DATE: 21-Jan-1998
/ APPLICATION NUMBER: US 60/036,139
/ FILING DATE: 21-JAN-1997
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Hibler, David W.
/ REGISTRATION NUMBER: 41,071
/ REFERENCE/DOCKET NUMBER: TAMK:189
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 512-418-3000
/ TELEFAX: 512-474-7577
/ INFORMATION FOR SEQ ID NO: 60:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 14 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: <Unknown>
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/ TOPOLOGY: linear
/ SEQUENCE DESCRIPTION: SEQ ID NO: 60:
US-10-731-238-60

Query Match      100.0%; Score 51; DB 18; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.015;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 IVDIDFDSVP 10
        |||||||
Db       5 IVDIDFDSVP 14

RESULT 3
US-10-731-238-5
/ Sequence 5, Application US/10731238
/ Publication No. US20050123552A1
/ GENERAL INFORMATION:
/ APPLICANT: Hook, Magnus
/      Patti, Joseph M.
/      House-Pompeo, Karen L.
/      Speziale, Pietro
/      Joh, Danny
/      McGavin, Martin J.
/ TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
/ AND METHODS OF USE
/ NUMBER OF SEQUENCES: 105
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Arnold, White & Durkee
/ STREET: P.O. Box 4433
/ CITY: Houston
/ STATE: TX
/ COUNTRY: USA
/ ZIP: 77210-4433
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patentin Releasee #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/10/731,238
/ FILING DATE: 10-Dec-2003
/ CLASSIFICATION: <Unknown>
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US/09/010,317
/ FILING DATE: 21-Jan-1998
/ APPLICATION NUMBER: US 60/036,139
/ FILING DATE: 21-JAN-1997
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Hibler, David W.
/ REGISTRATION NUMBER: 41,071
/ REFERENCE/DOCKET NUMBER: TAMK:189
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 512-418-3000
/ TELEFAX: 512-474-7577
/ INFORMATION FOR SEQ ID NO: 5:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 38 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: <Unknown>
/ TOPOLOGY: linear
/ SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-10-731-238-5

Query Match      100.0%; Score 51; DB 18; Length 38;
Best Local Similarity 100.0%; Pred. No. 0.045;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 IVDIDFDSVP 10
        |||||||
Db       25 IVDIDFDSVP 34
```

```
RESULT 4
US-10-731-238-6
; Sequence 6, Application US/10731238
; Publication No. US20050123552A1
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
Patli, Joseph M.
House-Pompeo, Karen L.
Speziale, Pietro
Joh, Danny
McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/731,238
FILING DATE: 10-Dec-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE: 21-Jan-1998
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TANK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-10-731-238-6
Query Match 100.0%; Score 51; DB 18; Length 38;
Best Local Similarity 100.0%; Pred. No. 0.045;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IVDIDFDSVP 10
| | | | | | | |
| | | | | | | |
Db 25 IVDIDFDSVP 34

RESULT 5
US-10-731-238-35
; Sequence 35, Application US/10731238
; Publication No. US20050123552A1
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
Patli, Joseph M.
House-Pompeo, Karen L.
Speziale, Pietro
Joh, Danny
McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
AND METHODS OF USE
```

```
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/731,238
FILING DATE: 10-Dec-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE: 21-Jan-1998
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TANK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 35:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 35:
US-10-731-238-35
Query Match 100.0%; Score 51; DB 18; Length 38;
Best Local Similarity 100.0%; Pred. No. 0.045;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IVDIDFDSVP 10
| | | | | | | |
| | | | | | | |
Db 25 IVDIDFDSVP 34

RESULT 6
US-10-731-238-36
; Sequence 36, Application US/10731238
; Publication No. US20050123552A1
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
Patli, Joseph M.
House-Pompeo, Karen L.
Speziale, Pietro
Joh, Danny
McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/731,238
FILING DATE: 10-Dec-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE: 21-Jan-1998
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-Jan-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAMK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 36:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 36:
US-10-731-238-36

Query Match 100.0%; Score 51; DB 18; Length 38;
Best Local Similarity 100.0%; Pred. No. 0.045;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IVDIDFDSVP 10
|||
Db 25 IVDIDFDSVP 34

RESULT 7
US-10-731-238-37
Sequence 37, Application US/10731238
Publication No. US20050123552A1
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
Patti, Joseph M.
House-Pompeo, Karen L.
Speziale, Pietro
Joh, Danny
McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/731,238
FILING DATE: 10-Dec-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE: 21-Jan-1998
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-Jan-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAMK:189

TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 37:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 37:
US-10-731-238-37

Query Match 100.0%; Score 51; DB 18; Length 38;
Best Local Similarity 100.0%; Pred. No. 0.045;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IVDIDFDSVP 10
|||
Db 25 IVDIDFDSVP 34

RESULT 8
US-10-731-238-38
Sequence 38, Application US/10731238
Publication No. US20050123552A1
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
Patti, Joseph M.
House-Pompeo, Karen L.
Speziale, Pietro
Joh, Danny
McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/731,238
FILING DATE: 10-Dec-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE: 21-Jan-1998
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-Jan-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAMK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 38:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 38:
US-10-731-238-38

Query Match 100.0%; Score 51; DB 18; Length 38;

Best Local Similarity 100.0%; Pred. No. 0.045;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 IVDIDFDSVP 10
|||
Db 25 IVDIDFDSVP 34

RESULT 9

US-10-731-238-39
; Sequence 39, Application US/10731238
; Publication No. US20050123552A1
; GENERAL INFORMATION:
; APPLICANT: Hook, Magnus
; Patti, Joseph M.
; House-Pompeo, Karen L.
; Speziale, Pietro
; Joh, Danny
; McGavin, Martin J.
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
; AND METHODS OF USE
; NUMBER OF SEQUENCES: 105
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: TX
; COUNTRY: USA
; ZIP: 77210-4433
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/731,238
; FILING DATE: 10-Dec-2003
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/010,317
; FILING DATE: 21-Jan-1998
; APPLICATION NUMBER: US 60/036,139
; FILING DATE: 21-JAN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Hibler, David W.
; REGISTRATION NUMBER: 41,071
; REFERENCE/DOCKET NUMBER: TAMK.189
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 512-418-3000
; TELEFAX: 512-474-7577
; INFORMATION FOR SEQ ID NO: 39:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 38 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 39:
US-10-731-238-39

Query Match 100.0%; Score 51; DB 18; Length 38;
Best Local Similarity 100.0%; Pred. No. 0.045;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 IVDIDFDSVP 10
|||
Db 25 IVDIDFDSVP 34

RESULT 10
US-10-731-238-40
; Sequence 40, Application US/10731238
; Publication No. US20050123552A1
; GENERAL INFORMATION:
; APPLICANT: Hook, Magnus
; Patti, Joseph M.
; House-Pompeo, Karen L.
; Speziale, Pietro
; Joh, Danny
; McGavin, Martin J.
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
; AND METHODS OF USE
; NUMBER OF SEQUENCES: 105
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: TX
; COUNTRY: USA
; ZIP: 77210-4433
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/731,238
; FILING DATE: 10-Dec-2003
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/010,317
; FILING DATE: 21-Jan-1998
; APPLICATION NUMBER: US 60/036,139
; FILING DATE: 21-JAN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Hibler, David W.
; REGISTRATION NUMBER: 41,071
; REFERENCE/DOCKET NUMBER: TAMK.189
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 512-418-3000
; TELEFAX: 512-474-7577
; INFORMATION FOR SEQ ID NO: 40:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 38 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 40:
US-10-731-238-40

Query Match 100.0%; Score 51; DB 18; Length 38;
Best Local Similarity 100.0%; Pred. No. 0.045;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 IVDIDFDSVP 10
|||
Db 25 IVDIDFDSVP 34

RESULT 11
US-10-731-238-41
; Sequence 41, Application US/10731238
; Publication No. US20050123552A1
; GENERAL INFORMATION:
; APPLICANT: Hook, Magnus
; Patti, Joseph M.
; House-Pompeo, Karen L.
; Speziale, Pietro
; Joh, Danny
; McGavin, Martin J.
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
; AND METHODS OF USE
; NUMBER OF SEQUENCES: 105
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: TX
; COUNTRY: USA
; ZIP: 77210-4433
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/731,238
; FILING DATE: 10-Dec-2003
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/010,317
; FILING DATE: 21-Jan-1998
; APPLICATION NUMBER: US 60/036,139
; FILING DATE: 21-JAN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Hibler, David W.
; REGISTRATION NUMBER: 41,071
; REFERENCE/DOCKET NUMBER: TAMK.189
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 512-418-3000
; TELEFAX: 512-474-7577
; INFORMATION FOR SEQ ID NO: 41:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 38 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 41:
US-10-731-238-41

STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/731,238
FILING DATE: 10-Dec-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE: 21-Jan-1998
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAMK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 41:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 41:
US-10-731-238-41

Query Match 100.0%; Score 51; DB 18; Length 38;
Beet Local Similarity 100.0%; Pred. No. 0.045;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 IVDIDFDSVP 10
Db 25 IVDIDFDSVP 34

RESULT 12
US-10-731-238-42
Sequence 42, Application US/10731238
Publication No. US2005012352A1
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
Patti, Joseph M.
House-Pompeo, Karen L.
Speziale, Pietro
John, Danny
McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/731,238
FILING DATE: 10-Dec-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/010,317
FILING DATE: 21-Jan-1998
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAMK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 42:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 42:
US-10-731-238-42

Query Match 100.0%; Score 51; DB 18; Length 38;
Beet Local Similarity 100.0%; Pred. No. 0.045;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 IVDIDFDSVP 10
Db 25 IVDIDFDSVP 34

RESULT 13
US-10-731-238-43
Sequence 43, Application US/10731238
Publication No. US2005012352A1
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
Patti, Joseph M.
House-Pompeo, Karen L.
Speziale, Pietro
John, Danny
McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/731,238
FILING DATE: 10-Dec-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE: 21-Jan-1998
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAMK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 43:
SEQUENCE CHARACTERISTICS:

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;
; LENGTH: 38 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 43:
US-10-731-238-43

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```

Query Match          100.0%; Score 51; DB 18; Length 38;
Best Local Similarity 100.0%; Pred. No. 0.045;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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```

QY 1 IVDIDPDSVP 10
    |||||
DB 25 IVDIDPDSVP 34

```

```

RESULT 14
US-10-731-238-44
; Sequence 44, Application US/10731238
; Publication No. US20050123552A1
; GENERAL INFORMATION:
; APPLICANT: Hook, Magnus
;             Patti, Joseph M.
;             House-Pompeo, Karen L.
;             Speziale, Pietro
;             John, Danny
;             McGavin, Martin J.
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
; AND METHODS OF USE
; NUMBER OF SEQUENCES: 105
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: TX
; COUNTRY: USA
; ZIP: 77210-4433
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/731,238
; FILING DATE: 10-Dec-2003
; CLASSIFICATION: <Unknown>
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: US/09/010,317
; FILING DATE: 21-Jan-1998
; APPLICATION NUMBER: US 60/036,139
; FILING DATE: 21-Jan-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Hibler, David W.
; REGISTRATION NUMBER: 41,071
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 512-418-3000
; TELEFAX: 512-474-7577
; INFORMATION FOR SEQ ID NO: 44:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 38 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 44:
US-10-731-238-44

```

```

Query Match          100.0%; Score 51; DB 18; Length 38;
Best Local Similarity 100.0%; Pred. No. 0.045;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 IVDIDPDSVP 10
    |||||

```

```

DB 25 IVDIDPDSVP 34

```

```

RESULT 15
US-09-813-820-8
; Sequence 8, Application US/09813820
; Patent No. US20020102262A1
; GENERAL INFORMATION:
; APPLICANT: Hook, Magnus
;             Patti, Joseph M.
;             House-Pompeo, Karen
;             Sthanam, Narayana
;             Symeraky, Jindrich
; TITLE OF INVENTION: COLLAGEN BINDING PROTEIN COMPOSITIONS
; AND METHODS OF USE
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: U.S.
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/813,820
; FILING DATE: 22-Mar-2001
; CLASSIFICATION: <Unknown>
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: 08/856,253
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Kirchell, Barbara S.
; REGISTRATION NUMBER: 33,928
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (512) 418-3000
; TELEFAX: (512) 474-7577
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 139 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-09-813-820-8

```

```

Query Match          100.0%; Score 51; DB 9; Length 139;
Best Local Similarity 100.0%; Pred. No. 0.19;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 IVDIDPDSVP 10
    |||||
DB 40 IVDIDPDSVP 49

```

Search completed: October 22, 2005, 12:39:45
Job time : 57.25 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 22, 2005, 06:10:10 ; Search time 11.45 Seconds
(without alignments)
84.032 Million cell updates/sec

Title: US-10-731-238-75

Perfect score: 51

Sequence: 1 IVDIDFDSVP 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :
1: pir1: *
2: pir2: *
3: pir3: *
4: pir4: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	51	100.0	940	2	S19702
2	51	100.0	961	2	G90053
3	51	100.0	1018	2	A32192
4	51	100.0	1038	2	H90053
5	38	74.5	430	1	Z4BP33
6	37	72.5	249	2	E90391
7	37	72.5	249	2	E49849
8	36	70.6	330	2	E98119
9	36	70.6	511	1	S31308
10	36	70.6	827	2	AB2764
11	36	70.6	832	2	A97545
12	36	70.6	1173	2	T42719
13	36	70.6	1195	2	E96615
14	36	70.6	1246	2	S60954
15	35	68.6	82	2	AD3161
16	35	68.6	102	2	S52711
17	35	68.6	185	2	AG0577
18	35	68.6	200	2	F97858
19	35	68.6	376	2	G84404
20	35	68.6	385	2	B84287
21	35	68.6	396	2	T33386
22	35	68.6	517	2	D72555
23	35	68.6	557	2	T40956
24	35	68.6	617	2	G70366
25	35	68.6	629	2	F72400
26	35	68.6	648	2	T44343
27	35	68.6	764	2	T39878
28	35	68.6	975	1	A28174
29	35	68.6	986	2	AB2209

30	35	68.6	995	2	C84145	hypothetical prote
31	35	68.6	2416	2	T13825	adenomatous poly
32	34	66.7	64	2	B81078	hypothetical prote
33	34	66.7	83	2	T07538	hypothetical prote
34	34	66.7	124	2	A84313	glycine decarboxyl
35	34	66.7	129	2	S73514	probable lipoprote
36	34	66.7	199	2	AF0947	probable haloacid
37	34	66.7	206	2	S40829	hypothetical 23.5k
38	34	66.7	206	2	G86076	probable phosphata
39	34	66.7	206	2	H91229	hypothetical prote
40	34	66.7	266	2	F75081	hypothetical prote
41	34	66.7	269	2	C86726	conserved hypochet
42	34	66.7	282	2	A84914	hypothetical prote
43	34	66.7	284	2	E72535	probable 4-hydroxy
44	34	66.7	284	2	E84616	probable bHLH tran
45	34	66.7	307	2	B40711	RNA polymerase II

ALIGNMENTS

RESULT 1
S19702
fibronectin-binding protein B - Staphylococcus aureus
C/Species: Staphylococcus aureus
C/Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #ext_change 09-Jul-2004
C/Accession: S19702
R/Joensson, K.; Signaes, C.; Mueller, H.P.; Lindberg, M.
Eur. J. Biochem. 202, 1041-1048, 1991
A/Title: Two different genes encode fibronectin binding proteins in Staphylococcus aure
A/Reference number: S19702; MUID:92111475; PMID:1837266
A/Accession: S19702
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-940 <JOB>
C/Cross-references: UNIPROT:Q53682; EMBL:X62992; NID:G49040; PIDN:CAA44726.1; PID:G5815
C/Keyword: fibronectin binding

Query Match
Best Local Similarity 100.0%; Score 51; DB 2; Length 940;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IVDIDFDSVP 10
DB 706 IVDIDFDSVP 715

RESULT 2

G90053
hypothetical protein fmb [imported] - Staphylococcus aureus (strain N315)
C/Species: Staphylococcus aureus
C/Date: 10-May-2001 #sequence_revision 10-May-2001 #ext_change 09-Jul-2004
C/Accession: G90053
R/Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Ogun
ma, A.; Mizutani, U.; Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kato, C.; Sekimizu, K.
C.; Shib, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiwamatsu, K.
Lancet 357, 1225-1240, 2001
A/Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.
A/Reference number: AB9758; MUID:21311952; PMID:11418146
A/Accession: G90053
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-961 <KUR>
A/Cross-references: UNIPROT:Q99RD3; GB:BA000018; PID:G13702452; PIDN:BAR43593.1; GSPDB:
A/Experimental source: strain N315
C/Genetics: fmb

Query Match
Best Local Similarity 100.0%; Score 51; DB 2; Length 961;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IVDIDFDSVP 10

Db 717 IVDIDFDSVP 726

RESULT 3

A32192

A: fibronectin-binding protein - Staphylococcus aureus

C: Species: Staphylococcus aureus

C: Date: 31-Jul-1989 #sequence_revision 31-Jul-1989 #text_change 16-Feb-1997

C: Accession: A32192

R: Sjognaes, C.; Raucci, G.; Joensen, K.; Lindgren, P.E.; Anantharamiah, G.M.; Hoesek, M

Proc. Natl. Acad. Sci. U.S.A. 86, 699-703, 1989

A: Title: Nucleotide sequence of the gene for a fibronectin-binding protein from Staphylo

A: Reference number: A32192; MUID:8908898; PMID:2521391

A: Accession: A32192

A: Status: preliminary

A: Molecule type: DNA

A: Residues: 1-1018 <SIG>

A: Cross-references: GB:J04151

C: Keywords: fibronectin binding

Query Match 100.0%; Score 51; DB 2; Length 1018;
Best Local Similarity 100.0%; Pred. No. 0.23;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IVDIDFDSVP 10
Db 770 IVDIDFDSVP 779

RESULT 4

H90053

A: hypothetical protein fnb [imported] - Staphylococcus aureus (strain N315)

C: Species: Staphylococcus aureus

C: Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004

C: Accession: H90053

R: Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguc

ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kato, C.; Sekimizu, K.;

C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.

Lancet 357, 1225-1240, 2001

A: Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.

A: Reference number: A89758; MUID:21311952; PMID:11418146

A: Accession: H90053

A: Status: preliminary

A: Molecule type: DNA

A: Residues: 1-1038 <KOR>

A: Cross-references: UNIPROT:Q99RD2; GB:BA000018; PID:G13702453; PIDN:BA843594.1; GSPDB:C

A: Experimental source: strain N315

C: Genetics:

A: Gene: fnb

Query Match 100.0%; Score 51; DB 2; Length 1038;
Best Local Similarity 100.0%; Pred. No. 0.23;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IVDIDFDSVP 10
Db 766 IVDIDFDSVP 775

RESULT 5

Z4BP33

A: gene 430 proteain - phage Pf3

C: Species: phage Pf3

A: Note: host Pseudomonas aeruginosa

C: Date: 28-May-1986 #sequence_revision 28-May-1986 #text_change 09-Jul-2004

C: Accession: A04270

R: Luiten, R.G.M.; Puterman, D.G.; Scheemakers, J.G.G.; Konings, R.N.H.; Day, L.A.

J. Virol. 56, 268-276, 1985

A: Title: Nucleotide sequence of the genome of Pf3, an IncP-1 plasmid-specific filamentou

A: Reference number: A94693; MUID:85293231; PMID:3928901

A: Accession: A04270

A: Molecule type: DNA

A: Residues: 1-430 <LUI>

A: Cross-references: UNIPROT:P03668; GB:M11912; NID:9215375; PIDN:AAA88381.1; PID:9215375

C: Comment: Bacteriophage Pf3 is a class II filamentous phage.

C: Comment: The host is strain O harboring IncPl plasmids.

C: Genetics:

A: Gene: 430

C: Superfamily: filamentous phage gene IV protein

C: Keywords: phage maturation

Query Match 74.5%; Score 38; DB 1; Length 430;
Best Local Similarity 60.0%; Pred. No. 23;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 IVDIDFDSVP 10
Db 57 VVSLDFDVP 66

RESULT 6

E90391

A: conserved hypothetical protein [imported] - Sulfolobus solfataricus

C: Species: Sulfolobus solfataricus

C: Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 16-Aug-2004

C: Accession: E90391

R: She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Chan-

Jong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, P

arrett, R.A.; Ragan, M.A.; Sensen, C.W.; Van der Oost, J.

submitted to Genbank, April 2001

A: Description: Sulfolobus solfataricus complete genome.

A: Reference number: A89139

A: Accession: E90391

A: Status: preliminary

A: Molecule type: DNA

A: Residues: 1-249 <KOR>

A: Cross-references: UNIPROT:Q97WJ8; GB:AE006641; NID:g13815518; PIDN:AAK42388.1; GSPDB:C

C: Genetics:

A: Gene: SS02219

C: Superfamily: ATP-NAD/NADH kinase

Query Match 72.5%; Score 37; DB 2; Length 249;
Best Local Similarity 77.8%; Pred. No. 19;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 IVDIDFDSVP 9
Db 31 VVDIDFDYV 39

RESULT 7

S49849

A: aconitate hydratase (EC 4.2.1.3) - muskmelon (fragment)

N: Alternate names: aconitase

C: Species: Cucumis melo (muskmelon)

C: Date: 05-Mar-1995 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004

C: Accession: S49849

R: Peyret, P.; Perez, P.; Alric, M.

submitted to the EMBL Data Library, November 1994

A: Description: Plant aconitase enzyme.

A: Reference number: S49847

A: Accession: S49849

A: Molecule type: mRNA

A: Residues: 1-764 <PEY>

A: Cross-references: UNIPROT:Q42669; EMBL:X82840; NID:g559722; PIDN:CAA58047.1; PID:g5597

A: Experimental source: variety Cantaloupe; pale ripening fruit; tissue type flesh

C: Genetics:

A: Gene: Aco

C: Function:

A: Description: reversibly catalyzes the hydration of cis-aconitate to citrate and also t

A: Pathway: glyoxylate bypass

C: Superfamily: iron-responsive element-binding protein

C: Keywords: 4Fe-4S; carbon-oxygen lyase; glyoxylate bypass; hydro-lyase; iron-sulfur pro

F: 349-492/Domain: RNA binding #status predicted <RNA>

F: 307,372,375/Binding site: 4Fe-4S cluster (Cys) (covalent) #status predicted

Query Match 72.5%; Score 37; DB 2; Length 764;
 Best Local Similarity 77.8%; Pred. No. 69;
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 VDIIDPDSVP 10
 |||||:|
 DB 435 VDIIDPDSVP 443

RESULT 8

E98119
 transposase, uncharacterized, truncation [imported] - Streptococcus pneumoniae (strain R
 C:Species: Streptococcus pneumoniae
 C:Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 09-Jul-2004
 C:Accession: E98119
 R:Hoeking, J.A.; Alborn Jr., W.; Arnold, J.; Blaszcak, L.; Burgett, S.; DeHoff, B.S.; E
 e, R.; LeBlanc, D.J.; Lee, L.N.; Lefkowitz, E.J.; Lu, J.; Matsushima, P.; McAhren, S.; M
 y, P.; Sun, P.M.; Winkler, M.E.
 J. Bacteriol. 183, 5709-5717, 2001
 A:Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaakunas, S.R.;
 A>Title: Genome of the Bacterium Streptococcus pneumoniae Strain R6.
 A:Reference number: A97872; PMID:21429245; PMID:11544234
 A:Accession: E98119
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-330 <KUR>
 A:Cross-references: UNIPROT:Q8DN10; GB:AE007317; PIDN:AAL00786.1; PID:G15459687; GSPDB:G
 C:Genetics:
 A:Gene: transposase H

Query Match 70.6%; Score 36; DB 2; Length 330;
 Best Local Similarity 64.3%; Pred. No. 41;
 Matches 9; Conservative 1; Mismatches 0; Indels 4; Gaps 1;

QY 1 IVDIDPDSVP 10
 |||||:|
 DB 40 IVDIDPDSVP 53

RESULT 9

S31308
 aldehyde dehydrogenase (NAD) (EC 1.2.1.3) 2 precursor, mitochondrial - yeast (Saccharomy
 C:Species: Saccharomyces cerevisiae
 C:Date: 28-May-1993 #sequence_revision 31-Jan-1997 #text_change 09-Jul-2004
 C:Accession: S31308
 R:Thielen, J.
 Submitted to the EMBL Data Library, October 1992
 A:Reference number: S31308
 A:Accession: S31308
 A:Molecule type: DNA
 A:Residues: 1-511 <THI>
 A:Cross-references: UNIPROT:P32872; EMBL:Z17314; NID:G3361; PIDN:CAA76962.1; PID:G3362
 C:Comment: This form is probably mitochondrial.
 C:Genetics:
 A:Gene: ALD2
 C:Function:
 A:Description: catalyzes the oxidation of an aldehyde to an acid using NAD+ and water
 A:Note: enzymes with this activity are involved in diverse metabolic pathways in various
 C:Superfamily: NAD-dependent aldehyde dehydrogenase; aldehyde dehydrogenase homology
 C:Keywords: alcohol metabolism; mitochondrion; NAD; oxidoreductase
 F:1-21/Domain: transit peptide (mitochondrion) #status predicted <TMP>
 F:22-511/Product: aldehyde dehydrogenase (NAD+) 2 #status predicted <MAT>
 F:80-351/Domain: aldehyde dehydrogenase homology <ALDD>
 F:297,331/Active site: Glu, Cys #status predicted
 F:483/Binding site: NAD (Cys) #status predicted

Query Match 70.6%; Score 36; DB 1; Length 511;
 Best Local Similarity 60.0%; Pred. No. 67;
 Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 IVDIDPDSVP 10
 |||||:|

DB 374 ILKIEPDSIP 383

RESULT 10

AB2764
 beta-mannosidase precursor [imported] - Agrobacterium tumefaciens (strain C58, Dupont)
 C:Species: Agrobacterium tumefaciens
 C:Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 09-Jul-2004
 C:Accession: AB2764
 R:Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, J
 erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kutyavlin, T.; Leroy, R.; Li, M.; McClell
 ; Karp, P.; Romero, P.; Zhang, S.
 Science 294, 2317-2323, 2001
 A:Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
 sier, E.W.
 A>Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
 A:Reference number: AB2777; PMID:21608550; PMID:11743193
 A:Accession: AB2764
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-827 <KUR>
 A:Cross-references: UNIPROT:Q8UF76; GB:AE008688; PIDN:AAL42528.1; PID:G1773949; GSPDB:G
 A:Experimental source: strain C58 (Dupont)
 C:Genetics:
 A:Gene: manA
 A:Map position: circular chromosome

Query Match 70.6%; Score 36; DB 2; Length 827;
 Best Local Similarity 60.0%; Pred. No. 1,2e+02;
 Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 IVDIDPDSVP 10
 |||||:|
 DB 696 IVDIDPDSVP 705

RESULT 11

A97545
 hypothetical protein AGR_C_2809 [imported] - Agrobacterium tumefaciens (strain C58, Cer
 C:Species: Agrobacterium tumefaciens
 C:Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 09-Jul-2004
 C:Accession: A97545
 R:Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman,
 A.; Liu, F.; Wolan, C.; Allinger, M.; Dougherty, D.; Scott, C.; Lappas, C.; Markelz, B.
 Science 294, 2323-2328, 2001
 A>Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tu
 A:Reference number: A97359; PMID:21608551; PMID:11743194
 A:Accession: A97545
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-832 <KUR>
 A:Cross-references: UNIPROT:Q8UF76; GB:AE007869; PIDN:AAK8714.1; PID:G15156611; GSPDB:G
 C:Genetics:
 A:Gene: AGR C 2809
 A:Map position: circular chromosome

Query Match 70.6%; Score 36; DB 2; Length 832;
 Best Local Similarity 60.0%; Pred. No. 1,2e+02;
 Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 IVDIDPDSVP 10
 |||||:|
 DB 701 IVDIDPDSVP 710

RESULT 12

T42719
 TPR-containing/SH2-binding phosphoprotein - mouse
 N:Alternate names: 150TSP protein
 C:Species: Mus musculus (house mouse)
 C:Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 09-Jul-2004
 C:Accession: T42719
 R:Malek, S.N.; Yang, C.H.; Barnshaw, W.E.; Kozak, C.A.; Desiderio, S.

J. Biol. Chem. 271, 6952-6962, 1996
 A>Title: P150-TSP, a conserved nuclear phosphoprotein that contains multiple tetrapeptide
 A:Reference number: 206712; MUID:96215125; PMID:8636124
 A:Accession: T42719
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-1173 <ML>
 A:Cross-references: UNIPROT:062018; EMBL:L49502; NID:g1236238; PID:g1236239; PIDN:AA0420
 A:Experimental source: lymphoma
 C:Genetics:
 A:Gene: 150TSP
 A:Map position: 7

Query Match 70.6%; Score 36; DB 2; Length 1173;
 Best Local Similarity 40.0%; Pred. No. 1.7e+02;
 Matches 4; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 1 VIDIDFDSVP 10
 :|:|:|:|:|:
 Db 16 VIELDFDQLP 25

RESULT 13
 E96615
 hypothetical protein F16M22.3 [imported] - Arabidopsis thaliana
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
 C:Accession: E96615
 R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
 Chiu, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;
 Jensen, N.F.; Hughes, B.; Huizar, L.
 Nature 408, 816-820, 2000
 A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
 C.A.; Li, J.H.; Lin, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziani,
 Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
 A:Authors: Salberg, S.L.; Schwartz, J.R.; Shih, P.; Southwick, A.M.; Sun, H.; Tallon,
 Ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
 A>Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
 A:Reference number: A66141; MUID:21016719; PMID:11130712
 A:Accession: E96615
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-1195 <SNO>
 A:Cross-references: UNIPROT:09C730; GB:AE005173; NID:g11055842; PIDN:AA028310.1; GSPDB:C
 C:Genetics:
 A:Gene: F16M22.3
 A:Map position: 1

Query Match 70.6%; Score 36; DB 2; Length 1195;
 Best Local Similarity 66.7%; Pred. No. 1.8e+02;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 VIDIDFDSVP 10
 :|:|:|:|:|:
 Db 165 VIDISFDIP 173

RESULT 14
 S60954
 probable membrane protein YOR227w - Yeast (Saccharomyces cerevisiae)
 N:Alternate names: hypothetical protein O5079; hypothetical protein YOR50-17
 C:Species: Saccharomyces cerevisiae
 C:Date: 15-Feb-1996 #sequence_revision 01-Mar-1996 #text_change 09-Jul-2004
 C:Accession: S60954; S67120; S71729
 R:Gallison, F.; Dujon, B.
 submitted to the EMBL Data Library, October 1995
 A:Description: Sequence and analysis of a 33 kb fragment from the right arm of chromosome
 A:Reference number: S60938
 A:Accession: S60954
 A:Molecule type: DNA
 A:Residues: 1-1246 <GAL>
 A:Cross-references: UNIPROT:012276; EMBL:X92441; NID:g1050762; PID:g1050779
 R:Boyer, J.; Fairhead, C.; Gallion, L.; Gallison, F.; Michaux, G.; Thierry, A.; Dujon, B

submitted to the Protein Sequence Database, July 1996
 A:Reference number: S67104
 A:Accession: S67120
 A:Molecule type: DNA
 A:Residues: 1-1246 <BOY>
 A:Cross-references: EMBL:Z75135; NID:g1420522; PID:e252401; PID:g1420523; MIPS:YOR227w
 A:Experimental source: strain S288C
 R:Gallison, F.; Dujon, B.
 Yeast 12, 877-885, 1996
 A>Title: Sequence and analysis of a 33 kb fragment from the right arm of chromosome XV o
 A:Reference number: S71713; MUID:96437977; PMID:8840505
 A:Accession: S71729
 A:Status: nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-1246 <GAW>
 A:Cross-references: EMBL:X92441; NID:g1050762; PIDN:CAA63190.1; PID:g1050779
 A>Note: The nucleotide sequence was submitted to the EMBL Data Library, October 1995
 C:Genetics:
 A:Cross-references: SGD:S0005753
 A:Map position: 15R
 C:Keywords: transmembrane protein
 F:518-534/Domain: transmembrane #status predicted <TM1>
 F:551-567/Domain: transmembrane #status predicted <TM2>

Query Match 70.6%; Score 36; DB 2; Length 1246;
 Best Local Similarity 55.6%; Pred. No. 1.9e+02;
 Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 2 VIDIDFDSVP 10
 :|:|:|:|:|:
 Db 864 LDVIDYQVP 872

RESULT 15
 AD3161
 conserved hypothetical protein Atus013 [imported] - Agrobacterium tumefaciens (strain C5
 C:Species: Agrobacterium tumefaciens
 C:Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 09-Jul-2004
 C:Accession: AD3161
 R:Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Moo, L.
 erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kutayavin, T.; Levy, R.; Li, M.; McCell
 ; Karp, P.; Romero, P.; Zhang, S.
 Science 294, 2317-2323, 2001
 A:Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
 ster, E.W.
 A>Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
 A:Reference number: AB2577; MUID:21608550; PMID:11743193
 A:Accession: AD3161
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-62 <KUR>
 A:Cross-references: UNIPROT:08UKT6; GB:AE008687; PIDN:AA145706.1; PID:g17743435; GSPDB:G
 A:Experimental source: strain C58 (Dupont)
 C:Genetics:
 A:Gene: Atus013
 A:Genome: plasmid

Query Match 68.6%; Score 35; DB 2; Length 82;
 Best Local Similarity 85.7%; Pred. No. 13;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 DIDPDSV 9
 :|:|:|:|:|:
 Db 63 DIDPDSI 69

Search completed: October 22, 2005, 08:04:31
 Job time : 12.45 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 22, 2005, 06:06:36 ; Search time 55.85 Seconds (without adjustments)

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Title: US-10-731-238-75
Perfect score: 51
Sequence: 1 IVDIDFDSVP 10
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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

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Searched:      1612378 beqs, 512079187 residues
Total number of hits satisfying chosen parameters:  1612378

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Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Post-processing: Minimum Match 0%
                  Maximum Match 100%
                  Listing first 45 summaries
```

```
1: uniprot_sprot:*
2: uniprot_trembl:
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

Result	\$				ID		Description
No.	Score	Match	Length	DB			
1	51	100.0	152	2	Q9AEP9	Q9AEP9	staphy10ccc
2	51	100.0	940	2	O53682	O53682	staphy10ccc
3	51	100.0	943	2	O8NU08	O8NU08	staphy10ccc
4	51	100.0	957	2	O6G6H4	O6G6H4	staphy10ccc
5	51	100.0	961	2	O99RD3	O99RD3	staphy10ccc
6	51	100.0	961	2	O7A3J8	O7A3J8	staphy10ccc
7	51	100.0	1015	2	O8NU07	O8NU07	staphy10ccc
8	51	100.0	1015	2	O6G6H3	O6G6H3	staphy10ccc
9	51	100.0	1018	1	FNBA_STANU	F14738	staphy10ccc
10	51	100.0	1038	2	O99RD2	O99RD2	staphy10ccc
11	51	100.0	1038	2	O7A3J7	O7A3J7	staphy10ccc
12	50	98.0	965	2	O6GDU5	O6gd45	staphy10ccc
13	39	76.5	421	2	O6N1E6	O6n1e6	rhodopsenda
14	38	74.5	266	2	O62A58	O62a58	burkholderia
15	38	74.5	266	2	O63AN1	O63n1	burkholderia
16	38	74.5	430	1	VP43_BPPE3	P03668	bacteriophan
17	38	74.5	467	1	ATPB_WOLSU	P42470	wolnelliella
18	38	74.5	522	2	O6BKX1	O6bk1	debaromyces
19	38	74.5	1243	2	O6BHL5	O6bhl5	debaromyces
20	38	74.5	1322	2	O8IBD7	O8ibd7	plasmodium
21	38	74.5	1453	2	O7S600	O7s600	neurospora
22	37	72.5	178	2	O6LI07	O6li07	phocobacter
23	37	72.5	249	1	PNK_SUISO	Q97w18	sulciolobus
24	37	72.5	764	1	ACOC_CUCMC	Q42669	cucumis meli
25	37	72.5	855	2	O97J3R5	O97j3r5	sulciolobus
26	37	72.5	1120	2	O84RP5	O84rp5	arabidopsis
27	37	72.5	1141	2	O9LHP4	O9lhp4	arabidopsis
28	37	72.5	1214	2	O7SCR3	O7scr3	neurospora
29	37	72.5	1800	2	O7PY03	O7py03	anopheles g
30	37	72.5	3481	2	O7QMH2	O7qmh2	giardia lam
31	37	72.5	4574	2	O63LX9	O63lx9	burkholderia

32	36	70.6	187	2	Q8XQM1	Q8XQM1	ralstonia	8
33	36	70.6	193	1	Y304_SULTO	Q975x4	sulfolobus	8
34	36	70.6	201	2	O54301	O54301	salmonella	8
35	36	70.6	211	2	Q8C9W7	Q8C9W7	mus musculus	8
36	36	70.6	230	2	Q92KT2	Q92KT2	rhizobium m	8
37	36	70.6	281	2	Q8RWD7	Q8RWD7	arabidopsis	8
38	36	70.6	294	2	Q6L0F6	Q6L0F6	microphilus	8
39	36	70.6	325	2	Q7WE76	Q7WE76	bordetella	8
40	36	70.6	329	2	O6AIA9	O6AIA9	desulfococcus	8
41	36	70.6	330	2	Q6NDN0	Q6NDN0	streplococcus	8
42	36	70.6	333	2	Q63FR9	Q63FR9	bacillus ce	8
43	36	70.6	333	2	Q73DB5	Q73DB5	bacillus ce	8
44	36	70.6	333	2	Q81UX8	Q81UX8	bacillus an	8
45	36	70.6	333	2	Q6NH88	Q6NH88	bacillus th	8

ALIGNMENTS

RESULT 1

Q9AEP9	Q9AEP9	Q9AEP9	Q9AEP9
ID	Q9AEP9	PRELIMINARY;	PT; 152 AA.
AC	Q9AEP9;		
DT	01-JUN-2001 (TREMBlrel. 17, Created)		
DT	01-JUN-2001 (TREMBlrel. 17, Last sequence update)		
DT	01-DEC-2001 (TREMBlrel. 19, Last annotation update)		
DE	Fibronectin-binding protein (Fragment).		
GN	Name=fnb;		
OS	Staphylococcus aureus.		
OC	Bacteria; Firmicutes; Bacillales; Staphylococcus.		
OX	NCBI_TaxID=1280;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=CMRSA-1;		
RX	MEDLINE=21246681; PubMed=11349044;		
RX	DOI=10.1128/JAI.69.6.3791-3799.2001;		
RA	Rice K., Huesca M., Vaz D., McGavin M.J.;		
RT	"Variance in fibronectin binding and fnb locus polymorphisms in		
RT	Staphylococcus aureus: identification of antigenic variation in a		
RT	fibronectin binding protein adhesion of the epidemic CMRSA-1 strain 05		
RT	methicillin-resistant S. aureus.";		
RL	Infect. Immun. 69:3791-3799 (2001).		
DR	EMBL; AY029184; AAK31588.1; -.		
FT	NON TER 1		
FT	NON TER 152		
SQ	SEQUENCE 152 AA; 17193 MW; CFA3913C2B11C025 CRG4;		

RESULT 2

053682			
ID	Q53682	PRELIMINARY;	PTT; 940 AA.
AC	Q53682;		
DT	01-NOV-1996 (TREMBLrel. 01, Created)		
DT	01-NOV-1996 (TREMBLrel. 01, Last sequence update)		
DT	01-MAR-2004 (TREMBLrel. 26, Last annotation update)		
DE	Fidronectin binding protein B.		
GN	Name=FnbB;		
OS	Staphylococcus aureus.		
OC	Bacteria; Firmicutes; Bacillales; Staphylococcus.		
OX	NCBI_TaxID=1280;		
RN	(1)		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=8325-4;		
RX	MEDLINE=92111475; PubMed=1837266;		
RA	Jonsson K., Sigmas C., Muller H.P., Lindberg M.;		

RT "Two different genes encode fibronectin binding proteins in
 RT Staphylococcus aureus. The complete nucleotide sequence and
 RT characterization of the second gene.";
 RL Eur. J. Biochem. 202;1041-1048(1991).
 CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
 CC an amide bond (By similarity).
 DR EMBL: X62992; CAA44726.1; -.
 DR PIR: S19702; S19702.
 DR HSSP: O53653; 1N67.
 DR GO: GO:0009986; C:cell surface; IEA.
 DR GO: GO:0005618; C:cell wall; IEA.
 DR GO: GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
 DR GO: GO:0016020; C:membrane; IEA.
 DR GO: GO:0007155; P:cell adhesion; IEA.
 DR InterPro: IPR008966; Adhes_bact.
 DR InterPro: IPR004237; Fn_bind.
 DR InterPro: IPR005877; Gpos_YsIRK.
 DR InterPro: IPR01899; Gram_pos_anchor.
 DR Pfam: PF02986; Fn_bind; 2.
 DR Pfam: PF00746; Gram_pos_anchor; 1.
 DR Pfam: PF04650; YsIRK_signal; 1.
 DR TIGRFAMs: TIGR01167; LpxTG_anchor; 1.
 DR TIGRFAMs: TIGR01168; YsIRK_signal; 1.
 DR PROSITE: PS50847; GRAM_POS_ANCHORING; 1.
 DR Cell wall; Peptidoglycan-anchor.
 KW CELL WALL; Peptidoglycan-anchor.
 SQ SEQUENCE 940 AA; 10355 MW; E35FBBCA307AE345 CRC64;

Query Match 100.0%; Score 51; DB 2; Length 940;
 Best Local Similarity 100.0%; Pred. No. 1.2;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 IVDIDFDSVP 10
 Db 706 IVDIDFDSVP 715

RESULT 3
 Q8NU8 PRELIMINARY; PRT; 943 AA.
 ID Q8NU8
 AC Q8NU8;
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Pnb protein.
 GN Name:fnb; OrderedlocusNames=MM2420;
 OS Staphylococcus aureus (strain MM2).
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 OX NCBI_TaxID=196620;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=MM2.
 RX MEDLINE=22040717; PubMed=12044378; DOI=10.1016/S0140-6736(02)08713-5;
 RA Baba T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Oguchi A.,
 RA Nagai Y., Iwama N., Asano K., Naimi T., Kuroda H., Cui L.,
 RA Yamamoto K., Hiramatsu K.;
 RT "Genome and virulence determinants of high virulence community-
 RT acquired MRSA.";
 RL Lancet 359;1819-1827(2002).
 CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
 CC an amide bond (By similarity).
 DR EMBL: AP004830; BAB96285.1; -.
 DR HSSP: O53653; 1N67.
 DR GO: GO:0009986; C:cell surface; IEA.
 DR GO: GO:0005618; C:cell wall; IEA.
 DR GO: GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
 DR GO: GO:0016020; C:membrane; IEA.
 DR GO: GO:0007155; P:cell adhesion; IEA.
 DR InterPro: IPR008966; Adhes_bact.
 DR InterPro: IPR004237; Fn_bind.
 DR InterPro: IPR005877; Gpos_YsIRK.
 DR InterPro: IPR01899; Gram_pos_anchor.
 DR Pfam: PF02986; Fn_bind; 1.
 DR Pfam: PF00746; Gram_pos_anchor; 1.

DR Pfam: PF04650; YsIRK_signal; 1.
 DR TIGRFAMs: TIGR01167; LpxTG_anchor; 1.
 DR TIGRFAMs: TIGR01168; YsIRK_signal; 1.
 DR PROSITE: PS50847; GRAM_POS_ANCHORING; 1.
 KW Cell wall; Complete proteome; Peptidoglycan-anchor.
 SQ SEQUENCE 943 AA; 104537 MW; DA8A5F31947E1B6A CRC64;

Query Match 100.0%; Score 51; DB 2; Length 943;
 Best Local Similarity 100.0%; Pred. No. 1.2;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 IVDIDFDSVP 10
 Db 713 IVDIDFDSVP 722

RESULT 4
 Q6G6H4 PRELIMINARY; PRT; 957 AA.
 ID Q6G6H4
 AC Q6G6H4;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Fibronectin-binding protein.
 GN Name:fnb; OrderedlocusNames=SAS2387;
 OS Staphylococcus aureus (strain MSSA476).
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 OX NCBI_TaxID=282459;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX PubMed=15213324; DOI=10.1073/pnas.0402521101;
 RA Holden M.T.G., Fell E.J., Lindsay J.A., Peacock S.J., Day N.P.J.,
 RA Enright M.C., Foster T.J., Moore C.E., Hurst L., Atkin R., Barron A.,
 RA Baeson N., Bentley S.D., Chillingworth C., Chillingworth T.,
 RA Churcher C., Clark L., Cotton C., Cronin A., Doggett J., Dowd L.,
 RA Felwell T., Hance Z., Harris B., Hauser H., Holroyd S., Jagsle K.,
 RA James K.D., Leonard N., Line A., Mayes R., Moule S., Mungall K.,
 RA Ormond D., Quail M.A., Rabinowitch E., Rutherford K.M., Sanders M.,
 RA Sharp S., Simmonds M., Stevens K., Whitehead S., Barrett B.G.,
 RA Spratt B.G., Parkhill J.;
 RT "Complete genomes of two clinical Staphylococcus aureus strains:
 RT evidence for the rapid evolution of virulence and drug resistance.";
 RL Proc. Natl. Acad. Sci. U.S.A. 101;9786-9791(2004).
 CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
 CC an amide bond (by similarity).
 DR EMBL: BX571857; CAG44201.1; -.
 DR GO: GO:0009986; C:cell surface; IEA.
 DR GO: GO:0005618; C:cell wall; IEA.
 DR GO: GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
 DR GO: GO:0016020; C:membrane; IEA.
 DR GO: GO:0007155; P:cell adhesion; IEA.
 DR InterPro: IPR008966; Adhes_bact.
 DR InterPro: IPR004237; Fn_bind.
 DR InterPro: IPR005877; Gpos_YsIRK.
 DR InterPro: IPR01899; Gram_pos_anchor.
 DR Pfam: PF02986; Fn_bind; 1.
 DR Pfam: PF00746; Gram_pos_anchor; 1.
 DR TIGRFAMs: TIGR01167; LpxTG_anchor; 1.
 DR TIGRFAMs: TIGR01168; YsIRK_signal; 1.
 DR PROSITE: PS50847; GRAM_POS_ANCHORING; 1.
 KW Cell wall; Complete proteome; Peptidoglycan-anchor.
 SQ SEQUENCE 957 AA; 105980 MW; 28F8BA7FFDF3EAF CRC64;

Query Match 100.0%; Score 51; DB 2; Length 957;
 Best Local Similarity 100.0%; Pred. No. 1.2;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 IVDIDFDSVP 10
 Db 713 IVDIDFDSVP 722

```
RESULT 5
Q99RD3 PRELIMINARY; PRT; 961 AA.
ID Q99RD3;
AC Q99RD3;
DT 01-JUN-2001 (TREMblrel. 17, Created)
DT 01-JUN-2001 (TREMblrel. 17, Last sequence update)
DT 01-JUN-2003 (TREMblrel. 24, Last annotation update)
DE Fibronectin-binding protein homolog.
GN Name=fnbB; OrderedLocustNames=SAV2502;
OS Staphylococcus aureus (strain Mu50 / ATCC 700699).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_Taxid=158878;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Mu50 / ATCC 700699;
RX MEDLINE=21311952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2;
RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Lian J.-Q., Ito T.,
RA Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,
RA Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
RA Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
RA Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
RA Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
RT "Whole genome sequencing of methicillin-resistant Staphylococcus
RT aureus."
RT Lancet 357:1225-1240(2001).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC an amide bond (By similarity).
DR EMBL: AP003137; BAB43593.1; -.
DR PIR: G90053; G90053.
DR HSSP: Q53653; IN67.
DR GO: GO:0009986; C:cell surface; IEA.
DR GO: GO:0005618; C:cell wall; IEA.
DR GO: GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO: GO:0016020; C:membrane; IEA.
DR GO: GO:0007155; P:cell adhesion; IEA.
DR InterPro: IPR008966; Adhes_bact.
DR InterPro: IPR004237; Fn_bind.
DR InterPro: IPR005877; Gpos_YsIRK.
DR InterPro: IPR001899; Gram_pos_anchor.
DR Pfam: PF02986; Fn_bind.1.
DR Pfam: PF00746; Gram_pos_anchor.1.
DR Pfam: PF04650; YsIRK_signal.1.
DR TIGRPFAMs: TIGR01167; LPXTG_anchor.1.
DR TIGRPFAMs: TIGR01168; YsIRK_signal.1.
DR PROSITE: PSS0847; GRAM_POS_ANCHORING.1.
KW Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ SEQUENCE 961 AA; 106010 MW; 364940F84EA4101 CRC64;

Query Match 100.0%; Score 51; DB 2; Length 961;
Best Local Similarity 100.0%; Pred. No. 1.3;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IVDIDFDSVP 10
Db 717 IVDIDFDSVP 726

RESULT 6
Q7A3J8 PRELIMINARY; PRT; 961 AA.
ID Q7A3J8;
AC Q7A3J8;
DT 05-JUL-2004 (TREMblrel. 27, Created)
DT 05-JUL-2004 (TREMblrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMblrel. 27, Last annotation update)
DE FnbB protein.
GN Name=fnbB; OrderedLocustNames=SA2290;
OS Staphylococcus aureus (strain N315).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_Taxid=158879;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21311952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2;
```

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RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Lian J.-Q., Ito T.,
RA Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,
RA Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
RA Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
RA Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
RA Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
RT "Whole genome sequencing of methicillin-resistant Staphylococcus
RT aureus."
RT Lancet 357:1225-1240(2001).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC an amide bond (By similarity).
DR EMBL: AP003137; BAB43593.1; -.
DR GO: GO:0009986; C:cell surface; IEA.
DR GO: GO:0005618; C:cell wall; IEA.
DR GO: GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO: GO:0016020; C:membrane; IEA.
DR GO: GO:0007155; P:cell adhesion; IEA.
DR InterPro: IPR008966; Adhes_bact.
DR InterPro: IPR004237; Fn_bind.
DR InterPro: IPR005877; Gpos_YsIRK.
DR InterPro: IPR001899; Gram_pos_anchor.
DR Pfam: PF02986; Fn_bind.1.
DR Pfam: PF00746; Gram_pos_anchor.1.
DR Pfam: PF04650; YsIRK_signal.1.
DR TIGRPFAMs: TIGR01167; LPXTG_anchor.1.
DR TIGRPFAMs: TIGR01168; YsIRK_signal.1.
DR PROSITE: PSS0847; GRAM_POS_ANCHORING.1.
KW Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ SEQUENCE 961 AA; 106010 MW; 364940F84EA4101 CRC64;
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Query Match 100.0%; Score 51; DB 2; Length 961;
Best Local Similarity 100.0%; Pred. No. 1.3;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IVDIDFDSVP 10
Db 717 IVDIDFDSVP 726

RESULT 7
Q8NUU7 PRELIMINARY; PRT; 1015 AA.
ID Q8NUU7;
AC Q8NUU7;
DT 01-OCT-2002 (TREMblrel. 22, Created)
DT 01-OCT-2002 (TREMblrel. 22, Last sequence update)
DT 01-OCT-2003 (TREMblrel. 25, Last annotation update)
DE Fnb protein.
GN Name=fnb; OrderedLocustNames=MW2421;
OS Staphylococcus aureus (strain MW2).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_Taxid=196620;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MW2;
RX MEDLINE=22040717; PubMed=12044378; DOI=10.1016/S0140-6736(02)08713-5;
RA Baba T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Oguchi A.,
RA Nagai Y., Iwama N., Asano K., Naimi T., Kuroda H., Cui L.,
RA Yamamoto K., Hiramatsu K.;
RT "Genome and virulence determinants of high virulence community-
RT acquired MRSA."
RT Lancet 359:1819-1827(2002).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC an amide bond (By similarity).
DR EMBL: AP004830; BAB96286.1; -.
DR GO: GO:0009986; C:cell surface; IEA.
DR GO: GO:0005618; C:cell wall; IEA.
DR GO: GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO: GO:0016020; C:membrane; IEA.
DR GO: GO:0007155; P:cell adhesion; IEA.
DR InterPro: IPR008966; Adhes_bact.
DR InterPro: IPR004237; Fn_bind.
DR InterPro: IPR005877; Gpos_YsIRK.
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DR InterPro: IPR001899; Gram_pos_anchor.
DR Pfam: PF02986; Fn_bind; 1.
DR Pfam: PF00746; Gram_pos_anchor; 1.
DR Pfam: PF04650; YSIRK_signal; 1.
DR TIGRFAMs: TIGR01167; LPXTG_anchor; 1.
DR TIGRFAMs: TIGR01168; YSIRK_signal; 1.
DR PROSITE: PS50847; GRAM_POS_ANCHORING; 1.
DR Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ SEQUENCE 1015 AA; 111145 MW; DQF9281BB64D442 CRC64;

Query Match          100.0%; Score 51; DB 2; Length 1015;
Best Local Similarity 100.0%; Pred. No. 1.3;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IVDIDPDSVP 10
   |||||
DB 771 IVDIDPDSVP 780

RESULT 8
AC Q6G6H3 PRELIMINARY; PRT; 1015 AA.
ID Q6G6H3;
DC 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DE 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DN Fibronectin-binding protein.
GN OrderedLocustNames=SAS2388;
OS Staphylococcus aureus (strain MSSA476).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=282459;
RN [1]
RP SEQUENCE FROM N.A.
RA PubMed=15213324; DOI=10.1073/pnas.0402521101;
RA Holden M.T.G., Fell E.J., Lindsay J.A., Peacock S.J., Day N.P.J.,
RA Enright M.C., Foster T.J., Moore C.E., Hurst L., Atkin R., Barron A.,
RA Bason N., Bentley S.D., Chillingworth C., Chillingworth T.,
RA Churcher C., Clark L., Corton C., Cronin A., Doggett J., Dowd L.,
RA Felwell T., Hance Z., Harris B., Hauser H., Holtroyd S., Jagels K.,
RA James K.D., Lennard N., Line A., Mayes R., Moule S., Mungall K.,
RA Ormond D., Quail M.A., Rabinovitch B., Rutherford K.M., Sanders M.,
RA Sharp S., Simmonds M., Stevens K., Whitehead S., Barrett B.G.,
RA Spratt B.G., Parkhill J.;
RT "Complete genomes of two clinical Staphylococcus aureus strains:
RT evidence for the rapid evolution of virulence and drug resistance.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:9786-9791(2004).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC an amide bond (By similarity).
EMBL: BX571857; CAG44202.1; -.
DR GO: GO:0009986; C:cell surface; IEA.
DR GO: GO:0005275; C:cell wall; IEA.
DR GO: GO:0016020; C:membrane; IEA.
DR GO: GO:0007155; P:cell adhesion; IEA.
DR InterPro: IPR008966; Adhes_bact.
DR InterPro: IPR004237; Fn_bind.
DR InterPro: IPR005877; Gpos_YSIRK.
DR InterPro: IPR001899; Gram_pos_anchor.
DR Pfam: PF02986; Fn_bind; 1.
DR Pfam: PF00746; Gram_pos_anchor; 1.
DR Pfam: PF04650; YSIRK_signal; 1.
DR TIGRFAMs: TIGR01167; LPXTG_anchor; 1.
DR TIGRFAMs: TIGR01168; YSIRK_signal; 1.
DR PROSITE: PS50847; GRAM_POS_ANCHORING; 1.
DR Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ SEQUENCE 1015 AA; 111145 MW; DQF9281BB64D442 CRC64;
```

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DB 771 IVDIDPDSVP 780

RESULT 9
AC FNBA STAAU STANDARD; PRT; 1018 AA.
ID FNBA STAAU
DC 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DE 25-OCT-2004 (Rel. 45, Last annotation update)
DN Fibronectin-binding protein precursor (FNBP).
GN Name=FNBP;
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1280;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=NCTC 8325-4; PubMed=2521391;
RX MEDLINE=8909898; PubMed=2521391;
RA Signaes C., Raucel G., Joensson K., Lindgren P.-E.,
RA Anantharamiah G.M., Hoceek M., Lindberg M.;
RT "Nucleotide sequence of the gene for a fibronectin-binding protein
RT from Staphylococcus aureus: use of this peptide sequence in the
RT synthesis of biologically active peptides.";
RL Proc. Natl. Acad. Sci. U.S.A. 86:699-703(1989).
CC -1- FUNCTION: The ability of bacteria to bind fibronectin has been
CC proposed as a virulence factor enabling bacteria to colonize wound
CC tissues and blood clots. Binding of plasma fibronectin to the
CC bacterial surface might block adhesion receptors on S.aureus, thus
CC representing an important defense mechanism against tissue
CC invasion.
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC an amide bond (Potential).
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (see http://www.isb-sib.ch/announce/
CC or send an email to license@sib-sib.ch).
CC -----
DR EMBL: J04151; AAA26632.1; -.
DR InterPro: IPR004237; Fn_bind.
DR InterPro: IPR005877; Gpos_YSIRK.
DR InterPro: IPR001899; Gram_pos_anchor.
DR Pfam: PF02986; Fn_bind; 1.
DR Pfam: PF00746; Gram_pos_anchor; 1.
DR Pfam: PF04650; YSIRK_signal; 1.
DR TIGRFAMs: TIGR01167; LPXTG_anchor; 1.
DR TIGRFAMs: TIGR01168; YSIRK_signal; 1.
DR PROSITE: PS50847; GRAM_POS_ANCHORING; 1.
DR Cell adhesion; Cell wall; Peptidoglycan-anchor; Repeat; Signal;
KW Virulence.
FT SIGNAL 1 36
FT CHAIN 37 985
FT PROPEP 986 1018
FT REPEAT 545 574
FT REPEAT 575 604
FT DOMAIN 745 878
FT REPEAT 745 782
FT REPEAT 783 820
FT REPEAT 821 859
FT REPEAT 860 878
FT DOMAIN 879 948
FT REPEAT 879 892
FT REPEAT 893 906
FT REPEAT 907 920
FT REPEAT 921 934
FT REPEAT 935 948
FT SITE 982 986
FT MOD_RES 985 985
FT -----
FT Fibronection-binding protein.
FT Removed by sortase (Potential).
FT B-1.
FT B-2.
FT 4 X approximate tandem repeats,
FT fibronection-binding domain.
FT D-1.
FT D-2.
FT D-3.
FT D-4 (incomplete).
FT 5 X tandem repeats, Pro-rich (WR).
FT WR 1.
FT WR 2.
FT WR 3.
FT WR 4.
FT WR 5.
FT LPXTG sorting signal (Potential).
FT Pentaglycyl murein peptidoglycan amidated
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FT SEQUENCE 1018 AA; 111780 MW; 58175E0020EB1F1F CRC64;
SQ

Query Match
Best Local Similarity 100.0%; Score 51; DB 1; Length 1018;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IVDIDFDSVP 10
Db 766 IVDIDFDSVP 779

RESULT 10
Q99RD2 PRELIMINARY; PRT; 1038 AA.
ID Q99RD2;
AC Q99RD2;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Fibronectin-binding protein homolog.
GN Name=fndb; OrderedlocusNames=SAV2503;
OS Staphylococcus aureus (strain Mu50 / ATCC 700699).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
NCBI_Taxid=158878;
[1]
SEQUENCE FROM N.A.
RC STRAIN=Mu50 / ATCC 700699;
RX MEDLINE=21311952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2;
RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Iian J.-Q., Ito T.,
RA Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,
RA Mizutani-Ul Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
RA Sekimizu K., Hirakawa H., Kihara S., Furuya K., Yoshino C., Shiba T.,
RA Kanehisa M., Yamashita A., Oshima K., Hara Y., Hiramatsu K.,
RA Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.,
RT "Whole genome sequencing of methicillin-resistant Staphylococcus
aureus.";
RL Lancet 357:1225-1240(2001).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
an amide bond (By similarity).
EMBL; AP003137; BAB3594.1; -;
DR PIR; H90053; H90053.
DR GO; GO:0009986; C:cell surface; IEA.
DR GO; GO:0005618; C:cell wall; IEA.
DR GO; GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0007155; P:cell adhesion; IEA.
DR InterPro; IPR008966; Adhes_bact.
DR InterPro; IPR004237; Fn_bind.
DR InterPro; IPR005877; Gpos_YsIRK.
DR InterPro; IPR001899; Gram_pos_anchor.
DR Pfam; PF02986; Fn_bind_1.
DR Pfam; PF00746; Gram_pos_anchor; 1.
DR Pfam; PF04650; YsIRK_signal; 1.
DR TIGRfams; TIGR01167; LPXTG_anchor; 1.
DR TIGRfams; TIGR01168; YsIRK_signal; 1.
DR PROSITE; PS50847; GRAM_POS_ANCHORING; 1.
KW Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ SEQUENCE 1038 AA; 113618 MW; 666BF6B2BFBB12 CRC64;

Query Match
Best Local Similarity 100.0%; Score 51; DB 2; Length 1038;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IVDIDFDSVP 10
Db 766 IVDIDFDSVP 775

RESULT 11
Q7A3J7 PRELIMINARY; PRT; 1038 AA.
ID Q7A3J7;
AC Q7A3J7;

DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Fnb protein.
GN Name=fndb; OrderedlocusNames=SA2291;
OS Staphylococcus aureus (strain N315).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
NCBI_Taxid=158879;
[1]
SEQUENCE FROM N.A.
RP MEDLINE=21311952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2;
RX Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Iian J.-Q., Ito T.,
RA Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,
RA Mizutani-Ul Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
RA Sekimizu K., Hirakawa H., Kihara S., Furuya K., Yoshino C., Shiba T.,
RA Kanehisa M., Yamashita A., Oshima K., Hara Y., Hiramatsu K.,
RA Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.,
RT "Whole genome sequencing of methicillin-resistant Staphylococcus
aureus.";
RL Lancet 357:1225-1240(2001).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
an amide bond (By similarity).
EMBL; AP003137; BAB3594.1; -;
DR GO; GO:0009986; C:cell surface; IEA.
DR GO; GO:0005618; C:cell wall; IEA.
DR GO; GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0007155; P:cell adhesion; IEA.
DR InterPro; IPR008966; Adhes_bact.
DR InterPro; IPR004237; Fn_bind.
DR InterPro; IPR005877; Gpos_YsIRK.
DR InterPro; IPR001899; Gram_pos_anchor.
DR Pfam; PF02986; Fn_bind_1.
DR Pfam; PF00746; Gram_pos_anchor; 1.
DR Pfam; PF04650; YsIRK_signal; 1.
DR TIGRfams; TIGR01167; LPXTG_anchor; 1.
DR TIGRfams; TIGR01168; YsIRK_signal; 1.
DR PROSITE; PS50847; GRAM_POS_ANCHORING; 1.
KW Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ SEQUENCE 1038 AA; 113618 MW; 666BF6B2BFBB12 CRC64;

Query Match
Best Local Similarity 100.0%; Score 51; DB 2; Length 1038;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IVDIDFDSVP 10
Db 766 IVDIDFDSVP 775

RESULT 12
Q6GDUS PRELIMINARY; PRT; 965 AA.
ID Q6GDUS;
AC Q6GDUS;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Fibronectin-binding protein.
GN Name=fndb; OrderedlocusNames=SA23580;
OS Staphylococcus aureus (strain MRS4252).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
NCBI_Taxid=282458;
[1]
SEQUENCE FROM N.A.
RP PubMed=15213324; DOI=10.1073/pnas.0402521101;
RX Holden M.T.G., Fell E.J., Lindsey J.A., Peacock S.J., Day N.P.J.,
RA Enright M.C., Foster T.J., Moore C.E., Hurst L., Atkin R., Barron A.,
RA Bason N., Bentley S.D., Chillingworth C., Chillingworth T.,
RA Churcher C., Clark L., Cotton C., Cronin A., Doggett J., Dowd L.,
RA Feltham T., Hance Z., Harris B., Hauser H., Holtroyd S., Jagsels K.,
RA James K.D., Lennard N., Line A., Mayes R., Moule S., Mungall K.,
RA Ormond D., Quail M.A., Rabinowitch E., Rutherford K.M., Sanders M.,

RA Sharp S., Simmonds M., Stevens K., Whitehead S., Barrell B.G.,
 RA Spratt B.G., Parkhill J.;
 RT "Complete genomes of two clinical *Staphylococcus aureus* strains:
 CC evidence for the rapid evolution of virulence and drug resistance.";
 RT Proc. Natl. Acad. Sci. U.S.A. 101:9786-9791(2004).
 CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
 CC an amide bond (By similarity).
 DR EMBL: BX571856; CAG41560.1; -;
 DR GO: GO:0009986; C:cell surface; IEA.
 DR GO: GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
 DR GO: GO:0016020; C:membrane; IEA.
 DR GO: GO:007155; P:cell adhesion; IEA.
 DR InterPro: IPR008966; Adhes_Bact.
 DR InterPro: IPR004237; Fn_bind.
 DR InterPro: IPR005877; Gpox_YsIRK.
 DR InterPro: IPR001899; Gram_pos_anchor.
 DR Pfam: PF02986; Fn_bind; 1.
 DR Pfam: PF00746; Gram_pos_anchor; 1.
 DR Pfam: PF04650; YsIRK_signal; 1.
 DR TIGRFAMs: TIGR01167; LPTXG_anchor; 1.
 DR TIGRFAMs: TIGR01168; YsIRK_signal; 1.
 DR PROSITE: PS50847; GRAM_POS_ANCHORING; 1.
 KW Cell wall; Complete proteome; Peptidoglycan-anchor.
 SQ SEQUENCE 965 AA; 105691 MW; 2982E132164D0551 CRC64;

Query Match 98.0%; Score 50; DB 2; Length 965;
 Best Local Similarity 90.0%; Pred. No. 1.9;
 Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 VDIDPDSVP 10
 Db 773 IDIDFDSVP 782

RESULT 13

ID Q6N1E6 PRELIMINARY; PRT; 421 AA.

AC Q6N1E6; 05-JUL-2004 (TREMBlrel. 27, Created)
 DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
 DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
 DE Putative flavocytochrome C sulfide dehydrogenase, flavoprotein subunit
 DE precursor.
 GN Name=dhsU1; OrderedLocustNames=RPA4460;
 OS Rhodopseudomonas palustris.
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
 OC Bradyrhizobiaceae; Rhodopseudomonas.
 OK NCBI_TaxID=1076;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CGA009 / ATCC BAA-98;
 RX PubMed=14704707; DOI=10.1038/nbt923;
 RA Larimer F.W., Chain P., Hauser L., Lamerdin J.E., Malfatti S., Do L.,
 RA Land M.L., Pelletier D.A., Beatty J.T., Lang A.S., Tabita F.R.,
 RA Gibson J.L., Hanson T.E., Bobet C., Torres y Torres J.L., Peres C.,
 RA Harrison F.H., Gibson J., Harwood C.S.;
 RT "Complete genome sequence of the metabolically versatile
 RT photosynthetic bacterium *Rhodopseudomonas palustris*.";
 RL Nat. Biotechnol. 22:55-61(2004).
 DR EMBL: BX572607; CAE29901.1; -;
 DR GO: GO:0015036; F:disulfide oxidoreductase activity; IEA.
 DR GO: GO:0006118; P:electron transport; IEA.
 DR InterPro: IPR001377; FAD_Pyr_redox.
 DR InterPro: IPR000103; Pyridine_redox_2.
 DR InterPro: IPR001665; Pyridine_redox.
 DR InterPro: IPR006311; Tat.
 DR PRINTS: PRO0358; RAMPNR.
 DR PRINTS: PRO0411; PNDRTNASEI.
 DR PRINTS: PRO0469; PNDRTNASEI.
 DR TIGRFAMs: TIGR01409; Tat_signal_seq; 1.
 DR PROSITE: PS00962; RIBOSOMAL_S2_1; UNKNOWN_1.
 KW Complete proteome; Signal.

FT SIGNAL 1 28 Potential.
 SQ SEQUENCE 421 AA; 45339 MW; 12906093C87E5A74 CRC64;

Query Match 76.5%; Score 39; DB 2; Length 421;
 Best Local Similarity 77.8%; Pred. No. 87;
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 VDIDPDSVP 10
 Db 134 IDIKFDSVP 142

RESULT 14

ID Q62A58 PRELIMINARY; PRT; 266 AA.

AC Q62A58; 25-OCT-2004 (TREMBlrel. 28, Created)
 DT 25-OCT-2004 (TREMBlrel. 28, Last sequence update)
 DT 25-OCT-2004 (TREMBlrel. 28, Last annotation update)
 DE Lamb/YcsF family protein.
 GN ORFNames=BMAA180;
 OS Burkholderia mallei ATCC 23344.
 OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
 OC Burkholderiaceae; Burkholderia.
 OK NCBI_TaxID=243160;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 23344;
 RA Nieman W.C.; Deshazer D., Kim H.S., Tetteijn H., Nelson K.E.,
 RA Feldblyum T., Ulrich R.L., Roming C.M., Brinkac L.M., Dougherty S.C.,
 RA Davidson T.D., DeBoy R.T., Dimitrov G., Dodson R.J., Durkin A.S.,
 RA Gwinn M.L., Haft D.H., Khouri H., Kolonay J.F., Madupu R.,
 RA Mohammed Y., Nelson W.C., Radune D., Romero C.M., Sarría S.,
 RA Selengut J., Shamblin C., Sullivan S.A., White O., Yu Y., Zafar N.,
 RA Zhou L., Fraser C.M.;
 RT "Structural flexibility in the *Burkholderia mallei* genome.";
 RL Proc. Natl. Acad. Sci. U.S.A. 101:14247-14251(2004).
 DR EMBL: CP000011; AAU45571.1; -;
 SQ SEQUENCE 266 AA; 28925 MW; 403FA6E015EBCA27 CRC64;

Query Match 74.5%; Score 38; DB 2; Length 266;
 Best Local Similarity 75.0%; Pred. No. 80;
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 VDIDPDSVP 9
 Db 216 IDIDFDSI 223

RESULT 15

ID Q63NV1 PRELIMINARY; PRT; 266 AA.

AC Q63NV1; 25-OCT-2004 (TREMBlrel. 28, Created)
 DT 25-OCT-2004 (TREMBlrel. 28, Last sequence update)
 DT 25-OCT-2004 (TREMBlrel. 28, Last annotation update)
 DE Lamb/YcsF family protein.
 GN ORFNames=BPS50198;
 OS Burkholderia pseudomallei K96243.
 OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
 OC Burkholderiaceae; Burkholderia.
 OK NCBI_TaxID=272560;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=K96243;
 RX PubMed=15377794;
 RA Holden M.T.G., Tibball R.W., Peacock S.J., Cerdano-Tarraga A.M.,
 RA Atkins T., Crossman L.C., Pitt T., Churcher C., Mungall K.,
 RA Bentley S.D., Sebahia M., Thomson N.R., Bason N., Beacham I.R.,
 RA Brooks K., Brown K.A., Brown N.F., Challis G.L., Cherevach I.,
 RA Chillingworth T., Cronin A., Crosset B., Davis P., Deshazer D.,
 RA Fellwell T., Fraser A., Hance Z., Hauser H., Holroyd S., Jørgels K.,
 RA Keith K.E., Maddison M., Moule S., Price C., Quail M.A.,

RA Rabinowitsch E., Rutherford K., Sanders M., Simmonds M.,
RA Songstivilai S., Stevens K., Tumapa S., Vesaratchaveest M.,
RA Whitehead S., Yeats C., Barrell B.G., Oyston P.C.F., Parkhill J.,
RT "Genomic plasticity of the causative agent of melioidosis,
RT Burkholderia pseudomallei.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:14240-14245(2004).
DR EMBL; BX571966; CAH37643.1; -. 51DDB4CFCSEC3709 CRC64;
SQ SEQUENCE 266 AA; 28867 MW; 51DDB4CFCSEC3709 CRC64;

Query Match 74.5%; Score 38; DB 2; Length 266;
Best Local Similarity 75.0%; Pred. No. 80;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VDIIDFDSV 9
:|||||:
Db 216 IDIDFDSI 223

Search completed: October 22, 2005, 08:00:43
Job time : 57.85 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 25, 2005, 20:21:18 ; Search time 63.2 Seconds
(without alignments)
61.196 Million cell updates/sec

Title: US-10-731-238-76

Perfect score: 52

Sequence: 1 DIDFSPVQI 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:*

1: geneseqp19808:***
2: geneseqp19908:***
3: geneseqp20008:***
4: geneseqp20018:***
5: geneseqp20028:***
6: geneseqp20038:***
7: geneseqp20048:***
8: geneseqp20048:***

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	52	100.0	10	2	AAW65732
2	52	100.0	38	1	AAW65732 Fibronect
3	52	100.0	38	1	AAW65732 Protein w
4	52	100.0	38	1	AAW65732 Fibronect
5	52	100.0	38	2	AAW65692
6	52	100.0	38	2	AAW65692 Fibronect
7	52	100.0	38	2	AAW65692 Fibronect
8	52	100.0	38	2	AAW65692 Fibronect
9	52	100.0	38	2	AAW65692 Fibronect
10	52	100.0	38	2	AAW65692 Fibronect
11	52	100.0	38	2	AAW65692 Fibronect
12	52	100.0	38	2	AAW65692 Fibronect
13	52	100.0	38	2	AAW65692 Fibronect
14	52	100.0	38	2	AAW65692 Fibronect
15	52	100.0	38	2	AAW65692 Fibronect
16	52	100.0	38	2	AAW65692 Fibronect
17	52	100.0	38	2	AAW65692 Fibronect
18	52	100.0	38	2	AAW65692 Fibronect
19	52	100.0	38	2	AAW65692 Fibronect
20	52	100.0	38	2	AAW65692 Fibronect
21	52	100.0	38	2	AAW65692 Fibronect
22	52	100.0	38	2	AAW65692 Fibronect
23	52	100.0	38	2	AAW65692 Fibronect
24	52	100.0	38	2	AAW65692 Fibronect
25	52	100.0	38	2	AAW65692 Fibronect

26	52	100.0	164	2	AAW65732	AAW65732 standard; peptide; 10 AA.
27	52	100.0	174	2	AAW65732	AAW65732 standard; peptide; 10 AA.
28	52	100.0	174	2	AAW65732	AAW65732 standard; peptide; 10 AA.
29	52	100.0	181	2	AAW65732	AAW65732 standard; peptide; 10 AA.
30	52	100.0	181	2	AAW65732	AAW65732 standard; peptide; 10 AA.
31	52	100.0	559	2	AAW65732	AAW65732 standard; peptide; 10 AA.
32	52	100.0	767	4	AAW65732	AAW65732 standard; peptide; 10 AA.
33	52	100.0	767	4	AAW65732	AAW65732 standard; peptide; 10 AA.
34	52	100.0	940	2	AAW65732	AAW65732 standard; peptide; 10 AA.
35	52	100.0	940	2	AAW65732	AAW65732 standard; peptide; 10 AA.
36	52	100.0	948	6	AAW65732	AAW65732 standard; peptide; 10 AA.
37	52	100.0	948	6	AAW65732	AAW65732 standard; peptide; 10 AA.
38	52	100.0	948	6	AAW65732	AAW65732 standard; peptide; 10 AA.
39	52	100.0	961	6	AAW65732	AAW65732 standard; peptide; 10 AA.
40	52	100.0	978	4	AAW65732	AAW65732 standard; peptide; 10 AA.
41	52	100.0	1001	4	AAW65732	AAW65732 standard; peptide; 10 AA.
42	52	100.0	1018	1	AAW65732	AAW65732 standard; peptide; 10 AA.
43	52	100.0	1018	1	AAW65732	AAW65732 standard; peptide; 10 AA.
44	52	100.0	1018	4	AAW65732	AAW65732 standard; peptide; 10 AA.
45	52	100.0	1018	6	AAW65732	AAW65732 standard; peptide; 10 AA.

ALIGNMENTS

RESULT 1
ID AAW65732
AAW65732 standard; peptide; 10 AA.

AC AAW65732;

DT 16-OCT-1998 (first entry)

DE Fibronectin binding protein-derived peptide #76.

KW microbial surface components recognising adhesive matrix molecule;

KW MSCRAMM; fibronectin; fibronectin-binding protein; antibody; epitope;

KW antibiotic; bacterial infection; antibiotic-resistant strain.

OS Synthetic.

OS Staphylococcus aureus.

PN MO9831389-A2.

PD 23-JUL-1998.

PF 21-JAN-1998; 98WC-US01222.

PR 21-JAN-1997; 97US-0036139P.

PA (TEXA) UNTV TEXAS A & M SYSTEM.

PI Hoeek M, Patti JM, House-Pompeo KL, Speziale P, Joh D;

PI McGavin MJ;

PI WPI; 1998-413816/35.

PT Antibody that binds to fibronectin-binding protein, preventing its

PT binding to fibronectin - used to treat or prevent bacterial infection,

PT especially by Staphylococci and Streptococci.

PT Example 9; Page 110; 20pp; English.

PS The invention relates to antibodies that bind to a fibronectin-binding

PS domain of a fibronectin-binding protein, and inhibit peptides of a

PS fibronectin-binding protein that do not bind to fibronectin; (2) fusion

PS protein containing at least one peptide of a fibronectin-binding protein

PS linked to a second amino acid sequence; (3) nucleic acid encoding the

PS isolated peptide of (1). Antibodies, the isolated peptides of (1) and the

PS nucleic acids are all useful for immunisation (active or passive) and (by

PS inhibiting binding of bacteria to fibronectin) for preventing or treating

PS infection in humans or other animals, particularly by staphylococci or

CC streptococci, e.g., meningitis, otitis media, pneumonia, endocarditis,
 CC mastitis in cattle, abortion in horses and many others. Since the
 CC antibodies block binding of bacteria, they should be effective against
 CC antibiotic-resistant strains, and may replace antibiotic therapy or
 CC increase its effectiveness. Sequences AAW65719-41 and AAW65658 represent
 CC peptides which were synthesised to span the D1 motif and the N-terminal
 CC 18 amino acids of D2, with each peptide overlapping by eight amino acids
 CC with the previous sequence
 XX
 SQ Sequence 10 AA;

Query Match 100.0%; Score 52; DB 2; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.0068;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DIDFDSVPQI 10
 |||||
 Db 1 DIDFDSVPQI 10

RESULT 2
 AAW60660
 ID AAW60660 standard; protein; 38 AA.

AC AAW60660;
 XX
 XX 25-MAR-2003 (revised)
 DT 07-OCT-1990 (first entry)
 DE Protein with fibronectin binding ability.

XX Hybrid DNA molecule; fibronectin binding; mastitis; ruminants;
 KW wound infection.

OS Staphylococcus aureus.
 XX
 XX EP294349-A.
 PN
 XX 07-DEC-1988.

XX 30-MAY-1988; 88EP-00850188.
 XX
 XX 01-JUN-1987; 87SE-00002272.
 XX

PA (ALFA) ALFA LAVAL AGRIC INT AB.

PI Lindberg MK, Signas LC, Wadstrom TM, Froman G;

DR WPI; 1988-347978/49.
 XX
 DR N-PSDB; AAN81097.

PT Hybrid DNA encoding Staphylococcus aureus fibronectin binding protein -
 PT useful for immunisation and topical application to prevent staphylococcal
 PT infections.

PS Claim 11; Page 12; 23pp; English.

CC The peptide has fibronectin binding ability. It is useful for immunising
 CC ruminants against staphylococcal mastitis, pref. when used at 0.5-5
 CC micrograms/kg, using 3 doses given at 1-3 week intervals; for topical
 CC application to prevent wound infection, using an isotonic saline soln. of
 CC concn. 25-250 micrograms/ml; and, when immobilised on a carrier, for
 CC diagnosing staphylococcal infections. (Updated on 25-MAR-2003 to correct
 CC Pf field.) (Updated on 25-MAR-2003 to correct PA field.)
 CC

SQ Sequence 38 AA;

Query Match 100.0%; Score 52; DB 1; Length 38;
 Best Local Similarity 100.0%; Pred. No. 0.028;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DIDFDSVPQI 10
 |||||

Db 28 DIDFDSVPQI 37

RESULT 3
 AAW82116
 ID AAW82116 standard; protein; 38 AA.

AC AAW82116;

DT 25-MAR-2003 (revised)
 DT 05-JAN-1990 (first entry)

DE Fibronectin binding protein.

XX Fibronectin binding protein; S.aureus; immunisation; mastitis; ruminants;
 KW wound infection; diagnosis.

OS Staphylococcus aureus.

XX EP294349-A.
 XX
 XX 07-DEC-1988.
 PD

XX 30-MAY-1988; 88EP-00850188.

XX 01-JUN-1987; 87SE-00002272.

XX (ALFA) ALFA LAVAL AGRIC INT AB.

PI Lindberg MK, Signas LC, Wadstrom TM, Froman G;

DR WPI; 1988-347978/49.
 XX
 DR N-PSDB; AAN82054.

PT Hybrid DNA encoding Staphylococcus aureus fibronectin binding protein -
 PT useful for immunisation and topical application to prevent staphylococcal
 PT infections.

PS Claim 11; Page 12; 23pp; English.

CC The S.aureus fibronectin binding protein may be included in a hybrid
 CC protein. The protein may be used to immunise ruminants against
 CC staphylococcal mastitis, pref. when given at 0.5-5 microg/kg, using 3
 CC doses at 1-3 week intervals; and for topical applicn. to prevent wound
 CC infection, pref. using isotonic saline soln. of concn. 25-250 microg/mg.
 CC The DNA encoding the binding protein and the hybrid protein may be
 CC immobilised on a carrier and used to diagnose staphylococcal infections.
 CC (Updated on 25-MAR-2003 to correct PA field.)
 CC

SQ Sequence 38 AA;

Query Match 100.0%; Score 52; DB 1; Length 38;
 Best Local Similarity 100.0%; Pred. No. 0.028;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DIDFDSVPQI 10
 |||||
 Db 28 DIDFDSVPQI 37

RESULT 4
 AAW65692
 ID AAW65692 standard; peptide; 38 AA.

AC AAW65692;

DT 16-OCT-1998 (first entry)

DE Fibronectin binding protein-derived peptide #36.

XX microbial surface components recognising adhesive matrix molecule;
 KW MSCRAMM; fibronectin; fibronectin-binding protein; antibody; epitope;
 KW antibiotic; bacterial infection; antibiotic-resistant strain.

XX OS Synthetic.
 XX OS Staphylococcus aureus.
 XX PN MO9831389-A2.
 XX PD 23-JUL-1998.
 XX PF 21-JAN-1998; 98WO-US001222.
 XX PR 21-JAN-1997; 97US-0036139P.
 XX PA (TEXA) UNIV TEXAS A & M SYSTEM.
 XX PI Hoecek M, Patti JM, House-Pompeo KL, Speciale P, Joh D;
 XX PI Mcgavin MJ;
 XX DR WPI; 1998-413816/35.
 XX PT Antibody that binds to fibronectin-binding protein, preventing its
 XX PT binding to fibronectin - used to treat or prevent bacterial infection,
 XX PT especially by Staphylococci and Streptococci.
 XX PS Example 8; Page 101; 201pp; English.
 XX CC The invention relates to antibodies that bind to a fibronectin-binding
 XX CC domain of a fibronectin-binding protein, and inhibit binding of the
 XX CC protein to fibronectin. Also claimed are: (1) isolated peptides of a
 XX CC fibronectin-binding protein that do not bind to fibronectin; (2) fusion
 XX CC protein containing at least one peptide of a fibronectin-binding protein
 XX CC linked to a second amino acid sequence; (3) nucleic acid encoding the
 XX CC isolated peptide of (1). Antibodies, the isolated peptides of (1) and (by
 XX CC nucleic acids are all useful for immunisation (active or passive) and (by
 XX CC inhibiting binding of bacteria to fibronectin) for preventing or treating
 XX CC infection in humans or other animals, particularly by staphylococci or
 XX CC streptococci, e.g. meningitis, otitis media, pneumonia, endocarditis,
 XX CC mastitis in cattle, abortion in horses and many others. Since the
 XX CC antibodies block binding of bacteria, they should be effective against
 XX CC antibiotic-resistant strains, and may replace antibiotic therapy or
 XX CC increase its effectiveness. Sequences AAW65691-700 represent a series of
 XX CC synthetic peptides based on the D1 region of S. aureus fibronectin
 XX CC binding protein A. They were synthesised to contain mutations
 XX SQ Sequence 38 AA;
 XX
 XX Query Match 100.0%; Score 52; DB 2; Length 38;
 XX Best Local Similarity 100.0%; Pred. No. 0.028;
 XX Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DIDFDSVPQI 10
 |||||
 DB 27 DIDFDSVPQI 36
 RESULT 5
 ID AAW65695
 DE AAW65695 standard; peptide; 38 AA.
 AC AAW65695;
 DT 16-OCT-1998 (first entry)
 XX Fibronectin binding protein-derived peptide #39.
 XX DE microbial surface components recognising adhesive matrix molecule;
 XX KM MSCRAMM; fibronectin; fibronectin-binding protein; antibody; epitope;
 XX KM antibiotic; bacterial infection; antibiotic-resistant strain.
 XX OS Synthetic.
 XX OS Staphylococcus aureus.
 XX PN MO9831389-A2.
 XX

PD 23-JUL-1998.
 XX PF 21-JAN-1998; 98WO-US001222.
 XX PR 21-JAN-1997; 97US-0036139P.
 XX PA (TEXA) UNIV TEXAS A & M SYSTEM.
 XX PI Hoecek M, Patti JM, House-Pompeo KL, Speciale P, Joh D;
 XX PI Mcgavin MJ;
 XX DR WPI; 1998-413816/35.
 XX PT Antibody that binds to fibronectin-binding protein, preventing its
 XX PT binding to fibronectin - used to treat or prevent bacterial infection,
 XX PT especially by Staphylococci and Streptococci.
 XX PS Example 8; Page 102; 201pp; English.
 XX CC The invention relates to antibodies that bind to a fibronectin-binding
 XX CC domain of a fibronectin-binding protein, and inhibit binding of the
 XX CC protein to fibronectin. Also claimed are: (1) isolated peptides of a
 XX CC fibronectin-binding protein that do not bind to fibronectin; (2) fusion
 XX CC protein containing at least one peptide of a fibronectin-binding protein
 XX CC linked to a second amino acid sequence; (3) nucleic acid encoding the
 XX CC isolated peptide of (1). Antibodies, the isolated peptides of (1) and (by
 XX CC nucleic acids are all useful for immunisation (active or passive) and (by
 XX CC inhibiting binding of bacteria to fibronectin) for preventing or treating
 XX CC infection in humans or other animals, particularly by staphylococci or
 XX CC streptococci, e.g. meningitis, otitis media, pneumonia, endocarditis,
 XX CC mastitis in cattle, abortion in horses and many others. Since the
 XX CC antibodies block binding of bacteria, they should be effective against
 XX CC antibiotic-resistant strains, and may replace antibiotic therapy or
 XX CC increase its effectiveness. Sequences AAW65691-700 represent a series of
 XX CC synthetic peptides based on the D1 region of S. aureus fibronectin
 XX CC binding protein A. They were synthesised to contain mutations
 XX SQ Sequence 38 AA;
 XX
 XX Query Match 100.0%; Score 52; DB 2; Length 38;
 XX Best Local Similarity 100.0%; Pred. No. 0.028;
 XX Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DIDFDSVPQI 10
 |||||
 DB 27 DIDFDSVPQI 36
 RESULT 6
 ID AAW65662
 DE AAW65662 standard; peptide; 38 AA.
 AC AAW65662;
 DT 16-OCT-1998 (first entry)
 XX Fibronectin binding protein-derived peptide #6.
 XX DE microbial surface components recognising adhesive matrix molecule;
 XX KM MSCRAMM; fibronectin; fibronectin-binding protein; antibody; epitope;
 XX KM antibiotic; bacterial infection; antibiotic-resistant strain.
 XX OS Synthetic.
 XX OS Staphylococcus aureus.
 XX PN MO9831389-A2.
 XX PD 23-JUL-1998.
 XX PF 21-JAN-1998; 98WO-US001222.
 XX PR 21-JAN-1997; 97US-0036139P.
 XX

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PA      (TEXA ) UNIV TEXAS A & M SYSTEM.
XX
XX   Hoesek M, Patti JM, House-Pompeo KL, Speziale P, Joh D;
PI   Mcgavin MJ;
XX
DR     WPI, 1998-413816/35.
XX
XX
PS     Example 2; Page 92; 201pp; English.
XX
XX   The invention relates to antibodies that bind to a fibronectin-binding
CC   domain of a fibronectin-binding protein, and inhibit binding of the
CC   protein to fibronectin. Also claimed are: (1) isolated peptides of a
CC   fibronectin-binding protein that do not bind to fibronectin; (2) fusion
CC   protein containing at least one peptide of a fibronectin-binding protein
CC   linked to a second amino acid sequence; (3) nucleic acid encoding the
CC   isolated peptide of (1). Antibodies, the isolated peptides of (1) and the
CC   nucleic acids are all useful for immunisation (active or passive) and
CC   inhibiting binding of bacteria to fibronectin) for preventing or treating
CC   infection in humans or other animals, particularly by staphylococci or
CC   streptococci, e.g. meningitis, otitis media, pneumonia, endocarditis,
CC   mastitis in cattle, abortion in horses and many others. Since the
CC   antibodies block binding of bacteria, they should be effective against
CC   antibiotic-resistant strains, and may replace antibiotic therapy or
CC   increase its effectiveness. Sequences AAW65659-68 represent synthetic
CC   epitopes from the fibronectin binding domains DU and DI-p4 of the S.
CC   aureus fnba gene
XX
SQ     Sequence 38 AA:
XX
XX   Query Match          100.0%; Score 52; DB 2; Length 38;
XX   Best Local Similarity 100.0%; Pred. No. 0.028;
XX   Matches    10; Conservative    0; Mismatches    0; Indels    0; Gaps    0
XX
OY     1 DIDPDSVPOI 10
XX       |||||
XX       27 DIDFDSVPQI 36
XX
DB     AAW65696 standard; peptide; 38 AA.
XX
AC     AAW65696;
XX
DT     16-OCT-1998 (first entry)
XX
DE     Fibronectin binding protein-derived peptide #40.
XX
KW     microbial surface components recognising adhesive matrix molecule;
KM     MSCRAMM; fibronectin; fibronectin-binding protein; antibody; epitope;
KK     antibiotic; bacterial infection; antibiotic-resistant strain.
XX
OS     Synthetic.
OS     Staphylococcus aureus.
XX
PN     WO9831389-A2.
XX
PD     23-JUL-1998.
XX
PF     21-JAN-1998; 98WO-US001222.
PR     21-JAN-1997; 97US-0036139P.
XX
XX   (TEXA ) UNIV TEXAS A & M SYSTEM.
XX
XX   Hoesek M, Patti JM, House-Pompeo KL, Speziale P, Joh D;
PI   Mcgavin MJ;
XX
DR     WPI, 1998-413816/35.

```

```

XX Antibody that binds to fibrinectin-binding protein, preventing its
PT binding to fibrinectin - used to treat or prevent bacterial infection,
PT especially by Staphylococci and Streptococci.
PS
XX Example 8; Page 102; 201pp; English.
XX
CC The invention relates to antibodies that bind to a fibrinectin-binding
CC domain of a fibrinectin-binding protein, and inhibit binding of the
CC protein to fibrinectin. Also claimed are: (1) isolated peptides of a
CC fibrinectin-binding protein that do not bind to fibrinectin; (2) fusion
CC protein containing at least one peptide of a fibrinectin-binding protein
CC linked to a second amino acid sequence; (3) nucleic acid encoding the
CC isolated peptide of (1). Antibodies, the isolated peptides of (1) and the
CC nucleic acids are all useful for immunisation (active or passive) and (by
CC infection binding of bacteria to fibrinectin) for preventing or treating
CC infection in humans or other animals, particularly by staphylococci or
CC streptococci, e.g. meningitis, otitis media, pneumonia, endocarditis,
CC mastitis in cattle, abortion in horses and many others. Since the
CC antibodies block binding of bacteria, they should be effective against
CC antibiotic-resistant strains, and may replace antibiotic therapy or
CC increase its effectiveness. Sequences AAW65691-700 represent a series of
CC synthetic peptides based on the D1 region of S. aureus fibrinectin
CC binding protein A. They were synthesised to contain mutations
SQ
XX
SQ Sequence 38 AA:
Query Match 100.0%; Score 52; DB 2; Length 38;
Beat Local Similarity 100.0%; Pred. No. 0.028;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 DIDFDSVPQI 10
| | | | | | |
| | | | | | |
Db 27 DIDFDSVPQI 36
AAW65697
ID AAW65697 standard; peptide; 38 AA.
XX
XX AAW65697;
AC
XX
XX 16-OCT-1998 (first entry)
DT
XX
XX Fibrinectin binding protein-derived peptide #41.
DE
XX
XX microbial surface components recognising adhesive matrix molecule;
KW MSCRAMM; fibrinectin; fibrinectin-binding protein; antibody; epitope;
KW antibiotic; bacterial infection; antibiotic-resistant strain.
XX
XX Synthetic.
OS
XX Staphylococcus aureus.
XX
XX MO9831389-A2.
XX
XX 23-OUL-1998.
PD
XX
XX 21-JAN-1998; 98WO-US001222.
PF
XX
XX 21-JAN-1997; 97US-0036139P.
PR
XX
XX (TEXA ) UNIV TEXAS A & M SYSTEM.
PA
XX
XX Hoecek M, Patci JM, House-Pompeo KL, Speziale P, Joh D;
PI Mcgavin M;
XX
XX WPI. 1998-413816/35.
XX
XX Antibody that binds to fibrinectin-binding protein, preventing its
PT binding to fibrinectin - used to treat or prevent bacterial infection,
PT especially by Staphylococci and Streptococci.
XX
XX Example 8; Page 102; 201pp; English.

```

XX The invention relates to antibodies that bind to a fibronectin-binding
 CC domain of a fibronectin-binding protein, and inhibit binding of the
 CC protein to fibronectin. Also claimed are: (1) isolated peptides of a
 CC fibronectin-binding protein that do not bind to fibronectin; (2) fusion
 CC protein containing at least one peptide of a fibronectin-binding protein
 CC linked to a second amino acid sequence; (3) nucleic acid encoding the
 CC isolated peptide of (1). Antibodies, the isolated peptides of (1) and the
 CC nucleic acids are all useful for immunisation (active or passive) and (by
 CC inhibiting binding of bacteria to fibronectin) for preventing or treating
 CC infection in humans or other animals, particularly by staphylococci or
 CC streptococci, e.g. meningitis, otitis media, pneumonia, endocarditis,
 CC mastitis in cattle, abortion in horses and many others. Since the
 CC antibodies block binding of bacteria, they should be effective against
 CC antibiotic-resistant strains, and may replace antibiotic therapy or
 CC increase its effectiveness. Sequences AAM65691-700 represent a series of
 CC synthetic peptides based on the DI region of *S. aureus* fibronectin
 CC binding protein A. They were synthesised to contain mutations

XX Sequence 38 AA;

Query Match 100.0%; Score 52; DB 2; Length 38;
 Best Local Similarity 100.0%; Pred. No. 0.028;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIDFDSVPQI 10
 |||||
 Db 27 DIDFDSVPQI 36

RESULT 9
 ID AAM65694 standard; peptide; 38 AA.

XX AAM65694;

XX 16-OCT-1998 (first entry)

XX Fibronectin binding protein-derived peptide #38.

XX microbial surface components recognising adhesive matrix molecule;

XX MSCRAMM; fibronectin; fibronectin-binding protein; antibody; epitope;

XX antibiotic; bacterial infection; antibiotic-resistant strain.

XX Synthetic.

XX Staphylococcus aureus.

XX WO9831389-A2.

XX 23-JUL-1998.

XX 21-JAN-1998; 98WO-US001222.

XX 21-JAN-1997; 97US-0036139P.

XX (TEXA) UNIV TEXAS A & M SYSTEM.

XX Hoeek M, Patli JM, House-Pompeo KL, Speziale P, Joh D;

XX Megavlin MJ;

XX WPI; 1998-413816/35.

XX Antibody that binds to fibronectin-binding protein, preventing its

XX binding to fibronectin - used to treat or prevent bacterial infection,

XX especially by Staphylococci and Streptococci.

XX Example 8; Page 102; 201pp; English.

CC linked to a second amino acid sequence; (3) nucleic acid encoding the
 CC isolated peptide of (1). Antibodies, the isolated peptides of (1) and the
 CC nucleic acids are all useful for immunisation (active or passive) and (by
 CC inhibiting binding of bacteria to fibronectin) for preventing or treating
 CC infection in humans or other animals, particularly by staphylococci or
 CC streptococci, e.g. meningitis, otitis media, pneumonia, endocarditis,
 CC mastitis in cattle, abortion in horses and many others. Since the
 CC antibodies block binding of bacteria, they should be effective against
 CC antibiotic-resistant strains, and may replace antibiotic therapy or
 CC increase its effectiveness. Sequences AAM65691-700 represent a series of
 CC synthetic peptides based on the DI region of *S. aureus* fibronectin
 CC binding protein A. They were synthesised to contain mutations

XX Sequence 38 AA;

Query Match 100.0%; Score 52; DB 2; Length 38;
 Best Local Similarity 100.0%; Pred. No. 0.028;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIDFDSVPQI 10
 |||||
 Db 27 DIDFDSVPQI 36

RESULT 10
 ID AAM65700 standard; peptide; 38 AA.

XX AAM65700;

XX 16-OCT-1998 (first entry)

XX Fibronectin binding protein-derived peptide #44.

XX microbial surface components recognising adhesive matrix molecule;

XX MSCRAMM; fibronectin; fibronectin-binding protein; antibody; epitope;

XX antibiotic; bacterial infection; antibiotic-resistant strain.

XX Synthetic.

XX Staphylococcus aureus.

XX WO9831389-A2.

XX 23-JUL-1998.

XX 21-JAN-1998; 98WO-US001222.

XX 21-JAN-1997; 97US-0036139P.

XX (TEXA) UNIV TEXAS A & M SYSTEM.

XX Hoeek M, Patli JM, House-Pompeo KL, Speziale P, Joh D;

XX Megavlin MJ;

XX WPI; 1998-413816/35.

XX Antibody that binds to fibronectin-binding protein, preventing its

XX binding to fibronectin - used to treat or prevent bacterial infection,

XX especially by Staphylococci and Streptococci.

XX Example 8; Page 102; 201pp; English.

XX The invention relates to antibodies that bind to a fibronectin-binding

XX domain of a fibronectin-binding protein, and inhibit binding of the

XX protein to fibronectin. Also claimed are: (1) isolated peptides of a

XX fibronectin-binding protein that do not bind to fibronectin; (2) fusion

XX protein containing at least one peptide of a fibronectin-binding protein

CC mastitis in cattle, abortion in horses and many others. Since the
 CC antibodies block binding of bacteria, they should be effective against
 CC antibiotic-resistant strains, and may replace antibiotic therapy or
 CC increase its effectiveness. Sequences AAW65691-700 represent a series of
 CC synthetic peptides based on the DI region of *S. aureus* fibronectin
 CC binding protein A. They were synthesised to contain mutations
 XX

Sequence 38 AA:

Query Match 100.0%; Score 52; DB 2; Length 38;
 Best Local Similarity 100.0%; Pred. No. 0.028;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIDPDSVPQI 10
 |||||
 DB 27 DIDPDSVPQI 36

RESULT 11
 AAW65691 standard; peptide; 38 AA.

XX AAW65691;
 AC
 DT 16-OCT-1998 (first entry)
 XX

DE Fibronectin binding protein-derived peptide #35.

XX
 XX microbial surface components recognising adhesive matrix molecule;
 KW MSCRAMM; fibronectin; fibronectin-binding protein; antibody; epitope;
 KW antibiotic; bacterial infection; antibiotic-resistant strain.
 XX

OS Synthetic.
 OS Staphylococcus aureus.
 XX

PN WO9831389-A2.
 XX

PD 23-JUL-1998.
 XX

PF 21-JAN-1998; 98WO-US001222.
 XX

PR 21-JAN-1997; 97US-0036139P.
 XX

PA (TEXA) UNIV TEXAS A & M SYSTEM.
 XX

PI Hoecek M, Patti JM, House-Pompeo KL, Speziale P, Joh D;
 PI McGavin MJ;
 XX

DR WPI; 1998-413816/35.
 XX

PT Antibody that binds to fibronectin-binding protein, preventing its
 PT binding to fibronectin - used to treat or prevent bacterial infection,
 PT especially by Staphylococci and Streptococci.
 XX

PS Example 8; Page 101; 201pp; English.
 XX

CC The invention relates to antibodies that bind to a fibronectin-binding
 CC domain of a fibronectin-binding protein, and inhibit binding of the
 CC protein to fibronectin. Also claimed are: (1) isolated peptides of a
 CC fibronectin-binding protein that do not bind to fibronectin; (2) fusion
 CC protein containing at least one peptide of a fibronectin-binding protein
 CC linked to a second amino acid sequence; (3) nucleic acid encoding the
 CC isolated peptide of (1). Antibodies, the isolated peptides of (1) and the
 CC nucleic acids are all useful for immunisation (active or passive) and (by
 CC inhibiting binding of bacteria to fibronectin) for preventing or treating
 CC infection in humans or other animals, particularly by staphylococci or
 CC streptococci, e.g. meningitis, otitis media, pneumonia, endocarditis,
 CC mastitis in cattle, abortion in horses and many others. Since the
 CC antibodies block binding of bacteria, they should be effective against
 CC antibiotic-resistant strains, and may replace antibiotic therapy or
 CC increase its effectiveness. Sequences AAW65691-700 represent a series of
 CC synthetic peptides based on the DI region of *S. aureus* fibronectin
 CC binding protein A. They were synthesised to contain mutations
 CC

XX
 SQ Sequence 38 AA;

Query Match 100.0%; Score 52; DB 2; Length 38;
 Best Local Similarity 100.0%; Pred. No. 0.028;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIDPDSVPQI 10
 |||||
 DB 27 DIDPDSVPQI 36

RESULT 12
 AAW65699 standard; peptide; 38 AA.

XX AAW65699;
 AC
 DT 16-OCT-1998 (first entry)
 XX

DE Fibronectin binding protein-derived peptide #43.

XX
 XX microbial surface components recognising adhesive matrix molecule;
 KW MSCRAMM; fibronectin; fibronectin-binding protein; antibody; epitope;
 KW antibiotic; bacterial infection; antibiotic-resistant strain.
 XX

OS Synthetic.
 OS Staphylococcus aureus.
 XX

PN WO9831389-A2.
 XX

PD 23-JUL-1998.
 XX

PF 21-JAN-1998; 98WO-US001222.
 XX

PR 21-JAN-1997; 97US-0036139P.
 XX

PA (TEXA) UNIV TEXAS A & M SYSTEM.
 XX

PI Hoecek M, Patti JM, House-Pompeo KL, Speziale P, Joh D;
 PI McGavin MJ;
 XX

DR WPI; 1998-413816/35.
 XX

PT Antibody that binds to fibronectin-binding protein, preventing its
 PT binding to fibronectin - used to treat or prevent bacterial infection,
 PT especially by Staphylococci and Streptococci.
 XX

PS Example 8; Page 102; 201pp; English.
 XX

CC The invention relates to antibodies that bind to a fibronectin-binding
 CC domain of a fibronectin-binding protein, and inhibit binding of the
 CC protein to fibronectin. Also claimed are: (1) isolated peptides of a
 CC fibronectin-binding protein that do not bind to fibronectin; (2) fusion
 CC protein containing at least one peptide of a fibronectin-binding protein
 CC linked to a second amino acid sequence; (3) nucleic acid encoding the
 CC isolated peptide of (1). Antibodies, the isolated peptides of (1) and the
 CC nucleic acids are all useful for immunisation (active or passive) and (by
 CC inhibiting binding of bacteria to fibronectin) for preventing or treating
 CC infection in humans or other animals, particularly by staphylococci or
 CC streptococci, e.g. meningitis, otitis media, pneumonia, endocarditis,
 CC mastitis in cattle, abortion in horses and many others. Since the
 CC antibodies block binding of bacteria, they should be effective against
 CC antibiotic-resistant strains, and may replace antibiotic therapy or
 CC increase its effectiveness. Sequences AAW65691-700 represent a series of
 CC synthetic peptides based on the DI region of *S. aureus* fibronectin
 CC binding protein A. They were synthesised to contain mutations
 XX

Sequence 38 AA:

Query Match 100.0%; Score 52; DB 2; Length 38;
 Best Local Similarity 100.0%; Pred. No. 0.028;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIDFDSVPQI 10
 |||||
 DB 27 DIDFDSVPQI 36

RESULT 13

AAW65661 standard; peptide; 38 AA.

AAW65661;

16-OCT-1998 (first entry)

Fibronectin binding protein-derived peptide #5.

microbial surface components recognising adhesive matrix molecule;

MSCRAMM; fibronectin; fibronectin-binding protein; antibody; epitope;

antibiotic; bacterial infection; antibiotic-resistant strain.

Synthetic.

Staphylococcus aureus.

WO9831389-A2.

23-JUL-1998.

21-JAN-1998; 98WO-US001222.

21-JAN-1997; 97US-0036139P.

(TEXA) UNIV TEXAS A & M SYSTEM.

Hoeck M, Patti JM, House-Pompeo KL, Speziale P, Joh D;

McGavin MJ;

WPI; 1998-413816/35.

Antibody that binds to fibronectin-binding protein, preventing its

binding to fibronectin - used to treat or prevent bacterial infection,

especially by Staphylococci and Streptococci.

Example 2; Page 92; 201pp; English.

The invention relates to antibodies that bind to a fibronectin-binding

domain of a fibronectin-binding protein, and inhibit binding of the

protein to fibronectin. Also claimed are: (1) isolated peptides of a

fibronectin-binding protein that do not bind to fibronectin; (2) fusion

protein containing at least one peptide of a fibronectin-binding protein

linked to a second amino acid sequence; (3) nucleic acid encoding the

isolated peptide of (1). Antibodies, the isolated peptides of (1) and the

nucleic acids are all useful for immunisation (active or passive) and (by

inhibiting binding of bacteria to fibronectin) for preventing or treating

infection in humans or other animals, particularly by staphylococci or

streptococci, e.g. meningitis, otitis media, pneumonia, endocarditis,

mastitis in cattle, abortion in horses and many others. Since the

antibodies block binding of bacteria, they should be effective against

antibiotic-resistant strains, and may replace antibiotic therapy or

increase its effectiveness. Sequences AAW65659-68 represent synthetic

epitopes from the fibronectin binding domains DU and DI-D4 of the S.

aureus fnbA gene

Sequence 38 AA;

Query Match 100.0%; Score 52; DB 2; Length 38;

Best Local Similarity 100.0%; Pred. No. 0.028;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIDFDSVPQI 10
 |||||
 DB 27 DIDFDSVPQI 36

RESULT 14

AAW65693 standard; peptide; 38 AA.

AAW65693;

16-OCT-1998 (first entry)

Fibronectin binding protein-derived peptide #37.

microbial surface components recognising adhesive matrix molecule;

MSCRAMM; fibronectin; fibronectin-binding protein; antibody; epitope;

antibiotic; bacterial infection; antibiotic-resistant strain.

Synthetic.

Staphylococcus aureus.

WO9831389-A2.

23-JUL-1998.

21-JAN-1998; 98WO-US001222.

21-JAN-1997; 97US-0036139P.

(TEXA) UNIV TEXAS A & M SYSTEM.

Hoeck M, Patti JM, House-Pompeo KL, Speziale P, Joh D;

McGavin MJ;

WPI; 1998-413816/35.

Antibody that binds to fibronectin-binding protein, preventing its

binding to fibronectin - used to treat or prevent bacterial infection,

especially by Staphylococci and Streptococci.

Example 8; Page 102; 201pp; English.

The invention relates to antibodies that bind to a fibronectin-binding

domain of a fibronectin-binding protein, and inhibit binding of the

protein to fibronectin. Also claimed are: (1) isolated peptides of a

fibronectin-binding protein that do not bind to fibronectin; (2) fusion

protein containing at least one peptide of a fibronectin-binding protein

linked to a second amino acid sequence; (3) nucleic acid encoding the

isolated peptide of (1). Antibodies, the isolated peptides of (1) and the

nucleic acids are all useful for immunisation (active or passive) and (by

inhibiting binding of bacteria to fibronectin) for preventing or treating

infection in humans or other animals, particularly by staphylococci or

streptococci, e.g. meningitis, otitis media, pneumonia, endocarditis,

mastitis in cattle, abortion in horses and many others. Since the

antibodies block binding of bacteria, they should be effective against

antibiotic-resistant strains, and may replace antibiotic therapy or

increase its effectiveness. Sequences AAW65691-700 represent a series of

synthetic peptides based on the DI region of S. aureus fibronectin

binding protein A. They were synthesised to contain mutations

Sequence 38 AA;

Query Match 100.0%; Score 52; DB 2; Length 38;

Best Local Similarity 100.0%; Pred. No. 0.028;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIDFDSVPQI 10
 |||||
 DB 27 DIDFDSVPQI 36

RESULT 15

AAW65698 standard; peptide; 38 AA.

AAW65698;

16-OCT-1998 (first entry)

Fibronectin binding protein-derived peptide #37.

microbial surface components recognising adhesive matrix molecule;

MSCRAMM; fibronectin; fibronectin-binding protein; antibody; epitope;

antibiotic; bacterial infection; antibiotic-resistant strain.

Synthetic.

Staphylococcus aureus.

WO9831389-A2.

23-JUL-1998.

21-JAN-1998; 98WO-US001222.

21-JAN-1997; 97US-0036139P.

(TEXA) UNIV TEXAS A & M SYSTEM.

Hoeck M, Patti JM, House-Pompeo KL, Speziale P, Joh D;

McGavin MJ;

WPI; 1998-413816/35.

Antibody that binds to fibronectin-binding protein, preventing its

binding to fibronectin - used to treat or prevent bacterial infection,

especially by Staphylococci and Streptococci.

Example 8; Page 102; 201pp; English.

The invention relates to antibodies that bind to a fibronectin-binding

domain of a fibronectin-binding protein, and inhibit binding of the

protein to fibronectin. Also claimed are: (1) isolated peptides of a

fibronectin-binding protein that do not bind to fibronectin; (2) fusion

protein containing at least one peptide of a fibronectin-binding protein

linked to a second amino acid sequence; (3) nucleic acid encoding the

isolated peptide of (1). Antibodies, the isolated peptides of (1) and the

nucleic acids are all useful for immunisation (active or passive) and (by

inhibiting binding of bacteria to fibronectin) for preventing or treating

infection in humans or other animals, particularly by staphylococci or

streptococci, e.g. meningitis, otitis media, pneumonia, endocarditis,

mastitis in cattle, abortion in horses and many others. Since the

antibodies block binding of bacteria, they should be effective against

antibiotic-resistant strains, and may replace antibiotic therapy or

increase its effectiveness. Sequences AAW65691-700 represent a series of

synthetic peptides based on the DI region of S. aureus fibronectin

binding protein A. They were synthesised to contain mutations

Sequence 38 AA;

Query Match 100.0%; Score 52; DB 2; Length 38;

Best Local Similarity 100.0%; Pred. No. 0.028;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIDFDSVPQI 10
 |||||
 DB 27 DIDFDSVPQI 36


```

DT 16-OCT-1998 (first entry)
XX
DE Fibronectin binding protein-derived peptide #42.
XX
KW microbial surface components recognising adhesive matrix molecule;
MSCRAM; fibronectin; fibronectin-binding protein; antibody; epitope;
KW antibiotic; bacterial infection; antibiotic-resistant strain.
XX
OS Synthetic.
OS Staphylococcus aureus.
XX
PN WO9831389-A2.
XX
PD 23-JUL-1998.
XX
PF 21-JAN-1998; 98WO-US001222.
XX
PR 21-JAN-1997; 97US-0036139P.
XX
PA (TEXA ) UNIV TEXAS A & M SYSTEM.
PI Hoecek M, Patti JM, House-Pompeo KL, Speziale P, Joh D;
PI McGavin MJ;
DR WPI; 1998-413816/35.
XX
PT Antibody that binds to fibronectin-binding protein, preventing its
PT binding to fibronectin - used to treat or prevent bacterial infection,
PT especially by Staphylococci and Streptococci.
XX
PS Example 8; Page 102; 201pp; English.
XX
CC The invention relates to antibodies that bind to a fibronectin-binding
CC domain of a fibronectin-binding protein, and inhibit binding of the
CC protein to fibronectin. Also claimed are: (1) isolated peptides of a
CC fibronectin-binding protein that do not bind to fibronectin; (2) fusion
CC protein containing at least one peptide of a fibronectin-binding protein
CC linked to a second amino acid sequence; (3) nucleic acid encoding the
CC isolated peptide of (1). Antibodies, the isolated peptides of (1) and the
CC nucleic acids are all useful for immunisation (active or passive) and (by
CC inhibiting binding of bacteria to fibronectin) for preventing or treating
CC infection in humans or other animals, particularly by staphylococci or
CC streptococci, e.g. meningitis, otitis media, pneumonia, endocarditis,
CC mastitis in cattle, abortion in horses and many others. Since the
CC antibodies block binding of bacteria, they should be effective against
CC antibiotic-resistant strains, and may replace antibiotic therapy or
CC increase its effectiveness. Sequences AAW65691-700 represent a series of
CC synthetic peptides based on the DI region of S. aureus fibronectin
CC binding protein A. They were synthesised to contain mutations
XX
SQ Sequence 38 AA;

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Query Match 100.0%; Score 52; DB 2; Length 38;
Best Local Similarity 100.0%; Pred. No. 0.028;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 DIDFDSVPQI 10
   |||||
DB 27 DIDFDSVPQI 36

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Search completed: October 25, 2005, 20:58:44
Job time : 63.2 secs

GenCore version 5.1.6
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OM protein - protein search, using SW model

Run on: October 22, 2005, 05:46:56 ; Search time 17.3 Seconds
(without alignments)
43.150 Million cell updates/sec

Title: US-10-731-238-76
Perfect score: 52
Sequence: 1 DIDPSPQI 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- 2: /cgn2_6/prodata/1/iaa/5B_COMB.pep:*
- 3: /cgn2_6/prodata/1/iaa/6A_COMB.pep:*
- 4: /cgn2_6/prodata/1/iaa/6B_COMB.pep:*
- 5: /cgn2_6/prodata/1/iaa/PCTUS_COMB.pep:*
- 6: /cgn2_6/prodata/1/iaa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	52	100.0	10	4	US-09-010-317-76
2	52	100.0	38	1	US-08-234-622A-2
3	52	100.0	38	1	US-08-729-767-3
4	52	100.0	38	4	US-09-010-317-5
5	52	100.0	38	4	US-09-010-317-6
6	52	100.0	38	4	US-09-010-317-35
7	52	100.0	38	4	US-09-010-317-36
8	52	100.0	38	4	US-09-010-317-37
9	52	100.0	38	4	US-09-010-317-38
10	52	100.0	38	4	US-09-010-317-39
11	52	100.0	38	4	US-09-010-317-40
12	52	100.0	38	4	US-09-010-317-41
13	52	100.0	38	4	US-09-010-317-42
14	52	100.0	38	4	US-09-010-317-43
15	52	100.0	38	4	US-09-010-317-44
16	52	100.0	114	1	US-08-259-000-3
17	52	100.0	130	2	US-08-459-135A-7
18	52	100.0	130	2	US-08-459-135A-8
19	52	100.0	130	2	US-08-495-559-7
20	52	100.0	130	3	US-08-495-559-8
21	52	100.0	139	3	US-08-856-253-8
22	52	100.0	174	2	US-08-459-135A-10
23	52	100.0	174	2	US-08-459-135A-13
24	52	100.0	174	3	US-08-495-559-10
25	52	100.0	174	3	US-08-495-559-13
26	52	100.0	176	3	US-08-495-559-6
27	52	100.0	178	2	US-08-459-135A-12

28	52	100.0	178	3	US-08-495-559-12	Sequence 12, Appl
29	52	100.0	181	2	US-08-459-135A-6	Sequence 6, Appl1
30	52	100.0	559	4	US-08-956-171E-5251	Sequence 5251, Ap
31	52	100.0	559	4	US-08-781-986A-5251	Sequence 5251, Ap
32	52	100.0	1027	4	US-08-956-171E-5254	Sequence 5254, Ap
33	52	100.0	1027	4	US-08-781-986A-5254	Sequence 5254, Ap
34	47	90.4	36	4	US-09-010-317-58	Sequence 58, Appl
35	47	90.4	36	4	US-09-010-317-59	Sequence 59, Appl
36	47	90.4	38	1	US-08-234-622A-3	Sequence 3, Appl1
37	47	90.4	38	1	US-08-729-767-4	Sequence 7, Appl1
38	47	90.4	38	4	US-09-010-317-7	Sequence 8, Appl1
39	47	90.4	38	4	US-09-010-317-8	Sequence 8, Appl1
40	47	90.4	38	4	US-09-010-317-45	Sequence 45, Appl
41	47	90.4	38	4	US-09-010-317-46	Sequence 46, Appl
42	47	90.4	38	4	US-09-010-317-47	Sequence 47, Appl
43	47	90.4	38	4	US-09-010-317-48	Sequence 48, Appl
44	47	90.4	38	4	US-09-010-317-49	Sequence 49, Appl
45	47	90.4	38	4	US-09-010-317-50	Sequence 50, Appl

ALIGNMENTS

RESULT 1
US-09-010-317-76
Sequence 76, Application US/09010317
Patent No. 6685943
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
APPLICANT: Patti, Joseph M.
APPLICANT: House-Pompeo, Karen L.
APPLICANT: Speziale, Pietro
APPLICANT: John, Danny
APPLICANT: McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
TITLE OF INVENTION: AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAMK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 76:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-09-010-317-76
Query Match 100.0%; Score 52; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0035;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DIDFDSVPQI 10
| | | | | | | | | |

Db 1 DIDFDSVPQI 10

RESULT 2

US-08-234-622A-2

; Sequence 2, Application US/08234622A

; Patent No. 5440014

; GENERAL INFORMATION:

; APPLICANT: HOOK, Magnus

; APPLICANT: MCGAVIN, Martin

; APPLICANT: RAUCCI, Giuseppe

; TITLE OF INVENTION: A FIBRONECTIN BINDING PEPTIDE

; NUMBER OF SEQUENCES: 4

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Burns, Doane, Swecker & Mathis

; STREET: P.O. Box 1404

; CITY: Alexandria

; STATE: Virginia

; COUNTRY: United States

; ZIP: 22313-1404

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Releasee #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/234,622A

; FILING DATE: 28-Apr-1994

; CLASSIFICATION: 530

; PRIORITY APPLICATION DATA:

; APPLICATION NUMBER: SE 9002617-0

; FILING DATE: 10-AUG-1990

; PRIORITY APPLICATION DATA:

; APPLICATION NUMBER: WO PCT/SE91/00534

; FILING DATE: 09-AUG-1991

; ATTORNEY/AGENT INFORMATION:

; NAME: Meuth, Donna M

; REGISTRATION NUMBER: 36,607

; REFERENCE/DOCKET NUMBER: 012885-044

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (703) 836-6620

; TELEFAX: (703) 836-2021

; INFORMATION FOR SEQ ID NO: 2:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 38 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

US-08-234-622A-2

Query Match 100.0%; Score 52; DB 1; Length 38;

Best Local Similarity 100.0%; Pred. No. 0.015;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DIDFDSVPQI 10
| | | | | | | | | |

Db 27 DIDFDSVPQI 36

RESULT 3

US-08-729-767-3

; Sequence 3, Application US/08729767

; Patent No. 5770702

; GENERAL INFORMATION:

; APPLICANT: HOOK, Magnus

; APPLICANT: LINDERBERG, Martin Kjell

; APPLICANT: SIGNAS, Lars Christer

; APPLICANT: MADSTROM, Torckel Mikael

; APPLICANT: FROMAN, Gunnar

; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN AS WELL AS

; TITLE OF INVENTION: ITS PREPARATION

; NUMBER OF SEQUENCES: 6

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Burns, Doane, Swecker & Mathis, L.L.P.

; STREET: P.O. Box 1404

; CITY: Alexandria

; STATE: Virginia

; COUNTRY: United States

; ZIP: 22313-1404

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Releasee #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/729,767

; FILING DATE: 07-OCT-1996

; CLASSIFICATION: 435

; PRIORITY APPLICATION DATA:

; APPLICATION NUMBER: US 08/259,000

; FILING DATE: 13-JUN-1994

; PRIORITY APPLICATION DATA:

; APPLICATION NUMBER: US 08/007,817

; FILING DATE: 22-JAN-1993

; PRIORITY APPLICATION DATA:

; APPLICATION NUMBER: US 07/201,028

; FILING DATE: 01-JUN-1988

; PRIORITY APPLICATION DATA:

; APPLICATION NUMBER: SE 8702272-9

; FILING DATE: 01-JUN-1987

; ATTORNEY/AGENT INFORMATION:

; NAME: McGowan, Malcolm K.

; REGISTRATION NUMBER: 39,300

; REFERENCE/DOCKET NUMBER: 012889-036

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (703) 836-6620

; TELEFAX: (703) 836-2021

; INFORMATION FOR SEQ ID NO: 3:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 38 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: protein

US-08-729-767-3

Query Match 100.0%; Score 52; DB 1; Length 38;

Best Local Similarity 100.0%; Pred. No. 0.015;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DIDFDSVPQI 10
| | | | | | | | | |

Db 28 DIDFDSVPQI 37

RESULT 4

US-09-010-317-5

; Sequence 5, Application US/09010317

; Patent No. 6685943

; GENERAL INFORMATION:

; APPLICANT: Hook, Magnus

; APPLICANT: Patti, Joseph M.

; APPLICANT: House-Pompeo, Karen L.

; APPLICANT: Speciale, Pietro

; APPLICANT: Joh, Danny

; APPLICANT: McGavin, Martin J.

; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS

; NUMBER OF SEQUENCES: 105

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Arnold, White & Durkee

STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAMK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-09-010-317-5

Query Match 100.0%; Score 52; DB 4; Length 38;
Best local Similarity 100.0%; Pred. No. 0.015;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIDFDSVPQI 10
Db 27 DIDFDSVPQI 36

RESULT 5
US-09-010-317-6
Sequence 6, Application US/09010317
Patent No. 6685943
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
APPLICANT: Patti, Joseph M.
APPLICANT: House-Pompeo, Karen L.
APPLICANT: Speziale, Pietro
APPLICANT: Joh, Danny
APPLICANT: McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
TITLE OF INVENTION: AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRES:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/036,139

FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAMK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-09-010-317-6

Query Match 100.0%; Score 52; DB 4; Length 38;
Best local Similarity 100.0%; Pred. No. 0.015;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIDFDSVPQI 10
Db 27 DIDFDSVPQI 36

RESULT 6
US-09-010-317-35
Sequence 35, Application US/09010317
Patent No. 6685943
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
APPLICANT: Patti, Joseph M.
APPLICANT: House-Pompeo, Karen L.
APPLICANT: Speziale, Pietro
APPLICANT: Joh, Danny
APPLICANT: McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
TITLE OF INVENTION: AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRES:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAMK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 35:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-09-010-317-35

Query Match 100.0%; Score 52; DB 4; Length 38;
Best Local Similarity 100.0%; Pred. No. 0.015;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIDFDSVPQI 10
| | | | | | | |
Db 27 DIDFDSVPQI 36

RESULT 7
US-09-010-317-36

; Sequence 36, Application US/09010317
; Patent No. 6685943

; GENERAL INFORMATION:

; APPLICANT: Hook, Magnus

; APPLICANT: Patti, Joseph M.

; APPLICANT: House-Pompeo, Karen L.

; APPLICANT: Speziale, Pietro

; APPLICANT: Job, Danny

; APPLICANT: McGavin, Martin J.

; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS

; TITLE OF INVENTION: AND METHODS OF USE

; NUMBER OF SEQUENCES: 105

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Arnold, White & Durkee

; STREET: P. O. Box 4433

; CITY: Houston

; STATE: TX

; COUNTRY: USA

; ZIP: 77210-4433

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/010,317

; FILING DATE:

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 60/036,139

; FILING DATE: 21-JAN-1997

; ATTORNEY/AGENT INFORMATION:

; NAME: Hibler, David W.

; REGISTRATION NUMBER: 41,071

; REFERENCE/DOCKET NUMBER: TANK:189

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 512-474-7577

; TELEFAX: 512-474-7577

; INFORMATION FOR SEQ ID NO: 36:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 38 amino acids

; TYPE: amino acid

; STRANDEDNESS:

; TOPOLOGY: linear

US-09-010-317-36

Query Match 100.0%; Score 52; DB 4; Length 38;
Best Local Similarity 100.0%; Pred. No. 0.015;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIDFDSVPQI 10
| | | | | | | |
Db 27 DIDFDSVPQI 36

RESULT 8
US-09-010-317-37

; Sequence 37, Application US/09010317
; Patent No. 6685943

; GENERAL INFORMATION:

; APPLICANT: Hook, Magnus

; APPLICANT: Patti, Joseph M.

; APPLICANT: House-Pompeo, Karen L.

; APPLICANT: Speziale, Pietro

; APPLICANT: Job, Danny

; APPLICANT: McGavin, Martin J.

; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS

; TITLE OF INVENTION: AND METHODS OF USE

; NUMBER OF SEQUENCES: 105

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Arnold, White & Durkee

; STREET: P. O. Box 4433

; CITY: Houston

; STATE: TX

; COUNTRY: USA

; ZIP: 77210-4433

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/010,317

; FILING DATE:

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 60/036,139

; FILING DATE: 21-JAN-1997

; ATTORNEY/AGENT INFORMATION:

; NAME: Hibler, David W.

; REGISTRATION NUMBER: 41,071

; REFERENCE/DOCKET NUMBER: TANK:189

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 512-418-3000

; TELEFAX: 512-474-7577

; INFORMATION FOR SEQ ID NO: 37:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 38 amino acids

; TYPE: amino acid

; STRANDEDNESS:

; TOPOLOGY: linear

US-09-010-317-37

Query Match 100.0%; Score 52; DB 4; Length 38;
Best Local Similarity 100.0%; Pred. No. 0.015;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIDFDSVPQI 10
| | | | | | | |
Db 27 DIDFDSVPQI 36

RESULT 9
US-09-010-317-38

; Sequence 38, Application US/09010317
; Patent No. 6685943

; GENERAL INFORMATION:

; APPLICANT: Hook, Magnus

; APPLICANT: Patti, Joseph M.

; APPLICANT: House-Pompeo, Karen L.

; APPLICANT: Speziale, Pietro

; APPLICANT: Job, Danny

; APPLICANT: McGavin, Martin J.

; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS

; TITLE OF INVENTION: AND METHODS OF USE

; NUMBER OF SEQUENCES: 105

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Arnold, White & Durkee

; STREET: P. O. Box 4433

; CITY: Houston

; STATE: TX

; COUNTRY: USA

; ZIP: 77210-4433

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

```
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAMK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 38:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-09-010-317-38

Query Match      100.0%; Score 52; DB 4; Length 38;
Best Local Similarity 100.0%; Pred. No. 0.015;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 DIDFDSVPQI 10
Db      27 DIDFDSVPQI 36

RESULT 10
US-09-010-317-39
Sequence 39, Application US/09010317
Patent No. 6685943
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
APPLICANT: Patti, Joseph M.
APPLICANT: House-Pompeo, Karen L.
APPLICANT: Speziale, Pietro
APPLICANT: McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
TITLE OF INVENTION: AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAMK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 40:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-09-010-317-40

Query Match      100.0%; Score 52; DB 4; Length 38;
Best Local Similarity 100.0%; Pred. No. 0.015;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 DIDFDSVPQI 10
Db      27 DIDFDSVPQI 36

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAMK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 40:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-09-010-317-40

Query Match      100.0%; Score 52; DB 4; Length 38;
Best Local Similarity 100.0%; Pred. No. 0.015;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 DIDFDSVPQI 10
Db      27 DIDFDSVPQI 36
```

```
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 39:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-09-010-317-39

Query Match      100.0%; Score 52; DB 4; Length 38;
Best Local Similarity 100.0%; Pred. No. 0.015;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 DIDFDSVPQI 10
Db      27 DIDFDSVPQI 36

RESULT 11
US-09-010-317-40
Sequence 40, Application US/09010317
Patent No. 6685943
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
APPLICANT: Patti, Joseph M.
APPLICANT: House-Pompeo, Karen L.
APPLICANT: Speziale, Pietro
APPLICANT: McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
TITLE OF INVENTION: AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAMK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 40:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-09-010-317-40

Query Match      100.0%; Score 52; DB 4; Length 38;
Best Local Similarity 100.0%; Pred. No. 0.015;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 DIDFDSVPQI 10
Db      27 DIDFDSVPQI 36
```

```
RESULT 12
US-09-010-317-41
; Sequence 41, Application US/09010317
; Patent No. 6685943
; GENERAL INFORMATION:
; APPLICANT: Hook, Magnus
; APPLICANT: Patti, Joseph M.
; APPLICANT: House-Pompeo, Karen L.
; APPLICANT: Speziale, Pietro
; APPLICANT: Joh, Danny
; APPLICANT: McGavin, Martin J.
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
; NUMBER OF SEQUENCES: 105
; TITLE OF INVENTION: AND METHODS OF USE
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: TX
; COUNTRY: USA
; ZIP: 77210-4433
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/010,317
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/036,139
; FILING DATE: 21-JAN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Hibler, David W.
; REGISTRATION NUMBER: 41,071
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 512-418-3000
; TELEFAX: 512-474-7577
; INFORMATION FOR SEQ ID NO: 41:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 38 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
US-09-010-317-41

Query Match      100.0%; Score 52; DB 4; Length 38;
Best Local Similarity 100.0%; Pred. No. 0.015;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 DIDPSVPOI 10
       |||||
Db      27 DIDPSVPOI 36

RESULT 13
US-09-010-317-42
; Sequence 42, Application US/09010317
; Patent No. 6685943
; GENERAL INFORMATION:
; APPLICANT: Hook, Magnus
; APPLICANT: Patti, Joseph M.
; APPLICANT: House-Pompeo, Karen L.
; APPLICANT: Speziale, Pietro
; APPLICANT: Joh, Danny
; APPLICANT: McGavin, Martin J.
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
; NUMBER OF SEQUENCES: 105
; TITLE OF INVENTION: AND METHODS OF USE
```

```
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: TX
; COUNTRY: USA
; ZIP: 77210-4433
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/010,317
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/036,139
; FILING DATE: 21-JAN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Hibler, David W.
; REGISTRATION NUMBER: 41,071
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 512-418-3000
; TELEFAX: 512-474-7577
; INFORMATION FOR SEQ ID NO: 42:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 38 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
US-09-010-317-42

Query Match      100.0%; Score 52; DB 4; Length 38;
Best Local Similarity 100.0%; Pred. No. 0.015;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 DIDPSVPOI 10
       |||||
Db      27 DIDPSVPOI 36

RESULT 14
US-09-010-317-43
; Sequence 43, Application US/09010317
; Patent No. 6685943
; GENERAL INFORMATION:
; APPLICANT: Hook, Magnus
; APPLICANT: Patti, Joseph M.
; APPLICANT: House-Pompeo, Karen L.
; APPLICANT: Speziale, Pietro
; APPLICANT: Joh, Danny
; APPLICANT: McGavin, Martin J.
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
; NUMBER OF SEQUENCES: 105
; TITLE OF INVENTION: AND METHODS OF USE
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: TX
; COUNTRY: USA
; ZIP: 77210-4433
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/010,317
; FILING DATE:
; CLASSIFICATION:
```

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAMK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 43:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-09-010-317-43

Query Match 100.0%; Score 52; DB 4; Length 38;
Best Local Similarity 100.0%; Pred. No. 0.015;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIDFDSVPQI 10
|||||
Db 27 DIDFDSVPQI 36

RESULT 15
US-09-010-317-44
Sequence 44, Application US/09010317
Patent No. 6685943
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
APPLICANT: Patti, Joseph M.
APPLICANT: House-Pompeo, Karen L.
APPLICANT: Speciale, Pietro
APPLICANT: McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
TITLE OF INVENTION: AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Releasee #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAMK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 44:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear

US-09-010-317-44
Query Match 100.0%; Score 52; DB 4; Length 38;
Best Local Similarity 100.0%; Pred. No. 0.015;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIDFDSVPQI 10
|||||
Db 27 DIDFDSVPQI 36

Search completed: October 22, 2005, 07:41:42
Job time : 17.35 secs

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OM protein - protein search, using sw model

Run on: October 22, 2005, 12:09:40 ; Search time 57.25 Seconds
(without alignments)
72.924 Million cell updates/sec

Title: US-10-731-238-76

Perfect score: 52

Sequence: 1 DIDPDSVPQI 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1862951 seqs, 417491010 residues

Total number of hits satisfying chosen parameters: 1862951

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA:*

1: /cgn2_6/prodata/2/pubppaa/US07_PUBCOMB.pep.*
2: /cgn2_6/prodata/2/pubppaa/PCT_NEW_PUB.pep.*
3: /cgn2_6/prodata/2/pubppaa/US06_NEW_PUB.pep.*
4: /cgn2_6/prodata/2/pubppaa/US06_PUBCOMB.pep.*
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10: /cgn2_6/prodata/2/pubppaa/US09C_PUBCOMB.pep.*
11: /cgn2_6/prodata/2/pubppaa/US09C_PUBCOMB.pep.*
12: /cgn2_6/prodata/2/pubppaa/US09_NEW_PUB.pep.*
13: /cgn2_6/prodata/2/pubppaa/US10_PUBCOMB.pep.*
14: /cgn2_6/prodata/2/pubppaa/US10C_PUBCOMB.pep.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	52	100.0	10	US-10-731-238-76	Sequence 76, Appl
2	52	100.0	38	US-10-731-238-5	Sequence 5, Appl
3	52	100.0	38	US-10-731-238-6	Sequence 6, Appl
4	52	100.0	38	US-10-731-238-35	Sequence 35, Appl
5	52	100.0	38	US-10-731-238-36	Sequence 36, Appl
6	52	100.0	38	US-10-731-238-37	Sequence 37, Appl
7	52	100.0	38	US-10-731-238-38	Sequence 38, Appl
8	52	100.0	38	US-10-731-238-39	Sequence 39, Appl
9	52	100.0	38	US-10-731-238-40	Sequence 40, Appl
10	52	100.0	38	US-10-731-238-41	Sequence 41, Appl
11	52	100.0	38	US-10-731-238-42	Sequence 42, Appl

12	52	100.0	38	18	US-10-731-238-43	Sequence 43, Appl
13	52	100.0	38	18	US-10-731-238-44	Sequence 44, Appl
14	52	100.0	139	9	US-09-813-820-8	Sequence 8, Appl
15	52	100.0	388	8	US-08-901-062-1	Sequence 1, Appl
16	52	100.0	559	8	US-08-781-986A-5251	Sequence 5251, Ap
17	52	100.0	559	15	US-10-329-624-5251	Sequence 5251, Ap
18	52	100.0	767	9	US-09-815-242-5899	Sequence 5899, Ap
19	52	100.0	767	9	US-09-815-242-13140	Sequence 13140, A
20	52	100.0	940	17	US-10-470-048B-424	Sequence 424, App
21	52	100.0	948	17	US-10-470-048B-69	Sequence 69, Appl
22	52	100.0	961	15	US-10-282-122A-43778	Sequence 43778, A
23	52	100.0	978	9	US-09-815-242-5456	Sequence 5456, Ap
24	52	100.0	1001	9	US-09-815-242-12686	Sequence 12686, A
25	52	100.0	1018	9	US-09-815-242-5797	Sequence 5797, Ap
26	52	100.0	1018	9	US-09-815-242-12838	Sequence 12838, A
27	52	100.0	1018	17	US-10-470-048B-68	Sequence 68, Appl
28	52	100.0	1027	8	US-08-781-986A-5254	Sequence 5254, Ap
29	52	100.0	1027	15	US-10-329-624-5254	Sequence 5254, Ap
30	52	100.0	1038	15	US-10-282-122A-43827	Sequence 43827, A
31	47	90.4	36	18	US-10-731-238-58	Sequence 59, Appl
32	47	90.4	36	18	US-10-731-238-59	Sequence 59, Appl
33	47	90.4	38	18	US-10-731-238-7	Sequence 7, Appl
34	47	90.4	38	18	US-10-731-238-8	Sequence 8, Appl
35	47	90.4	38	18	US-10-731-238-45	Sequence 45, Appl
36	47	90.4	38	18	US-10-731-238-46	Sequence 46, Appl
37	47	90.4	38	18	US-10-731-238-47	Sequence 47, Appl
38	47	90.4	38	18	US-10-731-238-48	Sequence 48, Appl
39	47	90.4	38	18	US-10-731-238-49	Sequence 49, Appl
40	47	90.4	38	18	US-10-731-238-50	Sequence 50, Appl
41	43	82.7	10	18	US-10-731-238-75	Sequence 75, Appl
42	43	82.7	14	18	US-10-731-238-103	Sequence 103, App
43	43	82.7	14	18	US-10-731-238-103	Sequence 103, App
44	42	80.8	10	18	US-10-731-238-77	Sequence 77, Appl
45	41.5	79.8	39	18	US-10-731-238-56	Sequence 56, Appl

ALIGNMENTS

RESULT 1
US-10-731-238-76
Sequence 76, Application US/10731238
Publication No. US20050123552A1
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
Patel, Joseph M.
House-Pompeo, Karen L.
Speziale, Pietro
Joh, Danny
McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSER: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/731.238
FILING DATE: 10-Dec-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/010.317
FILING DATE: 21-Jan-1998
APPLICATION NUMBER: US 60/036.139

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; FILING DATE: 21-JAN-1997
; ATTORNEY/AGENT INFORMATION:
;   NAME: Hibler, David W.
;   REGISTRATION NUMBER: 41,071
;   REFERENCE/DOCKET NUMBER: TAMK:189
; TELECOMMUNICATION INFORMATION:
;   TELEPHONE: 512-418-3000
;   TELEFAX: 512-474-7577
; INFORMATION FOR SEQ ID NO: 76:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH: 10 amino acids
;     TYPE: amino acid
;     STRANDEDNESS: <Unknown>
;     TOPOLOGY: linear
;
; SEQUENCE DESCRIPTION: SEQ ID NO: 76:
US-10-731-238-76

Query Match      100.0%; Score 52; DB 18; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0066;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 DIDFDSVPQI 10
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        1 DIDFDSVPQI 10

RESULT 2
US-10-731-238-5
; Sequence 5, Application US/10731238
; Publication No. US20050123552A1
; GENERAL INFORMATION:
;   APPLICANT: Hook, Magnus
;               Patti, Joseph M.
;               House-Pompeo, Karen L.
;               Speziale, Pietro
;               Joh, Danny
;               McGavin, Martin J.
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
; AND METHODS OF USE
;
; NUMBER OF SEQUENCES: 105
; CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Arnold, White & Durkee
;   STREET: P.O. Box 4433
;   CITY: Houston
;   STATE: TX
;   COUNTRY: USA
;   ZIP: 77210-4433
; COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/10/731,238
;   FILING DATE: 10-Dec-2003
;   CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US/09/010,317
;   FILING DATE: 21-Jan-1998
;   APPLICATION NUMBER: US 60/036,139
;   FILING DATE: 21-JAN-1997
; ATTORNEY/AGENT INFORMATION:
;   NAME: Hibler, David W.
;   REGISTRATION NUMBER: 41,071
;   REFERENCE/DOCKET NUMBER: TAMK:189
; TELECOMMUNICATION INFORMATION:
;   TELEPHONE: 512-418-3000
;   TELEFAX: 512-474-7577
; INFORMATION FOR SEQ ID NO: 5:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH: 38 amino acids
;     TYPE: amino acid
;     STRANDEDNESS: <Unknown>
;     TOPOLOGY: linear
;
; SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-10-731-238-6

Query Match      100.0%; Score 52; DB 18; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0066;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 DIDFDSVPQI 10
        |||
        1 DIDFDSVPQI 10

RESULT 3
US-10-731-238-6
; Sequence 6, Application US/10731238
; Publication No. US20050123552A1
; GENERAL INFORMATION:
;   APPLICANT: Hook, Magnus
;               Patti, Joseph M.
;               House-Pompeo, Karen L.
;               Speziale, Pietro
;               Joh, Danny
;               McGavin, Martin J.
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
; AND METHODS OF USE
;
; NUMBER OF SEQUENCES: 105
; CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Arnold, White & Durkee
;   STREET: P.O. Box 4433
;   CITY: Houston
;   STATE: TX
;   COUNTRY: USA
;   ZIP: 77210-4433
; COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/10/731,238
;   FILING DATE: 10-Dec-2003
;   CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US/09/010,317
;   FILING DATE: 21-Jan-1998
;   APPLICATION NUMBER: US 60/036,139
;   FILING DATE: 21-JAN-1997
; ATTORNEY/AGENT INFORMATION:
;   NAME: Hibler, David W.
;   REGISTRATION NUMBER: 41,071
;   REFERENCE/DOCKET NUMBER: TAMK:189
; TELECOMMUNICATION INFORMATION:
;   TELEPHONE: 512-418-3000
;   TELEFAX: 512-474-7577
; INFORMATION FOR SEQ ID NO: 6:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH: 38 amino acids
;     TYPE: amino acid
;     STRANDEDNESS: <Unknown>
;     TOPOLOGY: linear
;
; SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-10-731-238-6

Query Match      100.0%; Score 52; DB 18; Length 38;
Best Local Similarity 100.0%; Pred. No. 0.029;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 DIDFDSVPQI 10
        |||
        1 DIDFDSVPQI 10

Db      27 DIDFDSVPQI 36
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; TOPOLOGY: linear
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; SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-10-731-238-5

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Best Local Similarity 100.0%; Pred. No. 0.029;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 DIDFDSVPQI 10
        |||
        1 DIDFDSVPQI 10

Db      27 DIDFDSVPQI 36

RESULT 3
US-10-731-238-6
; Sequence 6, Application US/10731238
; Publication No. US20050123552A1
; GENERAL INFORMATION:
;   APPLICANT: Hook, Magnus
;               Patti, Joseph M.
;               House-Pompeo, Karen L.
;               Speziale, Pietro
;               Joh, Danny
;               McGavin, Martin J.
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
; AND METHODS OF USE
;
; NUMBER OF SEQUENCES: 105
; CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Arnold, White & Durkee
;   STREET: P.O. Box 4433
;   CITY: Houston
;   STATE: TX
;   COUNTRY: USA
;   ZIP: 77210-4433
; COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/10/731,238
;   FILING DATE: 10-Dec-2003
;   CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US/09/010,317
;   FILING DATE: 21-Jan-1998
;   APPLICATION NUMBER: US 60/036,139
;   FILING DATE: 21-JAN-1997
; ATTORNEY/AGENT INFORMATION:
;   NAME: Hibler, David W.
;   REGISTRATION NUMBER: 41,071
;   REFERENCE/DOCKET NUMBER: TAMK:189
; TELECOMMUNICATION INFORMATION:
;   TELEPHONE: 512-418-3000
;   TELEFAX: 512-474-7577
; INFORMATION FOR SEQ ID NO: 6:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH: 38 amino acids
;     TYPE: amino acid
;     STRANDEDNESS: <Unknown>
;     TOPOLOGY: linear
;
; SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-10-731-238-6

Query Match      100.0%; Score 52; DB 18; Length 38;
Best Local Similarity 100.0%; Pred. No. 0.029;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 DIDFDSVPQI 10
        |||
        1 DIDFDSVPQI 10

Db      27 DIDFDSVPQI 36
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RESULT 4
US-10-731-238-35
; Sequence 35, Application US/10731238
; Publication No. US20050123552A1
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
          Patti, Joseph M.
          House-Pompeo, Karen L.
          Speziale, Pietro
          Joh, Danny
          McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSER: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/731,238
FILING DATE: 10-Dec-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE: 21-Jan-1998
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAMK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 35:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 35:
US-10-731-238-35
Query Match      100.0%; Score 52; DB 18; Length 38;
Best Local Similarity 100.0%; Pred. No. 0.029;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 DIDFDSVPQI 10
   |||||
Db 27 DIDFDSVPQI 36
RESULT 5
US-10-731-238-36
; Sequence 36, Application US/10731238
; Publication No. US20050123552A1
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
          Patti, Joseph M.
          House-Pompeo, Karen L.
          Speziale, Pietro
          Joh, Danny
          McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
AND METHODS OF USE
```

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NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSER: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/731,238
FILING DATE: 10-Dec-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE: 21-Jan-1998
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAMK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 36:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 36:
US-10-731-238-36
Query Match      100.0%; Score 52; DB 18; Length 38;
Best Local Similarity 100.0%; Pred. No. 0.029;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 DIDFDSVPQI 10
   |||||
Db 27 DIDFDSVPQI 36
RESULT 6
US-10-731-238-37
; Sequence 37, Application US/10731238
; Publication No. US20050123552A1
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
          Patti, Joseph M.
          House-Pompeo, Karen L.
          Speziale, Pietro
          Joh, Danny
          McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSER: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/731,238
FILING DATE: 10-Dec-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE: 21-Jan-1998
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-Jan-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAMK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 37:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS: <unknown>
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 37:
US-10-731-238-37

Query Match 100.0%; Score 52; DB 18; Length 38;
Best Local Similarity 100.0%; Pred. No. 0.029;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DIDFSDVPQI 10
|||
Db 27 DIDFSDVPQI 36

RESULT 7
US-10-731-238-38
Sequence 38, Application US/10731238
Publication No. US20050123552A1
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
Pactl, Joseph M.
House-Pompeo, Karen L.
Speziale, Pietro
Joh, Danny
McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/731,238
FILING DATE: 10-Dec-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE: 21-Jan-1998
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-Jan-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAMK:189

TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 38:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 38:
US-10-731-238-38

Query Match 100.0%; Score 52; DB 18; Length 38;
Best Local Similarity 100.0%; Pred. No. 0.029;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DIDFSDVPQI 10
|||
Db 27 DIDFSDVPQI 36

RESULT 8
US-10-731-238-39
Sequence 39, Application US/10731238
Publication No. US20050123552A1
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
Pactl, Joseph M.
House-Pompeo, Karen L.
Speziale, Pietro
Joh, Danny
McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/731,238
FILING DATE: 10-Dec-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE: 21-Jan-1998
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-Jan-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAMK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 39:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 39:
US-10-731-238-39

Query Match 100.0%; Score 52; DB 18; Length 38;

Best Local Similarity 100.0%; Pred. No. 0.029;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIDFDSVPQI 10
|||||
Db 27 DIDFDSVPQI 36

RESULT 9
US-10-731-238-40
; Sequence 40, Application US/10731238
; Publication No. US20050123552A1
; GENERAL INFORMATION:
; APPLICANT: Hook, Magnus
; Patti, Joseph M.
; House-Pompeo, Karen L.
; Speziale, Pietro
; Joh, Danny
; McGavin, Martin J.
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
; AND METHODS OF USE
; NUMBER OF SEQUENCES: 105
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: TX
; COUNTRY: USA
; ZIP: 77210-4433
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/731,238
; FILING DATE: 10-Dec-2003
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/010,317
; FILING DATE: 21-Jan-1998
; APPLICATION NUMBER: US 60/036,139
; FILING DATE: 21-Jan-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Hibler, David W.
; REGISTRATION NUMBER: 41,071
; REFERENCE/DOCKET NUMBER: TAMK:189
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 512-418-3000
; TELEFAX: 512-474-7577
; INFORMATION FOR SEQ ID NO: 40:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 38 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 40:
US-10-731-238-40

Query Match 100.0%; Score 52; DB 18; Length 38;
Best Local Similarity 100.0%; Pred. No. 0.029;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIDFDSVPQI 10
|||||
Db 27 DIDFDSVPQI 36

RESULT 10
US-10-731-238-41
; Sequence 41, Application US/10731238
; Publication No. US20050123552A1
; GENERAL INFORMATION:

APPLICANT: Hook, Magnus
Patti, Joseph M.
House-Pompeo, Karen L.
Speziale, Pietro
Joh, Danny
McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/731,238
FILING DATE: 10-Dec-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE: 21-Jan-1998
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-Jan-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAMK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 41:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 41:
US-10-731-238-41

Query Match 100.0%; Score 52; DB 18; Length 38;
Best Local Similarity 100.0%; Pred. No. 0.029;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIDFDSVPQI 10
|||||
Db 27 DIDFDSVPQI 36

RESULT 11
US-10-731-238-42
; Sequence 42, Application US/10731238
; Publication No. US20050123552A1
; GENERAL INFORMATION:
; APPLICANT: Hook, Magnus
; Patti, Joseph M.
; House-Pompeo, Karen L.
; Speziale, Pietro
; Joh, Danny
; McGavin, Martin J.
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
; AND METHODS OF USE
; NUMBER OF SEQUENCES: 105
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston

STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/731,238
FILING DATE: 10-Dec-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE: 21-Jan-1998
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-Jan-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAMK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 42:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 42:
US-10-731-238-42

Query Match 100.0%; Score 52; DB 18; Length 38;
Best Local Similarity 100.0%; Pred. No. 0.029;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIDFDSVPOI 10
DB 27 DIDFDSVPOI 36

RESULT 12
US-10-731-238-43
Sequence 43, Application US/10731238
Publication No. US20050123552A1
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
Patli, Joseph M.
House-Pompeo, Karen L.
Speziale, Pietro
Joh, Danny
McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSER: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/731,238
FILING DATE: 10-Dec-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/010,317
FILING DATE: 21-Jan-1998
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-Jan-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAMK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 43:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 43:
US-10-731-238-43

Query Match 100.0%; Score 52; DB 18; Length 38;
Best Local Similarity 100.0%; Pred. No. 0.029;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIDFDSVPOI 10
DB 27 DIDFDSVPOI 36

RESULT 13
US-10-731-238-44
Sequence 44, Application US/10731238
Publication No. US20050123552A1
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
Patli, Joseph M.
House-Pompeo, Karen L.
Speziale, Pietro
Joh, Danny
McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSER: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/731,238
FILING DATE: 10-Dec-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE: 21-Jan-1998
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-Jan-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAMK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 44:
SEQUENCE CHARACTERISTICS:

LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 44:
US-10-731-238-44

Query Match 100.0%; Score 52; DB 18; Length 38;
Best Local Similarity 100.0%; Pred. No. 0.029;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIDFDSVPQI 10
DB 27 DIDFDSVPQI 36

RESULT 14
US-09-813-820-8
Sequence 8, Application US/09813820
Patent No. US20020102262A1
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
Patti, Joseph M.
House-Pompeo, Karen
Schnaum, Narayana
Symersky, Jindrich
TITLE OF INVENTION: COLLAGEN BINDING PROTEIN COMPOSITIONS
AND METHODS OF USE
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: Texas
COUNTRY: U.S.
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/813,820
FILING DATE: 22-Mar-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/856,253
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Kitchell, Barbara S.
REGISTRATION NUMBER: 33,928
REFERENCE/DOCKET NUMBER: TAMK.193
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
TELEFAX: (512) 474-7577
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 139 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-09-813-820-8

Query Match 100.0%; Score 52; DB 9; Length 139;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIDFDSVPQI 10
DB 42 DIDFDSVPQI 51

RESULT 15

US-08-901-062-1
Sequence 1, Application US/08901062
Publication No. US20020025324A1
GENERAL INFORMATION:
APPLICANT: SEALS, JONATHAN R.
TITLE OF INVENTION: RECOMBINANT BIVALENT BACTERIAL VACCINE
FOR THE PREVENTION OF MASTITIS
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: HALE AND DORR LLP
STREET: 60 State Street
CITY: Boston
STATE: MA
COUNTRY: United States Of America
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/901,062
FILING DATE: 25-JUL-1997
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Baker, Hollie L.
REGISTRATION NUMBER: 31,321
REFERENCE/DOCKET NUMBER: 106941.153
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 526-6000
TELEFAX: (617) 526-5000
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 388 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-901-062-1

Query Match 100.0%; Score 52; DB 8; Length 388;
Best Local Similarity 100.0%; Pred. No. 0.39;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIDFDSVPQI 10
DB 291 DIDFDSVPQI 300

Search completed: October 22, 2005, 12:39:46
Job time : 58.25 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 22, 2005, 06:10:10 ; Search time 11.45 Seconds
(without alignments)
84.032 Million cell updates/sec

Title: US-10-731-238-76

Perfect score: 52

Sequence: 1 DIDFDSVPQI 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	52	100.0	940	2	S19702 fibronectin-binding
2	52	100.0	961	2	G90053 fibronectin-binding
3	52	100.0	1018	2	A32192 fibronectin-binding
4	52	100.0	1038	2	H90053 fibronectin-binding
5	37	71.2	629	2	F72400 glucose-inhibited
6	37	71.2	2416	2	T13825 adenomatous polyp
7	36	69.2	114	2	F87314 conserved hypotet
8	36	69.2	360	2	T08677 conserved hypotet
9	36	69.2	488	1	S55874 sulfite oxidase (E
10	36	69.2	557	2	T40956 transcrition fact
11	36	69.2	975	1	A28174 methylenetetrahydr
12	36	69.2	1170	1	TSHUP1 chromopondin 1 p
13	35	67.3	82	2	AD3161 conserved hypotet
14	35	67.3	115	2	T08473 trao protein homol
15	35	67.3	239	2	AP0261 fatty acid metabol
16	35	67.3	345	2	T07839 ananin (EC 3.4.22
17	35	67.3	376	2	G84404 hypotetrical prote
18	35	67.3	396	2	T33386 hypotetrical prote
19	35	67.3	459	2	T48598 hypotetrical prote
20	35	67.3	511	1	S31308 aldehyde dehydrog
21	35	67.3	596	2	T23193 hypotetrical prote
22	35	67.3	617	2	G70366 glucose inhibited
23	35	67.3	726	2	A27602 complement C3 - ra
24	35	67.3	736	2	D90574 hypotetrical prote
25	35	67.3	764	2	T39878 hypotetrical prote
26	35	67.3	842	2	A87557 non-motile and pha
27	35	67.3	842	2	S27533 histidine protein
28	35	67.3	1246	2	S60954 probable membrane
29	35	67.3	1541	2	T30227 pipecolate-incorpo

30	35	67.3	1663	1	C3MS complement C3 prec
31	35	67.3	2824	2	C3RT complement C3 prec
32	35	67.3	2824	2	T18378 variant-specific s
33	35	67.3	3972	2	S75251 hypotetrical prote
34	34	65.4	148	2	S10238 legnemeogloblin glb3
35	34	65.4	200	2	F97858 hypotetrical prote
36	34	65.4	210	2	S73509 tRNA (guanine-N1) -
37	34	65.4	279	2	H83997 methylenetetrahydr
38	34	65.4	282	2	A84914 hypotetrical prote
39	34	65.4	284	2	AH1244 methylenetetrahydr
40	34	65.4	286	2	E89875 FOLD bifunctional
41	34	65.4	289	2	S74959 lipic acid synthe
42	34	65.4	449	2	D87362 hypotetrical prote
43	34	65.4	622	2	B86431 hypotetrical prote
44	34	65.4	680	2	T40827 probable phosphol
45	34	65.4	827	2	AB2764 beta-mannosidase p

ALIGNMENTS

RESULT 1
S19702 fibronectin-binding protein B - Staphylococcus aureus
C/Species: Staphylococcus aureus
C/Date: 13-Jan-1995 #sequence_revision.13-Jan-1995 #text_change 09-Jul-2004
C/Accession: S19702
R/Joensson, K.; Signaes, C.; Mueller, H.P.; Lindberg, M.
Eur. J. Biochem. 202, 1041-1048, 1991
A/Title: Two different genes encode fibronectin binding proteins in Staphylococcus aureus
A/Reference number: S19702; PMID:92111475; PMID:1837266
A/Accession: S19702
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-940 <JOB>
A/Cross-references: UNIPROT:Q53682; EMBL:X62992; NID:G49040; PIDN:CAA44726.1; PID:G5815
C/Keywords: fibronectin binding

Query Match 100.0%; Score 52; DB 2; Length 940;
Best Local Similarity 100.0%; Pred. No. 0.072;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIDFDSVPQI 10
DB 708 DIDFDSVPQI 717

RESULT 2

G90053 hypotetrical protein fmb (imported) - Staphylococcus aureus (strain N315)
C/Species: Staphylococcus aureus
C/Date: 10-May-2001 #sequence_revision.10-May-2001 #text_change 09-Jul-2004
C/Accession: G90053

R/Kuroda, M.; Uchiyama, T.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguni, A.; Mizutani, U.; Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kato, C.; Sekimizu, K.;
ma, A.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001

A/Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.
A/Reference number: AB9758; PMID:21311952; PMID:11418146

A/Accession: G90053
A/Status: preliminary
A/Molecule type: DNA

A/Residues: 1-961 <KUR>
A/Cross-references: UNIPROT:Q99RD3; GB:BA000018; PID:G13702452; PIDN:BAR43593.1; GSPDB:
A/Experimental source: strain N315

C/Genetics: fmb

Query Match 100.0%; Score 52; DB 2; Length 961;
Best Local Similarity 100.0%; Pred. No. 0.074;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIDFDSVPQI 10

Db 719 DIDFDSVPOI 728

RESULT 3

A32192

C:Species: Staphylococcus aureus

C:Date: 31-Jul-1989 #sequence_revision 31-Jul-1989 #text_change 16-Feb-1997

C:Accession: A32192

R:Signaase, C.; Raucchi, G.; Joensson, K.; Lindgren, P.E.; Anantharamaiah, G.M.; Hoecek, W

Proc. Natl. Acad. Sci. U.S.A. 86, 659-703, 1989

A:Title: Nucleotide sequence of the gene for a fibronectin-binding protein from Staphylo

A:Reference number: A32192; PMID:89098998; PMID:2521391

A:Accession: A32192

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-1018 <SIG>

A:Cross-references: GB:J04151

C:Keywords: fibronectin binding

Query Match 100.0%; Score 52; DB 2; Length 1018;
Best Local Similarity 100.0%; Pred. No. 0.079;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIDFDSVPOI 10
Db 772 DIDFDSVPOI 781

RESULT 4

H90053

C:Species: Staphylococcus aureus

C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004

C:Accession: H90053

R:Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguc

me, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.

C:Shiba, T.; Hatori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.

Lancet 357, 1225-1240, 2001

A:Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.

A:Reference number: A89758; PMID:21311952; PMID:11418146

A:Accession: H90053

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-1038 <KUR>

A:Cross-references: UNIPROT:Q99RD2; GB:BA000018; PID:gl3702453; PIDN:BA843594.1; GSPDB:G

A:Experimental source: strain N315

C:Genetics:

Query Match 100.0%; Score 52; DB 2; Length 1038;
Best Local Similarity 100.0%; Pred. No. 0.081;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIDFDSVPOI 10
Db 768 DIDFDSVPOI 777

RESULT 5

F72400

C:Species: Thermotoga maritima

C:Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004

C:Accession: F72400

R:Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hickey

Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.

C.M.

Nature 399, 323-329, 1999

A:Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome seq

A:Reference number: A72200; PMID:9287316; PMID:10360571

A:Accession: F72400

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-629 <ARN>

A:Cross-references: UNIPROT:Q9WYAL; GB:AE001708; GB:AE000512; NID:g4980740; PIDN:AAJ3535

A:Experimental source: strain MSB8

C:Genetics:

A:Gene: TM0263

C:Superfamily: gida protein

Query Match 71.2%; Score 37; DB 2; Length 629;
Best Local Similarity 50.0%; Pred. No. 39;
Matches 5; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 DIDFDSVPOI 10
Db 578 DIDYAVPNTL 587

RESULT 6

T13825

C:Species: Drosophila melanogaster

C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004

C:Accession: T13825

R:Hayashi, S.; Rubinfeld, B.; Souza, B.; Polakis, P.; Wieschaus, E.; Levine, A.J.

Proc. Natl. Acad. Sci. U.S.A. 94, 242-247, 1997

A:Title: A Drosophila homolog of the tumor suppressor gene adenomatous polyposis coli do

A:Reference number: Z17782; PMID:97144426; PMID:8990193

A:Accession: T13825

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-2416 <RAY>

A:Cross-references: UNIPROT:P91667; EMBL:U77947; NID:gl800228; PID:gl800229; PIDN:AA8414

C:Genetics:

A:Gene: D-APC

A:Cross-references: FlyBase:FBgn0015589

A:Map position: 3R

Query Match 71.2%; Score 37; DB 2; Length 2416;
Best Local Similarity 66.7%; Pred. No. 2e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 DIDFDSVPO 9
Db 21 DVDVDSVPE 29

RESULT 7

F87314

C:Species: Caulobacter crescentus

C:Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004

C:Accession: F87314

R:Nietman, W.C.; Feldblum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heideberg, J.

B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon

n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.

Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001

A:Title: Complete Genome Sequence of Caulobacter crescentus.

A:Reference number: A87249; PMID:21173698; PMID:11259647

A:Accession: F87314

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-114 <STO>

A:Cross-references: UNIPROT:Q9AAR9; GB:AE005673; NID:gl3421712; PIDN:AAK22514.1; GSPDB:G

C:Superfamily: Mycobacterium tuberculosis hypothetical protein RV2705c

Query Match 69.2%; Score 36; DB 2; Length 114;
Best Local Similarity 60.0%; Pred. No. 8;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 DIDFDSVPOI 10

Db 100 DLDADVPOI 109

RESULT 8

hypothetical protein F13H10.5 - *Caenorhabditis elegans*

C/Species: *Caenorhabditis elegans*

C/Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004

C/Accession: T20867, T26834

R/Cottage: A. Submitted to the EMBL Data Library, January 1996

A/Reference number: Z19335

A/Accession: T20867

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: DNA

A/Residues: 1-360 <MIL>

A/Cross-references: UNIPROT:O45359; EMBL:Z68748; PIDN:CAA92956.1; GSPDB:GN00022; CESP:FI

A/Experimental source: clone F13H10

R/lenard, N.

submitted to the EMBL Data Library, January 1998

A/Reference number: Z20274

A/Accession: T26834

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: DNA

A/Residues: 1-360 <W12>

A/Cross-references: EMBL:AL021176; PIDN:CAA15977.1; GSPDB:GN00022; CESP:FL3H10.5

A/Experimental source: clone Y43E12A

C/Genetics:

A/Gene: CESP:F13H10.5

A/Map position: 4

A/Introns: 79/1; 174/2; 245/2

Query Match 69.2%; Score 36; DB 2; Length 360;

Best Local Similarity 60.0%; Pred. No. 32;

Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 DIDFDSVPOI 10

Db 140 DVDMVDVAPQI 149

RESULT 9

S55874

sulfite oxidase (EC 1.8.3.1) precursor, mitochondrial [validated] - human

C/Species: *Homo sapiens* (man)

C/Date: 10-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 09-Jul-2004

C/Accession: S55874; S55875

R/Garrett, R.M.; Bellissimo, D.B.; Rajagopalan, K.V.

submitted to the EMBL Data Library, July 1994

A/Description: Molecular cloning of human sulfite oxidase.

A/Reference number: S55874

C/Accession: S55874

A/Molecule type: mRNA

A/Residues: 1-488 <GAR>

A/Cross-references: UNIPROT:P51687; EMBL:L31573; NID:G508501; PIDN:AAA74886.1; PID:G5085

A/Experimental source: liver

R/Garrett, R.M.; Bellissimo, D.B.; Rajagopalan, K.V.

Biochim. Biophys. Acta 1262, 147-149, 1995

A/Title: Molecular cloning of human liver sulfite oxidase.

A/Reference number: S55875; MUID:95322455; PMID:7599189

C/Accession: S55875

A/Status: nucleic acid sequence not shown

A/Molecule type: mRNA

A/Residues: 101-356 <GAR2>

A/Cross-references: EMBL:L31573; NID:G508501

A/Experimental source: liver

C/Genetics:

A/Gene: GDB:SUOX

A/Cross-references: GDB:S584405; OMIM:272300

C/Function:

A/Description: EC 1.8.3.1 [validated, MUID:95322455]; sulfite oxidase, catalyzes the ox

C/Superfamily: sulfite oxidase; cytochrome b5 core homology; molybdopterin-binding domain
C/Keywords: chromoprotein; heme; homodimer; iron; metalloprotein; mitochondrial; molybde
F/1-22/Domain: transit peptide (mitochondrion) #status predicted <TN>
F/25-103/Domain: cytochrome b5 core homology <CB>
F/107-481/Domain: molybdopterin-binding domain homology <PCO>
F/61.86/Binding site: heme iron (His) (axial ligands) #status predicted
F/207/Binding site: molybdopterin (Cys) (covalent) #status predicted

Query Match 69.2%; Score 36; DB 1; Length 488;

Best Local Similarity 66.7%; Pred. No. 46;

Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 DIDFDSVPOI 10

Db 355 VDFDSAPSI 363

RESULT 10

T40956

transcription factor gata-type - fission yeast (*Schizosaccharomyces pombe*)

C/Species: *Schizosaccharomyces pombe*

C/Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004

C/Accession: T40956

R/Wood, V.; Rajandream, M.A.; Barrell, B.G.; Volckaert, G.

submitted to the EMBL Data Library, February 1999

A/Reference number: Z21940

A/Accession: T40956

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: DNA

A/Residues: 1-557 <WOO>

A/Cross-references: UNIPROT:O94720; EMBL:AL035592; PIDN:CAB38164.1; GSPDB:GN00068; SPDB

A/Experimental source: strain 972h-; cosmid c1393

C/Genetics:

A/Gene: SPDB:SPCC1393.08

A/Map position: 3

Query Match 69.2%; Score 36; DB 2; Length 557;

Best Local Similarity 60.0%; Pred. No. 53;

Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 DIDFDSVPOI 10

Db 71 DVDFDSVSMU 80

RESULT 11

A28174

methylene-tetrahydrofolate dehydrogenase (NADP) (EC 1.5.1.5) - yeast (*Saccharomyces cere*

N/Alternate names: protein YBR0731; protein YBR084w

N/Contains: formate-tetrahydrofolate ligase (EC 6.3.4.3); methenyltetrahydrofolate cycl

C/Species: *Saccharomyces cerevisiae*

C/Date: 20-Jun-1989 #sequence_revision 05-Apr-1995 #text_change 09-Jul-2004

C/Accession: A28174; S45951

R/Shannon, K.W.; Rabinowitz, J.C.

J. Biol. Chem. 263, 7717-7725, 1988

A/Title: Isolation and characterization of the *Saccharomyces cerevisiae* M1S1 gene encod

A/Reference number: A28174; MUID:88227973; PMID:2836393

A/Molecule type: DNA

A/Residues: 1-975 <SHA>

A/Cross-references: UNIPROT:P09440; EMBL:J03724; NID:G171952; PIDN:AAA34781.1; PID:G171

R/Andre, B.; Czileplich, C.; Hein, C.; Jauniaux, J.C.; Urrestearazu, A.; Vlasova, S.

submitted to the Protein Sequence Database, August 1994

A/Reference number: S45893

A/Accession: S45951

A/Molecule type: DNA

A/Residues: 1-975 <AND>

A/Cross-references: EMBL:Z35953; NID:G536347; PIDN:CAA85029.1; PID:G536348; GSPDB:GN000

C/Genetics:

A/Gene: SGD:M1S1; MIPS:YBR084w

A/Cross-references: SGD:S0000288; MIPS:YBR084w

A/Map position: 2R

C/Superfamily: C1-tetrahydrofolate synthase; formate-tetrahydrofolate ligase homology;

C:Keywords: hydrolase; ligase; mitochondrion; multifunctional enzyme; NDP; one-carbon m
 F.1-34/Domains: transit peptide (mitochondrion) #status predicted <TNP>
 F.137-975/Product: C1-tetrahydrofolate synthase #status predicted <MAT>
 F.137-321/Domains: methyltetrahydrofolate dehydrogenase (NAD+) homology <MTFD>
 F.198-214/Domains: transmembrane #status predicted <TM1>
 F.231-247/Domains: transmembrane #status predicted <TM2>
 F.303-332/Domains: transmembrane #status predicted <TM3>
 F.334-975/Domains: formate-tetrahydrofolate ligase homology <FTL>
 F.592-608/Domains: transmembrane #status predicted <TM4>
 F.673-689/Domains: transmembrane #status predicted <TM5>
 F.729-745/Domains: transmembrane #status predicted <TM6>

Query Match 69.2% Score 36; DB 1; Length 975;
 Best Local Similarity 66.7%; Pred. No. 1e+02;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 DIDPDSVPQ 9
 Db 284 DDFDPSVKE 292

RESULT 12
 TSHUD1
 thombospondin 1 precursor - human
 C:Species: Homo sapiens (man)
 C>Date: 23-Aug-1987 #sequence_revision 03-Aug-1995 #text_change 09-Jul-2004
 C:Accession: A26155; A34274; A30140; A25812; A05172; A42927
 R:Lawler, J.; Hyne, R.O.
 J. Cell Biol. 103, 1635-1648, 1986
 A>Title: The structure of human thombospondin, an adhesive glycoprotein with multiple C
 A:Reference number: A26155; PMID:87057617; PMID:2430973
 A:Accession: A26155
 A:Molecule type: mRNA
 A:Residues: 1-1170 <LAW>
 A:Cross-references: UNIPROT:P07996; GB:X04665; NID:G37137; PIDN:CAA28370.1; PID:G37138
 A>Note: parts of this sequence, including the amino end of the mature protein, were dete
 R:laherty, C.D.; German, T.M.; Dixit, V.M.
 J. Biol. Chem. 264, 11222-11227, 1989
 A>Title: Characterization of the promoter region of the human thombospondin gene. DNA E
 A:Reference number: A34274; PMID:89291870; PMID:2544587
 A:Accession: A34274
 A:Molecule type: DNA
 A:Residues: 1-166 <LAH>
 A:Cross-references: GB:J04835
 R:Hennesy, S.W.; Frazier, B.A.; Kim, D.D.; Deckwerth, T.L.; Baumgartel, D.M.; Rotwein,
 J. Cell Biol. 108, 729-736, 1989
 A>Title: Complete thombospondin mRNA sequence includes potential regulatory sites in th
 A:Reference number: A30140; PMID:89139590; PMID:2918029
 A:Accession: A30140
 A:Molecule type: mRNA
 A:Residues: 1-83, 'A', 65-522, 'A', 524-1170 <HEN>
 A:Cross-references: EMBL:X14787; NID:G37464; PIDN:CAA32889.1; PID:G37465
 A>Note: parts of this sequence, including the amino end of the mature protein, were dete
 R:Kobayashi, S.; Eden-McCutchan, F.; Framson, P.; Bornstein, P.
 Biochemistry 25, 8418-8425, 1986
 A>Title: Partial amino acid sequence of human thombospondin as determined by analysis C
 A:Reference number: A25812; PMID:87157592; PMID:3030396
 A:Accession: A25812
 A:Molecule type: mRNA
 A:Residues: 1-83, 'A', 85-397 <KOB>
 A:Cross-references: GB:M25631; NID:G538353; PIDN:AAA6741.1; PID:G538354
 R:Dixit, V.M.; Hennesy, S.W.; Grant, G.A.; Rotwein, P.; Frazier, W.A.
 Proc. Natl. Acad. Sci. U.S.A. 83, 5449-5453, 1986
 A:Reference number: A05172; PMID:86287276; PMID:3461443
 A:Accession: A05172
 A:Molecule type: mRNA
 A:Residues: 1-83, 'A', 85-374, 'RC' <DIX>
 A:Cross-references: GB:M1326; NID:G340005; PIDN:AAA1237.1; PID:G553801
 A>Note: parts of this sequence, including the amino end of the mature protein, were dete
 R:Sun, X.; Skortenggaard, K.; Mosher, D.F.
 J. Cell Biol. 118, 693-701, 1992
 A>Title: Disulfide modulate RGD-inhibitable cell adhesive activity of thombospondin.
 A:Reference number: A42927; PMID:92348511; PMID:1379247

A:Accession: A42927
 A:Molecule type: protein
 A:Residues: 987-1003 <SUN>
 A>Note: Cys-992 is shown to have a free sulfhydryl
 C:Genetics:
 A:Gene: GDB:THBS1; TSP1; TSP
 A:Cross-references: GDB:120438; OMIM:188060
 A:Map position: 15q15-15q15
 A:Introns: 23/1
 A>Note: the list of introns may be incomplete
 C:Complex: homotrimer; disulfide linked
 C:Function:
 A:Description: participates in cell migration and adhesion, and in platelet aggregation
 C:Superfamily: thombospondin 1; EGF homology; thombospondin type 1 repeat homology; vo
 C:Keywords: beta-hydroxyasparagine; calcium binding; cell adhesion; glycoprotein; trimer
 F.1-18/Domains: signal sequence #status predicted <SIG>
 F.19-1170/Product: thombospondin 1 #status predicted <MAT>
 F.317-375/Domains: von Willebrand factor type C repeat homology <THR1>
 F.378-429/Domains: thombospondin type 1 repeat homology <THR1>
 F.434-490/Domains: thombospondin type 1 repeat homology <THR2>
 F.491-547/Domains: thombospondin type 1 repeat homology <THR3>
 F.551-586/Domains: EGF homology <EGF1>
 F.650-689/Domains: EGF homology <EGF2>
 F.926-928/Region: cell attachment (R-G-D) motif
 F.171-232/Disulfide bonds: #status predicted
 F.248,360,708,1067/Binding site: carbohydrate (asn) (covalent) #status predicted
 F.270,274/Disulfide bonds: interchain #status predicted
 F.610/Modified site: erythro-beta-hydroxyasparagine (asn) #status predicted
 F.1051/Binding site: carbohydrate (asn) (covalent) #status absent

Query Match 69.2% Score 36; DB 1; Length 1170;
 Best Local Similarity 70.0%; Pred. No. 1.3e+02;
 Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 DIDPDSVPQI 10
 Db 933 DDFDPSVPI 942

RESULT 13
 AD3161
 conserved hypothetical protein Atus013 [Imported] - Agrobacterium tumefaciens (strain C5
 C:Species: Agrobacterium tumefaciens
 C>Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 09-Jul-2004
 C:Accession: AD3161
 R:Wood, D.W.; Setubal, J.C.; Kaul, R.; Minks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Moo, L
 erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kutayavin, T.; Levy, R.; Li, M.; McClell
 ; Karp, P.; Romero, P.; Zhang, S.
 Science 294, 2317-2323, 2001
 A:Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
 ser, E.W.
 A>Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
 A:Reference number: AB2577; PMID:21608550; PMID:11743193
 A:Accession: AD3161
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-82 <KUR>
 A:Cross-references: UNIPROT:Q8UKT6; GB:AE006867; PIDN:AAA5706.1; PID:G17743435; GSPDB:G
 A:Experimental source: strain C58 (Dupont)
 C:Genetics:
 A:Gene: Atus013
 A:Genome: plasmid

Query Match 67.3% Score 35; DB 2; Length 82;
 Best Local Similarity 85.7%; Pred. No. 8.5;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DIDPDSV 7
 Db 63 DDFDPSI 69

RESULT 14

T08473
 ttaO protein homolog - Enterobacter aerogenes plasmid R751
 C:Species: Enterobacter aerogenes
 C:Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
 C:Accession: T08473
 R:Thorsted, P.B.; Shah, D.S.; Macartney, D.; Kostelidou, K.; Thomas, C.M.
 Plasmid 36, 95-111, 1996
 A:Title: Conservation of the genetic switch between replication and transfer genes of *E. coli*
 A:Reference number: Z16434; MUID:97118926; PMID:8954881
 A:Accession: T08473
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-115 <THO>
 A:Cross-references: UNIPROT:P71172; EMBL:U67194; NID:G1572520; PIDN:AA64417.1; PID:G1572520
 C:Genetics:
 A:Gene: upf54.8
 A:Genome: plasmid R751

Query Match 67.3%; Score 35; DB 2; Length 115;
 Best Local Similarity 75.0%; Pred. No. 13;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 DFDKVPQI 10
 |||||
 DB 79 DFDKVPQI 86

RESULT 15

AF0261
 fatty acid metabolism regulatory protein fadr [imported] - Yersinia pestis (strain CO92)
 C:Species: Yersinia pestis
 C:Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Jul-2004
 C:Accession: AF0261
 R:Parkhill, J.; Wren, B.W.; Thomson, N.R.; Tildall, R.W.; Holden, M.T.G.; Prentice, M.B.; deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Dougan, G.; Hill, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrett, N.
 Nature 413, 523-527, 2001
 A:Title: Genome sequence of Yersinia pestis, the causative agent of plague.
 A:Reference number: AB0001; MUID:21470413; PMID:11586360
 A:Accession: AF0261
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-239 <KUR>
 A:Cross-references: UNIPROT:Q8ZEL9; GB:AL590842; PIDN:CAC90954.1; PID:G15980150; GSPDB:G15980150
 C:Genetics:
 A:Gene: fadr
 C:Superfamily: pyruvate dehydrogenase complex repressor

Query Match 67.3%; Score 35; DB 2; Length 239;
 Best Local Similarity 66.7%; Pred. No. 31;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 IDPDVPOI 10
 :|||:
 DB 89 IDPDVPOI 97

Search completed: October 22, 2005, 08:04:32
 Job time : 12.45 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 22, 2005, 06:06:36 ; Search time 55.85 Seconds
(without alignment)
91.688 Million cell updates/sec

Title: US-10-731-238-76
Perfect score: 52
Sequence: 1 DIDFDSVPQI 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_03: *
1: uniprot_sprot: *
2: uniprot_trembl: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	52	100.0	152	2	Q9AEP9	Q9AEP9 staphylococ
2	52	100.0	940	2	O53682	O53682 staphylococ
3	52	100.0	943	2	O8NUU8	O8NUU8 staphylococ
4	52	100.0	957	2	O6G6H4	O6G6H4 staphylococ
5	52	100.0	961	2	O99RD3	O99RD3 staphylococ
6	52	100.0	961	2	Q7A3J8	Q7A3J8 staphylococ
7	52	100.0	965	2	O6GDU5	O6GDU5 staphylococ
8	52	100.0	1015	2	O8NUU7	O8NUU7 staphylococ
9	52	100.0	1015	2	O6G6H3	O6G6H3 staphylococ
10	52	100.0	1018	1	FNBA_STANU	P14738 staphylococ
11	52	100.0	1038	2	O99RD2	O99RD2 staphylococ
12	52	100.0	1038	2	Q7A3J7	Q7A3J7 staphylococ
13	52	100.0	1038	2	O6BSZ0	O6BSZ0 debaryomyce
14	40	76.9	399	2	O6FZU3	O6FZU3 neiseeria m
15	39	75.0	286	2	O67NB1	O67NB1 symbiobacte
16	39	75.0	290	2	O836D1	O836D1 enterococcu
17	38	73.1	431	2	O6INK4	O6INK4 xenopus lae
18	38	73.1	719	2	O6XQ07	O6XQ07 xenopus lae
19	37	71.2	108	2	O9F1A7	O9F1A7 uncultured
20	37	71.2	346	2	O6LP05	O6LP05 photobacter
21	37	71.2	408	2	O8K870	O8K870 streptococc
22	37	71.2	408	2	O8PIW1	O8PIW1 streptococc
23	37	71.2	408	2	O9A0U4	O9A0U4 streptococc
24	37	71.2	408	2	O878G1	O878G1 streptococc
25	37	71.2	416	2	O8CPE3	O8CPE3 streptococc
26	37	71.2	489	2	O7U9W7	O7U9W7 synecchococc
27	37	71.2	522	2	O6BKX1	O6BKX1 debaryomyce
28	37	71.2	524	2	O7X1G3	O7X1G3 oryza sativ
29	37	71.2	629	1	GIDA_THEMA	O9WY1 thermotoga
30	37	71.2	700	2	O7WFY0	O7WFY0 bordetella
31	37	71.2	753	2	O6ZSB4	O6ZSB4 homo sapien

32	37	71.2	937	2	O8IN69	O8IN69 drosophila
33	37	71.2	989	2	O9VDV0	O9VDV0 drosophila
34	37	71.2	1029	2	O7KSC1	O7KSC1 drosophila
35	37	71.2	1243	2	O6BHL5	O6BHL5 debaryomyce
36	37	71.2	1260	2	Q7Z305	Q7Z305 homo sapien
37	37	71.2	2416	2	Q7P167	Q7P167 drosophila
38	37	71.2	2417	2	O9VAS9	O9VAS9 drosophila
39	37	71.2	4574	2	O6JLK9	O6JLK9 burkholderi
40	36	69.2	114	2	O9AAR9	O9AAR9 cauliobacter
41	36	69.2	154	2	O29289	O29289 sus scrofa
42	36	69.2	280	2	O84FL7	O84FL7 panorea ag9
43	36	69.2	284	2	Q75TC1	Q75TC1 geobacillus
44	36	69.2	290	2	O7NJ88	O7NJ88 geobacter
45	36	69.2	329	2	O6AIA9	O6AIA9 desulfotale

ALIGNMENTS

RESULT 1
ID Q9AEP9 PRELIMINARY; PRT; 152 AA.
AC Q9AEP9;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Fibronectin-binding protein (Fragment).
GN Name=fnb;
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcu.
OX NCBI_TaxID=1280;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CMRSA-1;
RX MEDLINE=21246681; PubMed=11349044;
DOI=10.1128/IAI.69.6.3791-3799.2001;
RA Rice K., Huesca M., Vaz D., McGavin M.J.;
RT "Variance in fibronectin binding and fnb locus polymorphisms in
RT Staphylococcus aureus: identification of antigenic variation in a
RT fibronectin binding protein adhesin of the epidemic CMRSA-1 strain of
RT methicillin-resistant S. aureus.";
RL Infect. Immun. 69:3791-3799(2001).
DR EMBL: AY029184; AAK31588.1; -.
FT NON_TER
FT NON_TER
SQ SEQUENCE 152 AA; 17193 MW; CFA3913C2B11C025 CRC64;
Query Match 100.0%; Score 52; DB 2; Length 152;
Best Local Similarity 100.0%; Pred. No. 0.083;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 DIDFDSVPQI 10
Db 27 DIDFDSVPQI 36
RESULT 2
ID O53682 PRELIMINARY; PRT; 940 AA.
AC O53682;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Fibronectin binding protein B.
GN Name=fnb;
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1280;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=8325-4;
RX MEDLINE=92111475; PubMed=1837266;
RA Jonsson K., Sigmas C., Muller H.P., Lindberg M.;

RT "Two different genes encode fibronectin binding proteins in
RT Staphylococcus aureus. The complete nucleotide sequence and
RT characterization of the second gene."
RL Eur. J. Biochem. 202;1041-1048(1991).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC an amide bond (By similarity).
DR EMBL: X62992; CAA44726.1; -.
DR PIR: S19702; S19702.
DR HSP; O53653; 1N67.
DR GO: GO:0009986; C:cell surface; IEA.
DR GO: GO:0005618; C:cell wall; IEA.
DR GO: GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO: GO:0016020; C:membrane; IEA.
DR GO: GO:0007155; P:cell adhesion; IEA.
DR InterPro: IPR008966; Adhes_bact.
DR InterPro: IPR004237; Fn_bind.
DR InterPro: IPR005877; Gpos_YsIRK.
DR Pfam: PF02986; Fn_bind; 2.
DR Pfam: PF00746; Gram_pos_anchor; 1.
DR Pfam: PF04650; YsIRK_signal; 1.
DR TIGRfams; TIGR01167; LpxTG_anchor; 1.
DR TIGRfams; TIGR01168; YsIRK_signal; 1.
DR PROSITE; PS50847; GRAM_POS_ANCHORING; 1.
DR Cell wall; Peptidoglycan-anchor.
SQ SEQUENCE 940 AA; 103555 MW; E35FBBCA907AE345 CRC64;

Query Match 100.0%; Score 52; DB 2; Length 940;
Best Local Similarity 100.0%; Pred. No. 0.62;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 DIDPDSVPOI 10
|||||
Db 708 DIDFDSVPOI 717

RESULT 3
O6NUT8 PRELIMINARY; PRT; 943 AA.
ID O6NUT8
AC O6NUT8; 01-OCT-2002 (TREMBlrel. 22, Created)
DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Fndb protein.
GN Name=fndb; OrderedLocustNames=MM2420;
OS Staphylococcus aureus (strain MM2).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=196620;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MM2.
RX MEDLINE=22040717; PubMed=12044378; DOI=10.1016/S0140-6736(02)08713-5;
RA Baba T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Oguchi A.,
RA Nagai Y., Iwama N., Asano K., Naito T., Kuroda H., Cui L.,
RA Yamamoto K., Hiramoto K.;
RT "Genome and virulence determinants of high virulence community-
RT acquired MRSA".
RL Lancet 359;1819-1827(2002).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC an amide bond (By similarity).
DR EMBL: AP004830; BAB96285.1; -.
DR HSP; O53653; 1N67.
DR GO: GO:0009986; C:cell surface; IEA.
DR GO: GO:0005618; C:cell wall; IEA.
DR GO: GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO: GO:0016020; C:membrane; IEA.
DR GO: GO:0007155; P:cell adhesion; IEA.
DR InterPro: IPR008966; Adhes_bact.
DR InterPro: IPR004237; Fn_bind.
DR InterPro: IPR005877; Gpos_YsIRK.
DR Pfam: PF02986; Fn_bind; 1.
DR Pfam: PF00746; Gram_pos_anchor; 1.
SQ SEQUENCE 957 AA; 105980 MW; 28F8BA7FDFD3EAF CRC64;

DR Pfam: PF04650; YsIRK_signal; 1.
DR TIGRfams; TIGR01167; LpxTG_anchor; 1.
DR TIGRfams; TIGR01168; YsIRK_signal; 1.
DR PROSITE; PS50847; GRAM_POS_ANCHORING; 1.
DR Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ SEQUENCE 943 AA; 104537 MW; DA8A5F31947B1B6A CRC64;

Query Match 100.0%; Score 52; DB 2; Length 943;
Best Local Similarity 100.0%; Pred. No. 0.63;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 DIDPDSVPOI 10
|||||
Db 715 DIDFDSVPOI 724

RESULT 4
O6G6H4 PRELIMINARY; PRT; 957 AA.
ID O6G6H4
AC O6G6H4; 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE Fibronectin-binding protein.
GN Name=fndb; OrderedLocustNames=SA52387;
OS Staphylococcus aureus (strain MSSA476).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=282459;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=15213324; DOI=10.1073/pnas.0402521101;
RA Holden M.T.G., Fell E.J., Lindsey J.A., Peacock S.J., Day N.P.J.,
RA Enright M.C., Foster T.J., Moore C.E., Hurst L., Atkin R., Barton A.,
RA Bason N., Bentley S.D., Chillingworth C., Chillingworth T.,
RA Churcher C., Clark L., Cotton C., Cronin A., Doggett J., Dowd L.,
RA Feltham T., Hance Z., Harris B., Hauser H., Holroyd S., Jørgensen K.,
RA James K.D., Leonard N., Line A., Mayes R., Moule S., Mungall K.,
RA Ormond D., Quail M.A., Rabinowitch E., Rutherford K.M., Sanders M.,
RA Sharp S., Simmonds M., Stevens K., Whitehead S., Barrett B.G.,
RA Spratt B.G., Parkhill J.;
RT "Complete genomes of two clinical Staphylococcus aureus strains:
RT evidence for the rapid evolution of virulence and drug resistance".
RL Proc. Natl. Acad. Sci. U.S.A. 101:9786-9791(2004).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC an amide bond (By similarity).
DR EMBL: BX571857; CAG44201.1; -.
DR GO: GO:0009986; C:cell surface; IEA.
DR GO: GO:0005618; C:cell wall; IEA.
DR GO: GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO: GO:0016020; C:membrane; IEA.
DR GO: GO:0007155; P:cell adhesion; IEA.
DR InterPro: IPR008966; Adhes_bact.
DR InterPro: IPR004237; Fn_bind.
DR InterPro: IPR005877; Gpos_YsIRK.
DR InterPro: IPR001899; Gram_pos_anchor.
DR Pfam: PF02986; Fn_bind; 1.
DR Pfam: PF00746; Gram_pos_anchor; 1.
DR Pfam: PF04650; YsIRK_signal; 1.
DR TIGRfams; TIGR01167; LpxTG_anchor; 1.
DR TIGRfams; TIGR01168; YsIRK_signal; 1.
DR PROSITE; PS50847; GRAM_POS_ANCHORING; 1.
DR Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ SEQUENCE 957 AA; 105980 MW; 28F8BA7FDFD3EAF CRC64;

Query Match 100.0%; Score 52; DB 2; Length 957;
Best Local Similarity 100.0%; Pred. No. 0.64;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 DIDPDSVPOI 10
|||||
Db 715 DIDFDSVPOI 724

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RESULT 5
Q99RD3 PRELIMINARY: PRT; 961 AA.
ID Q99RD3;
AC Q99RD3;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DE Fibronectin-binding protein homolog.
GN Name=fnbB; OrderedlocusNames=SAV2502;
OS Staphylococcus aureus (strain Mu50 / ATCC 700699).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=158878;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=Mu50 / ATCC 700699;
RX MEDLINE=21311952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2;
RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Iino J.-O., Ito T.,
RA Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,
RA Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
RA Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
RA Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
RA Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
RT "Whole genome sequencing of methicillin-resistant Staphylococcus
RT aureus."
RL Lancet 357:1225-1240(2001).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC an amide bond (By similarity).
EMBL: AF003365; BAB58664.1; -.
DR PIR: G90053; G90053.
DR HSSP: O53653; 1N67.
DR GO: GO:0009986; C:cell surface; IEA.
DR GO: GO:0005618; C:cell wall; IEA.
DR GO: GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO: GO:0016020; C:membrane; IEA.
DR GO: GO:007155; P:cell adhesion; IEA.
DR InterPro: IPR008966; Adhes_bact.
DR InterPro: IPR004237; Fn_bind.
DR InterPro: IPR005877; Gpoe_YsIRK.
DR InterPro: IPR001899; Gram_pos_anchor.
DR Pfam: PF02986; Fn_bind_1.
DR Pfam: PF00746; Gram_pos_anchor_1.
DR Pfam: PF04650; YsIRK_signal; 1.
DR TIGRfams: TIGR01167; LPXTG_anchor; 1.
DR TIGRfams: TIGR01168; YsIRK_signal; 1.
DR PROSITE: PS50847; GRAM_POS_ANCHORING; 1.
DR KEGG: K01602; Complete proteome; Peptidoglycan-anchor.
SQ SEQUENCE 961 AA; 106010 MW; 364940F84EA4101 CRC64;

Query Match 100.0%; Score 52; DB 2; Length 961;
Best Local Similarity 100.0%; Pred. No. 0.64;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIDFDSVPOI 10
Db 719 DIDFDSVPOI 728

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RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Iino J.-O., Ito T.,
RA Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,
RA Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
RA Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
RA Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
RA Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
RT "Whole genome sequencing of methicillin-resistant Staphylococcus
RT aureus."
RL Lancet 357:1225-1240(2001).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC an amide bond (By similarity).
EMBL: AF003365; BAB58664.1; -.
DR GO: GO:0009986; C:cell surface; IEA.
DR GO: GO:0005618; C:cell wall; IEA.
DR GO: GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO: GO:0016020; C:membrane; IEA.
DR GO: GO:007155; P:cell adhesion; IEA.
DR InterPro: IPR008966; Adhes_bact.
DR InterPro: IPR004237; Fn_bind.
DR InterPro: IPR005877; Gpoe_YsIRK.
DR InterPro: IPR001899; Gram_pos_anchor.
DR Pfam: PF02986; Fn_bind_1.
DR Pfam: PF00746; Gram_pos_anchor_1.
DR Pfam: PF04650; YsIRK_signal; 1.
DR TIGRfams: TIGR01167; LPXTG_anchor; 1.
DR TIGRfams: TIGR01168; YsIRK_signal; 1.
DR PROSITE: PS50847; GRAM_POS_ANCHORING; 1.
DR KEGG: K01602; Complete proteome; Peptidoglycan-anchor.
SQ SEQUENCE 961 AA; 106010 MW; 364940F84EA4101 CRC64;

Query Match 100.0%; Score 52; DB 2; Length 961;
Best Local Similarity 100.0%; Pred. No. 0.64;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIDFDSVPOI 10
Db 719 DIDFDSVPOI 728

RESULT 7
Q6GDUS PRELIMINARY: PRT; 965 AA.
ID Q6GDUS;
AC Q6GDUS;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Fibronectin-binding protein.
GN Name=fnbA; OrderedlocusNames=SA2580;
OS Staphylococcus aureus (strain MRSA252).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=282458;
RN (1)
RP SEQUENCE FROM N.A.
RC PubMed=1521324; DOI=10.1073/pnas.0402521101;
RX Holden M.T.G., Fell E.J., Lindsey J.A., Peacock S.J., Day N.P.J.,
RA Highton M.C., Foster T.J., Moore C.B., Hurst L., Atkin R., Barron A.,
RA Bason N., Bentley S.D., Chillingworth C., Chillingworth T.,
RA Churcher C., Clark L., Cotton C., Cronin A., Doggett J., Dowd L.,
RA Felwell T., Hance Z., Harris B., Hauser H., Holtroyd S., Jagsels K.,
RA James K.D., Lennard N., Line A., Mayes R., Moulé S., Mungall K.,
RA Ormond D., Quail M.A., Rabinowitsch E., Rutherford K.M., Sanders M.,
RA Sharp S., Simmonds M., Stevens K., Whitehead S., Barrett B.G.,
RA Spratt B.G., Parkhill J.;
RT "Complete genomes of two clinical Staphylococcus aureus strains:
RT evidence for the rapid evolution of virulence and drug resistance."
RL Proc. Natl. Acad. Sci. U.S.A. 101:9786-9791(2004).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC an amide bond (By similarity).
EMBL: BX571856; CAG41560.1; -.
DR GO: GO:0009986; C:cell surface; IEA.
DR GO: GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO: GO:0016020; C:membrane; IEA.

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DR GO:0007155; P:cell adhesion; IEA.
DR InterPro; IPR008966; Adhes_bact.
DR InterPro; IPR004237; Fn_bind.
DR InterPro; IPR005877; Gpos_YsIRK.
DR InterPro; IPR001899; Gram_pos_anchor.
DR Pfam; PF02986; Fn_bind; 1.
DR Pfam; PF00746; Gram_pos_anchor; 1.
DR TIGRFAMs; TIGR01167; LpxTG_anchor; 1.
DR TIGRFAMs; TIGR01168; YsIRK_signal; 1.
DR PROSITE; PS50847; GRAM_POS_ANCHORING; 1.
DR Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ SEQUENCE 965 AA; 105691 MW; 2982E332164D0551 CRC64;

Query Match
Best Local Similarity 100.0%; Score 52; DB 2; Length 965;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DIDFSDVPQI 10
Db 773 DIDFSDVPQI 784

RESULT 8
08NUJ7 PRELIMINARY; PRT; 1015 AA.
ID 08NUJ7
AC 08NUJ7;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Fnb protein.
GN Name=fnb; Ordered locusNames=MM2423;
OS Staphylococcus aureus (strain MM2).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=196620;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MM2.
RX MEDLINE=22040717; PubMed=12044378; DOI=10.1016/S0140-6736(02)08713-5;
RA Baba T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Oguchi A.,
RA Nagai Y., Iwana N., Asano K., Naimi T., Kuroda H., Cui L.,
RA Yamamoto K., Hiramoto K.;
RT "Genome and virulence determinants of high virulence community-
acquired MRSA."
RL Lancet 359:1819-1827(2002).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
an amide bond (By similarity).
DR EMBL; AP004830; BAB96286.1; -.
DR GO; GO:0009986; C:cell surface; IEA.
DR GO; GO:0005618; C:cell wall; IEA.
DR GO; GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0007155; P:cell adhesion; IEA.
DR InterPro; IPR008966; Adhes_bact.
DR InterPro; IPR004237; Fn_bind.
DR InterPro; IPR005877; Gpos_YsIRK.
DR InterPro; IPR001899; Gram_pos_anchor.
DR Pfam; PF02986; Fn_bind; 1.
DR Pfam; PF00746; Gram_pos_anchor; 1.
DR TIGRFAMs; TIGR01167; LpxTG_anchor; 1.
DR TIGRFAMs; TIGR01168; YsIRK_signal; 1.
DR PROSITE; PS50847; GRAM_POS_ANCHORING; 1.
DR Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ SEQUENCE 1015 AA; 111145 MW; D0F9281BB64D44D2 CRC64;

Query Match
Best Local Similarity 100.0%; Score 53; DB 2; Length 1015;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DIDFSDVPQI 10
Db 773 DIDFSDVPQI 782

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RESULT 9
ID Q6G6H3 PRELIMINARY; PRT; 1015 AA.
AC Q6G6H3
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Fibronectin-binding protein.
GN Ordered locusNames=SAS2338;
OS Staphylococcus aureus (strain MSSA476).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=282459;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=15213324; DOI=10.1073/pnas.0402521101;
RA Holden M.T.G., Fell E.J., Lindsay J.A., Peacock S.J., Day N.P.J.,
RA Enright M.C., Foster T.J., Moore C.E., Hurst L., Atkin R., Barron A.,
RA Bason N., Bentley S.D., Chillingworth C., Chillingworth T.,
RA Churcher C., Clark L., Cronin A., Doggett J., Dowd L.,
RA Felwell T., Hance Z., Harris B., Hauser H., Holroyd S., Jags K.,
RA James K.D., Kennard N., Line A., Mayes R., Moule S., Mungall K.,
RA Ormond D., Quail M.A., Rabinovitch E., Rutherford K.M., Sanders M.,
RA Sharp S., Simmonds M., Stevens K., Whitehead S., Barrell B.G.,
RA Spratt B.G., Parkhill J.;
RT "Complete genomes of two clinical Staphylococcus aureus strains:
evidence for the rapid evolution of virulence and drug resistance."
Proc. Natl. Acad. Sci. U.S.A. 101:9786-9791(2004).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
an amide bond (By similarity).
DR EMBL; BX571857; CAG44202.1; -.
DR GO; GO:0009986; C:cell surface; IEA.
DR GO; GO:0005618; C:cell wall; IEA.
DR GO; GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0007155; P:cell adhesion; IEA.
DR InterPro; IPR008966; Adhes_bact.
DR InterPro; IPR004237; Fn_bind.
DR InterPro; IPR005877; Gpos_YsIRK.
DR InterPro; IPR001899; Gram_pos_anchor.
DR Pfam; PF02986; Fn_bind; 1.
DR Pfam; PF00746; Gram_pos_anchor; 1.
DR TIGRFAMs; TIGR01167; LpxTG_anchor; 1.
DR TIGRFAMs; TIGR01168; YsIRK_signal; 1.
DR PROSITE; PS50847; GRAM_POS_ANCHORING; 1.
DR Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ SEQUENCE 1015 AA; 111145 MW; D0F9281BB64D44D2 CRC64;

Query Match
Best Local Similarity 100.0%; Score 52; DB 2; Length 1015;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DIDFSDVPQI 10
Db 773 DIDFSDVPQI 782

RESULT 10
ID FNBA_STAAU STANDARD; PRT; 1016 AA.
AC FNBA_STAAU
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Fibronectin-binding protein precursor (FNBP).
GN Name=fnbA;
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1280;
RN [1]
RP SEQUENCE FROM N.A.

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RC STRAIN=NCTC 8325-4;
RX MEDLINE=8908998; PubMed=2521391;
RA Signaes C., Raucet G., Joeneson K., Lindgren P.-E.,
RA Anantharamiah G.M., Hoeck M., Lindberg M.;
RT "Nucleotide sequence of the gene for a fibronectin-binding protein
RT from Staphylococcus aureus: use of this peptide sequence in the
RT synthesis of biologically active peptides."
RL Proc. Natl. Acad. Sci. U.S.A. 86:699-703(1989).
CC -1- FUNCTION: The ability of bacteria to bind fibronectin has been
CC proposed as a virulence factor enabling bacteria to colonize wound
CC tissues and blood clots. Binding of plasma fibronectin to the
CC bacterial surface might block adhesion receptors on S. aureus, thus
CC representing an important defense mechanism against tissue
CC invasion.
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC an amide bond (Potential).
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@sib-sib.ch).
CC -----
CC EMBL, J04151; AAA26632.1; -
CC InterPro: IPR004237; Gp_bind.
CC InterPro: IPR005877; Gpos_YsIRK.
CC InterPro: IPR001899; Gram_pos_anchor.
CC Pfam: PF02986; Fn_bind.1.
CC Pfam: PF00746; Gram_pos_anchor.1.
CC DR PFam: PF04650; YsIRK_signal.1.
CC DR TIGRfams: TIGR01167; LPXTG_anchor.1.
CC DR TIGRfams: TIGR01168; YsIRK_signal.1.
CC DR PROSITE: PS50847; GRAM_POS_ANCHORING.1.
CC Cell adhesion; Cell wall; Peptidoglycan-anchor; Repeat; Signal;
CC Virulence.
KW SIGNAL.
FT 1 36
FT CHAIN 37 985
FT PROPEP 986 1018
FT REPEAT 545 574
FT REPEAT 575 604
FT DOMAIN 745 878
FT REPEAT 745 782
FT REPEAT 783 820
FT REPEAT 821 859
FT REPEAT 860 878
FT DOMAIN 879 948
FT REPEAT 879 892
FT REPEAT 893 906
FT REPEAT 907 920
FT REPEAT 921 934
FT REPEAT 935 948
FT SITE 982 986
FT MOD_RES 985 985
SQ SEQUENCE 1018 AA; 111780 MW; 58175E0020B81F1F CRC64;

Query Match 100.0%; Score 52; DB 1; Length 1018;
Best Local Similarity 100.0%; Pred. No. 0.68;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Fibronectin-binding protein homolog.
GN Name=fib; OrderedLocustNames=SAV2503;
OS Staphylococcus aureus (strain Mu50 / ATCC 700699).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxId=158878;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Mus0 / ATCC 700699;
RX MEDLINE=21111952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2;
RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Lian Y.-Q., Ito T.,
RA Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,
RA Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
RA Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
RA Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
RT "Whole genome sequencing of methicillin-resistant Staphylococcus
RT aureus."
RL Lancet 357:1225-1240(2001).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC an amide bond (By similarity).
CC EMBL, AF003365; BAB58665.1; -
CC PIR: H90053; H90053.
CC GO: GO:0009986; C:cell surface; IEA.
CC GO: GO:0005618; C:cell wall; IEA.
CC GO: GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
CC GO: GO:0016020; C:membrane; IEA.
CC GO: GO:0007155; P:cell adhesion; IEA.
CC InterPro: IPR008966; Adhes_bact.
CC InterPro: IPR004237; Fn_bind.
CC InterPro: IPR005877; Gpos_YsIRK.
CC InterPro: IPR001899; Gram_pos_anchor.
CC Pfam: PF02986; Fn_bind.1.
CC Pfam: PF00746; Gram_pos_anchor.1.
CC Pfam: PF04650; YsIRK_signal.1.
CC DR TIGRfams: TIGR01167; LPXTG_anchor.1.
CC DR TIGRfams: TIGR01168; YsIRK_signal.1.
CC DR PROSITE: PS50847; GRAM_POS_ANCHORING.1.
CC Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ SEQUENCE 1038 AA; 113618 MW; 666BF6BF2BFEB312 CRC64;

Query Match 100.0%; Score 52; DB 2; Length 1038;
Best Local Similarity 100.0%; Pred. No. 0.7;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 DIDFDSVPOI 10
DB 772 DIDFDSVPOI 781
RESULT 11
O99RD2 PRELIMINARY; PRT; 1038 AA.
AC O99RD2;
DT 01-JUN-2001 (TREMBLrel. 17, Created)

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RA Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
RT "Whole genome sequencing of methicillin-resistant Staphylococcus
RL aureus."
CC Lancel 357:1225-1240(2001).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC an amide bond (By similarity).
DR EMBL: AP003137; BAB3594.1; -.
DR GO: GO:0009986; C:cell surface; IEA.
DR GO: GO:0005618; C:cell wall; IEA.
DR GO: GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO: GO:0016020; C:membrane; IEA.
DR GO: GO:0007155; P:cell adhesion; IEA.
DR InterPro: IPR008966; Adhes_bact.
DR InterPro: IPR004237; Fn_bind.
DR InterPro: IPR005877; Gram_pos_anchor.
DR InterPro: IPR001899; Gram_pos_anchor.
DR Pfam: PF02986; Fn_bind; 1.
DR Pfam: PF00746; Gram_pos_anchor; 1.
DR Pfam: PF04650; YSIRK_signal; 1.
DR TIGRfam: TIGR01167; LPTXG_anchor; 1.
DR TIGRfam: TIGR01168; YSIRK_signal; 1.
DR PROSITE: PS50847; GRAM_POS_ANCHORING; 1.
KW Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ SEQUENCE 1038 AA; 113618 MW; 666BF6BF2BFEB12 CRC64;

Query Match 100.0%; Score 52; DB 2; Length 1038;
Best Local Similarity 100.0%; Pred. No. 0.7;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIDPDSVPOI 10
Db 768 DIDPDSVPOI 777

RESULT 13
O6BSZ0 PRELIMINARY; PRT; 399 AA.
ID O6BSZ0;
AC O6BSZ0;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DE 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Similar to CA3505|IPF11372 Candida albicans IPF11372 unknown
DE function.
GN ORFNames=DEHAD057099;
OS Debaryomyces hansenii CBS767.
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Debaryomycetes.
OX NCBI_TaxId=284592;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CBS767;
RG Genolevures;
RA Dujon B., Sherman D., Fischer G., Durrens P., Casaregola S.,
RA Lafontaine I., de Montigny J., Marcq C., Neuvéglise C., Talla E.,
RA Goffard N., Franseul L., Aigle M., Anhouard V., Babour A., Barbe V.,
RA Barnay S., Blanchin S., Beckerich J.M., Beyne E., Bleyaeren C.,
RA Borsari A., Boyer J., Catolico L., Confanieri F., de Darvar A.,
RA Despons L., Fabre E., Fairhead C., Ferry-Dunazet H., Gropfi A.,
RA Hantreuve F., Hennequin C., Jauniaux N., Joyet P., Kachouri R.,
RA Kerrest A., Koszul R., Lemaire M., Leduc I., Ma L., Muller H.,
RA Nicoud J.M., Nikolski M., Orlas S., Olier-Kalogeropoulos O.,
RA Pellenz S., Pottier S., Richard G.F., Strub M.L., Suleau A.,
RA Swennene D., Tekala F., Wesolowski-Louvel M., Westhof B., Wirth B.,
RA Zeniou-Meyer M., Zivanovic I., Bolotin-Fukuhara M., Thierry A.,
RA Bouchier C., Caudon B., Scarpelli C., Gallardin C., Weissenbach J.,
RA Winkler P., Souciet J.L.;
RT "Genome evolution in yeasts.";
RL Nature 430:35-44(2004).
RN
RN SEQUENCE FROM N.A.
RC STRAIN=CBS767;
RA Genomecope;
RL Submitted (JUL-2004) to the EMBL/Genbank/DBJ databases.

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DR EMBL: CR382136; CAG86819.1; -.
DR InterPro: IPR001917; Antictrns_II.
DR PROSITE: PS00599; AA_TRANSFERR_CLASS_2; UNKNOWN 1.
SQ SEQUENCE 399 AA; 44454 MW; B1C2E815A8DDA1 CRC64;

Query Match 76.9%; Score 40; DB 2; Length 399;
Best Local Similarity 77.8%; Pred. No. 47;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 DIDPDSVPO 9
Db 197 DIDPDSVPO 205

RESULT 14
ID Q9FZU3 PRELIMINARY; PRT; 1421 AA.
AC Q9FZU3;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE ORF 4.
OS Neisseria meningitidis phage 2120.
OC Viruses.
OX NCBI_TaxId=132905;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=2120;
RX MEDLINE=21172874; PubMed=11274117;
RX DOI=10.1128/JB.183.8.2570-2575.2001;
RA Claus H., Stoevesandt J., Froesch M., Vogel U.;
RT "Genetic isolation of meningococci of the electrophoretic type 37
RT complex."
RL J. Bacteriol. 183:2570-2575(2001).
DR EMBL: AJ278707; CAC19023.1; -.
DR InterPro: IPR003961; FN_III.
DR SMART: SM00060; FN3; 1.
DR PROSITE: PS50853; FN3; 1.
SQ SEQUENCE 1421 AA; 153412 MW; 7A17FDAAB6FA9A6 CRC64;

Query Match 76.9%; Score 40; DB 2; Length 1421;
Best Local Similarity 60.0%; Pred. No. 1.9e+02;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 DIDPDSVPOI 10
Db 171 DVEFDVPOV 180

RESULT 15
O67NB1 PRELIMINARY; PRT; 286 AA.
ID O67NB1;
AC O67NB1;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Methylaneotetrahydrofolate dehydrogenase/methylenetetrahydrofolate
DE cyclohydrolase.
GN ORFNames=STH1847;
OS Bacteroides thermophilum.
OC Bacteria; Actinobacteria; Syntrophobacterium.
OX NCBI_TaxId=2734;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=IM414863;
RA Ueda K., Yamashita A., Ishikawa J., Shinada M., Matsui T.,
RA Morimura K., Ikeda H., Hattori M., Beppu T.;
RT "Complete genome sequence of an uncultured bacterium Syntrophobacterium
RT thermophilum."
RL Submitted (APR-2004) to the EMBL/Genbank/DBJ databases.
DR EMBL: AP006840; BAD40832.1; -.
DR GO: GO:0016787; F:hydrolase activity; IEA.
DR InterPro: IPR000672; THPDhg/Cyc_hydro.

```

DR pEam; PF00763; THF_DHG_CYH; 1.
DR pEam; PF02882; THF_DHG_CYH_C; 1.
DR PRINTS; PR00085; THFDHGRGNASE.
DR ProDom; PD002300; THFDhg/Cyc_hydro; 1.
DR PROSITE; PS00767; THF_DHG_CYH_2; 1.
KW Hydrolyase.
SQ SEQUENCE 286 AA; 30374 MW; E3A018F64C3DB3C7 CRC64;

Query Match 75.0%; Score 39; DB 2; Length 286;
Best Local Similarity 60.0%; Pred. No. 50;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 DIDPDSVPQI 10
Db 244 DVDPDSVQEV 253

Search completed: October 22, 2005, 08:00:46
Job time : 58.85 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: October 25, 2005, 20:21:18 ; Search time 63.2 Seconds
(without alignments)
61.196 Million cell updates/sec

Title: US-10-731-238-77
Perfect score: 56
Sequence: 1 DFDSVPQIHG 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues
Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:.*
1: geneseqp1808:.*
2: geneseqp1908:.*
3: geneseqp2008:.*
4: geneseqp2001s:.*
5: geneseqp2002s:.*
6: geneseqp2003as:.*
7: geneseqp2003bs:.*
8: geneseqp2004s:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	56	100.0	10	2	AAW65733 Fibronec
2	56	100.0	38	2	AAW65692 Fibronec
3	56	100.0	38	2	AAW65695 Fibronec
4	56	100.0	38	2	AAW65662 Fibronec
5	56	100.0	38	2	AAW65696 Fibronec
6	56	100.0	38	2	AAW65697 Fibronec
7	56	100.0	38	2	AAW65694 Fibronec
8	56	100.0	38	2	AAW65700 Fibronec
9	56	100.0	38	2	AAW65691 Fibronec
10	56	100.0	38	2	AAW65699 Fibronec
11	56	100.0	38	2	AAW65661 Fibronec
12	56	100.0	38	2	AAW65693 Fibronec
13	56	100.0	38	2	AAW65698 Fibronec
14	56	100.0	113	2	AAW65698 Fibronec
15	56	100.0	130	2	AAW65698 Fibronec
16	56	100.0	130	2	AAW65698 Fibronec
17	56	100.0	130	2	AAW65698 Fibronec
18	56	100.0	130	2	AAW65698 Fibronec
19	56	100.0	130	2	AAW65698 Fibronec
20	56	100.0	134	2	AAW65698 Fibronec
21	56	100.0	134	2	AAW65698 Fibronec
22	56	100.0	139	2	AAW65698 Fibronec
23	56	100.0	162	2	AAW65698 Fibronec
24	56	100.0	164	2	AAW65698 Fibronec
25	56	100.0	174	2	AAW65698 Fibronec

26	56	100.0	174	2	AAW65733	AAW65733 standard; peptide; 10 AA.
27	56	100.0	181	2	AAW65733	AAW65733 standard; peptide; 10 AA.
28	56	100.0	181	2	AAW65733	AAW65733 standard; peptide; 10 AA.
29	56	100.0	559	2	AAW65733	AAW65733 standard; peptide; 10 AA.
30	56	100.0	767	4	AAW65733	AAW65733 standard; peptide; 10 AA.
31	56	100.0	767	4	AAW65733	AAW65733 standard; peptide; 10 AA.
32	56	100.0	940	2	AAW65733	AAW65733 standard; peptide; 10 AA.
33	56	100.0	940	2	AAW65733	AAW65733 standard; peptide; 10 AA.
34	56	100.0	948	6	AAW65733	AAW65733 standard; peptide; 10 AA.
35	56	100.0	948	6	AAW65733	AAW65733 standard; peptide; 10 AA.
36	56	100.0	948	6	AAW65733	AAW65733 standard; peptide; 10 AA.
37	56	100.0	961	6	AAW65733	AAW65733 standard; peptide; 10 AA.
38	56	100.0	978	4	AAW65733	AAW65733 standard; peptide; 10 AA.
39	56	100.0	1001	4	AAW65733	AAW65733 standard; peptide; 10 AA.
40	56	100.0	1018	1	AAW65733	AAW65733 standard; peptide; 10 AA.
41	56	100.0	1018	1	AAW65733	AAW65733 standard; peptide; 10 AA.
42	56	100.0	1018	6	AAW65733	AAW65733 standard; peptide; 10 AA.
43	56	100.0	1018	6	AAW65733	AAW65733 standard; peptide; 10 AA.
44	56	100.0	1018	6	AAW65733	AAW65733 standard; peptide; 10 AA.
45	56	100.0	1027	2	AAW65733	AAW65733 standard; peptide; 10 AA.

ALIGNMENTS

RESULT 1
ID AAW65733
AC AAW65733
XX AAW65733; 16-OCT-1998 (first entry)
DT 16-OCT-1998 (first entry)
XX
DE Fibronec binding protein-derived peptide #77.
XX
KW microbial surface components recognising adhesive matrix molecule;
KW MSCRAMM; fibronec; fibronec-binding protein; antibody; epitope;
KW antibiotic; bacterial infection; antibiotic-resistant strain.
XX
OS Synthetic.
OS Staphylococcus aureus.
XX
PN WO9831389-A2.
XX
PD 23-JUL-1998.
XX
PF 21-JAN-1998; 98WO-US001222.
XX
PR 21-JAN-1997; 97US-0036139P.
XX
XX (TEXA) UNIV TEXAS A & M SYSTEM.
XX Hoeek M, Patti JM, House-Pompeo KL, Speciale P, Joh D;
XX McGavin MJ;
XX WPI; 1998-413816/35.
XX
XX The invention relates to antibodies that bind to a fibronec-binding
XX domain of a fibronec-binding protein, and inhibit binding of the
XX protein to a fibronec. Also claimed are: (1) isolated peptides of a
XX fibronec-binding protein that do not bind to fibronec; (2) fusion
XX protein containing at least one peptide of a fibronec-binding protein
XX linked to a second amino acid sequence; (3) nucleic acid encoding the
XX isolated peptide of (1). Antibodies, the isolated peptides of (1) and the
XX nucleic acids are all useful for immunisation (active or passive) and (by
XX inhibiting binding of bacteria to fibronec) for preventing or treating
XX infection in humans or other animals, particularly by staphylococci or

CC streptococci, e.g. meningitis, otitis media, pneumonia, endocarditis,
CC mastitis in cattle, abortion in horses and many others. Since the
CC antibodies block binding of bacteria, they should be effective against
CC antibiotic-resistant strains, and may replace antibiotic therapy or
CC increase its effectiveness. Sequences AAW65719-41 and AAW65658 represent
CC peptides which were synthesised to span the D1 motif and the N-terminal
CC 18 amino acids of D2, with each peptide overlapping by eight amino acids
CC with the previous sequence

XX Sequence 10 AA;

Query Match 100.0%; Score 56; DB 2; Length 10;

Best Local Similarity 100.0%; Pred. No. 0.0011;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DFDSVPQIHG 10
|||
DB 1 DFDSVPQIHG 10

RESULT 2
AAW65692

ID AAW65692 standard; peptide; 38 AA.

XX AAW65692;

DT 16-OCT-1998 (first entry)

XX Fibronectin binding protein-derived peptide #36.

XX microbial surface components recognising adhesive matrix molecule;

KW MSCRAM; fibronectin; fibronectin-binding protein; antibody; epitope;

KM antibiotic; bacterial infection; antibiotic-resistant strain.

XX Synthetic.

OS Staphylococcus aureus.

XX WO9831389-A2.

XX 23-JUL-1998.

XX 21-JAN-1998; 98WO-US001222.

XX 21-JAN-1997; 97US-0036139P.

XX (TEXA) UNIV TEXAS A & M SYSTEM.

XX Hoeek M, Patti JM, House-Pompeo KL, Speziale P, Joh D;

PI McGavin MJ;

XX WPI, 1998-413816/35.

XX Antibody that binds to fibronectin-binding protein, preventing its
XX binding to fibronectin - used to treat or prevent bacterial infection,
XX especially by Staphylococci and Streptococci.

XX Example 8; Page 101; 201pp; English.

XX The invention relates to antibodies that bind to a fibronectin-binding
CC domain of a fibronectin-binding protein, and inhibit binding of the
CC protein to fibronectin. Also claimed are: (1) isolated peptides of a
CC fibronectin-binding protein that do not bind to fibronectin; (2) fusion
CC protein containing at least one peptide of a fibronectin-binding protein
CC linked to a second amino acid sequence; (3) nucleic acid encoding the
CC isolated peptide of (1). Antibodies, the isolated peptides of (1) and the
CC nucleic acids are all useful for immunisation (active or passive) and (by
CC inhibiting binding of bacteria to fibronectin) for preventing or treating
CC infection in humans or other animals, particularly by staphylococci or
CC streptococci, e.g. meningitis, otitis media, pneumonia, endocarditis,
CC mastitis in cattle, abortion in horses and many others. Since the
CC antibodies block binding of bacteria, they should be effective against
CC antibiotic-resistant strains, and may replace antibiotic therapy or
CC increase its effectiveness. Sequences AAW65691-700 represent a series of

CC synthetic peptides based on the D1 region of S. aureus fibronectin
CC binding protein A. They were synthesised to contain mutations

XX Sequence 38 AA;

Query Match 100.0%; Score 56; DB 2; Length 38;

Best Local Similarity 100.0%; Pred. No. 0.0046;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DFDSVPQIHG 10
|||
DB 29 DFDSVPQIHG 38

RESULT 3
AAW65695

ID AAW65695 standard; peptide; 38 AA.

XX AAW65695;

DT 16-OCT-1998 (first entry)

XX Fibronectin binding protein-derived peptide #39.

XX microbial surface components recognising adhesive matrix molecule;

KW MSCRAM; fibronectin; fibronectin-binding protein; antibody; epitope;

KM antibiotic; bacterial infection; antibiotic-resistant strain.

XX Synthetic.

OS Staphylococcus aureus.

XX WO9831389-A2.

XX 23-JUL-1998.

XX 21-JAN-1998; 98WO-US001222.

XX 21-JAN-1997; 97US-0036139P.

XX (TEXA) UNIV TEXAS A & M SYSTEM.

XX Hoeek M, Patti JM, House-Pompeo KL, Speziale P, Joh D;

PI McGavin MJ;

XX WPI, 1998-413816/35.

XX Antibody that binds to fibronectin-binding protein, preventing its
XX binding to fibronectin - used to treat or prevent bacterial infection,
XX especially by Staphylococci and Streptococci.

XX Example 8; Page 102; 201pp; English.

XX The invention relates to antibodies that bind to a fibronectin-binding
CC domain of a fibronectin-binding protein, and inhibit binding of the
CC protein to fibronectin. Also claimed are: (1) isolated peptides of a
CC fibronectin-binding protein that do not bind to fibronectin; (2) fusion
CC protein containing at least one peptide of a fibronectin-binding protein
CC linked to a second amino acid sequence; (3) nucleic acid encoding the
CC isolated peptide of (1). Antibodies, the isolated peptides of (1) and the
CC nucleic acids are all useful for immunisation (active or passive) and (by
CC inhibiting binding of bacteria to fibronectin) for preventing or treating
CC infection in humans or other animals, particularly by staphylococci or
CC streptococci, e.g. meningitis, otitis media, pneumonia, endocarditis,
CC mastitis in cattle, abortion in horses and many others. Since the
CC antibodies block binding of bacteria, they should be effective against
CC antibiotic-resistant strains, and may replace antibiotic therapy or
CC increase its effectiveness. Sequences AAW65691-700 represent a series of
CC synthetic peptides based on the D1 region of S. aureus fibronectin
CC binding protein A. They were synthesised to contain mutations

Query Match 100.0%; Score 56; DB 2; Length 38;

Best Local Similarity 100.0%; Pred. No. 0.0046;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DFDVSPQIHG 10
| | | | |
DB 29 DFDVSPQIHG 38

RESULT 4
AAW65662
ID AAW65662 standard; peptide; 38 AA.

XX AAW65662;

XX 16-OCT-1998 (first entry)

XX Fibronectin binding protein-derived peptide #6.

XX microbial surface components recognising adhesive matrix molecule;

KW MSCRAMM; fibronectin; fibronectin-binding protein; antibody; epitope;

KW antibiotic; bacterial infection; antibiotic-resistant strain.

XX Synthetic.

OS Staphylococcus aureus.

PN WO981389-A2.

PD 23-JUL-1998.

PF 21-JAN-1998; 98WO-US001222.

XX 21-JAN-1997; 97US-0036139P.

XX (TEXA) UNIV TEXAS A & M SYSTEM.

PI Hoeek M, Patci JM, House-Pompeo KL, Speziale P, Joh D;

PI Mcgavin MJ;

DR WPI; 1998-413816/35.

XX Antibody that binds to fibronectin-binding protein, preventing its

PT binding to fibronectin - used to treat or prevent bacterial infection,

PT especially by Staphylococci and Streptococci.

PS Example 2; Page 92; 201pp; English.

XX The invention relates to antibodies that bind to a fibronectin-binding

CC domain of a fibronectin-binding protein, and inhibit binding of the

CC protein to fibronectin. Also claimed are: (1) isolated peptides of a

CC fibronectin-binding protein that do not bind to fibronectin; (2) fusion

CC protein containing at least one peptide of a fibronectin-binding protein

CC linked to a second amino acid sequence; (3) nucleic acid encoding the

CC isolated peptide of (1). Antibodies, the isolated peptides of (1) and the

CC nucleic acids are all useful for immunisation (active or passive) and (by

CC inhibiting binding of bacteria to fibronectin) for preventing or treating

CC infection in humans or other animals, particularly by staphylococci or

CC streptococci, e.g. meningitis, otitis media, pneumonia, endocarditis,

CC mastitis in cattle, abortion in horses and many others. Since the

CC antibodies block binding of bacteria, they should be effective against

CC antibiotic-resistant strains, and may replace antibiotic therapy or

CC increase its effectiveness. Sequences AAW65659-68 represent synthetic

CC epitopes from the fibronectin binding domains DU and DI-D4 of the S.

CC aureus fmbA gene

XX Sequence 38 AA;

SO Query Match 100.0%; Score 56; DB 2; Length 38;

Best Local Similarity 100.0%; Pred. No. 0.0046;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DFDVSPQIHG 10
| | | | |
DB 29 DFDVSPQIHG 38

RESULT 5
AAW65696
ID AAW65696 standard; peptide; 38 AA.

XX AAW65696;

XX 16-OCT-1998 (first entry)

XX Fibronectin binding protein-derived peptide #40.

XX microbial surface components recognising adhesive matrix molecule;

KW MSCRAMM; fibronectin; fibronectin-binding protein; antibody; epitope;

KW antibiotic; bacterial infection; antibiotic-resistant strain.

XX Synthetic.

OS Staphylococcus aureus.

PN WO981389-A2.

PD 23-JUL-1998.

PF 21-JAN-1998; 98WO-US001222.

XX 21-JAN-1997; 97US-0036139P.

XX (TEXA) UNIV TEXAS A & M SYSTEM.

PI Hoeek M, Patci JM, House-Pompeo KL, Speziale P, Joh D;

PI Mcgavin MJ;

DR WPI; 1998-413816/35.

XX Antibody that binds to fibronectin-binding protein, preventing its

PT binding to fibronectin - used to treat or prevent bacterial infection,

PT especially by Staphylococci and Streptococci.

PS Example 8; Page 102; 201pp; English.

XX The invention relates to antibodies that bind to a fibronectin-binding

CC domain of a fibronectin-binding protein, and inhibit binding of the

CC protein to fibronectin. Also claimed are: (1) isolated peptides of a

CC fibronectin-binding protein that do not bind to fibronectin; (2) fusion

CC protein containing at least one peptide of a fibronectin-binding protein

CC linked to a second amino acid sequence; (3) nucleic acid encoding the

CC isolated peptide of (1). Antibodies, the isolated peptides of (1) and the

CC nucleic acids are all useful for immunisation (active or passive) and (by

CC inhibiting binding of bacteria to fibronectin) for preventing or treating

CC infection in humans or other animals, particularly by staphylococci or

CC streptococci, e.g. meningitis, otitis media, pneumonia, endocarditis,

CC mastitis in cattle, abortion in horses and many others. Since the

CC antibodies block binding of bacteria, they should be effective against

CC antibiotic-resistant strains, and may replace antibiotic therapy or

CC increase its effectiveness. Sequences AAW65691-700 represent a series of

CC synthetic peptides based on the DI region of S. aureus fibronectin

CC binding protein A. They were synthesised to contain mutations

XX Sequence 38 AA;

SO Query Match 100.0%; Score 56; DB 2; Length 38;

Best Local Similarity 100.0%; Pred. No. 0.0046;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DFDVSPQIHG 10
| | | | |
DB 29 DFDVSPQIHG 38

RESULT 6
AAW65697
ID AAW65697 standard; peptide; 38 AA.

```

AC  AAW65697;
XX  16-OCT-1998 (first entry)
XX  Fibronectin binding protein-derived peptide #41.
DE  microbial surface components recognising adhesive matrix molecule;
XX  MSCRAM; fibronectin; fibronectin-binding protein; antibody; epitope;
XX  antibiotic; bacterial infection; antibiotic-resistant strain.
KM  Synthetic.
OS  Staphylococcus aureus.
XX  WO9831389-A2.
XX  23-JUL-1998.
XX  21-JAN-1998; 98WO-US001222.
XX  21-JAN-1997; 97US-0036139P.
XX  (TEXA ) UNIV TEXAS A & M SYSTEM.
XX  Hoeoek M, Patti JM, House-Pompeo KL, Speziale P, Joh D;
XX  Mcgavin MJ;
XX  WPI; 1998-413816/35.
XX  Antibody that binds to fibronectin-binding protein, preventing its
XX  binding to fibronectin - used to treat or prevent bacterial infection,
XX  especially by Staphylococci and Streptococci.
XX  Example 8; Page 102; 201pp; English.
XX  The invention relates to antibodies that bind to a fibronectin-binding
XX  domain of a fibronectin-binding protein, and inhibit binding of the
XX  protein to fibronectin. Also claimed are: (1) isolated peptides of a
XX  fibronectin-binding protein that do not bind to fibronectin; (2) fusion
XX  protein containing at least one peptide of a fibronectin-binding protein
XX  linked to a second amino acid sequence; (3) nucleic acid encoding the
XX  isolated peptide of (1). Antibodies, the isolated peptides of (1) and the
XX  nucleic acids are all useful for immunisation (active or passive) and (by
XX  inhibiting binding of bacteria to fibronectin) for preventing or treating
XX  infection in humans or other animals, particularly by staphylococci or
XX  streptococci, e.g. meningitis, otitis media, pneumonia, endocarditis,
XX  mastitis in cattle, abortion in horses and many others. Since the
XX  antibodies block binding of bacteria, they should be effective against
XX  antibiotic-resistant strains, and may replace antibiotic therapy or
XX  increase its effectiveness. Sequences AAW65691-700 represent a series of
XX  synthetic peptides based on the D1 region of S. aureus fibronectin
XX  binding protein A. They were synthesised to contain mutations
XX  SQ Sequence 38 AA;

Query Match 100.0%; Score 56; DB 2; Length 38;
Best Local Similarity 100.0%; Pred. No. 0.0046;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DFDSVPQIHG 10
   |||||
   |||||
   |||||
   |||||
   |||||
Db 29 DFDSVPQIHG 38

```

```

KM  microbial surface components recognising adhesive matrix molecule;
XX  MSCRAM; fibronectin; fibronectin-binding protein; antibody; epitope;
XX  antibiotic; bacterial infection; antibiotic-resistant strain.
OS  Synthetic.
XX  Staphylococcus aureus.
XX  WO9831389-A2.
XX  23-JUL-1998.
XX  21-JAN-1998; 98WO-US001222.
XX  21-JAN-1997; 97US-0036139P.
XX  (TEXA ) UNIV TEXAS A & M SYSTEM.
XX  Hoeoek M, Patti JM, House-Pompeo KL, Speziale P, Joh D;
XX  Mcgavin MJ;
XX  WPI; 1998-413816/35.
XX  Antibody that binds to fibronectin-binding protein, preventing its
XX  binding to fibronectin - used to treat or prevent bacterial infection,
XX  especially by Staphylococci and Streptococci.
XX  Example 8; Page 102; 201pp; English.
XX  The invention relates to antibodies that bind to a fibronectin-binding
XX  domain of a fibronectin-binding protein, and inhibit binding of the
XX  protein to fibronectin. Also claimed are: (1) isolated peptides of a
XX  fibronectin-binding protein that do not bind to fibronectin; (2) fusion
XX  protein containing at least one peptide of a fibronectin-binding protein
XX  linked to a second amino acid sequence; (3) nucleic acid encoding the
XX  isolated peptide of (1). Antibodies, the isolated peptides of (1) and the
XX  nucleic acids are all useful for immunisation (active or passive) and (by
XX  inhibiting binding of bacteria to fibronectin) for preventing or treating
XX  infection in humans or other animals, particularly by staphylococci or
XX  streptococci, e.g. meningitis, otitis media, pneumonia, endocarditis,
XX  mastitis in cattle, abortion in horses and many others. Since the
XX  antibodies block binding of bacteria, they should be effective against
XX  antibiotic-resistant strains, and may replace antibiotic therapy or
XX  increase its effectiveness. Sequences AAW65691-700 represent a series of
XX  synthetic peptides based on the D1 region of S. aureus fibronectin
XX  binding protein A. They were synthesised to contain mutations
XX  SQ Sequence 38 AA;

Query Match 100.0%; Score 56; DB 2; Length 38;
Best Local Similarity 100.0%; Pred. No. 0.0046;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DFDSVPQIHG 10
   |||||
   |||||
   |||||
   |||||
   |||||
Db 29 DFDSVPQIHG 38

RESULT 8
AAW65700
ID AAW65700 standard; peptide; 38 AA.
XX
XX
XX
XX
XX
AC AAW65700;
XX
XX
XX 16-OCT-1998 (first entry)
XX
XX Fibronectin binding protein-derived peptide #44.
XX
XX microbial surface components recognising adhesive matrix molecule;
XX MSCRAM; fibronectin; fibronectin-binding protein; antibody; epitope;
XX antibiotic; bacterial infection; antibiotic-resistant strain.
XX
XX Synthetic.
XX Staphylococcus aureus.

```

XX WO9831389-A2.
 XX 23-JUL-1998.
 XX
 XX 21-JAN-1998; 98WO-US001222.
 XX 21-JAN-1997; 97US-0036139P.
 XX (TEXA) UNIV TEXAS A & M SYSTEM.
 XX Hoeoek M, Patti JM, House-Pompeo KL, Speziale P, Joh D;
 XX McGavin MJ;
 XX WPI; 1998-413816/35.
 XX
 XX Antibody that binds to fibronectin-binding protein, preventing its
 PT binding to fibronectin - used to treat or prevent bacterial infection,
 PT especially by Staphylococci and Streptococci.
 XX
 XX Example 8; Page 102; 201pp; English.
 XX
 XX The invention relates to antibodies that bind to a fibronectin-binding
 CC domain of a fibronectin-binding protein, and inhibit binding of the
 CC protein to fibronectin. Also claimed are: (1) isolated peptides of a
 CC fibronectin-binding protein that do not bind to fibronectin; (2) fusion
 CC protein containing at least one peptide of a fibronectin-binding protein
 CC linked to a second amino acid sequence; (3) nucleic acid encoding the
 CC isolated peptide of (1). Antibodies, the isolated peptides of (1) and the
 CC nucleic acids are all useful for immunisation (active or passive) and (by
 CC inhibiting binding of bacteria to fibronectin) for preventing or treating
 CC infection in humans or other animals, particularly by staphylococci or
 CC streptococci, e.g. meningitis, otitis media, pneumonia, endocarditis,
 CC mastitis in cattle, abortion in horses and many others. Since the
 CC antibodies block binding of bacteria, they should be effective against
 CC antibiotic-resistant strains, and may replace antibiotic therapy or
 CC increase its effectiveness. Sequences AAW65691-700 represent a series of
 CC synthetic peptides based on the DI region of S. aureus fibronectin
 CC binding protein A. They were synthesised to contain mutations
 XX
 XX Sequence 38 AA;
 SQ
 Query Match 100.0%; Score 56; DB 2; Length 38;
 Best Local Similarity 100.0%; Pred. No. 0.0046;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DFDSVPQIHG 10
 DB 29 DFDSVPQIHG 38
 XX
 XX RESULT 9
 XX AAW65691
 XX ID AAW65691 standard; peptide; 38 AA.
 XX AC AAW65691;
 XX DT 16-OCT-1998 (first entry)
 XX DE Fibronectin binding protein-derived peptide #35.
 XX
 XX microbial surface components recognising adhesive matrix molecule;
 KM MSCRAMM; fibronectin; fibronectin-binding protein; antibody; epitope;
 KM antibiotic; bacterial infection; antibiotic-resistant strain.
 XX
 XX Synthetic.
 OS Staphylococcus aureus.
 XX
 XX WO9831389-A2.
 XX 23-JUL-1998.
 XX 21-JAN-1998; 98WO-US001222.
 XX 21-JAN-1997; 97US-0036139P.
 XX (TEXA) UNIV TEXAS A & M SYSTEM.
 XX Hoeoek M, Patti JM, House-Pompeo KL, Speziale P, Joh D;
 XX McGavin MJ;
 XX WPI; 1998-413816/35.
 XX
 XX Antibody that binds to fibronectin-binding protein, preventing its
 PT binding to fibronectin - used to treat or prevent bacterial infection,
 PT especially by Staphylococci and Streptococci.
 XX
 XX Example 8; Page 101; 201pp; English.
 XX
 XX The invention relates to antibodies that bind to a fibronectin-binding
 CC domain of a fibronectin-binding protein, and inhibit binding of the
 CC protein to fibronectin. Also claimed are: (1) isolated peptides of a
 CC fibronectin-binding protein that do not bind to fibronectin; (2) fusion
 CC protein containing at least one peptide of a fibronectin-binding protein
 CC linked to a second amino acid sequence; (3) nucleic acid encoding the
 CC isolated peptide of (1). Antibodies, the isolated peptides of (1) and the
 CC nucleic acids are all useful for immunisation (active or passive) and (by
 CC inhibiting binding of bacteria to fibronectin) for preventing or treating
 CC infection in humans or other animals, particularly by staphylococci or
 CC streptococci, e.g. meningitis, otitis media, pneumonia, endocarditis,
 CC mastitis in cattle, abortion in horses and many others. Since the
 CC antibodies block binding of bacteria, they should be effective against
 CC antibiotic-resistant strains, and may replace antibiotic therapy or
 CC increase its effectiveness. Sequences AAW65691-700 represent a series of
 CC synthetic peptides based on the DI region of S. aureus fibronectin
 CC binding protein A. They were synthesised to contain mutations
 XX
 XX Sequence 38 AA;
 SQ
 Query Match 100.0%; Score 56; DB 2; Length 38;
 Best Local Similarity 100.0%; Pred. No. 0.0046;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DFDSVPQIHG 10
 DB 29 DFDSVPQIHG 38
 XX
 XX RESULT 10
 XX AAW65699
 XX ID AAW65699 standard; peptide; 38 AA.
 XX AC AAW65699;
 XX DT 16-OCT-1998 (first entry)
 XX DE Fibronectin binding protein-derived peptide #43.
 XX
 XX microbial surface components recognising adhesive matrix molecule;
 KM MSCRAMM; fibronectin; fibronectin-binding protein; antibody; epitope;
 KM antibiotic; bacterial infection; antibiotic-resistant strain.
 XX
 XX Synthetic.
 OS Staphylococcus aureus.
 XX
 XX WO9831389-A2.
 XX 23-JUL-1998.
 XX 21-JAN-1998; 98WO-US001222.
 XX 21-JAN-1997; 97US-0036139P.
 XX (TEXA) UNIV TEXAS A & M SYSTEM.
 XX Hoeoek M, Patti JM, House-Pompeo KL, Speziale P, Joh D;

XX 21-JAN-1997; 97US-0036139P.
 XX (TEXA) UNIV TEXAS A & M SYSTEM.
 XX Hoeoek M, Patti JM, House-Pompeo KL, Speziale P, Joh D;
 XX McGavin MJ;
 XX WPI; 1998-413816/35.
 XX
 XX Antibody that binds to fibronectin-binding protein, preventing its
 PT binding to fibronectin - used to treat or prevent bacterial infection,
 PT especially by Staphylococci and Streptococci.
 XX
 XX Example 8; Page 101; 201pp; English.
 XX
 XX The invention relates to antibodies that bind to a fibronectin-binding
 CC domain of a fibronectin-binding protein, and inhibit binding of the
 CC protein to fibronectin. Also claimed are: (1) isolated peptides of a
 CC fibronectin-binding protein that do not bind to fibronectin; (2) fusion
 CC protein containing at least one peptide of a fibronectin-binding protein
 CC linked to a second amino acid sequence; (3) nucleic acid encoding the
 CC isolated peptide of (1). Antibodies, the isolated peptides of (1) and the
 CC nucleic acids are all useful for immunisation (active or passive) and (by
 CC inhibiting binding of bacteria to fibronectin) for preventing or treating
 CC infection in humans or other animals, particularly by staphylococci or
 CC streptococci, e.g. meningitis, otitis media, pneumonia, endocarditis,
 CC mastitis in cattle, abortion in horses and many others. Since the
 CC antibodies block binding of bacteria, they should be effective against
 CC antibiotic-resistant strains, and may replace antibiotic therapy or
 CC increase its effectiveness. Sequences AAW65691-700 represent a series of
 CC synthetic peptides based on the DI region of S. aureus fibronectin
 CC binding protein A. They were synthesised to contain mutations
 XX
 XX Sequence 38 AA;
 SQ
 Query Match 100.0%; Score 56; DB 2; Length 38;
 Best Local Similarity 100.0%; Pred. No. 0.0046;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DFDSVPQIHG 10
 DB 29 DFDSVPQIHG 38
 XX
 XX RESULT 10
 XX AAW65699
 XX ID AAW65699 standard; peptide; 38 AA.
 XX AC AAW65699;
 XX DT 16-OCT-1998 (first entry)
 XX DE Fibronectin binding protein-derived peptide #43.
 XX
 XX microbial surface components recognising adhesive matrix molecule;
 KM MSCRAMM; fibronectin; fibronectin-binding protein; antibody; epitope;
 KM antibiotic; bacterial infection; antibiotic-resistant strain.
 XX
 XX Synthetic.
 OS Staphylococcus aureus.
 XX
 XX WO9831389-A2.
 XX 23-JUL-1998.
 XX 21-JAN-1998; 98WO-US001222.
 XX 21-JAN-1997; 97US-0036139P.
 XX (TEXA) UNIV TEXAS A & M SYSTEM.
 XX Hoeoek M, Patti JM, House-Pompeo KL, Speziale P, Joh D;

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PI   Mcgavin MJ;
XX
XX   WPI, 1998-413816/35.
DR
XX   Antibody that binds to fibronectin-binding protein, preventing its
XX   binding to fibronectin - used to treat or prevent bacterial infection,
XX   especially by Staphylococci and Streptococci.
XX
XX   Example 8; Page 102; 201pp; English.
XX
XX   The invention relates to antibodies that bind to a fibronectin-binding
XX   domain of a fibronectin-binding protein, and inhibit binding of the
XX   protein to fibronectin. Also claimed are: (1) isolated peptides of a
XX   fibronectin-binding protein that do not bind to fibronectin; (2) fusion
XX   protein containing at least one peptide of a fibronectin-binding protein
XX   linked to a second amino acid sequence; (3) nucleic acid encoding the
XX   isolated peptide of (1). Antibodies, the isolated peptides of (1) and the
XX   nucleic acids are all useful for immunisation (active or passive) and (by
XX   inhibiting binding of bacteria to fibronectin) for preventing or treating
XX   infection in humans or other animals, particularly by staphylococci or
XX   streptococci, e.g. meningitis, otitis media, pneumonia, endocarditis,
XX   mastitis in cattle, abortion in horses and many others. Since the
XX   antibodies block binding of bacteria, they should be effective against
XX   antibiotic-resistant strains, and may replace antibiotic therapy or
XX   increase its effectiveness. Sequences AAW65691-700 represent a series of
XX   synthetic peptides based on the D1 region of S. aureus fibronectin
XX   binding protein A. They were synthesised to contain mutations
XX
XX   Sequence 38 AA;
SQ
XX
XX   Query Match          100.0%; Score 56; DB 2; Length 38;
XX   Best Local Similarity 100.0%; Pred. No. 0.0046;
XX   Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
OY   1 DFDSVPQIHG 10
XX   |||||
XX   29 DFDSVPQIHG 38
DB
XX
XX   RESULT 11
XX   ID AAW65661 standard; peptide; 38 AA.
XX
XX   AAW65661;
XX
XX   16-OCT-1998 (first entry)
XX
XX   Fibronectin binding protein-derived peptide #5.
XX
XX   microbial surface components recognising adhesive matrix molecule;
XX   MSCRAMM; fibronectin; fibronectin-binding protein; antibody; epitope;
XX   antibiotic; bacterial infection; antibiotic-resistant strain.
XX
XX   Synthetic.
XX   Staphylococcus aureus.
XX
XX   WO9831389-A2.
XX
XX   23-JUL-1998.
XX
XX   21-JAN-1998; 98WO-US001222.
XX
XX   21-JAN-1997; 97US-0036139P.
XX
XX   (TEXA ) UNIV TEXAS A & M SYSTEM.
XX
XX   Hoeek M, Patti JM, House-Pompeo KL, Speziale P, Joh D;
XX   Mcgavin MJ;
XX
XX   WPI, 1998-413816/35.
XX
XX   Antibody that binds to fibronectin-binding protein, preventing its
XX   binding to fibronectin - used to treat or prevent bacterial infection,

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PT   especially by Staphylococci and Streptococci.
XX
XX   Example 2; Page 92; 201pp; English.
XX
XX   The invention relates to antibodies that bind to a fibronectin-binding
XX   domain of a fibronectin-binding protein, and inhibit binding of the
XX   protein to fibronectin. Also claimed are: (1) isolated peptides of a
XX   fibronectin-binding protein that do not bind to fibronectin; (2) fusion
XX   protein containing at least one peptide of a fibronectin-binding protein
XX   linked to a second amino acid sequence; (3) nucleic acid encoding the
XX   isolated peptide of (1). Antibodies, the isolated peptides of (1) and the
XX   nucleic acids are all useful for immunisation (active or passive) and (by
XX   inhibiting binding of bacteria to fibronectin) for preventing or treating
XX   infection in humans or other animals, particularly by staphylococci or
XX   streptococci, e.g. meningitis, otitis media, pneumonia, endocarditis,
XX   mastitis in cattle, abortion in horses and many others. Since the
XX   antibodies block binding of bacteria, they should be effective against
XX   antibiotic-resistant strains, and may replace antibiotic therapy or
XX   increase its effectiveness. Sequences AAW65659-68 represent synthetic
XX   epitopes from the fibronectin binding domains DU and D1-D4 of the S.
XX   aureus fnbA gene
XX
XX   Sequence 38 AA;
SQ
XX
XX   Query Match          100.0%; Score 56; DB 2; Length 38;
XX   Best Local Similarity 100.0%; Pred. No. 0.0046;
XX   Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
OY   1 DFDSVPQIHG 10
XX   |||||
XX   29 DFDSVPQIHG 38
DB
XX
XX   RESULT 12
XX   ID AAW65693 standard; peptide; 38 AA.
XX
XX   AAW65693;
XX
XX   16-OCT-1998 (first entry)
XX
XX   Fibronectin binding protein-derived peptide #37.
XX
XX   microbial surface components recognising adhesive matrix molecule;
XX   MSCRAMM; fibronectin; fibronectin-binding protein; antibody; epitope;
XX   antibiotic; bacterial infection; antibiotic-resistant strain.
XX
XX   Synthetic.
XX   Staphylococcus aureus.
XX
XX   WO9831389-A2.
XX
XX   23-JUL-1998.
XX
XX   21-JAN-1998; 98WO-US001222.
XX
XX   21-JAN-1997; 97US-0036139P.
XX
XX   (TEXA ) UNIV TEXAS A & M SYSTEM.
XX
XX   Hoeek M, Patti JM, House-Pompeo KL, Speziale P, Joh D;
XX   Mcgavin MJ;
XX
XX   WPI, 1998-413816/35.
XX
XX   Antibody that binds to fibronectin-binding protein, preventing its
XX   binding to fibronectin - used to treat or prevent bacterial infection,
XX   especially by Staphylococci and Streptococci.
XX
XX   Example 8; Page 102; 201pp; English.
XX
XX   The invention relates to antibodies that bind to a fibronectin-binding
XX   domain of a fibronectin-binding protein, and inhibit binding of the

```

CC protein to fibronectin. Also claimed are: (1) isolated peptides of a
 CC fibronectin-binding protein that do not bind to fibronectin; (2) fusion
 CC protein containing at least one peptide of a fibronectin-binding protein
 CC linked to a second amino acid sequence; (3) nucleic acid encoding the
 CC isolated peptide of (1). Antibodies, the isolated peptides of (1) and the
 CC nucleic acids are all useful for immunisation (active or passive) and (by
 CC inhibiting binding of bacteria to fibronectin) for preventing or treating
 CC infection in humans or other animals, particularly by staphylococci or
 CC streptococci, e.g. meningitis, otitis media, pneumonia, endocarditis,
 CC mastitis in cattle, abortion in horses and many others. Since the
 CC antibodies block binding of bacteria, they should be effective against
 CC antibiotic-resistant strains, and may replace antibiotic therapy or
 CC increase its effectiveness. Sequences AAW65691-700 represent a series of
 CC synthetic peptides based on the D1 region of S. aureus fibronectin
 CC binding protein A. They were synthesised to contain mutations

XX SQ Sequence 38 AA;

Query Match 100.0%; Score 56; DB 2; Length 38;

Best Local Similarity 100.0%; Pred. No. 0.0046; Mismatches 0; Indels 0; Gaps 0;

QY 1 DFDSVPQIHG 10

DB 29 DFDSVPQIHG 38

RESULT 13

AAW65698 AAW65698 standard; peptide; 38 AA.

XX AAW65698;

DT 16-OCT-1998 (first entry)

DE Fibronectin binding protein-derived peptide #42.

XX microbial surface components recognising adhesive matrix molecule;

KW MSCRAMM; fibronectin; fibronectin-binding protein; antibody; epitope;

XX antibiotic; bacterial infection; antibiotic-resistant strain.

OS Synthetic.

XX Staphylococcus aureus.

PN WO9831389-A2.

XX 23-UTL-1998.

PF 21-JAN-1998; 98WO-US001222.

XX 21-JAN-1997; 97US-0036139P.

PA (TEXA) UNIV TEXAS A & M SYSTEM.

PI Hoecek M, Patli JM, House-Pompeo KL, Speciale P, Joh D;

XX Mcgavin MJ;

DR WPI; 1998-413816/35.

XX Antibody that binds to fibronectin-binding protein, preventing its

PT binding to fibronectin - used to treat or prevent bacterial infection,

PT especially by Staphylococci and Streptococci.

XX Example 8; Page 102; 201pp; English.

XX The invention relates to antibodies that bind to a fibronectin-binding

CC domain of a fibronectin-binding protein, and inhibit binding of the

CC protein to fibronectin. Also claimed are: (1) isolated peptides of a

CC fibronectin-binding protein that do not bind to fibronectin; (2) fusion

CC protein containing at least one peptide of a fibronectin-binding protein

CC linked to a second amino acid sequence; (3) nucleic acid encoding the

CC isolated peptide of (1). Antibodies, the isolated peptides of (1) and the

CC nucleic acids are all useful for immunisation (active or passive) and (by

CC inhibiting binding of bacteria to fibronectin) for preventing or treating
 CC infection in humans or other animals, particularly by staphylococci or
 CC streptococci, e.g. meningitis, otitis media, pneumonia, endocarditis,
 CC mastitis in cattle, abortion in horses and many others. Since the
 CC antibodies block binding of bacteria, they should be effective against
 CC antibiotic-resistant strains, and may replace antibiotic therapy or
 CC increase its effectiveness. Sequences AAW65691-700 represent a series of
 CC synthetic peptides based on the D1 region of S. aureus fibronectin
 CC binding protein A. They were synthesised to contain mutations

XX SQ Sequence 38 AA;

Query Match 100.0%; Score 56; DB 2; Length 38;

Best Local Similarity 100.0%; Pred. No. 0.0046; Mismatches 0; Indels 0; Gaps 0;

QY 1 DFDSVPQIHG 10

DB 29 DFDSVPQIHG 38

RESULT 14

AAR90937 AAR90937 standard; peptide; 113 AA.

XX AAR90937;

DT 23-SEP-1996 (first entry)

DE D3D4 polypeptide #1.

XX Fibronectin binding protein; Fbp; S.aureus J2385; monoclonal antibody;

KW infection; surgical implant; antiaherent agent; hygiene; adhesion;

XX extracellular matrix protein; oral patchogen; oral cavity.

XX Staphylococcus aureus.

XX Key Location/Qualifiers

FT Region 1..21

FT /note= "D1 region fragment"

FT Region 22..59

FT /note= "D2 region"

FT Region 60..98

FT /note= "D3 region"

FT Region 99..113

FT /note= "D4 region"

FT Misc-difference 113

FT /note= "P113T"

XX WO9604381-A1.

XX 15-FEB-1996.

PF 28-UTL-1995; 95WO-EP003040.

XX 05-AUG-1994; 94GB-00015900.

XX (SMIK) SMITHKLINE BEECHAM PLC.

XX Crichtley IA, Dodd I, Barnett P, Mcday DL;

XX WPI; 1996-129397/13.

XX Polypeptide(s) derived from Staphylococcus aureus fibronectin binding

PT protein - inhibit binding of bacteria to extracellular matrix proteins,

PT for combating infection at the site of wounds and surgical implants, and

PT in oral hygiene.

XX Claim 6; Page 24; 35pp; English.

XX AAR90937-R90942 represent D3D4 polypeptides. These sequences correspond

CC to fragments of the Staphylococcus aureus fibronectin binding protein

CC (Fbp). This sequence corresponds to residues 18-130 of S.aureus J2385

CC Fbp, and also contains the D2 region, and a portion of the D1 region.
 CC These sequences, and monoclonal antibodies against them can be used to
 CC combat infection at the site of wounds, surgical implants and other in-
 CC dwelling devices (such as catheters), and as antiadherent agents in oral
 CC hygiene. They can also be used in the manufacture of a medicament for the
 CC prevention of adhesion of bacteria to extracellular matrix proteins
 CC present on in-dwelling devices or in wounds, or of oral pathogens to
 CC similar proteins on surfaces in the oral cavity

XX
 SQ Sequence 113 AA;

Query Match 100.0%; Score 56; DB 2; Length 113;
 Best Local Similarity 100.0%; Pred. No. 0.015;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DFDSVPQIHG 10
 |||||
 Db 13 DFDSVPQIHG 22

RESULT 15

AAR58806 AAR58806 standard; protein; 130 AA.

XX
 AC AAR58806;

XX
 DT 25-MAR-2003 (revised)

DT 30-MAR-1995 (first entry)

XX Fibronectin binding domain D1-D4(709-838(P838T)).

XX Fibronectin binding protein; Fbp; fibronectin binding domain;

KM monoclonal antibody; MAb; adhesion; Gram-positive bacterium; bacteremia;

KM Escherichia coli.

XX Staphylococcus aureus.

OS W09418327-A1.

XX 18-AUG-1994.

XX 04-FEB-1994; 94WO-GB000215.

XX 05-FEB-1993; 93GB-00002289.

XX 20-OCT-1993; 93GB-00021592.

XX (SMIK) SMITHKLINE BEECHAM PLC.

PI Burnham MKR, Chopra I, Critchley IA, Knowles DJC;

XX WPI; 1994-279748/34.

XX Fibronectin binding protein and monoclonal antibodies specific for Fbp -

PT useful to prevent adherence of Gram-positive bacteria to indwelling

XX devices or wounds.

XX Disclosure; Page 30; 40pp; English.

XX Polypeptides corresponding to residues G709-T886 plus PPIVPT, G709-

CC P838(P838T) and G709-P838 (AAR58805-07, respectively) of S. aureus J2385

CC (NCIMB 40532) Fbp type A fibronectin binding domain D1-D4 region

CC (AAR58808) were expressed in E. coli BL21(DE4) and used to raise Mabs

XX specific for Fbp. (Updated on 25-MAR-2003 to correct PN field.)

XX
 SQ Sequence 130 AA;

Search completed: October 25, 2005, 20:58:44
 UOB time : 63.2 secs

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OM protein - protein search, using sw model

Run on: October 22, 2005, 05:46:56 ; Search time 17.3 Seconds
(without alignments)
43.150 Million cell updates/sec

Title: US-10-731-238-77

Perfect score: 56

Sequence: 1 DFDVYPQIHG 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents, AA:*

- 1: /cgn2_6/prodata/1/1aa/5A_COMB.pep:*
- 2: /cgn2_6/prodata/1/1aa/5B_COMB.pep:*
- 3: /cgn2_6/prodata/1/1aa/5A_COMB.pep:*
- 4: /cgn2_6/prodata/1/1aa/5B_COMB.pep:*
- 5: /cgn2_6/prodata/1/1aa/5A_COMB.pep:*
- 6: /cgn2_6/prodata/1/1aa/5B_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	56	100.0	10	4	US-09-010-317-77
2	56	100.0	38	1	US-08-234-622A-2
3	56	100.0	38	4	US-09-010-317-5
4	56	100.0	38	4	US-09-010-317-6
5	56	100.0	38	4	US-09-010-317-35
6	56	100.0	38	4	US-09-010-317-36
7	56	100.0	38	4	US-09-010-317-37
8	56	100.0	38	4	US-09-010-317-38
9	56	100.0	38	4	US-09-010-317-39
10	56	100.0	38	4	US-09-010-317-40
11	56	100.0	38	4	US-09-010-317-41
12	56	100.0	38	4	US-09-010-317-42
13	56	100.0	38	4	US-09-010-317-43
14	56	100.0	38	4	US-09-010-317-44
15	56	100.0	114	1	US-08-259-000-3
16	56	100.0	130	2	US-08-459-135A-7
17	56	100.0	130	2	US-08-459-135A-8
18	56	100.0	130	3	US-08-495-559-7
19	56	100.0	130	3	US-08-495-559-8
20	56	100.0	139	3	US-08-856-253-8
21	56	100.0	174	2	US-08-459-135A-10
22	56	100.0	174	2	US-08-459-135A-13
23	56	100.0	174	3	US-08-495-559-10
24	56	100.0	174	3	US-08-495-559-13
25	56	100.0	176	3	US-08-495-559-6
26	56	100.0	178	2	US-08-459-135A-12
27	56	100.0	178	3	US-08-495-559-12

28	56	100.0	181	2	US-08-459-135A-6	Sequence 6, App1
29	56	100.0	559	4	US-08-956-171E-5251	Sequence 5251, Ap
30	56	100.0	559	4	US-08-781-986A-5251	Sequence 5251, Ap
31	56	100.0	1027	4	US-08-956-171E-5254	Sequence 5254, Ap
32	56	100.0	1027	4	US-08-781-986A-5254	Sequence 5254, Ap
33	51	91.1	36	4	US-09-010-317-58	Sequence 58, App1
34	51	91.1	36	4	US-09-010-317-59	Sequence 59, App1
35	51	91.1	38	1	US-08-234-622A-3	Sequence 3, App1
36	51	91.1	38	4	US-09-010-317-7	Sequence 7, App1
37	51	91.1	38	4	US-09-010-317-8	Sequence 8, App1
38	51	91.1	38	4	US-09-010-317-45	Sequence 45, App1
39	51	91.1	38	4	US-09-010-317-46	Sequence 46, App1
40	51	91.1	38	4	US-09-010-317-47	Sequence 47, App1
41	51	91.1	38	4	US-09-010-317-48	Sequence 48, App1
42	51	91.1	38	4	US-09-010-317-49	Sequence 49, App1
43	51	91.1	38	4	US-09-010-317-50	Sequence 50, App1
44	50	89.3	38	1	US-08-729-767-3	Sequence 3, App1
45	45.5	81.2	39	4	US-09-010-317-56	Sequence 56, App1

ALIGNMENTS

RESULT 1
US-09-010-317-77
Sequence 77, Application US/09010317
Patent No. 6685943
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
APPLICANT: Patti, Joseph M.
APPLICANT: House-Pompeo, Karen L.
APPLICANT: Speziale, Pietro
APPLICANT: Jon, Danny
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
TITLE OF INVENTION: AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAMK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 77:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-09-010-317-77
Query Match 100.0%; Score 56; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.00045;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DFDVPOIHG 10
|||||

Db 1 DFDVPOIHG 10

RESULT 2
US-08-234-622A-2

; Sequence 2, Application US/08234622A
; Patent No. 5440014

; GENERAL INFORMATION:

; APPLICANT: HOOK, Magnus

; APPLICANT: MCGAVIN, Martin

; APPLICANT: RAUCCI, Giuseppe

; TITLE OF INVENTION: A FIBRONECTIN BINDING PEPTIDE

; NUMBER OF SEQUENCES: 4

; CORRESPONDENCE ADDRESS:

; ADDRESSES: Burns, Doane, Swecker & Mathis

; STREET: P.O. Box 1404

; CITY: Alexandria

; STATE: Virginia

; COUNTRY: United States

; ZIP: 22113-1404

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; OPERATING SYSTEM: IBM PC compatible

; SOFTWARE: Patent Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/234,622A

; FILING DATE: 28-APR-1994

; CLASSIFICATION: 530

; PRIORITY APPLICATION DATA:

; APPLICATION NUMBER: SE 9002617-0

; FILING DATE: 10-AUG-1990

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: WO PCT/SE91/00534

; FILING DATE: 09-AUG-1991

; ATTORNEY/AGENT INFORMATION:

; NAME: Meuth, Donna M

; REGISTRATION NUMBER: 36, 607

; REFERENCE/DOCKET NUMBER: 012885-044

; TELEPHONE: (703) 836-6620

; TELEFAX: (703) 836-2021

; INFORMATION FOR SEQ ID NO: 2:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 38 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

; US-08-234-622A-2

Query Match 100.0%; Score 56; DB 1; Length 38;

Best Local Similarity 100.0%; Pred. No. 0.0019;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DFDVPOIHG 10
|||||

Db 29 DFDVPOIHG 38

RESULT 3
US-09-010-317-5

; Sequence 5, Application US/09010317

; Patent No. 6685943

; GENERAL INFORMATION:

; APPLICANT: HOOK, Magnus

; APPLICANT: Patti, Joseph M.

; APPLICANT: House-Pompeo, Karen L.

; APPLICANT: Speziale, Pietro

APPLICANT: Joh, Danny
APPLICANT: McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
TITLE OF INVENTION: AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:

ADDRESSES: Arnold, White & Durkee

STREET: P.O. Box 4433

CITY: Houston

STATE: TX

COUNTRY: USA

ZIP: 77210-4433

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/010,317

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 60/036,139

FILING DATE: 21-JAN-1997

ATTORNEY/AGENT INFORMATION:

NAME: Hibler, David W.

REGISTRATION NUMBER: 41, 071

REFERENCE/DOCKET NUMBER: TMK.189

TELEPHONE: 512-418-3000

TELEFAX: 512-474-7577

INFORMATION FOR SEQ ID NO: 5:

SEQUENCE CHARACTERISTICS:

LENGTH: 38 amino acids

TYPE: amino acid

STRANDEDNESS:

TOPOLOGY: linear

US-09-010-317-5

Query Match 100.0%; Score 56; DB 4; Length 38;

Best Local Similarity 100.0%; Pred. No. 0.0019;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DFDVPOIHG 10
|||||

Db 29 DFDVPOIHG 38

RESULT 4
US-09-010-317-6

; Sequence 6, Application US/09010317

; Patent No. 6685943

; GENERAL INFORMATION:

; APPLICANT: HOOK, Magnus

; APPLICANT: Patti, Joseph M.

; APPLICANT: House-Pompeo, Karen L.

; APPLICANT: Speziale, Pietro

; APPLICANT: Joh, Danny

; APPLICANT: McGavin, Martin J.

; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS

; TITLE OF INVENTION: AND METHODS OF USE

; NUMBER OF SEQUENCES: 105

; CORRESPONDENCE ADDRESS:

; ADDRESSES: Arnold, White & Durkee

; STREET: P.O. Box 4433

; CITY: Houston

; STATE: TX

; COUNTRY: USA

; ZIP: 77210-4433

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

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/
/   SOFTWARE: Patentin Release #1.0, Version #1.30
/   CURRENT APPLICATION DATA:
/   APPLICATION NUMBER: US/09/010,317
/   FILING DATE:
/   CLASSIFICATION:
/   PRIOR APPLICATION DATA:
/   APPLICATION NUMBER: US 60/036,139
/   FILING DATE: 21-JAN-1997
/   ATTORNEY/AGENT INFORMATION:
/   NAME: Hibler, David W.
/   REGISTRATION NUMBER: 41,071
/   REFERENCE/DOCKET NUMBER: TAMK:189
/   TELECOMMUNICATION INFORMATION:
/   TELEPHONE: 512-418-3000
/   TELEFAX: 512-474-7577
/   INFORMATION FOR SEQ ID NO: 6:
/   SEQUENCE CHARACTERISTICS:
/   LENGTH: 38 amino acids
/   TYPE: amino acid
/   STRANDEDNESS:
/   TOPOLOGY: linear
/
US-09-010-317-6

Query Match          100.0%; Score 56; DB 4; Length 38;
Best Local Similarity 100.0%; Pred. No. 0.0019;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DFDSVPQIHG 10
DB 29 DFDSVPQIHG 38

RESULT 5
US-09-010-317-35
/   Sequence 35, Application US/09010317
/   Patent No. 6685943
/   GENERAL INFORMATION:
/   APPLICANT: Hook, Magnus
/   APPLICANT: Patti, Joseph M.
/   APPLICANT: House-Pompeo, Karen L.
/   APPLICANT: Speziale, Pietro
/   APPLICANT: John, Danny
/   APPLICANT: McGavin, Martin J.
/   TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
/   NUMBER OF SEQUENCES: 105
/   CORRESPONDENCE ADDRESS:
/   ADDRESSEE: Arnold, White & Durkee
/   STREET: P.O. Box 4433
/   CITY: Houston
/   STATE: TX
/   COUNTRY: USA
/   ZIP: 77210-4433
/   COMPUTER READABLE FORM:
/   MEDIUM TYPE: Floppy disk
/   COMPUTER: IBM PC compatible
/   OPERATING SYSTEM: PC-DOS/MS-DOS
/   SOFTWARE: Patentin Release #1.0, Version #1.30
/   CURRENT APPLICATION DATA:
/   APPLICATION NUMBER: US/09/010,317
/   FILING DATE:
/   CLASSIFICATION:
/   PRIOR APPLICATION DATA:
/   APPLICATION NUMBER: US 60/036,139
/   FILING DATE: 21-JAN-1997
/   ATTORNEY/AGENT INFORMATION:
/   NAME: Hibler, David W.
/   REGISTRATION NUMBER: 41,071
/   REFERENCE/DOCKET NUMBER: TAMK:189
/   TELECOMMUNICATION INFORMATION:
/   TELEPHONE: 512-418-3000
/   TELEFAX: 512-474-7577
/   INFORMATION FOR SEQ ID NO: 35:
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/
/   SEQUENCE CHARACTERISTICS:
/   LENGTH: 38 amino acids
/   TYPE: amino acid
/   STRANDEDNESS:
/   TOPOLOGY: linear
/
US-09-010-317-35

Query Match          100.0%; Score 56; DB 4; Length 38;
Best Local Similarity 100.0%; Pred. No. 0.0019;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DFDSVPQIHG 10
DB 29 DFDSVPQIHG 38

RESULT 6
US-09-010-317-36
/   Sequence 36, Application US/09010317
/   Patent No. 6685943
/   GENERAL INFORMATION:
/   APPLICANT: Hook, Magnus
/   APPLICANT: Patti, Joseph M.
/   APPLICANT: House-Pompeo, Karen L.
/   APPLICANT: Speziale, Pietro
/   APPLICANT: John, Danny
/   APPLICANT: McGavin, Martin J.
/   TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
/   NUMBER OF SEQUENCES: 105
/   CORRESPONDENCE ADDRESS:
/   ADDRESSEE: Arnold, White & Durkee
/   STREET: P.O. Box 4433
/   CITY: Houston
/   STATE: TX
/   COUNTRY: USA
/   ZIP: 77210-4433
/   COMPUTER READABLE FORM:
/   MEDIUM TYPE: Floppy disk
/   COMPUTER: IBM PC compatible
/   OPERATING SYSTEM: PC-DOS/MS-DOS
/   SOFTWARE: Patentin Release #1.0, Version #1.30
/   CURRENT APPLICATION DATA:
/   APPLICATION NUMBER: US/09/010,317
/   FILING DATE:
/   CLASSIFICATION:
/   PRIOR APPLICATION DATA:
/   APPLICATION NUMBER: US 60/036,139
/   FILING DATE: 21-JAN-1997
/   ATTORNEY/AGENT INFORMATION:
/   NAME: Hibler, David W.
/   REGISTRATION NUMBER: 41,071
/   REFERENCE/DOCKET NUMBER: TAMK:189
/   TELECOMMUNICATION INFORMATION:
/   TELEPHONE: 512-418-3000
/   TELEFAX: 512-474-7577
/   INFORMATION FOR SEQ ID NO: 36:
/   SEQUENCE CHARACTERISTICS:
/   LENGTH: 38 amino acids
/   TYPE: amino acid
/   STRANDEDNESS:
/   TOPOLOGY: linear
/
US-09-010-317-36

Query Match          100.0%; Score 56; DB 4; Length 38;
Best Local Similarity 100.0%; Pred. No. 0.0019;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DFDSVPQIHG 10
DB 29 DFDSVPQIHG 38
```

RESULT 7
US-09-010-317-37
Sequence 37, Application US/09010317
Patent No. 6685943
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
APPLICANT: Patil, Joseph M.
APPLICANT: House-Pompeo, Karen L.
APPLICANT: Speziale, Pietro
APPLICANT: Jch, Danny
APPLICANT: McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
TITLE OF INVENTION: AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TANK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 37:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-09-010-317-37
Query Match 100.0%; Score 56; DB 4; Length 38;
Best Local Similarity 100.0%; Pred. No. 0.0019;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 DFDSPVQIHG 10
Db 29 DFDSPVQIHG 38
RESULT 8
US-09-010-317-38
Sequence 38, Application US/09010317
Patent No. 6685943
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
APPLICANT: Patil, Joseph M.
APPLICANT: House-Pompeo, Karen L.
APPLICANT: Speziale, Pietro
APPLICANT: Jch, Danny
APPLICANT: McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
TITLE OF INVENTION: AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Arnold, White & Durkee

STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TANK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 38:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-09-010-317-38
Query Match 100.0%; Score 56; DB 4; Length 38;
Best Local Similarity 100.0%; Pred. No. 0.0019;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 DFDSPVQIHG 10
Db 29 DFDSPVQIHG 38
RESULT 9
US-09-010-317-39
Sequence 39, Application US/09010317
Patent No. 6685943
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
APPLICANT: Patil, Joseph M.
APPLICANT: House-Pompeo, Karen L.
APPLICANT: Speziale, Pietro
APPLICANT: Jch, Danny
APPLICANT: McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
TITLE OF INVENTION: AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/036,139

FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TANK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 39:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-09-010-317-39

Query Match 100.0%; Score 56; DB 4; Length 38;
Best Local Similarity 100.0%; Pred. No. 0.0019;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DFDSVPQING 10
|||||
Db 29 DFDSVPQING 38

RESULT 10
US-09-010-317-40
Sequence 40, Application US/09010317
Patent No. 6685943
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
APPLICANT: Patti, Joseph M.
APPLICANT: House-Pompeo, Karen L.
APPLICANT: Speziale, Pietro
APPLICANT: Joh, Danny
APPLICANT: Mcgavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TANK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 40:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-09-010-317-40

Query Match 100.0%; Score 56; DB 4; Length 38;
Best Local Similarity 100.0%; Pred. No. 0.0019;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DFDSVPQING 10
|||||
Db 29 DFDSVPQING 38

RESULT 11
US-09-010-317-41
Sequence 41, Application US/09010317
Patent No. 6685943
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
APPLICANT: Patti, Joseph M.
APPLICANT: House-Pompeo, Karen L.
APPLICANT: Speziale, Pietro
APPLICANT: Joh, Danny
APPLICANT: Mcgavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TANK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 41:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-09-010-317-41

Query Match 100.0%; Score 56; DB 4; Length 38;
Best Local Similarity 100.0%; Pred. No. 0.0019;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DFDSVPQING 10
|||||
Db 29 DFDSVPQING 38

RESULT 12
US-09-010-317-42
Sequence 42, Application US/09010317
Patent No. 6685943
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
APPLICANT: Patti, Joseph M.

APPLICANT: House-Pompeo, Karen L.
APPLICANT: Speziale, Pietro
APPLICANT: Joh, Danny
APPLICANT: McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
TITLE OF INVENTION: AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TANK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 42:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-09-010-317-42
Query Match 100.0%; Score 56; DB 4; Length 38;
Best Local Similarity 100.0%; Pred. No. 0.0019;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 DFDSVPQIHG 10
Db 29 DFDSVPQIHG 38
RESULT 13
US-09-010-317-43
Sequence 43, Application US/09010317
Patent No. 6685943
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
APPLICANT: Patti, Joseph M.
APPLICANT: House-Pompeo, Karen L.
APPLICANT: Speziale, Pietro
APPLICANT: Joh, Danny
APPLICANT: McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
TITLE OF INVENTION: AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TANK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 43:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-09-010-317-43
Query Match 100.0%; Score 56; DB 4; Length 38;
Best Local Similarity 100.0%; Pred. No. 0.0019;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 DFDSVPQIHG 10
Db 29 DFDSVPQIHG 38
RESULT 14
US-09-010-317-44
Sequence 44, Application US/09010317
Patent No. 6685943
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
APPLICANT: Patti, Joseph M.
APPLICANT: House-Pompeo, Karen L.
APPLICANT: Speziale, Pietro
APPLICANT: Joh, Danny
APPLICANT: McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
TITLE OF INVENTION: AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TANK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000

Search completed: October 22, 2005, 07:41:43
Job time : 18.35 secs

TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 44:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-09-010-317-44

Query Match 100.0%; Score 56; DB 4; Length 38;
Best Local Similarity 100.0%; Pred. No. 0.0019;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DFDSVPOIHG 10
|||
Db 29 DFDSVPOIHG 38

RESULT 15
US-08-259-000-3
Sequence 3, Application US/08259000
Patent No. 5571514
GENERAL INFORMATION:
APPLICANT: HOOK, Magnus
APPLICANT: LINDBERG, Martin Kjell
APPLICANT: SIGNAS, Lars Christer
APPLICANT: MADSTROM, Torkel Mikael
APPLICANT: FROMAN, Gunnar
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN AS WELL AS
NUMBER OF INVENTION: ITS PREPARATION
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Burns, Doane, Swecker & Mathis
STREET: P.O. Box 1404
CITY: Alexandria
STATE: Virginia
COUNTRY: United States
ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/259,000
FILING DATE: 13-JUN-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: SE 8702272-9
FILING DATE: 01-JUN-1987
ATTORNEY/AGENT INFORMATION:
NAME: Meuth, Donna M
REGISTRATION NUMBER: 36,607
REFERENCE/DOCKET NUMBER: 012885-062
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 114 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-259-000-3

Query Match 100.0%; Score 56; DB 1; Length 114;
Best Local Similarity 100.0%; Pred. No. 0.0063;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DFDSVPOIHG 10
|||
Db 30 DFDSVPOIHG 39

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OM protein - protein search, using sw model

Run on: October 22, 2005, 12:09:40 ; Search time 57.25 Seconds
(without alignments)
72.924 Million cell updates/sec

Title: US-10-731-238-77

Perfect score: 56

Sequence: 1 DFDSVPQIHG 10

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Gapop 10.0 , Gapext 0.5

Searched: 1862951 seqs, 417491010 residues

Total number of hits satisfying chosen parameters: 1862951

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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17: /cgnt_6/ptodata/2/pubppa/US10F_PUBCOMB.pep.*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	56	100.0	38	US-10-731-238-5	Sequence 5, Appl
3	56	100.0	38	US-10-731-238-6	Sequence 6, Appl
4	56	100.0	38	US-10-731-238-35	Sequence 35, Appl
5	56	100.0	38	US-10-731-238-36	Sequence 36, Appl
6	56	100.0	38	US-10-731-238-37	Sequence 37, Appl
7	56	100.0	38	US-10-731-238-38	Sequence 38, Appl
8	56	100.0	38	US-10-731-238-39	Sequence 39, Appl
9	56	100.0	38	US-10-731-238-40	Sequence 40, Appl
10	56	100.0	38	US-10-731-238-41	Sequence 41, Appl
11	56	100.0	38	US-10-731-238-42	Sequence 42, Appl

12	56	100.0	38	US-10-731-238-43	Sequence 43, Appl
13	56	100.0	38	US-10-731-238-44	Sequence 44, Appl
14	56	100.0	139	US-09-813-820-8	Sequence 8, Appl
15	56	100.0	388	US-08-901-062-1	Sequence 1, Appl
16	56	100.0	559	US-08-781-966A-5251	Sequence 5251, Ap
17	56	100.0	559	US-10-329-624-5251	Sequence 5251, Ap
18	56	100.0	767	US-09-815-242-5899	Sequence 5899, Ap
19	56	100.0	767	US-09-815-242-11140	Sequence 11140, A
20	56	100.0	940	US-10-470-048B-424	Sequence 424, App
21	56	100.0	948	US-10-470-048B-69	Sequence 43778, A
22	56	100.0	961	US-10-282-122A-43778	Sequence 43778, A
23	56	100.0	978	US-09-815-242-5456	Sequence 5456, Ap
24	56	100.0	1001	US-09-815-242-12686	Sequence 12686, A
25	56	100.0	1018	US-09-815-242-5797	Sequence 5797, A
26	56	100.0	1018	US-09-815-242-12838	Sequence 12838, A
27	56	100.0	1018	US-10-470-048B-68	Sequence 68, Appl
28	56	100.0	1027	US-08-781-966A-5254	Sequence 5254, Ap
29	56	100.0	1027	US-10-329-624-5254	Sequence 43827, A
30	56	100.0	1038	US-10-282-122A-43827	Sequence 43827, A
31	51	91.1	36	US-10-731-238-58	Sequence 59, Appl
32	51	91.1	36	US-10-731-238-59	Sequence 7, Appl
33	51	91.1	38	US-10-731-238-7	Sequence 8, Appl
34	51	91.1	38	US-10-731-238-8	Sequence 45, Appl
35	51	91.1	38	US-10-731-238-45	Sequence 46, Appl
36	51	91.1	38	US-10-731-238-46	Sequence 47, Appl
37	51	91.1	38	US-10-731-238-47	Sequence 48, Appl
38	51	91.1	38	US-10-731-238-48	Sequence 49, Appl
39	51	91.1	38	US-10-731-238-49	Sequence 50, Appl
40	51	91.1	38	US-10-731-238-50	Sequence 56, Appl
41	45.5	81.2	39	US-10-731-238-56	Sequence 57, Appl
42	45.5	81.2	39	US-10-731-238-57	Sequence 78, Appl
43	44	78.6	10	US-10-731-238-78	Sequence 76, Appl
44	42	75.0	10	US-10-731-238-76	Sequence 140779, Sequence
45	40	71.4	324	US-10-437-963-140779	

ALIGNMENTS

RESULT 1
US-10-731-238-77
; Sequence 77, Application US/10731238
; Publication No. US20050123552A1
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
Pacifi, Joseph M.
House-Pompeo, Karen L.
Speziale, Pietro
Job, Danny
McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10731,238
FILING DATE: 10-Dec-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE: 21-Jan-1998
APPLICATION NUMBER: US 60/036,139

FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAMK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 77:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 77:
US-10-731-238-77

Query Match 100.0%; Score 56; DB 18; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.00093;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DFDSPVOIHG 10
Db 1 DFDSPVOIHG 10

RESULT 2
US-10-731-238-5
Sequence 5, Application US/10731238
Publication No. US20050123552A1
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
Patti, Joseph M.
House-Pompeo, Karen L.
Speziale, Pietro
Joh, Danny
McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Releasee #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/731,238
FILING DATE: 10-Dec-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE: 21-Jan-1998
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAMK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>

TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-10-731-238-5

Query Match 100.0%; Score 56; DB 18; Length 38;
Best Local Similarity 100.0%; Pred. No. 0.0041;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DFDSPVOIHG 10
Db 29 DFDSPVOIHG 38

RESULT 3
US-10-731-238-6
Sequence 6, Application US/10731238
Publication No. US20050123552A1
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
Patti, Joseph M.
House-Pompeo, Karen L.
Speziale, Pietro
Joh, Danny
McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Releasee #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/731,238
FILING DATE: 10-Dec-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE: 21-Jan-1998
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAMK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-10-731-238-6

Query Match 100.0%; Score 56; DB 18; Length 38;
Best Local Similarity 100.0%; Pred. No. 0.0041;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DFDSPVOIHG 10
Db 29 DFDSPVOIHG 38

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US-10-731-238-35
; Sequence 35, Application US/10731238
; Publication No. US20050123552A1
; GENERAL INFORMATION:
; APPLICANT: Hook, Magnus
;             Patti, Joseph M.
;             House-Pompeo, Karen L.
;             Speziale, Pietro
;             Joh, Danny
;             McGavin, Martin J.
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
; AND METHODS OF USE
; NUMBER OF SEQUENCES: 105
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: TX
; COUNTRY: USA
; ZIP: 77210-4433
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/731,238
; FILING DATE: 10-Dec-2003
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/010,317
; FILING DATE: 21-Jan-1998
; APPLICATION NUMBER: US 60/036,139
; FILING DATE: 21-JAN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Hibler, David W.
; REGISTRATION NUMBER: 41, 071
; REFERENCE/DOCKET NUMBER: TANK:189
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 512-418-3000
; TELEFAX: 512-474-7577
; INFORMATION FOR SEQ ID NO: 35:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 38 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 35:
US-10-731-238-35
;
; Query Match          100.0%; Score 56; DB 18; Length 38;
; Best Local Similarity 100.0%; Pred. No. 0.0041;
; Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0
;
Oy      1 DFDSPVQIHG 10
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        |||||
Db      29 DFDSPVQIHG 38

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NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/731,238
FILING DATE: 10-Dec-2003
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE: 21-Jan-1998
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997

ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TBMK.189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577

INFORMATION FOR SEQ ID NO: 36:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear

SEQUENCE DESCRIPTION: SEQ ID NO: 36:
US-10-731-238-36

Query Match      100.0%; Score 56; DB 18; Length 38;
Best Local Similarity 100.0%; Pred. NO. 0.0041;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0.

QY      1 DFDVSPQIHG 10
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      29 DFDVSPQIHG 38

RESULT 6
US-10-731-238-37
; Sequence 37, Application US/10731238
; Publication No. US20050123552A1
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
      Patti, Joseph M.
      House-Pompeo, Karen L.
      Speziale, Pietro
      Joh, Danny
      McGavin, Martin J.
TITLE OF INVENTION: FIBROBLAST BINDING PROTEIN COMPOSITIONS
AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30

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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/731,238
FILING DATE: 10-Dec-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE: 21-Jan-1998
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Habler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAMK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 37:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 37:
US-10-731-238-37

Query Match 100.0%; Score 56; DB 18; Length 38;
Best Local Similarity 100.0%; Pred. No. 0.0041;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DFDSVPQIHG 10
|||
Db 29 DFDSVPQIHG 38

RESULT 7
US-10-731-238-38
Sequence 38, Application US/10731238
Publication No. US20050123552A1
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
Pattl, Joseph M.
House-Pompeo, Karen L.
Speziale, Pietro
Joh, Danny
McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/731,238
FILING DATE: 10-Dec-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE: 21-Jan-1998
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Habler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAMK:189

TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 38:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 38:
US-10-731-238-38

Query Match 100.0%; Score 56; DB 18; Length 38;
Best Local Similarity 100.0%; Pred. No. 0.0041;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DFDSVPQIHG 10
|||
Db 29 DFDSVPQIHG 38

RESULT 8
US-10-731-238-39
Sequence 39, Application US/10731238
Publication No. US20050123552A1
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
Pattl, Joseph M.
House-Pompeo, Karen L.
Speziale, Pietro
Joh, Danny
McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/731,238
FILING DATE: 10-Dec-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE: 21-Jan-1998
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Habler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAMK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 39:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 39:
US-10-731-238-39

Query Match 100.0%; Score 56; DB 18; Length 38;

Best Local Similarity 100.0%; Pred. No. 0.0041;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DFDVPOIHG 10
|||||
Db 29 DFDVPOIHG 38

RESULT 9
US-10-731-238-40
; Sequence 40, Application US/10731238
; Publication No. US20050123552A1
; GENERAL INFORMATION:
; APPLICANT: Hook, Magnus
; Patti, Joseph M.
; House-Pompeo, Karen L.
; Speziale, Pietro
; Joh, Danny
; McGavin, Martin J.
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
; AND METHODS OF USE
; NUMBER OF SEQUENCES: 105
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: TX
; COUNTRY: USA
; ZIP: 77210-4433
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/731,238
; FILING DATE: 10-Dec-2003
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/010,317
; FILING DATE: 21-Jan-1998
; APPLICATION NUMBER: US 60/036,139
; FILING DATE: 21-Jan-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Hibler, David W.
; REGISTRATION NUMBER: 41,071
; REFERENCE/DOCKET NUMBER: TANK:189
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 512-418-3000
; TELEFAX: 512-474-7577
; INFORMATION FOR SEQ ID NO: 40:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 38 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 40:
US-10-731-238-40

Query Match 100.0%; Score 56; DB 18; Length 38;
Best Local Similarity 100.0%; Pred. No. 0.0041;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DFDVPOIHG 10
|||||
Db 29 DFDVPOIHG 38

RESULT 10
US-10-731-238-41
; Sequence 41, Application US/10731238
; Publication No. US20050123552A1
; GENERAL INFORMATION:

APPLICANT: Hook, Magnus
; Patti, Joseph M.
; House-Pompeo, Karen L.
; Speziale, Pietro
; Joh, Danny
; McGavin, Martin J.
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
; AND METHODS OF USE
; NUMBER OF SEQUENCES: 105
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: TX
; COUNTRY: USA
; ZIP: 77210-4433
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/731,238
; FILING DATE: 10-Dec-2003
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/010,317
; FILING DATE: 21-Jan-1998
; APPLICATION NUMBER: US 60/036,139
; FILING DATE: 21-Jan-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Hibler, David W.
; REGISTRATION NUMBER: 41,071
; REFERENCE/DOCKET NUMBER: TANK:189
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 512-418-3000
; TELEFAX: 512-474-7577
; INFORMATION FOR SEQ ID NO: 41:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 38 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 41:
US-10-731-238-41

Query Match 100.0%; Score 56; DB 18; Length 38;
Best Local Similarity 100.0%; Pred. No. 0.0041;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DFDVPOIHG 10
|||||
Db 29 DFDVPOIHG 38

RESULT 11
US-10-731-238-42
; Sequence 42, Application US/10731238
; Publication No. US20050123552A1
; GENERAL INFORMATION:
; APPLICANT: Hook, Magnus
; Patti, Joseph M.
; House-Pompeo, Karen L.
; Speziale, Pietro
; Joh, Danny
; McGavin, Martin J.
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
; AND METHODS OF USE
; NUMBER OF SEQUENCES: 105
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston

STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/731,238
FILING DATE: 10-Dec-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE: 21-Jan-1998
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-Jan-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAWK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 42:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 42:
US-10-731-238-42
Query Match 100.0%; Score 56; DB 18; Length 38;
Best Local Similarity 100.0%; Pred. No. 0.0041;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 DEDSVPOIHG 10
Db 29 DFDVSPQIHG 38
RESULT 12
US-10-731-238-43
Sequence 43, Application US/10731238
Publication No. US20050123552A1
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
Pattl, Joseph M.
House-Pompeo, Karen L.
Speziale, Pietro
Joh, Danny
McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/731,238
FILING DATE: 10-Dec-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/010,317
FILING DATE: 21-Jan-1998
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-Jan-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAWK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 43:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 43:
US-10-731-238-43
Query Match 100.0%; Score 56; DB 18; Length 38;
Best Local Similarity 100.0%; Pred. No. 0.0041;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 DEDSVPOIHG 10
Db 29 DFDVSPQIHG 38
RESULT 13
US-10-731-238-44
Sequence 44, Application US/10731238
Publication No. US20050123552A1
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
Pattl, Joseph M.
House-Pompeo, Karen L.
Speziale, Pietro
Joh, Danny
McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/731,238
FILING DATE: 10-Dec-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE: 21-Jan-1998
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-Jan-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAWK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 44:
SEQUENCE CHARACTERISTICS:

LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 44:
US-10-731-238-44

Query Match 100.0%; Score 56; DB 18; Length 38;
Best Local Similarity 100.0%; Pred. No. 0.0041;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DFDVSPQIHG 10
DB 29 DFDVSPQIHG 38

RESULT 14
US-09-813-820-8
Sequence 8, Application US/09813820
Patent No. US20020102262A1
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
Patel, Joseph M.
House-Pompeo, Karen
Sthanam, Narayana
Symersky, Jindrich
TITLE OF INVENTION: COLLAGEN BINDING PROTEIN COMPOSITIONS
AND METHODS OF USE
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: Texas
COUNTRY: U.S.
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/813,820
FILING DATE: 22-Mar-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/856,253
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Kitchell, Barbara S.
REGISTRATION NUMBER: 33,928
REFERENCE/DOCKET NUMBER: TAMK.193
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
TELEFAX: (512) 474-7577
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 139 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-09-813-820-8

Query Match 100.0%; Score 56; DB 9; Length 139;
Best Local Similarity 100.0%; Pred. No. 0.018;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DFDVSPQIHG 10
DB 44 DFDVSPQIHG 53

RESULT 15
US-08-901-062-1
Sequence 1, Application US/08901062
Publication No. US20020025324A1
GENERAL INFORMATION:
APPLICANT: SEALS, JONATHAN R.
TITLE OF INVENTION: RECOMBINANT BIVALENT BACTERIAL VACCINE
FOR THE PREVENTION OF MASTITIS
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: HALE AND DORR LLP
STREET: 60 State Street
CITY: Boston
STATE: MA
COUNTRY: United States Of America
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/901,062
FILING DATE: 25-JUL-1997
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Baker, Hollie L.
REGISTRATION NUMBER: 31,321
REFERENCE/DOCKET NUMBER: 106941.153
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 526-6000
TELEFAX: (617) 526-5000
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 388 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-901-062-1

Query Match 100.0%; Score 56; DB 8; Length 388;
Best Local Similarity 100.0%; Pred. No. 0.055;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DFDVSPQIHG 10
DB 293 DFDVSPQIHG 302

Search completed: October 22, 2005, 12:39:46
Job time : 57.25 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 22, 2005, 06:10:10 ; Search time 11.45 Seconds
(without alignments)
84.032 Million cell updates/sec

Title: US-10-731-238-77

Perfect score: 56

Sequence: 1 DFDSVPQIHG 10

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database :

1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	56	100.0	940	2	S19702	fibronectin-binding
2	56	100.0	961	2	G90053	hypothetical prote
3	56	100.0	1018	2	A32192	fibronectin-binding
4	56	100.0	1038	2	H90053	hypothetical prote
5	39	69.6	299	2	T16252	hypothetical prote
6	37	66.1	510	2	B83009	probable histidine
7	37	66.1	755	2	Fix12_E1-E2 type c	hypothetical prote
8	36	64.3	319	2	AH1247	hypothetical prote
9	36	64.3	668	2	T05257	probable disease r
10	36	64.3	643	2	C84464	mutator-like trans
11	35	62.5	115	2	T08473	trAO protein homol
12	35	62.5	135	2	S52080	ribosomal protein
13	35	62.5	289	2	P95250	ROK family protein
14	35	62.5	293	2	C98115	conserved hypotet
15	35	62.5	391	2	S15617	E2 protein - human
16	35	62.5	409	2	T117258	hypothetical prote
17	35	62.5	454	2	A82353	glutathione-disulf
18	35	62.5	459	2	T48598	hypothetical prote
19	35	62.5	493	2	P70841	probable lpda prot
20	35	62.5	586	2	AD1458	probable peptidogl
21	35	62.5	595	2	T31163	hypothetical prote
22	35	62.5	726	2	A27602	complement C3 - ra
23	35	62.5	775	2	C81594	hypothetical prote
24	35	62.5	775	2	D86549	hypothetical prote
25	35	62.5	775	2	B72074	hypothetical prote
26	35	62.5	857	2	S01864	lipoxygenase (EC 1
27	35	62.5	861	1	S01142	lipoxygenase (EC 1
28	35	62.5	1663	1	C3MS	complement C3 prec
29	35	62.5	1663	1	C3RT	complement C3 prec

30	34	60.7	131	2	A48527	photosystem I prot
31	34	60.7	137	2	PC4110	transcription regu
32	34	60.7	146	2	D86924	conserved hypotet
33	34	60.7	148	2	S10238	leghemoglobin glb3
34	34	60.7	162	2	AG0994	probable acetyltra
35	34	60.7	211	2	C90330	hypothetical prote
36	34	60.7	257	2	E90348	hypothetical prote
37	34	60.7	258	2	T34422	TPR-repeat-contain
38	34	60.7	273	2	D97353	hypothetical prote
39	34	60.7	282	2	B90348	partial transposas
40	34	60.7	288	2	D90345	partial transposas
41	34	60.7	310	2	E90334	partial transposas
42	34	60.7	318	2	A90154	partial transposas
43	34	60.7	320	2	T33303	hypothetical prote
44	34	60.7	332	2	C90497	transposase ISC135
45	34	60.7	350	2	A90279	transposase ISC135

ALIGNMENTS

RESULT 1

S19702

fibronectin-binding protein B - Staphylococcus aureus

C/Species: Staphylococcus aureus

C/Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #ext_change 09-Jul-2004

C/Accession: S19702

R/Joensson, K.; Stignae, C.; Mueller, H.P.; Lindberg, M.

Eur. J. Biochem. 202, 1041-1048, 1991

A/Title: Two different genes encode fibronectin binding proteins in Staphylococcus aure

A/Reference number: S19702; PMID:92111475; PMID:1837266

A/Accession: S19702

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-940 <JOB>

A/Cross-references: UNIPROT:Q53682; EMBL:X62992; NID:949040; PIDN:CAA44726.1; PID:95815

C/Keywords: fibronectin binding

Query Match

Best Local Similarity 100.0%; Score 56; DB 2; Length 940;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 710 DFDSVPQIHG 719

QY 1 DFDSVPQIHG 10

Db 710 DFDSVPQIHG 719

QY 1 DFDSVPQIHG 10

Db 710 DFDSVPQIHG 719

QY 1 DFDSVPQIHG 10

Db 710 DFDSVPQIHG 719

QY 1 DFDSVPQIHG 10

Db 710 DFDSVPQIHG 719

QY 1 DFDSVPQIHG 10

Db 710 DFDSVPQIHG 719

QY 1 DFDSVPQIHG 10

Db 710 DFDSVPQIHG 719

QY 1 DFDSVPQIHG 10

Db 710 DFDSVPQIHG 719

QY 1 DFDSVPQIHG 10

Db 710 DFDSVPQIHG 719

QY 1 DFDSVPQIHG 10

Db 710 DFDSVPQIHG 719

QY 1 DFDSVPQIHG 10

Db 710 DFDSVPQIHG 719

QY 1 DFDSVPQIHG 10

Db 710 DFDSVPQIHG 719

QY 1 DFDSVPQIHG 10

Db 710 DFDSVPQIHG 719

QY 1 DFDSVPQIHG 10

Db 710 DFDSVPQIHG 719

QY 1 DFDSVPQIHG 10

Db 710 DFDSVPQIHG 719

QY 1 DFDSVPQIHG 10

Db 710 DFDSVPQIHG 719

Db 721 DFDSVPQIHG 730

RESULT 3

A32192

fibronectin-binding protein - *Staphylococcus aureus*C:Species: *Staphylococcus aureus*

C:Date: 31-Jul-1989 #sequence_revision 31-Jul-1989 #text_change 16-Feb-1997

C:Accession: A32192

R:Signaee, C.; Raucel, G.; Jonsson, K.; Lindgren, P.E.; Anantharamaiah, G.M.; Hoecek, W

Proc. Natl. Acad. Sci. U.S.A. 86, 699-703, 1989

A:Title: Nucleotide sequence of the gene for a fibronectin-binding protein from *Staphylo*

A:Reference number: A32192; MUID:0908998; PMID:2521391

A:Accession: A32192

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-1018 <SIG>

A:Cross-references: GB:J04151

C:Keywords: fibronectin binding

Query Match 100.0%; Score 56; DB 2; Length 1018;
Best Local Similarity 100.0%; Pred. No. 0.0093;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DFDSVPQIHG 10
Db 774 DFDSVPQIHG 783

RESULT 4

H90053

hypothetical protein fnb [imported] - *Staphylococcus aureus* (strain N315)C:Species: *Staphylococcus aureus*

C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004

C:Accession: H90053

R:Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguc

ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.

C:Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.

Lancet 357, 1225-1240, 2001

A:Title: Whole genome sequencing of methicillin-resistant *Staphylococcus aureus*.

A:Reference number: A89758; MUID:21311952; PMID:1148146

A:Accession: H90053

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-1038 <KUR>

A:Cross-references: UNIPROT:Q99RD2; GB:BA000018; PID:G13702453; PIDN:BA843594.1; GSPDB:G

A:Experimental source: strain N315

C:Genetics:

A:Gene: fnb

Query Match 100.0%; Score 56; DB 2; Length 1038;
Best Local Similarity 100.0%; Pred. No. 0.0095;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DFDSVPQIHG 10
Db 770 DFDSVPQIHG 779

RESULT 5

T16252

hypothetical protein F35C8.4 - *Caenorhabditis elegans*C:Species: *Caenorhabditis elegans*

C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 17-Mar-2000

C:Accession: T16252

R:Wu, X.

submitted to the EMBL Data Library, November 1995

A:Description: The sequence of *C. elegans* cosmid F35C8.

A:Reference number: Z16486

A:Accession: T16252

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-299 <MUX>

A:Cross-references: EMBL:U40941; NID:G1072184; PID:G1072185; PIDN:AAA81707.1; CESP:F35C8

C:Genetics:

A:Gene: CESP:F35C8.4

A:Introns: 3/3; 39/3; 102/1; 161/1; 233/1

C:Superfamily: syntaxin

Query Match 69.6%; Score 39; DB 2; Length 299;
Best Local Similarity 60.0%; Pred. No. 5.7;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 DFDSVPQIHG 10
Db 57 DYDAVVLQIHG 66

RESULT 6

B83009

probable histidine/phenylalanine ammonia-lyase PA5093 [imported] - *Pseudomonas aeruginosa*C:Species: *Pseudomonas aeruginosa*

C:Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004

C:Accession: B83009

R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrenner, P.; Hickey, M.J.; Br

adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Lapidis, K.; Lim,

.; Lory, S.; Olson, M.V.

Nature 406, 959-964, 2000

A:Title: Complete genome sequence of *Pseudomonas aeruginosa* PA01, an opportunistic pathc

A:Reference number: A82950; MUID:20437337; PMID:10984043

A:Accession: B83009

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-510 <STO>

A:Cross-references: UNIPROT:Q9HU90; GB:AE004922; GB:AE004091; NID:G9951385; PIDN:AA60847

A:Experimental source: strain PA01

C:Genetics:

A:Superfamily: Bacillus subtilis histidine ammonia-lyase

Query Match 66.1%; Score 37; DB 2; Length 510;
Best Local Similarity 85.7%; Pred. No. 27;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 SVPQIHG 10
Db 283 STPQIHG 289

RESULT 7

E95302

Fix12 E1-E2 type cation ATPase [imported] - *Sinorhizobium meliloti* (strain 1021) magaplaC:Species: *Sinorhizobium meliloti*

C:Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 09-Jul-2004

C:Accession: E95302

R:Barrett, M.J.; Fisher, R.F.; Jones, T.; Komp, C.; Abola, A.P.; Barloy-Hubler, F.; Bows

.; Kalman, S.; Keating, D.H.; Palm, C.; Peck, M.C.; Surzycki, R.; Wells, D.H.; Yeh, K.C.

Proc. Natl. Acad. Sci. U.S.A. 98, 9883-9888, 2001

A:Title: Nucleotide sequence and predicted functions of the entire *Sinorhizobium meliloti*

A:Reference number: A85262; MUID:21396509; PMID:11481432

A:Accession: E95302

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-755 <KUR>

A:Cross-references: UNIPROT:Q922X3; GB:AE006469; PIDN:AAK64983.1; PID:G14523409; GSPDB:G

A:Experimental source: strain 1021, megaplasmid pSymA

R:Gallbert, F.; Finan, T.M.; Long, S.R.; Fuhrer, A.; Abola, P.; Ampe, F.; Barloy-Hubler,

peta, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.;

L.; Hyman, R.W.; Jones, T.

Science 293, 668-672, 2001

A:Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure,

hebaul, P.; Vandenbol, M.; Vornolter, F.J.; Weiner, S.; Wells, D.H.; Wong, K.; Yeh, K.

A:Title: The composite genome of the legume symbiont *Sinorhizobium meliloti*.

A:Reference number: A86039; MUID:21368234; PMID:11474104

A:Contents: annotation

C:Genetics:
A:Gene: fix12
A:Genome: plasmid
C:Superfamily: Enterococcus copper-transferring ATPase copA; ATPase nucleotide-binding d

Query Match 66.1%; Score 37; DB 2; Length 755;
Best Local Similarity 50.0%; Pred. No. 44;
Matches 5; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 DFDSVPQING 10
DB 504 EFDLSLEFVHG 513

RESULT 8
AH1247
hypochemical protein lmo1384 [imported] - Listeria monocytogenes (strain EGD-e)

C:Species: Listeria monocytogenes
C:Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #ext_change 09-Jul-2004

C:Accession: AH1247

R:Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloeker
; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussauguet, O.; Entlian, K.D.; Fshl, H.
D.; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001

A:Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkut, G.; Madueno, E.; Maitournam, A.; Ma
ok, C.; Schueller, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehlund,
A:Title: Comparative genomics of Listeria species.
A:Reference number: AB1077; MUID:21537279; PMID:11679669

A:Accession: AH1247

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-319 <GLA>

A:Cross-references: UNIPROT:Q8Y744; GB:NC_003210; PIDN:CAC99462.1; PID:G16410800; GSPDB:
A:Experimental source: strain EGD-e

C:Genetics:

A:Gene: lmo1384

C:Superfamily: Escherichia coli ycea protein

Query Match 64.3%; Score 36; DB 2; Length 319;
Best Local Similarity 66.7%; Pred. No. 25;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 FDSVPQING 10
DB 196 FDDVSQLHG 204

RESULT 9
T05257
probable disease resistance protein F18A5.270 - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)

C:Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #ext_change 09-Jul-2004

C:Accession: T05257

R:Bevan, M.; Weber, N.; Grueninger, D.; Schmidheini, T.; Bancroft, I.; Mewes, H.W.; Maye
submitted to the Protein Sequence Database, February 1999

A:Reference number: Z15405

A:Accession: T05257

A:Molecule type: DNA

A:Residues: 1-668 <BEV>

A:Cross-references: UNIPROT:Q9SVMS; EMBL:AL035528

A:Experimental source: cultivar Columbia; BAC clone F18A5

C:Genetics:

A:Map position: 4

A:Intons: 154/1

A:Note: F18A5.270

Query Match 64.3%; Score 36; DB 2; Length 668;
Best Local Similarity 62.5%; Pred. No. 60;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 FDSVPQIH 9
DB 461 FDTTPOVH 468

RESULT 10

C84464
Mutator-like transposase [imported] - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)

C:Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #ext_change 09-Jul-2004

C:Accession: C84464

R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanKen, S.E.; Umayam, L.; Tallon, L.
eus, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Frazer, C.M.; Venter, J.

Nature 402, 761-768, 1999

A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.

A:Reference number: A84420; MUID:20083487; PMID:10617197

A:Accession: C84464

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-731 <STO>

A:Cross-references: UNIPROT:Q9S125; GB:AE002093; NID:94585931; PIDN:AAD25591.1; GSPDB:GN

C:Genetics:

A:Gene: AT2905010

A:Map position: 2

Query Match 64.3%; Score 36; DB 2; Length 731;
Best Local Similarity 50.0%; Pred. No. 67;
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 DFDSVPQING 10
DB 676 DIDKIPCVHG 685

RESULT 11
T08473

trao Protein homolog - Enterobacter aerogenes plasmid R751

C:Species: Enterobacter aerogenes

C:Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #ext_change 09-Jul-2004

C:Accession: T08473

R:Thorsted, P.B.; Shah, D.S.; Macartney, D.; Kostelidou, K.; Thomas, C.M.
Plasmid 36, 95-111, 1996

A:Title: Conservation of the genetic switch between replication and transfer genes of T

A:Reference number: Z16434; MUID:97118926; PMID:8954881

A:Accession: T08473

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-115 <THO>

A:Cross-references: UNIPROT:P71172; EMBL:U67194; NID:G1572520; PIDN:AA64417.1; PID:G15

C:Genetics:

A:Gene: upf54.8

A:Genome: plasmid R751

Query Match 62.5%; Score 35; DB 2; Length 115;
Best Local Similarity 75.0%; Pred. No. 12;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 DFDSVPQI 8
DB 79 DFQKVPBI 86

RESULT 12

S52080
ribosomal protein S17.e, cytosolic - slime mold (Dictyostelium discoideum)

C:Species: Dictyostelium discoideum

C:Date: 14-Jul-1995 #sequence_revision 21-Jul-1995 #ext_change 09-Jul-2004

C:Accession: S52080

R:Beuerle, A.; Mutzel, R.

Biochim. Biophys. Acta 1260, 223-226, 1995

A:Title: Nucleotide sequence of the gene for ribosomal protein S17 from Dictyostelium d

A:Reference number: S52080; MUID:95143281; PMID:7841201

A:Accession: S52080

A:Molecule type: DNA

A:Residues: 1-135 <BAE>

A:Cross-references: UNIPROT:P42520; EMBL:J35173; NID:g521179; PIDN:AA67548.1; PID:g5211
C:Genetics:
A:Introns: 1/3, 117/1
A:Superfamily: rat ribosomal protein S17
C:Keywords: protein biosynthesis; ribosome

Query Match 62.5%; Score 35; DB 2; Length 135;
Best Local Similarity 55.6%; Pred. No. 14;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 FDSVPQIH 9
|:|:|:|:|
Db 111 EFPRIQIH 119

RESULT 13

F95250

ROK family protein [imported] - Streptococcus pneumoniae (strain TIGR4)

C:Species: Streptococcus pneumoniae

C>Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 09-Jul-2004

C:Accession: F95250

R:Retelien, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Heid
on, J.D.; Unayam, L.A.; White, O.; Salasberg, S.L.; Lewis, M.R.; Radune, D.; Holtzaple,
neon, T.; Hickey, E.K.; Holt, I.E.

Science 293, 498-506, 2001

A:Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison,
A:Title: Complete Genome Sequence of a virulent isolate of Streptococcus pneumoniae.

A:Reference number: A95000; MUID:2157209; PMID:11463916

A:Accession: F95250

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-289 <KUR>

A:Cross-references: UNIPROT:Q97NB0; GB:AE005672; PIDN:AAK76199.1; PID:g14973654; GSPDB:C

A:Experimental source: strain TIGR4

C:Genetics:

A:Gene: SP2142

C:Superfamily: glucose kinase; glucose kinase homology

A:Gene: SP2142

C:Superfamily: glucose kinase; glucose kinase homology

A:Gene: SP2142

C:Superfamily: glucose kinase; glucose kinase homology

A:Gene: SP2142

C:Superfamily: glucose kinase; glucose kinase homology

A:Gene: SP2142

C:Superfamily: glucose kinase; glucose kinase homology

A:Gene: SP2142

C:Superfamily: glucose kinase; glucose kinase homology

A:Gene: SP2142

C:Superfamily: glucose kinase; glucose kinase homology

A:Gene: SP2142

C:Superfamily: glucose kinase; glucose kinase homology

A:Gene: SP2142

C:Superfamily: glucose kinase; glucose kinase homology

A:Gene: SP2142

C:Superfamily: glucose kinase; glucose kinase homology

A:Gene: SP2142

C:Superfamily: glucose kinase; glucose kinase homology

A:Gene: SP2142

C:Superfamily: glucose kinase; glucose kinase homology

A:Gene: SP2142

C:Superfamily: glucose kinase; glucose kinase homology

A:Gene: SP2142

C:Superfamily: glucose kinase; glucose kinase homology

A:Gene: SP2142

C:Superfamily: glucose kinase; glucose kinase homology

A:Gene: SP2142

C:Superfamily: glucose kinase; glucose kinase homology

A:Gene: SP2142

C:Superfamily: glucose kinase; glucose kinase homology

A:Gene: SP2142

C:Superfamily: glucose kinase; glucose kinase homology

A:Gene: SP2142

C:Superfamily: glucose kinase; glucose kinase homology

A:Gene: SP2142

C:Superfamily: glucose kinase; glucose kinase homology

A:Gene: SP2142

C:Superfamily: glucose kinase; glucose kinase homology

A:Gene: SP2142

Qy 2 FDSVPQIH 10
|:|:|:|:|
Db 77 FSAVPYIH 85

RESULT 15

S15617

E2 protein - human papillomavirus type 2a

C:Species: human papillomavirus type 2a

A:Note: host Homo sapiens (man)

C>Date: 17-Feb-1994 #sequence_revision 17-Feb-1994 #text_change 09-Jul-2004

C:Accession: S15617

R:Hirsch-Behnam, A.; Delius, H.; de Villiers, E.M.

Virus Res. 18, 81-98, 1990

A:Title: A comparative sequence analysis of two human papillomavirus (HPV) types 2a and

A:Reference number: S15614; MUID:9118699; PMID:1964523

A:Accession: S15617

A:Molecule type: DNA

A:Residues: 1-391 <HIR>

A:Cross-references: UNIPROT:P25482; EMBL:X55964

C:Superfamily: papillomavirus E2 protein

C:Keywords: DNA binding; early protein; transcription regulation

Query Match 62.5%; Score 35; DB 1; Length 391;
Best Local Similarity 77.8%; Pred. No. 50;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 FDSVPQIH 9
|:|:|:|:|
Db 306 DTSVPYIH 314

Search completed: October 22, 2005, 08:04:33
Job time : 12.45 secs


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Q8NU8      PRELIMINARY;      PRT;      943 AA.
ID Q8NU8;
AC Q8NU8;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE FndB protein.
GN Name=fndB; OrderedLocustNames=MM2420;
OS Staphylococcus aureus (strain MM2).
OC Bacteria; Firmicutes; Bacilliales; Staphylococcus.
OX NCBI_TaxId=196620;
[1]
RN SEQUENCE FROM N.A.
RC STRAIN=MM2;
RX MEDLINE=2040717; PubMed=12044378; DOI=10.1016/S0140-6736(02)08713-5;
RA Baba T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Oguchi A.,
RA Nagai Y., Iwano N., Asano K., Naito T., Kuroda H., Cui L.,
RA Yamamoto K., Hiramoto K.;
RT "Genome and virulence determinants of high virulence community-
RT acquired MRSA.";
RL Lancet 359:1819-1827(2002).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC an amide bond (By similarity).
DR EMBL: AP004830; BAB96285.1; -.
DR HSSP: Q53653; 1N67.
DR GO: GO:0009986; C:cell surface; IEA.
DR GO: GO:0005618; C:cell wall; IEA.
DR GO: GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO: GO:0016020; C:membrane; IEA.
DR GO: GO:0007155; P:cell adhesion; IEA.
DR InterPro: IPR008966; Adhes_bact.
DR InterPro: IPR004237; Fn_bind.
DR InterPro: IPR005877; Gpos_YsIRK.
DR InterPro: IPR001899; Gram_pos_anchor.
DR Pfam: PF02986; Fn_bind. 1.
DR Pfam: PF00746; Gram_pos_anchor. 1.
DR TIGRfams: TIGR01167; LPTXG_anchor. 1.
DR TIGRfams: TIGR01168; YsIRK_signal. 1.
DR PROSITE: PS00847; GRAM_POS_ANCHORING. 1.
DR Cell wall; Complete proteome; Peptidoglycan-anchor.
DR SEQUENCE 943 AA; 104537 MW; DA8A5F31947E1B6A CRC64;

Query Match      100.0%; Score 56; DB 2; Length 943;
Best Local Similarity 100.0%; Pred. No. 0.062;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 DFDSPVQIHG 10
DB      717 DFDSPVQIHG 726

RESULT 3
Q6G6H4      PRELIMINARY;      PRT;      957 AA.
ID Q6G6H4;
AC Q6G6H4;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Fibronectin-binding protein.
GN Name=fndB; OrderedLocustNames=SAS2387;
OS Staphylococcus aureus (strain MSSA476).
OC Bacteria; Firmicutes; Bacilliales; Staphylococcus.
OX NCBI_TaxId=282459;
[1]
RN SEQUENCE FROM N.A.
RP PubMed=15213324; DOI=10.1073/pnas.0402521101;
RX Holden M.T.G., Fell E.J., Lindsey J.A., Peacock S.J., Day N.P.J.,
RX Enright M.C., Foster T.J., Moore C.E., Hurst L., Atkin R., Barron A.,
RX Baason N., Bentley S.D., Chillingworth C., Chillingworth T.,
RX Churcher C., Clark L., Cotton C., Cronin A., Doggett J., Dowd L.,
RX Felwell T., Hance Z., Harris B., Hauber H., Holtroyd S., Jagels K.,
RX James K.D., Lennard N., Line A., Mayes R., Moule S., Mungall K.,

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RA Ormond D., Quail M.A., Rabinowitch E., Rutherford K.M., Sanders M.,
RA Sharp S., Simmonds M., Stevens K., Whitehead S., Barrall B.G.,
RA Spratt B.G., Parkhill T.;
RT "Complete genomes of two clinical Staphylococcus aureus strains:
RT evidence for the rapid evolution of virulence and drug resistance.";
RT Proc. Natl. Acad. Sci. U.S.A. 101:9786-9791(2004).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC an amide bond (By similarity).
DR EMBL: BX571857; CAG4201.1; -.
DR GO: GO:0009986; C:cell surface; IEA.
DR GO: GO:0005618; C:cell wall; IEA.
DR GO: GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO: GO:0016020; C:membrane; IEA.
DR GO: GO:0007155; P:cell adhesion; IEA.
DR InterPro: IPR008966; Adhes_bact.
DR InterPro: IPR004237; Fn_bind.
DR InterPro: IPR005877; Gpos_YsIRK.
DR InterPro: IPR001899; Gram_pos_anchor.
DR Pfam: PF02986; Fn_bind. 1.
DR Pfam: PF00746; Gram_pos_anchor. 1.
DR Pfam: PF04650; YsIRK_signal. 1.
DR TIGRfams: TIGR01167; LPTXG_anchor. 1.
DR TIGRfams: TIGR01168; YsIRK_signal. 1.
DR PROSITE: PS00847; GRAM_POS_ANCHORING. 1.
DR Cell wall; Complete proteome; Peptidoglycan-anchor.
DR SEQUENCE 957 AA; 105980 MW; 28F8BA7FDFD3EAF CRC64;

Query Match      100.0%; Score 56; DB 2; Length 957;
Best Local Similarity 100.0%; Pred. No. 0.063;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 DFDSPVQIHG 10
DB      717 DFDSPVQIHG 726

RESULT 4
Q99RD3      PRELIMINARY;      PRT;      961 AA.
ID Q99RD3;
AC Q99RD3;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Fibronectin-binding protein homolog.
GN Name=fndB; OrderedLocustNames=SAV2502;
OS Staphylococcus aureus (strain MU50 / ATCC 700659).
OC Bacteria; Firmicutes; Bacilliales; Staphylococcus.
OX NCBI_TaxId=158878;
[1]
RN SEQUENCE FROM N.A.
RP STRAIN=MU50 / ATCC 700659;
RX MEDLINE=21311952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2;
RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Iian J.-Q., Ito T.,
RA Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hoshiyama C.,
RA Mizutani U.Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaio C.,
RA Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
RA Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
RA Hattori M., Ogasawara N., Hayashi H., Hiramoto K.;
RT "Whole genome sequencing of methicillin-resistant Staphylococcus
RT aureus.";
RL Lancet 357:1225-1240(2001).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC an amide bond (By similarity).
DR EMBL: AP003365; BAB58664.1; -.
DR PIR: G90053; G90053.
DR HSSP: Q53653; 1N67.
DR GO: GO:0009986; C:cell surface; IEA.
DR GO: GO:0005618; C:cell wall; IEA.
DR GO: GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO: GO:0016020; C:membrane; IEA.
DR GO: GO:0007155; P:cell adhesion; IEA.
DR InterPro: IPR008966; Adhes_bact.

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DR InterPro: IPR004237; Fn_bind.
 DR InterPro: IPR005877; Gpos_YsIRK.
 DR InterPro: IPR001899; Gram_pos_anchor.
 DR Pfam: PF02986; Fn_bind; 1.
 DR Pfam: PF00746; Gram_pos_anchor; 1.
 DR Pfam: PF04650; YsIRK_signal; 1.
 DR TIGRFAMs: TIGR01167; LpxTG_anchor; 1.
 DR TIGRFAMs: TIGR01168; YsIRK_signal; 1.
 DR PROSITE: PS50847; GRAM_POS_ANCHORING; 1.
 DR Cell wall; Complete proteome; Peptidoglycan-anchor.
 KW SEQUENCE 961 AA; 106010 MW; 364940F884EA4101 CRC64;

Query Match 100.0%; Score 56; DB 2; Length 961;
 Best Local Similarity 100.0%; Pred. No. 0.063;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DFDSVPQIHG 10
 Db 721 DFDSVPQIHG 730

RESULT 5
 ID 07A3J8 PRELIMINARY; PRT; 961 AA.
 AC 07A3J8;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DE FmbB protein.
 GN Name=fmbB; OrderedLocustNames=SA2290;
 OS Staphylococcus aureus (strain N315).
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 OX NCBI_TaxID=158879;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=1311992; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2;
 RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
 RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Iian J.-O., Ito T.,
 RA Kanamori M., Matsunaru H., Maruyama A., Murakami H., Hoshoyama A.,
 RA Mizunari-Ul Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
 RA Sekintzu K., Hirakawa H., Kubara S., Goto S., Yabuzaki J.,
 RA Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
 RA Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
 RT "Whole genome sequencing of methicillin-resistant Staphylococcus
 aureus."
 RL Lancet 357:1225-1240(2001).
 CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
 an amide bond (By similarity).
 DR EMBL: AP003137; BAB43593.1; -.
 DR GO: GO:0009986; C:cell surface; IEA.
 DR GO: GO:0005618; C:cell wall; IEA.
 DR GO: GO:0009375; C:cell wall (sensu Gram-positive Bacteria); IEA.
 DR GO: GO:0016020; C:membrane; IEA.
 DR GO: GO:0007155; P:cell adhesion; IEA.
 DR InterPro: IPR008966; Adhes_bact.
 DR InterPro: IPR004237; Fn_bind.
 DR InterPro: IPR005877; Gpos_YsIRK.
 DR InterPro: IPR001899; Gram_pos_anchor.
 DR Pfam: PF02986; Fn_bind; 1.
 DR Pfam: PF00746; Gram_pos_anchor; 1.
 DR Pfam: PF04650; YsIRK_signal; 1.
 DR TIGRFAMs: TIGR01167; LpxTG_anchor; 1.
 DR TIGRFAMs: TIGR01168; YsIRK_signal; 1.
 DR PROSITE: PS50847; GRAM_POS_ANCHORING; 1.
 DR Cell wall; Complete proteome; Peptidoglycan-anchor.
 KW SEQUENCE 961 AA; 106010 MW; 364940F884EA4101 CRC64;

Query Match 100.0%; Score 56; DB 2; Length 961;
 Best Local Similarity 100.0%; Pred. No. 0.063;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 DFDSVPQIHG 10
 Db 721 DFDSVPQIHG 730

Db 721 DFDSVPQIHG 730

RESULT 6
 ID 06GDU5 PRELIMINARY; PRT; 965 AA.
 AC 06GDU5;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DE Fibronectin-binding protein.
 GN Name=fmbA; OrderedLocustNames=SA2580;
 OS Staphylococcus aureus (strain MRSA252).
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 OX NCBI_TaxID=282458;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX PubMed=15213324; DOI=10.1073/pnas.0402521101;
 RA Holden M.T.G., Fell E.J., Lindsey J.A., Peacock S.J., Day N.P.J.,
 RA Enright M.C., Foster T.J., Moore C.E., Hurst L., Ackin R., Barron A.,
 RA Bason N., Bentley S.D., Chillingworth C., Chillingworth T.,
 RA Churcher C., Clark L., Corton C., Cronin A., Doggett J., Dowd L.,
 RA Feltham T., Hance Z., Harris B., Hauser H., Holtroyd S., Jagsels K.,
 RA James K.D., Leonard N., Line A., Mayes R., Moule S., Mungall K.,
 RA Ormond D., Quail M.A., Rabinowitsch B., Rutherford K.M., Sanders M.,
 RA Sharp S., Simmonds M., Stevens K., Whitehead S., Barrett B.G.,
 RA Spratt B.G., Parkhill J.;
 RT "Complete genomes of two clinical Staphylococcus aureus strains:
 evidence for the rapid evolution of virulence and drug resistance."
 RL Proc. Natl. Acad. Sci. U.S.A. 101:9786-9791(2004).
 CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
 an amide bond (By similarity).
 DR EMBL: BX571856; CAG41560.1; -.
 DR GO: GO:0009986; C:cell surface; IEA.
 DR GO: GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
 DR GO: GO:0016020; C:membrane; IEA.
 DR GO: GO:0007155; P:cell adhesion; IEA.
 DR InterPro: IPR008966; Adhes_bact.
 DR InterPro: IPR004237; Fn_bind.
 DR InterPro: IPR005877; Gpos_YsIRK.
 DR InterPro: IPR001899; Gram_pos_anchor.
 DR Pfam: PF02986; Fn_bind; 1.
 DR Pfam: PF00746; Gram_pos_anchor; 1.
 DR Pfam: PF04650; YsIRK_signal; 1.
 DR TIGRFAMs: TIGR01167; LpxTG_anchor; 1.
 DR TIGRFAMs: TIGR01168; YsIRK_signal; 1.
 DR PROSITE: PS50847; GRAM_POS_ANCHORING; 1.
 DR Cell wall; Complete proteome; Peptidoglycan-anchor.
 KW SEQUENCE 965 AA; 105691 MW; 2982E132164D0551 CRC64;

Query Match 100.0%; Score 56; DB 2; Length 965;
 Best Local Similarity 100.0%; Pred. No. 0.063;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DFDSVPQIHG 10
 Db 777 DFDSVPQIHG 786

RESULT 7
 ID 08NU7 PRELIMINARY; PRT; 1015 AA.
 AC 08NU7;
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DE Fmb protein.
 GN Name=fmb; OrderedLocustNames=MM2421;
 OS Staphylococcus aureus (strain MM2).
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 OX NCBI_TaxID=196620;
 RN [1]
 RP SEQUENCE FROM N.A.

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RC STRAIN=WM2;
RX MEDLINE=22040717; PubMed=12044378; DOI=10.1016/S0140-6736(02)08713-5;
RA Baba T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Oguchi A.,
RA Nagai Y., Iwano N., Asano K., Naimi T., Kuroda H., Cui L.,
RA Yamamoto K., Hiramatsu K.;
RT "Genome and virulence determinants of high virulence community-
RT acquired MRSA";
RL Lancet 359:1819-1827(2002).
CC -!- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC an amide bond (By similarity).
CC EMBL: AP04830; BAB96286.1; -.
DR GO: GO:0009986; C:cell surface; IEA.
DR GO: GO:0005618; C:cell wall; IEA.
DR GO: GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO: GO:0016020; C:membrane; IEA.
DR GO: GO:007155; P:cell adhesion; IEA.
DR InterPro: IPR008966; Adhes_bact.
DR InterPro: IPR004237; Fn_bind.
DR InterPro: IPR001899; Gram_pos_anchor.
DR Pfam: PF02986; Fn_bind; 1.
DR Pfam: PF00746; Gram_pos_anchor; 1.
DR Pfam: PF04650; YSIRK_signal; 1.
DR TIGRFAMs: TIGR01167; LpxTG_anchor; 1.
DR TIGRFAMs: TIGR01168; YSIRK_signal; 1.
DR PROSITE: PS50847; GRAM_POS_ANCHORING; 1.
KW Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ SEQUENCE 1015 AA; 111145 MW; D0F9281BB64D44D2 CRC64;

Query Match 100.0%; Score 56; DB 2; Length 1015;
Best Local Similarity 100.0%; Pred. No. 0.067;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DFDSVPOIHG 10
DB 813 DFDSVPOIHG 822

RESULT 8
O6G6H3 PRELIMINARY; PRT; 1015 AA.
ID O6G6H3;
AC O6G6H3;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Fibronectin-binding protein.
GN OrderedLocustNames=SAS2388;
OS Staphylococcus aureus (strain MSSA476).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxId=282459;
RN [1]
RP SEQUENCE FROM N.A.
RA PubMed=15213324; DOI=10.1073/pnas.0402521101;
RA Holden M.T.G., Fell E.J., Lindsay J.A., Peacock S.U., Day N.P.J.,
RA Enright M.C., Foster T.J., Moore C.E., Hurst L., Atkin R., Barron A.,
RA Baeson N., Bentley S.D., Chillingworth C., Chillingworth T.,
RA Churcher C., Clark L., Corton C., Cronin A., Doggett J., Dowd L.,
RA Fellwell T., Lennard N., Line A., Mayes B., Hauser H., Holtroyd S., Jagels K.,
RA James K.D., Leonard N., Line A., Mayes R., Moule S., Mungall K.,
RA Ormond D., Quail M.A., Rabinowitch E., Rutherford K.M., Sanders M.,
RA Sharp S., Simmonds M., Stevens K., Whitehead S., Barrett B.G.,
RA Spratt B.G., Parkhill J.;
RT "Complete genomes of two clinical Staphylococcus aureus strains:
RT evidence for the rapid evolution of virulence and drug resistance.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:9786-9791(2004).
CC -!- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC an amide bond (By similarity).
CC EMBL: X5571857; CAC44202.1; -.
DR GO: GO:0009986; C:cell surface; IEA.
DR GO: GO:0005618; C:cell wall; IEA.
DR GO: GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO: GO:0016020; C:membrane; IEA.
DR GO: GO:0007155; P:cell adhesion; IEA.

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DR InterPro: IPR008966; Adhes_bact.
DR InterPro: IPR004237; Fn_bind.
DR InterPro: IPR005877; Gpos_YSIRK.
DR InterPro: IPR001899; Gram_pos_anchor.
DR Pfam: PF02986; Fn_bind; 1.
DR Pfam: PF00746; Gram_pos_anchor; 1.
DR Pfam: PF04650; YSIRK_signal; 1.
DR TIGRFAMs: TIGR01167; LpxTG_anchor; 1.
DR TIGRFAMs: TIGR01168; YSIRK_signal; 1.
DR PROSITE: PS50847; GRAM_POS_ANCHORING; 1.
KW Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ SEQUENCE 1015 AA; 111145 MW; D0F9281BB64D44D2 CRC64;

Query Match 100.0%; Score 56; DB 2; Length 1015;
Best Local Similarity 100.0%; Pred. No. 0.067;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DFDSVPOIHG 10
DB 813 DFDSVPOIHG 822

RESULT 9
FNBA STAAU STANDARD; PRT; 1018 AA.
ID FNBA STAAU
AC P14738;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Fibronectin-binding protein precursor (FNBP).
GN Name=fnba;
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxId=1280;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=NCTC 8325-4;
RX MEDLINE=89098998; PubMed=2521391;
RA Signaes C., Raucel G., Joensson K., Lindgren P.-E.,
RA Anantharamaiah G.M., Hoeoek M., Lindberg M.,
RT "Nucleotide sequence of the gene for a fibronectin-binding protein
RT from Staphylococcus aureus: use of this peptide sequence in the
RT synthesis of biologically active peptides.";
RL Proc. Natl. Acad. Sci. U.S.A. 86:699-703(1989).
CC -!- FUNCTION: The ability of bacteria to bind fibronectin has been
CC proposed as a virulence factor enabling bacteria to colonize wound
CC tissues and blood clots. Binding of plasma fibronectin to the
CC bacterial surface might block adhesion receptors on S.aureus, thus
CC representing an important defense mechanism against tissue
CC invasion.
CC -!- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC an amide bond (Potential).
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial/
CC entities requires a license agreement (see http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: J04151; AAA26632.1; -.
DR InterPro: IPR004237; Fn_bind.
DR InterPro: IPR005877; Gpos_YSIRK.
DR InterPro: IPR001899; Gram_pos_anchor.
DR Pfam: PF02986; Fn_bind; 1.
DR Pfam: PF00746; Gram_pos_anchor; 1.
DR Pfam: PF04650; YSIRK_signal; 1.
DR TIGRFAMs: TIGR01167; LpxTG_anchor; 1.
DR TIGRFAMs: TIGR01168; YSIRK_signal; 1.
DR PROSITE: PS50847; GRAM_POS_ANCHORING; 1.
KW Cell adhesion; Cell wall; Peptidoglycan-anchor; Repeat; Signal;
KW Virulence.

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FT SIGNAL 1 36
 FT CHAIN 37 985 Fibronectin-binding protein.
 FT PROPEP 986 1018 Removed by sortase (Potential).
 FT REPEAT 545 574 B-1.
 FT REPEAT 575 604 B-2.
 FT DOMAIN 745 878 4 X approximate tandem repeats,
 FT REPEAT 745 782 Fibronectin-binding domain.
 FT REPEAT 783 820 D-1.
 FT REPEAT 821 859 D-2.
 FT REPEAT 860 878 D-3.
 FT DOMAIN 879 948 D-4 (incomplete).
 FT REPEAT 879 892 5 X tandem repeats, Pro-rich (WR).
 FT REPEAT 893 906 WR 1.
 FT REPEAT 907 920 WR 2.
 FT REPEAT 921 934 WR 3.
 FT REPEAT 935 948 WR 4.
 FT SITE 982 986 WR 5.
 FT MOD_RES 985 985 LpxTG sorting signal (potential).
 FT SEQUENCE 1018 AA; 111780 MW; 58175E020E81F1F CRC64; Pentaglycyl murein peptidoglycan amidated threonine (Potential).

Query Match 100.0%; Score 56; DB 1; Length 1018;
 Best Local Similarity 100.0%; Pred. No. 0.067; Indels 0; Gaps 0;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DFDSPVQING 10
 DB 774 DFDSPVQING 783

RESULT 10
 Q99RD2 PRELIMINARY; PRT; 1038 AA.

ID Q99RD2; AC Q99RD2; DT 01-JUN-2001 (TrEMBLrel. 17, Created)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DB Fibronectin-binding protein homolog.
 GN Name=fnb; OrderedLocustNames=SAV2503;
 OS Staphylococcus aureus (strain M50 / ATCC 700699).
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 OX NCBI_TaxID=158878;
 RX MEDLINE=21311952; Pubmed=11418146; DOI=10.1016/S0140-6736(00)04403-2;
 RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
 RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Iian J.-O., Ito T.,
 RA Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,
 RA Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
 RA Sekintzu K., Hirakawa H., Kohara S., Goto S., Yabuzaki J.,
 RA Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
 RA Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
 RT "Whole genome sequencing of methicillin-resistant Staphylococcus
 aureus.";
 RL Lancet 357:1225-1240(2001).
 CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
 an amide bond (By similarity).
 CC EMBL; AP003365; BAB58665.1; -.
 DR PIR; H90053; H90053.
 DR GO; GO:0009986; C:cell surface; IEA.
 DR GO; GO:0005618; C:cell wall; IEA.
 DR GO; GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0007155; P:cell adhesion; IEA.
 DR InterPro; IPR008966; Adhes_bact.
 DR InterPro; IPR004237; Fn_bind.
 DR InterPro; IPR005877; Gpos_Ysirk.
 DR InterPro; IPR001899; Gram_pos_anchor.
 DR Pfam; PF02986; Fn_bind; 1.
 DR Pfam; PF00746; Gram_pos_anchor; 1.
 DR Pfam; PF04650; Ysirk_signal; 1.

DR TIGRFAMs; TIGR01167; LpxTG_anchor; 1.
 DR TIGRFAMs; TIGR01168; Ysirk_signal; 1.
 DR PROSITE; PSS0847; GRAM_POS_ANCHORING; 1.
 KW Cell wall; Complete proteome; Peptidoglycan-anchor.
 SQ SEQUENCE 1038 AA; 113618 MW; 666BF6BF2BFEBB12 CRC64;

Query Match 100.0%; Score 56; DB 2; Length 1038;
 Best Local Similarity 100.0%; Pred. No. 0.069; Indels 0; Gaps 0;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DFDSPVQING 10
 DB 770 DFDSPVQING 779

RESULT 11
 Q7A3J7 PRELIMINARY; PRT; 1038 AA.

ID Q7A3J7; AC Q7A3J7; DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DB Fnb protein.
 GN Name=fnb; OrderedLocustNames=SA2291;
 OS Staphylococcus aureus (strain N315).
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 OX NCBI_TaxID=158879;
 RX MEDLINE=21311952; Pubmed=11418146; DOI=10.1016/S0140-6736(00)04403-2;
 RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
 RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Iian J.-O., Ito T.,
 RA Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,
 RA Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
 RA Sekintzu K., Hirakawa H., Kohara S., Goto S., Yabuzaki J.,
 RA Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
 RA Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
 RT "Whole genome sequencing of methicillin-resistant Staphylococcus
 aureus.";
 RL Lancet 357:1225-1240(2001).
 CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
 an amide bond (By similarity).
 CC EMBL; AP003337; BAB43594.1; -.
 DR GO; GO:0009986; C:cell surface; IEA.
 DR GO; GO:0005618; C:cell wall; IEA.
 DR GO; GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0007155; P:cell adhesion; IEA.
 DR InterPro; IPR008966; Adhes_bact.
 DR InterPro; IPR004237; Fn_bind.
 DR InterPro; IPR005877; Gpos_Ysirk.
 DR InterPro; IPR001899; Gram_pos_anchor.
 DR Pfam; PF02986; Fn_bind; 1.
 DR Pfam; PF00746; Gram_pos_anchor; 1.
 DR Pfam; PF04650; Ysirk_signal; 1.
 DR TIGRFAMs; TIGR01167; LpxTG_anchor; 1.
 DR TIGRFAMs; TIGR01168; Ysirk_signal; 1.
 DR PROSITE; PSS0847; GRAM_POS_ANCHORING; 1.
 KW Cell wall; Complete proteome; Peptidoglycan-anchor.
 SQ SEQUENCE 1038 AA; 113618 MW; 666BF6BF2BFEBB12 CRC64;

Query Match 100.0%; Score 56; DB 2; Length 1038;
 Best Local Similarity 100.0%; Pred. No. 0.069; Indels 0; Gaps 0;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DFDSPVQING 10
 DB 770 DFDSPVQING 779

RESULT 12
 Q9AEP9 PRELIMINARY; PRT; 152 AA.

AC 09ABP9;
 DT 01-JUN-2001 (TREMBlrel. 17, Created)
 DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE Fibronectin-binding protein (Fragment).
 GN Name=fnb;
 OS Staphylococcus aureus.
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 NC NCBI_TaxId=1280;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC STRAIN=CMRSA-1;
 RX MEDLINE=21246681; PubMed=11349044;
 DOI=10.1128/JAI.69.6.3791-3799.2001;
 RA Rice K., Huesca M., Vaz D., McGavin M.J.,
 RT "Variation in fibronectin binding and fnb locus polymorphisms in
 RT Staphylococcus aureus: identification of antigenic variation in a
 RT fibronectin binding protein adhesin of the epidemic CMRSA-1 strain of
 RT methicillin-resistant S. aureus."
 RT Infect. Immun. 69:3791-3799(2001).
 DR EMBL; AY029184; AAK31588.1; -.
 FT NON_TER 1
 FT NON_TER 152
 SQ SEQUENCE 152 AA; 17193 MW; CFA3913C2B11C025 CRC64;

Query Match 91.1%; Score 51; DB 2; Length 152;
 Best Local Similarity 90.0%; Pred. No. 0.079; Mismatches 1; Indels 0; Gaps 0;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 DFDSVPQING 10
 |||||
 Db 105 DFDSVPQING 114

RESULT 13
 OGIKGO PRELIMINARY; PRT; 85 AA.
 AC 06IKGO;
 DT 05-JUL-2004 (TREMBlrel. 27, Created)
 DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
 DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
 DE HDC12547.
 GN ORFNames=HDC12547;
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 NC NCBI_TaxId=7227;
 RN (1)
 RP SEQUENCE FROM N.A.
 RX PubMed=14709175; DOI=10.1186/gb-2003-5-1-r3;
 RA Hild M., Beckmann B., Haas S., Koch B., Solovyev V., Busold C.,
 RA Fellenberg K., Boutros M., Vingron M., Sauer F., Hohenberg J., Paro R.,
 RT "An integrated gene annotation and transcriptional profiling approach
 RT towards the full gene content of the Drosophila genome."
 RL Genome Biol. 5:R3-R3(2003).
 CC -1- MISCELLANEOUS: The sequence shown here is derived from an
 CC EMBL/GenBank/DBJ third party annotation (TPA) entry.
 DR EMBL; BK002406; DAA03912.1; -.
 DR InterPro; IPR009028; AP2_adap_apd.
 SQ SEQUENCE 85 AA; 10102 MW; 316B879BA6906C3 CRC64;

Query Match 75.0%; Score 42; DB 2; Length 85;
 Best Local Similarity 60.0%; Pred. No. 2.5; Mismatches 3; Indels 1; Gaps 0;
 Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Oy 1 DFDSVPQING 10
 |||||
 Db 7 DFHSIPKLHG 16

RESULT 14
 O66113

ID 066113 PRELIMINARY; PRT; 229 AA.
 AC 066113;
 DT 25-OCT-2004 (TREMBlrel. 28, Created)
 DT 25-OCT-2004 (TREMBlrel. 28, Last sequence update)
 DT 25-OCT-2004 (TREMBlrel. 28, Last annotation update)
 DE Hypothetical protein.
 OS Xenopus tropicalis (Western clawed frog) (Silurana tropicalis).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
 NC NCBI_TaxId=8364;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC TISSUE=Embryo;
 RX PubMed=12477932; DOI=10.1073/pnas.242603899.
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Foshayuk S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulik S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skalski U., Smalins D.E., Scherch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences."
 RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN (2)
 RP SEQUENCE FROM N.A.
 RC TISSUE=Embryo;
 RA Klein S., Gerard D.S.;
 RL Submitted (Aug-2004) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: Contains 2 SH3 domains.
 DR EMBL; BC081338; AAH81338.1; -.
 DR InterPro; IPR000108; Neu_cyt_fact_2.
 DR InterPro; IPR000980; SH2_
 DR InterPro; IPR001452; SH3_
 DR InterPro; IPR011511; SH3_2.
 DR Pfam; PF00017; SH2; 1.
 DR Pfam; PF00018; SH3_1; 2.
 DR Pfam; PF07653; SH3_2; 2.
 DR PRINTS; PR00489; P67PHOX.
 DR PRINTS; PR00401; SH2DOMAIN.
 DR PRINTS; PR00452; SH3DOMAIN.
 DR ProDom; PD000093; SH2; 1.
 DR ProDom; PD000066; SH3; 2.
 DR SMART; SM00252; SH2; 1.
 DR SMART; SM00326; SH3; 2.
 DR PROSITE; PS50001; SH2; 1.
 DR PROSITE; PS50002; SH3; 2.
 KW Hypothetical protein; SH3 domain.
 SQ SEQUENCE 229 AA; 26422 MW; ACC0DCFC344F154B CRC64;

Query Match 73.2%; Score 41; DB 2; Length 229;
 Best Local Similarity 60.0%; Pred. No. 12; Mismatches 2; Indels 0; Gaps 0;
 Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Oy 1 DFDSVPQING 10
 |||||
 Db 150 DIEQVPQVHG 159

RESULT 15
 O6GME6 PRELIMINARY; PRT; 229 AA.
 ID 06GME6

AC 06GME6;
 DT 05-JUL-2004 (TREMBlrel. 27, Created)
 DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
 DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
 DE Hypothetical protein.
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae;
 OC Xenopodinae; Xenopus.
 OX NCBI_TaxID=8355;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Kidney;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marzella K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ushin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mulhally S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywiński M.I., Skalska U., Smalins D.E., Schnerch A., Schein J.B.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Kidney;
 RX MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
 RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
 RA Richardson P.;
 RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus
 RT initiative.";
 RL Dev. Dyn. 225:384-391(2002).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Kidney;
 RA Klein S., Strausberg R.;
 RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: Contains 2 SH3 domains.
 DR EMBL; BC074118; AAH74118.1;
 DR GO; GO:0007242; P:intracellular signaling cascade; IEA.
 DR InterPro; IPR000108; Neu_cyt_fact_2.
 DR InterPro; IPR000980; SH2.
 DR InterPro; IPR001452; SH3.
 DR InterPro; IPR011511; SH3_2.
 DR Pfam; PF00017; SH2; 1.
 DR Pfam; PF00018; SH3; 1; 2.
 DR Pfam; PF07653; SH3_2; 2.
 DR PRINTS; PR00499; P67PHOX.
 DR PRINTS; PR00401; SH2DOMAIN.
 DR PRINTS; PR00452; SH3DOMAIN.
 DR ProDom; PD000093; SH2; 1.
 DR ProDom; PD000066; SH3; 2.
 DR SMART; SM00252; SH2; 1.
 DR SMART; SM00326; SH3; 2.
 DR PROSITE; PS50001; SH2; 1.
 DR PROSITE; PS50002; SH3; 2.
 KM Hypothetical protein; SH3 domain.
 SQ SEQUENCE 229 AA; 26383 MW; 7B278EDC6B3133 CRC64;

QY 1 DEDSVQPIHG 10
 DB 150 DIEQVPQVHG 159

Search completed: October 22, 2005, 08:00:47
 Job time : 56.85 secs

Query Match 73.2%; Score 41; DB 2; Length 229;
 Best Local Similarity 60.0%; Pred. No. 12;
 Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 25, 2005, 20:21:18 ; Search time 63.2 Seconds
(without alignments)
61.196 Million cell updates/sec

Title: US-10-731-238-78

Perfect score: 55
Sequence: 1 DSVPOIHQGN 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

A: Geneseq_16Dec04:*
1: geneseqp1808:*
2: geneseqp1908:*
3: geneseqp2008:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	55	100.0	10	2	AAW65734
2	55	100.0	113	2	AAAR90937
3	55	100.0	130	2	AAAR58806
4	55	100.0	130	2	AAAR58807
5	55	100.0	130	2	AAAR91202
6	55	100.0	130	2	AAAR91201
7	55	100.0	134	2	AAAY29089
8	55	100.0	134	2	AAAY29088
9	55	100.0	134	2	AAAY29087
10	55	100.0	139	2	AAAW1556
11	55	100.0	162	2	AAAR90942
12	55	100.0	164	2	AAAR90938
13	55	100.0	174	2	AAAR58808
14	55	100.0	174	2	AAAR91203
15	55	100.0	181	2	AAAR58805
16	55	100.0	181	2	AAAR91200
17	55	100.0	559	2	AAAR89803
18	55	100.0	767	4	AAU34403
19	55	100.0	767	4	AAU37547
20	55	100.0	940	2	AAAR07070
21	55	100.0	940	6	ABJ19111
22	55	100.0	948	6	ADA89470
23	55	100.0	948	6	ABJ18923
24	55	100.0	948	6	ABW72536
25	55	100.0	961	6	ABU15854

25	55	100.0	1018	1	AAAR82115
27	55	100.0	1018	4	AAU37245
28	55	100.0	1018	4	AAU34301
29	55	100.0	1018	6	ABJ18922
30	55	100.0	1018	6	ABW72537
31	55	100.0	1027	2	AAAR89806
32	55	100.0	1038	6	ABU15903
33	47	85.5	978	4	AAU33960
34	47	85.5	1001	4	AAU37093
35	45	81.8	10	2	AAW65735
36	44	80.0	10	2	AAW65733
37	44	80.0	38	2	AAW65692
38	44	80.0	38	2	AAW65695
39	44	80.0	38	2	AAW65662
40	44	80.0	38	2	AAW65696
41	44	80.0	38	2	AAW65697
42	44	80.0	38	2	AAW65694
43	44	80.0	38	2	AAW65700
44	44	80.0	38	2	AAW65691
45	44	80.0	38	2	AAW65699

ALIGNMENTS

RESULT 1
AAW65734
ID AAW65734 standard; peptide; 10 AA.
XX
AC AAW65734;
XX
DT 16-OCT-1998 (first entry)
XX
DE Fibronectin binding protein-derived peptide #78.
XX
XX microbial surface components recognising adhesive matrix molecule;
KW MSCRAMM; fibronectin; fibronectin-binding protein; antibody; epitope;
KW antidiabetic; bacterial infection; antibiotic-resistant strain.
XX
OS Synthetic.
OS Staphylococcus aureus.
XX
PN WO9831389-A2.
XX
PD 23-JUL-1998.
XX
PF 21-JAN-1998; 98WO-US001222.
XX
PR 21-JAN-1997; 97US-0036139P.
XX
PA (TEXA) UNIV TEXAS A & M SYSTEM.
XX
PI Hoeok M, Patli JM, House-Pompeo KL, Speziale P, Joh D;
PI Megavlin MJ;
XX
DR WPI; 1998-413816/35.
XX
XX Antibody that binds to fibronectin-binding protein, preventing its
PT binding to fibronectin - used to treat or prevent bacterial infection,
PT especially by Staphylococci and Streptococci.
XX
PS Example 9; Page 110; 201pp; English.
XX
XX The invention relates to antibodies that bind to a fibronectin-binding
CC domain of a fibronectin-binding protein, and inhibit binding of the
CC protein to fibronectin. Also claimed are: (1) isolated peptides of a
CC fibronectin-binding protein that do not bind to fibronectin; (2) fusion
CC protein containing at least one peptide of a fibronectin-binding protein
CC linked to a second amino acid sequence; (3) nucleic acid encoding the
CC isolated peptide of (1). Antibodies, the isolated peptides of (1) and the
CC nucleic acids are all useful for immunisation (active or passive) and (by
CC inhibiting binding of bacteria to fibronectin) for preventing or treating
CC infection in humans or other animals, particularly by staphylococci or

CC streptococci, e.g. meningitis, otitis media, pneumonia, endocarditis,
 CC mastitis in cattle, abortion in horses and many others. Since the
 CC antibodies block binding of bacteria, they should be effective against
 CC antibiotic-resistant strains, and may replace antibiotic therapy or
 CC increase its effectiveness. Sequences AAW65719-41 and AAW65658 represent
 CC peptides which were synthesised to span the D1 motif and the N-terminal
 CC 18 amino acids of D2, with each peptide overlapping by eight amino acids
 CC with the previous sequence

XX
 SQ Sequence 10 AA;

Query Match 100.0%; Score 55; DB 2; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.00079;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DSVPOIHGON 10
 |||||
 DB 1 DSVPOIHGON 10

RESULT 2
 AAR90937
 ID AAR90937 standard; peptide; 113 AA.
 XX
 AC AAR90937;
 XX
 DT 23-SEP-1996 (first entry)
 XX
 DE D3D4 polypeptide #1.

XX Fibronectin binding protein; Fbp; S.aureus J2385; monoclonal antibody;
 KM infection; surgical implant; antichaperon agent; hygiene; adhesion;
 KM extracellular matrix protein; oral pathogen; oral cavity.
 XX
 OS Staphylococcus aureus.

XX
 FH Key Location/Qualifiers
 FT Region 1..21
 FT Region /note= "D1 region fragment"
 FT Region 22..59
 FT Region /note= "D2 region"
 FT Region 60..98
 FT Region /note= "D3 region"
 FT Region 99..113
 FT Region /note= "D4 region"
 FT Misc-difference 113
 FT /note= "P113T"

XX WO9604381-A1.
 XX
 PD 15-FEB-1996.
 XX
 PF 28-JUL-1995; 95WO-EP003040.
 XX
 PR 05-AUG-1994; 94GB-00015900.
 XX
 PA (SMK) SMITHKLINE BEECHAM PLC.
 XX
 PI Critchley IA, Dodd I, Barnett P, Mcbay DL;
 XX
 DR WPI; 1996-129397/13.
 XX
 PT Polypeptide(s) derived from Staphylococcus aureus fibronectin binding
 PT protein - inhibit binding of bacteria to extracellular matrix proteins,
 PT for combating infection at the site of wounds and surgical implants, and
 PT in oral hygiene.
 XX
 PS Claim 6; Page 24; 35pp; English.

XX AAR90937-R30942 represent D3D4 polypeptides. These sequences correspond
 CC to fragments of the Staphylococcus aureus fibronectin binding protein
 CC (Fbp). This sequence corresponds to residues 18-130 of S.aureus J2385
 Fbp, and also contains the D2 region, and a portion of the D1 region.

CC These sequences, and monoclonal antibodies against them can be used to
 CC combat infection at the site of wounds, surgical implants and other in-
 CC dwelling devices (such as catheters), and as antichaperon agents in oral
 CC hygiene. They can also be used in the manufacture of a medicament for the
 CC prevention of adhesion of bacteria to extracellular matrix proteins
 CC present on in-dwelling devices or in wounds, or of oral pathogens to
 CC similar proteins on surfaces in the oral cavity

XX
 SQ Sequence 113 AA;

Query Match 100.0%; Score 55; DB 2; Length 113;
 Best Local Similarity 100.0%; Pred. No. 0.012;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DSVPOIHGON 10
 |||||
 DB 15 DSVPOIHGON 24

RESULT 3
 AAR58806
 ID AAR58806 standard; protein; 130 AA.
 XX
 AC AAR58806;
 XX
 DT 25-MAR-2003 (revised)
 DT 30-MAR-1995 (first entry)
 XX
 DE Fibronectin binding domain D1-D4(709-838(P838T)).

XX Fibronectin binding protein; Fbp; fibronectin binding domain;
 KM monoclonal antibody; MAb; adhesion; Gram-positive bacterium; bacteremia;
 KM Escherichia coli.
 XX
 OS Staphylococcus aureus.

XX
 PN WO9418327-A1.
 XX
 PD 18-AUG-1994.
 XX
 PF 04-FEB-1994; 94WO-GB000215.
 XX
 PR 05-FEB-1993; 93GB-00002289.
 PR 20-OCT-1993; 93GB-00021592.
 XX
 PA (SMK) SMITHKLINE BEECHAM PLC.

XX Burnham MKR, Chopra I, Critchley IA, Knowles DDC;
 XX
 PI WPI; 1994-279748/34.
 XX
 DR Fibronection binding protein and monoclonal antibodies specific for Fbp -
 PT useful to prevent adherence of Gram-positive bacteria to indwelling
 PT devices or wounds.
 XX
 PS Disclosure; Page 30; 40pp; English.

XX Polypeptides corresponding to residues G709-T886 plus PPIVPT, G709-
 CC P838(P838T) and G709-P838 (AAR58805-07, respectively) of S. aureus J2385
 CC (NCIMB 40532) Fbp type A fibronectin binding domain D1-D4 region
 CC (AAR58808) were expressed in E. coli BL21(DE4) and used to raise Mabs
 CC specific for Fbp. (Updated on 25-MAR-2003 to correct PN field.)

XX
 SQ Sequence 130 AA;

Query Match 100.0%; Score 55; DB 2; Length 130;
 Best Local Similarity 100.0%; Pred. No. 0.014;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DSVPOIHGON 10
 |||||
 DB 32 DSVPOIHGON 41

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RESULT 4
AA958807
ID AAR58807 standard; protein; 130 AA.
XX
AC AAR58807;
XX
DT 25-MAR-2003 (revised)
DT 30-MAR-1995 (first entry)
XX
DE Fibronectin binding domain D1-D4 (709-838).
XX
KW Fibronectin binding protein; Fbp; fibronectin binding domain;
KW monoclonal antibody; Mab; adhesion; Gram-positive Bacterium; bacteraemia;
KW Escherichia coli.
XX
OS Staphylococcus aureus.
XX
PN WO9418327-A1.
XX
PD 18-AUG-1994.
XX
PF 04-FEB-1994; 94MO-GB000215.
XX
PR 05-FEB-1993; 93GB-00002289.
PR 20-OCT-1993; 93GB-00021592.
XX
PA (SMIK ) SMITHKLINE BEECHAM PLC.
XX
PI Burnham MKR, Chopra I, Critchley IA, Knowles DJC;
XX
DR WPI; 1994-279748/34.
XX
PT Fibronectin binding protein and monoclonal antibodies specific for Fbp -
PT useful to prevent adherence of Gram-positive bacteria to indwelling
PT devices or wounds.
XX
PS Disclosure; Page 30; 40pp; English.
XX
CC Polypeptides corresponding to residues G709-T886 plus PIVPPT, G709-
CC P838(P838T) and G709-P838 (AAR58805-07, respectively) of S. aureus J2385
CC (NCIMB 40532) Fbp type A fibronectin binding domain D1-D4 region
CC (AAR58808) were expressed in E. coli Buz1(DB4) and used to raise Mabs
CC specific for Fbp. (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ Sequence 130 AA;
XX
Query Match 100.0%; Score 55; DB 2; Length 130;
Best Local Similarity 100.0%; Pred. No. 0.014;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 DSVPOIHGON 10
Db 32 DSVPOIHGON 41
XX
RESULT 5
AA91202
ID AAR91202 standard; peptide; 130 AA.
XX
AC AAR91202;
XX
DT 13-NOV-1996 (first entry)
XX
DE D1-D4 fibronectin binding domains.
XX
KW Fibronectin; oral hygiene; gingivitis; gum disease; adhesion;
KW periodontis; oral pathogen; caries; calculus; candidiasis; oral surgery;
KW tissue regeneration; irrigation; toothpaste; dentifrice; mouthwash;
XX
XX lozenge.
XX
OS Staphylococcus aureus.
XX

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PN WO9604003-A1.
XX
PD 15-FEB-1996.
XX
PF 18-JUL-1995; 95WO-EP002825.
XX
PR 05-AUG-1994; 94GB-00015902.
XX
PA (SMIK ) SMITHKLINE BEECHAM PLC.
XX
PI Barnett P, Critchley IA, Dodd I;
XX
DR WPI; 1996-129122/13.
XX
PT Prevention of adherence of oral pathogens in the oral cavity, partic.
PT tooth surfaces - by application of a fibronectin binding protein or
PT polypeptide or a monoclonal antibody or fragment against it.
XX
PS Claim 5; Page 32; 41pp; English.
XX
CC Adherence of oral pathogens, particularly to tooth surfaces, can be
CC prevented by application of a fibronectin binding protein or polypeptide.
CC The fibronectin binding protein or polypeptide is useful in the
CC manufacture of oral hygiene compositions, eg. toothpaste, liquid
CC dentifrice, mouthwash or lozenge. They are useful to prevent the plaque-
CC related development of carious lesions, gingivitis, calculus or
CC periodontal disease and to combat oral cavity infections, e.g.
CC candidiasis. They may also be useful in oral surgery e.g. in guided
CC tissue regeneration procedures to prevent subsequent bacterial infection,
CC and for irrigation of periodontal pockets. This sequence corresponds to
CC amino acids 709-838 of the D1-D4 fibronectin binding domain of
CC Staphylococcus aureus
XX
SQ Sequence 130 AA;
XX
Query Match 100.0%; Score 55; DB 2; Length 130;
Best Local Similarity 100.0%; Pred. No. 0.014;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 DSVPOIHGON 10
Db 32 DSVPOIHGON 41
XX
RESULT 6
AA91201
ID AAR91201 standard; peptide; 130 AA.
XX
AC AAR91201;
XX
DT 13-NOV-1996 (first entry)
XX
DE D1-D4 fibronectin binding domains.
XX
KW Fibronectin; oral hygiene; gingivitis; gum disease; adhesion;
KW periodontis; oral pathogen; caries; calculus; candidiasis; oral surgery;
KW tissue regeneration; irrigation; toothpaste; dentifrice; mouthwash;
XX
XX lozenge.
XX
OS Staphylococcus aureus.
XX
PN WO9604003-A1.
XX
PD 15-FEB-1996.
XX
PF 18-JUL-1995; 95WO-EP002825.
XX
PR 05-AUG-1994; 94GB-00015902.
XX
PA (SMIK ) SMITHKLINE BEECHAM PLC.
XX
PI Barnett P, Critchley IA, Dodd I;
XX

```

DR WPI: 1996-129122/13.
 XX Prevention of adherence of oral pathogens in the oral cavity, partic.
 PT tooth surfaces - by application of a fibronectin binding protein or
 XX polypeptide or a monoclonal antibody or fragment against it.
 PS Claim 5; Page 31-32; 41pp; English.
 CC Adherence of oral pathogens, particularly to tooth surfaces, can be
 CC prevented by application of a fibronectin binding protein or polypeptide.
 CC The fibronectin binding protein or polypeptide is useful in the
 CC manufacture of oral hygiene compositions, eg. toothpaste, liquid
 CC dentifrice, mouthwash or lozenge. They are useful to prevent the plaque-
 CC related development of carious lesions, gingivitis, calculus or
 CC periodontal disease and to combat oral cavity infections, e.g.
 CC candidiasis. They may also be useful in oral surgery e.g. in guided
 CC tissue regeneration procedures to prevent subsequent bacterial infection,
 CC and for irrigation of periodontal pockets. This sequence corresponds to
 CC amino acids 709-838 of the D1-D4 fibronectin binding domain of
 CC Staphylococcus aureus with a P838T substitution
 XX
 SQ Sequence 130 AA;
 Query Match 100.0%; Score 55; DB 2; Length 130;
 Best Local Similarity 100.0%; Pred. No. 0.014;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DSVPOIHGON 10
 DB 32 DSVPOIHGON 41
 RESULT 7
 AAY29089 standard; protein; 134 AA.
 XX AAY29089;
 XX 28-SEP-1999 (first entry)
 DT Cloned fibronectin binding protein binding domain (FnBAB) sequence.
 XX
 DE Bovine herpes virus-2; BHV-2; cytokine; immune response; immunogen; IL;
 XX Interleukin; colony stimulating factor; CSF; interferon; IFN; TNF;
 XX tumour necrosis factor; recombinant virus; vaccine; mucosal disease;
 KM mastitis; breast cancer; stress-induced disease; binding domain; FnBAB;
 KM fibronectin binding protein.
 XX
 OS Staphylococcus aureus.
 XX
 PN WO9916892-A1.
 XX
 PD 08-APR-1999.
 XX
 PF 29-SEP-1998; 98WO-GB002927.
 XX
 PR 29-SEP-1997; 97GB-00020633.
 XX
 PA (UYBR-) UNIV BRISTOL.
 XX
 PI Bradley AJ, Duffas WP;
 XX WPI: 1999-255101/21.
 DR N-PSDB; AAX91506.
 XX
 PT New bovine herpes virus-2 vectors.
 XX
 PS Example 2; Fig 8A-B; 130pp; English.
 CC The invention provides bovine herpes virus-2 (BHV-2) based vectors that
 CC comprise at least one cytokine-encoding DNA sequence. The expression of
 CC cytokines in mammals can up-regulate immune responses to the immunogens.
 CC The cytokine is selected from interleukins (IL), colony stimulating

CC factors (CSF), interferons (IFN) and tumour necrosis factors (TNF). The
 CC BHV-2 based vector or recombinant virus can be used as vaccines. They can
 CC be used for preventing or treating a mucosal disease in a subject, e.g.
 CC ruminants, cattle, sheep, goats, dogs, cats, horses, or man, particularly
 CC mastitis in cows or breast cancers in humans. They can also be used for
 CC preventing or treating a stress-induced disease. The present sequence
 CC represents a S. aureus fibronectin binding protein binding domain
 CC sequence FnBAB, the gene cloned for use in this invention. The gene has
 CC 97.8 percent identity when compared to the previously published sequences
 CC FnBA and FnBB
 XX
 SQ Sequence 134 AA;
 Query Match 100.0%; Score 55; DB 2; Length 134;
 Best Local Similarity 100.0%; Pred. No. 0.014;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DSVPOIHGON 10
 DB 32 DSVPOIHGON 41
 RESULT 8
 AAY29088 standard; protein; 134 AA.
 XX AAY29088;
 XX 28-SEP-1999 (first entry)
 DT S. aureus fibronectin binding protein B (FnBB) binding domain.
 DE
 XX Bovine herpes virus-2; BHV-2; cytokine; immune response; immunogen; IL;
 KM Interleukin; colony stimulating factor; CSF; interferon; IFN; TNF;
 KM tumour necrosis factor; recombinant virus; vaccine; mucosal disease;
 KM mastitis; breast cancer; stress-induced disease; binding domain; FnBB;
 KM fibronectin binding protein.
 XX
 OS Staphylococcus aureus.
 XX
 PN WO9916892-A1.
 XX
 PD 08-APR-1999.
 XX
 PF 29-SEP-1998; 98WO-GB002927.
 XX
 PR 29-SEP-1997; 97GB-00020633.
 XX
 PA (UYBR-) UNIV BRISTOL.
 XX
 PI Bradley AJ, Duffas WP;
 XX WPI: 1999-255101/21.
 DR N-PSDB; AAX91505.
 XX
 PT New bovine herpes virus-2 vectors.
 XX
 PS Example 2; Fig 8A-B; 130pp; English.
 CC The invention provides bovine herpes virus-2 (BHV-2) based vectors that
 CC comprise at least one cytokine-encoding DNA sequence. The expression of
 CC cytokines in mammals can up-regulate immune responses to the immunogen.
 CC The cytokine is selected from interleukins (IL), colony stimulating
 CC factors (CSF), interferons (IFN) and tumour necrosis factors (TNF). The
 CC BHV-2 based vector or recombinant virus can be used as vaccines. They can
 CC be used for preventing or treating a mucosal disease in a subject, e.g.
 CC ruminants, cattle, sheep, goats, dogs, cats, horses, or man, particularly
 CC mastitis in cows or breast cancers in humans. They can also be used for
 CC preventing or treating a stress-induced disease. The present sequence
 CC represents the binding domain of a previously published S. aureus
 CC fibronectin binding protein B (FnBB) sequence. The FnB binding domain
 CC gene sequence FnBAB, cloned for use in this invention has 97.8 percent
 CC identity when compared to the previously published FnBA and FnBB gene

CC sequences
XX
SQ Sequence 134 AA;

Query Match 100.0%; Score 55; DB 2; Length 134;
Best Local Similarity 100.0%; Pred. No. 0.014;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DSVPOIHGON 10
|||
Db 32 DSVPOIHGON 41

RESULT 9
AAV29087
ID AAV29087 standard; protein; 134 AA.

XX AC AAV29087;

XX DT 28-SBP-1999 (first entry)

XX DE S. aureus fibronectin binding protein A (FnBA) binding domain.

XX KW Bovine herpes virus-2; BHV-2; cytokine; immune response; immunogen; IL;
XX KW Interleukin; colony stimulating factor; CSF; interferon; IFN; TNF;
XX KW tumour necrosis factor; recombinant virus; vaccine; mucosal disease;
XX KW mastitis; breast cancer; stress-induced disease; binding domain; FnBA;
XX KW fibronectin binding protein.

XX OS Staphylococcus aureus.

XX PN WO9916892-A1.

XX PD 08-APR-1999.

XX PF 29-SEP-1998; 98WO-GB002927.

XX PR 29-SEP-1997; 97GB-00020633.

XX PS (UVR-) UNIT BRISTOL.

XX PI Bradley AJ, Duffas WPH;

XX DR WPI; 1999-255101/21.

XX DR N-PSDB; AAX91504.

XX PT New bovine herpes virus-2 vectors.

XX PS Example 2; Fig 8A-B; 130pp; English.

CC The invention provides bovine herpes virus-2 (BHV-2) based vectors that
CC comprise at least one cytokine-encoding DNA sequence. The expression of
CC cytokines in mammals can up-regulate immune responses to the immunogens.
CC The cytokine is selected from interleukins (IL), colony stimulating
CC factors (CSF), interferons (IFN) and tumour necrosis factors (TNF). The
CC BHV-2 based vector or recombinant virus can be used as vaccines. They can
CC be used for preventing or treating a mucosal disease in a subject, e.g.
CC ruminants, cattle, sheep, goats, dogs, cats, horses, or man, particularly
CC mastitis in cows or breast cancers in humans. They can also be used for
CC preventing or treating a stress-induced disease. The present sequence
CC represents the binding domain of a previously published S. aureus
CC fibronectin binding protein A (FnBA) sequence. The FnB binding domain
CC gene sequence FnBAB, cloned for use in this invention has 97.8 percent
CC identity when compared to the previously published FnBA and FnBB gene
CC sequences

XX Sequence 134 AA;

Query Match 100.0%; Score 55; DB 2; Length 134;
Best Local Similarity 100.0%; Pred. No. 0.014;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DSVPOIHGON 10

Db |||
32 DSVPOIHGON 41

RESULT 10
AAW31556
ID AAW31556 standard; protein; 139 AA.

XX AC AAW31556;

XX DT 27-AUG-2003 (revised)

XX DT 25-MAR-2003 (revised)

XX DT 21-MAY-1998 (first entry)

XX DE Fibronectin-binding MSCRAMM derivative pOD.
XX KW fibronectin; pOD; collagen binding protein; sepsis; infection;
XX KW microbial surface component recognising adhesive matrix molecule; MSCRAMM;
XX KW adhesin; vaccine; immunisation; diagnosis; therapy; mastitis.

XX OS Staphylococcus aureus.

XX FH Key Location/Qualifiers

XX FT Peptide 1..12 /note="vector pQE30-derived peptide"

XX PN WO9743314-A2.

XX PD 20-NOV-1997.

XX PF 14-MAY-1997; 97WO-US008210.

XX PR 16-MAY-1996; 96US-001678P.

XX PA (TEXA) UNIT TEXAS A & M SYSTEM.

XX PI (UABR-) UAB RES FOUND.

XX PI Hoeoek M, Patti JM, House-Pompeo K, Schanam N, Symersky J;

XX DR WPI; 1998-008801/01.

XX PT Antibody that interacts with collagen binding domain of Staphylococcal
XX PT cna gene product - useful to prevent bacterial sepsis in animal infected
XX PT with Staphylococcus aureus.

XX PS Disclosure; Page 91; 143pp; English.

CC This protein comprises Staphylococcus aureus fibronectin-binding
CC microbial surface component recognising adhesive matrix molecule (MSCRAMM)
CC derivative pOD, plus a vector-derived N-terminal peptide. The invention
CC relates to claimed nucleic acid sequences (see AAT93436-38) encoding S.
CC aureus collagen binding protein (CBP) epitopes M17, M31 and M55 (see
CC AAW31552-54) that confer protection against S. aureus infection. CBP
CC protein and antigenic epitopes are contemplated for use in the treatment
CC of pathological infections, especially to prevent bacterial adhesion to
CC collagen. The epitopes are also contemplated for use in the preparation
CC of vaccines and as carrier proteins in vaccine formulations, as well as
CC in the formulation of compositions for the prevention of S. aureus
CC infection. pCF33 and pOD (see AAW31556) were used to raise anti-MSCRAMM
CC polyclonal antibodies used in passive immunisation against bovine
CC mastitis. (Updated on 25-MAR-2003 to correct PI field.) (Updated on 27-
CC AUG-2003 to correct OS field.)

XX Sequence 139 AA;

Query Match 100.0%; Score 55; DB 2; Length 139;
Best Local Similarity 100.0%; Pred. No. 0.015;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DSVPOIHGON 10
|||
Db 46 DSVPOIHGON 55

RESULT 11
 AAR90942
 ID AAR90942 standard; peptide; 162 AA.
 XX AAR90942;
 AC 23-SEP-1996 (first entry)
 DT
 XX D3D4 polypeptide #6.
 DE
 XX Fibronectin binding protein; Fbp; S.aureus J2385; monoclonal antibody;
 KW infection; surgical implant; antiladherent agent; hygiene; adhesion;
 KW extracellular matrix protein; oral pathogen; oral cavity.
 XX
 OS Staphylococcus aureus.
 XX
 FH Key Location/Qualifiers
 FT Region 1..19
 FT /note= "D1 region fragment"
 FT 20..57
 FT Region /note= "D2 region"
 FT 58..96
 FT /note= "D3 region"
 FT 97..111
 FT /note= "D4 region"
 FT 111..162
 FT Region /note= "WRI region"
 FT
 XX
 PN WO9604381-A1.
 XX
 PD 15-FEB-1996.
 XX
 PF 28-JUL-1995; 95WO-EP003040.
 XX
 PR 05-AUG-1994; 94GB-00015900.
 XX
 PA (SMIK) SMITHKLINE BEECHAM PLC.
 XX
 PI Critchley IA, Dodd I, Barnett P, Mcday DL;
 DR WPI, 1996-129397/13.
 XX
 PT Polypeptide(s) derived from Staphylococcus aureus fibronectin binding
 PT protein - inhibit binding of bacteria to extracellular matrix proteins,
 PT for combating infection at the site of wounds and surgical implants, and
 PT in oral hygiene.
 PS
 PS Claim 6; Page 24; 35pp; English.
 XX
 CC AAR90937-R90942 represent D3D4 polypeptides. These sequences correspond
 CC to fragments of the Staphylococcus aureus fibronectin binding protein
 CC (Fbp). This sequence corresponds to residues 20-181 of S.aureus J2385
 CC (Fbp), and also contains the D2 region, a portion of the D1 region, and a
 CC portion of the wall region 1 (WRI). These sequences, and monoclonal
 CC antibodies against them can be used to combat infection at the site of
 CC wounds, surgical implants and other in-dwelling devices (such as
 CC catheters), and as antiladherent agents in oral hygiene. They can also be
 CC used in the manufacture of a medicament for the prevention of adhesion of
 CC bacteria to extracellular matrix proteins present on in-dwelling devices
 CC or in wounds, or of oral pathogens to similar proteins on surfaces in the
 CC oral cavity
 XX
 SQ Sequence 162 AA;

Query Match	100.0%	Score 55;	DB 2;	Length 162;
Best Local Similarity	100.0%	Pred. No. 0.017;		
Matches	10;	Conservative	0;	Mismatches 0; Indels 0; Gaps 0
QY	1	DSVDFIHHGN	10	
p	13	DSVDFIHHGN	22	

AC	AAAR09038;	
AD	23-SEP-1996 (first entry)	
AE	D3D4 polypeptide #2.	
AF	Fibronectin binding protein; Fbp; S.aureus J2385; monoclonal antibody;	
AG	infection; surgical implant; antiadherent agent; hygiene; adhesion;	
AH	extracellular matrix protein; oral pathogen; oral cavity.	
AI	Staphylococcus aureus.	
AK	Key	Location/Qualifiers
AL	Region	1. .21
AM	Region	/note= "D1 region fragment"
AN	Region	22. .59
AO	Region	/note= "D2 region"
AP	Region	60. .98
AQ	Region	/note= "D3 region"
AR	Region	99. .113
AS	Region	/note= "D4 region"
AT	Region	114. .164
AV	Region	/note= "WRI region"
AW	WO9604381-A1.	
AX	15-FEB-1996.	
AY	28-JUL-1995;	95WO-EP003040.
AZ	05-AUG-1994;	94GB-00015900.
BA	(SMIK) SMITHKLINE BEECHAM PLC.	
BB	Critchley IA, Dodd I, Barnett P, Mcbay DJ;	
BC	WPI; 1996-129397/13.	
BD	Polypeptide(s) derived from Staphylococcus aureus fibronectin binding	
BE	protein - inhibit binding of bacteria to extracellular matrix proteins,	
BF	for combatting infection at the site of wounds and surgical implants, and	
BG	in oral hygiene.	
BH	Claim 6; Page 24; 35pp; English.	
BI	AA90937-R09042 represent D3D4 polypeptides. These sequences correspond	
BJ	to fragments of the Staphylococcus aureus fibronectin binding protein	
BK	(Fbp). This sequence corresponds to residues 18-181 of S.aureus J2385	
BL	(Fbp), and also contains the D2 region, a portion of the D1 region, and a	
BM	portion of the wall region 1 (WRI1). These sequences, and monoclonal	
BN	antibodies against them can be used to combat infection at the site of	
BO	wounds, surgical implants and other in-dwelling devices (such as	
BP	catheters), and as antiadherent agents in oral hygiene. They can also be	
BQ	used in the manufacture of a medicament for the prevention of adhesion of	
BR	bacteria to extracellular matrix proteins present on in-dwelling devices	
BS	or in wounds, or of oral pathogens to similar proteins on surfaces in the	
BT	oral cavity	
BU	Sequence 164 AA;	

Query Match	100.0%;	Score 55;	DB 2;	Length 164;
Best Local Similarity	100.0%;	Pred. No. 0.018;		
Matches	10;	Conservative	0;	Mismatches 0; Indels 0; Gaps 0;
QY	1	DSVDPQIHQN	10	
Db	15	DSVDPQIHQN	24	

RESULT 13
 AAR58808
 ID AAR58808 standard; protein; 174 AA.
 XX
 AC AAR58808;
 XX
 DT 25-MAR-2003 (revised)
 DT 30-MAR-1995 (first entry)
 XX
 DE Fbp fibronectin binding domain.
 XX
 KW Fibronectin binding protein; Fbp; fibronectin binding domain;
 KW monoclonal antibody; Mab; adhesion; Gram-positive bacterium; bacteremia;
 KW Escherichia coli; pBROC531.
 XX
 OS Staphylococcus aureus.
 XX
 PN WO9418327-A1.
 XX
 PD 18-AUG-1994.
 XX
 PF 04-FEB-1994; 94WO-GB000215.
 XX
 PR 05-FEB-1993; 93GB-00002289.
 PR 20-OCT-1993; 93GB-00021592.
 XX
 PA (SMIK) SMITHKLINE BEECHAM PLC.
 XX
 PI Burnham MKR, Chopra I, Critchley IA, Knowles DUC;
 DR WPI; 1994-279748/34.
 DR N-PSDB; AAQ71838.
 XX
 PT Fibronectin binding protein and monoclonal antibodies specific for Fbp -
 PT useful to prevent adherence of Gram-positive bacteria to indwelling
 PT devices or wounds.
 XX
 PS Disclosure; Page 30; 40pp; English.
 XX
 CC The sequences of DNA encoding S. aureus Fbp type A fibronectin binding
 CC domain (D1-D4) and the encoded protein are provided. D1-D4 polypeptides
 CC have been expressed in E. coli BL21 (DE4) and used to raise Mabs specific
 CC for Fbp. (Updated on 25-MAR-2003 to correct PN field.)
 CC
 SO Sequence 174 AA:
 Query Match 100.0%; Score 55; DB 2; Length 174;
 Best Local Similarity 100.0%; Pred. No. 0.019;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DSVPOIHGON 10
 |||||
 32 DSVPOIHGON 41
 DB

RESULT 14
 AAR91203
 ID AAR91203 standard; protein; 174 AA.
 XX
 AC AAR91203;
 XX
 DT 16-OCT-2003 (revised)
 DT 13-NOV-1996 (first entry)
 XX
 DE D1-D4 fibronectin binding domains.
 XX
 KW Fibronectin; oral hygiene; gingivitis; gum disease; adhesion;
 KW periodontis; oral pathology; caries; calculus; candidiasis; oral surgery;
 KW tissue regeneration; irrigation; toothpaste; dentifrice; mouthwash;
 KW lozenge.
 XX
 OS Staphylococcus aureus; J2385.

XX
 PN WO9604003-A1.
 XX
 PD 15-FEB-1996.
 XX
 PF 18-JUL-1995; 95WO-EP002825.
 XX
 PR 05-AUG-1994; 94GB-00015902.
 XX
 PA (SMIK) SMITHKLINE BEECHAM PLC.
 XX
 PI Barnett P, Critchley IA, Dodd I;
 DR WPI; 1996-129122/13.
 DR N-PSDB; AAT18308.
 XX
 PT Prevention of adherence of oral pathogens in the oral cavity, partic.
 PT tooth surfaces - by application of a fibronectin binding protein or
 PT polypeptide or a monoclonal antibody or fragment against it.
 XX
 PS Claim 5; Page 32; 41pp; English.
 XX
 CC Adherence of oral pathogens, particularly to tooth surfaces, can be
 CC prevented by application of a fibronectin binding protein or polypeptide.
 CC The fibronectin binding protein or polypeptide is useful in the
 CC manufacture of oral hygiene compositions, eg. toothpaste, liquid
 CC dentifrice, mouthwash or lozenge. They are useful to prevent the plaque-
 CC related development of carious lesions, gingivitis, calculus or
 CC periodontal disease and to combat oral cavity infections, e.g.
 CC candidiasis. They may also be useful in oral surgery e.g. in guided
 CC tissue regeneration procedures to prevent subsequent bacterial infection,
 CC and for irrigation of periodontal pockets. This sequence corresponds to
 CC amino acids 709-838 of the D1-D4 fibronectin binding domain of
 CC Staphylococcus aureus with a P838T substitution. (Updated on 16-OCT-2003
 CC to standardise OS field)
 XX
 SO Sequence 174 AA:
 Query Match 100.0%; Score 55; DB 2; Length 174;
 Best Local Similarity 100.0%; Pred. No. 0.019;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DSVPOIHGON 10
 |||||
 32 DSVPOIHGON 41
 DB

RESULT 15
 AAR58805
 ID AAR58805 standard; protein; 181 AA.
 XX
 AC AAR58805;
 XX
 DT 25-MAR-2003 (revised)
 DT 30-MAR-1995 (first entry)
 XX
 DE Fibronectin binding domain D1-D4 (709-886).
 XX
 KW Fibronectin binding protein; Fbp; fibronectin binding domain;
 KW monoclonal antibody; Mab; adhesion; Gram-positive bacterium; bacteremia;
 KW Escherichia coli.
 XX
 OS Staphylococcus aureus.
 XX
 PN WO9418327-A1.
 XX
 PD 18-AUG-1994.
 XX
 PF 04-FEB-1994; 94WO-GB000215.
 XX
 PR 05-FEB-1993; 93GB-00002289.
 PR 20-OCT-1993; 93GB-00021592.
 XX

PA (SMIX) SMITHKLINE BEECHAM PLC.
 XX
 FI Burnham MKR, Chopra I, Critchley IA, Knowles DJC;
 XX
 DR WPI, 1994-279748/34.
 XX
 PT Fibronectin binding protein and monoclonal antibodies specific for Fbp -
 PT useful to prevent adherence of Gram-positive bacteria to indwelling
 PT devices or wounds.
 XX
 PS Disclosure; Page 29-30; 40pp; English.
 XX
 CC Polypeptides corresponding to residues G709-T886 plus PPIVPT, G709-
 CC P838(P838T) and G709-P838 (AAR58805-07, respectively) of S. aureus J2385
 CC (NCIMB 40532) Fbp type A fibronectin binding domain D1-D4 region MADS
 CC (AAR58808) were expressed in E. coli BL21(DE4) and used to raise MAb
 CC specific for Fbp. (Updated on 25-MAR-2003 to correct PN field.)
 XX
 SQ Sequence 181 AA;

Query Match 100.0%; Score 55; DB 2; Length 181;
 Best Local Similarity 100.0%; Pred. No. 0.02;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DSVPOIHGON 10
 |||||
 Db 32 DSVPOIHGON 41

Search completed: October 25, 2005, 20:58:45
 Job time : 64.2 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 22, 2005, 05:46:56 ; Search time 17.3 Seconds
(without alignments)
43.150 Million cell updates/sec

Title: US-10-731-238-78

Perfect score: 55

Sequence: 1 DSVPGIHGON 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

Issued Patents AA: *
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2: /cgn2_6/prodata/1/iaa/5B_COMB.pep.*
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4: /cgn2_6/prodata/1/iaa/6B_COMB.pep.*
5: /cgn2_6/prodata/1/iaa/PCTUS_COMB.pep.*
6: /cgn2_6/prodata/1/iaa/backfile1.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	55	100.0	10	4	US-09-010-317-78	Sequence 78, Appl
2	55	100.0	114	1	US-08-259-000-3	Sequence 3, Appl1
3	55	100.0	130	2	US-08-459-135A-7	Sequence 7, Appl1
4	55	100.0	130	2	US-08-459-135A-8	Sequence 8, Appl1
5	55	100.0	130	3	US-08-495-559-7	Sequence 7, Appl1
6	55	100.0	130	3	US-08-495-559-8	Sequence 8, Appl1
7	55	100.0	139	3	US-08-856-253-8	Sequence 8, Appl1
8	55	100.0	174	2	US-08-459-135A-10	Sequence 10, Appl
9	55	100.0	174	2	US-08-459-135A-13	Sequence 13, Appl
10	55	100.0	174	3	US-08-495-559-10	Sequence 10, Appl
11	55	100.0	174	3	US-08-495-559-13	Sequence 13, Appl
12	55	100.0	176	3	US-08-495-559-6	Sequence 6, Appl1
13	55	100.0	178	2	US-08-459-135A-12	Sequence 12, Appl
14	55	100.0	178	2	US-08-495-559-12	Sequence 12, Appl
15	55	100.0	181	2	US-08-459-135A-6	Sequence 6, Appl1
16	55	100.0	559	4	US-08-956-171E-5251	Sequence 5251, Ap
17	55	100.0	559	4	US-08-781-986A-5251	Sequence 5251, Ap
18	55	100.0	1027	4	US-08-956-171E-5254	Sequence 5254, Ap
19	55	100.0	1027	4	US-08-781-986A-5254	Sequence 5254, Ap
20	45	81.8	10	4	US-09-010-317-79	Sequence 79, Appl
21	44	80.0	10	4	US-09-010-317-77	Sequence 77, Appl
22	44	80.0	38	1	US-08-234-622A-2	Sequence 2, Appl1
23	44	80.0	38	1	US-09-010-317-5	Sequence 5, Appl1
24	44	80.0	38	4	US-09-010-317-6	Sequence 6, Appl1
25	44	80.0	38	4	US-09-010-317-15	Sequence 35, Appl
26	44	80.0	38	4	US-09-010-317-36	Sequence 36, Appl
27	44	80.0	38	4	US-09-010-317-37	Sequence 37, Appl

28	44	80.0	38	4	US-09-010-317-38	Sequence 38, Appl
29	44	80.0	38	4	US-09-010-317-39	Sequence 39, Appl
30	44	80.0	38	4	US-09-010-317-40	Sequence 40, Appl
31	44	80.0	38	4	US-09-010-317-41	Sequence 41, Appl
32	44	80.0	38	4	US-09-010-317-42	Sequence 42, Appl
33	44	80.0	38	4	US-09-010-317-43	Sequence 43, Appl
34	44	80.0	38	4	US-09-010-317-44	Sequence 44, Appl
35	44	80.0	39	4	US-09-010-317-55	Sequence 56, Appl
36	44	80.0	39	4	US-09-010-317-57	Sequence 57, Appl
37	39	70.9	36	4	US-09-010-317-58	Sequence 58, Appl
38	39	70.9	36	4	US-09-010-317-59	Sequence 59, Appl
39	39	70.9	38	1	US-08-234-622A-3	Sequence 3, Appl1
40	39	70.9	38	4	US-09-010-317-7	Sequence 7, Appl1
41	39	70.9	38	4	US-09-010-317-8	Sequence 8, Appl1
42	39	70.9	38	4	US-09-010-317-45	Sequence 45, Appl
43	39	70.9	38	4	US-09-010-317-46	Sequence 46, Appl
44	39	70.9	38	4	US-09-010-317-47	Sequence 47, Appl
45	39	70.9	38	4	US-09-010-317-48	Sequence 48, Appl

ALIGNMENTS

RESULT 1
US-09-010-317-78
Sequence 78, Application US/09010317
Patent No. 6685943
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
APPLICANT: Patti, Joseph M.
APPLICANT: House-Pompeo, Karen L.
APPLICANT: Speziale, Pietro
APPLICANT: Jon, Danny
APPLICANT: McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
TITLE OF INVENTION: AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAMK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 78:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-09-010-317-78
Query Match 100.0%; Score 55; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.00041;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DSVPOIHGN 10
| | | | | | | |
DB 1 DSVPOIHGN 10

RESULT 2
US-08-259-000-3
; Sequence 3, Application US/08259000
; Patent No. 5571514

; GENERAL INFORMATION:
; APPLICANT: HOOK, Magnus
; APPLICANT: LINDBERG, Martin Kjell
; APPLICANT: SIGNAS, Lars Christer
; APPLICANT: MADSTROM, Torkel Mikael
; APPLICANT: FROMAN, Gunnar
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN AS WELL AS
; TITLE OF INVENTION: ITS PREPARATION
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Doane, Swecker & Machis
; STREET: P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/259,000
; FILING DATE: 13-JUN-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: SE 8702272-9
; FILING DATE: 01-JUN-1987
; ATTORNEY/AGENT INFORMATION:
; NAME: Meuth, Donna M
; REGISTRATION NUMBER: 36,607
; REFERENCE/DOCKET NUMBER: 012885-062
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-2021

; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 114 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-259-000-3

Query Match 100.0%; Score 55; DB 1; Length 114;
Best Local Similarity 100.0%; Pred. No. 0.0055;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DSVPOIHGN 10
| | | | | | | |
DB 32 DSVPOIHGN 41

RESULT 3
US-08-459-135A-7
; Sequence 7, Application US/08459135A
; Patent No. 5955078

; GENERAL INFORMATION:
; APPLICANT: BURHAM, Martin Karl Russel
; APPLICANT: CHOPRA, Ian
; APPLICANT: CRITCHLEY, Ian Alfred
; APPLICANT: KNOWLES, David Justin Charles

; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN: MONOCLONAL ANTIBODY AND THEIR US
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corporation
; STREET: 709 Swedeland Road
; CITY: King of Prussia
; STATE: PA
; COUNTRY: U.S.A.
; ZIP: 19406-0939

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: Fastseq, Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/459,135A
; FILING DATE: 02-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB/94/00215
; FILING DATE: 04-Feb-1994

; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Gimm, Edward R
; REGISTRATION NUMBER: 38,891
; REFERENCE/DOCKET NUMBER: P30591C2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-270-4478
; TELEFAX: 610-270-5090
; TEXES:

; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 130 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-459-135A-7

Query Match 100.0%; Score 55; DB 2; Length 130;
Best Local Similarity 100.0%; Pred. No. 0.0064;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DSVPOIHGN 10
| | | | | | | |
DB 32 DSVPOIHGN 41

RESULT 4
US-08-459-135A-8
; Sequence 8, Application US/08459135A
; Patent No. 5955078

; GENERAL INFORMATION:
; APPLICANT: BURHAM, Martin Karl Russel
; APPLICANT: CHOPRA, Ian
; APPLICANT: CRITCHLEY, Ian Alfred
; APPLICANT: KNOWLES, David Justin Charles
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN: MONOCLONAL ANTIBODY AND THEIR US
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corporation
; STREET: 709 Swedeland Road
; CITY: King of Prussia
; STATE: PA
; COUNTRY: U.S.A.
; ZIP: 19406-0939

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: Fastseq, Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/459,135A
; FILING DATE: 02-JUN-1995

CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB/94/00215
FILING DATE: 04-Feb-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Gimmil, Edward R
REGISTRATION NUMBER: 38, 891
REFERENCE/DOCKET NUMBER: P30591C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-4478
TELEFAX: 610-270-5090
TELEX:
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 130 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-459-135A-8

Query Match 100.0%; Score 55; DB 3; Length 130;
Best Local Similarity 100.0%; Pred. No. 0.0064;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DSVPOIHGON 10
|||||
Db 32 DSVPOIHGON 41

RESULT 5
US-08-495-559-7
Sequence 7, Application US/08495559A
Patent No. 6054572
GENERAL INFORMATION:
APPLICANT: BURMAN, Martin Karl Russel
APPLICANT: CHOPRA, Ian
APPLICANT: CRITCHLEY, Ian Alfred
APPLICANT: KNOWLES, David Justin Charles
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN: MONOCLONAL
TITLE OF INVENTION: ANTIBODY AND THEIR USE IN PREVENTING BACTERIAL ADHESION
FILE REFERENCE: P30591
CURRENT APPLICATION NUMBER: US/08/495,559A
CURRENT FILING DATE: 1995-08-03
EARLIER APPLICATION NUMBER: GB 9302289.5
EARLIER FILING DATE: 1993-02-05
EARLIER APPLICATION NUMBER: GB 9321592.9
EARLIER FILING DATE: 1993-10-20
NUMBER OF SEQ ID NOS: 13
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 7
LENGTH: 130
TYPE: PRT
ORGANISM: Staphylococcus aureus
US-08-495-559-7

Query Match 100.0%; Score 55; DB 3; Length 130;
Best Local Similarity 100.0%; Pred. No. 0.0064;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DSVPOIHGON 10
|||||
Db 32 DSVPOIHGON 41

RESULT 6
US-08-495-559-8
Sequence 8, Application US/08495559A
Patent No. 6054572
GENERAL INFORMATION:
APPLICANT: BURMAN, Martin Karl Russel
APPLICANT: CHOPRA, Ian
APPLICANT: CRITCHLEY, Ian Alfred

APPLICANT: KNOWLES, David Justin Charles
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN: MONOCLONAL
TITLE OF INVENTION: ANTIBODY AND THEIR USE IN PREVENTING BACTERIAL ADHESION
FILE REFERENCE: P30591
CURRENT APPLICATION NUMBER: US/08/495,559A
CURRENT FILING DATE: 1995-08-03
EARLIER APPLICATION NUMBER: GB 9302289.5
EARLIER FILING DATE: 1993-02-05
EARLIER APPLICATION NUMBER: GB 9321592.9
EARLIER FILING DATE: 1993-10-20
NUMBER OF SEQ ID NOS: 13
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 8
LENGTH: 130
TYPE: PRT
ORGANISM: Staphylococcus aureus
US-08-495-559-8

Query Match 100.0%; Score 55; DB 3; Length 130;
Best Local Similarity 100.0%; Pred. No. 0.0064;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DSVPOIHGON 10
|||||
Db 32 DSVPOIHGON 41

RESULT 7
US-08-856-253-8
Sequence 8, Application US/08856253
Patent No. 6288214
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
APPLICANT: Patti, Joseph M.
APPLICANT: House-Pompeo, Karen
APPLICANT: Syhanam, Narayana
APPLICANT: Syteraky, Jindrich
TITLE OF INVENTION: COLLAGEN BINDING PROTEIN COMPOSITIONS
TITLE OF INVENTION: AND METHODS OF USE
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: Texas
COUNTRY: U.S.
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/856,253
FILING DATE: Concurrently Herewith
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/017,678
FILING DATE: 16-MAY-1996
ATTORNEY/AGENT INFORMATION:
NAME: Kitchell, Barbara S
REGISTRATION NUMBER: 33,928
REFERENCE/DOCKET NUMBER: TAMK:193
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
TELEFAX: (512) 474-7577
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 139 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-08-856-253-8

Query Match 100.0%; Score 55; DB 3; Length 139;
Best Local Similarity 100.0%; Pred. No. 0.0068;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DSVPOIHGON 10
|||
DB 46 DSVPOIHGON 55

RESULT 8
US-08-459-135A-10
Sequence 10, Application US/08459135A
Patent No. 5955078
GENERAL INFORMATION:
APPLICANT: BURNHAM, Martin Karl Russel
APPLICANT: CHOPRA, Ian
APPLICANT: CRITCHLEY, Ian Alfred
APPLICANT: KNOWLES, David Justin Charles
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN: MONOCLONAL ANTIBODY AND THEIR US
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
STATE: PA
COUNTRY: U.S.A.
ZIP: 19406-0939
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: Fastseq, Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/459,135A
FILING DATE: 02-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB/94/00215
FILING DATE: 04-Feb-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Gimm, Edward R
REGISTRATION NUMBER: 38,891
REFERENCE/DOCKET NUMBER: P30591C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-4478
TELEFAX: 610-270-5090
TELEX:
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 174 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: Protein
US-08-459-135A-10

Query Match 100.0%; Score 55; DB 2; Length 174;
Best Local Similarity 100.0%; Pred. No. 0.0087;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DSVPOIHGON 10
|||
DB 32 DSVPOIHGON 41

RESULT 9
US-08-459-135A-13
Sequence 13, Application US/08459135A
Patent No. 5955078
GENERAL INFORMATION:
APPLICANT: BURNHAM, Martin Karl Russel
APPLICANT: CHOPRA, Ian

APPLICANT: CRITCHLEY, Ian Alfred
APPLICANT: KNOWLES, David Justin Charles
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN: MONOCLONAL ANTIBODY AND THEIR US
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
STATE: PA
COUNTRY: U.S.A.
ZIP: 19406-0939
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: Fastseq, Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/459,135A
FILING DATE: 02-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB/94/00215
FILING DATE: 04-Feb-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Gimm, Edward R
REGISTRATION NUMBER: 38,891
REFERENCE/DOCKET NUMBER: P30591C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-4478
TELEFAX: 610-270-5090
TELEX:
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 174 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-459-135A-13

Query Match 100.0%; Score 55; DB 2; Length 174;
Best Local Similarity 100.0%; Pred. No. 0.0087;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DSVPOIHGON 10
|||
DB 32 DSVPOIHGON 41

RESULT 10
US-08-459-559-10
Sequence 10, Application US/08495559A
Patent No. 6054572
GENERAL INFORMATION:
APPLICANT: BURNHAM, Martin Karl Russel
APPLICANT: CHOPRA, Ian
APPLICANT: CRITCHLEY, Ian Alfred
APPLICANT: KNOWLES, David Justin Charles
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN: MONOCLONAL
TITLE OF INVENTION: ANTIBODY AND THEIR USE IN PREVENTING BACTERIAL ADHESION
FILE REFERENCE: P30591
CURRENT APPLICATION NUMBER: US/08/495,559A
CURRENT FILING DATE: 1995-08-03
EARLIER APPLICATION NUMBER: GB 9302289.5
EARLIER FILING DATE: 1993-02-05
EARLIER APPLICATION NUMBER: GB 9321592.9
EARLIER FILING DATE: 1993-10-20
NUMBER OF SEQ ID NOS: 13
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 10
LENGTH: 174
TYPE: PRT

ORGANISM: Staphylococcus aureus
US-08-495-559-10

Query Match 100.0%; Score 55; DB 3; Length 174;
Best Local Similarity 100.0%; Pred. No. 0.0087;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DSVPOIHGON 10
|||
Db 32 DSVPOIHGON 41

RESULT 11
US-08-495-559-13
; Sequence 13, Application US/08495559A
; Patent No. 6054572
; GENERAL INFORMATION:
; APPLICANT: BURHAM, Martin Karl Russel
; APPLICANT: CHOPRA, Ian
; APPLICANT: CRITCHLEY, Ian Alfred
; APPLICANT: KNOWLES, David Justin Charles
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN: MONOCLONAL
; TITLE OF INVENTION: ANTIBODY AND THEIR USE IN PREVENTING BACTERIAL ADHESION
; FILE REFERENCE: P30591
; CURRENT APPLICATION NUMBER: US/08/495,559A
; CURRENT FILING DATE: 1995-08-03
; EARLIER APPLICATION NUMBER: GB 9302289.5
; EARLIER FILING DATE: 1993-02-05
; EARLIER APPLICATION NUMBER: GB 9321592.9
; EARLIER FILING DATE: 1993-10-20
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 13
; LENGTH: 174
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-08-495-559-13

Query Match 100.0%; Score 55; DB 3; Length 174;
Best Local Similarity 100.0%; Pred. No. 0.0087;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DSVPOIHGON 10
|||
Db 32 DSVPOIHGON 41

RESULT 12
US-08-495-559-6
; Sequence 6, Application US/08495559A
; Patent No. 6054572
; GENERAL INFORMATION:
; APPLICANT: BURHAM, Martin Karl Russel
; APPLICANT: CHOPRA, Ian
; APPLICANT: CRITCHLEY, Ian Alfred
; APPLICANT: KNOWLES, David Justin Charles
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN: MONOCLONAL
; TITLE OF INVENTION: ANTIBODY AND THEIR USE IN PREVENTING BACTERIAL ADHESION
; FILE REFERENCE: P30591
; CURRENT APPLICATION NUMBER: US/08/495,559A
; CURRENT FILING DATE: 1995-08-03
; EARLIER APPLICATION NUMBER: GB 9302289.5
; EARLIER FILING DATE: 1993-02-05
; EARLIER APPLICATION NUMBER: GB 9321592.9
; EARLIER FILING DATE: 1993-10-20
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 176
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-08-495-559-6

Query Match 100.0%; Score 55; DB 3; Length 176;
Best Local Similarity 100.0%; Pred. No. 0.0088;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DSVPOIHGON 10
|||
Db 32 DSVPOIHGON 41

RESULT 13
US-08-459-135A-12
; Sequence 12, Application US/08459135A
; Patent No. 595078
; GENERAL INFORMATION:
; APPLICANT: BURHAM, Martin Karl Russel
; APPLICANT: CHOPRA, Ian
; APPLICANT: CRITCHLEY, Ian Alfred
; APPLICANT: KNOWLES, David Justin Charles
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN: MONOCLONAL ANTIBODY AND THEIR USE
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corporation
; STREET: 709 Swedeland Road
; CITY: King of Prussia
; STATE: PA
; COUNTRY: U.S.A.
; ZIP: 19406-0939
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: Fastseq, Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/459,135A
; FILING DATE: 02-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB/94/00215
; FILING DATE: 04-FEB-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Gimm, Edward R
; REGISTRATION NUMBER: 38,891
; REFERENCE/DOCKET NUMBER: P30591C2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-270-4478
; TELEFAX: 610-270-5090
; TELEX:
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 178 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Protein
US-08-459-135A-12

Query Match 100.0%; Score 55; DB 2; Length 178;
Best Local Similarity 100.0%; Pred. No. 0.0089;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DSVPOIHGON 10
|||
Db 32 DSVPOIHGON 41

RESULT 14
US-08-495-559-12
; Sequence 12, Application US/08495559A
; Patent No. 6054572
; GENERAL INFORMATION:
; APPLICANT: BURHAM, Martin Karl Russel
; APPLICANT: CHOPRA, Ian

APPLICANT: CRITCHLEY, Ian Alfred
APPLICANT: KNOWLES, David Justin Charles
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN: MONOCLONAL
TITLE OF INVENTION: ANTIBODY AND THEIR USE IN PREVENTING BACTERIAL ADHESION
FILE REFERENCE: P30591
CURRENT APPLICATION NUMBER: US/08/495,559A
CURRENT FILING DATE: 1995-08-03
EARLIER APPLICATION NUMBER: GB 9302289.5
EARLIER FILING DATE: 1993-02-05
EARLIER APPLICATION NUMBER: GB 9321592.9
EARLIER FILING DATE: 1993-10-20
NUMBER OF SEQ ID NOS: 13
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 12
LENGTH: 178
TYPE: PRT
ORGANISM: Staphylococcus aureus
US-08-495-559-12

Query Match 100.0%; Score 55; DB 3; Length 178;
Best Local Similarity 100.0%; Pred. No. 0.0089;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DSVPOIHGON 10
|||
Db 32 DSVPOIHGON 41

RESULT 15
US-08-459-135A-6
Sequence 6, Application US/08459135A
Patent No. 5955078
GENERAL INFORMATION:
APPLICANT: BURNHAM, Martin Karl Russel
APPLICANT: CHOPRA, Ian
APPLICANT: CRITCHLEY, Ian Alfred
APPLICANT: KNOWLES, David Justin Charles
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN: MONOCLONAL ANTIBODY AND THEIR US
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
STATE: PA
COUNTRY: U.S.A.
ZIP: 19406-0939
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: Fastseq, Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/459,135A
FILING DATE: 02-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB/94/00215
FILING DATE: 04-Feb-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Gimm, Edward R
REGISTRATION NUMBER: 38,891
REFERENCE/DOCKET NUMBER: P30591C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-4478
TELEFAX: 610-270-5090
TELEX:
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 181 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear

MOLECULE TYPE: Protein
US-08-459-135A-6
Query Match 100.0%; Score 55; DB 2; Length 181;
Best Local Similarity 100.0%; Pred. No. 0.0091;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DSVPOIHGON 10
|||
Db 32 DSVPOIHGON 41

Search completed: October 22, 2005, 07:41:43
Job time : 17.35 secs

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OM protein - protein search, using sw model

Run on: October 22, 2005, 12:09:40 ; Search time 57.25 Seconds
(without alignments)
72.924 Million cell updates/sec

Title: US-10-731-238-78

Perfect score: 55

Sequence: 1 DSVPGIHGQN 10

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 1862951 seqs, 417491010 residues

Total number of hits satisfying chosen parameters: 1862951

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications, AA.*
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3: /cgn2_6/ptodata/2/pubppaa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/2/pubppaa/US06_PUBCOMB.pep.*
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8: /cgn2_6/ptodata/2/pubppaa/US08_PUBCOMB.pep.*
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11: /cgn2_6/ptodata/2/pubppaa/US09B_PUBCOMB.pep.*
12: /cgn2_6/ptodata/2/pubppaa/US09_NEW_PUB.pep.*
13: /cgn2_6/ptodata/2/pubppaa/US10A_PUBCOMB.pep.*
14: /cgn2_6/ptodata/2/pubppaa/US10B_PUBCOMB.pep.*
15: /cgn2_6/ptodata/2/pubppaa/US10C_PUBCOMB.pep.*
16: /cgn2_6/ptodata/2/pubppaa/US10D_PUBCOMB.pep.*
17: /cgn2_6/ptodata/2/pubppaa/US10E_PUBCOMB.pep.*
18: /cgn2_6/ptodata/2/pubppaa/US10F_PUBCOMB.pep.*
19: /cgn2_6/ptodata/2/pubppaa/US11A_PUBCOMB.pep.*
20: /cgn2_6/ptodata/2/pubppaa/US11_NEW_PUB.pep.*
21: /cgn2_6/ptodata/2/pubppaa/US60_NEW_PUB.pep.*
22: /cgn2_6/ptodata/2/pubppaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	55	100.0	10	US-10-731-238-78	Sequence 78, Appl
2	55	100.0	139	US-09-813-820-8	Sequence 8, Appl
3	55	100.0	388	US-08-901-062-1	Sequence 1, Appl
4	55	100.0	359	US-08-781-986A-5251	Sequence 5251, Ap
5	55	100.0	559	US-10-329-624-5251	Sequence 5251, Ap
6	55	100.0	767	US-09-815-242-5899	Sequence 5899, Ap
7	55	100.0	767	US-09-815-242-13140	Sequence 13140, A
8	55	100.0	940	US-10-470-048B-424	Sequence 424, App
9	55	100.0	948	US-10-470-048B-69	Sequence 69, Appl
10	55	100.0	961	US-10-282-122A-43778	Sequence 43778, A
11	55	100.0	1018	US-09-815-242-5797	Sequence 5797, Ap

12	55	100.0	1018	9	US-09-815-242-12838	Sequence 12838, A
13	55	100.0	1018	17	US-10-470-048B-68	Sequence 68, Appl
14	55	100.0	1027	8	US-08-781-986A-5254	Sequence 5254, Ap
15	55	100.0	1027	15	US-10-329-624-5254	Sequence 5254, Ap
16	55	100.0	1038	15	US-10-282-122A-43827	Sequence 43827, A
17	55	100.0	978	9	US-09-815-242-5456	Sequence 5456, Ap
18	47	85.5	1001	9	US-09-815-242-12686	Sequence 12686, A
19	45	81.8	10	18	US-10-731-238-79	Sequence 79, Appl
20	44	80.0	10	18	US-10-731-238-77	Sequence 77, Appl
21	44	80.0	38	18	US-10-731-238-5	Sequence 5, Appl
22	44	80.0	38	18	US-10-731-238-6	Sequence 6, Appl
23	44	80.0	38	18	US-10-731-238-35	Sequence 35, Appl
24	44	80.0	38	18	US-10-731-238-36	Sequence 36, Appl
25	44	80.0	38	18	US-10-731-238-37	Sequence 37, Appl
26	44	80.0	38	18	US-10-731-238-38	Sequence 38, Appl
27	44	80.0	38	18	US-10-731-238-39	Sequence 39, Appl
28	44	80.0	38	18	US-10-731-238-40	Sequence 40, Appl
29	44	80.0	38	18	US-10-731-238-41	Sequence 41, Appl
30	44	80.0	38	18	US-10-731-238-42	Sequence 42, Appl
31	44	80.0	38	18	US-10-731-238-43	Sequence 43, Appl
32	44	80.0	38	18	US-10-731-238-44	Sequence 44, Appl
33	44	80.0	39	18	US-10-731-238-56	Sequence 56, Appl
34	44	80.0	39	18	US-10-731-238-57	Sequence 57, Appl
35	40	72.7	590	15	US-10-282-122A-65996	Sequence 65996, A
36	40	72.7	590	16	US-10-472-260-196	Sequence 196, App
37	39	70.9	36	18	US-10-731-238-58	Sequence 58, Appl
38	39	70.9	36	18	US-10-731-238-59	Sequence 59, Appl
39	39	70.9	38	18	US-10-731-238-7	Sequence 7, Appl
40	39	70.9	38	18	US-10-731-238-7	Sequence 8, Appl
41	39	70.9	38	18	US-10-731-238-8	Sequence 8, Appl
42	39	70.9	38	18	US-10-731-238-45	Sequence 45, Appl
43	39	70.9	38	18	US-10-731-238-46	Sequence 46, Appl
44	39	70.9	38	18	US-10-731-238-47	Sequence 47, Appl
45	39	70.9	38	18	US-10-731-238-48	Sequence 48, Appl
					US-10-731-238-49	Sequence 49, Appl

ALIGNMENTS

RESULT 1
US-10-731-238-78
; Sequence 78, Application US//10731238
; Publication No. US20050123552A1
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
Patel, Joseph M.
House-Pompeo, Karen L.
Speziale, Pietro
Joh, Danny
McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US//10-731,238
FILING DATE: 10-Dec-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US//09/010,317
FILING DATE: 21-Jan-1998
APPLICATION NUMBER: US 60/036,139

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; FILING DATE: 21-JAN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Hilder, David W.
; REGISTRATION NUMBER: 41,071
; REFERENCE/DOCKET NUMBER: TAMK:189
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 512-418-3000
; TELEFAX: 512-474-7577
; INFORMATION FOR SEQ ID NO: 78:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 78:
US-10-731-238-78

Query Match      100.0%; Score 55; DB 18; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0014;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 DSVPOIHGQN 10
        |||||
Db      1 DSVPOIHGQN 10

RESULT 2
US-09-813-820-8
; Sequence 8, Application US/09813820
; Patent No. US20020102262A1
; GENERAL INFORMATION:
; APPLICANT: Hook, Magnus
;          Patti, Joseph M.
;          House-Pompeo, Karen
;          Stanham, Narayana
;          Symeresky, Jindrich
; TITLE OF INVENTION: COLLAGEN BINDING PROTEIN COMPOSITIONS
; AND METHODS OF USE
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: U.S.
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/813,820
; FILING DATE: 22-Mar-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/856,253
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Kitchell, Barbara S.
; REGISTRATION NUMBER: 33,928
; REFERENCE/DOCKET NUMBER: TAMK:193
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (512) 418-3000
; TELEFAX: (512) 474-7577
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 139 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-09-813-820-8
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Query Match      100.0%; Score 55; DB 9; Length 139;
Best Local Similarity 100.0%; Pred. No. 0.024;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 DSVPOIHGQN 10
        |||||
Db      46 DSVPOIHGQN 55

RESULT 3
US-08-901-062-1
; Sequence 1, Application US/08901062
; Publication No. US20020025324A1
; GENERAL INFORMATION:
; APPLICANT: SEALS, JONATHAN R.
; TITLE OF INVENTION: RECOMBINANT BIVALENT BACTERIAL VACCINE
; AND METHODS OF USE
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HALE AND DORR LLP
; STREET: 60 State Street
; CITY: Boston
; STATE: MA
; COUNTRY: United States Of America
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/901,062
; FILING DATE: 25-JUL-1997
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Baker, Hollie L.
; REGISTRATION NUMBER: 31,321
; REFERENCE/DOCKET NUMBER: 106941.153
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 526-6000
; TELEFAX: (617) 526-6000
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 388 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; US-08-901-062-1

Query Match      100.0%; Score 55; DB 8; Length 388;
Best Local Similarity 100.0%; Pred. No. 0.073;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 DSVPOIHGQN 10
        |||||
Db      295 DSVPOIHGQN 304

RESULT 4
US-08-781-986A-5251
; Sequence 5251, Application US/08781986A
; Publication No. US20030054436A1
; GENERAL INFORMATION:
; APPLICANT: Charles Kunsch
; TITLE OF INVENTION: Steaphylococcus aureus Polynucleotides and Sequences
; AND METHODS OF USE
; NUMBER OF SEQUENCES: 5255
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
```

CITY: Rockville
STATE: Maryland
COUNTRY: USA
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/781,986A
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Benson, Bob
REGISTRATION NUMBER: 30,446
REFERENCE/DOCKET NUMBER: PB248PP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 5251:
SEQUENCE CHARACTERISTICS:
LENGTH: 559 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-781-986A-5251

Query Match 100.0%; Score 55; DB 8; Length 559;
Best Local Similarity 100.0%; Pred. No. 0.11;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DSVPOIHGON 10
|||
Db 331 DSVPOIHGON 340

RESULT 5
US-10-329-624-5251
Sequence 5251, Application US/10329624
Publication No. US2004004303A1
GENERAL INFORMATION:
APPLICANT: Charles Kunsch
Gill H. Choi
Patrick S. Dillon
Craig A. Rosen
Steven C. Barash
Michael R. Fannon
TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
NUMBER OF SEQUENCES: 5256
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COUNTRY: USA
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/329,624
FILING DATE: 27-Dec-2002
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/956,171
FILING DATE: October 20, 1997
APPLICATION NUMBER: 60/009,861

FILING DATE: January 5, 1996
APPLICATION NUMBER: 08/781,986
FILING DATE: January 3, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Mark J. Hyman
REGISTRATION NUMBER: 46,789
REFERENCE/DOCKET NUMBER: PB248P1D1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (240) 314-1224
TELEFAX: (301) 309-8439
INFORMATION FOR SEQ ID NO: 5251:
SEQUENCE CHARACTERISTICS:
LENGTH: 559 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 5251:
US-10-329-624-5251

Query Match 100.0%; Score 55; DB 15; Length 559;
Best Local Similarity 100.0%; Pred. No. 0.11;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DSVPOIHGON 10
|||
Db 331 DSVPOIHGON 340

RESULT 6
US-09-815-242-5899
Sequence 5899, Application US/09815242
Patent No. US20020061569A1
GENERAL INFORMATION:
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Karl L.
APPLICANT: Zyskind, Judith W.
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John D.
APPLICANT: Carr, Grant J.
APPLICANT: Yamamoto, Robert T.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in
FILE REFERENCE: ELITRA.01A
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 5899
LENGTH: 767
TYPE: PRT
ORGANISM: Staphylococcus aureus
US-09-815-242-5899

Query Match 100.0%; Score 55; DB 9; Length 767;
Best Local Similarity 100.0%; Pred. No. 0.15;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DSVPOIHGON 10
| | | | |
Db 712 DSVPOIHGON 721

RESULT 7
US-09-815-242-13140

/ Sequence 13140, Application US/09815242
/ Patent No. US2002061569A1
/ GENERAL INFORMATION:
/ APPLICANT: Haselbeck, Robert
/ APPLICANT: Ohlsen, Kari L.
/ APPLICANT: Zyskind, Judith W.
/ APPLICANT: Wall, Daniel
/ APPLICANT: Trawick, John D.
/ APPLICANT: Carr, Grant J.
/ APPLICANT: Yamamoto, Robert T.
/ APPLICANT: Xu, H. Howard
/ TITLE OF INVENTION: Identification of Essential Genes in
/ FILE REFERENCE: ELITRA.011A
/ CURRENT APPLICATION NUMBER: US/09/815,242
/ PRIOR FILING DATE: 2001-03-21
/ PRIOR APPLICATION NUMBER: 60/191,078
/ PRIOR FILING DATE: 2000-03-21
/ PRIOR APPLICATION NUMBER: 60/206,848
/ PRIOR FILING DATE: 2000-05-23
/ PRIOR APPLICATION NUMBER: 60/207,727
/ PRIOR FILING DATE: 2000-05-26
/ PRIOR APPLICATION NUMBER: 60/242,578
/ PRIOR FILING DATE: 2000-10-23
/ PRIOR APPLICATION NUMBER: 60/253,625
/ PRIOR FILING DATE: 2000-11-27
/ PRIOR APPLICATION NUMBER: 60/257,931
/ PRIOR FILING DATE: 2000-12-22
/ PRIOR APPLICATION NUMBER: 60/269,308
/ PRIOR FILING DATE: 2001-02-16
/ NUMBER OF SEQ ID NOS: 14110
/ SOFTWARE: FASTSEQ For Windows Version 4.0
/ SEQ ID NO 13140
/ LENGTH: 767
/ TYPE: PRT
/ ORGANISM: Staphylococcus aureus
US-09-815-242-13140

Query Match 100.0%; Score 55; DB 9; Length 767;
Best Local Similarity 100.0%; Pred. No. 0.15;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DSVPOIHGON 10
| | | | |
Db 712 DSVPOIHGON 721

RESULT 8
US-10-470-048B-424

/ Sequence 424, Application US/10470048B
/ Publication No. US2005003744A1
/ GENERAL INFORMATION:
/ APPLICANT: MEINKE ET AL.
/ TITLE OF INVENTION: A METHOD FOR IDENTIFICATION, ISOLATION AND PRODUCTION OF
/ FILE REFERENCE: SONN:035US
/ CURRENT APPLICATION NUMBER: US/10/470,048B
/ CURRENT FILING DATE: 2003-07-25
/ NUMBER OF SEQ ID NOS: 603
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 424
/ LENGTH: 940
/ TYPE: PRT
/ ORGANISM: Staphylococcus aureus
US-10-470-048B-424

Query Match 100.0%; Score 55; DB 17; Length 940;
Best Local Similarity 100.0%; Pred. No. 0.19;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DSVPOIHGON 10
| | | | |
Db 712 DSVPOIHGON 721

RESULT 9
US-10-470-048B-69

/ Sequence 69, Application US/10470048B
/ Publication No. US2005003744A1
/ GENERAL INFORMATION:
/ APPLICANT: MEINKE ET AL.
/ TITLE OF INVENTION: A METHOD FOR IDENTIFICATION, ISOLATION AND PRODUCTION OF
/ FILE REFERENCE: SONN:035US
/ CURRENT APPLICATION NUMBER: US/10/470,048B
/ CURRENT FILING DATE: 2003-07-25
/ NUMBER OF SEQ ID NOS: 603
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 69
/ LENGTH: 948
/ TYPE: PRT
/ ORGANISM: Staphylococcus aureus
US-10-470-048B-69

Query Match 100.0%; Score 55; DB 17; Length 948;
Best Local Similarity 100.0%; Pred. No. 0.19;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DSVPOIHGON 10
| | | | |
Db 720 DSVPOIHGON 729

RESULT 10
US-10-282-122A-43778

/ Sequence 43778, Application US/10282122A
/ Publication No. US20040029129A1
/ GENERAL INFORMATION:
/ APPLICANT: Wang, Liangsu
/ APPLICANT: Zamudio, Carlos
/ APPLICANT: Malone, Cheryl
/ APPLICANT: Haselbeck, Robert
/ APPLICANT: Ohlsen, Kari
/ APPLICANT: Zyskind, Judith
/ APPLICANT: Wall, Daniel
/ APPLICANT: Trawick, John
/ APPLICANT: Carr, Grant
/ APPLICANT: Yamamoto, Robert
/ APPLICANT: Forsyth, R.
/ APPLICANT: Xu, H.
/ TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
/ FILE REFERENCE: ELITRA.034A
/ CURRENT APPLICATION NUMBER: US/10/282,122A
/ CURRENT FILING DATE: 2003-02-20
/ PRIOR APPLICATION NUMBER: 60/191,078
/ PRIOR FILING DATE: 2000-03-21
/ PRIOR APPLICATION NUMBER: 60/206,848
/ PRIOR FILING DATE: 2000-05-23
/ PRIOR APPLICATION NUMBER: 60/207,727
/ PRIOR FILING DATE: 2000-05-26
/ PRIOR APPLICATION NUMBER: 60/230,335
/ PRIOR FILING DATE: 2000-09-06
/ PRIOR APPLICATION NUMBER: 60/230,347
/ PRIOR FILING DATE: 2000-09-09
/ PRIOR APPLICATION NUMBER: 60/242,578
/ PRIOR FILING DATE: 2000-10-23
/ PRIOR APPLICATION NUMBER: 60/253,625
/ PRIOR FILING DATE: 2000-11-27
/ PRIOR APPLICATION NUMBER: 60/257,931

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; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 43778
; LENGTH: 961
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-10-282-122A-43778
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Query Match          100.0%; Score 55; DB 15; Length 961;
Best Local Similarity 100.0%; Pred. No. 0.19;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy      1 DSVPOIHGON 10
Db      723 DSVPOIHGON 732
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RESULT 11
US-09-815-242-5797
; Sequence 5797, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Karl L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; FILE REFERENCE: ELITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5797
; LENGTH: 1018
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-09-815-242-5797
```

```
Query Match          100.0%; Score 55; DB 9; Length 1018;
Best Local Similarity 100.0%; Pred. No. 0.2;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
Qy      1 DSVPOIHGON 10
Db      776 DSVPOIHGON 785
```

RESULT 12

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US-09-815-242-12838
; Sequence 12838, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Karl L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; FILE REFERENCE: ELITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12838
; LENGTH: 1018
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-09-815-242-12838
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```
Query Match          100.0%; Score 55; DB 9; Length 1018;
Best Local Similarity 100.0%; Pred. No. 0.2;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
Qy      1 DSVPOIHGON 10
Db      776 DSVPOIHGON 785
```

```
RESULT 13
US-10-470-048B-68
; Sequence 68, Application US/10470048B
; Publication No. US2005003744A1
; GENERAL INFORMATION:
; APPLICANT: MEINKS ET AL.
; TITLE OF INVENTION: A METHOD FOR IDENTIFICATION, ISOLATION AND PRODUCTION OF
; FILE REFERENCE: SONN.035US
; CURRENT APPLICATION NUMBER: US/10/470,048B
; CURRENT FILING DATE: 2003-07-25
; NUMBER OF SEQ ID NOS: 603
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 68
; LENGTH: 1018
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-10-470-048B-68
```

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Query Match          100.0%; Score 55; DB 17; Length 1018;
Best Local Similarity 100.0%; Pred. No. 0.2;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
Qy      1 DSVPOIHGON 10
```

Db 776 DSVPOIHGON 785

RESULT 14

US-08-781-986A-5254

; Sequence 5254, Application US/08781986A

; Publication No. US20030054436A1

; GENERAL INFORMATION:

; APPLICANT: Charles Kunesh

; TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences

; NUMBER OF SEQUENCES: 5255

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Human Genome Sciences, Inc.

; STREET: 9410 Key West Avenue

; CITY: Rockville

; STATE: Maryland

; COUNTRY: USA

; ZIP: 20850

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage

; COMPUTER: HP Vectra 486/33

; OPERATING SYSTEM: MSDOS version 6.2

; SOFTWARE: ASCII text

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/781,986A

; FILING DATE:

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER:

; FILING DATE:

; ATTORNEY/AGENT INFORMATION:

; NAME: Benson, Bob

; REGISTRATION NUMBER: 30,446

; REFERENCE/DOCKET NUMBER: PB248PP

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (301) 309-8504

; TELEFAX: (301) 309-8512

; INFORMATION FOR SEQ ID NO: 5254:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 1027 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; US-08-781-986A-5254

Query Match 100.0%; Score 55; DB 8; Length 1027;

Best Local Similarity 100.0%; Pred. No. 0.21;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DSVPOIHGON 10

Db 785 DSVPOIHGON 794

RESULT 15

US-10-329-624-5254

; Sequence 5254, Application US/10329624

; Publication No. US20040043037A1

; GENERAL INFORMATION:

; APPLICANT: Charles Kunesh

; Gail H. Choi

; Patrick S. Dillon

; Craig A. Rosen

; Steven C. Barash

; Michael R. Pannoh

; TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences

; NUMBER OF SEQUENCES: 5256

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Human Genome Sciences, Inc.

; STREET: 9410 Key West Avenue

; CITY: Rockville

; STATE: Maryland

; COUNTRY: USA

; ZIP: 20850

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage

; COMPUTER: HP Vectra 486/33

; OPERATING SYSTEM: MSDOS version 6.2

; SOFTWARE: ASCII text

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/10/329,624

; FILING DATE: 27-Dec-2002

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/956,171

; FILING DATE: October 20, 1997

; APPLICATION NUMBER: 60/009,861

; FILING DATE: January 5, 1996

; APPLICATION NUMBER: 08/781,986

; FILING DATE: January 3, 1997

; ATTORNEY/AGENT INFORMATION:

; NAME: Mark J. Hyman

; REGISTRATION NUMBER: 46,789

; REFERENCE/DOCKET NUMBER: PB248P1D1

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (240) 314-1224

; TELEFAX: (301) 309-8439

; INFORMATION FOR SEQ ID NO: 5254:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 1027 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; SEQUENCE DESCRIPTION: SEQ ID NO: 5254:

US-10-329-624-5254

Query Match 100.0%; Score 55; DB 15; Length 1027;

Best Local Similarity 100.0%; Pred. No. 0.21;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DSVPOIHGON 10

Db 785 DSVPOIHGON 794

Search completed: October 22, 2005, 12:39:47
Job time : 58.25 secs

GenCore version 5.1.6
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OM protein - protein search, using SW model

Run on: October 22, 2005, 06:10:10 ; Search time 11.45 Seconds
(without alignments)
84.032 Million cell updates/sec

Title: US-10-731-238-78

Perfect score: 55
Sequence: 1 DSVPOIHGON 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 791*
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	55	100.0	940	2	S19702 fibronectin-binding
2	55	100.0	961	2	G90053 hypochetinal prote
3	55	100.0	1018	2	A32192 fibronectin-binding
4	55	100.0	1038	2	H90053 hypochetinal prote
5	40	72.7	590	2	E81072 DNA primase NMB153
6	40	72.7	590	2	H81797 conserved hypochet
7	38	69.1	584	2	B89772 hypochetinal prote
8	37	67.3	409	2	T17258 hypochetinal prote
9	37	67.3	510	2	B83009 probable histidine
10	36	65.5	71	2	E82610 hypochetinal prote
11	36	65.5	137	2	PC4110 transcriptions regu
12	36	65.5	172	2	T34227 23K phosphatidyle
13	36	65.5	187	2	A36126 inosine-uridine nu
14	35	63.6	309	2	A83702 Dpp receptor TRV,
15	35	63.6	509	2	T45713 catechol oxidase (
16	35	63.6	583	2	S34785 catechol oxidase (
17	35	63.6	583	2	S30930 catechol oxidase (
18	35	63.6	585	1	S33544 catechol oxidase (
19	35	63.6	587	1	S33543 catechol oxidase (
20	35	63.6	588	2	S34786 catechol oxidase (
21	35	63.6	588	2	S30929 catechol oxidase (
22	35	63.6	592	2	T03682 catechol oxidase (
23	35	63.6	805	2	T06657 hypochetinal prote
24	34	61.8	131	2	A48527 photosystem I prot
25	34	61.8	321	2	A95182 hypochetinal prote
26	34	61.8	322	2	D98049 thioredoxin-disulf
27	34	61.8	361	2	T49337 hypochetinal prote
28	34	61.8	366	2	T44174 DNA polymerase pro
29	34	61.8	367	2	C70820 Probable alcohohde

30	34	61.8	368	1	Q0B8HG early nuclear anti
31	34	61.8	391	2	T43987 pp41, pol processi
32	34	61.8	403	2	T09322 DNA polymerase pro
33	34	61.8	500	2	B98260 hypochetinal prote
34	34	61.8	500	2	AG3024 histidine huch [lm
35	34	61.8	524	2	F75610 histidine ammonia-
36	34	61.8	675	2	T30708 probable major cor
37	34	61.8	692	2	T28783 hypochetinal prote
38	34	61.8	742	2	T23226 hypochetinal prote
39	34	61.8	805	2	C88628 protein W03G1.4 [l
40	34	61.8	805	2	C88037 protein K02E7.3 [l
41	34	61.8	805	2	T03896 hypochetinal prote
42	34	61.8	895	2	I54343 dyseroglycan - hum
43	34	61.8	1217	2	D88966 protein C17B7.7 [l
44	34	61.8	1307	2	T21283 hypochetinal prote
45	33	60.0	188	2	PS0039 methionyl aminopep

ALIGNMENTS

RESULT 1
S19702
fibronectin-binding protein B - Staphylococcus aureus
C/Species: Staphylococcus aureus
C/Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #ext_change 09-Jul-2004
C/Accession: S19702
R/Joenson, K.; Signaes, C.; Mueller, H.P.; Lindberg, M.
Eur. J. Biochem. 202, 1041-1048, 1991
A/Title: Two different genes encode fibronectin binding proteins in Staphylococcus aure
A/Reference number: S19702, PMID:92111475, PMID:1837266
A/Accession: S19702
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-940 <JOE>
A/Cross-references: UNIPROT:Q53682; EMBL:X62992; NID:949040; PIDN:CA44726.1; PID:95815
C/Keywords: fibronectin binding

Query Match 100.0%; Score 55; DB 2; Length 940;
Best Local Similarity 100.0%; Pred. No. 0.011;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DSVPOIHGON 10

DB 712 DSVPOIHGON 721

RESULT 2

G90053
hypochetinal protein fnbB [imported] - Staphylococcus aureus (strain N315)
C/Species: Staphylococcus aureus
C/Date: 10-May-2001 #sequence_revision 10-May-2001 #ext_change 09-Jul-2004
C/Accession: G90053
R/Kuroda, M.; Ohba, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Ogu-
ma, A.; Mizutani, U.; Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.;
C.; Shibata, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
A/Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.
A/Reference number: A89758; PMID:11418146
A/Accession: G90053
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-961 <KUR>
A/Cross-references: UNIPROT:Q99RD3; GB:BA000018; PID:913702452; PIDN:BAB43593.1; GSPDB:
A/Experimental source: strain N315
C/Genetics:
A/Genes: fnbB

Query Match 100.0%; Score 55; DB 2; Length 961;
Best Local Similarity 100.0%; Pred. No. 0.012;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DSVPOIHGON 10

Db 723 DSVPOIHGON 732

RESULT 3

A32192

C:Species: Staphylococcus aureus

C:Date: 31-Jul-1989 #sequence_revision 31-Jul-1989 #text_change 16-Feb-1997

C:Accession: A32192

R:Signaase, C.; Raucel, G.; Joansson, K.; Lindgren, P.E.; Anantharamiah, G.M.; Hoecek, M. Proc. Natl. Acad. Sci. U.S.A. 86, 699-703, 1989

A:Title: Nucleotide sequence of the gene for a fibronectin-binding protein from Staphylococcus aureus

A:Reference number: A32192; MUID:8908998; PMID:2521391

A:Accession: A32192

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-1018 <SIG>

A:Cross-references: GB:J04151

C:Keywords: fibronectin binding

Query Match 100.0%; Score 55; DB 2; Length 1018;
Best Local Similarity 100.0%; Pred. No. 0.012;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DSVPOIHGON 10
Db 776 DSVPOIHGON 785

RESULT 4

H90053

hypothetical protein fnb [imported] - Staphylococcus aureus (strain N315)

C:Species: Staphylococcus aureus

C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004

C:Accession: H90053

R:Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguc ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.; C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K. Lancet 357, 1225-1240, 2001

A:Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.

A:Reference number: A89758; MUID:21311952; PMID:1148146

A:Accession: H90053

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-1038 <KUR>

A:Cross-references: UNIPROT:Q99RD2; GB:BA000018; PID:G13702453; PIDN:BA843594.1; GSPDB:G

A:Experimental source: strain N315

C:Genetics:

A:Gene: fnb

Query Match 100.0%; Score 55; DB 2; Length 1038;
Best Local Similarity 100.0%; Pred. No. 0.013;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DSVPOIHGON 10
Db 772 DSVPOIHGON 781

RESULT 5

E81072

DNA primase NMB1537 [imported] - Neisseria meningitidis (strain MCS8 serogroup B)

C:Species: Neisseria meningitidis

C:Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004

C:Accession: E81072

R:Retcelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.B.; Bisen, J.A. Hickey, E.K.; Haft, D.H.; Salberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.; et al.; Qin, H.; Vanachavan, J.; Gill, J.; Scarlato, V.; Maignani, V.; Pizzi, M. Science 287, 1809-1815, 2000

A:Authors: Grand, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; Ve

A:Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MCS8.

A:Reference number: A81000; MUID:2015755; PMID:10710307

A:Accession: E81072

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-590 <TEF>

A:Cross-references: UNIPROT:P57029; GB:AE002503; GB:AE002098; NID:G7226775; PIDN:AAF4189

A:Experimental source: serogroup B, strain MCS8

C:Genetics:

A:Gene: NMB1537

C:Superfamily: DNA primase

Query Match 72.7%; Score 40; DB 2; Length 590;
Best Local Similarity 75.0%; Pred. No. 7;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 VPQIHGON 10
Db 94 VPKVHGON 101

RESULT 6

H81797

DNA primase (EC 2.7.7.-) NMA1736 [imported] - Neisseria meningitidis (strain Z2491 serog

C:Species: Neisseria meningitidis

C:Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 09-Jul-2004

C:Accession: H81797

R:Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morel ; Holroyd, S.; Jagers, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandream, Nature 404, 502-506, 2000

A:Title: Complete DNA sequence of a serogroup A strain of Neisseria meningitidis Z2491.

A:Reference number: A81775; MUID:20222556; PMID:10761919

A:Accession: H81797

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-590 <PAR>

A:Cross-references: UNIPROT:P57028; GB:AL162757; GB:AL157959; NID:G7380371; PIDN:CB8496

A:Experimental source: serogroup A, strain Z2491

C:Genetics:

A:Gene: dnaG; NMA1736

C:Superfamily: DNA primase

C:Keywords: nucleotidyltransferase

Query Match 72.7%; Score 40; DB 2; Length 590;
Best Local Similarity 75.0%; Pred. No. 7;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 VPQIHGON 10
Db 94 VPKVHGON 101

RESULT 7

B89772

conserved hypothetical protein SA0114 [imported] - Staphylococcus aureus (strain N315)

C:Species: Staphylococcus aureus

C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004

C:Accession: B89772

R:Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguc ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.; C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K. Lancet 357, 1225-1240, 2001

A:Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.

A:Reference number: A89758; MUID:21311952; PMID:1148146

A:Accession: B89772

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-584 <KUR>

A:Cross-references: UNIPROT:Q99X97; GB:BA000018; PID:G13700034; PIDN:BA841333.1; GSPDB:G

A:Experimental source: strain N315

C:Genetics:

A:Gene: SA0114

Query Match 69.1%; Score 38; DB 2; Length 584;
Best Local Similarity 55.6%; Pred. No. 17;

Matches 5; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 2 SVPQIHGN 10
:::|:|:|

Db 419 ALPELHGN 427

RESULT 8

T17258

hypothetical protein DKFZp727A071.1 - human (fragment)

C:Species: Homo sapiens (man)

C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004

C:Accession: T17258

R:Poucka, A.; Klein, M.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.

A:Reference number: Z18723

A:Accession: T17258

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-409 <POU>

A:Cross-references: UNIPROT:Q9UFT1; EMBL:AL117473

A:Experimental source: adult breast cancer; clone DKFZp727A071

C:Genetics:

A:Note: DKFZp727A071.1

C:Superfamily: proline-cRNA ligase pros

Query Match 67.3%; Score 37; DB 2; Length 409;
Best Local Similarity 55.6%; Pred. No. 19;
Matches 5; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 DSVPOIHQ 9
:::|:|:|

Db 333 EAVPQLHGE 341

RESULT 9

B83009

probable histidine/phenylalanine ammonia-lyase PA5093 [imported] - Pseudomonas aeruginosa

C:Species: Pseudomonas aeruginosa

C>Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004

C:Accession: B83009

R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.; Bz

adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Hardy, K.; Lim,

.; Lory, S.; Olson, M.V.

Nature 406, 959-964, 2000

A:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patho

A:Reference number: A82950; MUID:20437337; PMID:10984043

A:Accession: B83009

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-510 <STO>

A:Cross-references: UNIPROT:Q9HU90; GB:AE004922; GB:AE004091; NID:g9951385; PIDN:AG0847

A:Experimental source: strain PA01

C:Genetics:

A:Gene: PA5093

C:Superfamily: Bacillus subtilis histidine ammonia-lyase

Query Match 67.3%; Score 37; DB 2; Length 510;
Best Local Similarity 85.7%; Pred. No. 24;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 SVPQIHG 8
|:|:|:|

Db 283 SIFQIHG 289

RESULT 10

E82610

hypothetical protein XP2016 [imported] - Xylella fastidiosa (strain 9a5c)

C:Species: Xylella fastidiosa

C>Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004

C:Accession: E82610

R:anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequen

Nature 406, 151-157, 2000

A:Title: The genome sequence of the plant pathogen Xylella fastidiosa.

A:Reference number: A82515; MUID:20365717; PMID:10910347

A:Note: for a complete list of authors see reference number A59328 below

A:Accession: E82610

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-71 <SIM>

A:Cross-references: UNIPROT:Q9PBW9; GB:AE004020; GB:AE003849; NID:g9107122; PIDN:AAF8481

A:Experimental source: strain 9a5c

R:Simpton, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.;

Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carter, i

as-Neco, E.; Docena, C.; El-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S.

submitted to GenBank, June 2000

A:Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohm

J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laig

chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, P

A:Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.;

, F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.

Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawa

A:Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silve

M.; Teuhako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.;

A:Reference number: A59328

A:Contents: annotation

C:Genetics:

A:Gene: XF2016

Query Match 65.5%; Score 36; DB 2; Length 71;
Best Local Similarity 60.0%; Pred. No. 4.3;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 DSVPOIHQ 10
|:|:|:|

Db 15 DSVPEIHQS 24

RESULT 11

PC4110

transcription regulator homolog - Streptomyces aureofaciens (fragment)

N:Alternate names: hypothetical 137 protein

C:Species: Streptomyces aureofaciens

C>Date: 10-Jan-1996 #sequence_revision 08-Feb-1996 #text_change 09-Jul-2004

C:Accession: PC4110

R:Kornane, J.; Lempelova, A.; Farkasovsky, M.; Homeroova, D.

Gene 165, 77-80, 1995

A:Title: Cloning, sequencing and expression in Escherichia coli of a Streptomyces aureo

A:Reference number: J04373; MUID:96084956; PMID:7489920

A:Accession: PC4110

A:Molecule type: DNA

A:Residues: 1-137 <ROR>

A:Cross-references: UNIPROT:Q53603; GB:U21191; NID:g706951; PIDN:AAA91363.1; PID:g70695

C:Comment: This protein has a helix-turn-helix DNA-binding domain in the carboxyl-termi

C:Superfamily: Mycobacterium tuberculosis hypothetical protein Rv1931c

C:Keywords: transcription

RESULT 12

T34227

hypothetical protein F20B6.4 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C>Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004

C:Accession: T34227

R:Minx, P.

submitted to the EMBL Data Library, November 1995

A:Description: The sequence of C. elegans cosmid F20B6.

A:Reference number: Z21491
A:Accession: T34227
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-172 <MIN>
A:Cross-references: UNIPROT:Q19627; EMBL:U41015; PIDN:AAA82312.1; CESP:F20B6.4
A:Experimental source: strain Bristol N2
C:Genetics:
A:Gene: CESP:F20B6.4
A:Introns: 57/3; 90/1; 114/3; 139/3
C:Superfamily: Caenorhabditis elegans hypothetical protein F20B6.4

Query Match
Best Local Similarity 65.5%; Score 36; DB 2; Length 172;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4 POIHGON 10
DB 118 PQVHGRN 124

RESULT 13
A36126
23X phosphatidyethanolamine-binding protein - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 28-Mar-1991 #sequence revision 28-Mar-1991 #text_change 09-Jul-2004
C:Accession: A36126; S46484; S37556; I84473; S37555
R:Grandy, D.K.; Hanneman, E.; Bunzow, J.; Shin, M.; Machida, C.A.; Bidlack, J.M.; Civej
Mol. Endocrinol. 4, 1370-1376, 1990
A:Title: Purification, cloning, and tissue distribution of a 23-kDa rat protein isolated
A:Reference number: A36126; MUID:91042640; PMID:1978248
A:Accession: A36126
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-187 <GRA>
A:Cross-references: UNIPROT:P31044
R:Perry, A.C.F.; Hall, L.; Bell, A.E.; Jones, R.
Biochem. J. 301, 235-242, 1994
A:Title: Sequence analysis of a mammalian phospholipid-binding protein from testis and e
A:Reference number: S46484; MUID:9431839; PMID:8037677
A:Accession: S46484
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-187 <PER>
A:Cross-references: EMBL:X71873; NID:9510338; PIDN:CAA50708.1; PID:9510339
R:Todoh, N.; Agui, H.; Ojika, K.
Submitted to the EMBL Data Library, September 1993
A:Description: Sequences of rat HCNP precursor protein promoter region.
A:Reference number: S37556
A:Accession: S37556
A:Molecule type: DNA
A:Residues: 1-45 <TOD>
A:Cross-references: EMBL:X75254
R:Todoh, N.; Tojo, S.; Agui, H.; Ojika, K.
Brain Res. Mol. Brain Res. 30, 381-384, 1995
A:Title: Sequence homology of rat and human HCNP precursor proteins, bovine phosphatidyl
A:Reference number: I38109; MUID:95364631; PMID:7637590
A:Accession: I84473
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-187 <RES>
A:Cross-references: EMBL:X75253; NID:9406291; PIDN:CAA53032.1; PID:9406292
C:Superfamily: Caenorhabditis elegans hypothetical protein Y69E1A.5

Query Match
Best Local Similarity 65.5%; Score 36; DB 2; Length 187;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 DSVPOIHGO 9
DB 175 DSVPLHGO 183

RESULT 14
A83702
inosine-uridine nucleoside hydrolase BH0417 [imported] - Bacillus halodurans (strain C-1
C:Species: Bacillus halodurans
C:Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004
C:Accession: A83702
R:Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, F.; Hira
Nucleic Acids Res. 28, 4317-4331, 2000
A:Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and
A:Reference number: A83650; MUID:20512582; PMID:11058132
A:Accession: A83702
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-309 <STO>
A:Cross-references: UNIPROT:Q9KFR1; GB:AP001508; GB:BA000004; NID:g10172890; PIDN:BA8041
A:Experimental source: strain C-125
C:Genetics:
A:Gene: BH0417
C:Superfamily: yaaf protein

Query Match
Best Local Similarity 63.6%; Score 35; DB 2; Length 309;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4 POIHGON 10
DB 79 PEIHGEN 85

RESULT 15
I45713
Dpp receptor TKV, splice form 1 - fruit fly (Drosophila melanogaster)
C:Species: Drosophila melanogaster
C:Date: 09-Mar-1996 #sequence_revision 09-Mar-1996 #text_change 16-Aug-2004
C:Accession: I45713
R:Brimmel, T.J.; Twombly, V.; Marques, G.; Wrana, J.L.; Newfield, S.J.; Attisano, L.; Ma
Cell 78, 251-261, 1994
A:Title: Characterization and relationship of Dpp receptors encoded by the saxophone and
A:Reference number: A54829; MUID:94320137; PMID:8044839
A:Accession: I45713
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-509 <RES>
A:Cross-references: UNIPROT:Q95S10; EMBL:U11442; NID:9523341; PIDN:AAA53243.1; PID:95233
C:Genetics:
A:Gene: FlyBase:tkv; thickveins
A:Cross-references: FlyBase:FBgn0003716
C:Superfamily: protein kinase homology
C:Keywords: alternative splicing; ATP
F:198-500/Domain: protein kinase homology <KIN>
F:206-214/Region: protein kinase ATP-binding motif

Query Match
Best Local Similarity 63.6%; Score 35; DB 2; Length 509;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 2 SVPOIHGON 10
DB 79 AVPHLHGRN 87

Search completed: October 22, 2005, 08:04:33
Job time : 11.45 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 22, 2005, 06:06:36 ; Search time 55.85 Seconds
(without alignments)
91.688 Million cell updates/sec

Title: US-10-731-238-78
Perfect score: 55
Sequence: 1 DSVPOIHGON 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues
Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : uniprot_03: *
1: uniprot_sprot: *
2: uniprot_trembl: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	55.100.0	940	2	Q53682	Q53682 staphylococ
2	55.100.0	943	2	Q8NUU8	Q8NUU8 staphylococ
3	55.100.0	957	2	Q6G6H4	Q6G6H4 staphylococ
4	55.100.0	961	2	Q99RD3	Q99RD3 staphylococ
5	55.100.0	961	2	Q7A3U8	Q7A3U8 staphylococ
6	55.100.0	1018	1	FNBA_STRAU	P14738 staphylococ
7	55.100.0	1038	2	Q99RD2	Q99RD2 staphylococ
8	55.100.0	1038	2	Q7A3J7	Q7A3J7 staphylococ
9	47.85.5	152	2	Q9AEP9	Q9AEP9 staphylococ
10	47.85.5	965	2	Q6GDU5	Q6GDU5 staphylococ
11	47.85.5	1015	2	Q8NUU7	Q8NUU7 staphylococ
12	47.85.5	1015	2	Q6G6H3	Q6G6H3 staphylococ
13	41.74.5	346	2	Q99LN2	Q99LN2 mus musculu
14	41.74.5	353	2	Q8BTT8	Q8BTT8 mus musculu
15	41.74.5	354	2	Q9H8B2	Q9H8B2 homo sapien
16	41.74.5	614	2	Q8NDE9	Q8NDE9 homo sapien
17	41.74.5	807	2	Q8C037	Q8C037 mus musculu
18	41.74.5	1268	2	Q6DID3	Q6DID3 mus musculu
19	41.74.5	1271	1	RBNG_HUMAN	Q9UPH6 homo sapien
20	41.74.5	1271	1	Q6NSK3	Q6NSK3 homo sapien
21	41.74.5	1362	2	Q80RT3	Q80RT3 mus musculu
22	40.72.7	290	2	Q8P5Q3	Q8P5Q3 xanthomonas
23	40.72.7	455	2	Q64EV0	Q64EV0 vibrio chol
24	40.72.7	590	1	PRIM_NEIMA	P57028 neisseria m
25	40.72.7	590	1	PRIM_NEIMB	P57029 neisseria m
26	39.70.9	2058	2	Q9LGG0	Q9LGG0 oryza sativ
27	38.69.1	335	2	Q24112	Q24112 drosophila
28	38.69.1	359	2	Q9VER8	Q9VER8 drosophila
29	38.69.1	584	2	Q6X7U5	Q6X7U5 staphylococ
30	38.69.1	584	2	Q8NYS6	Q8NYS6 staphylococ
31	38.69.1	584	2	Q99X97	Q99X97 etaphylococ

32	38.69.1	584	2	Q7A867	Q7A867 staphylococ
33	38.69.1	584	2	Q6GDU7	Q6GDU7 staphylococ
34	38.69.1	584	2	Q6GK17	Q6GK17 staphylococ
35	38.69.1	690	2	Q82RY5	Q82RY5 streptomyce
36	37.67.3	375	2	Q82G88	Q82G88 streptomyce
37	37.67.3	402	2	Q9H6S5	Q9H6S5 homo sapien
38	37.67.3	409	2	Q9JFT1	Q9JFT1 homo sapien
39	37.67.3	475	2	Q7L3T8	Q7L3T8 homo sapien
40	37.67.3	510	2	Q9HU90	Q9HU90 pseudomonas
41	37.67.3	629	2	Q8XSP8	Q8XSP8 ralbstonia s
42	37.67.3	784	2	Q6YGU2	Q6YGU2 rattus norv
43	37.67.3	5987	2	Q8IDN3	Q8IDN3 plasmodium
44	36.65.5	71	2	Q9PBM9	Q9PBM9 xylella fas
45	36.65.5	145	2	Q93QL6	Q93QL6 erwania car

ALIGNMENTS

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RESULT 1
Q53682 ID Q53682 PRELIMINARY; PRT; 940 AA.
AC Q53682;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Fibronectin binding protein B.
GN Name=fnbB;
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1280;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=8325-4;
RX MEDLINE=92111475; PubMed=1837266;
RA Jonsson K., Sigman C., Muller H.P., Lindberg M.;
RT "Two different genes encode fibronectin binding proteins in
RT Staphylococcus aureus. The complete nucleotide sequence and
RT characterization of the second gene.";
RL Eur. J. Biochem. 202:1041-1048 (1991).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC an amide bond (By similarity).
DR EMBL: X62992; CAA44726.1; -.
DR FTR; S19702; S19702.
DR HSSP; Q53653; IN67.
DR GO; GO:0009986; C:cell surface; IEA.
DR GO; GO:0005618; C:cell wall; IEA.
DR GO; GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0007155; P:cell adhesion; IEA.
DR InterPro; IPR008966; Adhes_Dact.
DR InterPro; IPR004237; Fn_bind.
DR InterPro; IPR005877; Gpos_YsIRK.
DR InterPro; IPR001899; Gram_pos_anchor.
DR Pfam; PR02986; Fn_bind_2.
DR Pfam; PR00746; Gram_pos_anchor_1.
DR Pfam; PF04650; YsIRK_signal_1.
DR TIGRFAMs; TIGR01167; LpXTG_anchor_1.
DR TIGRFAMs; TIGR01168; YsIRK_signal_1.
DR PROSITE; PSS0847; GRAM_POS_ANCHORING; 1.
KW Cell wall; Peptidoglycan-anchor.
SQ
SEQUENCE 940 AA; 103555 MW; E35FBBCA907A8345 CRC64;

Query Match 100.0%; Score 55; DB 2; Length 940;
Best Local Similarity 100.0%; Pred. No. 0.066;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 DSVPOIHGON 10
DB 712 DSVPOIHGON 721
RESULT 2

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O8NU8
ID O8NU8 PRELIMINARY; PRT; 943 AA.
AC O8NU8;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE PubB protein.
GN Name=fnbB; Ordered locus names=MM2420;
OS Staphylococcus aureus (strain MM2).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=196620;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MM2.
RX MEDLINE=22040717; PubMed=12044378; DOI=10.1016/S0140-6736(02)08713-5;
RA Baba T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Oguchi A.,
RA Nagai Y., Iwama N., Asano K., Naimi T., Kuroda H., Cui L.,
RA Yamamoto K., Hiramatsu K.;
RT "Genome and virulence determinants of high virulence community-
acquired MRSA.";
RL Lancet 359:1819-1827(2002).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
an amide bond (By similarity).
EMBL; AP004830; BAB96285.1; -.
DR HSP; O53653; IN67.
DR GO; GO:0009986; C:cell surface; IEA.
DR GO; GO:0005618; C:cell wall; IEA.
DR GO; GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0007155; P:cell adhesion; IEA.
DR InterPro; IPR008966; Adhes_bact.
DR InterPro; IPR004237; Fn_bind.
DR InterPro; IPR005877; Gpos_YsIRK.
DR InterPro; IPR001899; Gram_pos_anchor.
DR Pfam; PF02986; Fn_bind; 1.
DR Pfam; PF00746; Gram_pos_anchor; 1.
DR Pfam; PF04650; YsIRK_signal; 1.
DR TIGRFAMs; TIGR01167; LPXG_anchor; 1.
DR TIGRFAMs; TIGR01168; YsIRK_signal; 1.
DR PROSITE; PS50847; GRAM_POS_ANCHORING; 1.
DR Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ SEQUENCE 943 AA; 104537 MW; DA8A5F31947E1B6A CRC64;

Query Match 100.0%; Score 55; DB 2; Length 943;
Best Local Similarity 100.0%; Pred. No. 0.066;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DSVPOIHGON 10
DB 719 DSVPOIHGON 728

RESULT 3
O6G6H4 PRELIMINARY; PRT; 957 AA.
ID O6G6H4;
AC O6G6H4;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Fibronectin-binding protein.
GN Name=fnbB; Ordered locus names=SAS2387;
OS Staphylococcus aureus (strain MSSA476).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=282459;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=15213324; DOI=10.1073/pnas.0402521101;
RA Holden M.T.G., Fell E.J., Lindsey J.A., Peacock S.J., Day N.P.J.,
RA Enright M.C., Foster T.J., Moore C.E., Hurst L., Atkin R., Barron A.,
RA Bason N., Bentley S.D., Chillingworth C., Chillingworth T.,
RA Churcher C., Clark L., Cotton C., Cronin A., Doggett J., Dowd L.,
RA Felwell T., Hance Z., Harris B., Hauber H., Holtroyd S., Jagsis K.,
RA James K.D., Lennard N., Line A., Mayes R., Moule S., Mungall K.,

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RA Ormond D., Quail M.A., Rabinowitch E., Rutherford K.M., Sanders M.,
RA Sharp S., Simmonds M., Stevens K., Whitehead S., Bartell B.G.,
RA Spratt B.G., Parkhill J.;
RT "Complete genomes of two clinical Staphylococcus aureus strains:
RT evidence for the rapid evolution of virulence and drug resistance.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:9786-9791(2004).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
an amide bond (By similarity).
EMBL; BX571857; CAG44201.1; -.
DR GO; GO:0009986; C:cell surface; IEA.
DR GO; GO:0005618; C:cell wall; IEA.
DR GO; GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0007155; P:cell adhesion; IEA.
DR InterPro; IPR008966; Adhes_bact.
DR InterPro; IPR004237; Fn_bind.
DR InterPro; IPR005877; Gpos_YsIRK.
DR InterPro; IPR001899; Gram_pos_anchor.
DR Pfam; PF02986; Fn_bind; 1.
DR Pfam; PF00746; Gram_pos_anchor; 1.
DR Pfam; PF04650; YsIRK_signal; 1.
DR TIGRFAMs; TIGR01167; LPXG_anchor; 1.
DR TIGRFAMs; TIGR01168; YsIRK_signal; 1.
DR PROSITE; PS50847; GRAM_POS_ANCHORING; 1.
DR Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ SEQUENCE 957 AA; 105980 MW; 28F8BA7FFDFD3EAF CRC64;

Query Match 100.0%; Score 55; DB 2; Length 957;
Best Local Similarity 100.0%; Pred. No. 0.067;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DSVPOIHGON 10
DB 719 DSVPOIHGON 728

RESULT 4
O99RD3 PRELIMINARY; PRT; 961 AA.
ID O99RD3;
AC O99RD3;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Fibronectin-binding protein homolog.
GN Name=fnbB; Ordered locus names=SAV2502;
OS Staphylococcus aureus (strain Mu50 / ATCC 700639).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=158878;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Mu50 / ATCC 700639;
RX MEDLINE=21311952; PubMed=1418146; DOI=10.1016/S0140-6736(00)04403-2;
RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Iian J.-Q., Ito T.,
RA Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hasegawa A.,
RA Mizutani-Uji Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
RA Sekimizu K., Hiraoka H., Kuhara S., Goto S., Yabuzaki J.,
RA Kamehisa M., Yameshita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
RA Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
RT "Whole genome sequencing of methicillin-resistant Staphylococcus
RT aureus.";
RL Lancet 357:1225-1240(2001).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
an amide bond (By similarity).
EMBL; AP003365; BAB58664.1; -.
DR PIR; G90053; G90053.
DR HSP; O53653; IN67.
DR GO; GO:0009986; C:cell surface; IEA.
DR GO; GO:0005618; C:cell wall; IEA.
DR GO; GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0007155; P:cell adhesion; IEA.
DR InterPro; IPR008966; Adhes_bact.

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DR InterPro; IPR004237; Fn_bind.
 DR InterPro; IPR005877; Gpos_YsIRK.
 DR InterPro; IPR001899; Gram_pos_anchor.
 DR Pfam; PF02986; Fn_bind; 1.
 DR Pfam; PF00746; Gram_pos_anchor; 1.
 DR Pfam; PF04650; YsIRK_signal; 1.
 DR TIGRfams; TIGR01167; LpXTG_anchor; 1.
 DR TIGRfams; TIGR01168; YsIRK_signal; 1.
 DR PROSITE; PS50847; GRAM_POS_ANCHORING; 1.
 DR Cell wall; Complete proteome; Peptidoglycan-anchor.
 KW SEQUENCE 961 AA; 106010 MW; 364940F884EA4101 CRC64;

Query Match 100.0%; Score 55; DB 2; Length 961;
 Best Local Similarity 100.0%; Pred. No. 0.068;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DSVPOIHGON 10
 DB 723 DSVPOIHGON 732

RESULT 5
 ID Q7A3J8 PRELIMINARY; PRT; 961 AA.
 AC Q7A3J8;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE FndB protein.
 GN Name=fndB; Ordered locus names=SA2290;
 OS Staphylococcus aureus (strain N315).
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 OX NCBI_TaxID=158879; OX
 RN [1]

RP SEQUENCE FROM N.A.
 RX MEDLINE=21311952; PubMed=1141816; DOI=10.1016/S0140-6736(00)04403-2;
 RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
 RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Iian J.-O., Ito T.,
 RA Kanamori M., Matsunaru H., Maruyama A., Murakami H., Hoshiyama A.,
 RA Mizunuma-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kato C.,
 RA Sekintzu K., Hirakawa H., Kubara S., Goto S., Yabuzaki J.,
 RA Kanehisa M., Yamashita A., Ohshima K., Furuya K., Yoshino C., Shida T.,
 RA Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.,
 RT "Whole genome sequencing of methicillin-resistant Staphylococcus
 aureus."
 RL Lancet 357:1225-1240(2001).
 CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
 an amide bond (By similarity).

CC EMBL; AP003137; BAB43593.1; -
 DR GO; GO:0009986; C:cell surface; IEA.
 DR GO; GO:0005618; C:cell wall; IEA.
 DR GO; GO:000975; C:cell wall (sensu Gram-positive Bacteria); IEA.
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0007155; P:cell adhesion; IEA.
 DR InterPro; IPR008966; Adhes_bact.
 DR InterPro; IPR004237; Fn_bind.
 DR InterPro; IPR005877; Gpos_YsIRK.
 DR InterPro; IPR001899; Gram_pos_anchor.
 DR Pfam; PF02986; Fn_bind; 1.
 DR Pfam; PF00746; Gram_pos_anchor; 1.
 DR Pfam; PF04650; YsIRK_signal; 1.
 DR TIGRfams; TIGR01167; LpXTG_anchor; 1.
 DR TIGRfams; TIGR01168; YsIRK_signal; 1.
 DR PROSITE; PS50847; GRAM_POS_ANCHORING; 1.
 KW Cell wall; Complete proteome; Peptidoglycan-anchor.
 SQ SEQUENCE 961 AA; 106010 MW; 364940F884EA4101 CRC64;

Query Match 100.0%; Score 55; DB 2; Length 961;
 Best Local Similarity 100.0%; Pred. No. 0.068;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DSVPOIHGON 10
 DB 723 DSVPOIHGON 732

DB 723 DSVPOIHGON 732

RESULT 6
 ID FNBA_STAAU STANDARD; PRT; 1018 AA.
 AC P14738;
 DT 01-APR-1990 (Rel. 14, Created)
 DT 01-APR-1990 (Rel. 14, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Fibronectin-binding protein precursor (FNBP).
 GN Name=fnbp;
 OS Staphylococcus aureus.
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 OX NCBI_TaxID=1280; OX
 RN [1]

RP SEQUENCE FROM N.A.
 RX STRAIN=NCTC 8325-4;
 RX MEDLINE=89098998; PubMed=2521391;
 RA Signaes C., Raucel G., Jensonson K., Lindgren P.-E.,
 RA Anantharamaiah G.M., Hoeck M., Lindberg M.,
 RT "Nucleotide sequence of the gene for a fibronectin-binding protein
 from Staphylococcus aureus: use of this peptide sequence in the
 synthesis of biologically active peptides."
 RT Proc. Natl. Acad. Sci. U.S.A. 86:699-703(1989).
 RL -1- FUNCTION: The ability of bacteria to bind fibronectin has been
 proposed as a virulence factor enabling bacteria to colonize wound
 tissues and blood clots. Binding of plasma fibronectin to the
 bacterial surface might block adhesion receptors on S. aureus, thus
 representing an important defense mechanism against tissue
 invasion.
 CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
 an amide bond (Potential).

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 or send an email to license@isb-sib.ch).

CC EMBL; J04151; AAA26632.1; -
 DR InterPro; IPR004237; Fn_bind.
 DR InterPro; IPR005877; Gpos_YsIRK.
 DR InterPro; IPR001899; Gram_pos_anchor.
 DR Pfam; PF02986; Fn_bind; 1.
 DR Pfam; PF00746; Gram_pos_anchor; 1.
 DR Pfam; PF04650; YsIRK_signal; 1.
 DR TIGRfams; TIGR01167; LpXTG_anchor; 1.
 DR TIGRfams; TIGR01168; YsIRK_signal; 1.
 DR PROSITE; PS50847; GRAM_POS_ANCHORING; 1.
 KW Cell adhesion; Cell wall; Peptidoglycan-anchor; Repeat; Signal;
 virulence.

KW SIGNAL 1 36
 FT CHAIN 37 985 Fibronectin-binding protein.
 FT REPEAT 986 1018 Removed by sortase (Potential).
 FT REPEAT 545 574 B-1.
 FT REPEAT 575 604 B-2.
 FT DOMAIN 745 878 4 X approximate tandem repeats,
 fibronectin-binding domain.
 FT REPEAT 745 782 D-1.
 FT REPEAT 783 820 D-2.
 FT REPEAT 821 859 D-3.
 FT REPEAT 860 878 D-4 (incomplete).
 FT DOMAIN 879 948 5 X tandem repeats, Pro-rich (WR).
 FT REPEAT 879 892 WR 1.
 FT REPEAT 893 906 WR 2.
 FT REPEAT 907 920 WR 3.
 FT REPEAT 921 934 WR 4.
 FT REPEAT 935 948 WR 5.
 FT SITE 982 986 LpXTG sorting signal (Potential).
 FT MOD_RES 985 985 Pentaglycyl murein peptidoglycan amidated

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FT      SEQUENCE      1018 AA; 111780 MW; 58175E0020BE1F1F CRC64;
SQ      Query Match
        Best Local Similarity 100.0%; Score 55; DB 1; Length 1018;
        Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 DSVPOIHGON 10
        |||||
Db      776 DSVPOIHGON 785

RESULT 7
Q99RD2 PRELIMINARY; PRT; 1038 AA.
ID      Q99RD2
AC      Q99RD2;
DT      01-JUN-2001 (TREMBLrel. 17, Created)
DT      01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT      01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE      Fibronectin-binding protein homolog.
GN      Name=fnb; OrderedlocusNames=SAV2503;
OS      Staphylococcus aureus (strain Mu50 / ATCC 700699).
OC      Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX      NCBI_TaxId=158878;
RN      [1]
RP      STRAIN=Mu50 / ATCC 700699;
RX      MEDLINE=21311952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2;
RA      Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
RA      Cui L., Oguchi A., Aoki K.-I., Nagai Y., Iano J.-Q., Ito T.,
RA      Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hoshoyama A.,
RA      Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
RA      Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
RA      Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
RA      Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
RT      "Whole genome sequencing of methicillin-resistant Staphylococcus
RT      aureus.";
RL      Lancet 357:1225-1240(2001).
CC      -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC      an amide bond (By similarity).
DR      EMBL; AP003365; BAB58665.1; -.
DR      PIR; H90053; H90053.
DR      GO; GO:0009986; C:cell surface; IEA.
DR      GO; GO:0005618; C:cell wall; IEA.
DR      GO; GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR      GO; GO:0016020; C:membrane; IEA.
DR      GO; GO:0007155; P:cell adhesion; IEA.
DR      InterPro; IPR008966; Adhes_bact.
DR      InterPro; IPR004237; Fn_bind.
DR      InterPro; IPR005877; Gpos_YsIRK.
DR      InterPro; IPR001899; Gram_pos_anchor.
DR      Pfam; PF02986; Fn_bind.1.
DR      Pfam; PF00746; Gram_pos_anchor.1.
DR      Pfam; PF04650; YsIRK_signal.1.
DR      TIGRFAMs; TIGR01167; LpxTG_anchor.1.
DR      TIGRFAMs; TIGR01168; YsIRK_signal.1.
DR      PROSITE; PS50847; GRAM_POS_ANCHORING.1.
KW      Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ      SEQUENCE 1038 AA; 113618 MW; 666B6BF2BFBEB12 CRC64;

Query Match
Best Local Similarity 100.0%; Score 55; DB 2; Length 1038;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 DSVPOIHGON 10
        |||||
Db      772 DSVPOIHGON 781

RESULT 8
Q7A3J7 PRELIMINARY; PRT; 1038 AA.
ID      Q7A3J7
AC      Q7A3J7;

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DT      05-JUL-2004 (TREMBLrel. 27, Created)
DT      05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DT      05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE      Fnb protein.
GN      Name=fnb; OrderedlocusNames=SA2291;
OS      Staphylococcus aureus (strain N315).
OC      Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX      NCBI_TaxId=158879;
RN      [1]
RP      SEQUENCE FROM N.A.
RX      MEDLINE=21311952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2;
RA      Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
RA      Cui L., Oguchi A., Aoki K.-I., Nagai Y., Iano J.-Q., Ito T.,
RA      Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hoshoyama A.,
RA      Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
RA      Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
RA      Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
RA      Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
RT      "Whole genome sequencing of methicillin-resistant Staphylococcus
RT      aureus.";
RL      Lancet 357:1225-1240(2001).
CC      -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC      an amide bond (By similarity).
DR      EMBL; AP003373; BAB43594.1; -.
DR      GO; GO:0009986; C:cell surface; IEA.
DR      GO; GO:0005618; C:cell wall; IEA.
DR      GO; GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR      GO; GO:0016020; C:membrane; IEA.
DR      GO; GO:0007155; P:cell adhesion; IEA.
DR      InterPro; IPR008966; Adhes_bact.
DR      InterPro; IPR004237; Fn_bind.
DR      InterPro; IPR005877; Gpos_YsIRK.
DR      InterPro; IPR001899; Gram_pos_anchor.
DR      Pfam; PF02986; Fn_bind.1.
DR      Pfam; PF00746; Gram_pos_anchor.1.
DR      Pfam; PF04650; YsIRK_signal.1.
DR      TIGRFAMs; TIGR01167; LpxTG_anchor.1.
DR      TIGRFAMs; TIGR01168; YsIRK_signal.1.
DR      PROSITE; PS50847; GRAM_POS_ANCHORING.1.
KW      Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ      SEQUENCE 1038 AA; 113618 MW; 666B6BF2BFBEB12 CRC64;

Query Match
Best Local Similarity 100.0%; Score 55; DB 2; Length 1038;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 DSVPOIHGON 10
        |||||
Db      772 DSVPOIHGON 781

RESULT 9
Q9AEP9 PRELIMINARY; PRT; 152 AA.
ID      Q9AEP9
AC      Q9AEP9;
DT      01-JUN-2001 (TREMBLrel. 17, Created)
DT      01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT      01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE      Fibronectin-binding protein (Fragment).
GN      Name=fnb;
OS      Staphylococcus aureus.
OC      Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX      NCBI_TaxId=1280;
RN      [1]
RP      SEQUENCE FROM N.A.
RX      STRAIN=CMRSA-1;
RX      MEDLINE=21246681; PubMed=11349044;
RX      DOI=10.1128/IAI.69.6.3791-3799.2001;
RA      Rice K., Huebner M., Vaz D., McGavin M.J.;
RT      "Variance in fibronectin binding and fnb locus polymorphisms in
RT      Staphylococcus aureus: identification of antigenic variation in a
RT      fibronectin binding protein adhesin of the epidemic CMRSA-1 strain of
RT      methicillin-resistant S. aureus.";

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RL Infect. Immun. 69:3791-3799(2001).
DR EMBL; AY029184; AAK31588.1; -.
FT NON TER 1
FT NON TER 152
SQ SEQUENCE 152 AA; 17193 MW; CFA3913C2B11C025 CRC64;

Query Match
Best Local Similarity 90.0%; Score 47; DB 2; Length 152;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DSVPOIQGN 10
DB 31 DSVPOIQGN 40

RESULT 10
Q6GDU5 PRELIMINARY; PRT; 965 AA.
ID 06GDU5
AC 06GDU5;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Fibronectin-binding protein.
GN Name=fndA; OrderedLocustNames=SAR2580;
OS Staphylococcus aureus (strain MRSA252).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=282458;
[1]
RP SEQUENCE FROM N.A.
RX PubMed=15213324; DOI=10.1073/pnas.0402521101;
RA Holden M.T.G., Fell E.J., Lindsay J.A., Peacock S.J., Day N.P.J.,
RA Enright M.C., Foster T.J., Moore C.E., Hurst L., Atkin R., Barton A.,
RA Baeson N., Bentley S.D., Chillingworth C., Chillingworth T.,
RA Churcher C., Clark L., Corton C., Cronin A., Doggett J., Dowd L.,
RA Peitwell T., Hance Z., Harris B., Hauser H., Holtroyd S., Jørgels K.,
RA James K.D., Lennard N., Line A., Mayes R., Mølle S., Mungall K.,
RA Ormond D., Quail M.A., Rabinowitsch E., Rutherford K.M., Sanders M.,
RA Sharp S., Simmonds M., Stevens K., Whitehead S., Barrell B.G.,
RA Spratt B.G., Parkhill J.;
RT "Complete genomes of two clinical Staphylococcus aureus strains:
RT evidence for the rapid evolution of virulence and drug resistance.";
RC Proc. Natl. Acad. Sci. U.S.A. 101:9786-9791(2004).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC an amide bond (By similarity).
DR EMBL; BX571856; CAG41560.1; -.
DR GO; GO:0009986; C:cell surface; IEA.
DR GO; GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0007155; P:cell adhesion; IEA.
DR InterPro; IPR008966; Adhes_bact.
DR InterPro; IPR004237; Fn_bind.
DR InterPro; IPR005877; Gpos_YsIRK.
DR InterPro; IPR001899; Gram_pos_anchor.
DR Pfam; PF02986; Fn_bind.1.
DR Pfam; PF00746; Gram_pos_anchor.1.
DR Pfam; PF04650; YsIRK_signal.1.
DR TIGRFAMs; TIGR01167; LPXTG_anchor.1.
DR TIGRFAMs; TIGR01168; YsIRK_signal.1.
DR PROSITE; PS50847; GRAM_POS_ANCHORING.1.
KM Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ SEQUENCE 965 AA; 105691 MW; 2982E13164D0551 CRC64;

Query Match
Best Local Similarity 85.5%; Score 47; DB 2; Length 965;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DSVPOIQGN 10
DB 779 DSVPOIQGN 788

RESULT 11
Q8NUU7

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ID Q8NUU7 PRELIMINARY; PRT; 1015 AA.
AC Q8NUU7;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Fmb protein.
GN Name=fmb; OrderedLocustNames=MM2421;
OS Staphylococcus aureus (strain MM2).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=196620;
[1]
RP SEQUENCE FROM N.A.
RX PubMed=15213324; DOI=10.1073/pnas.0402521101;
RA Holden M.T.G., Fell E.J., Lindsay J.A., Peacock S.J., Day N.P.J.,
RA Enright M.C., Foster T.J., Moore C.E., Hurst L., Atkin R., Barton A.,
RA Baeson N., Bentley S.D., Chillingworth C., Chillingworth T.,
RA Churcher C., Clark L., Corton C., Cronin A., Doggett J., Dowd L.,
RA Peitwell T., Hance Z., Harris B., Hauser H., Holtroyd S., Jørgels K.,
RA James K.D., Lennard N., Line A., Mayes R., Mølle S., Mungall K.,
RA Ormond D., Quail M.A., Rabinowitsch E., Rutherford K.M., Sanders M.,
RA Sharp S., Simmonds M., Stevens K., Whitehead S., Barrell B.G.,
RA Spratt B.G., Parkhill J.;
RT "Genome and virulence determinants of high virulence community-
RT acquired MRSA";
RC Lancet 359:1819-1827(2002).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC an amide bond (By similarity).
DR EMBL; AF004830; BAB96286.1; -.
DR GO; GO:0009986; C:cell surface; IEA.
DR GO; GO:0005618; C:cell wall; IEA.
DR GO; GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0007155; P:cell adhesion; IEA.
DR InterPro; IPR008966; Adhes_bact.
DR InterPro; IPR004237; Fn_bind.
DR InterPro; IPR005877; Gpos_YsIRK.
DR InterPro; IPR001899; Gram_pos_anchor.
DR Pfam; PF02986; Fn_bind.1.
DR Pfam; PF00746; Gram_pos_anchor.1.
DR Pfam; PF04650; YsIRK_signal.1.
DR TIGRFAMs; TIGR01167; LPXTG_anchor.1.
DR TIGRFAMs; TIGR01168; YsIRK_signal.1.
DR PROSITE; PS50847; GRAM_POS_ANCHORING.1.
KM Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ SEQUENCE 1015 AA; 111145 MW; D0F9281B864D44D2 CRC64;

Query Match
Best Local Similarity 90.0%; Score 47; DB 2; Length 1015;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DSVPOIQGN 10
DB 777 DSVPOIQGN 786

RESULT 12
Q6G6H3 PRELIMINARY; PRT; 1015 AA.
ID Q6G6H3
AC Q6G6H3;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Fibronectin-binding protein.
GN Name=fndA; OrderedLocustNames=SAS2388;
OS Staphylococcus aureus (strain MSSA476).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=282459;
[1]
RP SEQUENCE FROM N.A.
RX PubMed=15213324; DOI=10.1073/pnas.0402521101;
RA Holden M.T.G., Fell E.J., Lindsay J.A., Peacock S.J., Day N.P.J.,
RA Enright M.C., Foster T.J., Moore C.E., Hurst L., Atkin R., Barton A.,
RA Baeson N., Bentley S.D., Chillingworth C., Chillingworth T.,
RA Churcher C., Clark L., Corton C., Cronin A., Doggett J., Dowd L.,
RA Peitwell T., Hance Z., Harris B., Hauser H., Holtroyd S., Jørgels K.,
RA James K.D., Lennard N., Line A., Mayes R., Mølle S., Mungall K.,
RA Ormond D., Quail M.A., Rabinowitsch E., Rutherford K.M., Sanders M.,
RA Sharp S., Simmonds M., Stevens K., Whitehead S., Barrell B.G.,
RA Spratt B.G., Parkhill J.;
RT "Complete genomes of two clinical Staphylococcus aureus strains:
RT evidence for the rapid evolution of virulence and drug resistance.";
RC Proc. Natl. Acad. Sci. U.S.A. 101:9786-9791(2004).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC an amide bond (By similarity).
DR EMBL; AF004830; BAB96286.1; -.
DR GO; GO:0009986; C:cell surface; IEA.
DR GO; GO:0005618; C:cell wall; IEA.
DR GO; GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0007155; P:cell adhesion; IEA.
DR InterPro; IPR008966; Adhes_bact.
DR InterPro; IPR004237; Fn_bind.
DR InterPro; IPR005877; Gpos_YsIRK.
DR InterPro; IPR001899; Gram_pos_anchor.
DR Pfam; PF02986; Fn_bind.1.
DR Pfam; PF00746; Gram_pos_anchor.1.
DR Pfam; PF04650; YsIRK_signal.1.
DR TIGRFAMs; TIGR01167; LPXTG_anchor.1.
DR TIGRFAMs; TIGR01168; YsIRK_signal.1.
DR PROSITE; PS50847; GRAM_POS_ANCHORING.1.
KM Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ SEQUENCE 1015 AA; 111145 MW; D0F9281B864D44D2 CRC64;

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RA Spratt B.G., Parkhill J.;
RT "Complete genomes of two clinical Staphylococcus aureus strains:
RT evidence for the rapid evolution of virulence and drug resistance.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:9786-9791(2004).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC an amide bond (By similarity).
DR EMBL: BX571857; CAC44202.1; -.
DR GO: GO:0009986; C:cell surface; IEA.
DR GO: GO:0005618; C:cell wall; IEA.
DR GO: GO:0005275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO: GO:0016020; C:membrane; IEA.
DR GO: GO:0007155; P:cell adhesion; IEA.
DR InterPro: IPR008966; Adhes_bact.
DR InterPro: IPR004237; Pn_bind.
DR InterPro: IPR005877; Gpos_YsIRK.
DR InterPro: IPR001899; Gram_pos_anchor.
DR Pfam: PF02986; Pn_bind; 1.
DR Pfam: PF00746; Gram_pos_anchor; 1.
DR TIGRPFAM: TIGR01167; LpxTG_anchor; 1.
DR TIGRPFAM: TIGR01168; YsIRK_signal; 1.
DR PROSITE: PS00847; GRAM_POS_ANCHORING; 1.
KW Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ SEQUENCE 1015 AA; 111145 MW; D0F9281BB64D4D2 CRC64;

Query Match 85.5%; Score 47; DB 2; Length 1015;
Best Local Similarity 90.0%; Pred. No. 2.8;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 DSVPOIHGQN 10
Db 777 DSVPOIHGQN 786

RESULT 13
Q99LN2 PRELIMINARY; PRT; 346 AA.
ID 099LN2;
AC 099LN2;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Rbm16 protein (Fragment).
DE Rbm16 protein (Fragment).
GN Name=Rbm16;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_Taxid=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CZECH II; TISSUE=Mammary tumor;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heish F.,
RA Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.V., Usslin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Lovellano N.A., Peters G.J., Abramson R.D., Millhys S.J.,
RA Bosak S.A., McMan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richardson S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Murry D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kerteman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Kravinsky M.I., Skalska U., Smalish D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
```

```
RC STRAIN=CZECH II; TISSUE=Mammary tumor;
RA Strausberg R.;
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: BC002302; AA02302.1; -.
DR MGI: MGI:1925212; Rbm16.
FT NON_TER 1
FT SEQUENCE 346 AA; 39305 MW; 2CB318DECTEDA21 CRC64;

Query Match 74.5%; Score 41; DB 2; Length 346;
Best Local Similarity 60.0%; Pred. No. 14;
Matches 6; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DSVPOIHGQN 10
Db 284 DNPVQNGEN 293

RESULT 14
Q8BTT8 PRELIMINARY; PRT; 353 AA.
ID 08BTT8;
AC 08BTT8;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Mus musculus 2 days neonate thymus thymic cell cDNA, RIKEN full-
DE length enriched library, clone:E43024N19 product:UNKNOWN PROTEIN
DE homolog.
GN Name=Rbm16;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_Taxid=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NOD; TISSUE=Thymus;
RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Meth. Enzymol. 303:19-44(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=NOD; TISSUE=Thymus;
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA RIKEN FANTOM Consortium;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=NOD; TISSUE=Thymus;
RA The FANTOM Consortium;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=NOD; TISSUE=Thymus;
RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata Y., Hayatsu N., Suganuma Y., Shibata K., Itoh M.,
RA Kono H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630(2000).
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=NOD; TISSUE=Thymus;
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA Kono H., Akiyama J., Nishi K., Kitasuna T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishino T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kaibuchi K.,
RA Fujiwara S., Inoue K., Togawa Y., Izawa M., Ohara E., Watanabe M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,
```

RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
 RT "RIKEN integrated sequence analysis (RISA) system-364-Format
 RT sequencing pipeline with 384 multicapillary sequencer";
 RL Genome Res. 10:1757-1771(2000).
 RN [6]
 RP SEQUENCE FROM N.A.
 RC STRAIN=MOD; TISSUE=Thymus;
 RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
 RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
 RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
 RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
 RA Katoh H., Kawai J., Kojima Y., Kondo S., Kono H., Kouda M., Koya S.,
 RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
 RA Nishi K., Nomura K., Numazaki R., Ono M., Ono M., Okazaki Y.,
 RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
 RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
 RA Tagawa A., Takahashi F., Takeku-Akahira S., Takeda Y., Tanaka T.,
 RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
 RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AK088735; BAC40537.1; -;
 DR MGD; MGI:1925212; Rbm16.
 SQ SEQUENCE 353 AA; 40032 MW; DCB92564407BCA2C CRC64;

Query Match 74.5%; Score 41; DB 2; Length 353;
 Best Local Similarity 60.0%; Pred. No. 15;
 Matches 6; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DSVPOIHGON 10
 Db 291 DNPQVNGEN 300

RESULT 15

Q9H8B2 PRELIMINARY; PRT; 354 AA.
 AC Q9H8B2;
 DT 01-MAR-2001 (TrEMBL). 16, Created
 DT 01-MAR-2001 (TrEMBL). 16, Last sequence update)
 DT 01-OCT-2002 (TrEMBL). 22, Last annotation update)
 DE Hypothetical protein FLJ13797.
 OS Homo sapiens (Human)
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Thyroid gland;
 RX PubMed=14702039; DOI=10.1038/ng1285;
 RA Ota T., Suzuki Y., Nishikawa T., Otsuki T., Sugiyama T., Irie R.,
 RA Wakamatsu A., Hayashi K., Sato H., Nagai K., Kimura K., Makita H.,
 RA Sekine M., Oobayashi M., Nishi T., Shibahara T., Tanaka T., Ishii S.,
 RA Yamamoto J., Saito K., Kawai Y., Isono Y., Nakamura Y., Nagahara K.,
 RA Murakami K., Yasuda T., Iwayanagi T., Magatsuna M., Shiratori A.,
 RA Sudo H., Hosoiri T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,
 RA Takahashi M., Kanda K., Yokoi T., Furuya T., Kikkawa E., Omura Y.,
 RA Abe K., Kamihara K., Katsuta N., Sato K., Tanikawa M., Yamazaki M.,
 RA Ninomiya K., Ishibashi T., Yamashita H., Murakawa K., Fujimori K.,
 RA Tanai H., Kimura M., Watanabe M., Hirakawa S., Chiba Y., Ishida S.,
 RA Ono Y., Takiguchi S., Watanabe S., Yosida M., Horita T., Kusano J.,
 RA Kanehori K., Takahashi-Fujii A., Hara H., Tanase T., Nomura Y.,
 RA Togliya S., Komai F., Hara R., Takeuchi K., Arita M., Imose N.,
 RA Yoshikawa Y., Matsunawa H., Ichihara T., Shionohara N., Sano S.,
 RA Moriya S., Momiyama H., Satoh N., Takami S., Terashima N., Sano S.,
 RA Nakagawa S., Senoh A., Mizoguchi H., Goto Y., Shimizu F., Wakebe H.,
 RA Hishigaki H., Watanabe K., Kumagai A., Takemoto M., Kawakami B.,
 RA Yamazaki M., Watanabe K., Kumagai A., Itakura S., Fukuzumi Y.,
 RA Fujimori Y., Komiyama M., Tashiro H., Tanigami A., Fujiwara T.,
 RA Ono T., Yamada K., Fujii Y., Ozaki K., Hirao M., Ohmori Y.,
 RA Kawabata A., Hikiji T., Kobayashi N., Inagaki H., Ikema Y., Okamoto S.,
 RA Okitani R., Kawakami T., Noguchi S., Itoh T., Shigeta K., Senba T.,
 RA Matsunura K., Nakajima Y., Mizuno T., Morinaga M., Sasaki M.,
 RA Togashi T., Oyama M., Hata H., Watanabe M., Komatsu T.,

RA Mizushima-Sugano J., Satoh T., Shirai Y., Takahashi Y., Nakagawa K.,
 RA Okumura K., Nagase T., Nomura N., Kikuchi H., Masuo Y., Yamashita R.,
 RA Nakai K., Yada T., Nakamura Y., Ohara O., Isegai T., Sugano S.;
 RT "Complete sequencing and characterization of 21,243 full-length human
 RT cDNAs";
 RL Nat. Genet. 36:40-45(2004).
 DR EMBL; AK023859; BAB14705.1; -;
 SQ SEQUENCE 354 AA; 40468 MW; 64E779AB5D5CF3FE CRC64;

Query Match 74.5%; Score 41; DB 2; Length 354;
 Best Local Similarity 60.0%; Pred. No. 15;
 Matches 6; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DSVPOIHGON 10
 Db 292 DNPQVNGEN 301

Search completed: October 22, 2005, 08:00:49
 Job time : 57.85 secs

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CC streptococci, e.g., meningitis, otitis media, pneumonia, endocarditis,
 CC mastitis in cattle, abortion in horses and many others. Since the
 CC antibodies block binding of bacteria, they should be effective against
 CC antibiotic-resistant strains, and may replace antibiotic therapy or
 CC increase its effectiveness. Sequences AAW65719-41 and AAW65658 represent
 CC peptides which were synthesised to span the D1 motif and the N-terminal
 CC 18 amino acids of D2, with each peptide overlapping by eight amino acids
 CC with the previous sequence

XX
 SQ Sequence 10 AA;

Query Match 100.0%; Score 56; DB 2; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.00076;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPOIHGQKNG 10
 |||||
 DB 1 VPOIHGQKNG 10

RESULT 2

AAAR90937
 ID AAR90937 standard; peptide; 113 AA.

XX AAR90937;

XX 23-SEP-1996 (first entry)

XX D3D4 polypeptide #1.

XX Fibronectin binding protein; Fbp; S.aureus J2385; monoclonal antibody;
 KW infection; surgical implant; antiadherent agent; hygiene; adhesion;
 KM extracellular matrix protein; oral pathogen; oral cavity.

XX Staphylococcus aureus.

XX Key Location/Qualifiers

FT Region 1..21
 /note= "D1 region fragment"

FT Region 22..59
 /note= "D2 region"

FT Region 60..98
 /note= "D3 region"

FT Region 99..113
 /note= "D4 region"

FT Misc-difference 113
 /note= "P113T"

XX WO9604381-A1.

XX 15-FEB-1996.

XX 28-JUL-1995; 95WO-EP003040.

XX 05-AUG-1994; 94GB-00015900.

XX (SMTK) SMITHKLINE BEECHAM PLC.

XX Critchley IA, Dodd I, Barnett P, Mcbay DL;

XX WPI; 1996-129397/13.

XX Polyepitide(s) derived from Staphylococcus aureus fibronectin binding
 PT protein - inhibit binding of bacteria to extracellular matrix proteins,
 PT for combating infection at the site of wounds and surgical implants, and
 PT in oral hygiene.

XX Claim 6; Page 24; 35pp; English.

XX AAR90937-R30942 represent D3D4 polypeptides. These sequences correspond
 CC to fragments of the Staphylococcus aureus fibronectin binding protein
 CC (Fbp). This sequence corresponds to residues 18-130 of S.aureus J2385
 CC Fbp, and also contains the D2 region, and a portion of the D1 region.

CC These sequences, and monoclonal antibodies against them can be used to
 CC combat infection at the site of wounds, surgical implants and other in-
 CC dwelling devices (such as catheters), and as antiadherent agents in oral
 CC hygiene. They can also be used in the manufacture of a medicament for the
 CC prevention of adhesion of bacteria to extracellular matrix proteins
 CC present on in-dwelling devices or in wounds, or of oral pathogens to
 CC similar proteins on surfaces in the oral cavity

XX
 SQ Sequence 113 AA;

Query Match 100.0%; Score 56; DB 2; Length 113;
 Best Local Similarity 100.0%; Pred. No. 0.012;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPOIHGQKNG 10
 |||||
 DB 17 VPOIHGQKNG 26

RESULT 3

AAAR58806
 ID AAR58806 standard; protein; 130 AA.

XX AAR58806;

XX 25-MAR-2003 (revised)

XX 30-MAR-1995 (first entry)

XX Fibronectin binding domain D1-D4(709-838(P838T)).

XX Fibronectin binding protein; Fbp; fibronectin binding domain;
 KW monoclonal antibody; MAb; adhesion; Gram-positive bacterium; bacteremia;
 KM Escherichia coli.

XX Staphylococcus aureus.

XX WO9418327-A1.

XX 18-AUG-1994.

XX 04-FEB-1994; 94WO-GB000215.

XX 05-FEB-1993; 93GB-00002289.

XX 20-OCT-1993; 93GB-00021592.

XX (SMTK) SMITHKLINE BEECHAM PLC.

XX Burnham MKR, Chopra I, Critchley IA, Knowles DUC;

XX WPI; 1994-279748/34.

XX Fibronectin binding protein and monoclonal antibodies specific for Fbp -
 PT useful to prevent adherence of Gram-positive bacteria to indwelling
 PT devices or wounds.

XX Disclosure; Page 30; 40pp; English.

XX Polyepitides corresponding to residues G709-T886 plus PPIVPT, G709-
 CC P838(P838T) and G709-P838 (AAR58805-07, respectively) of S. aureus J2385
 CC (NCIMB 40532) Fbp type A fibronectin binding domain D1-D4 region
 CC (AAR58808) were expressed in E. coli BL21(DE4) and used to raise MAb
 CC specific for Fbp. (Updated on 25-MAR-2003 to correct PN field.)

XX
 SQ Sequence 130 AA;

Query Match 100.0%; Score 56; DB 2; Length 130;
 Best Local Similarity 100.0%; Pred. No. 0.012;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPOIHGQKNG 10
 |||||
 DB 34 VPOIHGQKNG 43

```

RESULT 4
ID AAR58807 standard; protein; 130 AA.
XX
AC AAR58807;
XX
DT 25-MAR-2003 (revised)
DT 30-MAR-1995 (first entry)
XX
DE Fibronectin binding domain D1-D4 (709-838).
XX
KW Fibronectin binding protein; Fbp; fibronectin binding domain;
KW monoclonal antibody; Mab; adhesion; Gram-positive Bacterium; Bacteremia;
KW Escherichia coli.
XX
OS Staphylococcus aureus.
XX
PN WO9418327-A1.
XX
PD 18-AUG-1994.
XX
PF 04-FEB-1994; 94WO-GB000215.
XX
PR 05-FEB-1993; 93GB-00002289.
XX
PR 20-OCT-1993; 93GB-00021592.
XX
PA (SMIK ) SMITHKLINE BEECHAM PLC.
XX
PI Burnham MKR, Chopra I, Critchley IA, Knowles DGC;
XX
DR WPI; 1994-279748/34.
XX
PT Fibronectin binding protein and monoclonal antibodies specific for Fbp -
PT useful to prevent adherence of Gram-positive bacteria to indwelling
PT devices or wounds.
XX
PS Disclosure; Page 30; 40pp; English.
XX
CC Polypeptides corresponding to residues G709-T886 plus PPIVPT, G709-
CC P838(P838T) and G709-P838 (AAR58805-07, respectively) of S. aureus J2385
CC (NCIMB 40532) Fbp type A fibronectin binding domain D1-D4 region
CC (AAR58808) were expressed in E. coli Buz1 (DS4) and used to raise Mabs
CC specific for Fbp. (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ Sequence 130 AA;

Query Match          100.0%; Score 56; DB 2; Length 130;
Best Local Similarity 100.0%; Pred. No. 0.012;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPOIHGONGK 10
   |||||
Db 34 VPOIHGONGK 43

RESULT 5
ID AAR91202 standard; peptide; 130 AA.
XX
AC AAR91202;
XX
DT 13-NOV-1996 (first entry)
XX
DE D1-D4 fibronectin binding domains.
XX
KW Fibronectin; oral hygiene; gingivitis; gum disease; adhesion;
KW periodontitis; oral pathogen; caries; calculus; candidiasis; oral surgery;
KW tissue regeneration; irrigation; toothpaste; dentifrice; mouthwash;
KW lozenge.
XX
OS Staphylococcus aureus.
XX

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PN WO9604003-A1.
XX
PD 15-FEB-1996.
XX
PF 18-JUL-1995; 95WO-EP002825.
XX
PR 05-AUG-1994; 94GB-00015902.
XX
PA (SMIK ) SMITHKLINE BEECHAM PLC.
XX
PI Barnett P, Critchley IA, Dodd I;
XX
DR WPI; 1996-129122/13.
XX
PT Prevention of adherence of oral pathogens in the oral cavity, partic.
PT tooth surfaces - by application of a fibronectin binding protein or
PT polypeptide or a monoclonal antibody or fragment against it.
XX
PS Claim 5; Page 32; 41pp; English.
XX
CC Adherence of oral pathogens, particularly to tooth surfaces, can be
CC prevented by application of a fibronectin binding protein or polypeptide.
CC The fibronectin binding protein or polypeptide is useful in the
CC manufacture of oral hygiene compositions, eg. toothpaste, liquid
CC dentifrice, mouthwash or lozenge. They are useful to prevent the plaque-
CC related development of carious lesions, gingivitis, calculus or
CC periodontal disease and to combat oral cavity infections, e.g.
CC candidiasis. They may also be useful in oral surgery e.g. in guided
CC tissue regeneration procedures to prevent subsequent bacterial infection,
CC and for irrigation of periodontal pockets. This sequence corresponds to
CC amino acids 709-838 of the D1-D4 fibronectin binding domain of
CC Staphylococcus aureus
XX
SQ Sequence 130 AA;

Query Match          100.0%; Score 56; DB 2; Length 130;
Best Local Similarity 100.0%; Pred. No. 0.012;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPOIHGONGK 10
   |||||
Db 34 VPOIHGONGK 43

RESULT 6
ID AAR91201 standard; peptide; 130 AA.
XX
AC AAR91201;
XX
DT 13-NOV-1996 (first entry)
XX
DE D1-D4 fibronectin binding domains.
XX
KW Fibronectin; oral hygiene; gingivitis; gum disease; adhesion;
KW periodontitis; oral pathogen; caries; calculus; candidiasis; oral surgery;
KW tissue regeneration; irrigation; toothpaste; dentifrice; mouthwash;
KW lozenge.
XX
OS Staphylococcus aureus.
XX
PN WO9604003-A1.
XX
PD 15-FEB-1996.
XX
PF 18-JUL-1995; 95WO-EP002825.
XX
PR 05-AUG-1994; 94GB-00015902.
XX
PA (SMIK ) SMITHKLINE BEECHAM PLC.
XX
PI Barnett P, Critchley IA, Dodd I;
XX

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DR WPI: 1996-129122/13.
 XX
 XX Prevention of adherence of oral pathogens in the oral cavity, partic.
 PT tooth surfaces - by application of a fibronectin binding protein or
 PT polypeptide or a monoclonal antibody or fragment against it.
 XX
 PS Claim 5, Page 31-32; 41pp; English.
 XX
 CC Adherence of oral pathogens, particularly to tooth surfaces, can be
 CC prevented by application of a fibronectin binding protein or polypeptide.
 CC The fibronectin binding protein or polypeptide is useful in the
 CC manufacture of oral hygiene compositions, eg. toothpaste, liquid
 CC dentifrice, mouthwash or lozenge. They are useful to prevent the plaque-
 CC related development of carious lesions, gingivitis, calculus or
 CC periodontal disease and to combat oral cavity infections, e.g.
 CC candidiasis. They may also be useful in oral surgery e.g. in guided
 CC tissue regeneration procedures to prevent subsequent bacterial infection,
 CC and for irrigation of periodontal pockets. This sequence corresponds to
 CC amino acids 709-838 of the D1-D4 fibronectin binding domain of
 CC Staphylococcus aureus with a P838T substitution
 CC
 XX Sequence 130 AA;
 SQ
 Query Match 100.0%; Score 56; DB 2; Length 130;
 Best Local Similarity 100.0%; Pred. No. 0.012;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 VPOIHGQNGK 10
 |||||
 DB 34 VPOIHGQNGK 43
 RESULT 7
 AAY29087
 ID AAY29087 standard; protein; 134 AA.
 XX
 AC AAY29087;
 XX
 DT 28-SEP-1999 (first entry)
 XX
 DE S. aureus fibronectin binding protein A (FnBA) binding domain.
 XX
 KM Bovine herpes virus-2; BHV-2; cytokine; immune response; immunogen; IL;
 KM Interleukin; colony stimulating factor; CSF; interferon; IFN; TNF;
 KM Tumour necrosis factor; recombinant virus; vaccine; mucosal disease;
 KM mastitis; breast cancer; stress-induced disease; binding domain; FnBA;
 KM fibronectin binding protein.
 XX
 OS Staphylococcus aureus.
 XX
 FN WO9916892-A1.
 PD 08-APR-1999.
 XX
 PF 29-SEP-1998; 98WO-GB002927.
 XX
 PR 29-SEP-1997; 97GB-00020633.
 XX
 PA (UYBR-) UNIV BRISTOL.
 XX
 PI Bradley AJ, Duffas WP;
 XX
 DR WPI: 1999-255101/21.
 XX
 DR N-PSDB; AAX91504.
 XX
 PT New bovine herpes virus-2 vectors.
 XX
 PS Example 2; Fig 8A-B; 130pp; English.
 CC The invention provides bovine herpes virus-2 (BHV-2) based vectors that
 CC comprise at least one cytokine-encoding DNA sequence. The expression of
 CC cytokines in mammals can up-regulate immune responses to the immunogens.
 CC The cytokine is selected from interleukins (IL), colony stimulating

CC factors (CSF), interferons (IFN) and tumour necrosis factors (TNF). The
 CC BHV-2 based vector or recombinant virus can be used as vaccines. They can
 CC be used for preventing or treating a mucosal disease in a subject, e.g.
 CC ruminants, cattle, sheep, goats, dogs, cats, horses, or man, particularly
 CC mastitis in cows or breast cancers in humans. They can also be used for
 CC preventing or treating a stress-induced disease. The present sequence
 CC represents the binding domain of a previously published S. aureus
 CC fibronectin binding protein A (FnBA) sequence. The FnB binding domain
 CC gene sequence FnBAB, cloned for use in this invention has 97.8 percent
 CC identity when compared to the previously published FnBA and FnBB gene
 CC sequences
 XX
 SQ Sequence 134 AA;
 Query Match 100.0%; Score 56; DB 2; Length 134;
 Best Local Similarity 100.0%; Pred. No. 0.012;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 VPOIHGQNGK 10
 |||||
 DB 34 VPOIHGQNGK 43
 RESULT 8
 AAW31556
 ID AAW31556 standard; protein; 139 AA.
 XX
 AC AAW31556;
 XX
 DT 27-AUG-2003 (revised)
 DT 25-MAR-2003 (revised)
 DT 21-MAY-1998 (first entry)
 XX
 DE Fibronectin-binding MSCRAMM derivative pOD.
 XX
 KM Fibronectin; pOD; collagen binding protein; sepsis; infection;
 KM microbial surface component recognising adhesive matrix molecule; MSCRAMM;
 KM adhesin; vaccine; immunisation; diagnosis; therapy; mastitis.
 XX
 OS Staphylococcus aureus.
 XX
 FN Key Location/Qualifiers
 FT Peptide 1..12
 FT /note="vector pOE30-derived peptide"
 XX
 PN WO9743314-A2.
 XX
 PD 20-NOV-1997.
 XX
 PF 14-MAY-1997; 97WO-US008210.
 XX
 PR 16-MAY-1996; 96US-0017678P.
 XX
 PA (TEXA) UNIV TEXAS A & M SYSTEM.
 PA (UABR-) UAB RES FOUND.
 XX
 PI Hoeoek M, Patli JM, House-Pompeo K, Sthanam N, Symersky J;
 XX
 DR WPI: 1998-008801/01.
 XX
 PT Antibody that interacts with collagen binding domain of Staphylococcal
 PT cna gene product - useful to prevent bacterial sepsis in animal infected
 PT with Staphylococcus aureus.
 XX
 PS Disclosure; Page 91; 143pp; English.
 XX
 CC This protein comprises Staphylococcus aureus fibronectin-binding
 CC microbial surface component recognising adhesive matrix molecule (MSCRAMM)
 CC derivative pOD, plus a vector-derived N-terminal peptide. The invention
 CC relates to claimed nucleic acid sequences (see AAT93436-38) encoding S.
 CC aureus collagen binding protein (CBP) epitopes M17, M31 and M55 (see
 CC AAW1552-54) that confer protection against S. aureus infection. CBP
 CC protein and antigenic epitopes are contemplated for use in the treatment

CC of pathological infections, especially to prevent bacterial adhesion to
CC collagen. The epitopes are also contemplated for use in the preparation
CC of vaccines and as carrier proteins in vaccine formulations, as well as
CC in the formulation of compositions for the prevention of S. aureus
CC infection. PCP33 and POD (see AAW31556) were used to raise anti-MSCRAMM
CC polyclonal antibodies used in passive immunisation against bovine
CC mastitis. (Updated on 25-MAR-2003 to correct PI field.) (Updated on 27-
CC AUG-2003 to correct OS field.)
XX

SQ Sequence 139 AA;

Query Match 100.0%; Score 56; DB 2; Length 139;
Best Local Similarity 100.0%; Pred. No. 0.012; Mismatches 0; Indels 0; Gaps 0;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPQIHGQNGK 10
| | | | |
Db 48 VPQIHGQNGK 57

RESULT 9

AAR90942 standard; peptide; 162 AA.

AAR90942;

23-SEP-1996 (first entry)

D3D4 polypeptide #6.

KW Fibronectin binding protein; Fbp; S. aureus J2385; monoclonal antibody;
KM infection; surgical implant; antiadherent agent; hygiene; adhesion;
XX extracellular matrix protein; oral pathogen; oral cavity.

OS Staphylococcus aureus.

FH Key Location/Qualifiers

FT Region 1..19 /note= "D1 region fragment"

FT Region 20..57 /note= "D2 region"

FT Region 58..96 /note= "D3 region"

FT Region 97..111 /note= "D4 region"

FT Region 111..162 /note= "D4 region"

FT Region /note= "WRI region"

XX MO9604381-A1.

XX 15-FEB-1996.

XX 28-JUL-1995; 95MO-EP003040.

XX 05-AUG-1994; 94GB-00015900.

XX (SMIK) SMITHKLINE BEECHAM PLC.

XX Critchley IA, Dodd I, Barnett P, Mcbay DL;

XX WPI; 1996-129397/13.

XX Polypeptide(s) derived from Staphylococcus aureus fibronectin binding

XX protein - inhibit binding of bacteria to extracellular matrix proteins,
XX for combating infection at the site of wounds and surgical implants, and
XX in oral hygiene.

XX Claim 6; Page 24; 35pp; English.

CC AAR90937-R90942 represent D3D4 polypeptides. These sequences correspond
CC to fragments of the Staphylococcus aureus fibronectin binding protein
CC (Fbp). This sequence corresponds to residues 20-181 of S. aureus J2385
CC Fbp, and also contains the D2 region, a portion of the D1 region, and a

CC portion of the wall region 1 (WRI). These sequences, and monoclonal
CC antibodies against them can be used to combat infection at the site of
CC wounds, surgical implants and other in-dwelling devices (such as
CC catheters), and as antiadherent agents in oral hygiene. They can also be
CC used in the manufacture of a medicament for the prevention of adhesion of
CC bacteria to extracellular matrix proteins present on in-dwelling devices
CC or in wounds, or of oral pathogens to similar proteins on surfaces in the
CC oral cavity
XX

SQ Sequence 162 AA;

Query Match 100.0%; Score 56; DB 2; Length 162;
Best Local Similarity 100.0%; Pred. No. 0.015; Mismatches 0; Indels 0; Gaps 0;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPQIHGQNGK 10
| | | | |
Db 15 VPQIHGQNGK 24

RESULT 10

AAR90938 standard; peptide; 164 AA.

AAR90938;

23-SEP-1996 (first entry)

D3D4 polypeptide #2.

KW Fibronectin binding protein; Fbp; S. aureus J2385; monoclonal antibody;
KM infection; surgical implant; antiadherent agent; hygiene; adhesion;
XX extracellular matrix protein; oral pathogen; oral cavity.

OS Staphylococcus aureus.

FH Key Location/Qualifiers

FT Region 1..21 /note= "D1 region fragment"

FT Region 22..59 /note= "D2 region"

FT Region 60..98 /note= "D3 region"

FT Region 99..113 /note= "D4 region"

FT Region 114..164 /note= "D4 region"

FT Region /note= "WRI region"

XX MO9604381-A1.

XX 15-FEB-1996.

XX 28-JUL-1995; 95MO-EP003040.

XX 05-AUG-1994; 94GB-00015900.

XX (SMIK) SMITHKLINE BEECHAM PLC.

XX Critchley IA, Dodd I, Barnett P, Mcbay DL;

XX WPI; 1996-129397/13.

XX Polypeptide(s) derived from Staphylococcus aureus fibronectin binding

XX protein - inhibit binding of bacteria to extracellular matrix proteins,
XX for combating infection at the site of wounds and surgical implants, and
XX in oral hygiene.

XX Claim 6; Page 24; 35pp; English.

CC AAR90937-R90942 represent D3D4 polypeptides. These sequences correspond
CC to fragments of the Staphylococcus aureus fibronectin binding protein
CC (Fbp). This sequence corresponds to residues 18-181 of S. aureus J2385
CC Fbp, and also contains the D2 region, a portion of the D1 region, and a

CC portion of the wall region 1 (WR1). These sequences, and monoclonal
 CC antibodies against them can be used to combat infection at the site of
 CC wounds, surgical implants and other in-dwelling devices (such as
 CC catheters), and as antiadherent agents in oral hygiene. They can also be
 CC used in the manufacture of a medicament for the prevention of adhesion of
 CC bacteria to extracellular matrix proteins present on in-dwelling devices
 CC or in wounds, or of oral pathogens to similar proteins on surfaces in the
 CC oral cavity

XX
 XX Sequence 164 AA;

Query Match 100.0%; Score 56; DB 2; Length 164;
 Best Local Similarity 100.0%; Pred. No. 0.015;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 VPOIHGQNGK 10
 |||||
 DB 17 VPOIHGQNGK 26

RESULT 11

AAR58808
 ID AAR58808 standard; protein; 174 AA.

XX AAR58808;

DT 25-MAR-2003 (revised)
 DT 30-MAR-1995 (first entry)

XX Fbp fibronectin binding domain.

XX Fibronectin binding protein; Fbp; fibronectin binding domain;
 KM monoclonal antibody; MAb; adhesion; Gram-positive bacterium; bacteraemia;
 KW Escherichia coli; PBROC351.

XX Staphylococcus aureus.

XX WO9418327-A1.

XX 18-AUG-1994.

XX 04-FEB-1994; 94WO-GB000215.

XX 05-FEB-1993; 93GB-00002289.

PR 20-OCT-1993; 93GB-00021592.

XX (SMIK) SMITHKLINE BEECHAM PLC.

XX Burnham MKR, Chopra I, Critchley IA, Knowles DJC;

DR WPI, 1994-279748/34.

DR N-PSDB; AAO71838.

XX Fibronectin binding protein and monoclonal antibodies specific for Fbp -
 PT useful to prevent adherence of Gram-positive bacteria to indwelling
 PT devices or wounds.

XX Disclosure; Page 30; 40pp; English.

XX The sequences of DNA encoding S. aureus Fbp type A fibronectin binding
 CC domain (DI-D4) and the encoded protein are provided. DI-D4 polypeptides
 CC have been expressed in E. coli BL21(DE4) and used to raise Mabs specific
 CC for Fbp. (Updated on 25-MAR-2003 to correct FN field.)

XX Sequence 174 AA;

Query Match 100.0%; Score 56; DB 2; Length 174;
 Best Local Similarity 100.0%; Pred. No. 0.016;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 VPOIHGQNGK 10
 |||||
 DB 34 VPOIHGQNGK 43

RESULT 12

AAR91203
 ID AAR91203 standard; protein; 174 AA.

XX AAR91203;

XX 16-OCT-2003 (revised)

DT 13-NOV-1996 (first entry)

XX DI-D4 fibronectin binding domains.

XX Fibronectin; oral hygiene; gingivitis; gum disease; adhesion;
 KM periodontitis; oral pathogens; caries; calculus; candidiasis; oral surgery;
 KM tissue regeneration; irrigation; toothpaste; dentifrice; mouthwash;
 KW lozenge.

XX Staphylococcus aureus; J2385.

XX WO9604003-A1.

XX 15-FEB-1996.

XX 18-JUL-1995; 95WO-EP002825.

XX 05-AUG-1994; 94GB-00015902.

XX (SMIK) SMITHKLINE BEECHAM PLC.

XX Barnett P, Critchley IA, Dodd I;

XX WPI: 1996-129122/13.

DR N-PSDB; AAT18308.

XX Prevention of adherence of oral pathogens in the oral cavity, partic.
 PT tooth surfaces - by application of a fibronectin binding protein or
 PT polypeptide or a monoclonal antibody or fragment against it.

XX Claim 5; Page 32; 41pp; English.

XX Adherence of oral pathogens, particularly to tooth surfaces, can be

XX prevented by application of a fibronectin binding protein or polypeptide.

XX The fibronectin binding protein or polypeptide is useful in the

XX manufacture of oral hygiene compositions, eg. toothpaste, liquid

XX dentifrice, mouthwash or lozenge. They are useful to prevent the plaque-

XX related development of carious lesions, gingivitis, calculus or

XX periodontal disease and to combat oral cavity infections, e.g.

XX tissue regeneration procedures to prevent subsequent bacterial infection,

XX and for irrigation of periodontal pockets. This sequence corresponds to

XX amino acids 709-838 of the DI-D4 fibronectin binding domain of

XX Staphylococcus aureus with a P838T substitution. (Updated on 16-OCT-2003

XX to standardise OS field)

XX Sequence 174 AA;

Query Match 100.0%; Score 56; DB 2; Length 174;
 Best Local Similarity 100.0%; Pred. No. 0.016;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 VPOIHGQNGK 10
 |||||
 DB 34 VPOIHGQNGK 43

RESULT 13

AAR58805
 ID AAR58805 standard; protein; 181 AA.

XX AAR58805;

DT 25-MAR-2003 (revised)

DT 30-MAR-1995 (first entry)
 XX Fibronectin binding domain D1-D4 (709-886).
 DE Fibronectin binding protein; Fbp; fibronectin binding domain;
 XX monoclonal antibody; Mab; adhesion; Gram-positive bacterium; bacteraemia;
 KW Escherichia coli.
 XX Staphylococcus aureus.
 OS
 XX WO9418327-A1.
 PN
 XX 18-AUG-1994.
 PD
 XX 04-FEB-1994; 94WO-GB000215.
 PF
 XX 05-FEB-1993; 93GB-00002289.
 PR
 XX 20-OCT-1993; 93GB-00021592.
 PA (SMIK) SMITHKLINE BEECHAM PLC.
 PI Burnham MKR, Chopra I, Critchley IA, Knowles DJC;
 XX WPI; 1994-279748/34.
 DR
 XX Fibronectin binding protein and monoclonal antibodies specific for Fbp -
 PT useful to prevent adherence of Gram-positive bacteria to indwelling
 PT devices or wounds.
 PS
 XX disclosure, Page 29-30; 40pp; English.
 XX
 CC Polypeptides corresponding to residues G709-1886 plus PEIVPPT, G709-
 CC P638(P838T) and G709-P838 (AARS8805-07, respectively) of S. aureus J2385
 CC (NCIMB 40532) Fbp type A fibronectin binding domain D1-D4 region
 CC (AARS8808) were expressed in E. coli BL21(DE4) and used to raise Mabs
 CC specific for Fbp. (Updated on 25-MAR-2003 to correct PN field.)
 CC
 SQ Sequence 181 AA;
 XX
 XX
 Query Match 100.0%; Score 56; DB 2; Length 181;
 Best Local Similarity 100.0%; Pred. No. 0.016;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 VPGIHGQNGK 10
 |||||
 DB 34 VPGIHGQNGK 43

RESULT 14
 AAR91200
 ID AAR91200 standard; peptide; 181 AA.
 XX
 AC AAR91200;
 XX
 DT 13-NOV-1996 (first entry)
 XX
 DE D1-D4 fibronectin binding domains.
 XX
 KW Fibronectin; oral hygiene; gingivitis; gum disease; adhesion;
 KW periodontitis; oral pathogen; caries; calculus; candidiasis; oral surgery;
 KW tissue regeneration; irrigation; toothpaste; dentifrice; mouthwash;
 KM lozenge.
 XX
 XX Staphylococcus aureus.
 OS
 XX WO9604003-A1.
 PN
 XX 15-FEB-1996.
 PD
 XX 18-JUL-1995; 95WO-EP002825.
 PF
 XX 05-AUG-1994; 94GB-00015902.
 PR
 XX

PA (SMIK) SMITHKLINE BEECHAM PLC.
 XX
 XX Barnett P, Critchley IA, Dodd I;
 PI
 XX WPI; 1996-129122/13.
 DR
 XX N-PSDB; AAT18307.
 PT Prevention of adherence of oral pathogens in the oral cavity, partic-
 PT tooth surfaces - by application of a fibronectin binding protein or
 PT polypeptide or a monoclonal antibody or fragment against it.
 PS
 XX Claim 5; Page 31; 41pp; English.
 XX
 CC Adherence of oral pathogens, particularly to tooth surfaces, can be
 CC prevented by application of a fibronectin binding protein or polypeptide.
 CC The fibronectin binding protein or polypeptide is useful in the
 CC manufacture of oral hygiene compositions, eg. toothpaste, liquid
 CC dentifrice, mouthwash or lozenge. They are useful to prevent the plaque-
 CC related development of carious lesions, gingivitis, calculus or
 CC periodontal disease and to combat oral cavity infections, eg.
 CC candidiasis. They may also be useful in oral surgery e.g. in guided
 CC tissue regeneration procedures to prevent subsequent bacterial infection,
 CC and for irrigation of periodontal pockets. This sequence corresponds to
 CC amino acids 709-886 of the D1-D4 fibronectin binding domain of
 CC Staphylococcus aureus
 CC
 SQ Sequence 181 AA;
 XX
 XX
 Query Match 100.0%; Score 56; DB 2; Length 181;
 Best Local Similarity 100.0%; Pred. No. 0.016;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 VPGIHGQNGK 10
 |||||
 DB 34 VPGIHGQNGK 43

RESULT 15
 AAP82115
 ID AAP82115 standard; protein; 1018 AA.
 XX
 AC AAP82115;
 XX
 DT 25-MAR-2003 (revised)
 DT 05-JAN-1990 (first entry)
 XX
 DE Fibronectin binding protein.
 XX
 KW Fibronectin binding protein; S.aureus; immunisation; mastitis; ruminants;
 KW wound infection; diagnosis.
 XX
 XX Staphylococcus aureus.
 OS
 XX EP294349-A.
 PN
 XX 07-DEC-1988.
 PD
 XX 30-MAY-1988; 88EP-00850188.
 PF
 XX 01-JUN-1987; 87SE-00002272.
 PR
 XX (ALFA) ALFA LAVAL AGRIC INT AB.
 PA
 XX Lindberg MK, Signas LC, Wadstrom TM, Froman G;
 PI WPI; 1988-347978/49.
 DR
 XX P-PSDB; AAP82115.
 DR
 XX Hybrid DNA encoding Staphylococcus aureus fibronectin binding protein -
 PT useful for immunisation and topical application to prevent staphylococcal
 PT infections.
 PS
 XX disclosure, Fig. 8A:1-8A:2; 23pp; English.

XX The S.aureus fibronectin binding protein may be included in a hybrid
CC protein. The protein may be used to immunise ruminants against
CC staphylococcal mastitis, pref. when given at 0.5-5 microg/kg, using 3
CC doses at 1-3 week intervals; and for topical applicn. to prevent wound
CC infection, pref. using isotonic saline soln. of concn. 25-250 microg/mg.
CC The DNA encoding the binding protein and the hybrid protein may be
CC immobilised on a carrier and used to diagnose staphylococcal infections.
CC (Updated on 25-MAR-2003 to correct PA field.)
XX

SQ Sequence 1018 AA;

Query Match 100.0%; Score 56; DB 1; Length 1018;

Best Local Similarity 100.0%; Pred No. 0.1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VPOIHGQNK 10
|||
Db 778 VPOIHGQNK 787

Search completed: October 25, 2005, 20:58:46
Job time : 64.2 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 22, 2005, 05:46:56 ; Search time 17.3 Seconds
(without alignments)
43.150 Million cell updates/sec

Title: US-10-731-238-79

Perfect score: 56

Sequence: 1 VPQIHQNGK 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA: *
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2: /cgn2_6/prodata/1/iaa/5B_COMB.pep: *
3: /cgn2_6/prodata/1/iaa/6A_COMB.pep: *
4: /cgn2_6/prodata/1/iaa/6B_COMB.pep: *
5: /cgn2_6/prodata/1/iaa/PCOTUS_COMB.pep: *
6: /cgn2_6/prodata/1/iaa/backfile1.pep: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	56	100.0	10	4	US-09-010-317-79	Sequence 79, Appl
2	56	100.0	114	1	US-08-259-000-3	Sequence 3, Appl
3	56	100.0	130	2	US-08-459-135A-7	Sequence 7, Appl
4	56	100.0	130	2	US-08-459-135A-8	Sequence 8, Appl
5	56	100.0	130	3	US-08-495-559-7	Sequence 7, Appl
6	56	100.0	130	3	US-08-495-559-8	Sequence 8, Appl
7	56	100.0	139	3	US-08-856-253-8	Sequence 8, Appl
8	56	100.0	174	2	US-08-459-135A-10	Sequence 10, Appl
9	56	100.0	174	2	US-08-459-135A-13	Sequence 13, Appl
10	56	100.0	174	3	US-08-495-559-10	Sequence 10, Appl
11	56	100.0	174	3	US-08-495-559-13	Sequence 13, Appl
12	56	100.0	176	3	US-08-495-559-6	Sequence 6, Appl
13	56	100.0	178	2	US-08-459-135A-12	Sequence 12, Appl
14	56	100.0	178	2	US-08-495-559-12	Sequence 12, Appl
15	56	100.0	181	2	US-08-459-135A-6	Sequence 6, Appl
16	56	100.0	1027	4	US-08-956-171E-5254	Sequence 5254, Ap
17	56	100.0	1027	4	US-08-781-986A-5254	Sequence 5254, Ap
18	56	100.0	1027	4	US-08-956-171E-5251	Sequence 5251, Ap
19	51	91.1	559	4	US-08-781-986A-5251	Sequence 5251, Ap
20	45	80.4	10	4	US-09-010-317-78	Sequence 78, Appl
21	45	80.4	10	4	US-09-010-317-80	Sequence 80, Appl
22	38	67.9	12	4	US-09-748-114A-13	Sequence 13, Appl
23	36	64.3	10	4	US-09-010-317-81	Sequence 81, Appl
24	36	64.3	91	4	US-09-134-000C-6592	Sequence 6592, Ap
25	35	62.5	38	4	US-08-294-189-8	Sequence 8, Appl
26	35	62.5	69	1	US-09-248-796A-27835	Sequence 27835, A
27	35	62.5	116	4	US-09-270-767-34192	Sequence 34192, A

28	35	62.5	116	4	US-09-270-767-49409	Sequence 49409, A
29	35	62.5	420	4	US-09-252-991A-19389	Sequence 19389, A
30	35	62.5	527	4	US-09-252-991A-21680	Sequence 21680, A
31	35	62.5	700	4	US-09-620-412C-345	Sequence 345, App
32	35	62.5	700	4	US-09-598-419-345	Sequence 345, App
33	35	62.5	1752	4	US-09-556-877-180	Sequence 180, App
34	35	62.5	1752	4	US-09-620-412C-180	Sequence 180, App
35	35	62.5	1752	4	US-09-598-419-180	Sequence 180, App
36	35	60.7	10	4	US-09-010-317-77	Sequence 77, Appl
37	34	60.7	38	1	US-08-234-622A-2	Sequence 2, Appl
38	34	60.7	38	4	US-09-010-317-5	Sequence 5, Appl
39	34	60.7	38	4	US-09-010-317-6	Sequence 6, Appl
40	34	60.7	38	4	US-09-010-317-35	Sequence 35, Appl
41	34	60.7	38	4	US-09-010-317-36	Sequence 36, Appl
42	34	60.7	38	4	US-09-010-317-37	Sequence 37, Appl
43	34	60.7	38	4	US-09-010-317-38	Sequence 38, Appl
44	34	60.7	38	4	US-09-010-317-39	Sequence 39, Appl
45	34	60.7	38	4	US-09-010-317-40	Sequence 40, Appl

ALIGNMENTS

```
RESULT 1
US-09-010-317-79
Sequence 79, Application US/09010317
Patent No. 6685943
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
APPLICANT: Patti, Joseph M.
APPLICANT: House-Pompeo, Karen L.
APPLICANT: Speciale, Pietro
APPLICANT: Joh, Danny
APPLICANT: McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
TITLE OF INVENTION: AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAMK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 79:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-09-010-317-79
Query Match 100.0%; Score 56; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.00029;
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Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 VPOIHQNGK 10
Db 1 VPOIHQNGK 10

RESULT 2
US-08-259-000-3
; Sequence 3, Application US/08259000
; Patent No. 5571514
; GENERAL INFORMATION:
; APPLICANT: HOOK, Magnus
; APPLICANT: LINDBERG, Martin Kjell
; APPLICANT: SIGNAS, Lars Christer
; APPLICANT: MADSTROM, Torkel Mikael
; APPLICANT: FROMAN, Gunnar
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN AS WELL AS
; TITLE OF INVENTION: ITS PREPARATION
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Doane, Swecker & Mathis
; STREET: P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22113-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/259,000
; FILING DATE: 13-JUN-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: SE 8702272-9
; FILING DATE: 01-JUN-1987
; ATTORNEY/AGENT INFORMATION:
; NAME: Meuth, Donna M
; REGISTRATION NUMBER: 36,607
; REFERENCE/DOCKET NUMBER: 012885-062
; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 114 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-259-000-3

Query Match 100.0%; Score 56; DB 1; Length 114;
Best Local Similarity 100.0%; Pred. No. 0.0037;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 VPOIHQNGK 10
Db 34 VPOIHQNGK 43

RESULT 3
US-08-459-135A-7
; Sequence 7, Application US/08459135A
; Patent No. 5955078
; GENERAL INFORMATION:
; APPLICANT: BURNHAM, Martin Karl Russel
; APPLICANT: CHOPRA, Ian
; APPLICANT: CRITCHLEY, Ian Alfred
; APPLICANT: KNOWLES, David Justin Charles
;

TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN: MONOCLONAL ANTIBODY AND THEIR US
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
STATE: PA
COUNTRY: U.S.A.
ZIP: 19406-0939
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: Fastseq, Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/459,135A
; FILING DATE: 02-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB/94/00215
; FILING DATE: 04-Feb-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Gimmil, Edward R
; REGISTRATION NUMBER: 38,891
; REFERENCE/DOCKET NUMBER: P30591C2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-270-4478
; TELEFAX: 610-270-5090
; TELEX:
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 130 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-459-135A-7

Query Match 100.0%; Score 56; DB 2; Length 130;
Best Local Similarity 100.0%; Pred. No. 0.0043;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 VPOIHQNGK 10
Db 34 VPOIHQNGK 43

RESULT 4
US-08-459-135A-8
; Sequence 8, Application US/08459135A
; Patent No. 5955078
; GENERAL INFORMATION:
; APPLICANT: BURNHAM, Martin Karl Russel
; APPLICANT: CHOPRA, Ian
; APPLICANT: CRITCHLEY, Ian Alfred
; APPLICANT: KNOWLES, David Justin Charles
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN: MONOCLONAL ANTIBODY AND THEIR US
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corporation
; STREET: 709 Swedeland Road
; CITY: King of Prussia
; STATE: PA
; COUNTRY: U.S.A.
; ZIP: 19406-0939
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: Fastseq, Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/459,135A
; FILING DATE: 02-JUN-1995
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; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB/94/00215
; FILING DATE: 04-Feb-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Gimm, Edward R
; REGISTRATION NUMBER: 38,891
; REFERENCE/DOCKET NUMBER: P30591C2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-270-4478
; TELEFAX: 610-270-5090
;
;
;
; TELETYPE:
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 130 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
;
US-08-459-135A-8

Query Match          100.0%; Score 56; DB 3; Length 130;
Best Local Similarity 100.0%; Pred. No. 0.0043;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 VPQIHGQNGK 10
        |||||
        34 VPQIHGQNGK 43

Db

RESULT 5
US-08-495-559-7
; Sequence 7, Application US/08495559A
;
; GENERAL INFORMATION:
; APPLICANT: BURMAN, Martin Karl Russel
; APPLICANT: CHOPRA, Ian
; APPLICANT: CRITCHLEY, Ian Alfred
; APPLICANT: KNOWLES, David Justin Charles
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN: MONOCLONAL
; TITLE OF INVENTION: ANTIBODY AND THEIR USE IN PREVENTING BACTERIAL ADHESION
; FILE REFERENCE: P30591
; CURRENT APPLICATION NUMBER: US/08/495,559A
; CURRENT FILING DATE: 1995-08-03
; EARLIER APPLICATION NUMBER: GB 9302289.5
; EARLIER FILING DATE: 1993-02-05
; EARLIER APPLICATION NUMBER: GB 9321592.9
; EARLIER FILING DATE: 1993-10-20
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 7
; LENGTH: 130
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
;
US-08-495-559-7

Query Match          100.0%; Score 56; DB 3; Length 130;
Best Local Similarity 100.0%; Pred. No. 0.0043;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 VPQIHGQNGK 10
        |||||
        34 VPQIHGQNGK 43

Db

RESULT 6
US-08-495-559-8
; Sequence 8, Application US/08495559A
; Patent No. 6054572
;
; GENERAL INFORMATION:
; APPLICANT: BURMAN, Martin Karl Russel
; APPLICANT: CHOPRA, Ian
; APPLICANT: CRITCHLEY, Ian Alfred
; APPLICANT: KNOWLES, David Justin Charles
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN: MONOCLONAL
; TITLE OF INVENTION: ANTIBODY AND THEIR USE IN PREVENTING BACTERIAL ADHESION
; FILE REFERENCE: P30591
; CURRENT APPLICATION NUMBER: US/08/495,559A
; CURRENT FILING DATE: 1995-08-03
; EARLIER APPLICATION NUMBER: GB 9302289.5
; EARLIER FILING DATE: 1993-02-05
; EARLIER APPLICATION NUMBER: GB 9321592.9
; EARLIER FILING DATE: 1993-10-20
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 7
; LENGTH: 130
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
;
US-08-495-559-7

Query Match          100.0%; Score 56; DB 3; Length 130;
Best Local Similarity 100.0%; Pred. No. 0.0043;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 VPQIHGQNGK 10
        |||||
        34 VPQIHGQNGK 43

Db

RESULT 7
US-08-856-253-8
; Sequence 8, Application US/08856253
; Patent No. 6288214
;
; GENERAL INFORMATION:
; APPLICANT: HOOK, Magnus
; APPLICANT: Patti, Joseph M.
; APPLICANT: House-Pompeo, Karen
; APPLICANT: Symanak, Narayana
; APPLICANT: Symanak, Jindrich
; TITLE OF INVENTION: COLLAGEN BINDING PROTEIN COMPOSITIONS
; TITLE OF INVENTION: AND METHODS OF USE
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: U.S.
; ZIP: 77210
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/856,253
; FILING DATE: Concurrently Herewith
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/017,678
; FILING DATE: 16-MAY-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Kitchell, Barbara S
; REGISTRATION NUMBER: 33,928
; REFERENCE/DOCKET NUMBER: TAMK:193
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (512) 418-3000
; TELEFAX: (512) 474-7577
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 139 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
;
US-08-856-253-8
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; APPLICANT: KNOWLES, David Justin Charles
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN: MONOCLONAL
; TITLE OF INVENTION: ANTIBODY AND THEIR USE IN PREVENTING BACTERIAL ADHESION
; FILE REFERENCE: P30591
; CURRENT APPLICATION NUMBER: US/08/495,559A
; CURRENT FILING DATE: 1995-08-03
; EARLIER APPLICATION NUMBER: GB 9302289.5
; EARLIER FILING DATE: 1993-02-05
; EARLIER APPLICATION NUMBER: GB 9321592.9
; EARLIER FILING DATE: 1993-10-20
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 8
; LENGTH: 130
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
;
US-08-495-559-8

Query Match          100.0%; Score 56; DB 3; Length 130;
Best Local Similarity 100.0%; Pred. No. 0.0043;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 VPQIHGQNGK 10
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        34 VPQIHGQNGK 43

Db

RESULT 7
US-08-856-253-8
; Sequence 8, Application US/08856253
; Patent No. 6288214
;
; GENERAL INFORMATION:
; APPLICANT: HOOK, Magnus
; APPLICANT: Patti, Joseph M.
; APPLICANT: House-Pompeo, Karen
; APPLICANT: Symanak, Narayana
; APPLICANT: Symanak, Jindrich
; TITLE OF INVENTION: COLLAGEN BINDING PROTEIN COMPOSITIONS
; TITLE OF INVENTION: AND METHODS OF USE
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: U.S.
; ZIP: 77210
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/856,253
; FILING DATE: Concurrently Herewith
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/017,678
; FILING DATE: 16-MAY-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Kitchell, Barbara S
; REGISTRATION NUMBER: 33,928
; REFERENCE/DOCKET NUMBER: TAMK:193
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (512) 418-3000
; TELEFAX: (512) 474-7577
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 139 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
;
US-08-856-253-8
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Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPOIHGQNGK 10
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DB 48 VPOIHGQNGK 57

RESULT 8
US-08-459-135A-10
; Sequence 10, Application US/08459135A
; Patent No. 5955078
; GENERAL INFORMATION:
; APPLICANT: BURHAM, Martin Karl Russel
; APPLICANT: CHOPRA, Ian
; APPLICANT: CRITCHLEY, Ian Alfred
; APPLICANT: KNOWLES, David Justin Charles
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN: MONOCLONAL ANTIBODY AND THEIR US
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corporation
; STREET: 709 Swedeland Road
; CITY: King of Prussia
; STATE: PA
; COUNTRY: U.S.A.
; ZIP: 19406-0939
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: Pastseq, Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/459,135A
; FILING DATE: 02-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB/94/00215
; FILING DATE: 04-Feb-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Gimmil, Edward R
; REGISTRATION NUMBER: 38,891
; REFERENCE/DOCKET NUMBER: P30591C2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-270-4478
; TELEFAX: 610-270-5090
; TELEX:
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 174 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: Protein
US-08-459-135A-10
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Best Local Similarity 100.0%; Pred. No. 0.0058;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPOIHGQNGK 10
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DB 34 VPOIHGQNGK 43

RESULT 9
US-08-459-135A-13
; Sequence 13, Application US/08459135A
; Patent No. 5955078
; GENERAL INFORMATION:
; APPLICANT: BURHAM, Martin Karl Russel
; APPLICANT: CHOPRA, Ian

APPLICANT: CRITCHLEY, Ian Alfred
; APPLICANT: KNOWLES, David Justin Charles
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN: MONOCLONAL ANTIBODY AND THEIR US
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corporation
; STREET: 709 Swedeland Road
; CITY: King of Prussia
; STATE: PA
; COUNTRY: U.S.A.
; ZIP: 19406-0939
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: Pastseq, Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/459,135A
; FILING DATE: 02-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB/94/00215
; FILING DATE: 04-Feb-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Gimmil, Edward R
; REGISTRATION NUMBER: 38,891
; REFERENCE/DOCKET NUMBER: P30591C2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-270-4478
; TELEFAX: 610-270-5090
; TELEX:
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 174 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-459-135A-13
Query Match 100.0%; Score 56; DB 2; Length 174;
Best Local Similarity 100.0%; Pred. No. 0.0058;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPOIHGQNGK 10
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DB 34 VPOIHGQNGK 43

RESULT 10
US-08-459-559-10
; Sequence 10, Application US/08495559A
; Patent No. 6054572
; GENERAL INFORMATION:
; APPLICANT: BURHAM, Martin Karl Russel
; APPLICANT: CHOPRA, Ian
; APPLICANT: CRITCHLEY, Ian Alfred
; APPLICANT: KNOWLES, David Justin Charles
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN: MONOCLONAL
; TITLE OF INVENTION: ANTIBODY AND THEIR USE IN PREVENTING BACTERIAL ADHESION
; FILE REFERENCE: P30591
; CURRENT APPLICATION NUMBER: US/08/495,559A
; CURRENT FILING DATE: 1995-08-03
; EARLIER APPLICATION NUMBER: GB 9302289.5
; EARLIER FILING DATE: 1993-02-05
; EARLIER APPLICATION NUMBER: GB 9321592.9
; EARLIER FILING DATE: 1993-10-20
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 10
; LENGTH: 174
; TYPE: PRT

ORGANISM: Staphylococcus aureus
US-08-495-559-10

Query Match 100.0%; Score 56; DB 3; Length 174;
Best Local Similarity 100.0%; Pred. No. 0.0058;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPOIHGQNGK 10
|||||
Db 34 VPOIHGQNGK 43

RESULT 11
US-08-495-559-13
Sequence 13, Application US/08495559A
Patent No. 6054572

GENERAL INFORMATION:
APPLICANT: BURHAM, Martin Karl Russel
APPLICANT: CHOPRA, Ian
APPLICANT: CRITCHLEY, Ian Alfred
APPLICANT: KNOWLES, David Justin Charles
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN: MONOCLONAL
TITLE OF INVENTION: ANTIBODY AND THEIR USE IN PREVENTING BACTERIAL ADHESION
FILE REFERENCE: P30591
CURRENT APPLICATION NUMBER: US/08/495,559A
CURRENT FILING DATE: 1995-08-03
EARLIER APPLICATION NUMBER: GB 9302289.5
EARLIER FILING DATE: 1993-02-05
EARLIER APPLICATION NUMBER: GB 9321592.9
EARLIER FILING DATE: 1993-10-20
NUMBER OF SEQ ID NOS: 13
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 13
LENGTH: 174
TYPE: PRT
ORGANISM: Staphylococcus aureus
US-08-495-559-13

Query Match 100.0%; Score 56; DB 3; Length 174;
Best Local Similarity 100.0%; Pred. No. 0.0058;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 34 VPOIHGQNGK 43

RESULT 12
US-08-495-559-6
Sequence 6, Application US/08495559A
Patent No. 6054572

GENERAL INFORMATION:
APPLICANT: BURHAM, Martin Karl Russel
APPLICANT: CHOPRA, Ian
APPLICANT: CRITCHLEY, Ian Alfred
APPLICANT: KNOWLES, David Justin Charles
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN: MONOCLONAL
TITLE OF INVENTION: ANTIBODY AND THEIR USE IN PREVENTING BACTERIAL ADHESION
FILE REFERENCE: P30591
CURRENT APPLICATION NUMBER: US/08/495,559A
CURRENT FILING DATE: 1995-08-03
EARLIER APPLICATION NUMBER: GB 9302289.5
EARLIER FILING DATE: 1993-02-05
EARLIER APPLICATION NUMBER: GB 9321592.9
EARLIER FILING DATE: 1993-10-20
NUMBER OF SEQ ID NOS: 13
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 6
LENGTH: 176
TYPE: PRT
ORGANISM: Staphylococcus aureus
US-08-495-559-6

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Best Local Similarity 100.0%; Pred. No. 0.0059;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 34 VPOIHGQNGK 43

RESULT 13
US-08-459-135A-12
Sequence 12, Application US/08459135A
Patent No. 5955078

GENERAL INFORMATION:
APPLICANT: BURHAM, Martin Karl Russel
APPLICANT: CHOPRA, Ian
APPLICANT: CRITCHLEY, Ian Alfred
APPLICANT: KNOWLES, David Justin Charles
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN: MONOCLONAL ANTIBODY AND THEIR USE
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
STATE: PA
COUNTRY: U.S.A.
ZIP: 19406-0939
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: Fastseq, Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/459,135A
FILING DATE: 02-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB/94/00215
FILING DATE: 04-FEB-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Glimmi, Edward R
REGISTRATION NUMBER: 38,891
REFERENCE/DOCKET NUMBER: P30591C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-4478
TELEFAX: 610-270-5090
TELEX:
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 178 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: Protein
US-08-459-135A-12

Query Match 100.0%; Score 56; DB 2; Length 178;
Best Local Similarity 100.0%; Pred. No. 0.0059;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPOIHGQNGK 10
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Db 34 VPOIHGQNGK 43

RESULT 14
US-08-495-559-12
Sequence 12, Application US/08495559A
Patent No. 6054572

GENERAL INFORMATION:
APPLICANT: BURHAM, Martin Karl Russel
APPLICANT: CHOPRA, Ian

APPLICANT: CRITCHLEY, Ian Alfred
APPLICANT: KNOWLES, David Justin Charles
TITLE OF INVENTION: FIBROBLAST BINDING PROTEIN: MONOCLONAL
FILE REFERENCE: P30591
CURRENT APPLICATION NUMBER: US/08/495,559A
CURRENT FILING DATE: 1995-08-03
EARLIER APPLICATION NUMBER: GB 9302289.5
EARLIER FILING DATE: 1993-02-05
EARLIER APPLICATION NUMBER: GB 9321592.9
EARLIER FILING DATE: 1993-10-20
NUMBER OF SEQ ID NOS: 13
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO: 12
LENGTH: 178
TYPE: PRT
ORGANISM: Staphylococcus aureus
US-08-495-559-12

Query Match
Best Local Similarity 100.0%; Score 56; DB 3; Length 178;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPQIHGQNGK 10
|||
Db 34 VPQIHGQNGK 43

RESULT 15
US-08-459-135A-6
Sequence 6, Application US/08459135A
Patent No. 5955078
GENERAL INFORMATION:
APPLICANT: BURNHAM, Martin Karl Russel
APPLICANT: CHOPRA, Ian
APPLICANT: CRITCHLEY, Ian Alfred
APPLICANT: KNOWLES, David Justin Charles
TITLE OF INVENTION: FIBROBLAST BINDING PROTEIN: MONOCLONAL ANTIBODY AND THEIR US
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
STATE: PA
COUNTRY: U.S.A.
ZIP: 19406-0939
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: Fastseq, Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/459,135A
FILING DATE: 02-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB/94/00215
FILING DATE: 04-Feb-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Gimm1, Edward R
REGISTRATION NUMBER: 38,891
REFERENCE/DOCKET NUMBER: P30591C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-4478
TELEFAX: 610-270-5090
TELEX:
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 181 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear

MOLECULE TYPE: Protein
US-08-459-135A-6
Query Match
Best Local Similarity 100.0%; Score 56; DB 2; Length 181;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPQIHGQNGK 10
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Db 34 VPQIHGQNGK 43

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Job time : 18.35 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 22, 2005, 12:09:40 : Search time 57.25 Seconds
(without alignments)
72.924 Million cell updates/sec

Title: US-10-731-238-79

Perfect score: 56
Sequence: 1 VPOIHQNKKG 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1862951 seqs, 417491010 residues

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Minimum DB seq length: 0
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Maximum Match 100%
Listing first 45 summaries

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Published Applications AA:*
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17: /cgn2_6/prodata/2/pubppaa/US10F_PUBCOMB.pep:*
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19: /cgn2_6/prodata/2/pubppaa/US11_NEW_PUB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	56	100.0	10	US-10-731-238-79	Sequence 79, Appl
2	56	100.0	139	US-09-813-820-8	Sequence 8, Appl
3	56	100.0	1018	US-09-815-242-5797	Sequence 5797, Ap
4	56	100.0	1018	US-09-815-242-12838	Sequence 12838, A
5	56	100.0	1018	US-10-470-048B-68	Sequence 68, Appl
6	56	100.0	1027	US-08-781-986A-5254	Sequence 5254, Ap
7	56	100.0	1027	US-10-329-624-5254	Sequence 5254, Ap
8	56	100.0	1038	US-10-282-122A-43827	Sequence 43827, A
9	51	91.1	388	US-08-901-062-1	Sequence 1, Appl
10	51	91.1	359	US-08-781-986A-5251	Sequence 5251, Ap
11	51	91.1	559	US-10-329-624-5251	Sequence 5251, Ap

Result No.	Score	Query Match	Length	ID	Description
12	51	91.1	767	US-09-815-242-5899	Sequence 5899, Ap
13	51	91.1	767	US-09-815-242-13140	Sequence 13140, A
14	51	91.1	940	US-10-470-048B-424	Sequence 424, App
15	51	91.1	948	US-10-470-048B-69	Sequence 69, Appl
16	51	91.1	961	US-10-282-122A-43778	Sequence 43778, A
17	45	80.4	10	US-10-731-238-78	Sequence 78, Appl
18	45	80.4	10	US-10-731-238-80	Sequence 80, Appl
19	43	76.8	978	US-09-815-242-5456	Sequence 5456, Ap
20	43	76.8	1001	US-09-815-242-12686	Sequence 12686, A
21	41	73.2	258	US-10-264-227-1813	Sequence 1813, Ap
22	41	73.2	277	US-10-461-862-156	Sequence 156, App
23	41	73.2	327	US-10-220-335-334	Sequence 334, App
24	41	73.2	331	US-10-461-862-154	Sequence 154, App
25	40	71.4	213	US-10-425-115-202183	Sequence 202183, A
26	40	71.4	431	US-10-424-599-259925	Sequence 259925, A
27	40	71.4	500	US-10-450-763-48313	Sequence 48313, A
28	40	71.4	590	US-10-282-122A-65996	Sequence 65996, A
29	40	71.4	590	US-10-472-260-196	Sequence 196, App
30	38	67.9	12	US-09-748-114-13	Sequence 13, Appl
31	38	67.9	12	US-10-742-864-13	Sequence 13, Appl
32	38	67.9	359	US-11-097-143-36564	Sequence 36564, A
33	38	67.9	1098	US-10-450-763-33706	Sequence 33706, A
34	37	66.1	126	US-10-767-701-58864	Sequence 58864, A
35	37	66.1	437	US-09-815-242-5664	Sequence 5664, Ap
36	37	66.1	469	US-10-282-122A-74536	Sequence 74536, A
37	37	66.1	520	US-09-815-242-12205	Sequence 12205, A
38	37	66.1	584	US-10-282-122A-43890	Sequence 43890, A
39	37	66.1	1071	US-10-425-115-303876	Sequence 303876, A
40	36	64.3	10	US-10-731-238-81	Sequence 81, Appl
41	36	64.3	115	US-10-425-115-354344	Sequence 354344, A
42	36	64.3	132	US-10-425-115-253339	Sequence 253339, A
43	36	64.3	135	US-10-425-115-198808	Sequence 198808, A
44	36	64.3	158	US-09-890-688-12	Sequence 12, Appl
45	36	64.3	206	US-10-282-122A-68056	Sequence 68056, A

ALIGNMENTS

RESULT 1
US-10-731-238-79
Sequence 79, Appl
Publication No. US20050123552A1
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
Patel, Joseph M.
House-Pompeo, Karen L.
Speziale, Pietro
Joh, Danny
McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSER: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: US
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/731.238
FILING DATE: 10-Dec-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/010.317
FILING DATE: 21-Jan-1998
APPLICATION NUMBER: US 60/036.139

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; FILING DATE: 21-JAN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Hibler, David W.
; REGISTRATION NUMBER: 41,071
; REFERENCE/DOCKET NUMBER: TAMK:189
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 512-418-3000
; TELEFAX: 512-474-7577
; INFORMATION FOR SEQ ID NO: 79:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 79:
US-10-731-238-79

Query Match      100.0%; Score 56; DB 18; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.00083;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 VPQIHGQNGK 10
DB      1 VPQIHGQNGK 10

RESULT 2
US-09-813-820-8
; Sequence 8, Application US/09813820
; Patent No. US20020102262A1
; GENERAL INFORMATION:
; APPLICANT: Hook, Magnus
;             Patti, Joseph M.
;             House-Pompeo, Karen
;             Sthanam, Narayana
;             Symersky, Jindrich
; TITLE OF INVENTION: COLLAGEN BINDING PROTEIN COMPOSITIONS
; AND METHODS OF USE
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: U.S.
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/813,820
; FILING DATE: 22-Mar-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/856,253
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Kitchell, Barbara S.
; REGISTRATION NUMBER: 33,928
; REFERENCE/DOCKET NUMBER: TAMK:193
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (512) 418-3000
; TELEFAX: (512) 474-7577
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 139 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-09-813-820-8
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Query Match      100.0%; Score 56; DB 9; Length 139;
Best Local Similarity 100.0%; Pred. No. 0.013;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 VPQIHGQNGK 10
DB      48 VPQIHGQNGK 57

RESULT 3
US-09-815-242-5797
; Sequence 5797, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Karl L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; PROKARYOTES
; FILE REFERENCE: ELITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5797
; LENGTH: 1018
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-09-815-242-5797

Query Match      100.0%; Score 56; DB 9; Length 1018;
Best Local Similarity 100.0%; Pred. No. 0.11;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 VPQIHGQNGK 10
DB      778 VPQIHGQNGK 787

RESULT 4
US-09-815-242-12838
; Sequence 12838, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Karl L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 22, 2005, 12:09:40 ; Search time 57.25 Seconds
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72.924 Million cell updates/sec

Title: US-10-731-238-71

Perfect score: 55
Sequence: 1 PXYEQGNIV 10

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Gapop 10.0 , Gapext 0.5

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Total number of hits satisfying chosen parameters: 1862951

Minimum DB seq length: 0

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Post-Processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Published Applications AA: *
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11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep: *
12: /cgn2_6/ptodata/2/pubpaa/US09A_NEW_PUB.pep: *
13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep: *
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15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep: *
16: /cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pep: *
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18: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep: *
19: /cgn2_6/ptodata/2/pubpaa/US11A_PUBCOMB.pep: *
20: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep: *
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22: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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3	55	100.0	38	18	US-10-731-238-35
4	55	100.0	38	18	US-10-731-238-36
5	55	100.0	38	18	US-10-731-238-37
6	55	100.0	38	18	US-10-731-238-38
7	55	100.0	38	18	US-10-731-238-39
8	55	100.0	38	18	US-10-731-238-40
9	55	100.0	38	18	US-10-731-238-41
10	55	100.0	38	18	US-10-731-238-42
11	55	100.0	39	18	US-10-731-238-56

12	55	100.0	139	9	US-09-813-820-8
13	55	100.0	388	8	US-08-901-062-1
14	55	100.0	559	8	US-08-781-966A-5251
15	55	100.0	559	15	US-10-329-624-5251
16	55	100.0	767	9	US-09-815-242-5899
17	55	100.0	767	9	US-09-815-242-13140
18	55	100.0	948	17	US-10-470-048B-424
19	55	100.0	948	17	US-10-470-048B-69
20	55	100.0	961	15	US-10-282-122A-43778
21	55	100.0	978	9	US-09-815-242-5456
22	55	100.0	1001	9	US-09-815-242-14866
23	55	100.0	1018	9	US-09-815-242-5797
24	55	100.0	1018	9	US-09-815-242-12838
25	55	100.0	1018	17	US-10-470-048B-68
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28	55	100.0	1038	15	US-10-282-122A-43827
29	54	98.2	30	14	US-10-287-821-1
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31	49	89.1	38	18	US-10-731-238-7
32	49	89.1	38	18	US-10-731-238-45
33	49	89.1	38	18	US-10-731-238-46
34	49	89.1	38	18	US-10-731-238-47
35	49	89.1	38	18	US-10-731-238-48
36	47	85.5	10	18	US-10-731-238-70
37	47	85.5	38	18	US-10-731-238-6
38	47	85.5	38	18	US-10-731-238-43
39	47	85.5	39	18	US-10-731-238-57
40	43	78.2	10	18	US-10-731-238-72
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42	41	74.5	38	18	US-10-731-238-8
43	41	74.5	38	18	US-10-731-238-49
44	40	72.7	591	15	US-10-282-122A-53313
45	39	70.9	38	18	US-10-731-238-44

ALIGNMENTS

Sequence 8, Appli
Sequence 1, Appli
Sequence 5251, Ap
Sequence 5251, Ap
Sequence 5899, Ap
Sequence 13140, A
Sequence 424, App
Sequence 69, Appl
Sequence 43778, A
Sequence 5456, Ap
Sequence 12838, A
Sequence 5797, Ap
Sequence 12838, A
Sequence 68, Appl
Sequence 5254, Ap
Sequence 5254, Ap
Sequence 43827, A
Sequence 1, Appli
Sequence 2, Appli
Sequence 7, Appli
Sequence 45, Appl
Sequence 46, Appl
Sequence 47, Appl
Sequence 48, Appl
Sequence 70, Appl
Sequence 6, Appli
Sequence 43, Appl
Sequence 57, Appl
Sequence 72, Appl
Sequence 58, Appl
Sequence 8, Appl
Sequence 49, Appl
Sequence 53113, A
Sequence 44, Appl

RESULT 1
US-10-731-238-71
; Sequence 71, Application US/10731238
; Publication No. US20050123552A1
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
Pattl, Joseph M.
House-Pompeo, Karen L.
Speziale, Pietro
Job, Danny
McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSER: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/731,238
FILING DATE: 10-Dec-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE: 21-Jan-1998
APPLICATION NUMBER: US 60/036,139

FILED DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAMK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 71:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 71:
US-10-731-238-71

Query Match 100.0%; Score 55; DB 18; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0019;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PRYEOGGNIV 10
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Db 1 PRYEOGGNIV 10

RESULT 2
US-10-731-238-5
Sequence 5, Application US/10731238
Publication No. US20050123552A1
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
Patti, Joseph M.
House-Pompeo, Karen L.
Speziale, Pietro
Joh, Danny
McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/731,238
FILING DATE: 10-Dec-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE: 21-Jan-1998
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAMK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>

TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-10-731-238-5

Query Match 100.0%; Score 55; DB 18; Length 38;
Best Local Similarity 100.0%; Pred. No. 0.0078;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PRYEOGGNIV 10
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Db 17 PRYEOGGNIV 26

RESULT 3
US-10-731-238-35
Sequence 35, Application US/10731238
Publication No. US20050123552A1
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
Patti, Joseph M.
House-Pompeo, Karen L.
Speziale, Pietro
Joh, Danny
McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/731,238
FILING DATE: 10-Dec-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE: 21-Jan-1998
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAMK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 35:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 35:
US-10-731-238-35

Query Match 100.0%; Score 55; DB 18; Length 38;
Best Local Similarity 100.0%; Pred. No. 0.0078;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PRYEOGGNIV 10
|||
Db 17 PRYEOGGNIV 26

```
APPLICANT: Charles Kunsch
TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
NUMBER OF SEQUENCES: 5255
CORRESPONDENCE ADDRESS:
ADDRESSER: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COUNTRY: USA
ZIP: 20850

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/781,986A
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
ATTORNEY/AGENT INFORMATION:
NAME: Benson, Bob
REGISTRATION NUMBER: 30,446
REFERENCE/DOCKET NUMBER: PB248PP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 5251:
SEQUENCE CHARACTERISTICS:
LENGTH: 559 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-781-986A-5251

Query Match          91.1%; Score 51; DB 8; Length 559;
Best Local Similarity 90.0%; Pred. No. 0.52;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 VPQIHGQNGK 10
Db 333 VPQIHGQNGK 342

RESULT 11
US-10-329-624-5251
Sequence 5251, Application US/10329624
Publication No. US20040043037A1
GENERAL INFORMATION:
APPLICANT: Charles Kunsch
Gil H. Choi
Patrick S. Dillon
Craig A. Rosen
Steven C. Barash
Michael R. Fannon
TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
NUMBER OF SEQUENCES: 5256
CORRESPONDENCE ADDRESS:
ADDRESSER: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COUNTRY: USA
ZIP: 20850

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
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APPLICATION NUMBER: US/10/329,624
FILING DATE: 27-Dec-2002
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/956,171
FILING DATE: October 20, 1997
APPLICATION NUMBER: 60/009,861
FILING DATE: January 5, 1996
APPLICATION NUMBER: 08/781,986
FILING DATE: January 3, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Mark J. Hyman
REGISTRATION NUMBER: 46,789
REFERENCE/DOCKET NUMBER: PB248P1D1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (240) 314-1224
TELEFAX: (301) 309-8439
INFORMATION FOR SEQ ID NO: 5251:
SEQUENCE CHARACTERISTICS:
LENGTH: 559 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 5251:
US-10-329-624-5251

Query Match          91.1%; Score 51; DB 15; Length 559;
Best Local Similarity 90.0%; Pred. No. 0.52;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 VPQIHGQNGK 10
Db 333 VPQIHGQNGK 342

RESULT 12
US-09-815-242-5899
Sequence 5899, Application US/09815242
Patent No. US20020061569A1
GENERAL INFORMATION:
APPLICANT: Haeselbeck, Robert
APPLICANT: Ohlsen, Karl L.
APPLICANT: Zyskind, Judith W.
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John D.
APPLICANT: Carr, Grant J.
APPLICANT: Yamamoto, Robert T.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in
FILE REFERENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 5899
LENGTH: 767
TYPE: PRT
ORGANISM: Staphylococcus aureus
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US-09-815-242-5899

Query Match 91.1%; Score 51; DB 9; Length 767;
Best Local Similarity 90.0%; Pred. No. 0.73;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 VPOIHGQNGK 10
|||
Db 714 VPOIHGQNGG 723

RESULT 13

US-09-815-242-13140
; Sequence 13140, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Karl L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; FILE REFERENCE: ELITRA, 011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13140
; LENGTH: 767
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-09-815-242-13140

Query Match 91.1%; Score 51; DB 9; Length 767;
Best Local Similarity 90.0%; Pred. No. 0.73;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 VPOIHGQNGK 10
|||
Db 714 VPOIHGQNGG 723

RESULT 14

US-10-470-048B-424
; Sequence 424, Application US/10470048B
; Publication No. US2005003744A1
; GENERAL INFORMATION:
; APPLICANT: MEINKE ET AL.
; TITLE OF INVENTION: A METHOD FOR IDENTIFICATION, ISOLATION AND PRODUCTION OF
; FILE REFERENCE: SONN:035US
; CURRENT APPLICATION NUMBER: US/10/470,048B
; NUMBER OF SEQ ID NOS: 603
; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 424
; LENGTH: 940
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-10-470-048B-424

Query Match 91.1%; Score 51; DB 17; Length 940;
Best Local Similarity 90.0%; Pred. No. 0.9;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 VPOIHGQNGK 10
|||
Db 714 VPOIHGQNGG 723

RESULT 15

US-10-470-048B-69
; Sequence 69, Application US/10470048B
; Publication No. US2005003744A1
; GENERAL INFORMATION:
; APPLICANT: MEINKE ET AL.
; TITLE OF INVENTION: A METHOD FOR IDENTIFICATION, ISOLATION AND PRODUCTION OF
; FILE REFERENCE: SONN:035US
; CURRENT APPLICATION NUMBER: US/10/470,048B
; CURRENT FILING DATE: 2003-07-25
; NUMBER OF SEQ ID NOS: 603
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 69
; LENGTH: 948
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-10-470-048B-69

Query Match 91.1%; Score 51; DB 17; Length 948;
Best Local Similarity 90.0%; Pred. No. 0.91;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 VPOIHGQNGK 10
|||
Db 722 VPOIHGQNGG 731

Search completed: October 22, 2005, 12:39:48
Job time : 58.25 secs

GenCore version 5.1.6
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OW protein - protein search, using SW model

Run on: October 22, 2005, 06:10:10 ; Search time 11.45 Seconds
(without alignments)
84.032 Million cell updates/sec

Title: US-10-731-238-79

Perfect score: 56
Sequence: 1 VPOIHQNGK 10

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database:

1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	56	100.0	1018	2	A32192	fibronectin-binding
2	56	100.0	1038	2	H90053	hypothetical prote
3	51	91.1	940	2	S19702	fibronectin-binding
4	51	91.1	961	2	G90053	hypothetical prote
5	40	71.4	590	2	H81072	DNA primase NMB153
6	40	71.4	590	2	H81797	DNA primase (EC 2.
7	37	66.1	302	2	AD3106	hypothetical prote
8	37	66.1	305	2	H98180	hypothetical prote
9	37	66.1	332	2	S39657	undecaprenol-phosp
10	37	66.1	584	2	H89772	conserved hypochet
11	36	64.3	53	2	T07225	hypothetical prote
12	36	64.3	90	2	C56272	PGS protein - Ent
13	36	64.3	90	2	E41662	probable pheromone
14	36	64.3	172	2	T34227	hypothetical prote
15	36	64.3	364	2	I45915	interstitial retin
16	36	64.3	370	2	D83818	heat-shock protein
17	36	64.3	1286	1	RJBOF	interphotoreceptor
18	36	64.3	2715	1	T13049	eyelid - fruit fly
19	35	62.5	102	2	S33337	proteasome p2 - rhe
20	35	62.5	103	2	S33337	proteasome p2 - pig
21	35	62.5	295	2	S77111	transcription regu
22	35	62.5	309	2	A83702	inosine-uridine nu
23	35	62.5	360	2	F90505	glucose 1-dehydrog
24	35	62.5	599	2	AG1964	hypothetical prote
25	35	62.5	689	2	F84389	excision nuclease
26	35	62.5	1245	2	H87340	hypothetical prote
27	35	62.5	1672	2	C81675	polymorphic membra
28	35	62.5	1751	2	G71518	hypothetical prote
29	34	60.7	99	2	T45405	hypothetical prote

30	34	60.7	167	2	J02258	dehydroin-like prot
31	34	60.7	358	2	T02903	hypothetical prote
32	34	60.7	361	2	T49337	hypothetical prote
33	34	60.7	392	2	H71526	probable heat choc
34	34	60.7	409	2	T17258	hypothetical prote
35	34	60.7	509	2	I45713	DPP receptor TKV,
36	34	60.7	534	2	F69263	conserved hypochet
37	34	60.7	564	2	S57124	CTP synthase (EC 6
38	34	60.7	579	2	S50291	CTP synthase (EC 6
39	34	60.7	634	2	F82079	probable 2',3'-cyc
40	34	60.7	680	2	C82905	hypothetical prote
41	34	60.7	769	2	F81415	DNA topoisomerase
42	34	60.7	820	2	G81733	DNA mismatch repai
43	34	60.7	1079	1	TVPFVMI	gag-Rml1-env polyP
44	34	60.7	1736	2	T05174	hypothetical prote
45	33.5	59.8	249	2	G97110	ATPase component o

ALIGNMENTS

RESULT 1
A32192
fibronectin-binding protein - Staphylococcus aureus
C/Species: Staphylococcus aureus
C/Date: 31-Jul-1989 #sequence_revision 31-Jul-1989 #text_change 16-Feb-1997
C/Accession: A32192
R/Signaes, C.; Raucel, G.; Joensson, K.; Lindgren, P.E.; Anantharamiah, G.M.; Hoecek, J.
Proc. Natl. Acad. Sci. U.S.A. 86, 699-703, 1989
A/Title: Nucleotide sequence of the gene for a fibronectin-binding protein from Staphylo
A/Reference number: A32192; MUID:89098998; PMID:2521391
A/Accession: A32192
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-1018 <SIG>
A/Cross-references: GB:J04151
C/Keywords: fibronectin binding

Query Match 100.0%; Score 56; DB 2; Length 1018;
Best Local Similarity 100.0%; Pred. No. 0.014;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPOIHQNGK 10
DB 778 VPOIHQNGK 787

RESULT 2

H90053
hypothetical protein fmb [imported] - Staphylococcus aureus (strain N315)
C/Species: Staphylococcus aureus
C/Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C/Accession: H90053
R/Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; O
ma, A.; Mizutani, U.; Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.
C.; Shibb, T.; Hattori, M.; Ogasawara, N.; Hayaishi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
A/Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.
A/Reference number: A89758; MUID:21311952; PMID:11418146
A/Accession: H90053
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-1038 <KUN>
A/Cross-references: UNIPROT:Q99RD2; GB:BA000018; PID:G13702453; PIDN:BA843594.1; GS
C/Genetics:
A/Experimental source: strain N315

A/Gene: fmb

Query Match 100.0%; Score 56; DB 2; Length 1038;
Best Local Similarity 100.0%; Pred. No. 0.014;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPOIHQNGK 10

Db 774 VPOIHGQNGK 783

RESULT 3

fibronectin-binding protein B - Staphylococcus aureus
C:Species: Staphylococcus aureus
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
C:Accession: S19702
R:Joensen, K.; Signaess, C.; Mueller, H.P.; Lindberg, M.
Eur. J. Biochem. 202, 1041-1048, 1991
A:Title: Two different genes encode fibronectin binding proteins in Staphylococcus aureus
A:Reference number: S19702; MUID:92111475; PMID:1837266
A:Accession: S19702
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-940 <JOB>
A:Cross-references: UNIPROT:Q53682; EMBL:X62992; NID:G49040; PIDN:CAA44726.1; PID:G58156
C:Keywords: fibronectin binding

Query Match 91.1%; Score 51; DB 2; Length 940;
Best Local Similarity 90.0%; Pred. No. 0.12;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 VPOIHGQNGK 10
Db 714 VPOIHGQNGK 723

RESULT 4

hypothetical protein fnbB [imported] - Staphylococcus aureus (strain N315)
C:Species: Staphylococcus aureus
C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C:Accession: G90053
R:Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguc, A.; Mizutani-Uji, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.; C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
A:Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.
A:Reference number: A89758; MUID:21311952; PMID:11418146
A:Accession: G90053
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-961 <KUR>
A:Cross-references: UNIPROT:Q99RD3; GB:BA000018; PID:G13702452; PIDN:BA843593.1; GSPDB:C
A:Experimental source: strain N315
C:Genetics:
A:Gene: fnbB

Query Match 91.1%; Score 51; DB 2; Length 961;
Best Local Similarity 90.0%; Pred. No. 0.12;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 VPOIHGQNGK 10
Db 725 VPOIHGQNGK 734

RESULT 5

DNA primase NMB1537 [imported] - Neisseria meningitidis (strain MC58 serogroup B)
C:Species: Neisseria meningitidis
C:Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004
C:Accession: E81072
R:Teitelin, H.; Saunders, N.U.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Bisen, J.A.; Hickey, E.K.; Haft, D.H.; Salberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.; et al.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Maignan, V.; Pizzi, M.
Science 287, 1809-1815, 2000
A:Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58.
A:Reference number: A81000; MUID:20175755; PMID:10710307

A:Accession: E81072
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-590 <TET>
A:Cross-references: UNIPROT:P57029; GB:AE002503; GB:AE002098; NID:G7226775; PIDN:AA
A:Experimental source: serogroup B, strain MC58
C:Genetics:
A:Gene: NMB1537
C:Superfamily: DNA primase

Query Match 71.4%; Score 40; DB 2; Length 590;
Best Local Similarity 75.0%; Pred. No. 9.9;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPOIHGQNGK 8
Db 94 VPKVHGQNGK 101

RESULT 6

DNA primase (EC 2.7.7.-) NMA1736 [imported] - Neisseria meningitidis (strain Z2491 sero
C:Species: Neisseria meningitidis
C:Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 09-Jul-2004
C:Accession: H81797
R:Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morel
Nature 404, 502-506, 2000
A:Title: Complete DNA sequence of a serogroup A strain of Neisseria meningitidis Z2491.
A:Reference number: A81775; MUID:20222556; PMID:10761919
A:Accession: H81797
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-590 <PAR>
A:Cross-references: UNIPROT:P57028; GB:AL162757; GB:AL157959; NID:G7380371; PIDN:CAB8496
A:Experimental source: serogroup A, strain Z2491
C:Genetics:
A:Gene: dnaG; NMA1736
C:Superfamily: DNA primase
C:Keywords: nucleotidyltransferase

Query Match 71.4%; Score 40; DB 2; Length 590;
Best Local Similarity 75.0%; Pred. No. 9.9;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPOIHGQNGK 8
Db 94 VPKVHGQNGK 101

RESULT 7

hypothetical protein Atu4472 [imported] - Agrobacterium tumefaciens (strain C58, Dupont)
C:Species: Agrobacterium tumefaciens
C:Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 09-Jul-2004
C:Accession: AD3106
R:Wood, D.W.; Setubal, J.C.; Kaul, R.; Moks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, L.
erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kutayav, T.; Levy, R.; Li, M.; McClell
; Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A:Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krepan, W.; Perry, M.; Gordon-Kamm,
ster, E.W.
A:Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A:Reference number: AB2577; MUID:21608550; PMID:11743193
A:Accession: AD3106
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-302 <KUR>
A:Cross-references: UNIPROT:Q8U7H7; GB:AE008669; PIDN:AA145266.1; PID:G17742951; GSPDB G
A:Experimental source: strain C58 (Dupont)
C:Genetics:
A:Gene: Atu4472
A:Map position: linear chromosome

Query Match 66.1%; Score 37; DB 2; Length 302;
Best Local Similarity 66.7%; Pred. No. 19;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 PQIHGONK 10
DB 203 PKGHGKNKG 211

RESULT 8
H98180
hypothetical protein AGR_L_796 [imported] - Agrobacterium tumefaciens (strain C58, Cere
C/Species: Agrobacterium tumefaciens
C/Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 09-Jul-2004
C/Accession: H98180
R/Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman,
A.; Liu, F.; Wollam, C.; Allinger, M.; Doughy, D.; Scott, C.; Lappas, C.; Markelz, B.;
Science 294, 2323-2328, 2001
A/Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum
A/Reference number: A97359; MUID:21608551; PMID:11743194
A/Accession: H98180
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-305 <KUR>
A/Cross-references: UNIPROT:Q8U7H7; GB:AE007870; PIDN:AAK8970.1; PID:G15158752; GSPDB:C
A/Genetic: AGR_L_796
A/Map position: linear chromosome

Query Match 66.1%; Score 37; DB 2; Length 305;
Best Local Similarity 66.7%; Pred. No. 19;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 PQIHGONK 10
DB 206 PKGHGKNKG 214

RESULT 9
S39657
Nucleoside-phosphate-poly(glycophosphate chain) D-alanine transfer protein dltD - Ba
N/Alternate names: protein ipa-2r
C/Species: Bacillus subtilis
C/Date: 07-Oct-1994 #sequence_revision 26-May-1995 #text_change 09-Jul-2004
C/Accession: S39657; F69616
R/Glaeser, P.; Kunst, F.; Arnand, M.; Coudart, M.P.; Gonzalez, W.; Hullo, M.F.; Ionescu,
A.; Rapoport, G.; Danchin, A.
Mol. Microbiol. 10, 371-384, 1993
A/Title: Bacillus subtilis genome project: cloning and sequencing of the 97 kb region fr
A/Reference number: S39655; MUID:95020537; PMID:7934828
A/Accession: S39657
A/Status: preliminary; nucleic acid sequence not shown; translation not shown
A/Cross-references: UNIPROT:P39578; EMBL:X73124; NID:9413923; PIDN:CAA51558.1; PID:94139
A/Residues: 1-392 <GAA>
A/Molecule type: DNA
A/Cross-references: UNIPROT:P39578; EMBL:X73124; NID:9413923; PIDN:CAA51558.1; PID:94139
A/Note: The nucleotide sequence was submitted to the EMBL Data Library, June 1993
R/Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Allion, G.; Azevedo, V.; Berta
C.; Bron, S.; Brouillet, S.; Brusch, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Chd
A.; Ehlich, S.D.; Emmerison, P.T.; Entian, K.D.; Errington, J.; Fabis, C.; Ferrari, E.
Nature 390, 249-256, 1997
A/Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Gallazzi, A.; Gall
leth, J.; Harwood, C.R.; Hanaul, A.; Hilbert, H.; Holleppel, S.; Hosono, S.; Hullo, M.F.
Koeter, P.; Koninger, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois,
A/Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Maeda, S.; Maue
Y., M.; Ogawa, K.; Ogawa, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetel
Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadale, Y.; Sato, T.; Scanton
A/Authors: Schleicher, S.; Schroeter, R.; Scoffone, P.; Sekiguchi, J.; Sekowska, A.; Ser
A/Authors: Schleicher, S.; Schroeter, R.; Scoffone, P.; Sekiguchi, J.; Sekowska, A.; Ser
A/Authors: Schleicher, S.; Schroeter, R.; Scoffone, P.; Sekiguchi, J.; Sekowska, A.; Ser
T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K
A/Authors: Yoshikawa, H.F.; Zundstein, E.; Yoshikawa, H.; Danchin, A.
A/Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.
A/Reference number: A69580; MUID:98044033; PMID:9384377

A/Accession: F69616
A/Status: preliminary; nucleic acid sequence not shown; translation not shown
A/Molecule type: DNA
A/Residues: 1-392 <KUN>
A/Cross-references: GB:Z99123; GB:AL009126; NID:92636240; PIDN:CAB15879.1; PID:ell186352,
A/Experimental source: strain 168
C/Genetics:
A/Genetic: dltD

Query Match 66.1%; Score 37; DB 2; Length 392;
Best Local Similarity 60.0%; Pred. No. 25;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 VPQIHGONK 10
DB 274 VPQIHGONK 283

RESULT 10
B89772
conserved hypothetical protein SA0114 [imported] - Staphylococcus aureus (strain N315)
C/Species: Staphylococcus aureus
C/Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C/Accession: B89772
R/Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Ogu
ma, A.; Mizutani-U, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.
C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiratsuku, K.
Lancet 357, 1225-1240, 2001
A/Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.
A/Reference number: A89758; MUID:21311952; PMID:11418146
A/Accession: B89772
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-584 <KUR>
A/Cross-references: UNIPROT:Q99X97; GB:BA000018; PID:G13700034; PIDN:BA841333.1; GSPDB (C
A/Experimental source: strain N315
C/Genetics:
A/Genetic: SA0114

Query Match 66.1%; Score 37; DB 2; Length 584;
Best Local Similarity 62.5%; Pred. No. 38;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPQIHGON 8
DB 420 LPEIHGON 427

RESULT 11
T07225
hypothetical protein 53 - Chlorella vulgaris chloroplast
C/Species: Chlorella vulgaris
C/Date: 14-May-1999 #sequence_revision 14-May-1999 #text_change 21-Jul-2000
C/Accession: T07225
R/Makaguchi, T.; Nagai, T.; Kapoor, M.; Sugita, M.; Ito, M.; Ito, S.; Tsudzuki, J.; Nak
Proc. Natl. Acad. Sci. U.S.A. 94, 5967-5972, 1997
A/Title: Complete nucleotide sequence of the chloroplast genome from the green alga Ch
A/Reference number: Z15985; MUID:97303241; PMID:9159184
A/Accession: T07225
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-53 <WAK>
A/Cross-references: EMBL:AB001684; NID:92224352; PIDN:BA57872.1; PID:92224388
C/Genetics:
A/Genetic: chloroplast

Query Match 64.3%; Score 36; DB 2; Length 53;
Best Local Similarity 66.7%; Pred. No. 5;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 VPQIHGONK 9
DB 111

Db 5 IPOPHONK 13

RESULT 12

C56272

prgs protein - Enterococcus faecalis plasmid pCF10

C:Species: Enterococcus faecalis

C:Date: 03-Oct-1995 #sequence_revision 03-Oct-1995 #text_change 07-May-1999

C:Accession: C56272

R:Chung, J.W.; Bensing, B.A.; Dunny, G.M.

J. Bacteriol. 177, 2107-2117, 1995

A:Title: Genetic analysis of a region of the Enterococcus faecalis plasmid pCF10 involve

A:Reference number: A56272; MUID:95238283; PMID:7721703

A:Accession: C56272

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-90 <CHU>

A:Cross-references: GB:M64978

C:Genetics:

A:Gene: prgs

A:Genome: plasmid

Query Match 64.3%; Score 36; DB 2; Length 90;

Best Local Similarity 60.0%; Pred. No. 8.6;

Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 VPQIHGQNGK 10

Db 79 LPKEYGQNGK 88

RESULT 13

E41662

Probable pheromone-responsive regulatory protein S - Enterococcus faecalis plasmid pCF10

C:Species: Enterococcus faecalis

C:Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 18-Jun-1993

C:Accession: E41662

R:Kao, S.M.; Olmsted, S.B.; Viksning, A.S.; Gallo, J.C.; Dunny, G.M.

J. Bacteriol. 173, 7650-7664, 1991

A:Title: Molecular and genetic analysis of a region of plasmid pCF10 containing positive

terococcus faecalis.

A:Reference number: A41662; MUID:92041679; PMID:1938961

A:Accession: E41662

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-90 <KAO>

A:Cross-references: GB:M64978

C:Genetics:

A:Genome: plasmid

Query Match 64.3%; Score 36; DB 2; Length 90;

Best Local Similarity 60.0%; Pred. No. 8.6;

Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 VPQIHGQNGK 10

Db 79 LPKEYGQNGK 88

RESULT 14

T34227

hypothetical protein F20B6.4 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C:Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004

C:Accession: T34227

R:Mink, P.

submitted to the EMBL Data Library, November 1995

A:Description: The sequence of C. elegans cosmid F20B6.

A:Reference number: Z21491

A:Accession: T34227

A:Status: preliminary; translated from GB/EMBL/DBD

A:Molecule type: DNA

Residues: 1-172 <MIN>

A:Cross-references: UNIPROT:Q19627; EMBL:U41015; PIDN:AAA82312.1; CESP:F20B6.4

A:Experimental source: strain Bristol N2

C:Genetics:

A:Gene: CESP:F20B6.4

A:Insertions: 57/3; 90/1; 114/3; 139/3

C:Superfamily: Caenorhabditis elegans hypothetical protein F20B6.4

Query Match 64.3%; Score 36; DB 2; Length 172;

Best Local Similarity 71.4%; Pred. No. 17;

Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 PQIHGQNG 8

Db 118 PQVHGRN 124

RESULT 15

I45915

interstitial retinol binding protein - bovine (fragment)

C:Species: Bos primigenius taurus (cattle)

C:Date: 16-Aug-1996 #sequence_revision 16-Aug-1996 #text_change 09-Jul-2004

C:Accession: I45915

R:Liou, G.I.; Fong, S.

Vision Res. 26, 1645-1653, 1986

A:Title: Bovine interstitial retinol-binding protein (IRBP) -isolation and sequence analy

A:Reference number: I45915; MUID:87293907; PMID:3617506

A:Accession: I45915

A:Status: preliminary; translated from GB/EMBL/DBD

A:Molecule type: mRNA

A:Residues: 1-364 <LIO>

A:Cross-references: UNIPROT:Q28129; GB:M19390; NID:G163232; PIDN:AAA30592.1; PID:G163235

C:Superfamily: interphotoreceptor retinoid-binding protein

C:Keywords: duplication

Query Match 64.3%; Score 36; DB 2; Length 364;

Best Local Similarity 55.6%; Pred. No. 36;

Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 2 PQIHGQNGK 10

Db 317 PRLHGRNGK 325

Search completed: October 22, 2005, 08:04:34
Job time : 12.45 secs


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O6G6H4 PRELIMINARY; PRT; 957 AA.
ID O6G6H4
AC O6G6H4;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Fibronectin-binding protein.
GN Name=fnbB; OrderedLocName=SAS2387;
OS Staphylococcus aureus (strain MSSA476).
OC Bacteria; Firmicutes; Bacillales; Staphylococcaceae.
OX NCBI_TaxId=282459;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=15213324; DOI=10.1073/pnas.0402521101;
RA Holden M.T.G., Fell E.J., Lindsay J.A., Peacock S.J., Day N.P.J.,
RA Enright M.C., Foster T.U., Moore C.E., Hurst L., Atkin R., Barton A.,
RA Baeson N., Bentley S.D., Chillingworth C., Chillingworth T.,
RA Churcher C., Clark L., Corton C., Cronin A., Duggett J., Dowd L.,
RA Felwell T., Hance Z., Harris B., Hauser H., Holtroyd S., Jagels K.,
RA James K.D., Lennard N., Line A., Mayes R., Moule S., Mungall K.,
RA Ormond D., Quail M.A., Rabinowitch E., Rutherford K.M., Sanders M.,
RA Sharp S., Simmonds M., Stevens K., Whittread S., Barrell B.G.,
RA Spratt B.G., Parkhill J.;
RT "Complete genomes of two clinical Staphylococcus aureus strains:
RT evidence for the rapid evolution of virulence and drug resistance.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:9786-9791(2004).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC an amide bond (By similarity).
CC EMBL; BX571857; CAG44201.1; -
DR GO; GO:0009986; C:cell surface; IEA.
DR GO; GO:0005618; C:cell wall; IEA.
DR GO; GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0071353; P:cell adhesion; IEA.
DR InterPro; IPR008966; Adhes. bact.
DR InterPro; IPR004237; Fn_bind.
DR InterPro; IPR005877; Gpos_YsIRK.
DR InterPro; IPR001899; Gram_pos_anchor.
DR Pfam; PF02986; Fn_bind; 1.
DR Pfam; PF00746; Gram_pos_anchor; 1.
DR Pfam; PF04650; YsIRK_signal; 1.
DR TIGRFAMs; TIGR01167; LPXTG_anchor; 1.
DR TIGRFAMs; TIGR01168; YsIRK_signal; 1.
DR PROSITE; PS50847; GRAM_POS_ANCHORING; 1.
KW Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ SEQUENCE 957 AA; 105960 MW; 2878BA7FFDFD3EAF CRC64;
Query Match 100.0%; Score 56; DB 2; Length 957;
Best Local Similarity 100.0%; Pred. No. 0.059;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 VQIHGQNGK 10
DB 721 VQIHGQNGK 730

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RA Anantharamaiah G.M., Hoocek M., Lindberg M.;
RT "Nucleotide sequence of the gene for a fibronectin-binding protein
RT from Staphylococcus aureus: use of this peptide sequence in the
RT synthesis of biologically active peptides."
RL Proc. Natl. Acad. Sci. U.S.A. 86:699-703(1989).
CC -1- FUNCTION: The ability of bacteria to bind fibronectin has been
CC proposed as a virulence factor enabling bacteria to colonize wound
CC tissues and blood clots. Binding of plasma fibronectin to the
CC bacterial surface might block adhesion receptors on S.aureus, thus
CC representing an important defense mechanism against tissue
CC invasion.
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC an amide bond (Potential).
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@sib-sib.ch).
CC -----
DR EMBL; J04151; AA26632.1; -
DR InterPro; IPR004237; Fn_bind.
DR InterPro; IPR005877; Gpos_YsIRK.
DR InterPro; IPR001899; Gram_pos_anchor.
DR Pfam; PF02986; Fn_bind; 1.
DR Pfam; PF00746; Gram_pos_anchor; 1.
DR Pfam; PF04650; YsIRK_signal; 1.
DR TIGRFAMs; TIGR01167; LPXTG_anchor; 1.
DR TIGRFAMs; TIGR01168; YsIRK_signal; 1.
DR PROSITE; PS50847; GRAM_POS_ANCHORING; 1.
KW Cell adhesion; Cell wall; Peptidoglycan-anchor; Repeat; Signal;
KW Virulence.
FT SIGNAL 1 36
FT CHAIN 37 985
FT PROPEP 986 1018
FT REPEAT 545 574
FT REPEAT 575 604
FT DOMAIN 745 878
FT FT 745 782
FT REPEAT 783 820
FT REPEAT 821 859
FT REPEAT 860 878
FT DOMAIN 879 948
FT REPEAT 879 892
FT REPEAT 893 906
FT REPEAT 907 920
FT REPEAT 921 934
FT REPEAT 935 948
FT SITE 982 986
FT MOD_RES 985 985
FT FT 985 985
SQ SEQUENCE 1018 AA; 111780 MW; 58175E0D20E81P1F CRC64;
Query Match 100.0%; Score 56; DB 1; Length 1018;
Best Local Similarity 100.0%; Pred. No. 0.063;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 VQIHGQNGK 10
DB 778 VQIHGQNGK 787

```

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RESULT 4
ID O99RD2 PRELIMINARY; PRT; 1038 AA.
AC O99RD2;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Fibronectin-binding protein homolog.

```

GN Name=fnb; OrderedLocusNames=SAV2503;
 OS Staphylococcus aureus (strain Mu50 / ATCC 700699).
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 NCBI_TaxID=158878;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Mu50 / ATCC 700699;
 RX MEDLINE=21311952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2;
 RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
 RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Lian J.-Q., Ito T.,
 RA Kanemori M., Matsunari H., Maruyama A., Murakami H., Hosoyama A.,
 RA Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
 RA Sekimizu K., Hirakawa H., Kihara S., Goto S., Yabuzaki J.,
 RA Sekimizu K., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
 RA Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.,
 RA "Whole genome sequencing of methicillin-resistant Staphylococcus
 RT aureus".
 RL Lancel 357.1225-1240(2001).
 CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
 an amide bond (By similarity).
 CC EMBL: AP003365; BAB58665.1; -.
 CC PIR: H90053; H90053.
 DR GO: GO:0009986; C:cell surface; IEA.
 DR GO: GO:0005618; C:cell wall; IEA.
 DR GO: GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
 DR GO: GO:0016020; C:membrane; IEA.
 DR GO: GO:0007155; P:cell adhesion; IEA.
 DR InterPro: IPR008966; Adhes_bact.
 DR InterPro: IPR004237; Fn_bind.
 DR InterPro: IPR005877; Gpos_YsIRK.
 DR InterPro: IPR001899; Gram_pos_anchor.
 DR Pfam: PF00746; Gram_pos_anchor; 1.
 DR Pfam: PF04650; YsIRK_signal; 1.
 DR TIGRPFAMs: TIGR01167; LPXTG_anchor; 1.
 DR TIGRPFAMs: TIGR01168; YsIRK_signal; 1.
 DR PROSITE: PS50847; GRAM_POS_ANCHORING; 1.
 KM Cell wall; Complete proteome; Peptidoglycan-anchor.
 SQ SEQUENCE 1038 AA; 113618 MW; 666BF6BF2BFBEB12 CRC64;

Query Match 100.0%; Score 56; DB 2; Length 1038;
 Best Local Similarity 100.0%; Pred. No. 0.064;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPOIHGQNGK 10
 DB 774 VPOIHGQNGK 783

RESULT 5
 ID Q7A3J7 PRELIMINARY; PRT; 1038 AA.
 AC Q7A3J7;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Fnb protein.
 GN Name=fnb; OrderedLocusNames=SA2291;
 OS Staphylococcus aureus (strain NJ15).
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 NCBI_TaxID=158879;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC MEDLINE=21311952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2;
 RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
 RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Lian J.-Q., Ito T.,
 RA Kanemori M., Matsunari H., Maruyama A., Murakami H., Hosoyama A.,
 RA Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
 RA Sekimizu K., Hirakawa H., Kihara S., Goto S., Yabuzaki J.,
 RA Kanemizu M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
 RA Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.,
 RA "Whole genome sequencing of methicillin-resistant Staphylococcus
 RT aureus".

RL Lancel 357.1225-1240(2001).
 CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
 an amide bond (By similarity).
 CC EMBL: AP003377; BAB4594.1; -.
 CC DR GO: GO:0009986; C:cell surface; IEA.
 DR GO: GO:0005618; C:cell wall; IEA.
 DR GO: GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
 DR GO: GO:0016020; C:membrane; IEA.
 DR GO: GO:0007155; P:cell adhesion; IEA.
 DR InterPro: IPR008966; Adhes_bact.
 DR InterPro: IPR004237; Fn_bind.
 DR InterPro: IPR005877; Gpos_YsIRK.
 DR InterPro: IPR001899; Gram_pos_anchor.
 DR Pfam: PF02986; Fn_bind; 1.
 DR Pfam: PF00746; Gram_pos_anchor; 1.
 DR Pfam: PF04650; YsIRK_signal; 1.
 DR TIGRPFAMs: TIGR01167; LPXTG_anchor; 1.
 DR TIGRPFAMs: TIGR01168; YsIRK_signal; 1.
 DR PROSITE: PS50847; GRAM_POS_ANCHORING; 1.
 KM Cell wall; Complete proteome; Peptidoglycan-anchor.
 SQ SEQUENCE 1038 AA; 113618 MW; 666BF6BF2BFBEB12 CRC64;

Query Match 100.0%; Score 56; DB 2; Length 1038;
 Best Local Similarity 100.0%; Pred. No. 0.064;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPOIHGQNGK 10
 DB 774 VPOIHGQNGK 783

RESULT 6
 ID Q53682 PRELIMINARY; PRT; 940 AA.
 AC Q53682;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Fibronectin binding protein B.
 GN Name=fnb;
 OS Staphylococcus aureus.
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 NCBI_TaxID=1280;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=8325-4;
 RX MEDLINE=92111475; PubMed=1837266;
 RA Jonsson K., Signas C., Muller H.P., Lindberg M.,
 RA "Two different genes encode fibronectin binding proteins in
 RT Staphylococcus aureus. The complete nucleotide sequence and
 RT characterization of the second gene".
 RL Eur. J. Biochem. 202:1041-1048 (1991).
 CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
 an amide bond (By similarity).
 CC EMBL: X62392; CAA44726.1; -.
 CC PIR: S19702; S19702.
 DR HSSP: Q53653; 1N67.
 DR GO: GO:0009986; C:cell surface; IEA.
 DR GO: GO:0005618; C:cell wall; IEA.
 DR GO: GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
 DR GO: GO:0016020; C:membrane; IEA.
 DR GO: GO:0007155; P:cell adhesion; IEA.
 DR InterPro: IPR008966; Adhes_bact.
 DR InterPro: IPR004237; Fn_bind.
 DR InterPro: IPR005877; Gpos_YsIRK.
 DR InterPro: IPR001899; Gram_pos_anchor.
 DR Pfam: PF02986; Fn_bind; 2.
 DR Pfam: PF00746; Gram_pos_anchor; 1.
 DR Pfam: PF04650; YsIRK_signal; 1.
 DR TIGRPFAMs: TIGR01167; LPXTG_anchor; 1.
 DR TIGRPFAMs: TIGR01168; YsIRK_signal; 1.
 DR PROSITE: PS50847; GRAM_POS_ANCHORING; 1.
 KM Cell wall; Peptidoglycan-anchor.

SQ SEQUENCE 940 AA; 103555 MW; E35FBBCA907AE345 CRC64;
 Query Match 91.1%; Score 51; DB 2; Length 940;
 Best Local Similarity 90.0%; Pred. No. 0.57;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 VPOIHGQNGK 10
 DB 714 VPOIHGQNGG 723
 RESULT 7
 Q99RD3 PRELIMINARY; PRT; 961 AA.
 AC Q99RD3; 01-JUN-2001 (TrEMBLrel. 17, Created)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
 DE Fibronection-binding protein homologous.
 GN Name=fndb; OrderedLocustNames=SAV2502;
 OS Staphylococcus aureus (strain Mu50 / ATCC 700699).
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 OX NCBI_TaxId=158878;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Mu50 / ATCC 700699;
 RX MEDLINE=21311952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2;
 RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
 RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Iian J.-Q., Ito T.,
 RA Kanemori M., Matsumaru H., Maruyama A., Murakami H., Hoshoyama A.,
 RA Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
 RA Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
 RA Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
 RA Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
 RT "Whole genome sequencing of methicillin-resistant Staphylococcus
 aureus";
 RL Lancet 357:1225-1240(2001).
 CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
 an amide bond (By similarity).
 CC EMBL; AP003137; BAB43593.1; -;
 DR HSRP; O53653; IN67.
 DR GO; GO:0009986; C:cell surface; IEA.
 DR GO; GO:0005618; C:cell wall; IEA.
 DR GO; GO:0009275; C:cell wall (benu Gram-positive Bacteria); IEA.
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:007155; P:cell adhesion; IEA.
 DR InterPro; IPR008966; Adhes_bact.
 DR InterPro; IPR004237; Fn_bind.
 DR InterPro; IPR005877; Gpos_YsIRK.
 DR InterPro; IPR001899; Gram_pos_anchor.
 DR Pfam; PF02986; Fn_bind; 1.
 DR Pfam; PF00746; Gram_pos_anchor; 1.
 DR Pfam; PF04650; YsIRK_signal; 1.
 DR TIGRFAMs; TIGR01167; LpxTG_anchor; 1.
 DR TIGRFAMs; TIGR01168; YsIRK_signal; 1.
 DR PROSITE; PS50847; GRAM_POS_ANCHORING; 1.
 DR Cell wall; Complete proteome; Peptidoglycan-anchor.
 KW SEQUENCE 961 AA; 106010 MW; 364940F884EA4101 CRC64;
 Query Match 91.1%; Score 51; DB 2; Length 961;
 Best Local Similarity 90.0%; Pred. No. 0.57;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 VPOIHGQNGK 10
 DB 725 VPOIHGQNGG 734
 RESULT 8
 Q7A3J8 PRELIMINARY; PRT; 961 AA.
 AC Q7A3J8; 07A3J8;

DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DE Fndb protein.
 GN Name=fndb; OrderedLocustNames=SA2290;
 OS Staphylococcus aureus (strain N315).
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 OX NCBI_TaxId=158879;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC MEDLINE=21311952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2;
 RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
 RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Iian J.-Q., Ito T.,
 RA Kanemori M., Matsumaru H., Maruyama A., Murakami H., Hoshoyama A.,
 RA Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
 RA Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
 RA Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
 RA Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
 RT "Whole genome sequencing of methicillin-resistant Staphylococcus
 aureus";
 RL Lancet 357:1225-1240(2001).
 CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
 an amide bond (By similarity).
 CC EMBL; AP003137; BAB43593.1; -;
 DR GO; GO:0009986; C:cell surface; IEA.
 DR GO; GO:0005618; C:cell wall; IEA.
 DR GO; GO:0009275; C:cell wall (benu Gram-positive Bacteria); IEA.
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:007155; P:cell adhesion; IEA.
 DR InterPro; IPR008966; Adhes_bact.
 DR InterPro; IPR004237; Fn_bind.
 DR InterPro; IPR005877; Gpos_YsIRK.
 DR InterPro; IPR001899; Gram_pos_anchor.
 DR Pfam; PF02986; Fn_bind; 1.
 DR Pfam; PF00746; Gram_pos_anchor; 1.
 DR Pfam; PF04650; YsIRK_signal; 1.
 DR TIGRFAMs; TIGR01167; LpxTG_anchor; 1.
 DR TIGRFAMs; TIGR01168; YsIRK_signal; 1.
 DR PROSITE; PS50847; GRAM_POS_ANCHORING; 1.
 DR Cell wall; Complete proteome; Peptidoglycan-anchor.
 KW SEQUENCE 961 AA; 106010 MW; 364940F884EA4101 CRC64;
 Query Match 91.1%; Score 51; DB 2; Length 961;
 Best Local Similarity 90.0%; Pred. No. 0.57;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 VPOIHGQNGK 10
 DB 725 VPOIHGQNGG 734
 RESULT 9
 Q9AEP9 PRELIMINARY; PRT; 152 AA.
 AC Q9AEP9; 01-JUN-2001 (TrEMBLrel. 17, Created)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
 DE Fibronection-binding protein (Fragment).
 GN Name=fndb;
 OS Staphylococcus aureus.
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 OX NCBI_TaxId=1280;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CMRSA-1;
 RX MEDLINE=21246681; PubMed=11349044;
 RX DOI=10.1128/IAI.69.6.3791-3799.2001;
 RA Rice K., Huesca M., Vaz D., McGavin M.J.;
 RT "Variance in Fibronection binding and fnd locus polymorphisms in
 Staphylococcus aureus: identification of antigenic variation in a
 fibronection binding protein adhesin of the epidemic CMRSA-1 strain of
 methicillin-resistant S. aureus";

RL Infect. Immun. 69:3791-3799(2001).
 DR EMBL: AY029184; AAK31588.1; -.
 FT NON TER 1
 FT NON TER 152 152
 SO SEQUENCE 152 AA; 17193 MW; CFAJ913C2B11C025 CRC64;

Query Match 85.7%; Score 48; DB 2; Length 152;
 Best Local Similarity 90.0%; Pred. No. 0.35;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 VPOIHGONKG 10
 |||||
 Db 33 VPOIQGONKG 42

RESULT 10

Q8NUU7 PRELIMINARY; PRT; 1015 AA.

AC Q8NUU7;
 DT 01-OCT-2002 (TREMBlrel. 22, Created)
 DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
 DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
 DE Pnb protein.
 GN Name-fnb; OrderedlocusNames=MM2421;
 OS Staphylococcus aureus (strain MM2).
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 OX NCBI_TaxID=196620;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=MM2;
 RX MEDLINE=22040717; PubMed=12044378; DOI=10.1016/S0140-6736(02)08713-5;
 RA Baba T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Oguchi A.,
 RA Nagai Y., Iwano N., Amano K., Naimi T., Kuroda H., Cui L.,
 RA Yamamoto K., Hiramatsu K.;
 RT Genome and virulence determinants of high virulence community-

RT acquired MRSA. "1827(2002).
 RL Lancet 359:1819-1827(2002).
 CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
 an amide bond (By similarity).
 DR EMBL: AP004830; BAB96286.1; -;
 DR GO: GO:0009986; C:cell surface; IEA.

DR GO: GO:0005618; C:cell wall; IEA.
 DR GO: GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
 DR GO: GO:0016020; C:membrane; IEA.
 DR GO: GO:0007155; P:cell adhesion; IEA.
 DR InterPro: IPR008966; Adhes_bact.
 DR InterPro: IPR004237; Fn_bind.
 DR InterPro: IPR005877; Gpos_YsIRK.
 DR InterPro: IPR001899; Gram_pos_anchor.
 DR Pfam: PF02986; Fn_bind.1.
 DR Pfam: PF00746; Gram_pos_anchor.1.
 DR Pfam: PF04650; YsIRK_signal.1.
 DR TIGRPFAM: TIGR01167; LPXTG_anchor.1.
 DR TIGRPFAM: TIGR01168; YsIRK_signal.1.
 DR TIGRPFAM: TIGR01168; YsIRK_signal.1.
 DR POSTITE; PSS0847; GRAM_POS_ANCHORING.1.
 DR Cell wall; Complete proteome; Peptidoglycan-anchor.
 DR Cell wall; Complete proteome; Peptidoglycan-anchor.
 SO SEQUENCE 1015 AA; 111145 MW; D0F9281B64D44D2 CRC64;

Query Match 76.8%; Score 43; DB 2; Length 1015;
 Best Local Similarity 80.0%; Pred. No. 22;
 Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 VPOIHGONKG 10
 |||||
 Db 779 VPOIQGONKG 788

RESULT 11

Q6G6H3 PRELIMINARY; PRT; 1015 AA.

ID Q6G6H3;
 AC Q6G6H3;
 DT 05-JUL-2004 (TREMBlrel. 27, Created)
 DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)

DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
 DE Fibronectin-binding protein.
 GN OrderedlocusNames=SA52388;
 OS Staphylococcus aureus (strain MSSA476).
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 OX NCBI_TaxID=282459;
 RN [1]
 RP SEQUENCE FROM N.A.

RX PubMed=15213324; DOI=10.1073/pnas.0402521101;
 RA Holden M.T.G., Fell E.J., Lindsey J.A., Peacock S.J., Day N.P.J.,
 RA Enright M.C., Foster T.J., Moore C.E., Hurst L., Atkin R., Barron A.,
 RA Bason N., Bentley S.D., Chillingworth C., Chillingworth T.,
 RA Churcher C., Clark L., Cotton C., Cronin A., Doggett J., Dowd L.,
 RA Felwell T., Hance Z., Harris B., Hauser H., Holtroyd S., Jagsels K.,
 RA James K.D., Lennard N., Line A., Mayes R., Moul S., Mungall K.,
 RA Ormond D., Quail M.A., Rabinowitch E., Rutherford K.M., Sanders M.,
 RA Sharp S., Simmonds M., Stevens K., Whitehead S., Barrett B.G.,
 RA Spratt B.G., Parkhill J.;
 RT Complete genomes of two clinical Staphylococcus aureus strains:
 RT evidence for the rapid evolution of virulence and drug resistance."
 RL Proc. Natl. Acad. Sci. U.S.A. 101:9786-9791(2004).
 CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
 an amide bond (By similarity).
 DR EMBL: BX571857; CAG44202.1; -;
 DR GO: GO:0009986; C:cell surface; IEA.

DR GO: GO:0005618; C:cell wall; IEA.
 DR GO: GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
 DR GO: GO:0016020; C:membrane; IEA.
 DR GO: GO:0007155; P:cell adhesion; IEA.
 DR InterPro: IPR008966; Adhes_bact.
 DR InterPro: IPR004237; Fn_bind.
 DR InterPro: IPR005877; Gpos_YsIRK.
 DR InterPro: IPR001899; Gram_pos_anchor.
 DR Pfam: PF02986; Fn_bind.1.
 DR Pfam: PF00746; Gram_pos_anchor.1.
 DR Pfam: PF04650; YsIRK_signal.1.
 DR TIGRPFAM: TIGR01167; LPXTG_anchor.1.
 DR TIGRPFAM: TIGR01168; YsIRK_signal.1.
 DR TIGRPFAM: TIGR01168; YsIRK_signal.1.
 DR POSTITE; PSS0847; GRAM_POS_ANCHORING.1.
 DR Cell wall; Complete proteome; Peptidoglycan-anchor.
 DR Cell wall; Complete proteome; Peptidoglycan-anchor.
 SO SEQUENCE 1015 AA; 111145 MW; D0F9281B64D44D2 CRC64;

Query Match 76.8%; Score 43; DB 2; Length 1015;
 Best Local Similarity 80.0%; Pred. No. 22;
 Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 VPOIHGONKG 10
 |||||
 Db 779 VPOIQGONKG 788

RESULT 12

Q6GDU5 PRELIMINARY; PRT; 965 AA.

DT 05-JUL-2004 (TREMBlrel. 27, Created)
 DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
 DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
 DE Fibronectin-binding protein.
 GN Name=fnbA; OrderedlocusNames=SA52580;
 OS Staphylococcus aureus (strain MSSA252).
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 OX NCBI_TaxID=282458;
 RN [1]
 RP SEQUENCE FROM N.A.

RX PubMed=15213324; DOI=10.1073/pnas.0402521101;
 RA Holden M.T.G., Fell E.J., Lindsey J.A., Peacock S.J., Day N.P.J.,
 RA Enright M.C., Foster T.J., Moore C.E., Hurst L., Atkin R., Barron A.,
 RA Bason N., Bentley S.D., Chillingworth C., Chillingworth T.,
 RA Churcher C., Clark L., Cotton C., Cronin A., Doggett J., Dowd L.,
 RA Felwell T., Hance Z., Harris B., Hauser H., Holtroyd S., Jagsels K.,
 RA James K.D., Lennard N., Line A., Mayes R., Moul S., Mungall K.,
 RA Ormond D., Quail M.A., Rabinowitch E., Rutherford K.M., Sanders M.,


```
RA Sharp S., Simmonds M., Stevens K., Whitehead S., Barrell B.G.,
RA Spratt B.G., Parkhill J.,
RT "Complete genomes of two clinical Staphylococcus aureus strains:
RT evidence for the rapid evolution of virulence and drug resistance."
RT Proc. Natl. Acad. Sci. U.S.A. 101:9786-9791(2004).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC an amide bond (By similarity).
CC EMBL: BX571856; CACG41560.1; -.
DR GO: GO:0008986; C:cell surface; IEA.
DR GO: GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO: GO:0016020; C:membrane; IEA.
DR GO: GO:007155; P:cell adhesion; IEA.
DR InterPro: IPR008966; Adhes_bact.
DR InterPro: IPR004237; Fn_bind.
DR InterPro: IPR005877; Gpos_YSTRK.
DR InterPro: IPR001899; Gram_pos_anchor.
DR Pfam: PF02986; Fn_bind; 1.
DR Pfam: PF04650; YSTRK_signal; 1.
DR TIGRfam: TIGR01167; LPXNG_anchor; 1.
DR TIGRfam: TIGR01168; YSTRK_signal; 1.
DR PROSITE: PS50847; GRAM_POS_ANCHORING; 1.
DR Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ SEQUENCE 965 AA; 105691 MW; 2982E132164D0551 CRC64;

Query Match 75.0%; Score 42; DB 2; Length 965;
Best Local Similarity 88.9%; Pred. No. 33;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 VPOIHGQNK 9
Db 781 VPOIHGQNK 789

RESULT 13
O6PCB8 PRELIMINARY; PRT; 327 AA.
ID O6PCB8
AC O6PCB8:
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Similar to embigin.
GN Name=MGC71745;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OC NCB1_TaxID=9606;
OX [1]
RN SEQUENCE FROM N.A.
RP TISSUE=Placenta;
RC MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buettow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.F., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.U., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loguelli N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Scherch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
```

```
RC TISSUE=Placenta;
RA Strausberg R.;
RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL: BC059398; AAH59398.1; -.
DR InterPro: IPR003599; IG.
DR InterPro: IPR007110; IG-like.
DR Pfam: PF00047; IG; 2.
DR SMART: SM00409; IG; 2.
DR PROSITE: PS50835; IG_LIKE; 2.
SQ SEQUENCE 327 AA; 36881 MW; E6B933DAF6A3B0D4 CRC64;

Query Match 73.2%; Score 41; DB 2; Length 327;
Best Local Similarity 66.7%; Pred. No. 17;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VPOIHGQNK 9
Db 158 VPELHGQNK 166

RESULT 14
ID O88775 PRELIMINARY; PRT; 328 AA.
AC O88775;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Embigin protein precursor.
GN Name=embigin; Synonyms=Emb;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCB1_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=spague dawley; TISSUE=regressing prostate;
RX MEDLINE=98101284; PubMed=9438341;
RX DOI=10.1002/(SICI)1520-6408(1997)21:4<268::AID-DVG4>3.0.CO;2-5;
RA Guenette R., Strihar S., Herley M., Woolbrock M., Wong P.,
RA Tenniswood M.,
RT "Embigin, a developmentally expressed member of the immunoglobulin
RT super family, is also expressed during regression of prostate and
RT mammary gland."
RL Dev. Genet. 21:268-278(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=spague dawley; TISSUE=regressing prostate;
RA Guenette R.;
RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Prostate;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buettow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loguelli N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Scherch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
```

```

RN (4)
RP SEQUENCE FROM N.A.
RC TISSUE=Prostate;
RA Strausberg R.;
RL Submitted (NOV-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL: AJ009698; CA008796.1; -.
DR EMBL: BC061846; AAH61846.1; -.
DR InterPro: IPR007110; IG-1like.
DR Pfam: PF00047; 1g; 1.
DR PROSITE: PS50835; IG_LIKE; 2.
KW Signal.
FT SIGNAL.
FT CHAIN 1 23
FT SEQUENCE 328 AA; 37005 MW; C749A847ACE374B1 CRC64;

Query Match
Best Local Similarity 66.7%; Pred. No. 17;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPGHGNK 9
Db 158 VPKHGK 166

RESULT 15
DEGP BUCBP
ID DEGP BUCBP STANDARD; PRT; 465 AA.
AC 089AB5;
DT 05-JUL-2004 (Rel. 44, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Probable serine protease do-like precursor (EC 3.4.21.-).
GN Name=degp; Synonyms=htra; OrderedLocustNames=bpp210;
OS Buchnera aphidicola (subsp. Baizongia distictae).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Buchnera.
OX NCBI_TaxID=135842;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=12523265; DOI=10.1073/pnas.0235981100;
RA van Ham R.C.H.J., Kamerbeek J., Palacios C., Rausell C., Abascal F.,
RA Bastolla U., Fernandez J.M., Jimenez L., Postigo M., Silva F.J.,
RA Tamames J., Viguera E., Latorre A., Valencia A., Moran F., Moya A.;
RT "Reductive genome evolution in Buchnera aphidicola."
Proc. Natl. Acad. Sci. U.S.A. 100:581-586(2003).
CC -1- SIMILARITY: Belongs to the peptidase S1C family.
CC -1- SIMILARITY: Contains 2 PDZ/DHR domains.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: AB014016; AAO26942.1; -.
DR HSSP: P09376; 1KY9.
DR InterPro: IPR001478; PDZ.
DR InterPro: IPR009003; Pept_Ser_Cys.
DR InterPro: IPR001254; Peptidase_S1.
DR InterPro: IPR001940; Peptidase_S1C.
DR Pfam: PF00595; PDZ; 2.
DR Pfam: PF00089; Trypsin; 1.
DR PRINTS: PR00834; PROTEASES2C.
DR SMART; SM00228; PDZ; 2.
DR PROSITE; PS50106; PDZ; 2.
KM Complete proteome; Hydrolyase; Repeat; Serine protease; Signal.
FT SIGNAL.
FT CHAIN 1 26
FT DOMAIN 27 465 Potential.
FT DOMAIN 102 240 Probable serine protease do-like.
FT DOMAIN 268 359 PDZ 1.
FT DOMAIN 365 457 PDZ 2.

```

```

FT ACT SITE 119 119 Charge relay system (Potential).
FT ACT_SITE 149 149 Charge relay system (Potential).
FT ACT_SITE 224 224 Charge relay system (Potential).
FT DISULFID 85 91 By similarity.
SQ SEQUENCE 465 AA; 51085 MW; 57B3677C05838E78 CRC64;

Query Match
Best Local Similarity 73.2%; Score 41; DB 1; Length 465;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 QIHGNKG 10
Db 394 RIHGNKG 401

Search completed: October 22, 2005, 08:00:51
Job time : 57.85 secs

```

Handwritten text, possibly a signature or name, oriented diagonally.

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 25, 2005, 20:21:18 ; Search time 63.2 Seconds
(without alignments)
61.196 Million cell updates/sec

Title: US-10-731-238-80

Perfect score: 56

Sequence: 1 QIHGQKNGNQ 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

1: A_Geneseq_16Dec04:*
2: geneseqp19808:*
3: geneseqp19908:*
4: geneseqp20008:*
5: geneseqp20018:*
6: geneseqp20028:*
7: geneseqp20038:*
8: geneseqp20048:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	56	100.0	10	2 AAW65736	Aaw65736 Fibronect
2	56	100.0	134	2 AAY29087	Aay29087 S. aureus
3	56	100.0	139	2 AAW31556	Aaw31556 Fibronect
4	56	100.0	1018	1 AAP82115	Aap82115 Fibronect
5	56	100.0	1018	4 AAU37245	Aau37245 Staphyloc
6	56	100.0	1018	4 AAU34301	Aau34301 Staphyloc
7	56	100.0	1018	6 ABU18922	Abu18922 Patnogen
8	56	100.0	1018	6 ABM72537	Abm72537 Staphyloc
9	56	100.0	1027	2 AAW89806	Aaw89806 Staphyloc
10	51	91.1	113	2 AAR90937	Aar90937 D3D4 poly
11	51	91.1	130	2 AAR58806	Aar58806 Fibronect
12	51	91.1	130	2 AAR58807	Aar58807 Fibronect
13	51	91.1	130	2 AAR91202	Aar91202 D1-D4 fib
14	51	91.1	130	2 AAR91201	Aar91201 D1-D4 fib
15	51	91.1	134	2 AAY29088	Aay29088 S. aureus
16	51	91.1	162	2 AAR90942	Aar90942 D3D4 poly
17	51	91.1	164	2 AAR90938	Aar90938 D3D4 poly
18	51	91.1	174	2 AAR58808	Aar58808 Fbp fibro
19	51	91.1	174	2 AAR51203	Aar51203 D1-D4 fib
20	51	91.1	181	2 AAR58805	Aar58805 Fibronect
21	51	91.1	181	2 AAR91200	Aar91200 D1-D4 fib
22	51	91.1	559	2 AAW89803	Aaw89803 Staphyloc
23	51	91.1	767	4 AAU34403	Aau34403 Staphyloc
24	51	91.1	767	4 AAU37547	Aau37547 Staphyloc
25	51	91.1	940	2 AAR07070	Aar07070 Fibronect

26	51	91.1	940	6 ABJ19111	Abj19111 Pathogen
27	51	91.1	948	6 ADA89470	Ada89470 Staphyloc
28	51	91.1	948	6 ABJ18923	Abj18923 Pathogen
29	51	91.1	948	6 ABM72536	Abm72536 Staphyloc
30	51	91.1	961	6 ABU15854	Abu15854 Protein e
31	51	91.1	1038	6 ABU15903	Abu15903 Protein e
32	49	87.5	1098	4 ABG03347	Abg03347 Novel hum
33	47	82.1	109	2 AAW65737	Aaw65737 Fibronect
34	46	82.1	134	2 AAY29089	Aay29089 Cloned f1
35	45	80.4	10	2 AAW65735	Aaw65735 Fibronect
36	45	76.8	978	4 AAU33960	Aau33960 Staphyloc
37	43	76.8	1001	4 AAU37093	Aau37093 Staphyloc
38	40	71.4	734	4 ABG06491	Abg06491 Novel hum
39	40	71.4	1241	4 ABB71273	Abb71273 Drosophila
40	39	69.6	38	1 AAR80661	Aar80661 Protein w
41	39	69.6	38	1 AAR82117	Aar82117 Fibronect
42	37	66.1	164	5 ABP31449	Abp31449 Human ORF
43	37	66.1	318	4 ABB68750	Abb68750 Drosophila
44	37	66.1	320	4 AAU65372	Aau65372 Proplonab
45	37	66.1	320	6 ABM61891	Abm61891 Proplonab

ALIGNMENTS

RESULT 1
AAW65736 standard; peptide, 10 AA.
XX
XX
AC AAW65736;
XX
XX
DT 16-OCT-1998 (first entry)
XX
XX DE Fibronectin binding protein-derived peptide #80.
XX
XX KM Microbial surface components recognising adhesive matrix molecule;
KM MSCRAMM: fibronectin; fibronectin-binding protein; antibody; epitope;
KW antibiotic; bacterial infection; antibiotic-resistant strain.
XX
XX OS Synthetic.
OS Staphylococcus aureus.
XX
XX PN W09831389-A2.
XX
XX PD 23-JUL-1998.
XX
XX PF 21-JAN-1998; 98WO-US001222.
XX
XX PR 21-JAN-1997; 97US-0036139P.
XX
XX PA (TEXA) UNIV TEXAS A & M SYSTEM.
XX
XX PI Hoeoek M, Patti JM, House-Pompeo KL, Speciale P, Joh D;
PI Megavlin MJ;
XX
XX DR WPI, 1998-413816/35.
XX
XX PT Antibody that binds to fibronectin-binding protein, preventing its
PT binding to fibronectin - used to treat or prevent bacterial infection,
PT especially by Staphylococci and Streptococci.
XX
XX PS Example 9, Page 110; 20pp; English.
XX
XX CC The invention relates to antibodies that bind to a fibronectin-binding
CC domain of a fibronectin-binding protein, and inhibit binding of the
CC protein to fibronectin. Also claimed are: (1) isolated peptides of a
CC fibronectin-binding protein that do not bind to fibronectin; (2) fusion
CC protein containing at least one peptide of a fibronectin-binding protein
CC linked to a second amino acid sequence; (3) nucleic acid encoding the
CC isolated peptide of (1). Antibodies, the isolated peptides of (1) and the
CC nucleic acids are all useful for immunisation (active or passive) and (by
CC inhibiting binding of bacteria to fibronectin) for preventing or treating
CC infection in humans or other animals, particularly by staphylococci or

CC streptococci, e.g. meningitis, otitis media, pneumonia, endocarditis,
 CC mastitis in cattle, abortion in horses and many others. Since the
 CC antibodies block binding of bacteria, they should be effective against
 CC antibiotic-resistant strains, and may replace antibiotic therapy or
 CC increase its effectiveness. Sequences AAW65719-41 and AAW65658 represent
 CC peptides which were synthesised to span the D1 motif and the N-terminal
 CC 18 amino acids of D2, with each peptide overlapping by eight amino acids
 CC with the previous sequence
 CC
 XX
 SQ Sequence 10 AA;

Query Match 100.0%; Score 56; DB 2; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.00075;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QIHGQKNGQ 10
 |||||
 Db 1 QIHGQKNGQ 10

RESULT 2
 AAY29087
 ID AAY29087 standard; protein; 134 AA.

XX AAY29087;

XX 28-SEP-1999 (first entry)

XX S. aureus fibronectin binding protein A (FnBA) binding domain.

XX Bovine herpes virus-2; BHV-2; cytokine; immune response; immunogen; IL;
 XX Interleukin; colony stimulating factor; CSF; interferon; IFN; TNF;
 XX tumor necrosis factor; recombinant virus; vaccine; mucosal disease;
 XX mastitis; breast cancer; stress-induced disease; binding domain; FnBA;
 XX fibronectin binding protein.

XX Staphylococcus aureus.

XX WO9916892-A1.

XX 08-APR-1999.

XX 29-SEP-1998; 98WO-GB002927.

XX 29-SEP-1997; 97GB-00020633.

XX (UYBR-) UNIV BRISTOL.

XX Bradley AJ, Duffas WPB;

XX WPI: 1999-255101/21.

XX N-PSDB; AAX91504.

XX New bovine herpes virus-2 vectors.

XX Example 2; Fig 8A-B; 130pp; English.

CC The invention provides bovine herpes virus-2 (BHV-2) based vectors that
 CC comprise at least one cytokine-encoding DNA sequence. The expression of
 CC cytokines in mammals can up-regulate immune responses to the immunogens.
 CC The cytokine is selected from interleukin (IL), colony stimulating
 CC factors (CSF), interferons (IFN) and tumor necrosis factors (TNF). The
 CC BHV-2 based vector or recombinant virus can be used as vaccines. They can
 CC be used for preventing or treating a mucosal disease in a subject, e.g.
 CC tumourants, cattle, sheep, goats, dogs, cats, horses, or man, particularly
 CC mastitis in cows or breast cancers in humans. They can also be used for
 CC preventing or treating a stress-induced disease. The present sequence
 CC represents the binding domain of a previously published S. aureus
 CC fibronectin binding protein A (FnBA) sequence. The FnB binding domain
 CC gene sequence FNBA, cloned for use in this invention has 97.8 percent
 CC identity when compared to the previously published FnBA and FNBB gene
 CC sequences

SQ Sequence 134 AA;

Query Match 100.0%; Score 56; DB 2; Length 134;
 Best Local Similarity 100.0%; Pred. No. 0.012;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QIHGQKNGQ 10
 |||||
 Db 36 QIHGQKNGQ 45

RESULT 3
 AAW31556
 ID AAW31556 standard; protein; 139 AA.

XX AAW31556;

XX 27-AUG-2003 (revised)

XX 25-MAR-2003 (revised)

XX 21-MAY-1998 (first entry)

XX Fibronectin-binding MSCRAMM derivative pOD.

XX Fibronectin; pOD; collagen binding protein; sepsis; infection;
 XX microbial surface component recognising adhesive matrix molecule; MSCRAMM;
 XX adhesin; vaccine; immunisation; diagnosis; therapy; mastitis.

XX Staphylococcus aureus.

XX Key Location/Qualifiers

XX Peptide 1..12 /note="vector pQE30-derived peptide"

XX WO9743314-A2.

XX 20-NOV-1997.

XX 14-MAY-1997; 97WO-US008210.

XX 16-MAY-1996; 96US-0017678P.

XX (TEXA) UNIV TEXAS A & M SYSTEM.

XX (UABR-) UAB RES FOUND.

XX Hoeek M, Patti JM, House-Pompeo K, Sthanam N, Symersky J;

XX WPI: 1998-008801/01.

XX Antibody that interacts with collagen binding domain of Staphylococcal
 XX cna gene product - useful to prevent bacterial sepsis in animal infected
 XX with Staphylococcus aureus.

XX Disclosure; Page 91; 143pp; English.

CC This protein comprises Staphylococcus aureus fibronectin-binding
 CC microbial surface component recognising adhesive matrix molecule (MSCRAMM)
 CC derivative pOD, plus a vector-derived N-terminal peptide. The invention
 CC relates to claimed nucleic acid sequences (see AA193436-38) encoding S.
 CC aureus collagen binding protein (CBP) epitopes M17, M1 and M5 (see
 CC AAW31552-54) that confer protection against S. aureus infection. CBP
 CC protein and antigenic epitopes are contemplated for use in the treatment
 CC of pathological infections, especially to prevent bacterial adhesion to
 CC collagen. The epitopes are also contemplated for use in the preparation
 CC of vaccines and as carrier proteins in vaccine formulations, as well as
 CC in the formulation of compositions for the prevention of S. aureus
 CC infection. pCF33 and pOD (see AAW31556) were used to raise anti-MSCRAMM
 CC polyclonal antibodies used in passive immunisation against bovine
 CC mastitis. (Updated on 25-MAR-2003 to correct PI field.) (Updated on 27-
 CC AUG-2003 to correct OS field.)

XX Sequence 139 AA;

Query Match 100.0%; Score 56; DB 2; Length 139;


```

XX Antisense; prokaryotic cellular proliferation protein; antibiotic;
KM antibacterial; drug design.
XX
XX Staphylococcus aureus.
OS
XX WO200170955-A2.
XX
XX 27-SEP-2001.
XX
XX 21-MAR-2001; 2001WO-US009180.
XX
XX 21-MAR-2000; 2000US-0191078P.
XX
XX 23-MAY-2000; 2000US-0206848P.
XX
XX 26-MAY-2000; 2000US-0207727P.
XX
XX 23-OCT-2000; 2000US-0242578P.
XX
XX 27-NOV-2000; 2000US-0253625P.
XX
XX 22-DEC-2000; 2000US-0257931P.
XX
XX 16-FEB-2001; 2001US-0269308P.
XX
XX (ELIT-) ELITRA PHARM INC.
XX
XX Haselbeck R, Ohlsen KL, Zyskind JW, Wall D, Trawick JD, Carr GU;
PI Yamamoto RT, Xu HH;
XX
XX WPI; 2001-611495/70.
XX
XX N-PSDB; AAS52160.
XX
XX New polynucleotides for the identification and development of
PT antibiotics, comprise sequences of antisense nucleic acids.
XX
XX Example 3; SEQ ID NO 5797; 51pp; English.
XX
XX The invention relates to antisense inhibitors of genes essential to
CC prokaryotic cellular proliferation, their use in identifying the genes,
CC their use in the discovery of novel antibiotics, the essential genes
CC themselves and the encoded proteins. The prokaryotes used are Escherichia
CC coli, Staphylococcus aureus, Salmonella typhi, Klebsiella pneumoniae,
CC Pseudomonas aeruginosa and Enterococcus faecalis. The invention is also
CC useful for the identification of potential new targets for antibiotic
CC development. The antisense nucleic acids can also be used to identify
CC proteins used in proliferation, to express these proteins, and to obtain
CC antibodies capable of binding to the expressed proteins. The proteins can
CC be used to screen compounds in rational drug discovery programmes. The
CC antisense nucleic acid sequence is also useful to screen for homologous
CC nucleic acids which are required for cell proliferation in a wide variety
CC of organisms. The present sequence represents an essential prokaryotic
CC cellular proliferation protein. Note: The sequence data for this patent
CC did not form part of the printed specification, but was obtained in
CC electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX
XX Sequence 1018 AA;
SQ
Query Match 100.0%; Score 56; DB 4; Length 1018;
Best Local Similarity 100.0%; Pred. No. 0.11;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 QIHGQNKGNQ 10
DB 780 QIHGQNKGNQ 789

```

```

KM Antibacterial; virucide; fungicide; protozoacide; cytostatic; anti-HIV;
KM hyperimmune; serum-reactive; antigen; pathogen; tumour; allergen;
KM auto-immunity; vaccine; staphylococcal infection; antibody; cancer;
KM autoimmune disease; HIV; hepatitis.
XX
XX Staphylococcus sp.
OS
XX WO200259148-A2.
XX
XX 01-AUG-2002.
XX
XX 21-JAN-2002; 2002WO-EP000546.
XX
XX 26-JAN-2001; 2001AT-00000130.
XX
XX (CIST-) CISTEM BIOTECHNOLOGIES GMBH.
XX
XX Meinke A, Nagy E, Von Ahse U, Klade C, Henice T, Zauner W;
PI Minh DB, Vytvyetka O, Etz H, Dryla A, Weichart T, Hafner M;
PI Tempelmaier B;
XX
XX WPI; 2003-075410/07.
XX
XX Identifying, isolating and producing hyperimmune serum-reactive antigens
PT from a pathogen, for preparing vaccine or medicament for treating or
PT preventing e.g. staphylococcal infections, comprises providing antibody
PT preparation.
XX
XX Example 7; Page 157; 252pp; English.
XX
XX The invention relates to a novel method for identifying, isolating and
CC producing hyperimmune serum-reactive antigens from a pathogen, tumour,
CC allergen, a tissue or host prone to auto-immunity, where the antigens are
CC used in a vaccine, comprises providing antibody preparation from a plasma
CC pool of a type of animal, or individual sera with antibodies against the
CC specific pathogen, tumour, allergen, tissue or host prone to auto-
CC immunity. The hyperimmune serum-reactive antigens comprising any of the
CC 62 sequences of 53-2261 amino acids fully defined in the specification,
CC or their hyperimmune fragments are useful for the manufacture of a
CC pharmaceutical preparation, particularly a vaccine against staphylococcal
CC infections or colonisation against S. aureus or S. epidermidis. The
CC preparation of antibodies is useful for the manufacture of a medicament
CC for treating or preventing staphylococcal infections or colonisation
CC against S. aureus or S. epidermidis. The antibody preparations may also
CC be used for diagnostic and imaging purposes. Other conditions that can be
CC treated include cancer, autoimmune diseases or infections caused by viral
CC (e.g. HIV, hepatitis A, B or C), fungal or protozoan pathogens. This
CC sequence represents a staphylococcal protein relating to the method for
CC identifying and producing pathogen specific antigens of the invention
XX
XX
XX Sequence 1018 AA;
SQ
Query Match 100.0%; Score 56; DB 6; Length 1018;
Best Local Similarity 100.0%; Pred. No. 0.11;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 QIHGQNKGNQ 10
DB 780 QIHGQNKGNQ 789

```

```

RESULT 7
ABJ18922
ID ABJ18922 standard; protein; 1018 AA.
XX
XX AC ABJ18922;
XX
XX 06-MAR-2003 (first entry)
XX
XX Pathogen specific antigen related staphylococcal protein SEQ ID No 68.
DE
XX
XX

```

```

RESULT 8
ABM72537
ID ABM72537 standard; protein; 1018 AA.
XX
XX AC ABM72537;
XX
XX 20-NOV-2003 (first entry)
XX
XX Staphylococcus aureus protein #1777.
XX
XX Antibacterial; vaccine; gene therapy; infection; sepsis; diagnosis;
KM enzymatic assay; antibiotic target.
KM

```



```
XX 05-AUG-1994; 94GB-00015900.
XX (SMIK ) SMITHKLINE BEECHAM PLC.
XX Critchley IA, Dodd I, Barnett P, Mcbay DL;
XX WPI, 1996-129397/13.
XX
XX Polypeptide(s) derived from Staphylococcus aureus fibronectin binding
XX protein - inhibit binding of bacteria to extracellular matrix proteins,
XX for combating infection at the site of wounds and surgical implants, and
XX in oral hygiene.
XX Claim 6; Page 24; 35pp; English.
XX
XX AAR90937-R90942 represent D3D4 polypeptides. These sequences correspond
XX to fragments of the Staphylococcus aureus fibronectin binding protein
XX (Fbp). This sequence corresponds to residues 18-130 of S. aureus J2385
XX (Fbp). and also contains the D2 region, and a portion of the D1 region.
XX These sequences, and monoclonal antibodies against them can be used to
XX combat infection at the site of wounds, surgical implants and other in-
XX dwelling devices (such as catheters), and as antiadherent agents in oral
XX hygiene. They can also be used in the manufacture of a medicament for the
XX prevention of adhesion of bacteria to extracellular matrix proteins
XX present on in-dwelling devices or in wounds, or of oral pathogens to
XX similar proteins on surfaces in the oral cavity
XX
XX Sequence 113 AA;
SQ
Query Match          91.1%; Score 51; DB 2; Length 113;
Best Local Similarity 90.0%; Pred. No. 0.092;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 QIHGQNKGNQ 10
   |||||:|
Db 19 QIHGQNKGDQ 28

RESULT 11
AAR58806
ID AAR58806 standard; protein; 130 AA.
XX
XX AAR58806;
AC
XX 25-MAR-2003 (revised)
DT 30-MAR-1995 (first entry)
XX
XX Fibronectin binding domain D1-D4(709-838)(P838T).
DE
XX Fibronectin binding protein; Fbp; fibronectin binding domain;
XX monoclonal antibody; Mab; adhesion; Gram-positive bacterium; bacteremia;
XX Escherichia coli.
XX
XX Staphylococcus aureus.
OS
XX WO9418327-A1.
XX
XX 18-AUG-1994.
XX
XX 04-FEB-1994; 94WO-GB000215.
XX
XX 05-FEB-1993; 93GB-00002289.
XX
XX 20-OCT-1993; 93GB-00021592.
XX
XX (SMIK ) SMITHKLINE BEECHAM PLC.
XX
XX Burnham MKR, Chopra I, Critchley IA, Knowles DJC;
XX WPI, 1994-279748/34.
XX
XX Fibronectin binding protein and monoclonal antibodies specific for Fbp -
XX useful to prevent adherence of Gram-positive bacteria to indwelling
```

```
PT devices or wounds.
XX
XX Disclosure; Page 30; 40pp; English.
XX
XX Polypeptides corresponding to residues G709-T886 plus PPIVPT, G709-
XX P838(P838T) and G709-P838 (AAR58805-07, respectively) of S. aureus J2385
XX (NCIMB 40532) Fbp type A fibronectin binding domain D1-D4 region
XX (AAR58808) were expressed in E. coli BL21(DE4) and used to raise Mabs
XX specific for Fbp. (Updated on 25-MAR-2003 to correct PN field.)
XX
XX Sequence 130 AA;
SQ
Query Match          91.1%; Score 51; DB 2; Length 130;
Best Local Similarity 90.0%; Pred. No. 0.11;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 QIHGQNKGNQ 10
   |||||:|
Db 36 QIHGQNKGDQ 45

RESULT 12
AAR58807
ID AAR58807 standard; protein; 130 AA.
XX
XX AAR58807;
AC
XX 25-MAR-2003 (revised)
DT 30-MAR-1995 (first entry)
XX
XX Fibronectin binding domain D1-D4(709-838).
DE
XX Fibronectin binding protein; Fbp; fibronectin binding domain;
XX monoclonal antibody; Mab; adhesion; Gram-positive bacterium; bacteremia;
XX Escherichia coli.
XX
XX Staphylococcus aureus.
OS
XX WO9418327-A1.
XX
XX 18-AUG-1994.
XX
XX 04-FEB-1994; 94WO-GB000215.
XX
XX 05-FEB-1993; 93GB-00002289.
XX
XX 20-OCT-1993; 93GB-00021592.
XX
XX (SMIK ) SMITHKLINE BEECHAM PLC.
XX
XX Burnham MKR, Chopra I, Critchley IA, Knowles DJC;
XX WPI, 1994-279748/34.
XX
XX Fibronectin binding protein and monoclonal antibodies specific for Fbp -
XX useful to prevent adherence of Gram-positive bacteria to indwelling
XX devices or wounds.
XX
XX Disclosure; Page 30; 40pp; English.
XX
XX Polypeptides corresponding to residues G709-T886 plus PPIVPT, G709-
XX P838(P838T) and G709-P838 (AAR58805-07, respectively) of S. aureus J2385
XX (NCIMB 40532) Fbp type A fibronectin binding domain D1-D4 region
XX (AAR58808) were expressed in E. coli BL21(DE4) and used to raise Mabs
XX specific for Fbp. (Updated on 25-MAR-2003 to correct PN field.)
XX
XX Sequence 130 AA;
SQ
Query Match          91.1%; Score 51; DB 2; Length 130;
Best Local Similarity 90.0%; Pred. No. 0.11;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 QIHGQNKGNQ 10
   |||||:|
```

Db 36 QIHGONKGDQ 45

RESULT 13
AAR91202
ID AAR91202 standard; peptide; 130 AA.

XX
XX AAR91202;
XX
XX 13-NOV-1996 (first entry)
XX
XX
XX D1-D4 fibronectin binding domains.
XX
XX Fibronectin; oral hygiene; gingivitis; gum disease; adhesion;
XX
XX periodontitis; oral pathogen; caries; calculus; candidiasis; oral surgery;
XX
XX tissue regeneration; irrigation; toothpaste; dentifrice; mouthwash;
XX
XX lozenge.
XX
XX Staphylococcus aureus.
XX
XX WO9604003-A1.
XX
XX 15-FEB-1996.
XX
XX 18-JUL-1995; 95WO-EP002825.
XX
XX 05-AUG-1994; 94GB-00015902.
XX
XX (SMIK) SMITHKLINE BEECHAM PLC.
XX
XX Barnett P, Critchley IA, Dodd I;
XX
XX WPI; 1996-129122/13.
XX
XX Prevention of adherence of oral pathogens in the oral cavity, partic.
XX
XX tooth surfaces - by application of a fibronectin binding protein or
XX
XX polypeptide or a monoclonal antibody or fragment against it.
XX
XX
XX Claim 5; Page 32; 41pp; English.

CC Adherence of oral pathogens, particularly to tooth surfaces, can be
CC
CC prevented by application of a fibronectin binding protein or polypeptide.
CC
CC The fibronectin binding protein or polypeptide is useful in the
CC
CC manufacture of oral hygiene compositions, eg. toothpaste, liquid
CC
CC dentifrice, mouthwash or lozenge. They are useful to prevent the plaque-
CC
CC related development of carious lesions, gingivitis, calculus or
CC
CC periodontal disease and to combat oral cavity infections, e.g.
CC
CC candidiasis. They may also be useful in oral surgery e.g. in guided
CC
CC tissue regeneration procedures to prevent subsequent bacterial infection,
CC
CC and for irrigation of periodontal pockets. This sequence corresponds to
CC
CC amino acids 709-838 of the D1-D4 fibronectin binding domain of
CC
CC Staphylococcus aureus
XX
XX
XX Sequence 130 AA;
SQ

Query Match 91.1%; Score 51; DB 2; Length 130;
Best Local Similarity 90.0%; Pred. No. 0.11;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 QIHGONKGNQ 10
DB 36 QIHGONKGDQ 45

RESULT 14
AAR91201
ID AAR91201 standard; peptide; 130 AA.

XX
XX AAR91201;
XX
XX 13-NOV-1996 (first entry)
XX
XX
XX D1-D4 fibronectin binding domains.
XX

XX
XX Fibronectin; oral hygiene; gingivitis; gum disease; adhesion;
XX
XX periodontitis; oral pathogen; caries; calculus; candidiasis; oral surgery;
XX
XX tissue regeneration; irrigation; toothpaste; dentifrice; mouthwash;
XX
XX lozenge.
XX
XX Staphylococcus aureus.
XX
XX WO9604003-A1.
XX
XX 15-FEB-1996.
XX
XX 18-JUL-1995; 95WO-EP002825.
XX
XX 05-AUG-1994; 94GB-00015902.
XX
XX (SMIK) SMITHKLINE BEECHAM PLC.
XX
XX Barnett P, Critchley IA, Dodd I;
XX
XX WPI; 1996-129122/13.
XX
XX Prevention of adherence of oral pathogens in the oral cavity, partic.
XX
XX tooth surfaces - by application of a fibronectin binding protein or
XX
XX polypeptide or a monoclonal antibody or fragment against it.
XX
XX
XX Claim 5; Page 31-32; 41pp; English.

CC Adherence of oral pathogens, particularly to tooth surfaces, can be
CC
CC prevented by application of a fibronectin binding protein or polypeptide.
CC
CC The fibronectin binding protein or polypeptide is useful in the
CC
CC manufacture of oral hygiene compositions, eg. toothpaste, liquid
CC
CC dentifrice, mouthwash or lozenge. They are useful to prevent the plaque-
CC
CC related development of carious lesions, gingivitis, calculus or
CC
CC periodontal disease and to combat oral cavity infections, e.g.
CC
CC candidiasis. They may also be useful in oral surgery e.g. in guided
CC
CC tissue regeneration procedures to prevent subsequent bacterial infection,
CC
CC and for irrigation of periodontal pockets. This sequence corresponds to
CC
CC amino acids 709-838 of the D1-D4 fibronectin binding domain of
CC
CC Staphylococcus aureus with a P638T substitution
XX
XX
XX Sequence 130 AA;
SQ

Query Match 91.1%; Score 51; DB 2; Length 130;
Best Local Similarity 90.0%; Pred. No. 0.11;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 QIHGONKGNQ 10
DB 36 QIHGONKGDQ 45

RESULT 15
AAV29088
ID AAV29088 standard; protein; 134 AA.

XX
XX AAV29088;
XX
XX 28-SEP-1999 (first entry)
XX
XX
XX S. aureus fibronectin binding protein B (FnBB) binding domain.
XX
XX Bovine herpes virus-2; BHV-2; cytokine; immune response; immunogen; IL;
XX
XX interleukin; colony stimulating factor; CSF; interferon; IFN; TNF;
XX
XX tumour necrosis factor; recombinant virus; vaccine; mucosal disease;
XX
XX mastitis; breast cancer; stress-induced disease; binding domain; FnBB;
XX
XX fibronectin binding protein.
XX
XX Staphylococcus aureus.
XX
XX WO916892-A1.
XX
XX 08-APR-1999.
PD

XX 29-SEP-1998; 98WO-GB002927.
PF
XX 29-SEP-1997; 97GB-00020633.
PR
XX (UYBR-) UNIV BRISTOL.
PA
XX Bradley AJ, Duffas WPH;
PI
XX WPI, 1999-255101/21.
DR
XX N-PSDB; AAX91505.
PT
XX New bovine herpes virus-2 vectors.
PS
XX Example 2; Fig 8A-B; 130pp; English.
XX
XX The invention provides bovine herpes virus-2 (BHV-2) based vectors that
CC comprise at least one cytokine-encoding DNA sequence. The expression of
CC cytokines in mammals can up-regulate immune responses to the immunogens.
CC The cytokine is selected from interleukins (IL), colony stimulating
CC factors (CSF), interferons (IFN) and tumour necrosis factors (TNF). The
CC BHV-2 based vector or recombinant virus can be used as vaccines. They can
CC be used for preventing or treating a mucosal disease in a subject, e.g.
CC ruminants, cattle, sheep, goats, dogs, cats, horses, or man, particularly
CC mastitis in cows or breast cancers in humans. They can also be used for
CC preventing or treating a stress-induced disease. The present sequence
CC represents the binding domain of a previously published S. aureus
CC fibronectin binding protein B (FnBB) sequence. The FnB binding domain
CC gene sequence FNBBAB, cloned for use in this invention has 97.8 percent
CC identity when compared to the previously published FnBB and FnBB gene
CC sequences
SQ Sequence 134 AA;

Query Match 91.1%; Score 51; DB 2; Length 134;
Best Local Similarity 90.0%; Pred. No. 0.11;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 QIHGQNGNQ 10
Db 36 QIHGQNGNQ 45

Search completed: October 25, 2005, 20:58:47
Job time : 64.2 secs

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OM protein - protein search, using SW model

Run on: October 22, 2005, 05:46:56 ; Search time 17.3 Seconds
(without alignments)
43.150 Million cell updates/sec

Title: US-10-731-238-80

Perfect score: 56

Sequence: 1 QIHGQNKGNQ 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*
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3: /cgn2_6/prodata/1/iaa/5A_COMB.pep.*
4: /cgn2_6/prodata/1/iaa/5B_COMB.pep.*
5: /cgn2_6/prodata/1/iaa/PCTUS_COMB.pep.*
6: /cgn2_6/prodata/1/iaa/backfile1.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	56	100.0	10	US-09-010-317-80	Sequence 80, Appl
2	56	100.0	114	US-08-259-000-3	Sequence 3, Appl1
3	56	100.0	139	US-08-856-253-8	Sequence 8, Appl1
4	56	100.0	1027	US-08-956-171E-5254	Sequence 5254, Ap
5	56	100.0	1027	US-08-781-986A-5254	Sequence 5254, Ap
6	51	91.1	130	US-08-459-135A-7	Sequence 7, Appl1
7	51	91.1	130	US-08-459-135A-8	Sequence 8, Appl1
8	51	91.1	130	US-08-495-559-7	Sequence 7, Appl1
9	51	91.1	130	US-08-495-559-8	Sequence 8, Appl1
10	51	91.1	174	US-08-459-135A-10	Sequence 10, Appl
11	51	91.1	174	US-08-459-135A-13	Sequence 13, Appl
12	51	91.1	174	US-08-485-559-10	Sequence 10, Appl
13	51	91.1	174	US-08-485-559-13	Sequence 13, Appl
14	51	91.1	176	US-08-495-559-6	Sequence 6, Appl1
15	51	91.1	178	US-08-459-135A-12	Sequence 12, Appl
16	51	91.1	178	US-08-495-559-12	Sequence 12, Appl
17	51	91.1	181	US-08-459-135A-6	Sequence 6, Appl1
18	51	91.1	559	US-08-956-171E-5251	Sequence 5251, Ap
19	51	91.1	559	US-08-781-986A-5251	Sequence 5251, Ap
20	47	83.9	10	US-09-010-317-81	Sequence 81, Appl
21	45	80.4	10	US-09-010-317-79	Sequence 79, Appl
22	39	69.6	38	US-08-729-767-4	Sequence 4, Appl1
23	37	66.1	643	US-09-252-991A-18482	Sequence 18482, A
24	36	64.3	252	US-09-134-001C-3754	Sequence 3754, Ap
25	35	62.5	12	US-08-748-114A-13	Sequence 13, Appl
26	35	62.5	425	US-09-540-236-2538	Sequence 2538, Ap
27	35	62.5	446	US-09-252-991A-27399	Sequence 27399, A

28	35	62.5	683	US-09-252-991A-29859	Sequence 29859, A
29	35	62.5	785	US-09-733-643B-2	Sequence 2, Appl1
30	35	62.5	900	US-09-328-352-8072	Sequence 8072, Ap
31	34	60.7	10	US-09-010-317-78	Sequence 78, Appl
32	34	60.7	38	US-08-729-767-3	Sequence 8026, Ap
33	34	60.7	102	US-09-513-999C-8026	Sequence 11187, A
34	34	60.7	129	US-09-949-016-11187	Sequence 20430, A
35	34	60.7	168	US-09-248-796A-20430	Sequence 18039, A
36	34	60.7	191	US-09-248-796A-18039	Sequence 1658, Ap
37	34	60.7	245	US-09-710-279-1658	Sequence 4787, Ap
38	34	60.7	246	US-09-134-001C-4787	Sequence 956, App
39	34	60.7	822	US-09-198-452A-956	Sequence 896, App
40	34	60.7	822	US-09-438-185A-889	Sequence 82, Appl
41	33	58.9	10	US-09-010-317-82	Sequence 58, Appl
42	33	58.9	36	US-09-010-317-58	Sequence 59, Appl
43	33	58.9	36	US-09-010-317-59	Sequence 3, Appl1
44	33	58.9	38	US-08-234-622A-3	Sequence 7, Appl1
45	33	58.9	38	US-09-010-317-7	

ALIGNMENTS

RESULT 1
US-09-010-317-80
; Sequence 80, Application US/09010317
; Patent No. 6685943
; GENERAL INFORMATION:
; APPLICANT: Hook, Magnus
; APPLICANT: Patti, Joseph M.
; APPLICANT: House-Pompeo, Karen L.
; APPLICANT: Speziale, Pietro
; APPLICANT: John, Danny
; APPLICANT: McGavin, Martin J.
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
; TITLE OF INVENTION: AND METHODS OF USE
; NUMBER OF SEQUENCES: 105
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: TX
; COUNTRY: USA
; ZIP: 77210-4433
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/010,317
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/036,139
; FILING DATE: 21-JAN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Hibler, David W.
; REGISTRATION NUMBER: 41,071
; REFERENCE/DOCKET NUMBER: TAMK:189
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 512-418-3000
; TELEFAX: 512-474-7577
; INFORMATION FOR SEQ ID NO: 80:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; US-09-010-317-80
Query Match 100.0%; Score 56; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0065;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 QIHGKNGNQ 10
|||||

Db 1 QIHGKNGNQ 10

RESULT 2
US-08-259-000-3
; Sequence 3, Application US/08259000
; Patent No. 5571514
; GENERAL INFORMATION:
; APPLICANT: HOOK, Magnus
; APPLICANT: LINDERBERG, Martin Kjell
; APPLICANT: SIGMANS, Lars Christer
; APPLICANT: WADSTROM, Torkel Mikael
; APPLICANT: FROMAN, Gunnar
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN AS WELL AS
; TITLE OF INVENTION: ITS PREPARATION
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSES: Burns, Doane, Swecker & Mathis
; STREET: P. O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22113-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/259,000
; FILING DATE: 13-JUN-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: SE 8702272-9
; FILING DATE: 01-JUN-1987
; ATTORNEY/AGENT INFORMATION:
; NAME: Neulth, Donna M
; REGISTRATION NUMBER: 36,607
; REFERENCE/DOCKET NUMBER: 012885-062
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 114 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-259-000-3

Query Match 100.0%; Score 56; DB 1; length 114;
Best Local Similarity 100.0%; Pred. No. 0.0074;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 QIHGKNGNQ 10
|||||

Db 36 QIHGKNGNQ 45

RESULT 3
US-08-856-253-8
; Sequence 8, Application US/08856253
; Patent No. 6288214
; GENERAL INFORMATION:
; APPLICANT: HOOK, Magnus
; APPLICANT: Patcl, Joseph M.
; APPLICANT: House-Pompeo, Karen
; APPLICANT: Sthanam, Narayana

APPLICANT: Sytersky, Jindrich
; TITLE OF INVENTION: COLLAGEN BINDING PROTEIN COMPOSITIONS
; TITLE OF INVENTION: AND METHODS OF USE
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P. O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: U.S.
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/856,253
; FILING DATE: Concurrently Herewith
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/017,678
; FILING DATE: 16-MAY-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Kitchell, Barbara S.
; REGISTRATION NUMBER: 33,928
; REFERENCE/DOCKET NUMBER: TMK.193
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (512) 418-3000
; TELEFAX: (512) 474-7577
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 139 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; US-08-856-253-8

Query Match 100.0%; Score 56; DB 3; length 139;
Best Local Similarity 100.0%; Pred. No. 0.009;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 QIHGKNGNQ 10
|||||

Db 50 QIHGKNGNQ 59

RESULT 4
US-08-956-171E-5254
; Sequence 5254, Application US/08956171E
; Patent No. 6593114
; GENERAL INFORMATION:
; APPLICANT: Charles Kunach
; Gail H. Choi
; Patrick S. Dillon
; Craig A. Rosen
; Steven C. Barash
; Michael R. Fannon
; TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
; NUMBER OF SEQUENCES: 5256
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4mb storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/956,171E
FILING DATE: 20-Oct-1997
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/009,861
FILING DATE: January 5, 1996
APPLICATION NUMBER: 08/781,986
FILING DATE: January 3, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Mark J. Hyman
REGISTRATION NUMBER: 46,789
REFERENCE/DOCKET NUMBER: PB248P1
TELEPHONE: (240) 314-1224
TELEFAX: (301) 309-8439
INFORMATION FOR SEQ ID NO: 5254:
SEQUENCE CHARACTERISTICS:
LENGTH: 1027 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 5254:
US-08-956-171E-5254

Query Match : 100.0%; Score 56; DB 4; Length 1027;
Best Local Similarity 100.0%; Pred. No. 0.066;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QIHGONKGNQ 10
DB 789 QIHGONKGNQ 798

RESULT 5
US-08-781-986A-5254
Sequence 5254, Application US/08781986A
Patent No. 6737248
GENERAL INFORMATION:
APPLICANT: Charles Kunsch
TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
NUMBER OF SEQUENCES: 5255
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
City: Rockville
STATE: Maryland
COUNTRY: USA
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/781,986A
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Benson, Bob
REGISTRATION NUMBER: 30,446
REFERENCE/DOCKET NUMBER: PB248PP
TELEPHONE: (301) 309-8504
TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 5254:
SEQUENCE CHARACTERISTICS:
LENGTH: 1027 amino acids
TYPE: amino acid
STRANDEDNESS: single

TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-781-986A-5254

Query Match : 100.0%; Score 56; DB 4; Length 1027;
Best Local Similarity 100.0%; Pred. No. 0.066;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QIHGONKGNQ 10
DB 789 QIHGONKGNQ 798

RESULT 6
US-08-459-135A-7
Sequence 7, Application US/08459135A
Patent No. 5955078
GENERAL INFORMATION:
APPLICANT: BURHAM, Martin Karl Russel
APPLICANT: CHOPRA, Ian
APPLICANT: CRITCHLEY, Ian Alfred
APPLICANT: KNOWLES, David Justin Charles
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN: MONOCLONAL ANTIBODY AND THEIR US
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
City: King of Prussia
STATE: PA
COUNTRY: U.S.A.
ZIP: 19406-0939
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: Fastseq, Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/459,135A
FILING DATE: 02-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB/94/00215
FILING DATE: 04-Feb-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Gimmil, Edward R
REGISTRATION NUMBER: 38,891
REFERENCE/DOCKET NUMBER: P30591C2
TELEPHONE: 610-270-4478
TELEFAX: 610-270-5090
TELEX:
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 130 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-459-135A-7

Query Match : 91.1%; Score 51; DB 2; Length 130;
Best Local Similarity 90.0%; Pred. No. 0.066;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 QIHGONKGNQ 10
DB 36 QIHGONKGDQ 45

RESULT 7
US-08-459-135A-8
Sequence 8, Application US/08459135A
Patent No. 5955078

```

; GENERAL INFORMATION:
; APPLICANT: BURHAM, Martin Karl Russel
; APPLICANT: CHOPRA, Ian
; APPLICANT: CRITCHLEY, Ian Alfred
; APPLICANT: KNOWLES, David Justin Charles
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN: MONOCLONAL ANTIBODY AND THEIR US
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corporation
; STREET: 709 Swedeland Road
; CITY: King of Prussia
; STATE: PA
; COUNTRY: U.S.A.
; ZIP: 19406-0939
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq, Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/459,135A
; FILING DATE: 02-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB/94/00215
; FILING DATE: 04-Feb-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Gimmi, Edward R
; REGISTRATION NUMBER: 38,891
; REFERENCE/DOCKET NUMBER: P30591C2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-270-4478
; TELEFAX: 610-270-5090
; TELEX:
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 130 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-459-135A-8

Query Match          91.1%; Score 51; DB 2; Length 130;
Best Local Similarity 90.0%; Pred. No. 0.066;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 QIHGQNKGNQ 10
Db 36 QIHGQNKGDQ 45

RESULT 8
; US-08-459-559-7
; Sequence 7, Application US/08495559A
; Patent No. 6054572
; GENERAL INFORMATION:
; APPLICANT: BURHAM, Martin Karl Russel
; APPLICANT: CHOPRA, Ian
; APPLICANT: CRITCHLEY, Ian Alfred
; APPLICANT: KNOWLES, David Justin Charles
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN: MONOCLONAL
; APPLICANT: ANTIBODY AND THEIR USE IN PREVENTING BACTERIAL ADHESION
; FILE REFERENCE: P30591
; CURRENT APPLICATION NUMBER: US/08/495,559A
; CURRENT FILING DATE: 1995-08-03
; EARLIER APPLICATION NUMBER: GB 9302289.5
; EARLIER FILING DATE: 1993-02-05
; EARLIER APPLICATION NUMBER: GB 9321592.9
; EARLIER FILING DATE: 1993-10-20
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 7
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; LENGTH: 130
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
; US-08-495-559-7

Query Match          91.1%; Score 51; DB 3; Length 130;
Best Local Similarity 90.0%; Pred. No. 0.066;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 QIHGQNKGNQ 10
Db 36 QIHGQNKGDQ 45

RESULT 9
; US-08-495-559-8
; Sequence 8, Application US/08495559A
; Patent No. 6054572
; GENERAL INFORMATION:
; APPLICANT: BURHAM, Martin Karl Russel
; APPLICANT: CHOPRA, Ian
; APPLICANT: CRITCHLEY, Ian Alfred
; APPLICANT: KNOWLES, David Justin Charles
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN: MONOCLONAL
; FILE REFERENCE: P30591
; CURRENT APPLICATION NUMBER: US/08/495,559A
; CURRENT FILING DATE: 1995-08-03
; EARLIER APPLICATION NUMBER: GB 9302289.5
; EARLIER FILING DATE: 1993-02-05
; EARLIER APPLICATION NUMBER: GB 9321592.9
; EARLIER FILING DATE: 1993-10-20
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 8
; LENGTH: 130
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
; US-08-495-559-8

Query Match          91.1%; Score 51; DB 3; Length 130;
Best Local Similarity 90.0%; Pred. No. 0.066;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 QIHGQNKGNQ 10
Db 36 QIHGQNKGDQ 45

RESULT 10
; US-08-459-135A-10
; Sequence 10, Application US/08459135A
; Patent No. 5955078
; GENERAL INFORMATION:
; APPLICANT: BURHAM, Martin Karl Russel
; APPLICANT: CHOPRA, Ian
; APPLICANT: CRITCHLEY, Ian Alfred
; APPLICANT: KNOWLES, David Justin Charles
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN: MONOCLONAL ANTIBODY AND THEIR US
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corporation
; STREET: 709 Swedeland Road
; CITY: King of Prussia
; STATE: PA
; COUNTRY: U.S.A.
; ZIP: 19406-0939
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq, Version 2.0
; CURRENT APPLICATION DATA:
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; APPLICATION NUMBER: US/08/459,135A
; FILING DATE: 02-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB/94/00215
; FILING DATE: 04-Feb-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Gimmil, Edward R
; REGISTRATION NUMBER: 38,891
; REFERENCE/DOCKET NUMBER: P30591C2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-270-4478
; TELEFAX: 610-270-5090
;
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 174 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: Protein
;
US-08-459-135A-10

Query Match          91.1%; Score 51; DB 2; Length 174;
Best Local Similarity 90.0%; Pred. No. 0.088;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 QIHGONKGNQ 10
Db      36 QIHGONKGDQ 45

RESULT 11
; US-08-459-135A-13
; Sequence 13, Application US/08/459135A
; Patent No. 5955078
; GENERAL INFORMATION:
; APPLICANT: BURHAM, Martin Karl Russel
; APPLICANT: CHOPRA, Ian
; APPLICANT: CRITCHLEY, Ian Alfred
; APPLICANT: KNOWLES, David Justin Charles
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN: MONOCLONAL ANTIBODY AND THEIR USE
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corporation
; STREET: 709 Swedeland Road
; CITY: King of Prussia
; STATE: PA
; COUNTRY: U.S.A.
; ZIP: 19406-0939
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq, Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/459,135A
; FILING DATE: 02-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB/94/00215
; FILING DATE: 04-Feb-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Gimmil, Edward R
; REGISTRATION NUMBER: 38,891
; REFERENCE/DOCKET NUMBER: P30591C2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-270-4478
; TELEFAX: 610-270-5090
;
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 174
```

```

; LENGTH: 174 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
;
US-08-459-135A-13

Query Match          91.1%; Score 51; DB 2; Length 174;
Best Local Similarity 90.0%; Pred. No. 0.088;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 QIHGONKGNQ 10
Db      36 QIHGONKGDQ 45

RESULT 12
; US-08-495-559-10
; Sequence 10, Application US/08/495559A
; Patent No. 6054572
; GENERAL INFORMATION:
; APPLICANT: BURHAM, Martin Karl Russel
; APPLICANT: CHOPRA, Ian
; APPLICANT: CRITCHLEY, Ian Alfred
; APPLICANT: KNOWLES, David Justin Charles
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN: MONOCLONAL ANTIBODY AND THEIR USE IN PREVENTING BACTERIAL ADHESION
; FILE REFERENCE: P30591
; CURRENT APPLICATION NUMBER: US/08/495,559A
; CURRENT FILING DATE: 1995-08-03
; EARLIER APPLICATION NUMBER: GB 9302289.5
; EARLIER FILING DATE: 1993-02-05
; EARLIER APPLICATION NUMBER: GB 9321592.9
; EARLIER FILING DATE: 1993-10-20
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 10
; LENGTH: 174
; TYPE: PRT
; ORGANISM: Staphylococcus aureus

US-08-495-559-10

Query Match          91.1%; Score 51; DB 3; Length 174;
Best Local Similarity 90.0%; Pred. No. 0.088;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 QIHGONKGNQ 10
Db      36 QIHGONKGDQ 45

RESULT 13
; US-08-495-559-13
; Sequence 13, Application US/08/495559A
; Patent No. 6054572
; GENERAL INFORMATION:
; APPLICANT: BURHAM, Martin Karl Russel
; APPLICANT: CHOPRA, Ian
; APPLICANT: CRITCHLEY, Ian Alfred
; APPLICANT: KNOWLES, David Justin Charles
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN: MONOCLONAL ANTIBODY AND THEIR USE IN PREVENTING BACTERIAL ADHESION
; FILE REFERENCE: P30591
; CURRENT APPLICATION NUMBER: US/08/495,559A
; CURRENT FILING DATE: 1995-08-03
; EARLIER APPLICATION NUMBER: GB 9302289.5
; EARLIER FILING DATE: 1993-02-05
; EARLIER APPLICATION NUMBER: GB 9321592.9
; EARLIER FILING DATE: 1993-10-20
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 13
; LENGTH: 174
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; TYPE: PR1
; ORGANISM: Staphylococcus aureus
US-08-495-559-13
Query Match
Best Local Similarity 91.1%; Score 51; DB 3; Length 174;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 QIHGONKGNQ 10
   |||||:|
Db 36 QIHGONKGDQ 45

RESULT 14
US-08-495-559-6
; Sequence 6, Application US/08495559A
; Patent No. 6054572
; GENERAL INFORMATION:
; APPLICANT: BURHAM, Martin Karl Russel
; APPLICANT: CHOPRA, Ian
; APPLICANT: CRITCHLEY, Ian Alfred
; APPLICANT: KNOWLES, David Justin Charles
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN: MONOCLONAL
; FILE REFERENCE: P30591
; CURRENT APPLICATION NUMBER: US/08/495,559A
; EARLIER FILING DATE: 1995-08-03
; EARLIER APPLICATION NUMBER: GB 9302289.5
; EARLIER FILING DATE: 1993-02-05
; EARLIER APPLICATION NUMBER: GB 9321592.9
; EARLIER FILING DATE: 1993-10-20
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 176
; TYPE: PR1
; ORGANISM: Staphylococcus aureus
US-08-495-559-6
Query Match
Best Local Similarity 91.1%; Score 51; DB 3; Length 176;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 QIHGONKGNQ 10
   |||||:|
Db 36 QIHGONKGDQ 45

RESULT 15
US-08-459-135A-12
; Sequence 12, Application US/08459135A
; Patent No. 5955078
; GENERAL INFORMATION:
; APPLICANT: BURHAM, Martin Karl Russel
; APPLICANT: CHOPRA, Ian
; APPLICANT: CRITCHLEY, Ian Alfred
; APPLICANT: KNOWLES, David Justin Charles
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN: MONOCLONAL ANTIBODY AND THEIR US
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corporation
; STREET: 709 Swedeland Road
; CITY: King of Prussia
; STATE: PA
; COUNTRY: U.S.A.
; ZIP: 19406-0939
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq, Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/459,135A
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; FILING DATE: 02-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB/94/00215
; FILING DATE: 04-Feb-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Gimm1, Edward R
; REGISTRATION NUMBER: 38, 891
; REFERENCE/DOCKET NUMBER: P30591C2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-270-4478
; TELEFAX: 610-270-5090
; TELEX:
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 178 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Protein
US-08-459-135A-12
Query Match
Best Local Similarity 91.1%; Score 51; DB 2; Length 178;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 QIHGONKGNQ 10
   |||||:|
Db 36 QIHGONKGDQ 45
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Search completed: October 22, 2005, 07:41:45
Job time : 18.35 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 22, 2005, 12:09:40 ; Search time 57.25 Seconds
(without alignments)
72.924 Million cell updates/sec

Title: US-10-731-238-80

Perfect score: 56

Sequence: 1 QIHGKNKGNO 10

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1862951 seqs, 417491010 residues

Total number of hits satisfying chosen parameters: 1862951

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-Processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	100.0	10	18	US-10-731-238-80	Sequence 80, Appl
2	100.0	139	9	US-09-813-820-8	Sequence 8, Appl
3	100.0	1018	9	US-09-815-242-12838	Sequence 5797, Ap
4	100.0	1018	9	US-09-815-242-12838	Sequence 12838, A
5	100.0	1018	9	US-10-470-0488-69	Sequence 68, Appl
6	100.0	1027	8	US-08-781-986A-5254	Sequence 5254, Ap
7	100.0	1027	15	US-10-329-624-5254	Sequence 5254, Ap
8	91.1	388	8	US-08-901-062-1	Sequence 1, Appl
9	91.1	558	8	US-08-781-986A-5251	Sequence 5251, Ap
10	91.1	559	15	US-10-329-624-5251	Sequence 5251, Ap
11	91.1	767	9	US-09-815-242-5899	Sequence 5899, Ap

12	51	91.1	767	9	US-09-815-242-13140	Sequence 13140, A
13	51	91.1	940	17	US-10-470-0488-424	Sequence 424, App
14	51	91.1	948	17	US-10-470-0488-69	Sequence 69, Appl
15	51	91.1	961	15	US-10-282-122A-43778	Sequence 43778, A
16	51	91.1	1038	15	US-10-282-122A-43827	Sequence 43827, A
17	49	87.5	1098	18	US-10-450-763-33706	Sequence 33706, A
18	47	83.9	10	18	US-10-731-238-81	Sequence 81, Appl
19	45	80.4	10	18	US-10-731-238-79	Sequence 79, Appl
20	43	76.8	978	9	US-09-815-242-5456	Sequence 5456, Ap
21	43	76.8	1001	9	US-09-815-242-13686	Sequence 12686, A
22	40	71.4	734	18	US-10-450-763-36850	Sequence 36850, A
23	40	71.4	1241	20	US-11-097-143-40611	Sequence 40611, A
24	39	69.6	269	16	US-10-739-930-8413	Sequence 8413, Ap
25	39	69.6	319	16	US-10-425-115-361327	Sequence 361327, A
26	37	66.1	164	11	US-09-864-408A-844	Sequence 844, App
27	37	66.1	318	20	US-11-097-143-33042	Sequence 33042, A
28	36	64.3	71	15	US-10-424-599-147719	Sequence 147719, A
29	36	64.3	99	16	US-10-425-115-334727	Sequence 334727, A
30	36	64.3	206	15	US-10-282-122A-68056	Sequence 68056, A
31	36	64.3	206	15	US-10-282-122A-70093	Sequence 70093, A
32	36	64.3	239	15	US-10-282-122A-70765	Sequence 70765, Ap
33	36	64.3	252	18	US-10-724-972A-5028	Sequence 5028, Ap
34	36	64.3	411	17	US-10-732-923-11868	Sequence 11868, A
35	36	64.3	411	17	US-10-732-923-11869	Sequence 11869, A
36	36	64.3	725	15	US-10-467-433-3	Sequence 3, Appl
37	36	64.3	733	13	US-10-001-857-145	Sequence 145, App
38	35	62.5	12	9	US-09-748-114-13	Sequence 13, Appl
39	35	62.5	12	16	US-10-742-864-13	Sequence 13, Appl
40	35	62.5	12	16	US-10-742-864-13	Sequence 44415, A
41	35	62.5	45	9	US-09-864-761-44415	Sequence 1074, Ap
42	35	62.5	56	10	US-09-925-299-1074	Sequence 1074, Ap
43	35	62.5	67	16	US-10-425-115-241355	Sequence 241355, A
44	35	62.5	118	16	US-10-767-701-34928	Sequence 34928, A
45	35	62.5	185	18	US-10-450-763-36841	Sequence 36841, A

ALIGNMENTS

RESULT 1
US-10-731-238-80
Sequence 80, Application US/10731238
Publication No. US20050123552A1
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
Patell, Joseph M.
House-Pompeo, Karen L.
Speziale, Pietro
Job, Danny
McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 443
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/107/731.238
FILING DATE: 10-Dec-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/010.317
FILING DATE: 21-Jan-1998
APPLICATION NUMBER: US 60/036.139

FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hblder, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAMK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 80:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 80:
US-10-731-238-80

Query Match 100.0%; Score 56; DB 18; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0021;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QIHGONKGNQ 10
Db 1 QIHGONKGNQ 10

RESULT 2
US-09-813-820-8
Sequence 8, Application US/09813820
Patent No. US20020102262A1
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
Patti, Joseph M.
House-Pompeo, Karen
Sthanam, Narayana
Symeraky, Jindrich
TITLE OF INVENTION: COLLAGEN BINDING PROTEIN COMPOSITIONS
AND METHODS OF USE
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: Texas
COUNTRY: U.S.
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/813,820
FILING DATE: 22-Mar-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/856,253
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Kitchell, Barbara S.
REGISTRATION NUMBER: 33,928
REFERENCE/DOCKET NUMBER: TAMK:193
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
TELEFAX: (512) 474-7577
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 139 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-09-813-820-8

Query Match 100.0%; Score 56; DB 9; Length 139;
Best Local Similarity 100.0%; Pred. No. 0.031;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QIHGONKGNQ 10
Db 50 QIHGONKGNQ 59

RESULT 3
US-09-815-242-5797
Sequence 5797, Application US/09815242
Patent No. US20020061569A1
GENERAL INFORMATION:
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Karl L.
APPLICANT: Zyskind, Judith W.
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John D.
APPLICANT: Carr, Grant J.
APPLICANT: Yamamoto, Robert T.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in
FILE REFERENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 5797
LENGTH: 1018
TYPE: PRT
ORGANISM: Staphylococcus aureus
US-09-815-242-5797

Query Match 100.0%; Score 56; DB 9; Length 1018;
Best Local Similarity 100.0%; Pred. No. 0.24;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QIHGONKGNQ 10
Db 760 QIHGONKGNQ 789

RESULT 4
US-09-815-242-12838
Sequence 12838, Application US/09815242
Patent No. US20020061569A1
GENERAL INFORMATION:
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Karl L.
APPLICANT: Zyskind, Judith W.
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John D.
APPLICANT: Carr, Grant J.
APPLICANT: Yamamoto, Robert T.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in

```
/ TITLE OF INVENTION: Prokaryotes
/ FILE REFERENCE: ELITRA.011A
/ CURRENT APPLICATION NUMBER: US/09/815,242
/ CURRENT FILING DATE: 2001-03-21
/ PRIOR APPLICATION NUMBER: 60/191,078
/ PRIOR FILING DATE: 2000-03-21
/ PRIOR APPLICATION NUMBER: 60/206,848
/ PRIOR FILING DATE: 2000-05-23
/ PRIOR APPLICATION NUMBER: 60/207,727
/ PRIOR FILING DATE: 2000-05-26
/ PRIOR APPLICATION NUMBER: 60/242,578
/ PRIOR FILING DATE: 2000-10-23
/ PRIOR APPLICATION NUMBER: 60/253,625
/ PRIOR FILING DATE: 2000-11-27
/ PRIOR APPLICATION NUMBER: 60/257,931
/ PRIOR FILING DATE: 2000-12-22
/ PRIOR APPLICATION NUMBER: 60/269,308
/ PRIOR FILING DATE: 2001-02-16
/ NUMBER OF SEQ ID NOS: 14110
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO: 12838
/ LENGTH: 1018
/ TYPE: PRT
/ ORGANISM: Staphylococcus aureus
US-09-815-242-12838

Query Match          100.0%; Score 56; DB 9; Length 1018;
Best Local Similarity 100.0%; Pred. No. 0.24;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QIHGONKGNQ 10
DB 780 QIHGONKGNQ 789

RESULT 5
US-10-470-048B-68
/ Sequence 68, Application US/10470048B
/ Publication No. US20050037444A1
/ GENERAL INFORMATION:
/ APPLICANT: MEINKE ET AL.
/ TITLE OF INVENTION: A METHOD FOR IDENTIFICATION, ISOLATION AND PRODUCTION OF
/ FILE REFERENCE: SONN:035US
/ CURRENT APPLICATION NUMBER: US/10/470,048B
/ CURRENT FILING DATE: 2003-07-25
/ NUMBER OF SEQ ID NOS: 603
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO: 68
/ LENGTH: 1018
/ TYPE: PRT
/ ORGANISM: Staphylococcus aureus
US-10-470-048B-68

Query Match          100.0%; Score 56; DB 17; Length 1018;
Best Local Similarity 100.0%; Pred. No. 0.24;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QIHGONKGNQ 10
DB 780 QIHGONKGNQ 789

RESULT 6
US-08-781-986A-5254
/ Sequence 5254, Application US/08781986A
/ Publication No. US20030054436A1
/ GENERAL INFORMATION:
/ APPLICANT: Charles Kunsch
/ TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
/ NUMBER OF SEQUENCES: 5255
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Human Genome Sciences, Inc.
```

```
/ STREET: 9410 Key West Avenue
/ CITY: Rockville
/ STATE: Maryland
/ COUNTRY: USA
/ ZIP: 20850
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Diskette, 3.50 inch, 1.4mb storage
/ COMPUTER: HP Vectra 486/33
/ OPERATING SYSTEM: MSDOS version 6.2
/ SOFTWARE: ASCII Text
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/781,986A
/ FILING DATE:
/ CLASSIFICATION: 435
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER:
/ FILING DATE:
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Benson, Bob
/ REGISTRATION NUMBER: 30,446
/ REFERENCE/DOCKET NUMBER: PB248PP
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (301) 309-8504
/ TELEFAX: (301) 309-8512
/ INFORMATION FOR SEQ ID NO: 5254:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 1027 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
US-08-781-986A-5254

Query Match          100.0%; Score 56; DB 8; Length 1027;
Best Local Similarity 100.0%; Pred. No. 0.24;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QIHGONKGNQ 10
DB 789 QIHGONKGNQ 788

RESULT 7
US-10-329-624-5254
/ Sequence 5254, Application US/10329624
/ Publication No. US20040043037A1
/ GENERAL INFORMATION:
/ APPLICANT: Charles Kunsch
/ GIL H. Choi
/ PATRICK S. DILLON
/ CRAIG A. ROSEN
/ STEVEN C. BARASH
/ MICHAEL R. FANNON
/ TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
/ NUMBER OF SEQUENCES: 5256
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Human Genome Sciences, Inc.
/ STREET: 9410 Key West Avenue
/ CITY: Rockville
/ STATE: Maryland
/ COUNTRY: USA
/ ZIP: 20850
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Diskette, 3.50 inch, 1.4mb storage
/ COMPUTER: HP Vectra 486/33
/ OPERATING SYSTEM: MSDOS version 6.2
/ SOFTWARE: ASCII Text
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/10/329,624
/ FILING DATE: 27-Dec-2002
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/956,171
/ FILING DATE: October 20, 1997
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APPLICATION NUMBER: 60/009,861
FILING DATE: January 5, 1996
APPLICATION NUMBER: 08/781,986
FILING DATE: January 3, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Mark J. Hyman
REGISTRATION NUMBER: 46,789
REFERENCE/DOCKET NUMBER: PB248P1D1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (240) 314-1224
TELEFAX: (301) 309-8439
INFORMATION FOR SEQ ID NO: 5254:
SEQUENCE CHARACTERISTICS:
LENGTH: 1027 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 5254:
US-10-329-624-5254

Query Match 100.0%; Score 56; DB 15; Length 1027;
Best Local Similarity 100.0%; Pred. No. 0.24;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QIHGONKNGQ 10
Db 789 QIHGONKNGQ 798

RESULT 8
US-08-901-062-1
Sequence 1, Application US/08901062
GENERAL INFORMATION:
APPLICANT: SEALS, JONATHAN R.
TITLE OF INVENTION: RECOMBINANT BIVALENT BACTERIAL VACCINE
TITLE OF INVENTION: FOR THE PREVENTION OF MASTITIS
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: HALE AND DORR LLP
STREET: 60 State Street
CITY: Boston
STATE: MA
COUNTRY: United States Of America
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/901,062
FILING DATE: 25-JUL-1997
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Baker, Hollie L.
REGISTRATION NUMBER: 31,321
REFERENCE/DOCKET NUMBER: 106941.153
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 526-6000
TELEFAX: (617) 526-5000
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 388 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-901-062-1

Query Match 91.1%; Score 51; DB 8; Length 388;
Best Local Similarity 90.0%; Pred. No. 0.71;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QIHGONKNGQ 10
Db 299 QIHGONKNGQ 308

RESULT 9
US-08-781-986A-5251
Sequence 5251, Application US/08781986A
Publication No. US20030054436A1
GENERAL INFORMATION:
APPLICANT: Charles Kunsch
TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
NUMBER OF SEQUENCES: 5255
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COUNTRY: USA
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/781,986A
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Benson, Bob
REGISTRATION NUMBER: 30,446
REFERENCE/DOCKET NUMBER: PB248PP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 5251:
SEQUENCE CHARACTERISTICS:
LENGTH: 559 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-781-986A-5251

Query Match 91.1%; Score 51; DB 8; Length 559;
Best Local Similarity 90.0%; Pred. No. 1;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QIHGONKNGQ 10
Db 335 QIHGONKNGQ 344

RESULT 10
US-10-329-624-5251
Sequence 5251, Application US/10329624
Publication No. US20040043037A1
GENERAL INFORMATION:
APPLICANT: Charles Kunsch
Gill H. Choi
Patrick S. Dillon
Craig A. Rosen
Steven C. Barash
Michael R. Fannon
TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences

```

;
; NUMBER OF SEQUENCES: 5256
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4MB storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/329,624
; FILING DATE: 27-Dec-2002
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/956,171
; FILING DATE: October 20, 1997
; APPLICATION NUMBER: 60/009,861
; FILING DATE: January 5, 1996
; APPLICATION NUMBER: 08/781,986
; FILING DATE: January 3, 1997
;
; ATTORNEY/AGENT INFORMATION:
; NAME: Mark J. Hyman
; REGISTRATION NUMBER: 46,789
; REFERENCE/DOCKET NUMBER: PB248P1D1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (240) 314-1224
; TELEFAX: (301) 309-8439
;
; INFORMATION FOR SEQ ID NO: 5251:
;
; SEQUENCE CHARACTERISTICS:
; LENGTH: 559 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
;
; MOLECULE TYPE: protein
;
; SEQUENCE DESCRIPTION: SEQ ID NO: 5251:
;
US-10-329-624-5251
;
Query Match          91.1%; Score 51; DB 15; Length 559;
Best Local Similarity 90.0%; Pred. No. 1;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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QY      1 QIHGQNGNQ 10
Db      335 QIHGQNGNQ 344
;
RESULT 11
US-09-815-242-5899
; Sequence 5899, Application US/09815242
; Patent No. US20020061569A1
;
GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Karl L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
;
TITLE OF INVENTION: Identification of Essential Genes in
;
FILE REFERENCE: ELITRA.011A
;
CURRENT APPLICATION NUMBER: US/09/815,242
;
PRIOR FILING DATE: 2001-03-21
;
PRIOR APPLICATION NUMBER: 60/191,078
;
PRIOR FILING DATE: 2000-03-21
;
PRIOR APPLICATION NUMBER: 60/206,848
;
PRIOR FILING DATE: 2000-05-23
;
PRIOR APPLICATION NUMBER: 60/207,727
;
PRIOR FILING DATE: 2000-05-26
;

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; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
;
; NUMBER OF SEQ ID NOS: 14110
;
; SOFTWARE: FastSeq for Windows Version 4.0
;
; SEQ ID NO 5899
; LENGTH: 767
; TYPE: PRT
;
; ORGANISM: Staphylococcus aureus
;
US-09-815-242-5899
;
Query Match          91.1%; Score 51; DB 9; Length 767;
Best Local Similarity 90.0%; Pred. No. 1.4;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
;
QY      1 QIHGQNGNQ 10
Db      716 QIHGQNGNQ 725
;
RESULT 12
US-09-815-242-13140
; Sequence 13140, Application US/09815242
; Patent No. US20020061569A1
;
GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Karl L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
;
TITLE OF INVENTION: Identification of Essential Genes in
;
FILE REFERENCE: ELITRA.011A
;
CURRENT APPLICATION NUMBER: US/09/815,242
;
PRIOR FILING DATE: 2001-03-21
;
PRIOR APPLICATION NUMBER: 60/191,078
;
PRIOR FILING DATE: 2000-03-21
;
PRIOR APPLICATION NUMBER: 60/206,848
;
PRIOR FILING DATE: 2000-05-23
;
PRIOR APPLICATION NUMBER: 60/207,727
;
PRIOR FILING DATE: 2000-05-26
;
PRIOR APPLICATION NUMBER: 60/242,578
;
PRIOR FILING DATE: 2000-10-23
;
PRIOR APPLICATION NUMBER: 60/253,625
;
PRIOR FILING DATE: 2000-11-27
;
PRIOR APPLICATION NUMBER: 60/257,931
;
PRIOR FILING DATE: 2000-12-22
;
PRIOR APPLICATION NUMBER: 60/269,308
;
PRIOR FILING DATE: 2001-02-16
;
; NUMBER OF SEQ ID NOS: 14110
;
; SOFTWARE: FastSeq for Windows Version 4.0
;
; SEQ ID NO 13140
; LENGTH: 767
; TYPE: PRT
;
; ORGANISM: Staphylococcus aureus
;
US-09-815-242-13140
;
Query Match          91.1%; Score 51; DB 9; Length 767;
Best Local Similarity 90.0%; Pred. No. 1.4;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
;
QY      1 QIHGQNGNQ 10
Db      716 QIHGQNGNQ 725
;

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RESULT 13
US-10-470-048B-424
; Sequence 424, Application US/10470048B
; Publication No. US20050037444A1
; GENERAL INFORMATION:
; APPLICANT: MEINKE ET AL.
; TITLE OF INVENTION: A METHOD FOR IDENTIFICATION, ISOLATION AND PRODUCTION OF
; FILE OF INVENTION: ANTIGENS TO A SPECIFIC PATHOGEN
; FILE REFERENCE: SONN:03505
; CURRENT APPLICATION NUMBER: US/10/470,048B
; CURRENT FILING DATE: 2003-07-25
; NUMBER OF SEQ ID NOS: 603
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 424
; LENGTH: 940
; TYPE: PRN
; ORGANISM: Staphylococcus aureus
US-10-470-048B-424

Query Match          91.1%; Score 51; DB 17; Length 940;
Best Local Similarity 90.0%; Pred. No. 1.8;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 OIHGONKGNQ 10
DB      716 QIHGONNGNQ 725

RESULT 14
US-10-470-048B-69
; Sequence 69, Application US/10470048B
; Publication No. US20050037444A1
; GENERAL INFORMATION:
; APPLICANT: MEINKE ET AL.
; TITLE OF INVENTION: A METHOD FOR IDENTIFICATION, ISOLATION AND PRODUCTION OF
; FILE OF INVENTION: ANTIGENS TO A SPECIFIC PATHOGEN
; FILE REFERENCE: SONN:03505
; CURRENT APPLICATION NUMBER: US/10/470,048B
; CURRENT FILING DATE: 2003-07-25
; NUMBER OF SEQ ID NOS: 603
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 69
; LENGTH: 948
; TYPE: PRN
; ORGANISM: Staphylococcus aureus
US-10-470-048B-69

Query Match          91.1%; Score 51; DB 17; Length 948;
Best Local Similarity 90.0%; Pred. No. 1.8;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 OIHGONKGNQ 10
DB      724 QIHGONNGNQ 733

RESULT 15
US-10-282-122A-43778
; Sequence 43778, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haseibeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zykand, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Foreyth, R.

```

```

; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: EUTRA.034A US/10/282,122A
; CURRENT APPLICATION NUMBER: 2003-02-20
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 43778
; LENGTH: 961
; TYPE: PRN
; ORGANISM: Staphylococcus aureus
US-10-282-122A-43778

Query Match          91.1%; Score 51; DB 15; Length 961;
Best Local Similarity 90.0%; Pred. No. 1.8;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 OIHGONKGNQ 10
DB      727 QIHGONNGNQ 736

```

Search completed: October 22, 2005, 12:39:49
Job time : 58.25 secs

GenCore version 5.1.6
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OM protein - protein search, using SW model

Run on: October 22, 2005, 06:10:10 ; Search time 11.45 Seconds
(without alignments)
84.032 Million cell updates/sec

Title: US-10-731-238-80

Perfect score: 56
Sequence: 1 QIHGQNGNQ 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79:***
1: p1r1:***
2: p1r2:***
3: p1r3:***
4: p1r4:***

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	56	100.0	1018	2 A32192	fibronectin-binding
2	51	91.1	940	2 S19702	fibronectin-binding
3	51	91.1	961	2 G90053	hypothetical prote
4	51	91.1	1038	2 H90053	hypothetical prote
5	36	64.3	102	2 S33336	protamine P2 - r
6	36	64.3	103	2 S33337	protamine P2 - p
7	35	62.5	467	2 S39193	royal jelly protei
8	35	62.5	879	2 T22033	hypothetical prote
9	35	62.5	1012	2 T00958	hypothetical prote
10	34	60.7	102	1 HSHUP2	sperm histone P2 p
11	34	60.7	102	2 S33333	protamine P2 - gor
12	34	60.7	102	2 S33332	protamine P2 - pig
13	34	60.7	102	2 S33331	protamine P2 - chi
14	34	60.7	102	2 S33334	protamine P2 - ora
15	34	60.7	133	2 F95312	hypothetical prote
16	34	60.7	147	2 C84049	hypothetical prote
17	34	60.7	167	2 UQ2258	dehydrin-like prot
18	34	60.7	283	2 S39602	class I histocompa
19	34	60.7	434	2 T47575	hypothetical prote
20	34	60.7	450	2 S42825	serum response fac
21	34	60.7	515	2 T46610	cellulase (EC 3.2.
22	34	60.7	523	2 T47560	serine protease kin
23	34	60.7	626	2 H82147	methy1-accepting c
24	34	60.7	680	2 C82905	hypothetical prote
25	34	60.7	822	2 E86601	CHLTR probable pho
26	34	60.7	822	2 B81518	conserved hypochet
27	34	60.7	822	2 C72023	chltr probable pho
28	34	60.7	905	2 T00475	probable disease r
29	34	60.7	1018	2 T13525	hypothetical prote

30	33.5	59.8	292	1 D55582	cytochrome-c oxida
31	33	58.9	109	2 T47696	hypothetical prote
32	33	58.9	227	2 S35240	heat shock protein
33	33	58.9	302	2 AD3106	hypothetical prote
34	33	58.9	305	2 H98180	hypothetical prote
35	33	58.9	463	2 T39004	probable histone a
36	33	58.9	497	2 AB0700	probable outer mem
37	33	58.9	604	2 T37870	RNA-binding / Ran
38	33	58.9	640	2 S35734	DNA topoisomerase
39	33	58.9	679	2 C71413	hypothetical prote
40	33	58.9	698	2 JH0163	No-on-transient A
41	33	58.9	700	2 JH0162	No-on-transient A
42	33	58.9	731	2 JC7919	1,4-alpha-glucan b
43	33	58.9	733	2 F84476	probable Achilla re
44	33	58.9	784	2 H83158	Fe(III) dicitrate
45	33	58.9	785	2 A82123	chemotaxis protein

ALIGNMENTS

RESULT 1

A32192

fibronectin-binding protein B - Staphylococcus aureus

C:Species: Staphylococcus aureus

C>Date: 31-Jul-1989 #sequence_revision 31-Jul-1989 #text_change 16-Feb-1997

C/Accession: A32192

R:Signaes, C.; Raucchi, G.; Joensson, K.; Lindgren, P.E.; Anantharamaiah, G.M.; Hoeoek, i

Proc. Natl. Acad. Sci. U.S.A. 86, 699-703, 1989

A>Title: Nucleotide sequence of the gene for a fibronectin-binding protein from Staphyl

A/Reference number: A32192; MID:8908998; PMID:2521391

A/Accession: A32192

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-1018 <SIG>

A/Cross-references: GB:J04151

C/Keywords: fibronectin binding

Query Match

Best Local Similarity 100.0%; Score 56; DB 2; Length 1018;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QIHGQNGNQ 10
|||||
Db 780 QIHGQNGNQ 789

RESULT 2

fibronectin-binding protein B - Staphylococcus aureus

C:Species: Staphylococcus aureus

C>Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004

C/Accession: S19702

R:Joensson, K.; Signaes, C.; Mueller, H.P.; Lindberg, M.

Eur. J. Biochem. 202, 1041-1048, 1991

A>Title: Two different genes encode fibronectin binding proteins in Staphylococcus aure

A/Reference number: S19702; MID:9211475; PMID:1637266

A/Accession: S19702

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-940 <JOE>

A/Cross-references: UNIPROT:Q53682; EMBL:X62992; MID:949040; PDB:CAA4726.1; PDB:95815

C/Keywords: fibronectin binding

Query Match

Best Local Similarity 91.1%; Score 51; DB 2; Length 940;

Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QIHGQNGNQ 10
|||||
Db 716 QIHGQNGNQ 725


```
RESULT 3
G90053
Hypothetical protein fnbB [imported] - Staphylococcus aureus (strain N315)
C:Species: Staphylococcus aureus
C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C:Accession: G90053
R:Kurita, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Ogo
ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.;
C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
L:ncet 357, 1225-1240, 2001
A:Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.
A:Reference number: A89758; PMID:21311952; PMID:11418146
A:Accession: G90053
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-961 <KUR>
A:Cross-references: UNIPROT:Q99RD3; GB:BA000018; PID:G13702452; PIDN:BA843593.1; GSPDB:G
A:Experimental source: strain N315
C:Genetics:
A:Gene: fnbB

Query Match          91.1%; Score 51; DB 2; Length 961;
Best Local Similarity 90.0%; Pred. No. 0.13;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QIHGONKGN 10
|:|:|:|:|:|
DB 727 QIHGONNGNQ 736

RESULT 4
H90053
Hypothetical protein fnbB [imported] - Staphylococcus aureus (strain N315)
C:Species: Staphylococcus aureus
C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C:Accession: H90053
R:Kurita, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Ogo
ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.;
C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
L:ncet 357, 1225-1240, 2001
A:Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.
A:Reference number: A89758; PMID:21311952; PMID:11418146
A:Accession: H90053
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1038 <KUR>
A:Cross-references: UNIPROT:Q99RD2; GB:BA000018; PID:G13702453; PIDN:BA843594.1; GSPDB:G
A:Experimental source: strain N315
C:Genetics:
A:Gene: fnbB

Query Match          91.1%; Score 51; DB 2; Length 1038;
Best Local Similarity 90.0%; Pred. No. 0.14;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 QIHGONKGN 10
|:|:|:|:|:|
DB 776 QIHGONKGDQ 785

RESULT 5
S33336
Protamine P2 - rhesus macaque
C:Species: Macaca mulatta (rhesus macaque)
C:Date: 08-Dec-1993 #sequence_revision 26-May-1995 #text_change 09-Jul-2004
C:Accession: S33336
R:Retief, J.D.; Dixon, G.H.
L:ur J. Biochem. 214, 609-615, 1993
A:Title: Evolution of pro-protamine P2 genes in primates.
A:Reference number: S33331; PMID:93292525; PMID:8513810
A:Accession: S33336
A:Status: preliminary
A:Molecule type: DNA
```

```
A:Residues: 1-102 <RET>
A:Cross-references: UNIPROT:P35297; EMBL:X71338; NID:9296755; PIDN:CA850478.1; PID:92967
A:Note: the authors did not translate the codon for residue 1
C:Genetics:
A:Introns: 91/1
C:Superfamily: sperm histone
C:Keywords: DNA binding; nucleus

Query Match          64.3%; Score 36; DB 2; Length 102;
Best Local Similarity 55.6%; Pred. No. 10;
Matches 5; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 QIHGONKGN 9
|:|:|:|:|:|
DB 20 QVHGQDQGH 28

RESULT 6
S33337
Protamine P2 - pig-tailed macaque
C:Species: Macaca nemestrina (pig-tailed macaque)
C:Date: 08-Dec-1993 #sequence_revision 26-May-1995 #text_change 09-Jul-2004
C:Accession: S33337
R:Retief, J.D.; Dixon, G.H.
L:ur J. Biochem. 214, 609-615, 1993
A:Title: Evolution of pro-protamine P2 genes in primates.
A:Reference number: S33331; PMID:93292525; PMID:8513810
A:Accession: S33337
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-103 <RET>
A:Cross-references: UNIPROT:P35298; EMBL:X71340; NID:9296760; PIDN:CA850480.1; PID:92967
A:Note: the authors did not translate the codon for residue 1
C:Genetics:
A:Introns: 92/1
C:Superfamily: sperm histone
C:Keywords: DNA binding; nucleus

Query Match          64.3%; Score 36; DB 2; Length 103;
Best Local Similarity 55.6%; Pred. No. 10;
Matches 5; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 QIHGONKGN 9
|:|:|:|:|:|
DB 20 QVHGQDQGH 28

RESULT 7
S39193
royal jelly protein RJP57-1 - honeybee
C:Species: Apis mellifera (honeybee)
C:Date: 05-Mar-1995 #sequence_revision 12-May-1995 #text_change 12-May-1995
C:Accession: S39193
R:Klaidiny, J.; Hanes, J.; Kulifajova, J.; Albert, S.; Stimuth, J.
L:ubmitted to the EMBL Data Library, September 1993
A:Description: Molecular cloning of two cDNAs from the head of the nurse honey bee (Apis
A:Reference number: S39193
A:Accession: S39193
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-467 <KLA>
A:Cross-references: EMBL:Z26318

Query Match          62.5%; Score 35; DB 2; Length 467;
Best Local Similarity 75.0%; Pred. No. 71;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 HGONKGNQ 10
|:|:|:|:|
DB 421 HMONNAGNQ 428

RESULT 8
```

T22033
 hypothetical protein F40F8.5 - *Caenorhabditis elegans*
 C:Species: *Caenorhabditis elegans*
 C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
 C:Accession: T22033
 R:MacDougall, R.
 submitted to the EMBL Data Library, February 1996
 A:Reference number: Z19505
 A:Accession: T22033
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-879 <MTL>
 A:Cross-references: UNIPROT:Q02027; EMBL:Z69302; PIDN:CAA93261.1; GSPDB:GN00020; CESP:F4
 A:Experimental source: clone F40F8
 C:Genetic:
 A:Gene: CESP:F40F8.5
 A:Map position: 2
 A:Introns: 63/1; 149/1; 173/1; 217/1; 262/1; 306/1; 347/1; 381/2; 422/2; 440/3; 461/3; 5

Query Match 62.5%; Score 35; DB 2; Length 879;
 Best Local Similarity 55.6%; Pred. No. 1.3e+02;
 Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 1 QIHGKNKN 9
 :|||:|
 DB 421 KLRHGSSGN 429

RESULT 9
 T00958
 hypothetical protein F20D22.8 - *Arabidopsis thaliana*
 C:Species: *Arabidopsis thaliana* (mouse-ear cress)
 C:Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 09-Jul-2004
 C:Accession: T00958
 R:Vybotskaja, V.S.; Osborne, B.I.; Schwartz, J.R.; Tortum, M.; Kwan, A.; Yu, G.; Oji, C.
 K.; Feng, J.; Kim, C.; Kutz, D.; Li, Y.; Palm, C.J.; Shinn, P.; Sun, H.; Davis, R.W.;
 submitted to the EMBL Data Library, May 1998
 A:Description: *Arabidopsis thaliana* chromosome 1 BAC F20D22 complete sequence.
 A:Reference number: Z14214
 A:Accession: T00958
 A:Status: translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-1012 <VYS>
 A:Cross-references: UNIPROT:O64492; EMBL:AC002411; NID:93570223; PID:93142295; GSPDB:GN0
 C:Genetic:
 A:Gene: ARSP:F20D22.8
 A:Map position: 1
 C:Superfamily: *Arabidopsis thaliana* hypothetical protein F20D22.8

Query Match 62.5%; Score 35; DB 2; Length 1012;
 Best Local Similarity 55.6%; Pred. No. 1.5e+02;
 Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 2 IHGQKGNQ 10
 :|||:|
 DB 183 LHNHNGNQ 191

RESULT 10
 HSHUP2
 sperm histone P2 precursor [validated] - human
 N:Alternate names: protamine; protamine 2 (P2); protamine 3 (P3)
 N:Containing: intermediate nuclear basic protein P11; intermediate nuclear basic protein P
 tone P3; sperm histone P4
 C:Species: *Homo sapiens* (man)
 C:Date: 30-Jun-1987 #sequence_revision 12-Apr-1996 #text_change 09-Jul-2004
 C:Accession: B38515; I38871; A02651; A25395; B25395; S10801; S17219; S01953; S02056; A25
 R:Domenjoud, L.; Nusbaum, G.; Adham, I.M.; Greeske, G.; Engel, W.
 Genomics 8, 127-133, 1990
 A:Title: Genomic sequences of human protamines whose genes, PRM1 and PRM2, are clustered
 A:Reference number: A38515; MUID:91184796; PMID:2081589
 A:Accession: B38515
 A:Molecule type: DNA

A:Residues: 1-102 <DOM>
 A:Cross-references: UNIPROT:P04554; GB:M60332; NID:9190455
 A:Note: translation of initiator Met is not shown
 R:Nelson, J.E.; Krawetz, S.A.
 J. Biol. Chem. 269, 31067-31073, 1994
 A:Title: Characterization of a human locus in transition.
 A:Reference number: A55329; MUID:95074145; PMID:7983046
 A:Accession: I38871
 A:Molecule type: DNA
 A:Residues: 1-102 <RES>
 A:Cross-references: EMBL:U15422; NID:9642458; PIDN:AAC50487.1; PID:9642460
 R:Ammer, H.; Henschen, A.; Lee, C.H.
 Biol. Chem. Hoppe-Seyler 367, 515-522, 1986
 A:Title: Isolation and amino-acid sequence analysis of human sperm protamines P1 and P2.
 A:Reference number: A90708; MUID:86296190; PMID:3527226
 A:Accession: A02651
 A:Molecule type: protein
 A:Residues: 46-102 <THE>
 A:Note: form designated P2'; form designated P2'' lacked the 3 amino-terminal residues
 R:McKay, D.J.; Renaux, B.S.; Dixon, G.H.
 Eur. J. Biochem. 156, 5-8, 1986
 A:Title: Human sperm protamines. Amino-acid sequences of two forms of protamine P2.
 A:Reference number: A91168; MUID:86164351; PMID:3956509
 A:Accession: A25395
 A:Molecule type: protein
 A:Residues: 46-102 <MCK>
 A:Note: form P2a
 A:Accession: B25395
 A:Molecule type: protein
 A:Residues: 49-102 <MC2>
 A:Note: form P2b
 R:Marinage, A.; Arkhis, A.; Alimi, E.; Sautiere, P.; Chevallier, P.
 Eur. J. Biochem. 191, 449-451, 1990
 A:Title: Molecular characterization of nuclear basic protein HP11, a putative precursor
 A:Reference number: S10801; MUID:90345953; PMID:2384091
 A:Accession: S10801
 A:Molecule type: protein
 A:Residues: 2-102 <MAR>
 R:Arkhis, A.; Marinage, A.; Sautiere, P.; Chevallier, P.
 Eur. J. Biochem. 200, 387-392, 1991
 A:Title: Molecular structure of human protamine P4 (HP4), a minor basic protein of human
 A:Reference number: S17219; MUID:91364687; PMID:1889406
 A:Accession: S17219
 A:Molecule type: protein
 A:Residues: 45-102 <ARK>
 A:Note: minor form designated protamine P4
 R:Domenjoud, L.; Fronia, C.; Uhde, F.; Engel, W.
 Nucleic Acids Res. 16, 7733, 1988
 A:Title: Sequence of human protamine 2 cDNA.
 A:Reference number: S01953; MUID:8831971; PMID:3412906
 A:Accession: S01953
 A:Molecule type: mRNA
 A:Residues: 1-37, 'RM', 40-102 <DO2>
 A:Cross-references: EMBL:X07862
 A:Note: translation of initiator Met is not shown
 R:Domenjoud, L.
 submitted to the EMBL Data Library, June 1988
 A:Reference number: S02056
 A:Accession: S02056
 A:Molecule type: mRNA
 A:Residues: 1-37, 'RM', 40-51, 'Q', 53-102 <DO3>
 R:Sautiere, P.; Marinage, A.; Belaiche, D.; Arkhis, A.; Chevallier, P.
 J. Biol. Chem. 263, 11059-11062, 1988
 A:Title: Comparison of the amino acid sequences of human protamines HP2 and HP3 and of
 A:Reference number: A29222; MUID:88298740; PMID:3403514
 A:Accession: A29222
 A:Molecule type: protein
 A:Residues: 'E', 35-63 <SAU>
 R:Alimi, E.; Marinage, A.; Arkhis, A.; Belaiche, D.; Sautiere, P.; Chevallier, P.
 Eur. J. Biochem. 214, 445-450, 1993
 A:Title: Amino acid sequence of the human intermediate basic protein 2 (HP12) from sper
 A:Reference number: S33299; MUID:93292505; PMID:8513794
 A:Accession: S33299

A:Molecule type: protein
A:Residues: 22-46 <ALI>
R:Chirac, F.; Arthie, A.; Martinge, A.; Jaquinod, M.; Chevallier, P.; Sautiere, P.
Biochim. Biophys. Acta 1203, 109-114, 1993
A:Title: Phosphorylation of human sperm protamines HPI and HP2: identification of phosph
A:Reference number: A57865; MUID:94032442; PMID:8218377
A:Content: annotation; phosphorylation site
C:Genetics:
A:Gene: GDB:PRM2
A:Cross-references: GDB:125271; OMIM:182890
A:Map position: 16p13.3-16p13.3
A:Introns: 91/1
C:Function:
A:Description: binds to and packages sperm DNA in a condensed form of chromatin that is
C:Superfamily: sperm histone
C:Keyword: chromosomal protein; DNA binding; nucleosome core; phosphoprotein; spermatog
F:2-102/Product: intermediate nuclear basic protein P11 #status experimental <P11>
F:22-102/Product: intermediate nuclear basic protein P12 #status experimental <P12>
F:34-102/Product: intermediate nuclear basic protein P31 #status experimental <P31>
F:37-102/Product: intermediate nuclear basic protein P32 #status experimental <P32>
F:45-102/Product: sperm histone P4 #status experimental <HP4>
F:46-102/Product: sperm histone P2 #status experimental <HP2>
F:49-102/Product: sperm histone P3 #status experimental <HP3>
F:59/Binding site: phosphate (Ser) (covalent) (partial) #status experimental
Query Match Best Local Similarity 60.7%; Score 34; DB 1; Length 102;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
Qy 1 QIHGQNGN 9
Db 20 QIHGQNGH 28
RESULT 11
S33333
protamine P2 - gorilla
C:Species: Gorilla gorilla (gorilla)
C:Date: 08-Dec-1993 #sequence_revision 26-May-1995 #text_change 09-Jul-2004
C:Accession: S33333
R:Retief, J.D.; Dixon, G.H.
Eur. J. Biochem. 214, 609-615, 1993
A:Title: Evolution of pro-protamine P2 genes in primates.
A:Reference number: S33331; MUID:93292525; PMID:8513810
A:Accession: S33333
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-102 <RET>
A:Cross-references: UNIPROT:P35313; EMBL:X71336; NID:G296723; PIDN:CAA50476.1; PID:G2967
A>Note: the authors did not translate the codon for residue 1
C:Genetics:
A:Introns: 91/1
C:Superfamily: sperm histone
C:Keywords: DNA binding; nucleus
Query Match Best Local Similarity 60.7%; Score 34; DB 2; Length 102;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
Qy 1 QIHGQNGN 9
Db 20 QIHGQNGH 28
RESULT 12
S33332
protamine P2 - pygmy chimpanzee
C:Species: Pan paniscus (pygmy chimpanzee, bonobo)
C:Date: 08-Dec-1993 #sequence_revision 26-May-1995 #text_change 09-Jul-2004
C:Accession: S33332
R:Retief, J.D.; Dixon, G.H.
Eur. J. Biochem. 214, 609-615, 1993
A:Title: Evolution of pro-protamine P2 genes in primates.

A:Reference number: S33331; MUID:93292525; PMID:8513810
A:Accession: S33332
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-102 <RET>
A:Cross-references: UNIPROT:P35299; EMBL:X71334; NID:G296766; PIDN:CAA50474.1; PID:G2967
A>Note: the authors did not translate the codon for residue 1
C:Genetics:
A:Introns: 91/1
C:Superfamily: sperm histone
C:Keywords: DNA binding; nucleus
Query Match Best Local Similarity 60.7%; Score 34; DB 2; Length 102;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
Qy 1 QIHGQNGN 9
Db 20 QIHGQNGH 28
RESULT 13
S33331
protamine P2 - chimpanzee
C:Species: Pan troglodytes (chimpanzee)
C:Date: 08-Dec-1993 #sequence_revision 26-May-1995 #text_change 09-Jul-2004
C:Accession: S33331
R:Retief, J.D.; Dixon, G.H.
Eur. J. Biochem. 214, 609-615, 1993
A:Title: Evolution of pro-protamine P2 genes in primates.
A:Reference number: S33331; MUID:93292525; PMID:8513810
A:Accession: S33331
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-102 <RET>
A:Cross-references: UNIPROT:P35300; EMBL:X72968; NID:G296074; PIDN:CAA51474.1; PID:G2960
A>Note: the authors did not translate the codon for residue 1
C:Genetics:
A:Introns: 91/1
C:Superfamily: sperm histone
C:Keywords: DNA binding; nucleus
Query Match Best Local Similarity 60.7%; Score 34; DB 2; Length 102;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
Qy 1 QIHGQNGN 9
Db 20 QIHGQNGH 28
RESULT 14
S33334
protamine P2 - orangutan
C:Species: Pongo pygmaeus (orangutan)
C:Date: 08-Dec-1993 #sequence_revision 26-May-1995 #text_change 09-Jul-2004
C:Accession: S33334
R:Retief, J.D.; Dixon, G.H.
Eur. J. Biochem. 214, 609-615, 1993
A:Title: Evolution of pro-protamine P2 genes in primates.
A:Reference number: S33331; MUID:93292525; PMID:8513810
A:Accession: S33334
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-102 <RET>
A:Cross-references: UNIPROT:P35301; EMBL:X71337; NID:G296768; PIDN:CAA50477.1; PID:G2967
A>Note: the authors did not translate the codon for residue 1
C:Genetics:
A:Introns: 91/1
C:Superfamily: sperm histone
C:Keywords: DNA binding; nucleus
Query Match Best Local Similarity 60.7%; Score 34; DB 2; Length 102;

Best Local Similarity 55.6%; Pred. No. 24;
 Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
 QY 1 QIHGQKGN 9
 |.:|||.:|:
 |.:|||.:|:
 Db 20 QIHGQEGH 28

RESULT 15

F95312
 hypothetical protein Sma0759 [imported] - Sinorhizobium meliloti (strain 1021) magaplaasm
 C/Spectes: Sinorhizobium meliloti
 C/Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 09-Jul-2004
 C/Accession: F95312
 R/Barnett, M.J.; Fisher, R.F.; Jones, T.; Komp, C.; Abola, A.P.; Barloy-Hubler, F.; Bowe
 .; Kalman, S.; Keating, D.H.; Palm, C.; Peck, M.C.; Surzycki, R.; Wells, D.H.; Yeh, K.C.
 Proc. Natl. Acad. Sci. U.S.A. 98, 9883-9888, 2001
 A/Title: Nucleotide sequence and predicted functions of the entire Sinorhizobium melilot
 A/Reference number: A95262; MUID:21396509; PMID:11481432
 A/Accession: F95312
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-133 <RUB>
 A/Cross-references: UNIPROT:Q92ZP4; GB:AB06469; PIDN:AAK65064.1; PID:G14523497; GSPDB:G
 A/Experimental source: strain 1021, megaplaasmid pSymA
 R/Galibert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubler,
 pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.;
 L.; Hyman, R.W.; Jones, T.
 Science 293, 668-672, 2001
 A/Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure,
 hebaull, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K.
 A/Title: The composite genome of the legume symbiont Sinorhizobium meliloti.
 A/Reference number: A96039; MUID:21368234; PMID:11474104
 A/Contents: annotation
 C/Genetics:
 A/Gene: Sma0759
 A/Genome: plasmid

Query Match 60.7%; Score 34; DB 2; Length 133;
 Best Local Similarity 62.5%; Pred. No. 32;
 Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 HGOQKGNQ 10
 |.:|||.:|:
 |.:|||.:|:
 Db 93 HGOQEGGE 100

Search completed: October 22, 2005, 08:04:35
 Job time : 12.45 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 22, 2005, 06:06:36 ; Search time 55.85 Seconds
(without alignments)
91.688 Million cell updates/sec

Title: US-10-731-238-80
Perfect score: 56
Sequence: 1 QIHGQNGNQ 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : uniprot_03:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	56	100.0	1018	1 FNB_A_STAUV	P14738 staphylococ
2	51	91.1	940	2 Q53682	O53682 staphylococ
3	51	91.1	943	2 Q8NTU8	O8NTU8 staphylococ
4	51	91.1	957	2 Q6G6H4	O6G6H4 staphylococ
5	51	91.1	961	2 Q99RD3	O99RD3 staphylococ
6	51	91.1	961	2 Q7A3J8	Q7A3J8 staphylococ
7	51	91.1	1038	2 Q99RD2	Q99RD2 staphylococ
8	51	91.1	1038	2 Q7A3J7	Q7A3J7 staphylococ
9	43	76.8	152	2 Q9AEP9	Q9AEP9 staphylococ
10	43	76.8	1015	2 Q8NTU7	O8NTU7 staphylococ
11	43	76.8	1015	2 Q6G6H3	O6G6H3 staphylococ
12	41	73.2	465	1 DEGP_BUCBP	O89AP5 buchnera ap
13	40	71.4	1241	2 Q9BP41	Q9BP41 drosophila
14	40	71.4	1241	2 Q9VWE7	Q9VWE7 drosophila
15	39	69.6	1285	2 Q7MKL1	Q7MKL1 vibrio vuln
16	39	69.6	1233	2 Q7PZF9	Q7PZF9 anopheles g
17	38	67.9	599	2 Q7PM78	Q7PM78 anopheles g
18	37	66.1	106	2 Q8PVT1	O8PVT1 methanosarc
19	37	66.1	292	2 Q7S6U5	Q7S6U5 neurospora
20	37	66.1	318	2 Q9W0P3	Q9W0P3 drosophila
21	37	66.1	378	2 Q6LTS1	Q6LTS1 photobacter
22	37	66.1	415	2 Q6SPY3	Q6SPY3 manheimia
23	37	66.1	474	2 Q6G6C0	Q6G6C0 yarrowia li
24	37	66.1	627	2 Q7RFM0	Q7RFM0 plasmodium
25	37	66.1	654	2 Q6A756	Q6A756 propionibac
26	37	66.1	837	2 Q6BYQ1	Q6BYQ1 debaryomyce
27	37	66.1	844	2 Q6A8X0	Q6A8X0 propionibac
28	37	66.1	965	2 Q6GDU5	Q6GDU5 staphylococ
29	36	64.3	74	2 Q52159	Q52159 pseudomonas
30	36	64.3	102	2 HSP2_MACMU	P35297 macaca mlla
31	36	64.3	103	1 HSP2_ERYPA	Q9gkno erythrocebu

32	36	64.3	103	1 HSP2_MACFU	P61253 macaca fusc
33	36	64.3	103	1 HSP2_MACNE	P35298 macaca neme
34	36	64.3	206	1 R54_PSEPK	O88G12 pseudomonas
35	36	64.3	206	1 R54_PSESM	O889U7 pseudomonas
36	36	64.3	239	1 LEXA_AGRU	P61605 agrobacteri
37	36	64.3	239	2 O8CN68	O8CN68 staphylococ
38	36	64.3	340	2 O8BGL2	O8BGL2 paramecium
39	36	64.3	411	2 O8KON0	O8KON0 anaplasmia p
40	36	64.3	411	2 O8RR42	O8RR42 anaplasmia p
41	36	64.3	411	2 O8JZF6	O8JZF6 anaplasmia p
42	36	64.3	440	2 Q6APG2	Q6APG2 desulfoleale
43	36	64.3	450	2 Q69D87	Q69D87 rabies viru
44	36	64.3	526	2 Q9H703	Q9H703 homo sapien
45	36	64.3	591	2 Q7M515	Q7M515 fowl adenov

ALIGNMENTS

RESULT 1
ID FNB_A_STAUV STANDARD; PRT; 1018 AA.
AC P14738;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Fibronectin-binding protein precursor (FNBP).
GN Name=fnbp;
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1280;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=NCTC 8325-4;
RX MEDLINE=8908998; PubMed=2521391;
RA Signes C., Raucel G., Joensson K., Lindgren P.-E.,
RANantharamaiah G.M., Hoeck M., Lindberg M.;
RT "Nucleotide sequence of the gene for a fibronectin-binding protein
from Staphylococcus aureus: use of this peptide sequence in the
synthesis of biologically active peptides."
RL Proc. Natl. Acad. Sci. U.S.A. 86:699-703(1989).
CC -1- FUNCTION: The ability of bacteria to bind fibronectin has been
proposed as a virulence factor enabling bacteria to colonize wound
tissues and blood clots. Binding of plasma fibronectin to the
bacterial surface might block adhesion receptors on S.aureus, thus
representing an important defense mechanism against tissue
invasion.
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
an amide bond (Potential).
CC -----
CC THIS SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
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CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: J04151; AAA26632.1; -;
DR InterPro: IPR004237; Fn_bind.
DR InterPro: IPR005877; Gpob_YsIRK.
DR InterPro: IPR001899; Gram_pos_anchor.
DR Pfam: PF02986; Fn_bind_1.
DR Pfam: PF00746; Gram_pos_anchor; 1.
DR Pfam: PF04650; YsIRK_signal; 1.
DR TIGRfam: TIGR01167; Lptxg_anchor; 1.
DR TIGRfam: TIGR01168; YsIRK_signal; 1.
DR POSTITE; PSS0847; GRAM_POS_ANCHORING; 1.
KW Cell adhesion; Cell wall; Peptidoglycan-anchor; Repeat; Signal;
KW virulence.
FT STGNL 1 36
FT CHAIN 37 985 Fibronectin-binding protein.
FT PROPEP 986 1018 Removed by sortase (Potential).
FT

```
FT REPEAT 545 574 B-1.
FT REPEAT 575 604 B-2.
FT DOMAIN 745 878 4 X approximate tandem repeats,
  fibronectin-binding domain.
FT REPEAT 745 782 D-1.
FT REPEAT 783 820 D-2.
FT REPEAT 821 859 D-3.
FT REPEAT 860 878 D-4 (incomplete).
FT DOMAIN 879 948 5 X tandem repeats, Pro-rich (WR).
FT REPEAT 879 892 WR 1.
FT REPEAT 893 906 WR 2.
FT REPEAT 907 920 WR 3.
FT REPEAT 921 934 WR 4.
FT REPEAT 935 948 WR 5.
FT SITE 962 986 LpXTG sorting signal (Potential).
FT MOD_RES 985 985 Pentaglycyl murein peptidoglycan amidated
  threonine (Potential).
SQ SEQUENCE 1018 AA; 111780 MW; 58175E0020E81F1F CRC64;

Query Match 100.0%; Score 56; DB 1; Length 1018;
Best Local Similarity 100.0%; Pred. No. 0.047;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QIHGONKGNQ 10
Db 780 QIHGONKGNQ 789

RESULT 2
OS3682 PRELIMINARY; PRT; 940 AA.
AC OS3682;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Fibronectin binding protein B.
GN Name=fnbB;
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxId=1280;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=8325-4;
RX MEDLINE=92111475; PubMed=1837266;
RA Johnson K., Signae C., Muller H.P., Lindberg M.;
RT "Two different genes encode fibronectin binding proteins in
  Staphylococcus aureus. The complete nucleotide sequence and
  characterization of the second gene."
RU Eur. J. Biochem. 202;1041-1048(1991).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
  an amide bond (By similarity).
DR EMBL; X62992; CAA44726.1; -.
DR PIR; S19702; S19702.
DR HSP; OS3653; IN67.
DR GO; GO:0009986; C:cell surface; IEA.
DR GO; GO:0005618; C:cell wall; IEA.
DR GO; GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0007155; P:cell adhesion; IEA.
DR InterPro; IPR008966; Adhes_bact.
DR InterPro; IPR004237; Fn_bind.
DR InterPro; IPR005877; Gpos_YsIRK.
DR InterPro; IPR001899; Gram_pos_anchor.
DR Pfam; PF02986; Fn_bind_2.
DR Pfam; PF00746; Gram_pos_anchor_1.
DR Pfam; PF04650; YsIRK_signal_1.
DR TIGRFAMs; TIGR01167; LpXTG_anchor_1.
DR TIGRFAMs; TIGR01168; YsIRK_signal_1.
DR PROSITE; PS50847; GRAM_POS_ANCHORING; 1.
KW Cell wall; Peptidoglycan-anchor.
SQ SEQUENCE 940 AA; 103555 MW; E35FBBCA907AE345 CRC64;

Query Match 91.1%; Score 51; DB 2; Length 940;
```

```
Best Local Similarity 90.0%; Pred. No. 0.42;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QIHGONKGNQ 10
Db 716 QIHGONKGNQ 725

RESULT 3
OS8NTU8 PRELIMINARY; PRT; 943 AA.
ID Q8NTU8
AC Q8NTU8;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE FnbB protein.
GN Name=fnbB; OrderedLocustNames=MM2420;
OS Staphylococcus aureus (strain MM2).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxId=196620;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MM2;
RX MEDLINE=22040717; PubMed=12044378; DOI=10.1016/S0140-6736(02)08713-5;
RA Baba T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Oguchi A.,
RA Nagai Y., Iwama N., Asano K., Naimi T., Kuroda H., Cui L.,
RA Yamamoto K., Hiramatsu K.;
RT "Genome and virulence determinants of high virulence community-
  acquired MRSA."
RT Lancet 359;1819-1827(2002).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
  an amide bond (By similarity).
DR EMBL; AP004830; BAB96285.1; -.
DR HSP; OS3653; IN67.
DR GO; GO:0009986; C:cell surface; IEA.
DR GO; GO:0005618; C:cell wall; IEA.
DR GO; GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0007155; P:cell adhesion; IEA.
DR InterPro; IPR008966; Adhes_bact.
DR InterPro; IPR004237; Fn_bind.
DR InterPro; IPR005877; Gpos_YsIRK.
DR InterPro; IPR001899; Gram_pos_anchor.
DR Pfam; PF02986; Fn_bind_1.
DR Pfam; PF00746; Gram_pos_anchor_1.
DR Pfam; PF04650; YsIRK_signal_1.
DR TIGRFAMs; TIGR01167; LpXTG_anchor_1.
DR TIGRFAMs; TIGR01168; YsIRK_signal_1.
DR PROSITE; PS50847; GRAM_POS_ANCHORING; 1.
KW Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ SEQUENCE 943 AA; 104537 MW; DA8A5F31947E1B8A CRC64;

Query Match 91.1%; Score 51; DB 2; Length 943;
Best Local Similarity 90.0%; Pred. No. 0.42;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QIHGONKGNQ 10
Db 723 QIHGONKGNQ 732

RESULT 4
OS6G6H4 PRELIMINARY; PRT; 957 AA.
ID Q6G6H4
AC Q6G6H4;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Fibronectin-binding protein.
GN Name=fnbB; OrderedLocustNames=SAS2387;
OS Staphylococcus aureus (strain MSSA476).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxId=282459;
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[1]
RN SEQUENCE FROM N.A.
RP PubMed=15213324; DOI=10.1073/pnas.0402521101;
RX Holden M.T.G., Fell E.J., Lindsey J.A., Peacock S.J., Day N.P.J.,
RA Enright M.C., Foster T.J., Moore C.E., Hurst L., Alkin R., Barton A.,
RA Baeson N., Bentley S.D., Chillingworth C., Chillingworth T.,
RA Churcher C., Clark L., Cotton C., Cronin A., Doggett J., Dowd L.,
RA Feltwell T., Hance Z., Harris B., Hauser H., Holtroyd S., Jagels K.,
RA James K.D., Lennard N., Line A., Mayes R., Moule S., Mungall K.,
RA Ormond D., Quail M.A., Rabinowitch E., Rutherford K.M., Sanders M.,
RA Sharp S., Simmonds M., Stevens K., Whitehead S., Barrell B.G.,
RA Spratt B.G., Parkhill J.,
RT "Complete genomes of two clinical Staphylococcus aureus strains:
RT evidence for the rapid evolution of virulence and drug resistance.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:9786-9791(2004).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC an amide bond (By similarity).
CC EMBL, BK571857; CNG44201.1; -.
DR GO; GO:0009986; C:cell surface; IEA.
DR GO; GO:0005618; C:cell wall; IEA.
DR GO; GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0007155; P:cell adhesion; IEA.
DR InterPro; IPR008966; Adhes_bact.
DR InterPro; IPR004237; Fn_bind.
DR InterPro; IPR005877; Gpos_YsIRK.
DR Pfam; PF02986; Fn_bind; 1.
DR Pfam; PF00746; Gram_pos_anchor; 1.
DR TIGRFAMs; TIGR01167; LpXTG_anchor; 1.
DR TIGRFAMs; TIGR01168; YsIRK_signal; 1.
DR PROSITE; PS50847; GRAM_POS_ANCHORING; 1.
KW Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ SEQUENCE 957 AA; 105980 MW; 28F8BA7FDFD3EAF CRC64;

Query Match 91.1%; Score 51; DB 2; Length 957;
Best Local Similarity 90.0%; Pred. No. 0.43;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 QIHGONKGNQ 10
DB 723 QIHGONKGNQ 732

RESULT 5
Q99RD3 PRELIMINARY; PRT; 961 AA.
AC Q99RD3;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Ribonectin-binding protein homolog.
GN Name=fnbB; Ordered locus names=SAV2502;
OS Staphylococcus aureus (strain Mu50 / ATCC 700699).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_Taxid=158878;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=Mu50 / ATCC 700699;
RX MEDLINE=21311952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2;
RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Lian J.-Q., Ito T.,
RA Kanamori M., Matsunaru H., Maruyama A., Murakami H., Hoshoyama A.,
RA Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
RA Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
RA Kanehisa M., Yamashita A., Ohshima K., Furuya K., Yoshino C., Shiba T.,
RA Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
RT "Whole genome sequencing of methicillin-resistant Staphylococcus
RT aureus".
RL Lancet 357:1225-1240(2001).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC an amide bond (By similarity).

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DR EMBL, AP003365; BAB58664.1; -.
DR PIR, G90053; G90053.
DR HSRP, Q53653; 1n67.
DR GO; GO:0009986; C:cell surface; IEA.
DR GO; GO:0005618; C:cell wall; IEA.
DR GO; GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0007155; P:cell adhesion; IEA.
DR InterPro; IPR008966; Adhes_bact.
DR InterPro; IPR004237; Fn_bind.
DR InterPro; IPR005877; Gpos_YsIRK.
DR InterPro; IPR001899; Gram_pos_anchor.
DR Pfam; PF02986; Fn_bind; 1.
DR Pfam; PF00746; Gram_pos_anchor; 1.
DR TIGRFAMs; TIGR01167; LpXTG_anchor; 1.
DR TIGRFAMs; TIGR01168; YsIRK_signal; 1.
DR PROSITE; PS50847; GRAM_POS_ANCHORING; 1.
KW Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ SEQUENCE 961 AA; 106010 MW; 364940F884EA4101 CRC64;

Query Match 91.1%; Score 51; DB 2; Length 961;
Best Local Similarity 90.0%; Pred. No. 0.43;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QIHGONKGNQ 10
DB 727 QIHGONKGNQ 736

RESULT 6
Q7A3J8 PRELIMINARY; PRT; 961 AA.
AC Q7A3J8;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE fnbB protein.
GN Name=fnbB; Ordered locus names=SA2290;
OS Staphylococcus aureus (strain N315).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_Taxid=158879;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21311952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2;
RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Lian J.-Q., Ito T.,
RA Kanamori M., Matsunaru H., Maruyama A., Murakami H., Hoshoyama A.,
RA Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
RA Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
RA Kanehisa M., Yamashita A., Ohshima K., Furuya K., Yoshino C., Shiba T.,
RA Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
RT "Whole genome sequencing of methicillin-resistant Staphylococcus
RT aureus".
RL Lancet 357:1225-1240(2001).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC an amide bond (By similarity).
CC EMBL, AP003137; BAB43593.1; -.
DR GO; GO:0009986; C:cell surface; IEA.
DR GO; GO:0005618; C:cell wall; IEA.
DR GO; GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0007155; P:cell adhesion; IEA.
DR InterPro; IPR008966; Adhes_bact.
DR InterPro; IPR004237; Fn_bind.
DR InterPro; IPR005877; Gpos_YsIRK.
DR InterPro; IPR001899; Gram_pos_anchor.
DR Pfam; PF02986; Fn_bind; 1.
DR Pfam; PF00746; Gram_pos_anchor; 1.
DR TIGRFAMs; TIGR01167; LpXTG_anchor; 1.
DR TIGRFAMs; TIGR01168; YsIRK_signal; 1.
DR PROSITE; PS50847; GRAM_POS_ANCHORING; 1.

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KW Cell wall; Complete proteome: Peptidoglycan-anchor.
SQ SEQUENCE 961 AA; 106010 MW; 364940F884EA4101 CRC64;

Query Match
Best Local Similarity 91.1%; Score 51; DB 2; Length 961;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QIHGONKGNQ 10
DB 727 QIHGONKGNQ 736

RESULT 7
Q99RD2 PRELIMINARY; PRT; 1038 AA.
ID Q99RD2;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Fibronectin-binding protein homolog.
GN Name=fnb; OrderedLocustNames=SAV2503;
OS Staphylococcus aureus (strain Mu50 / ATCC 700699).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxId=158878;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=Mu50 / ATCC 700699;
RX MEDLINE=21111952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2;
RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Iian J.-Q., Ito T.,
RA Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,
RA Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
RA Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
RA Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
RT "Whole genome sequencing of methicillin-resistant Staphylococcus
aureus.";
RL Lancet 357:1225-1240(2001).
CC -!- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
an amide bond (By similarity).
EMBL: AP003365; BAB5865.1; -.
DR GO: GO:0009986; C:cell surface; IEA.
DR GO: GO:0005618; C:cell wall; IEA.
DR GO: GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO: GO:0016020; C:membrane; IEA.
DR GO: GO:007155; P:cell adhesion; IEA.
DR InterPro: IPR008966; Adhes_bact.
DR InterPro: IPR004237; Fn_bind.
DR InterPro: IPR005877; Gpos_YsIRK.
DR InterPro: IPR001899; Gram_pos_anchor.
DR Pfam: PF02986; Fn_bind. 1.
DR Pfam: PF00746; Gram_pos_anchor. 1.
DR Pfam: PF04650; YsIRK_signal. 1.
DR TIGRFAMs: TIGR01167; LpxTG_anchor. 1.
DR TIGRFAMs: TIGR01168; YsIRK_signal. 1.
DR PROSITE: PS50847; GRAM_POS_ANCHORING. 1.
KW Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ SEQUENCE 1038 AA; 113618 MW; 666BF6BF2BFBEB12 CRC64;

Query Match
Best Local Similarity 91.1%; Score 51; DB 2; Length 1038;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 QIHGONKGNQ 10
DB 776 QIHGONKGNQ 785

RESULT 8
Q7A3J7 PRELIMINARY; PRT; 1038 AA.
AC Q7A3J7;

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DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Fnb protein.
GN Name=fnb; OrderedLocustNames=SA2291;
OS Staphylococcus aureus (strain N315).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxId=158879;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=21111952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2;
RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Iian J.-Q., Ito T.,
RA Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,
RA Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
RA Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
RA Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
RA Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
RT "Whole genome sequencing of methicillin-resistant Staphylococcus
aureus.";
RL Lancet 357:1225-1240(2001).
CC -!- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
an amide bond (By similarity).
EMBL: AP003137; BAB43594.1; -.
DR GO: GO:0009986; C:cell surface; IEA.
DR GO: GO:0005618; C:cell wall; IEA.
DR GO: GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO: GO:0016020; C:membrane; IEA.
DR GO: GO:007155; P:cell adhesion; IEA.
DR InterPro: IPR008966; Adhes_bact.
DR InterPro: IPR004237; Fn_bind.
DR InterPro: IPR005877; Gpos_YsIRK.
DR InterPro: IPR001899; Gram_pos_anchor.
DR Pfam: PF02986; Fn_bind. 1.
DR Pfam: PF00746; Gram_pos_anchor. 1.
DR Pfam: PF04650; YsIRK_signal. 1.
DR TIGRFAMs: TIGR01167; LpxTG_anchor. 1.
DR TIGRFAMs: TIGR01168; YsIRK_signal. 1.
DR PROSITE: PS50847; GRAM_POS_ANCHORING. 1.
KW Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ SEQUENCE 1038 AA; 113618 MW; 666BF6BF2BFBEB12 CRC64;

Query Match
Best Local Similarity 91.1%; Score 51; DB 2; Length 1038;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 QIHGONKGNQ 10
DB 776 QIHGONKGNQ 785

RESULT 9
Q9AEP9 PRELIMINARY; PRT; 152 AA.
ID Q9AEP9;
AC Q9AEP9;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Fibronectin-binding protein (Fragment).
GN Name=fnb;
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxId=1280;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=CMRSA-1;
RX MEDLINE=21246681; PubMed=11349044;
RX DOI=10.1128/IAI.59.6.3791-3799.2001;
RA Rice K., Huesca M., Vaz D., McGavin M.J.;
RT "Variance in fibronectin binding and fnb locus polymorphisms in
Staphylococcus aureus: identification of antigenic variation in a
fibronectin binding protein adhesin of the epidemic CMRSA-1 strain of
methicillin-resistant S. aureus.";

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RL Infect Immun. 69:3791-3799(2001).
DR EMBL: AY029184; AAK31588.1; -.
FT NON TER 1
FT 152 152
SQ SEQUENCE 152 AA; 17193 MW; CFA3913C2B11C025 CRC64;

Query Match 76.8%; Score 43; DB 2; Length 152;
Best Local Similarity 80.0%; Pred. No. 2.2;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 QIHGONKGNQ 10
DB 35 QIOGONKGDQ 44

RESULT 10
08NUU7 PRELIMINARY; PRT; 1015 AA.
AC 08NUU7;
DT 01-OCT-2002 (TREMBlrel. 22, Created)
DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Pnb protein.
GN Name=fnb; OrderedlocusNames=MM2421;
OS Staphylococcus aureus (Strain MM2).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxId=196620;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MM2;
RX MEDLINE=22040717; PubMed=12044378; DOI=10.1016/S0140-6736(02)08713-5;
RA Baba T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Oguchi A.,
RA Nagai Y., Iwama N., Asano K., Naimi T., Kuroda H., Cui L.,
RA Yamamoto K., Hiramatsu K.;
RT "Genome and virulence determinants of high virulence community-
RT acquired MRSA.";
RL Lancet 359:1819-1827(2002).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
an amide bond (By similarity).
EMBL: AP004830; BAB96286.1; -.
DR GO: GO:0009986; C:cell surface; IEA.
DR GO: GO:0005618; C:cell wall; IEA.
DR GO: GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO: GO:0016020; C:membrane; IEA.
DR GO: GO:0007155; P:cell adhesion; IEA.
DR InterPro: IPR008966; Adhes_bact.
DR InterPro: IPR004237; Fn_bind.
DR InterPro: IPR005877; Gpos_YsIRK.
DR InterPro: IPR001899; Gram_pos_anchor.
DR Pfam: PF02986; Fn_bind.1.
DR Pfam: PF00746; Gram_pos_anchor.1.
DR Pfam: PF04650; YsIRK_signal.1.
DR TIGRfams: TIGR01167; LPXTG_anchor.1.
DR TIGRfams: TIGR01168; YsIRK_signal.1.
DR PROSITE: PS50847; GRAM_POS_ANCHORING.1.
KW Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ SEQUENCE 1015 AA; 11145 MW; D0F9281BB64D4D2 CRC64;

Query Match 76.8%; Score 43; DB 2; Length 1015;
Best Local Similarity 80.0%; Pred. No. 17;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 QIHGONKGNQ 10
DB 781 QIOGONKGNQ 790

RESULT 11
06G6H3 PRELIMINARY; PRT; 1015 AA.
AC 06G6H3;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
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DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE Fibronectin-binding protein.
GN OrderedlocusNames=SA52398;
OS Staphylococcus aureus (Strain MSSA476).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxId=282459;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=15233324; DOI=10.1073/pnas.0402521101;
RA Holden M.T.G., Fell E.U., Lindsay J.A., Peacock S.J., Day N.P.J.,
RA Holten M.C., Foster T.J., Moore C.E., Horst L., Atkin R., Barron A.,
RA Bason N., Bentley S.D., Chillingworth C., Chillingworth T.,
RA Churcher C., Clark L., Cotton C., Cronin A., Doggett J., Dowd L.,
RA Felwell T., Hance Z., Harris B., Hauser H., Holroyd S., Jagsels K.,
RA James K.D., Lennard N., Line A., Mayes R., Moule S., Mungall K.,
RA Ormond D., Quail M.A., Rabinovitch E., Rutherford K.M., Sanders M.,
RA Sharp S., Simmonds M., Stevens K., Whitehead S., Barrett B.G.,
RA Spratt B.G., Parkhill J.;
RT "Complete genomes of two clinical Staphylococcus aureus strains:
RT evidence for the rapid evolution of virulence and drug resistance.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:9786-9791(2004).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
an amide bond (By similarity).
EMBL: BX571857; CAG44202.1; -.
DR GO: GO:0009986; C:cell surface; IEA.
DR GO: GO:0005618; C:cell wall; IEA.
DR GO: GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO: GO:0016020; C:membrane; IEA.
DR GO: GO:0007155; P:cell adhesion; IEA.
DR InterPro: IPR008966; Adhes_bact.
DR InterPro: IPR005877; Gpos_YsIRK.
DR InterPro: IPR001899; Gram_pos_anchor.
DR Pfam: PF02986; Fn_bind.1.
DR Pfam: PF00746; Gram_pos_anchor.1.
DR Pfam: PF04650; YsIRK_signal.1.
DR TIGRfams: TIGR01167; LPXTG_anchor.1.
DR TIGRfams: TIGR01168; YsIRK_signal.1.
DR PROSITE: PS50847; GRAM_POS_ANCHORING.1.
KW Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ SEQUENCE 1015 AA; 11145 MW; D0F9281BB64D4D2 CRC64;

Query Match 76.8%; Score 43; DB 2; Length 1015;
Best Local Similarity 80.0%; Pred. No. 17;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 QIHGONKGNQ 10
DB 781 QIOGONKGNQ 790

RESULT 12
DEGP_BUCBP STANDARD; PRT; 465 AA.
AC 089AF5;
DT 05-JUL-2004 (Rel. 44, Created)
DT 05-JUL-2004 (Rel. 44, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Probable serine protease do-like precursor (EC 3.4.21.-).
GN Name=degp; Synonyms=htpA; OrderedlocusNames=bbp210;
OS Buchnera aphidicola (subsp. Baizongia pteractia);
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Buchnera.
OX NCBI_TaxId=135842;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=12522265; DOI=10.1073/pnas.0235981100;
RA van Ham R.C.H.J., Kamerbeek J., Palacios C., Rausell C., Abascal F.,
RA Bastolla U., Fernandez J.M., Jimenez R., Postigo M., Silva F.J.,
RA Tamames J., Viguera E., Latorre A., Valencia A., Moran F., Moya A.;
RT "Reductive genome evolution in Buchnera aphidicola.";
RL Proc. Natl. Acad. Sci. U.S.A. 100:581-586(2003).
CC -1- SIMILARITY: Belongs to the peptidase S1C family.
```

CC -!- SIMILARITY: Contains 2 PDZ/DHR domains.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation
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 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL: AE014016; AAO26942.1; -.
 CC
 CC DR HSSP; P09376; 1KY9.
 CC DR InterPro; IPR001478; PDZ.
 CC DR InterPro; IPR001254; Peptidase_S1.
 CC DR InterPro; IPR001940; Peptidase_S1C.
 CC DR Pfam; PF00595; PDZ; 2.
 CC DR Pfam; PF00089; Trypsin; 1.
 CC DR PRINTS; PR00834; PROTEASES2C.
 CC DR SMART; SM00228; PDZ; 2.
 CC DR PROSITE; PS50106; PDZ; 2.
 CC KW Complete proteome; Hydrolase; Repeat; Serine protease; Signal.
 CC FT SIGNAL 1 26 Potential.
 CC FT CHAIN 27 465 Probable serine protease do-like.
 CC FT DOMAIN 102 240 Catalytic.
 CC FT DOMAIN 268 359 PDZ 1.
 CC FT DOMAIN 365 457 PDZ 2.
 CC FT ACT_SITE 119 119 Charge relay system (potential).
 CC FT ACT_SITE 149 149 Charge relay system (potential).
 CC FT ACT_SITE 224 224 Charge relay system (potential).
 CC FT DISULFID 85 91 By similarity.
 CC SQ SEQUENCE 465 AA; 51085 MW; 5783677C05838E78 CRC64;
 CC
 CC Query Match 73.2%; Score 41; DB 1; Length 465;
 CC Best Local Similarity 87.5%; Pred. No. 19;
 CC Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 CC
 CC QY 1 QIHGQNGK 8
 CC Db 394 RIHGQNGK 401
 CC
 CC RESULT 13
 CC ID Q9BP41 PRELIMINARY; PRT; 1241 AA.
 CC AC Q9BP41;
 CC DT 01-JUN-2001 (TrEMBLrel. 17, Created)
 CC DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
 CC DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 CC DE RANBP21.
 CC GN Name=Ranbp21;
 CC OS Drosophila melanogaster (Fruit fly).
 CC OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 CC OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 CC OC Ephydroidea; Drosophilidae; Drosophila.
 CC OC NCBI_Taxid=7227;
 CC RN [1]
 CC RP SEQUENCE FROM N.A.
 CC RA MEDLINE=2213332; PubMed=12426392; DOI=10.1093/emboj/cdf613;
 CC RA Bohnsack M.T., Regener K., Schwappach B., Saffrich R., Paraskeva E.,
 CC RA Hartman E., Gorlich D.;
 CC RT "Exs exports eEF1A via tRNA from nuclei and synergizes with other
 CC RT transport pathways to confine translation to the cytoplasm.";
 CC RT EMBO J. 21:6205-6215(2002).
 CC RL [2]
 CC RP SEQUENCE FROM N.A.
 CC RA Goerlich D., Hartman E.;
 CC RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
 CC DR EMBL; AF222746; AAG53520.1; -.
 CC DR Inctact; Q9BP41; -.
 CC DR Flybase; Fgn0031051; Ranbp21.
 CC DR GO; GO:0005737; Cytoplasm; IEA.
 CC DR GO; GO:0005643; C:nuclear pore; IEA.

DR GO; GO:0005634; C:nucleus; IEA.
 DR GO; GO:0008565; F:protein transporter activity; IEA.
 DR GO; GO:0000059; P:protein-nucleus import, docking; IEA.
 DR InterPro; IPR00938; ARM.
 DR InterPro; IPR00194; Importinb_N.
 DR Pfam; PF03810; IBN_N; 1.
 DR SQ SEQUENCE 1241 AA; 139293 MW; 9BAF36ACF348502 CRC64;
 DR
 DR Query Match 71.4%; Score 40; DB 2; Length 1241;
 DR Best Local Similarity 60.0%; Pred. No. 85;
 DR Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
 DR
 DR QY 1 QIHGQNGK 10
 DR Db 1111 QVHGHEANQ 1120
 DR
 DR RESULT 14
 DR ID Q9VME7 PRELIMINARY; PRT; 1241 AA.
 DR AC Q9VME7;
 DR DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DR DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DR DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
 DR DE CG12234-PA (LD26789p).
 CC GN Name=Ranbp21; ORFNames=CG12234;
 CC OS Drosophila melanogaster (Fruit fly).
 CC OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 CC OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 CC OC Ephydroidea; Drosophilidae; Drosophila.
 CC OC NCBI_Taxid=7227;
 CC RN [1]
 CC RP SEQUENCE FROM N.A.
 CC RA MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;
 CC RA Adams M.D., Celinker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 CC RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,
 CC RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 CC RA Sutton R.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 CC RA Brandon R.C., Rogers Y.H., Blazey R.G., Champe M., Pfeiffer B.D.,
 CC RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Gabor G.L.,
 CC RA Abril J.F., Agbayani A., An H.J., Andrews-Pfannkoch C., Baldwin D.,
 CC RA Ballew R.M., Basu P.V., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 CC RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 CC RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Broctier P.,
 CC RA Burris K.C., Busan D.A., Butler H., Cadieu E., Center A., Chandra I.,
 CC RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 CC RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 CC RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 CC RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 CC RA Fostel C., Gabrieli A.E., Garg N.S., Gilbert W.M., Glasser K.,
 CC RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 CC RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
 CC RA Hostin D., Houston K.A., Howland T.J., Wei M.H., Ibegam C.,
 CC RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 CC RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 CC RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 CC RA Liu X., Martel B., McIntosh T.C., McLeod M.P., McPherson D.,
 CC RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 CC RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D., Nelson D.L.,
 CC RA Nelson D.R., Nelson K.A., Nixon K., Nuskern D.R., Pauleb J.M.,
 CC RA Palazzolo M., Peltcan G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 CC RA Reinert K., Remington K., Saunders R.D., Scheefel F., Shen H.,
 CC RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 CC RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 CC RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 CC RA Wang Z.Y., Wasserman D.A., Weinstein G.M., Weissbach J.,
 CC RA Williams S.M., Woodgerf, Worley K.C., Wu D., Yang S., Yao Q.A., Ye J.,
 CC RA Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 CC RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 CC RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 CC RT "The genome sequence of Drosophila melanogaster.";
 CC RL Science 287:2185-2195(2000).
 CC RN [2]

RP SEQUENCE FROM N.A.
 RX MEDLINE=22426065; PubMed=12537568;
 RA Celinker S.E., Wheeler D.A., Krommiller B., Carlson J.W., Halpern A.,
 RA Patel S., Adams M., Champagne M., Dugan S.P., Frise E., Hodgson A.,
 RA George R.A., Hoskins R.A., Lavery T., Muzny D.M., Nelson C.R.,
 RA Pacle J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,
 RA Svirskas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,
 RA Weinstein G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.,
 RT "Finishing a whole-genome shotgun: Release 3 of the Drosophila
 RT melanogaster euchromatic genome sequence."
 RT Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22426070; PubMed=12537573;
 RA Kaminker J.S., Bergman C.M., Krommiller B., Carlson J., Svirskas R.,
 RA Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,
 RA Ashburner M., Celinker S.E.;
 RT "The transposable elements of the Drosophila melanogaster euchromatin:
 RT a genome Biol. 3:RESEARCH0084-RESEARCH0084(2002).
 RN [4]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22426069; PubMed=12537572;
 RA Mista S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
 RA Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochownik S.B.,
 RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,
 RA Belencourt B.R., Celinker S.E., de Grey A.D., Drysdale R.A.,
 RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
 RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
 RA Lewis S.E.;
 RT "Annotation of the Drosophila melanogaster euchromatic genome: a
 RT systematic review."
 RT Genome Biol. 3:RESEARCH0083-RESEARCH0083(2002).
 RN [5]
 RP SEQUENCE FROM N.A.
 RX FlyBase;
 RT Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
 RN [6]
 RP SEQUENCE FROM N.A.
 RX FlyBase;
 RT Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
 RN [7]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Berkeley;
 RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
 RA Champagne M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E.,
 RA George R., Gonzalez M., Guatin H., Krommiller B., Li P., Liao G.,
 RA Miranda A., Mungall C.J., Nunoo J., Pacle J., Paragas V., Park S.,
 RA Patel S., Phouanavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
 RA Celinker S.;
 RT Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
 RN EMBL: AE003512; AAF48995.1; -;
 DR EMBL: AY118535; AAM49904.1; -;
 DR FlyBase; FBgn0031051; Rarbp21.
 DR GO; GO:0005737; C:cytoplasm; IEA.
 DR GO; GO:0005634; C:nuclear pore; IEA.
 DR GO; GO:0008565; P:protein-nucleus import; IEA.
 DR GO; GO:0000559; P:protein-nucleus import, docking; IEA.
 DR InterPro; IPR008938; ARM.
 DR InterPro; IPR001494; Importinb_N.
 DR Pfam; PF03810; IBN_N; 1.
 SQ SEQUENCE 1241 AA; 139188 MW; D665A929CB148500 CRC64;

Query Match 71.4%; Score 40; DB 2; Length 1241;
 Best Local Similarity 60.0%; Pred. No. 85;
 Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 1 QHGNKGNQ 10
 DB 1111 QHGNKGNQ 1120

RESULT 15
 ID Q7MKL1 PRELIMINARY; PRT; 285 AA.
 AC Q7MKL1;
 DT 01-MAR-2004 (TrEMBLrel. 26, Created)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Probable transmembrane protein.
 GN OrderedLocNames=VY1772;
 OS Vibrio vulnificus (strain YJ016).
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
 OC Vibrionaceae; Vibrio.
 OX NCBI_Taxid=196600;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX PubMed=14656965; DOI=10.1101/gr.1295503;
 RA Chen C.-Y., Wu K.-M., Chang Y.-C., Chang C.-H., Tsai H.-C.,
 RA Liao T.-L., Liu Y.-M., Chen H.-J., Shen A.B.-T., Li J.-C., Su T.-L.,
 RA Shao C.-P., Lee C.-T., Hor L.-I., Tsai S.-F.;
 RT "Comparative genome analysis of Vibrio vulnificus, a marine
 RT pathogen."
 RT Genome Res. 13:2577-2587(2003).
 RN EMBL: AP005337; BAC94536.1; -;
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0003677; F:DNA binding; IEA.
 DR GO; GO:0003917; F:DNA topoisomerase type I activity; IEA.
 DR GO; GO:0006265; P:DNA topological change; IEA.
 DR GO; GO:0006268; P:DNA unwinding; IEA.
 DR InterPro; IPR007380; DNA_topoisomerase.
 DR InterPro; IPR007560; Mtr_cat.
 DR Pfam; PF04471; Mtr_cat; 1.
 DR Pfam; PF01396; zf-C4_Topoisom; 1.
 KW Complete proteome; Transmembrane.
 SQ SEQUENCE 285 AA; 32103 MW; 051P9525370AC978 CRC64;

Query Match 69.6%; Score 39; DB 2; Length 285;
 Best Local Similarity 100.0%; Pred. No. 27;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 GGNKGNQ 10
 DB 260 GGNKGNQ 266

Search completed: October 22, 2005, 08:00:52
 Job time : 56.85 secs

The Bank (usps)

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 25, 2005, 20:21:18 ; Search time 63.2 Seconds
(without alignment)
61.196 Million cell updates/sec

Title: US-10-731-238-81

Perfect score: 57
Sequence: 1 HGONKGNQSF 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-Processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: A_Geneseq_16Dec04:*
2: geneseqp19808:*
3: geneseqp19908:*
4: geneseqp20008:*
5: geneseqp20028:*
6: geneseqp20038:*
7: geneseqp20038:*
8: geneseqp20048:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	57	100.0	10	2	AAW65737
2	57	100.0	134	2	AAW29087
3	57	100.0	139	2	AAW31556
4	57	100.0	1018	1	AAW82115
5	57	100.0	1018	4	AAU37245
6	57	100.0	1018	4	AAU37245
7	57	100.0	1018	6	AAU34301
8	57	100.0	1018	6	AAU34301
9	57	100.0	1027	6	AAW72537
10	57	100.0	1027	6	AAW72537
11	52	91.2	113	2	AAW90937
12	52	91.2	130	2	AAW88806
13	52	91.2	130	2	AAW88806
14	52	91.2	130	2	AAW88806
15	52	91.2	134	2	AAW91201
16	52	91.2	134	2	AAW91201
17	52	91.2	164	2	AAW90942
18	52	91.2	164	2	AAW90942
19	52	91.2	174	2	AAW90942
20	52	91.2	181	2	AAW90942
21	52	91.2	181	2	AAW90942
22	52	91.2	559	2	AAW90942
23	52	91.2	767	4	AAU34403
24	52	91.2	767	4	AAU34403
25	52	91.2	940	2	AAW07070

26	52	91.2	940	6	ABJ19111	Abj19111 Pathogen
27	52	91.2	948	6	ADA89470	Ada89470 Staphyloc
28	52	91.2	948	6	ABJ18923	Abj18923 Pathogen
29	52	91.2	948	6	ABW72536	Abw72536 Staphyloc
30	52	91.2	961	6	ABU15854	Abu15854 Protein e
31	52	91.2	1038	6	ABU15903	Abu15903 Protein e
32	49	86.0	38	1	AAW80661	AAW80661 Protein w
33	49	86.0	38	1	AAW82117	AAW82117 Protein w
34	47	82.5	10	2	AAW65736	AAW65736 Fibronect
35	47	82.5	134	2	AAW29089	AAW29089 Cloned fi
36	47	82.5	1098	4	AAW03347	AAW03347 Novel hum
37	44	77.2	30	4	AAW82164	AAW82164 Peptide f
38	44	77.2	30	7	ADC69221	ADC69221 Fibronect
39	44	77.2	31	7	ADC69222	ADC69222 Fibronect
40	44	77.2	38	1	AAW80660	AAW80660 Protein w
41	44	77.2	38	1	AAW82116	AAW82116 Fibronect
42	44	77.2	77	2	AAW88749	AAW88749 S. aureus
43	44	77.2	978	4	AAU33960	AAU33960 Staphyloc
44	44	77.2	1001	4	AAU37093	AAU37093 Staphyloc
45	43	75.4	10	2	AAW65738	AAW65738 Fibronect

ALIGNMENTS

RESULT 1
ID AAW65737 standard; peptide; 10 AA.
AC
XX
XX

AAW65737;

16-OCT-1998 (first entry)

Fibronectin binding protein-derived peptide #81.

microbial surface components recognising adhesive matrix molecule;

MSCRAMM; fibronectin; fibronectin-binding protein; antibody; epitope;

antibiotic; bacterial infection; antibiotic-resistant strain.

Synthetic.

Staphylococcus aureus.

MO981389-A2.

23-JUL-1998.

21-JAN-1998; 98WC-US001222.

21-JAN-1997; 97US-0036139P.

(TEXA) UNIV TEXAS A & M SYSTEM.

Hoeek M, Patti JM, House-Pompeo KL, Speziale P, Joh D;

Megavin MJ;

WPI, 1998-413816/35.

Antibody that binds to fibronectin-binding protein, preventing its

binding to fibronectin - used to treat or prevent bacterial infection,

especially by Staphylococci and Streptococci.

Example 9; Page 110; 201pp; English.

The invention relates to antibodies that bind to a fibronectin-binding domain of a fibronectin-binding protein, and inhibit binding of the protein to a fibronectin. Also claimed are: (1) isolated peptides of a fibronectin-binding protein that do not bind to fibronectin; (2) fusion protein containing at least one peptide of a fibronectin-binding protein linked to a second amino acid sequence; (3) nucleic acid encoding the isolated peptide of (1). Antibodies, the isolated peptides of (1) and the nucleic acids are all useful for immunisation (active or passive) and (by inhibiting binding of bacteria to fibronectin) for preventing or treating infection in humans or other animals, particularly by staphylococci or

SQ	Sequence	134 AA;
	Query Match	100.0%; Score 57; DB 2; Length 134;
	Best Local Similarity	100.0%; Pred. No. 0.0071;
	Matches	10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY	1 HGONKGNOSF	10
Db	38 HGONKGNOSF	47

RESULT 3	
AAW31556	
ID	AAW31556 standard; protein; 139 AA

AC	AAW31556;
XX	
DT	27-AUG-2003 (revised)

XX	Fibronectin-binding MSCRAM derivative pDB
DE	
XX	

KW microbial surface component recognising adhesive matrix molecule; MSCRAMM
KW adhesin; vaccine; immunisation; diagnosis; therapy; mastitis.
XX

XX

FT	Peptide	1.12	"vector pQE30-derived peptide"
FT			
XX			
XX			
PN	W09743314-A2.		
XX			

XX 5
4
3
2
1

XX :

XX

PA (UABR-) UAB RES FOUND.

PI Hoeek M, Patti JM, House-Pompeo K, Sthanam N, Symersky J;

WPI; 1998-008801/01.

PT Antibody that interacts with collagen binding domain of Staphylococcal

PT with *Staphylococcus aureus*.

PS Disclosure; Page 91; 143pp; English.

CC This protein comprises Staphylococcus aureus fibronectin-binding
CC microbial surface component registering adhesive matrix molecule (MSCRAMM)

CC relates to claimed nucleic acid sequences (see AWP3456-38) encoding *S.*
CC aureus collagen binding protein (CBP) epitopes M17, M31 and M55 (see
CC AWP3152-54) that confer protection against *S. aureus* infection. CBP
CC protein and antigenic epitopes are contemplated for use in the treatment
CC of pathological infections, especially to prevent bacterial adhesion to
CC collagen. The epitopes are also contemplated for use in the preparation
CC of vaccines and as carrier proteins in vaccine formulations, as well as
CC in the formulation of compositions for the prevention of *S. aureus*
CC infection. pCBF3 and pOD (see AWP3155) were used to raise anti-M5CGRAM
CC polyclonal antibodies used in passive immunisation against bovine
CC mastitis. (Updated on 25-MAR-2003 to correct PI field.) (Updated on 27-
CC AUG-2003 to correct OS field.)

Best Local Similarity 100.0%; Pred. No. 0.0074;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HGONKGNQSF 10
|||
Db 52 HGONKGNQSF 61

RESULT 4

AAPE2115
ID AAP82115 standard; protein; 1018 AA.

AC AAP82115;

DT 25-MAR-2003 (revised)
DT 05-JAN-1990 (first entry)

XX Fibronectin binding protein.

XX Fibronectin binding protein; S. aureus; immunisation; mastitis; ruminants;
XX wound infection; diagnosis.

XX Staphylococcus aureus.

XX EP294349-A.

XX 07-DEC-1988.

PF 30-MAY-1988; 88EP-00850188.

XX 01-JUN-1987; 87SE-00002272.

XX (ALFA) ALFA LAVAL AGRIC INT AB.

XX Lindberg MK, Sigmas LC, Madstrom TM, Froman G;

XX WPI; 1988-347978/49.

XX P-PSDB; AAP82115.

PT Hybrid DNA encoding Staphylococcus aureus fibronectin binding protein -
PT useful for immunisation and topical application to prevent staphylococcal
PT infections.

XX Disclosure; Fig. 8A:1-8A:2; 23pp; English.

XX The S. aureus fibronectin binding protein may be included in a hybrid

XX protein. The protein may be used to immunise ruminants against

XX staphylococcal mastitis, pref. when given at 0.5-5 microg/kg, using 3

XX doses at 1-3 week intervals; and for topical applicn. to prevent wound

XX infection, pref. using isotonic saline soln. of concn. 25-250 microg/mg.

XX The DNA encoding the binding protein and the hybrid protein may be

XX immobilised on a carrier and used to diagnose staphylococcal infections.

XX (Updated on 25-MAR-2003 to correct PA field.)

XX SQ Sequence 1018 AA;

QY 1 HGONKGNQSF 10
|||
Db 782 HGONKGNQSF 791

RESULT 5
ID AAU37245 standard; protein; 1018 AA.

XX AAU37245;

XX 14-FEB-2002 (first entry)

XX

DE Staphylococcus aureus cellular proliferation protein #1415.

XX Antisense; prokaryotic cellular proliferation protein; antibiotic;
XX antibacterial; drug design.

XX Staphylococcus aureus.

XX WO200170955-A2.

XX 27-SEP-2001.

XX 21-MAR-2001; 2001WO-US009180.

XX 21-MAR-2000; 2000US-0191078P.

XX 23-MAY-2000; 2000US-0206848P.

XX 26-MAY-2000; 2000US-0207727P.

XX 23-OCT-2000; 2000US-024578P.

XX 27-NOV-2000; 2000US-0253625P.

XX 22-DEC-2000; 2000US-0257931P.

XX 16-FEB-2001; 2001US-0269308P.

XX (ELIT-) ELITRA PHARM INC.

XX Haselbeck R, Ohlsen KL, Zyskind JW, Wall D, Trawick JD, Carr GJ;

XX Yamamoto RT, Xu HH;

XX WPI; 2001-611495/70.

XX N-PSDB; AAS55104.

XX New polynucleotides for the identification and development of
XX antibiotics, comprise sequences of antisense nucleic acids.

XX Example 3; SEQ ID NO 12838; 51pp; English.

XX The invention relates to antisense inhibitors of genes essential to

XX prokaryotic cellular proliferation, their use in identifying the genes,

XX their use in the discovery of novel antibiotics, the essential genes

XX themselves and the encoded proteins. The prokaryotes used are Escherichia

XX coli, Staphylococcus aureus, Salmonella typhi, Klebsiella pneumoniae,

XX Pseudomonas aeruginosa and Enterococcus faecalis. The invention is also

XX useful for the identification of potential new targets for antibiotic

XX development. The antisense nucleic acids can also be used to identify

XX proteins used in proliferation, to express these proteins, and to obtain

XX antibodies capable of binding to the expressed proteins. The proteins can

XX be used to screen compounds in rational drug discovery programmes. The

XX antisense nucleic acid sequence is also useful to screen for homologous

XX CC nucleic acids which are required for cell proliferation in a wide variety

XX of organisms. The present sequence represents an essential prokaryotic

XX cellular proliferation protein. Note: The sequence data for this patent

XX did not form part of the printed specification, but was obtained in

XX electronic format directly from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 1018 AA;

QY 1 HGONKGNQSF 10
|||
Db 782 HGONKGNQSF 791

Query Match 100.0%; Score 57; DB 4; Length 1018;
Best Local Similarity 100.0%; Pred. No. 0.063; Mismatches 0; Indels 0; Gaps 0;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HGONKGNQSF 10
|||
Db 782 HGONKGNQSF 791

RESULT 6

AAU34301
ID AAU34301 standard; protein; 1018 AA.

XX AAU34301;

XX 14-FEB-2002 (first entry)

XX Staphylococcus aureus cellular proliferation protein #577.

XX Antisense; prokaryotic cellular proliferation protein; antibiotic;
KM antibacterial; drug design.
XX
XX Staphylococcus aureus.
XX
XX WO200170955-A2.
XX
XX 27-SEP-2001.
XX
XX 21-MAR-2001; 2001WO-US009180.
XX
XX 21-MAR-2000; 2000US-0191078P.
XX PR 23-MAY-2000; 2000US-0206848P.
XX PR 26-MAY-2000; 2000US-0207727P.
XX PR 23-OCT-2000; 2000US-0242578P.
XX PR 27-NOV-2000; 2000US-0253625P.
XX PR 22-DEC-2000; 2000US-0257931P.
XX PR 16-FEB-2001; 2001US-0269308P.
XX
XX (ELITR-) ELITRA PHARM INC.
XX
XX Haselebeck R, Ohlsen KL, Zyskind JW, Wall D, Trawick JD, Carr GU;
PI Yamamoto RT, Xu HH;
XX
XX WPI: 2001-611495/70.
XX
XX N-PSDB; AMS52160.
XX
XX New polynucleotides for the identification and development of
PT antibiotics, comprise sequences of antisense nucleic acids.
XX
XX Example 3; SEQ ID NO 5797; 511pp; English.
XX
XX The invention relates to antisense inhibitors of genes essential to
CC prokaryotic cellular proliferation, their use in identifying the genes,
CC their use in the discovery of novel antibiotics, the essential genes
CC themselves and the encoded proteins. The prokaryotes used are Escherichia
CC coli, Staphylococcus aureus, Salmonella typhi, Klebsiella pneumoniae,
CC Pseudomonas aeruginosa and Enterococcus faecalis. The invention is also
CC useful for the identification of potential new targets for antibiotic
CC development. The antisense nucleic acids can also be used to identify
CC proteins used in proliferation, to express these proteins, and to obtain
CC antibodies capable of binding to the expressed proteins. The proteins can
CC be used to screen compounds in rational drug discovery programmes. The
CC antisense nucleic acid sequence is also useful to screen for homologous
CC nucleic acids which are required for cell proliferation in a wide variety
CC of organisms. The present sequence represents an essential prokaryotic
CC cellular proliferation protein. Note: The sequence data for this patent
CC did not form part of the printed specification, but was obtained in
CC electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX SQ Sequence 1018 AA;
XX
XX Query Match 100.0%; Score 57; DB 4; Length 1018;
XX Best Local Similarity 100.0%; Pred. No. 0.063;
XX Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HGQNKGNQSF 10
DB 782 HGQNKGNQSF 791

RESULT 7
ID ABJ18922 standard; protein; 1018 AA.
XX
XX ABJ18922;
XX
XX 06-MAR-2003 (first entry)
XX
XX Pathogen specific antigen related staphylococcal protein SEQ ID No 68.
DE
XX

KM Antibacterial; virucide; fungicide; protozoacide; cytostatic; anti-HIV;
KM hyperimmune; serum-reactive; antigen; pathogen; tumour; allergen;
KM auto-immunity; vaccine; staphylococcal infection; antibody; cancer;
KM autoimmune disease; HIV; hepatitis.
XX
XX Staphylococcus sp.
XX
XX WO200259148-A2.
XX
XX 01-AUG-2002.
XX
XX 21-JAN-2002; 2002WO-EP000546.
XX
XX 26-JAN-2001; 2001AT-0000130.
XX
XX (CIST-) CISTEM BIOTECHNOLOGIES GMBH.
XX
XX Meinke A, Nagy B, Von Ahnen U, Klade C, Henics T, Zauner W;
PI Minh DB, Vytvyetka O, Etz H, Dryla A, Weichart T, Hafner M;
PI Tempelmaier B;
XX
XX WPI: 2003-075410/07.
XX
XX Identifying, isolating and producing hyperimmune serum-reactive antigens
PT from a pathogen, for preparing vaccine or medicament for treating or
PT preventing e.g. staphylococcal infections, comprises providing antibody
PT preparation.
XX
XX Example 7; Page 157; 252pp; English.
XX
XX The invention relates to a novel method for identifying, isolating and
CC producing hyperimmune serum-reactive antigens from a pathogen, tumour,
CC allergen, a tissue or host prone to auto-immunity, where the antigens are
CC used in a vaccine, comprises providing antibody preparation from a plasma
CC pool of a type of animal, or individual sera with antibodies against the
CC specific pathogen, tumour, allergen, tissue or host prone to auto-
CC immunity. The hyperimmune serum-reactive antigens comprising any of the
CC 62 sequences of 53-2261 amino acids fully defined in the specification,
CC or their hyperimmune fragments are useful for the manufacture of a
CC pharmaceutical preparation, particularly a vaccine against staphylococcal
CC infections or colonisation against S. aureus or S. epidermidis. The
CC preparation of antibodies is useful for the manufacture of a medicament
CC for treating or preventing staphylococcal infections or colonisation
CC against S. aureus or S. epidermidis. The antibody preparations may also
CC be used for diagnostic and imaging purposes. Other conditions that can be
CC treated include cancer, autoimmune diseases or infections caused by viral
CC (e.g. HIV, hepatitis A, B or C), fungal or protozoan pathogens. This
CC sequence represents a staphylococcal protein relating to the method for
CC identifying and producing pathogen specific antigens of the invention
XX
XX SQ Sequence 1018 AA;
XX
XX Query Match 100.0%; Score 57; DB 6; Length 1018;
XX Best Local Similarity 100.0%; Pred. No. 0.063;
XX Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HGQNKGNQSF 10
DB 782 HGQNKGNQSF 791

RESULT 8
ID ABM72537 standard; protein; 1018 AA.
XX
XX ABM72537;
XX
XX 20-NOV-2003 (first entry)
XX
XX Staphylococcus aureus protein #1777.
XX
XX Antibacterial; vaccine; gene therapy; infection; sepsis; diagnosis;
KM enzymatic assay; antibiotic target.
KM

XX Staphylococcus aureus.
OS WO200294868-A2.
XX 28-NOV-2002.
XX 27-MAR-2002; 2002WO-IB002637.
XX 27-MAR-2001; 2001GB-00007661.
XX (CHIR-) CHIRON SPA.
XX Masignani V, Mora M, Scarselli M;
XX MPI; 2003-120786/11.
XX N-PSDB; ACF74097.
XX New Staphylococcus aureus protein, useful as a vaccine for treating or
PT preventing Staphylococcal infection, specifically an infection caused by
PT S. aureus, e.g. sepsis.
XX
XX Claim 1; SEQ ID NO 3554; 49pp; English.
XX
XX The invention relates to novel genes and encoded proteins from
XX Staphylococcus aureus. A composition comprising the S. aureus protein, a
XX nucleic acid encoding the protein, or an antibody to the protein, is
XX useful as a pharmaceutical, particularly as a vaccine for treating or
XX preventing infection due to Staphylococcus bacteria, specifically an
XX infection caused by S. aureus. The composition is particularly useful for
XX treating or preventing sepsis in a patient. The composition can also be
XX used for diagnostics. The protein is also used in an assay for enzymatic
XX studies and as a target for antibiotics. This sequence represents one of
XX the novel S. aureus proteins of the invention
SQ
Sequence 1018 AA;
Query Match 100.0%; Score 57; DB 6; Length 1018;
Best Local Similarity 100.0%; Pred. No. 0.063;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 HGONKGNOSF 10
DB 782 HGONKGNOSF 791
RESULT 9
AAW89806
ID AAW89806 standard; protein; 1027 AA.
XX
XX AAW89806;
AC
XX
XX 16-MAR-1999 (first entry)
DT
XX
XX Staphylococcus aureus protein SEQ ID #5254.
DE
XX
XX Computer readable medium; vaccine; S. aureus infection; immunodetection;
KW cellulitis; eyelid infection; food poisoning; osteomyelitis; therapy;
KW skin infection; surgical wound infection; scalded skin syndrome;
KW toxic shock syndrome.
XX
XX Staphylococcus aureus.
OS
XX
XX EP786519-A2.
PN
XX
XX 30-JUL-1997.
PD
XX
XX 07-JAN-1997; 97BP-00100117.
PF
XX
XX 05-JAN-1996; 96US-0009861P.
PR
XX
XX (HUMA-) HUMAN GENOME SCI INC.
PA
XX

PI Kunsch CA, Choi GH, Barash SC, Dillon PJ, Fannon MR, Rosen CA;
XX
XX MPI; 1997-374922/35.
XX
XX Polynucleotide(s) and proteins derived from Staphylococcus aureus -
PT stored on computer readable medium and used in the production of anti-
PT S. aureus vaccines.
XX
XX
XX Claim 23; Page 3263-3267; 3271pp; English.
XX
XX This sequence represents a Staphylococcus aureus protein sequence of the
CC invention. The DNA sequences encoding the S. aureus proteins are recorded
CC on a computer readable medium, preferably selected from a floppy or hard
CC disk, random access memory (RAM), read-only memory (ROM) or CD-ROM.
CC Homology searches using the S. aureus DNA sequences allows putative
CC functions to be assigned so that protein-encoding or regulatory regions
CC of commercial, therapeutic or industrial importance can be obtained.
CC Specifically, sequences which are likely to encode antigens have been
CC identified and these polypeptides can be used in a vaccine composition
CC against S. aureus infection. The polypeptides can also be used in a kit
CC for the immunodetection of S. aureus in a sample. S. aureus is implicated
CC in numerous human diseases, including cellulitis, eyelid infections, food
CC poisoning, osteomyelitis, skin and surgical wound infections, scalded
CC skin syndrome, toxic shock syndrome, etc. Organisms transformed with the
CC DNA sequences can be used for recombinant production of the polypeptides.
CC The new DNA sequences (and their fragments) are useful as primers or
CC probes for isolating homologues of any of the 5191 S. aureus DNA sequences
XX contained on the computer readable medium
SQ
Sequence 1027 AA;
Query Match 100.0%; Score 57; DB 2; Length 1027;
Best Local Similarity 100.0%; Pred. No. 0.064;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 HGONKGNOSF 10
DB 791 HGONKGNOSF 800
RESULT 10
AAR90937
ID AAR90937 standard; peptide; 113 AA.
XX
XX AAR90937;
AC
XX
XX 23-SEP-1996 (first entry)
DT
XX
XX D3D4 polypeptide #1.
DE
XX
XX Fibronectin binding protein; Fbp; S. aureus J2385; monoclonal antibody;
KW infection; surgical implant; antiadherent agent; hygiene; adhesion;
KW extracellular matrix protein; oral pathogen; oral cavity.
XX
XX Staphylococcus aureus.
OS
XX
XX
FH Key Location/Qualifiers
FH Region 1..21
FT /note= "D1 region fragment"
FT Region 22..59
FT /note= "D2 region"
FT Region 60..98
FT /note= "D3 region"
FT Region 99..113
FT /note= "D4 region"
FT Misc-difference 113
FT /note= "P113T"
XX
XX
XX WO9604381-A1.
PN
XX
XX 15-FEB-1996.
PD
XX
XX 28-JUL-1995; 95WO-EP003040.
PF

```
XX 05-AUG-1994; 94GB-00015900.
PR
XX
XX (SMIK ) SMITHKLINE BEECHAM PLC.
XX Critchley IA, Dodd I, Barnett P, Mcbay DL;
XX WPI; 1996-129397/13.
XX
XX Polypeptide(s) derived from Staphylococcus aureus fibronectin binding
PT protein - inhibit binding of bacteria to extracellular matrix proteins,
PT for combating infection at the site of wounds and surgical implants, and
PT in oral hygiene.
XX Claim 6; Page 24; 35pp; English.
XX
XX AAR90937-R90942 represent D3D4 polypeptides. These sequences correspond
CC to fragments of the Staphylococcus aureus fibronectin binding protein
CC (Fbp). This sequence corresponds to residues 18-130 of S. aureus J2385
CC (Fbp), and also contains the D2 region, and a portion of the D1 region.
CC These sequences, and monoclonal antibodies against them can be used to
CC combat infection at the site of wounds, surgical implants and other in-
CC dwelling devices (such as catheters), and as antiadherent agents in oral
CC hygiene. They can also be used in the manufacture of a medicament for the
CC prevention of adhesion of bacteria to extracellular matrix proteins
CC present on in-dwelling devices or in wounds, or of oral pathogens to
CC similar proteins on surfaces in the oral cavity
XX
XX SQ Sequence 113 AA;
XX
XX Query Match 91.2%; Score 52; DB 2; Length 113;
XX Best Local Similarity 90.0%; Pred. No. 0.054;
XX Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 HGQNGKNGSF 10
XX |||||:|
XX Db 21 HGQNGKGDQSF 30
XX
XX RESULT 11
XX AAR58806
XX ID AAR58806 standard; protein; 130 AA.
XX
XX AAR58806;
XX
XX 25-MAR-2003 (revised)
XX 30-MAR-1995 (first entry)
XX
XX Fibronectin binding domain D1-D4(709-838(P838T)).
XX
XX Fibronectin binding protein; Fbp; fibronectin binding domain;
XX monoclonal antibody; Mab; adhesion; Gram-positive bacterium; bacteremia;
XX Escherichia coli.
XX
XX Staphylococcus aureus.
XX
XX WO9418327-A1.
XX
XX 18-AUG-1994.
XX
XX 04-FEB-1994; 94WO-GB000215.
XX
XX 05-FEB-1993; 93GB-00002289.
XX 20-OCT-1993; 93GB-00021592.
XX
XX (SMIK ) SMITHKLINE BEECHAM PLC.
XX
XX Burnham MKR, Chopra I, Critchley IA, Knowles DJC;
XX WPI; 1994-279748/34.
XX
XX Fibronectin binding protein and monoclonal antibodies specific for Fbp -
PT useful to prevent adherence of Gram-positive bacteria to indwelling
```

```
PT devices or wounds.
XX
XX PS Disclosure; Page 30; 40pp; English.
XX
XX Polypeptides corresponding to residues G709-T886 plus PPIVPT, G709-
CC P838(P838T) and G709-P838 (AAR58805-07, respectively) of S. aureus J2385
CC (NCIMB 40532) Fbp type A fibronectin binding domain D1-D4 region
CC (AAR58808) were expressed in E. coli BL21(DE4) and used to raise Mabs
XX specific for Fbp. (Updated on 25-MAR-2003 to correct PN field.)
XX
XX SQ Sequence 130 AA;
XX
XX Query Match 91.2%; Score 52; DB 2; Length 130;
XX Best Local Similarity 90.0%; Pred. No. 0.062;
XX Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 HGQNGKNGSF 10
XX |||||:|
XX Db 38 HGQNGKGDQSF 47
XX
XX RESULT 12
XX AAR58807
XX ID AAR58807 standard; protein; 130 AA.
XX
XX AAR58807;
XX
XX 25-MAR-2003 (revised)
XX 30-MAR-1995 (first entry)
XX
XX Fibronectin binding domain D1-D4(709-838).
XX
XX Fibronectin binding protein; Fbp; fibronectin binding domain;
XX monoclonal antibody; Mab; adhesion; Gram-positive bacterium; bacteremia;
XX Escherichia coli.
XX
XX Staphylococcus aureus.
XX
XX WO9418327-A1.
XX
XX 18-AUG-1994.
XX
XX 04-FEB-1994; 94WO-GB000215.
XX
XX 05-FEB-1993; 93GB-00002289.
XX 20-OCT-1993; 93GB-00021592.
XX
XX (SMIK ) SMITHKLINE BEECHAM PLC.
XX
XX Burnham MKR, Chopra I, Critchley IA, Knowles DJC;
XX WPI; 1994-279748/34.
XX
XX Fibronectin binding protein and monoclonal antibodies specific for Fbp -
PT useful to prevent adherence of Gram-positive bacteria to indwelling
PT devices or wounds.
XX
XX Disclosure; Page 30; 40pp; English.
XX
XX Polypeptides corresponding to residues G709-T886 plus PPIVPT, G709-
CC P838(P838T) and G709-P838 (AAR58805-07, respectively) of S. aureus J2385
CC (NCIMB 40532) Fbp type A fibronectin binding domain D1-D4 region
CC (AAR58808) were expressed in E. coli BL21(DE4) and used to raise Mabs
XX specific for Fbp. (Updated on 25-MAR-2003 to correct PN field.)
XX
XX SQ Sequence 130 AA;
XX
XX Query Match 91.2%; Score 52; DB 2; Length 130;
XX Best Local Similarity 90.0%; Pred. No. 0.062;
XX Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 HGQNGKNGSF 10
XX |||||:|
```

DB 38 HGONKGDQSF 47

RESULT 13
AAR91202
ID AAR91202 standard; peptide; 130 AA.

XX
XX AAR91202;
XX
XX
XX
XX 13-NOV-1996 (first entry)
XX
XX
XX D1-D4 fibronectin binding domains.
XX
XX Fibronectin; oral hygiene; gingivitis; gum disease; adhesion;
XX periodontitis; oral pathogens; caries; calculus; candidiasis; oral surgery;
XX tissue regeneration; irrigation; toothpaste; dentifrice; mouthwash;
XX lozenge.
XX
XX Staphylococcus aureus.
XX
XX WO9604003-A1.
XX
XX 15-FEB-1996.
XX
XX 18-JUL-1995; 95WO-EP002825.
XX
XX 05-AUG-1994; 94GB-00015902.
XX
XX (SMTK) SMITHKLINE BEECHAM PLC.
XX
XX Barnett P, Critchley IA, Dodd I;
XX
XX WPI; 1996-129122/13.
XX
XX Prevention of adherence of oral pathogens in the oral cavity, partic.
XX tooth surfaces - by application of a fibronectin binding protein or
XX polypeptide or a monoclonal antibody or fragment against it.
XX
XX Claim 5; Page 32; 41pp; English.

CC Adherence of oral pathogens, particularly to tooth surfaces, can be
CC prevented by application of a fibronectin binding protein or polypeptide.
CC The fibronectin binding protein or polypeptide is useful in the
CC manufacture of oral hygiene compositions, eg. toothpaste, liquid
CC dentifrice, mouthwash or lozenge. They are useful to prevent the plaque-
CC related development of carious lesions, gingivitis, calculus or
CC periodontal disease and to combat oral cavity infections, e.g.
CC candidiasis. They may also be useful in oral surgery e.g. in guided
CC tissue regeneration procedures to prevent subsequent bacterial infection,
CC and for irrigation of periodontal pockets. This sequence corresponds to
CC amino acids 709-838 of the D1-D4 fibronectin binding domain of
CC Staphylococcus aureus

XX
XX SQ Sequence 130 AA;

Query Match 91.2%; Score 52; DB 2; Length 130;
Best Local Similarity 90.0%; Pred. No. 0.062;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 HGONKGNQSF 10
DB 38 HGONKGDQSF 47

RESULT 14
AAR91201
ID AAR91201 standard; peptide; 130 AA.

XX
XX AAR91201;
XX
XX
XX
XX 13-NOV-1996 (first entry)
XX
XX
XX D1-D4 fibronectin binding domains.

XX
XX Fibronectin; oral hygiene; gingivitis; gum disease; adhesion;
XX periodontitis; oral pathogens; caries; calculus; candidiasis; oral surgery;
XX tissue regeneration; irrigation; toothpaste; dentifrice; mouthwash;
XX lozenge.
XX
XX Staphylococcus aureus.
XX
XX WO9604003-A1.
XX
XX 15-FEB-1996.
XX
XX 18-JUL-1995; 95WO-EP002825.
XX
XX 05-AUG-1994; 94GB-00015902.
XX
XX (SMTK) SMITHKLINE BEECHAM PLC.
XX
XX Barnett P, Critchley IA, Dodd I;
XX
XX WPI; 1996-129122/13.
XX
XX Prevention of adherence of oral pathogens in the oral cavity, partic.
XX tooth surfaces - by application of a fibronectin binding protein or
XX polypeptide or a monoclonal antibody or fragment against it.
XX
XX Claim 5; Page 31-32; 41pp; English.

CC Adherence of oral pathogens, particularly to tooth surfaces, can be
CC prevented by application of a fibronectin binding protein or polypeptide.
CC The fibronectin binding protein or polypeptide is useful in the
CC manufacture of oral hygiene compositions, eg. toothpaste, liquid
CC dentifrice, mouthwash or lozenge. They are useful to prevent the plaque-
CC related development of carious lesions, gingivitis, calculus or
CC periodontal disease and to combat oral cavity infections, e.g.
CC candidiasis. They may also be useful in oral surgery e.g. in guided
CC tissue regeneration procedures to prevent subsequent bacterial infection,
CC and for irrigation of periodontal pockets. This sequence corresponds to
CC amino acids 709-838 of the D1-D4 fibronectin binding domain of
CC Staphylococcus aureus with a P838T substitution

XX
XX SQ Sequence 130 AA;

Query Match 91.2%; Score 52; DB 2; Length 130;
Best Local Similarity 90.0%; Pred. No. 0.062;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 HGONKGNQSF 10
DB 38 HGONKGDQSF 47

RESULT 15
AAV29088
ID AAV29088 standard; protein; 134 AA.

XX
XX AAV29088;
XX
XX
XX 28-SEP-1999 (first entry)
XX
XX
XX S. aureus fibronectin binding protein B (FnBB) binding domain.
XX
XX Bovine herpes virus-2; BHV-2; cytokine; immune response; immunogen; IL;
XX interleukin; colony stimulating factor; CSF; interferon; IFN; TNF;
XX tumour necrosis factor; recombinant virus; vaccine; mucosal disease;
XX mastitis; breast cancer; stress-induced disease; binding domain; FnBB;
XX fibronectin binding protein.
XX
XX Staphylococcus aureus.
XX
XX WO916892-A1.
XX
XX 08-APR-1999.

```

XX 29-SEP-1998; 98WO-GB002927.
PF
XX 29-SEP-1997; 97GB-0020633.
PR
XX (UYBR-) UNIV BRISTOL.
PA
XX
XX Bradley AJ, Duffas WP;
PI
XX WPI, 1999-255101/21.
DR
XX N-PSDB; AAX91505.
PT
XX
XX New bovine herpes virus-2 vectors.
PS
XX Example 2; Fig 8A-B; 130pp; English.
XX
XX The invention provides bovine herpes virus-2 (BHV-2) based vectors that
CC comprise at least one cytokine-encoding DNA sequence. The expression of
CC cytokines in mammals can up-regulate immune responses to the immunogens.
CC The cytokine is selected from interleukins (IL), colony stimulating
CC factors (CSF), interferons (IFN) and tumour necrosis factors (TNF). The
CC BHV-2 based vector or recombinant virus can be used as vaccines. They can
CC be used for preventing or treating a mucosal disease in a subject, e.g.
CC ruminants, cattle, sheep, goats, dogs, cats, horses, or man, particularly
CC mastitis in cows or breast cancers in humans. They can also be used for
CC preventing or treating a stress-induced disease. The present sequence
CC represents the binding domain of a previously published S. aureus
CC fibronectin binding protein B (FnBB) sequence. The FnB binding domain
CC gene sequence FNBBAB, cloned for use in this invention has 97.8 percent
CC identity when compared to the previously published FNBA and FnBB gene
CC sequences
XX
SQ Sequence 134 AA;

```

Query Match 91.2%; Score 52; DB 2; Length 134;
Best Local Similarity 90.0%; Pred. No. 0.064;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

QY 1 HQQNKGNQSF 10
   |||||
Db 38 HQQNNGNQSF 47

```

Search completed: October 25, 2005, 20:58:47
Job time : 63.2 secs

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OM protein - protein search, using sw model

Run on: October 22, 2005, 05:46:56 ; Search time 17.3 Seconds

(without alignments)
43.150 Million cell updates/sec

Title: US-10-731-238-81

Perfect score: 57
Sequence: 1 HGQNKGNQSF 10Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 200000000Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

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- 3: /cgn2_6/prodata/1/1aa/6A_COMB.pep:*
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- 5: /cgn2_6/prodata/1/1aa/PCTUS_COMB.pep:*
- 6: /cgn2_6/prodata/1/1aa/backfillseq1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	57	100.0	10	4	US-09-010-317-81
2	57	100.0	114	1	US-08-259-000-3
3	57	100.0	139	3	US-08-856-253-8
4	57	100.0	1027	4	US-08-956-171E-5254
5	57	100.0	1027	4	US-08-781-986A-5254
6	52	91.2	130	2	US-08-459-135A-7
7	52	91.2	130	2	US-08-459-135A-8
8	52	91.2	130	3	US-08-495-559-7
9	52	91.2	130	3	US-08-495-559-8
10	52	91.2	174	2	US-08-459-135A-10
11	52	91.2	174	2	US-08-459-135A-13
12	52	91.2	174	3	US-08-495-559-10
13	52	91.2	174	3	US-08-495-559-13
14	52	91.2	176	3	US-08-495-559-6
15	52	91.2	178	2	US-08-459-135A-12
16	52	91.2	181	2	US-08-495-559-12
17	52	91.2	181	2	US-08-459-135A-6
18	52	91.2	559	4	US-08-956-171E-5251
19	52	91.2	559	4	US-08-781-986A-5251
20	49	86.0	38	1	US-08-729-767-4
21	47	82.5	10	4	US-09-010-317-80
22	44	77.2	38	1	US-08-729-767-3
23	43	75.4	10	4	US-09-010-317-82
24	43	75.4	36	4	US-09-010-317-58
25	43	75.4	36	4	US-09-010-317-59
26	43	75.4	38	1	US-08-234-622A-3
27	43	75.4	38	4	US-09-010-317-7

28	43	75.4	38	4	US-09-010-317-8	Sequence 8, Appl
29	43	75.4	38	4	US-09-010-317-46	Sequence 46, Appl
30	43	75.4	38	4	US-09-010-317-47	Sequence 47, Appl
31	43	75.4	38	4	US-09-010-317-48	Sequence 48, Appl
32	43	75.4	38	4	US-09-010-317-49	Sequence 49, Appl
33	43	75.4	38	4	US-09-010-317-50	Sequence 50, Appl
34	39	68.4	785	4	US-09-733-643B-2	Sequence 2, Appl
35	38	66.7	10	4	US-09-010-317-63	Sequence 63, Appl
36	38	66.7	38	1	US-08-234-622A-2	Sequence 2, Appl
37	38	66.7	38	4	US-09-010-317-5	Sequence 5, Appl
38	38	66.7	38	4	US-09-010-317-6	Sequence 6, Appl
39	38	66.7	38	4	US-09-010-317-36	Sequence 36, Appl
40	38	66.7	38	4	US-09-010-317-37	Sequence 37, Appl
41	38	66.7	38	4	US-09-010-317-38	Sequence 38, Appl
42	38	66.7	38	4	US-09-010-317-39	Sequence 39, Appl
43	38	66.7	38	4	US-09-010-317-40	Sequence 40, Appl
44	38	66.7	38	4	US-09-010-317-41	Sequence 41, Appl
45	38	66.7	38	4	US-09-010-317-42	Sequence 42, Appl

ALIGNMENTS

RESULT 1
US-09-010-317-81
Sequence 81, Application US/09010317
Patent No. 6685943
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
APPLICANT: Patti, Joseph M.
APPLICANT: House-Pompeo, Karen L.
APPLICANT: Speziale, Pietro
APPLICANT: Jon, Danny
APPLICANT: Mcgavlin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
TITLE OF INVENTION: AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Habler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TANK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 81:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-09-010-317-81
Query Match 100.0%; Score 57; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.00031;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 HGONKGNOSF 10

Db 1 HGONKGNOSF 10

RESULT 2
US-08-259-000-3

; Sequence 3, Application US/08259000

; Patent No. 5571514

; GENERAL INFORMATION:

; APPLICANT: HOOK, Magnus

; APPLICANT: LINDBERG, Martin Kjell

; APPLICANT: SIGNAS, Lars Christer

; APPLICANT: WADSTROM, Torke Mikael

; APPLICANT: FROMAN, Gunnar

; TITLE OF INVENTION: FIBROBLAST BINDING PROTEIN AS WELL AS

; TITLE OF INVENTION: ITS PREPARATION

; NUMBER OF SEQUENCES: 4

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Burns, Doane, Swecker & Mathis

; STREET: P. O. Box 1404

; CITY: Alexandria

; STATE: Virginia

; COUNTRY: United States

; ZIP: 22131-1404

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/259,000

; FILING DATE: 13-JUN-1994

; CLASSIFICATION: 435

; PRIORITY APPLICATION DATA:

; FILING DATE: 01-JUN-1987

; ATTORNEY/AGENT INFORMATION:

; NAME: Meuth, Donna M

; REGISTRATION NUMBER: 36,607

; REFERENCE/DOCKET NUMBER: 012885-062

; TELEPHONE: (703) 836-6620

; TELEFAX: (703) 836-2021

; INFORMATION FOR SEQ ID NO: 3:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 114 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: protein

US-08-259-000-3

Query Match 100.0%; Score 57; DB 1; Length 114;

Best Local Similarity 100.0%; Pred. No. 0.0037;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 HGONKGNOSF 10

Db 38 HGONKGNOSF 47

RESULT 3

US-08-856-253-8

; Sequence 8, Application US/08856253

; Patent No. 6286214

; GENERAL INFORMATION:

; APPLICANT: Hook, Magnus

; APPLICANT: Patti, Joseph M.

; APPLICANT: House-Pompeo, Karen

; APPLICANT: Schanam, Narayana

; APPLICANT: Symersky, Jindrich

; TITLE OF INVENTION: COLLAGEN BINDING PROTEIN COMPOSITIONS

; TITLE OF INVENTION: AND METHODS OF USE

; NUMBER OF SEQUENCES: 8

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Arnold, White & Durkee

; STREET: P. O. Box 4433

; CITY: Houston

; STATE: Texas

; COUNTRY: U.S.

; ZIP: 77210

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; OPERATING SYSTEM: IBM PC compatible

; SOFTWARE: Patent Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/856,253

; FILING DATE: Concurrently Herewith

; CLASSIFICATION: 514

; PRIORITY APPLICATION DATA:

; APPLICATION NUMBER: US 60/017,678

; FILING DATE: 16-MAY-1996

; ATTORNEY/AGENT INFORMATION:

; NAME: Kitchell, Barbara S.

; REGISTRATION NUMBER: 33,928

; REFERENCE/DOCKET NUMBER: TANK:193

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (512) 418-3000

; TELEFAX: (512) 474-7577

; INFORMATION FOR SEQ ID NO: 8:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 139 amino acids

; TYPE: amino acid

; STRANDEDNESS:

; TOPOLOGY: linear

US-08-856-253-8

Query Match 100.0%; Score 57; DB 3; Length 139;

Best Local Similarity 100.0%; Pred. No. 0.0046;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 HGONKGNOSF 10

Db 52 HGONKGNOSF 61

RESULT 4

US-08-956-171E-5254

; Sequence 5254, Application US/08956171E

; Patent No. 6593114

; GENERAL INFORMATION:

; APPLICANT: Charles Kunsch

; APPLICANT: Gil H. Choi

; APPLICANT: Patrick S. Dillon

; APPLICANT: Steven C. Barash

; APPLICANT: Michael R. Fannon

; TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences

; NUMBER OF SEQUENCES: 5256

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Human Genome Sciences, Inc.

; STREET: 9410 Key West Avenue

; CITY: Rockville

; STATE: Maryland

; COUNTRY: USA

; ZIP: 20850

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette, 3.50 inch, 1.4mb storage

; OPERATING SYSTEM: HP Vectra 486/33

; SOFTWARE: MSDOS version 6.2

; CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/956,171E
FILING DATE: 20-Oct-1997
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/009,861
FILING DATE: January 5, 1996
APPLICATION NUMBER: 08/781,986
FILING DATE: January 3, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Mark J. Hyman
REGISTRATION NUMBER: 46,789
REFERENCE/DOCKET NUMBER: PB248P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (240) 314-1224
TELEFAX: (301) 309-8439
INFORMATION FOR SEQ ID NO: 5254:
SEQUENCE CHARACTERISTICS:
LENGTH: 1027 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 5254:
US-08-956-171E-5254

Query Match 100.0%; Score 57; DB 4; Length 1027;
Best Local Similarity 100.0%; Pred. No. 0.035;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HGQKNGNSF 10
DB 791 HGQKNGNSF 800

RESULT 5
US-08-781-986A-5254
Sequence 5254, Application US/08781986A
Patent No. 6737248
GENERAL INFORMATION:
APPLICANT: Charles Kunsch
TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
NUMBER OF SEQUENCES: 5255
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COUNTRY: USA
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/781,986A
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Benson, Bob
REGISTRATION NUMBER: 30,446
REFERENCE/DOCKET NUMBER: PB248PP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 5254:
SEQUENCE CHARACTERISTICS:
LENGTH: 1027 amino acids
TYPE: amino acid
STRANDEDNESS: single

TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-781-986A-5254

Query Match 100.0%; Score 57; DB 4; Length 1027;
Best Local Similarity 100.0%; Pred. No. 0.035;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HGQKNGNSF 10
DB 791 HGQKNGNSF 800

RESULT 6
US-08-459-135A-7
Sequence 7, Application US/08459135A
Patent No. 5955078
GENERAL INFORMATION:
APPLICANT: BURNHAM, Martin Karl Russel
APPLICANT: CHOPRA, Ian
APPLICANT: CRITCHLEY, Ian Alfred
APPLICANT: KNOWLES, David Justin Charles
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN: MONOCLONAL ANTIBODY AND THEIR US
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
STATE: PA
COUNTRY: U.S.A.
ZIP: 19406-0939
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: Fastseq, Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/459,135A
FILING DATE: 02-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB/94/00215
FILING DATE: 04-Feb-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: GIMMI, Edward R
REGISTRATION NUMBER: 38,891
REFERENCE/DOCKET NUMBER: P30591C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-4478
TELEFAX: 610-270-5090
TELEX:
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 130 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-459-135A-7

Query Match 91.2%; Score 52; DB 2; Length 130;
Best Local Similarity 90.0%; Pred. No. 0.035;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HGQKNGNSF 10
DB 38 HGQKNGNSF 47

RESULT 7
US-08-459-135A-8
Sequence 8, Application US/08459135A
Patent No. 5955078


```

; GENERAL INFORMATION:
; APPLICANT: BURHAM, Martin Karl Russel
; APPLICANT: CHOPRA, Ian
; APPLICANT: CRITCHLEY, Ian Alfred
; APPLICANT: KNOWLES, David Justin Charles
; TITLE OF INVENTION: FIBROBLAST BINDING PROTEIN: MONOCLONAL ANTIBODY AND THEIR US
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corporation
; STREET: 709 Swedeland Road
; CITY: King of Prussia
; STATE: PA
; COUNTRY: U.S.A.
; ZIP: 19406-0939
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq, Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/459,135A
; FILING DATE: 02-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB/94/00215
; FILING DATE: 04-Feb-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Gimml, Edward R
; REGISTRATION NUMBER: 38,891
; REFERENCE/DOCKET NUMBER: P30591C2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-270-4478
; TELEFAX: 610-270-5090
; TELEX:
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 130 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-459-135A-8

Query Match          91.2%; Score 52; DB 2; Length 130;
Best Local Similarity 90.0%; Pred. No. 0.035;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 HGQNKGNQSF 10
       |||||:||||
Db      38 HGQNKGDQSF 47

RESULT 8
US-08-495-559-7
; Sequence 7, Application US/08495559A
; Patent No. 6054572
; GENERAL INFORMATION:
; APPLICANT: BURHAM, Martin Karl Russel
; APPLICANT: CHOPRA, Ian
; APPLICANT: CRITCHLEY, Ian Alfred
; APPLICANT: KNOWLES, David Justin Charles
; TITLE OF INVENTION: FIBROBLAST BINDING PROTEIN: MONOCLONAL
; TITLE OF INVENTION: ANTIBODY AND THEIR USE IN PREVENTING BACTERIAL ADHESION
; FILE REFERENCE: P30591
; CURRENT APPLICATION NUMBER: US/08/495,559A
; EARLIER FILING DATE: 1995-08-03
; EARLIER APPLICATION NUMBER: GB 9302289.5
; EARLIER FILING DATE: 1993-02-05
; EARLIER APPLICATION NUMBER: GB 9321592.9
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 7
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; LENGTH: 130
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
; US-08-495-559-7

Query Match          91.2%; Score 52; DB 3; Length 130;
Best Local Similarity 90.0%; Pred. No. 0.035;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 HGQNKGNQSF 10
       |||||:||||
Db      38 HGQNKGDQSF 47

RESULT 9
US-08-495-559-8
; Sequence 8, Application US/08495559A
; Patent No. 6054572
; GENERAL INFORMATION:
; APPLICANT: BURHAM, Martin Karl Russel
; APPLICANT: CHOPRA, Ian
; APPLICANT: CRITCHLEY, Ian Alfred
; APPLICANT: KNOWLES, David Justin Charles
; TITLE OF INVENTION: FIBROBLAST BINDING PROTEIN: MONOCLONAL
; TITLE OF INVENTION: ANTIBODY AND THEIR USE IN PREVENTING BACTERIAL ADHESION
; FILE REFERENCE: P30591
; CURRENT APPLICATION NUMBER: US/08/495,559A
; EARLIER FILING DATE: 1995-08-03
; EARLIER APPLICATION NUMBER: GB 9302289.5
; EARLIER FILING DATE: 1993-02-05
; EARLIER APPLICATION NUMBER: GB 9321592.9
; EARLIER FILING DATE: 1993-10-20
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 8
; LENGTH: 130
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
; US-08-495-559-8

Query Match          91.2%; Score 52; DB 3; Length 130;
Best Local Similarity 90.0%; Pred. No. 0.035;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 HGQNKGNQSF 10
       |||||:||||
Db      38 HGQNKGDQSF 47

RESULT 10
US-08-459-135A-10
; Sequence 10, Application US/08459135A
; Patent No. 5955078
; GENERAL INFORMATION:
; APPLICANT: BURHAM, Martin Karl Russel
; APPLICANT: CHOPRA, Ian
; APPLICANT: CRITCHLEY, Ian Alfred
; APPLICANT: KNOWLES, David Justin Charles
; TITLE OF INVENTION: FIBROBLAST BINDING PROTEIN: MONOCLONAL ANTIBODY AND THEIR US
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corporation
; STREET: 709 Swedeland Road
; CITY: King of Prussia
; STATE: PA
; COUNTRY: U.S.A.
; ZIP: 19406-0939
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq, Version 2.0
; CURRENT APPLICATION DATA:
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APPLICATION NUMBER: US/08/459,135A
FILING DATE: 02-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB/94/00215
FILING DATE: 04-Feb-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Gimm, Edward R
REGISTRATION NUMBER: 38,891
REFERENCE/DOCKET NUMBER: P30591C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-4478
TELEFAX: 610-270-5090
TELEX:
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 174 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: Protein
US-08-459-135A-10

Query Match 91.2%; Score 52; DB 2; Length 174;
Best Local Similarity 90.0%; Pred. No. 0.047;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HGONKGNQSF 10
|||||:
DB 38 HGONKGDQSF 47

RESULT 11
US-08-459-135A-13
Sequence 13, Application US/08459135A
Patent No. 5955078
GENERAL INFORMATION:
APPLICANT: BURHAM, Martin Karl Russel
APPLICANT: CHOPRA, Ian
APPLICANT: CRITCHLEY, Ian Alfred
APPLICANT: KNOWLES, David Justin Charles
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN: MONOCLONAL ANTIBODY AND THEIR USE
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSER: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
STATE: PA
COUNTRY: U.S.A.
ZIP: 19406-0939
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq, Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/459,135A
FILING DATE: 02-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB/94/00215
FILING DATE: 04-Feb-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Gimm, Edward R
REGISTRATION NUMBER: 38,891
REFERENCE/DOCKET NUMBER: P30591C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-4478
TELEFAX: 610-270-5090
TELEX:
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:

LENGTH: 174 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: Protein
US-08-459-135A-13

Query Match 91.2%; Score 52; DB 2; Length 174;
Best Local Similarity 90.0%; Pred. No. 0.047;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HGONKGNQSF 10
|||||:
DB 38 HGONKGDQSF 47

RESULT 12
US-08-495-559-10
Sequence 10, Application US/08495559A
Patent No. 6054572
GENERAL INFORMATION:
APPLICANT: BURHAM, Martin Karl Russel
APPLICANT: CHOPRA, Ian
APPLICANT: CRITCHLEY, Ian Alfred
APPLICANT: KNOWLES, David Justin Charles
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN: MONOCLONAL ANTIBODY AND THEIR USE IN PREVENTING BACTERIAL ADHESION
FILE REFERENCE: P30591
CURRENT APPLICATION NUMBER: US/08/495,559A
EARLIER FILING DATE: 1995-08-03
EARLIER APPLICATION NUMBER: GB 9302289.5
EARLIER FILING DATE: 1993-02-05
EARLIER APPLICATION NUMBER: GB 9321592.9
EARLIER FILING DATE: 1993-10-20
NUMBER OF SEQ ID NOS: 13
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 10
LENGTH: 174
TYPE: PRT
ORGANISM: Staphylococcus aureus
US-08-495-559-10

Query Match 91.2%; Score 52; DB 3; Length 174;
Best Local Similarity 90.0%; Pred. No. 0.047;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HGONKGNQSF 10
|||||:
DB 38 HGONKGDQSF 47

RESULT 13
US-08-495-559-13
Sequence 13, Application US/08495559A
Patent No. 6054572
GENERAL INFORMATION:
APPLICANT: BURHAM, Martin Karl Russel
APPLICANT: CHOPRA, Ian
APPLICANT: CRITCHLEY, Ian Alfred
APPLICANT: KNOWLES, David Justin Charles
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN: MONOCLONAL ANTIBODY AND THEIR USE IN PREVENTING BACTERIAL ADHESION
FILE REFERENCE: P30591
CURRENT APPLICATION NUMBER: US/08/495,559A
EARLIER FILING DATE: 1995-08-03
EARLIER APPLICATION NUMBER: GB 9302289.5
EARLIER FILING DATE: 1993-02-05
EARLIER APPLICATION NUMBER: GB 9321592.9
EARLIER FILING DATE: 1993-10-20
NUMBER OF SEQ ID NOS: 13
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 13
LENGTH: 174

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; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-08-495-559-13
Query Match          91.2%; Score 52; DB 3; Length 174;
Best Local Similarity 90.0%; Pred. No. 0.047;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 HGQKNGDSF 10
       |||||:||||
Db      38 HGQKNGDSF 47

RESULT 14
US-08-495-559-6
; Sequence 6, Application US/08495559A
; Patent No. 6054572
; GENERAL INFORMATION:
; APPLICANT: BURHAM, Martin Karl Russel
; APPLICANT: CHOPRA, Ian
; APPLICANT: CRITCHLEY, Ian Alfred
; APPLICANT: KNOWLES, David Justin Charles
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN: MONOCLONAL
; FILE REFERENCE: P30591
; CURRENT APPLICATION NUMBER: US/08/495,559A
; EARLIER FILING DATE: 1995-08-03 9302289.5
; EARLIER FILING DATE: 1993-02-05
; EARLIER APPLICATION NUMBER: GB 9321592.9
; EARLIER FILING DATE: 1993-10-20
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 176
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-08-495-559-6
Query Match          91.2%; Score 52; DB 3; Length 176;
Best Local Similarity 90.0%; Pred. No. 0.048;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 HGQKNGDSF 10
       |||||:||||
Db      38 HGQKNGDSF 47

RESULT 15
US-08-459-135A-12
; Sequence 12, Application US/08459135A
; Patent No. 5955078
; GENERAL INFORMATION:
; APPLICANT: BURHAM, Martin Karl Russel
; APPLICANT: CHOPRA, Ian
; APPLICANT: CRITCHLEY, Ian Alfred
; APPLICANT: KNOWLES, David Justin Charles
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN: MONOCLONAL ANTIBODY AND THEIR US
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corporation
; STREET: 709 Swedeland Road
; CITY: King of Prussia
; STATE: PA
; COUNTRY: U.S.A.
; ZIP: 19406-0939
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: Fastseq, Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/459,135A
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; FILING DATE: 02-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB/94/00215
; FILING DATE: 04-Feb-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Gimmil, Edward R
; REGISTRATION NUMBER: 38,891
; REFERENCE/DOCKET NUMBER: P30591C2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-270-4478
; TELEFAX: 610-270-5090
; TELEX:
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 178 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Protein
US-08-459-135A-12
Query Match          91.2%; Score 52; DB 2; Length 178;
Best Local Similarity 90.0%; Pred. No. 0.048;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 HGQKNGDSF 10
       |||||:||||
Db      38 HGQKNGDSF 47
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Search completed: October 22, 2005, 07:41:46
Job time : 18.35 secs

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OM protein - protein search, using sw model

Run on: October 22, 2005, 12:09:40 ; Search time 57.25 Seconds
(without alignments)
72.924 Million cell updates/sec

Title: US-10-731-238-81

Perfect score: 57

Sequence: 1 HGONKGNOSF 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1862951 seqs, 417491010 residues

Total number of hits satisfying chosen parameters: 1862951

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Published Applications_AA:*
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2: /cgn2_6/ptodata/2/pubppa/PCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/2/pubppa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/2/pubppa/US06_PUBCOMB.pep.*
5: /cgn2_6/ptodata/2/pubppa/US07_NEW_PUB.pep.*
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9: /cgn2_6/ptodata/2/pubppa/US09_PUBCOMB.pep.*
10: /cgn2_6/ptodata/2/pubppa/US09B_PUBCOMB.pep.*
11: /cgn2_6/ptodata/2/pubppa/US09C_PUBCOMB.pep.*
12: /cgn2_6/ptodata/2/pubppa/US09_NEW_PUB.pep.*
13: /cgn2_6/ptodata/2/pubppa/US10_PUBCOMB.pep.*
14: /cgn2_6/ptodata/2/pubppa/US10B_PUBCOMB.pep.*
15: /cgn2_6/ptodata/2/pubppa/US10C_PUBCOMB.pep.*
16: /cgn2_6/ptodata/2/pubppa/US10D_PUBCOMB.pep.*
17: /cgn2_6/ptodata/2/pubppa/US10E_PUBCOMB.pep.*
18: /cgn2_6/ptodata/2/pubppa/US10_NEW_PUB.pep.*
19: /cgn2_6/ptodata/2/pubppa/US11_PUBCOMB.pep.*
20: /cgn2_6/ptodata/2/pubppa/US11_NEW_PUB.pep.*
21: /cgn2_6/ptodata/2/pubppa/US60_NEW_PUB.pep.*
22: /cgn2_6/ptodata/2/pubppa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	57	100.0	10	US-10-731-238-81	Sequence 81, Appl
2	57	100.0	139	US-09-813-820-8	Sequence 8, Appl1
3	57	100.0	1018	US-09-815-242-5797	Sequence 5797, Ap
4	57	100.0	1018	US-09-815-242-12838	Sequence 12838, A
5	57	100.0	1018	US-10-470-048B-68	Sequence 68, Appl
6	57	100.0	1027	US-08-781-986A-5254	Sequence 5254, Ap
7	57	100.0	1027	US-10-329-624-5254	Sequence 5254, Ap
8	52	91.2	388	US-08-901-062-1	Sequence 1, Appl1
9	52	91.2	559	US-08-781-986A-5251	Sequence 5251, Ap
10	52	91.2	559	US-10-329-624-5251	Sequence 5251, Ap
11	52	91.2	767	US-09-815-242-5899	Sequence 5899, Ap

12	52	91.2	767	9	US-09-815-242-13140	Sequence 13140, A
13	52	91.2	940	17	US-10-470-048B-424	Sequence 424, App
14	52	91.2	948	17	US-10-470-048B-69	Sequence 69, Appl
15	52	91.2	961	15	US-10-282-122A-43778	Sequence 43778, A
16	52	91.2	1038	18	US-10-282-122A-43827	Sequence 43827, A
17	47	82.5	10	18	US-10-731-238-80	Sequence 80, Appl
18	47	82.5	1098	18	US-10-450-763-33706	Sequence 33706, A
19	44	77.2	30	14	US-10-287-821-1	Sequence 1, Appl1
20	44	77.2	31	14	US-10-287-821-2	Sequence 2, Appl1
21	44	77.2	978	9	US-09-815-242-5456	Sequence 5456, Ap
22	44	77.2	1001	9	US-09-815-242-1686	Sequence 12686, A
23	43	75.4	10	18	US-10-731-238-52	Sequence 82, Appl
24	43	75.4	36	18	US-10-731-238-58	Sequence 58, Appl
25	43	75.4	36	18	US-10-731-238-59	Sequence 59, Appl
26	43	75.4	38	18	US-10-731-238-7	Sequence 7, Appl1
27	43	75.4	38	18	US-10-731-238-8	Sequence 8, Appl1
28	43	75.4	38	18	US-10-731-238-46	Sequence 46, Appl
29	43	75.4	38	18	US-10-731-238-47	Sequence 47, Appl
30	43	75.4	38	18	US-10-731-238-48	Sequence 48, Appl
31	43	75.4	38	18	US-10-731-238-49	Sequence 49, Appl
32	43	75.4	38	18	US-10-731-238-50	Sequence 50, Appl
33	39	68.4	269	16	US-10-733-930-8413	Sequence 8413, Ap
34	39	68.4	319	16	US-10-425-115-361327	Sequence 361327, A
35	39	68.4	785	10	US-09-733-643-2	Sequence 2, Appl1
36	38	66.7	10	18	US-10-731-238-63	Sequence 63, Appl
37	38	66.7	38	18	US-10-731-238-5	Sequence 5, Appl1
38	38	66.7	38	18	US-10-731-238-6	Sequence 6, Appl1
39	38	66.7	38	18	US-10-731-238-36	Sequence 36, Appl
40	38	66.7	38	18	US-10-731-238-37	Sequence 37, Appl
41	38	66.7	38	18	US-10-731-238-38	Sequence 38, Appl
42	38	66.7	38	18	US-10-731-238-39	Sequence 39, Appl
43	38	66.7	38	18	US-10-731-238-40	Sequence 40, Appl
44	38	66.7	38	18	US-10-731-238-41	Sequence 41, Appl
45	38	66.7	38	18	US-10-731-238-42	Sequence 42, Appl

ALIGNMENTS

RESULT 1
US-10-731-238-81
Sequence 81, Application US/10731238
Publication No. US20050123552A1
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
Pacifi, Joseph M.
House-Pompeo, Karen L.
Speziale, Pietro
Joh, Danny
McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/107/731,238
FILING DATE: 10-Dec-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE: 21-Jan-1998
APPLICATION NUMBER: US 60/036,139

```

; FILING DATE: 21-JAN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Hibler, David W.
; REGISTRATION NUMBER: 41,071
; REFERENCE/DOCKET NUMBER: TAMK:169
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 512-418-3000
; TELEFAX: 512-474-7577
; INFORMATION FOR SEQ ID NO: 81:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 81:
US-10-731-238-81

Query Match      100.0%; Score 57; DB 18; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.00084;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 HGONKGNOSF 10
Db      1 HGONKGNOSF 10

RESULT 2
US-09-813-820-8
; Sequence 8, Application US/09813820
; Patent No. US20020102262A1
; GENERAL INFORMATION:
; APPLICANT: Hook, Magnus
;          Pacil, Joseph M.
;          House-Pompeo, Karen
;          Schanam, Narayana
;          Symersky, Jindrich
; TITLE OF INVENTION: COLLAGEN BINDING PROTEIN COMPOSITIONS
; AND METHODS OF USE
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: U.S.
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/813,820
; FILING DATE: 22-Mar-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/856,253
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Kitchell, Barbara S.
; REGISTRATION NUMBER: 33,928
; REFERENCE/DOCKET NUMBER: TAMK:193
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (512) 418-3000
; TELEFAX: (512) 474-7577
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 139 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-09-813-820-8
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Query Match      100.0%; Score 57; DB 9; Length 139;
Best Local Similarity 100.0%; Pred. No. 0.013;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 HGONKGNOSF 10
Db      52 HGONKGNOSF 61

RESULT 3
US-09-815-242-5797
; Sequence 5797, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; FILE REFERENCE: EITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5797
; LENGTH: 1018
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-09-815-242-5797

Query Match      100.0%; Score 57; DB 9; Length 1018;
Best Local Similarity 100.0%; Pred. No. 0.11;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 HGONKGNOSF 10
Db      782 HGONKGNOSF 791

RESULT 4
US-09-815-242-12838
; Sequence 12838, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
```

```

; TITLE OF INVENTION: Prokaryotes
; FILE REFERENCE: ELITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 12838
; LENGTH: 1018
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
; US-09-815-242-12838

Query Match          100.0%; Score 57; DB 9; Length 1018;
Best Local Similarity 100.0%; Pred. No. 0.11;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 HGQNKGNQSF 10
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Db       782 HGQNKGNQSF 791

RESULT 5
US-10-470-048B-68
; Sequence 68, Application US/10470048B
; Publication No. US20050037444A1
; GENERAL INFORMATION:
; APPLICANT: MEINKE ET AL.
; TITLE OF INVENTION: A METHOD FOR IDENTIFICATION, ISOLATION AND PRODUCTION OF
; FILE REFERENCE: SONN:035US
; CURRENT APPLICATION NUMBER: US/10/470,048B
; CURRENT FILING DATE: 2003-07-25
; NUMBER OF SEQ ID NOS: 603
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 68
; LENGTH: 1018
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
; US-10-470-048B-68

Query Match          100.0%; Score 57; DB 17; Length 1018;
Best Local Similarity 100.0%; Pred. No. 0.11;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 HGQNKGNQSF 10
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Db       782 HGQNKGNQSF 791

RESULT 6
US-08-781-986A-5254
; Sequence 5254, Application US/08781986A
; Publication No. US20030054436A1
; GENERAL INFORMATION:
; APPLICANT: Charles Kunsch
; TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
; NUMBER OF SEQUENCES: 5255
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; US-08-781-986A-5254
```

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; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4mb storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/781,986A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; ATTORNEY/AGENT INFORMATION:
; NAME: Benson, Bob
; REGISTRATION NUMBER: 30,445
; REFERENCE/DOCKET NUMBER: PB248PP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 5254:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1027 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-781-986A-5254

Query Match          100.0%; Score 57; DB 8; Length 1027;
Best Local Similarity 100.0%; Pred. No. 0.11;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 HGQNKGNQSF 10
        |||||
Db       791 HGQNKGNQSF 800

RESULT 7
US-10-329-624-5254
; Sequence 5254, Application US/10329624
; Publication No. US20040043037A1
; GENERAL INFORMATION:
; APPLICANT: Charles Kunsch
; Gil H. Choi
; Patrick S. Dillon
; Craig A. Rosen
; Steven C. Barash
; Michael R. Fannon
; TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
; NUMBER OF SEQUENCES: 5256
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4mb storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/329,624
; FILING DATE: 27-Dec-2002
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/956,171
; FILING DATE: October 20, 1997
; US-10-329-624-5254
```

APPLICATION NUMBER: 60/009,861
FILING DATE: January 5, 1996
APPLICATION NUMBER: 08/781,986
FILING DATE: January 3, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Mark J. Hyman
REGISTRATION NUMBER: 46,789
REFERENCE/DOCKET NUMBER: PB248PDI
TELECOMMUNICATION INFORMATION:
TELEPHONE: (240) 314-1224
TELEFAX: (301) 309-8439
INFORMATION FOR SEQ ID NO: 5254:
SEQUENCE CHARACTERISTICS:
LENGTH: 1027 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 5254:
US-10-329-624-5254

Query Match 100.0%; Score 57; DB 15; Length 1027;
Best Local Similarity 100.0%; Pred. No. 0.11;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HGONKGNOSF 10
DB 791 HGONKGNOSF 800

RESULT 8
US-08-901-062-1
Sequence 1, Application US/08901062
Publication No. US20020025324A1
GENERAL INFORMATION:
APPLICANT: SEALS, JONATHAN R.
TITLE OF INVENTION: RECOMBINANT BIVALENT BACTERIAL VACCINE
TITLE OF INVENTION: FOR THE PREVENTION OF MASTITIS
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: HALE AND DORR LLP
STREET: 60 State Street
CITY: Boston
STATE: MA
COUNTRY: United States Of America
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/901,062
FILING DATE: 25-JUL-1997
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Baker, Hollie L.
REGISTRATION NUMBER: 31,321
REFERENCE/DOCKET NUMBER: 106941.153
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 526-6000
TELEFAX: (617) 526-5000
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 388 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-901-062-1

Query Match 91.2%; Score 52; DB 8; Length 388;
Best Local Similarity 90.0%; Pred. No. 0.33;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 HGONKGNOSF 10
DB 301 HGONKGNOSF 310

RESULT 9
US-08-781-986A-5251
Sequence 5251, Application US/08781986A
Publication No. US20030054436A1
GENERAL INFORMATION:
APPLICANT: Charles Kunach
TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
NUMBER OF SEQUENCES: 525
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COUNTRY: USA
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/781,986A
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Benson, Bob
REGISTRATION NUMBER: 30,446
REFERENCE/DOCKET NUMBER: PB248BP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 5251:
SEQUENCE CHARACTERISTICS:
LENGTH: 559 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-781-986A-5251

Query Match 91.2%; Score 52; DB 8; Length 559;
Best Local Similarity 90.0%; Pred. No. 0.48;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 HGONKGNOSF 10
DB 337 HGONKGNOSF 346

RESULT 10
US-10-329-624-5251
Sequence 5251, Application US/10329624
Publication No. US20040043037A1
GENERAL INFORMATION:
APPLICANT: Charles Kunach
Gill H. Choi
Patrick S. Dillon
Craig A. Rosen
Steven C. Barash
Michael R. Pannon
TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences

NUMBER OF SEQUENCES: 5256
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COUNTRY: USA
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4MB storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/329,624
FILING DATE: 27-Dec-2002
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/956,171
FILING DATE: October 20, 1997
APPLICATION NUMBER: 60/009,861
FILING DATE: January 5, 1996
APPLICATION NUMBER: 08/781,986
FILING DATE: January 3, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Mark J. Hyman
REGISTRATION NUMBER: 46,789
REFERENCE/DOCKET NUMBER: PB248P1D1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (240) 314-1224
TELEFAX: (301) 309-8439
INFORMATION FOR SEQ ID NO: 5251:
SEQUENCE CHARACTERISTICS:
LENGTH: 559 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 5251:
US-10-329-624-5251
Query Match 91.2%; Score 52; DB 15; Length 559;
Best Local Similarity 90.0%; Pred. No. 0.48; 1; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 HGQKNGNSF 10
Db 337 HGQKNGNSF 346
RESULT 11
US-09-815-242-5899
Sequence 5899, Application US/09815242
Patent No. US2002061569A1
GENERAL INFORMATION:
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Karl L.
APPLICANT: Zyskind, Judith W.
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John D.
APPLICANT: Carr, Grant J.
APPLICANT: Yamamoto, Robert T.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26

PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 1410
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 5899
LENGTH: 767
TYPE: PRT
ORGANISM: Staphylococcus aureus
US-09-815-242-5899
Query Match 91.2%; Score 52; DB 9; Length 767;
Best Local Similarity 90.0%; Pred. No. 0.67;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 HGQKNGNSF 10
Db 718 HGQKNGNSF 727
RESULT 12
US-09-815-242-13140
Sequence 13140, Application US/09815242
Patent No. US2002061569A1
GENERAL INFORMATION:
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Karl L.
APPLICANT: Zyskind, Judith W.
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John D.
APPLICANT: Carr, Grant J.
APPLICANT: Yamamoto, Robert T.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 1410
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 13140
LENGTH: 767
TYPE: PRT
ORGANISM: Staphylococcus aureus
US-09-815-242-13140
Query Match 91.2%; Score 52; DB 9; Length 767;
Best Local Similarity 90.0%; Pred. No. 0.67;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 HGQKNGNSF 10
Db 718 HGQKNGNSF 727


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RESULT 13
US-10-470-048B-424
; Sequence 424, Application US/10470048B
; Publication No. US20050037444A1
; GENERAL INFORMATION:
; APPLICANT: MEINKE ET AL.
; TITLE OF INVENTION: A METHOD FOR IDENTIFICATION, ISOLATION AND PRODUCTION OF
; FILE REFERENCE: SONN:035US
; CURRENT FILING DATE: 2003-07-25
; NUMBER OF SEQ ID NOS: 603
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 424
; LENGTH: 940
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-10-470-048B-424

Query Match          91.2%; Score 52; DB 17; Length 940;
Best Local Similarity 90.0%; Pred. No. 0.83; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY      1 HGQNKGNOSF 10
      |||||
Db      718 HGQNNGNOSF 727

RESULT 14
US-10-470-048B-69
; Sequence 69, Application US/10470048B
; Publication No. US20050037444A1
; GENERAL INFORMATION:
; APPLICANT: MEINKE ET AL.
; TITLE OF INVENTION: A METHOD FOR IDENTIFICATION, ISOLATION AND PRODUCTION OF
; FILE REFERENCE: SONN:035US
; CURRENT FILING DATE: 2003-07-25
; NUMBER OF SEQ ID NOS: 603
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 69
; LENGTH: 948
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-10-470-048B-69

Query Match          91.2%; Score 52; DB 17; Length 948;
Best Local Similarity 90.0%; Pred. No. 0.84; Indels 1; Gaps 0;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY      1 HGQNKGNOSF 10
      |||||
Db      726 HGQNNGNOSF 735

RESULT 15
US-10-282-122A-43778
; Sequence 43778, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zysek, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Foreyth, R.

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; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT FILING DATE: 2003-02-20
; CURRENT FILING DATE: 2003-02-20
; PRIOR FILING DATE: 2000-03-21
; PRIOR FILING DATE: 2000-03-21
; PRIOR FILING DATE: 2000-05-23
; PRIOR FILING DATE: 2000-05-23
; PRIOR FILING DATE: 2000-05-26
; PRIOR FILING DATE: 2000-10-23
; PRIOR FILING DATE: 2000-09-06
; PRIOR FILING DATE: 2000-09-06
; PRIOR FILING DATE: 2000-09-09
; PRIOR FILING DATE: 2000-12-22
; PRIOR FILING DATE: 2000-12-22
; PRIOR FILING DATE: 2001-02-09
; PRIOR FILING DATE: 2001-02-09
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See file Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 43778
; LENGTH: 961
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-10-282-122A-43778

Query Match          91.2%; Score 52; DB 15; Length 961;
Best Local Similarity 90.0%; Pred. No. 0.85; Indels 1; Gaps 0;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY      1 HGQNKGNOSF 10
      |||||
Db      729 HGQNNGNOSF 738

Search completed: October 22, 2005, 12:39:49
Job time : 57.25 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 22, 2005, 06:10:10 ; Search time 11.45 Seconds
(without alignments)
84.032 Million cell updates/sec

Title: US-10-731-238-81

Perfect score: 57
Sequence: 1 HGONKGNOSF 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-Processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	57	100.0	1018	2	A32192	fibronectin-bindin
2	52	91.2	940	2	S19702	fibronectin-bindin
3	52	91.2	961	2	G90053	hypothetical prote
4	52	91.2	1038	2	H90053	hypothetical prote
5	37	64.9	463	2	T39004	probable histone a
6	37	64.9	879	2	T22033	hypothetical prote
7	37	64.9	1223	2	T15316	hypothetical prote
8	36	63.2	390	2	TS1197	hypothetical prote
9	36	63.2	467	2	S39193	royal jelly protei
10	35	61.4	626	2	H82147	methy1-accepting c
11	35	61.4	822	2	E86601	CHLNR probable pho
12	35	61.4	822	2	B81518	conserved hypochet
13	35	61.4	822	2	C72023	chltr probable pho
14	35	61.4	1035	2	IS8490	integrin alpha-9 c
15	35	61.4	1086	2	T18523	integrin alpha cha
16	35	61.4	1390	2	T14004	trfA protein - sli
17	34	59.6	114	2	T117927	hypothetical prote
18	34	59.6	133	2	P95312	hypothetical prote
19	34	59.6	210	2	A49180	glutathione transf
20	34	59.6	215	2	A59428	glutathione B (EC 3
21	34	59.6	270	2	S71191	hypothetical prote
22	34	59.6	310	2	JL0091	beta-lactamase (EC
23	34	59.6	427	2	T00465	RNA-binding / Ran
24	34	59.6	604	2	T37870	finger protein HZF
25	34	59.6	732	2	S47073	hypothetical prote
26	34	59.6	854	2	T23837	hypothetical prote
27	34	59.6	917	2	A84690	hypothetical prote
28	34	59.6	1018	2	T13525	hypothetical prote
29	34	59.6	1082	2	H81962	hypothetical prote

30	34	59.6	2902	2	C71953
31	33.5	58.8	292	1	D55582
32	33	57.9	109	2	B82210
33	33	57.9	195	2	B86204
34	33	57.9	227	2	S35240
35	33	57.9	267	2	H86548
36	33	57.9	302	2	AD3106
37	33	57.9	305	2	H98180
38	33	57.9	348	1	BUC5B
39	33	57.9	357	2	F83537
40	33	57.9	369	2	C82211
41	33	57.9	494	2	A99683
42	33	57.9	494	2	E85533
43	33	57.9	520	2	F90596
44	33	57.9	520	2	S49395
45	33	57.9	520	2	A99566

ALIGNMENTS

RESULT 1

A32192
fibronectin-binding protein - Staphylococcus aureus
C:Species: Staphylococcus aureus
C>Date: 31-Jul-1989 #sequence_revision 31-Jul-1989 #text_change 16-Feb-1997
C:Accession: A32192
R:Signaes, C.; Raucel, G.; Joensson, K.; Lindgren, P.E.; Anantharamaiah, G.M.; Hoeck, J.
Proc. Natl. Acad. Sci. U.S.A. 86, 699-703, 1989
A>Title: Nucleotide sequence of the gene for a fibronectin-binding protein from Staphyl.
A:Reference number: A32192; PMID:89098998; PMID:2521391
A:Accession: A32192
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1018 <SIG>
A:Cross-references: GB:J04151
C:Keywords: fibronectin binding

Query Match 100.0%; Score 57; DB 2; Length 1018;
Best Local Similarity 100.0%; Pred. No. 0.0079;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HGONKGNOSF 10
DB 782 HGONKGNOSF 791

RESULT 2

S19702
fibronectin-binding protein B - Staphylococcus aureus
C:Species: Staphylococcus aureus
C>Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
R:Joensson, K.; Signaes, C.; Mueller, H.P.; Lindberg, M.
Eur. J. Biochem. 202, 1041-1048, 1991
A>Title: Two different genes encode fibronectin binding proteins in Staphylococcus aure
A:Reference number: S19702; PMID:92111475; PMID:1837266
A:Accession: S19702
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-940 <JOB>
A:Cross-references: UNIPROT:Q53682; EMBL:X62992; NID:949040; PIDD:CAA44726.1; PID:95815
C:Keywords: fibronectin binding

Query Match 91.2%; Score 52; DB 2; Length 940;
Best Local Similarity 90.0%; Pred. No. 0.068;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 HGONKGNOSF 10
DB 718 HGONKGNOSF 727

```
RESULT 3
G90053
Hypothetical protein fnbB [imported] - Staphylococcus aureus (strain N315)
C:Species: Staphylococcus aureus
C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C:Accession: G90053
R:Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguo
ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.;
C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
A:Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.
A:Reference number: A89758; MUID:21311952; PMID:11418146
A:Accession: G90053
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-961 <KUR>
A:Cross-references: UNIPROT:Q99RD3; GB:BA000018; PID:G13702452; PIDN:BA843593.1; GSPDB:G
A:Experimental source: strain N315
C:Genetics:
A:Gene: fnbB

Query Match          91.2%; Score 52; DB 2; Length 961;
Best Local Similarity 90.0%; Pred. No. 0.069;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 HGONKGNOSF 10
    |||||
Db 729 HGONKGNOSF 738

RESULT 4
H90053
Hypothetical protein fnbB [imported] - Staphylococcus aureus (strain N315)
C:Species: Staphylococcus aureus
C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C:Accession: H90053
R:Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguo
ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.;
C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
A:Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.
A:Reference number: A89758; MUID:21311952; PMID:11418146
A:Accession: H90053
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1038 <KUR>
A:Cross-references: UNIPROT:Q99RD2; GB:BA000018; PID:G13702453; PIDN:BA843594.1; GSPDB:G
A:Experimental source: strain N315
C:Genetics:
A:Gene: fnbB

Query Match          91.2%; Score 52; DB 2; Length 1038;
Best Local Similarity 90.0%; Pred. No. 0.075;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HGONKGNOSF 10
    |||||
Db 778 HGONKGNOSF 787

RESULT 5
T39004
Probable histone acetyl transferase - fission yeast (Schizosaccharomyces pombe)
C:Species: Schizosaccharomyces pombe
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C:Accession: T39004
R:Purrelle, B.; Goffeau, A.; Wood, V.; Rajandream, M.A.; Barrell, B.G.
submitted to the EMBL Data Library, December 1998
A:Reference number: Z21823
A:Accession: T39004
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-463 <PUR>
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A:Cross-references: UNIPROT:O94446; EMBL:AL034583; PIDN:CAA22591.1; GSPDB:GN00066; SPDB:
A:Experimental source: strain 972h-; cosmid c637
C:Genetics:
A:Gene: SPDB:SPAC637.12c
A:Map position: 1

Query Match          64.9%; Score 37; DB 2; Length 463;
Best Local Similarity 66.7%; Pred. No. 27;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 HGONKGNOS 9
    |||||
Db 135 HGONKGNOS 143

RESULT 6
T22033
Hypothetical protein F40F8.5 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T22033
R:MacDougall, R.
submitted to the EMBL Data Library, February 1996
A:Reference number: Z19505
A:Accession: T22033
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-879 <WIL>
A:Cross-references: UNIPROT:Q20227; EMBL:Z69302; PIDN:CAA93261.1; GSPDB:GN00020; CESP:F4
A:Experimental source: clone F40F8
C:Genetics:
A:Gene: CESP:F40F8.5
A:Map position: 2
A:introns: 63/1; 149/1; 173/1; 217/1; 262/1; 306/1; 347/1; 381/2; 422/2; 440/3; 461/3; 5

Query Match          64.9%; Score 37; DB 2; Length 879;
Best Local Similarity 60.0%; Pred. No. 50;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 HGONKGNOSF 10
    |||||
Db 423 HGONKGNOSF 432

RESULT 7
T15316
Hypothetical protein B0302.1 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C:Accession: T15316
R:Du, Z.
submitted to the EMBL Data Library, November 1995
A:Description: The sequence of C. elegans cosmid B0302.
A:Reference number: Z18328
A:Accession: T15316
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-1223 <DUZ>
A:Cross-references: UNIPROT:Q10925; EMBL:U41032; NID:G1086728; PID:G1086729; PIDN:AAA823
A:Experimental source: strain Bristol N2
C:Genetics:
A:Gene: CESP:B0302.1
A:introns: 50/3; 106/3; 153/3; 180/3; 243/3; 399/2; 438/3; 482/1; 520/2; 545/1; 589/1; 6

Query Match          64.9%; Score 37; DB 2; Length 1223;
Best Local Similarity 77.8%; Pred. No. 69;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 GONKGNOSF 10
    |||||
Db 405 GONKGNOSF 413
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C:Species: Chlamydia pneumoniae, Chlamydia pneumoniae
 C>Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #ext_change 09-Jul-2004
 C:Accession: C72023
 R:Kallman, S.; Mitchell, W.; Marathe, R.; Lammel, C.; Pan, J.; Olinger, I.; Grimwood, J.;
 Nature Genet. 21, 385-389, 1999
 A:Title: Comparative genomes of Chlamydia pneumoniae and C. trachomatis.
 A:Reference number: A72000; MUID:99206606; PMID:10192388
 A:Accession: C72023
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-822 <ARN>
 A:Cross-references: UNIPROT:Q92719; GB:AE001669; GB:AE001363; NID:94377199; PIDN:AAD1902
 A:Experimental source: strain Cw1029
 C:Genetics:
 A:Gene: Cpn0887

Query Match 61.4%; Score 35; DB 2; Length 822;
 Best Local Similarity 55.6%; Pred. No. 1.1e+02;
 Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 HQGNKGNOS 9
 |||||:
 DB 466 HQGNKGNOS 474

RESULT 14

158409
 Integrin alpha-9 chain precursor - human
 C:Species: Homo sapiens (man)
 C>Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #ext_change 09-Jul-2004
 C:Accession: I58409; A49459
 R:Hibb, K.; Yamakawa, K.; Ueda, R.; Horio, Y.; Murata, Y.; Tamari, M.; Uchida, K.; Takah
 Onoegne 9, 611-619, 1994
 A:Title: Aberrant upregulation of a novel integrin alpha subunit gene at 3p21.3 in small
 A:Reference number: I58409; MUID:94119603; PMID:8290272
 A:Accession: I58409
 A:Status: preliminary; translated from GB/EMBL/DBDJ
 A:Molecule type: mRNA
 A:Residues: 1-1035 <RES>
 A:Cross-references: UNIPROT:Q13797; GB:D25303; NID:9464180; PIDN:BA04984.1; PID:G533327
 R:Palmer, E. L.; Ruegg, C.; Ferrando, R.; Pytela, R.; Sheppard, D.
 J. Cell Biol. 123, 1289-1297, 1993
 A:Title: Sequence and tissue distribution of the integrin alpha9 subunit, a novel partic
 A:Reference number: A49459; MUID:94064789; PMID:8245132
 A:Accession: A49459
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 30-1035 <PAL>
 A:Cross-references: GB:L24158
 C:Superfamily: Integrin alpha-4 chain
 C:Keywords: glycoprotein; metal binding; transmembrane protein
 F:1-27/Domain: signal sequence #status predicted <Sig>

Query Match 61.4%; Score 35; DB 2; Length 1035;
 Best Local Similarity 77.8%; Pred. No. 1.4e+02;
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 GONKGNOSF 10
 |||||:
 DB 849 GONKGNOSF 857

RESULT 15

118523
 Integrin alpha chain - Geodia cydonium
 C:Species: Geodia cydonium
 C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #ext_change 09-Jul-2004
 C:Accession: T18523
 R:Pancer, Z.; Kruse, M.; Mueller, I.; Mueller, W. E. G.
 Mol. Biol. Evol. 14, 391-398, 1997
 A:Title: On the origin of adhesion receptors of metazoa: Cloning of the integrin alpha B
 A:Reference number: Z18946; MUID:97254987; PMID:9100369
 A:Accession: T18523

A:Status: preliminary; translated from GB/EMBL/DBDJ
 A:Molecule type: mRNA
 A:Residues: 1-1086 <PAN>
 A:Cross-references: UNIPROT:O18428; EMBL:X97283; PIDN:CAA65943.1
 C:Function:
 A:Description: signal transduction
 C:Superfamily: Integrin alpha-4 chain

Query Match 61.4%; Score 35; DB 2; Length 1086;
 Best Local Similarity 75.0%; Pred. No. 1.5e+02;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 ONKGNOSF 10
 |||||:
 DB 668 ONKGNOSF 675

Search completed: October 22, 2005, 08:04:36
 Job time : 12.45 secs

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OM protein - protein search, using sw model

Run on: October 22, 2005, 06:06:36 ; Search time 55.85 Seconds
(without alignments)
91.688 Million cell updates/sec

Title: US-10-731-238-81

Perfect score: 57
Sequence: 1 HGONKGNQSF 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_03: *
1: uniprot_sprot: *
2: uniprot_trembl: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	57	100.0	1018	1 FNBA_STRAU	P14738 staphylococ
2	52	91.2	940	2 Q53682	Q53682 staphylococ
3	52	91.2	943	2 Q8NTU8	Q8NTU8 staphylococ
4	52	91.2	957	2 Q6G6H4	Q6G6H4 staphylococ
5	52	91.2	961	2 Q99RD3	Q99RD3 staphylococ
6	52	91.2	961	2 Q7A3I8	Q7A3I8 staphylococ
7	52	91.2	1038	2 Q99RD2	Q99RD2 staphylococ
8	52	91.2	1038	2 Q7A3J7	Q7A3J7 staphylococ
9	44	77.2	152	2 Q9AEP9	Q9AEP9 staphylococ
10	44	77.2	965	2 Q6GDU5	Q6GDU5 staphylococ
11	44	77.2	1015	2 Q8NTU7	Q8NTU7 staphylococ
12	44	77.2	1015	2 Q6G6H3	Q6G6H3 staphylococ
13	41	71.9	654	2 Q6A756	Q6A756 propionibac
14	40	70.2	285	2 Q7MKL1	Q7MKL1 vibrio vuln
15	39.5	69.3	500	2 Q6BGL7	Q6BGL7 parametium
16	39	68.4	269	2 Q9NJV8	Q9NJV8 penaeus sem
17	39	68.4	371	2 Q6SKD0	Q6SKD0 bacillus li
18	39	68.4	1576	2 Q6IRN6	Q6IRN6 xenopus lae
19	38	66.7	363	2 Q8PKN9	Q8PKN9 methanosa
20	38	66.7	410	2 Q9P868	Q9P868 piroplasma e
21	38	66.7	837	2 Q6BY01	Q6BY01 debaryomye
22	37	64.9	107	2 Q8B791	Q8B791 chimpanzee
23	37	64.9	239	2 Q8CNE6	Q8CNE6 staphylococ
24	37	64.9	292	2 Q7S6U5	Q7S6U5 neurospora
25	37	64.9	318	2 Q9W0P3	Q9W0P3 dirosophila
26	37	64.9	463	1 MST1_SCHPO	O54446 schizosacch
27	37	64.9	639	2 Q6Y7B3	Q6Y7B3 staphylococ
28	37	64.9	844	2 Q6A8X0	Q6A8X0 propionibac
29	37	64.9	877	2 Q20227	Q20227 caenorhabdi
30	37	64.9	1130	2 Q7JPS8	Q7JPS8 caenorhabdi
31	37	64.9	1223	1 K125_CABEL	Q10925 caenorhabdi

32	37	64.9	1237	2 Q7JPS9	Q7JPS9 caenorhabdi
33	36	63.2	206	1 RS4_PSPK	Q86412 pseudomonas
34	36	63.2	206	1 RS4_PBSM	Q86412 pseudomonas
35	36	63.2	345	2 Q7RU21	Q7RU21 neurospora
36	36	63.2	390	2 Q9P3C0	Q9P3C0 neurospora
37	36	63.2	411	2 Q8KQNO	Q8KQNO anaplasmata p
38	36	63.2	411	2 Q8KRA2	Q8KRA2 anaplasmata p
39	36	63.2	411	2 Q832F6	Q832F6 anoplhelas g
40	36	63.2	421	2 Q7PRJ7	Q7PRJ7 xenopus lae
41	36	63.2	430	2 Q6DCK0	Q6DCK0 xenopus lae
42	36	63.2	465	1 DEGP_BUCBP	Q89ap5 buchnera ap
43	36	63.2	543	2 Q8JHF9	Q8JHF9 xenopus lae
44	36	63.2	543	2 Q7ZMU1	Q7ZMU1 xenopus lae
45	36	63.2	544	1 MRJ3_APIME	Q17060 apis mellif

ALIGNMENTS

RESULT 1

ID	FNBA_STRAU	STANDARD	PRT	1018 AA.
AC	P14738;			
DT	01-APR-1990 (Rel. 14, Created)			
DT	01-APR-1990 (Rel. 14, Last sequence update)			
DT	25-OCT-2004 (Rel. 45, Last annotation update)			
DE	Fibronectin-binding protein precursor (FNBP).			
GN	Name=fnba;			
OS	Staphylococcus aureus.			
OC	Bacteria; Firmicutes; Bacillales; Staphylococcus.			
OX	NCBI_TaxID=1280;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=NCTC 8325-4;			
RX	MEDLINE=8908998; PubMed=2521391;			
RA	Signaes C., Raucel G., Joenson K., Lindgren P.-E.,			
RA	Anantharamiah G.M., Hoeck M., Lindberg M.;			
RT	"Nucleotide sequence of the gene for a fibronectin-binding protein			
RT	from Staphylococcus aureus: use of this peptide sequence in the			
RT	synthesis of biologically active peptides."			
RL	Proc. Natl. Acad. Sci. U.S.A. 86:699-703(1989).			
CC	-1- FUNCTION: The ability of bacteria to bind fibronectin has been			
CC	proposed as a virulence factor enabling bacteria to colonize wound			
CC	tissues and blood clots. Binding of plasma fibronectin to the			
CC	bacterial surface might block adhesion receptors on S.aureus, thus			
CC	representing an important defense mechanism against tissue			
CC	invasion.			
CC	-1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by			
CC	an amide bond (Potential).			
CC	-----			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration			
CC	between the Swiss Institute of Bioinformatics and the EMBL Outstation -			
CC	the European Bioinformatics Institute. There are no restrictions on its			
CC	use by non-profit institutions as long as its content is in no way			
CC	modified and this statement is not removed. Usage by and for commercial			
CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/			
CC	or send an email to license@isb-sib.ch).			
CC	-----			
DR	EMBL; J04151; AAA26632.1; -			
DR	InterPro; IPR004237; Fn bind.			
DR	InterPro; IPR005877; Gpos_YsIRK.			
DR	InterPro; IPR001899; Gram_pos_anchor.			
DR	Pfam; PF02986; Fn_bind_1.			
DR	Pfam; PF00746; Gram_pos_anchor; 1.			
DR	Pfam; PF04650; YsIRK_signal; 1.			
DR	TIGRfam; TIGR01167; LPXTG_anchor; 1.			
DR	TIGRfam; TIGR01168; YsIRK_signal; 1.			
DR	TRAM; PSS0847; GRAM_POS_ANCHORING; 1.			
KW	Cell adhesion; Cell wall; Peptidoglycan-anchor; Repeat; Signal;			
KW	Virulence.			
FT	SIGNAL	1	36	
FT	CHAIN	37	985	Fibronectin-binding protein.
FT	PROPEP	986	1018	Removed by sortase (Potential).

```
FT REPEAT 545 574 B-1.
FT REPEAT 575 604 B-2.
FT DOMAIN 745 878 4 X approximate tandem repeats,
  fibronectin-binding domain.
FT REPEAT 745 782 D-1.
FT REPEAT 783 820 D-2.
FT REPEAT 821 859 D-3.
FT REPEAT 860 878 D-4 (incomplete).
FT DOMAIN 879 948 5 X tandem repeats, Pro-rich (WR).
FT REPEAT 879 892 WR 1.
FT REPEAT 893 906 WR 2.
FT REPEAT 907 920 WR 3.
FT REPEAT 921 934 WR 4.
FT REPEAT 935 948 WR 5.
FT SITE 982 985 LpXTG sorting signal (Potential).
FT MOD_RES 985 Pentaglycyl murein peptidoglycan amidated
  threonine (Potential).
SQ SEQUENCE 1018 AA; 111780 MW; 58175E0020E81F1F CRC64;

Query Match 100.0%; Score 57; DB 1; Length 1018;
Best Local Similarity 100.0%; Pred. No. 0.028;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HGONKNGNSF 10
  |||||
Db 782 HGONKNGNSF 791

RESULT 2
053682 PRELIMINARY; PRT; 940 AA.
ID 053682;
AC 053682;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Fibronectin binding protein B.
GN Name=fnbB;
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxId=1280;
CC [1]
  SEQUENCE FROM N.A.
  RC STRAIN=8325-4;
  RX MEDLINE=92111475; PubMed=1837266;
  RA Johnson K., Signas C., Muller H.P., Lindberg M.;
  RT "Two different genes encode fibronectin binding proteins in
  RT Staphylococcus aureus. The complete nucleotide sequence and
  RT characterization of the second gene.";
  RL Eur. J. Biochem. 202;1041-1048(1991).
  CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
  CC an amide bond (By similarity).
  DR EMBL: X62992; CAA44726.1; -.
  DR PIR: S19702; S19702.
  DR HSSP: O53653; 1N67.
  DR GO: GO:0009986; C:cell surface; IEA.
  DR GO: GO:0005618; C:cell wall (sensu Gram-positive Bacteria); IEA.
  DR GO: GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
  DR GO: GO:0016020; C:membrane; IEA.
  DR GO: GO:007155; P:cell adhesion; IEA.
  DR InterPro: IPR008966; Adhes_bact.
  DR InterPro: IPR004237; Fn_bind.
  DR InterPro: IPR005877; Gpos_YsIRK.
  DR InterPro: IPR001899; Gram_pos_anchor.
  DR Pfam: PF02986; Fn_bind_2.
  DR Pfam: PF00746; Gram_pos_anchor; 1.
  DR Pfam: PF04650; YsIRK_signal; 1.
  DR TIGRFAMs: TIGR01167; LpXTG_anchor; 1.
  DR TIGRFAMs: TIGR01168; YsIRK_signal; 1.
  DR PROSITE: PS50847; GRAM_POS_ANCHORING; 1.
  GN Cell wall, peptidoglycan-anchor.
  KW SEQUENCE 940 AA; 103555 MW; E35FBBCA907AE345 CRC64;
  OX NCBI_TaxId=282459;

Query Match 91.2%; Score 52; DB 2; Length 940;
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Best Local Similarity 90.0%; Pred. No. 0.25;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 HGONKNGNSF 10
  |||||
Db 718 HGONKNGNSF 727

RESULT 3
Q8NTU8 PRELIMINARY; PRT; 943 AA.
ID Q8NTU8;
AC Q8NTU8;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE FnbB protein.
GN Name=fnbB; OrderedLocustNames=MM2420;
OS Staphylococcus aureus (strain MM2).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxId=196620;
CC [1]
  SEQUENCE FROM N.A.
  RC STRAIN=MM2;
  RX MEDLINE=22040717; PubMed=12044378; DOI=10.1016/S0140-6736(02)08713-5;
  RA Baba T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Oguchi A.,
  RA Nagai Y., Iwama N., Asano K., Naimi T., Kuroda H., Cui L.,
  RA Yamamoto K., Hiramatsu K.;
  RT "Genome and virulence determinants of high virulence community-
  RT acquired MRSA.";
  RT Lancet 359;1819-1827(2002).
  CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
  CC an amide bond (By similarity).
  DR EMBL: AP004830; BAB96285.1; -.
  DR HSSP: O53653; 1N67.
  DR GO: GO:0009986; C:cell surface; IEA.
  DR GO: GO:0005618; C:cell wall; IEA.
  DR GO: GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
  DR GO: GO:0016020; C:membrane; IEA.
  DR GO: GO:007155; P:cell adhesion; IEA.
  DR InterPro: IPR008966; Adhes_bact.
  DR InterPro: IPR004237; Fn_bind.
  DR InterPro: IPR005877; Gpos_YsIRK.
  DR InterPro: IPR001899; Gram_pos_anchor.
  DR Pfam: PF02986; Fn_bind_1.
  DR Pfam: PF00746; Gram_pos_anchor; 1.
  DR Pfam: PF04650; YsIRK_signal; 1.
  DR TIGRFAMs: TIGR01167; LpXTG_anchor; 1.
  DR TIGRFAMs: TIGR01168; YsIRK_signal; 1.
  DR PROSITE: PS50847; GRAM_POS_ANCHORING; 1.
  KW Cell wall; Complete proteome; Peptidoglycan-anchor.
  KW SEQUENCE 943 AA; 104537 MW; DA8A5F31947E1B8A CRC64;

Query Match 91.2%; Score 52; DB 2; Length 943;
Best Local Similarity 90.0%; Pred. No. 0.25;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HGONKNGNSF 10
  |||||
Db 725 HGONKNGNSF 734

RESULT 4
Q6G6H4 PRELIMINARY; PRT; 957 AA.
ID Q6G6H4;
AC Q6G6H4;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Fibronectin-binding protein.
GN Name=fnbB; OrderedLocustNames=SAS2387;
OS Staphylococcus aureus (strain MSSA476).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxId=282459;
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RN      [1]
RP      SEQUENCE FROM N.A.
RX      Pubmed=15213324; DOI=10.1073/pnas.0402521101;
RA      Holden M.T.G., Fell B.J., Lindsay J.A., Peacock S.J., Day N.P.J.,
RA      Enright M.C., Foster T.J., Moore C.E., Hurst L., Actin R., Barron A.,
RA      Bason N., Bentley S.D., Chillingworth C., Chillingworth T.,
RA      Churcher C., Clark L., Cotton C., Cronin A., Duggett J., Dowd L.,
RA      Felwell T., Hance Z., Harris B., Hauser H., Holroyd S., Jagels K.,
RA      James K.D., Lennard N., Line A., Mayes R., Moule S., Mungall K.,
RA      Ormond D., Quail M.A., Rabinowitsch E., Rutherford K.M., Sanders M.,
RA      Sharp S., Simmonds M., Stevens K., Whitehead S., Barrett B.G.,
RA      Spratt B.G., Parkhill J.;
RT      "Complete genomes of two clinical Staphylococcus aureus strains:
RT      evidence for the rapid evolution of virulence and drug resistance.";
RL      Proc. Natl. Acad. Sci. U.S.A. 101:9786-9791(2004).
CC      -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC      an amide bond (By similarity).
DR      EMBL: BX571857; CAC44201.1; -
DR      GO: GO:0009986; C:cell surface; IEA.
DR      GO: GO:0005618; C:cell wall; IEA.
DR      GO: GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR      GO: GO:0016020; C:membrane; IEA.
DR      GO: GO:0007155; P:cell adhesion; IEA.
DR      InterPro: IPR008966; Adhes_Bact.
DR      InterPro: IPR004237; Fn_bind.
DR      InterPro: IPR005877; Gpos_YsIRK.
DR      InterPro: IPR001899; Gram_pos_anchor.
DR      Pfam: PF02986; Fn_bind_1.
DR      Pfam: PF00746; Gram_pos_anchor; 1.
DR      Pfam: PF04650; YsIRK_signal; 1.
DR      TIGRFAMs: TIGR01167; LPXTG_anchor; 1.
DR      TIGRFAMs: TIGR01168; YsIRK_signal; 1.
DR      PROSITE: PS50847; GRAM_POS_ANCHORING; 1.
KM      Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ      SEQUENCE 957 AA; 105980 MW; 28F6BAFFPFDJ3EAF CRC64;

Query Match          91.2%; Score 52; DB 2; Length 957;
Best Local Similarity 90.0%; Pred. No. 0.25;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 HGONKGNQSF 10
DB      725 HGONKGDQSF 734

RESULT 5
Q99RD3 PRELIMINARY; PRT; 961 AA.
AC      Q99RD3;
DT      01-JUN-2001 (TrEMBLrel. 17, Created)
DT      01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT      01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE      Fibronectin-binding protein homolog.
GN      Name=fnb3; OrderedLocustNames=SAV2502;
OS      Staphylococcus aureus (strain MU50 / ATCC 700699).
OC      Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX      NCBI_TaxID=158878;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN=MU50 / ATCC 700699;
RX      MEDLINE=21311952; Pubmed=11418146; DOI=10.1016/S0140-6736(00)04403-2;
RA      Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
RA      Cui L., Oguchi A., Aoki K.-I., Nagai Y., Iian J.-Q., Ito T.,
RA      Kanamori M., Matsunaru H., Maruyama A., Murakami H., Hosooyama A.,
RA      Mizutani U.I., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
RA      Sekimizu K., Hatakawa H., Kihara S., Goto S., Yabuzaki J.,
RA      Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
RA      Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
RT      "Whole genome sequencing of methicillin-resistant Staphylococcus
RT      aureus.";
RL      Lancet 357:1225-1240(2001).
CC      -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC      an amide bond (By similarity).

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DR      EMBL: AP003365; BAB58664.1; -
DR      PIR; G90053; G90053.
DR      HSSP; Q53653; 1N67.
DR      GO: GO:0009986; C:cell surface; IEA.
DR      GO: GO:0005618; C:cell wall; IEA.
DR      GO: GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR      GO: GO:0016020; C:membrane; IEA.
DR      GO: GO:0007155; P:cell adhesion; IEA.
DR      InterPro: IPR008966; Adhes_Bact.
DR      InterPro: IPR004237; Fn_bind.
DR      InterPro: IPR005877; Gpos_YsIRK.
DR      InterPro: IPR001899; Gram_pos_anchor.
DR      Pfam: PF02986; Fn_bind_1.
DR      Pfam: PF00746; Gram_pos_anchor; 1.
DR      Pfam: PF04650; YsIRK_signal; 1.
DR      TIGRFAMs: TIGR01167; LPXTG_anchor; 1.
DR      TIGRFAMs: TIGR01168; YsIRK_signal; 1.
DR      PROSITE: PS50847; GRAM_POS_ANCHORING; 1.
KM      Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ      SEQUENCE 961 AA; 106010 MW; 364940F884E8A101 CRC64;

Query Match          91.2%; Score 52; DB 2; Length 961;
Best Local Similarity 90.0%; Pred. No. 0.26;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 HGONKGNQSF 10
DB      729 HGONKGNQSF 738

RESULT 6
Q7A3J8 PRELIMINARY; PRT; 961 AA.
AC      Q7A3J8;
DT      05-JUL-2004 (TrEMBLrel. 27, Created)
DT      05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT      05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE      FndB protein.
GN      Name=fndB; OrderedLocustNames=SA2290;
OS      Staphylococcus aureus (strain N315).
OC      Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX      NCBI_TaxID=158879;
RN      [1]
RP      SEQUENCE FROM N.A.
RX      MEDLINE=21311952; Pubmed=11418146; DOI=10.1016/S0140-6736(00)04403-2;
RA      Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
RA      Cui L., Oguchi A., Aoki K.-I., Nagai Y., Iian J.-Q., Ito T.,
RA      Kanamori M., Matsunaru H., Maruyama A., Murakami H., Hosooyama A.,
RA      Mizutani U.I., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
RA      Sekimizu K., Hatakawa H., Kihara S., Goto S., Yabuzaki J.,
RA      Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
RA      Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
RT      "Whole genome sequencing of methicillin-resistant Staphylococcus
RT      aureus.";
RL      Lancet 357:1225-1240(2001).
CC      -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC      an amide bond (By similarity).
DR      EMBL: AP003137; BAB43593.1; -
DR      GO: GO:0009986; C:cell surface; IEA.
DR      GO: GO:0005618; C:cell wall; IEA.
DR      GO: GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR      GO: GO:0016020; C:membrane; IEA.
DR      GO: GO:0007155; P:cell adhesion; IEA.
DR      InterPro: IPR008966; Adhes_Bact.
DR      InterPro: IPR004237; Fn_bind.
DR      InterPro: IPR005877; Gpos_YsIRK.
DR      InterPro: IPR001899; Gram_pos_anchor.
DR      Pfam: PF02986; Fn_bind_1.
DR      Pfam: PF00746; Gram_pos_anchor; 1.
DR      Pfam: PF04650; YsIRK_signal; 1.
DR      TIGRFAMs: TIGR01167; LPXTG_anchor; 1.
DR      TIGRFAMs: TIGR01168; YsIRK_signal; 1.
DR      PROSITE: PS50847; GRAM_POS_ANCHORING; 1.

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KW Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ SEQUENCE 961 AA; 106010 MW; 364940F868EA101 CRC64;

Query Match          91.2%; Score 52; DB 2; Length 961;
Best Local Similarity 90.0%; Pred. No. 0.26;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 HGONKGNOSF 10
   |||||
Db 729 HGONKGNOSF 738

RESULT 7
ID Q99RD2 PRELIMINARY; PRT; 1038 AA.
AC Q99RD2;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Fibronectin-binding protein homolog.
GN Name=fnb; OrderedlocusNames=SAV2503;
OS Staphylococcus aureus (strain Mu50 / ATCC 700699).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=158878;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=21111952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2;
RX Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Lian J.-Q., Ito T.,
RA Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosooyama A.,
RA Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
RA Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
RA Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
RA Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
RT "Whole genome sequencing of methicillin-resistant Staphylococcus
RT aureus.";
RL Lancet 357:1225-1240(2001).
CC -!- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC an amide bond (By similarity).
EMBL; AP003365; BAB58665.1; -.
DR GO; GO:0009986; C:cell surface; IEA.
DR GO; GO:0005618; C:cell wall; IEA.
DR GO; GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:007155; P:cell adhesion; IEA.
DR InterPro; IPR008966; Adhes_bact.
DR InterPro; IPR004237; Fn_bind.
DR InterPro; IPR005877; Gpos_YsIRK.
DR InterPro; IPR001899; Gram_pos_anchor.
DR Pfam; PF02986; Fn_bind; 1.
DR Pfam; PF00746; Gram_pos_anchor; 1.
DR Pfam; PF04650; YsIRK_signal; 1.
DR TIGRFAMs; TIGR01167; LpxTG_anchor; 1.
DR TIGRFAMs; TIGR01168; YsIRK_signal; 1.
DR PROSITE; PS50847; GRAM_POS_ANCHORING; 1.
KW Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ SEQUENCE 1038 AA; 113618 MW; 666B6BF2BFBEB12 CRC64;

Query Match          91.2%; Score 52; DB 2; Length 1038;
Best Local Similarity 90.0%; Pred. No. 0.28;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HGONKGNOSF 10
   |||||
Db 778 HGONKGNOSF 787

RESULT 8
ID Q7A3J7 PRELIMINARY; PRT; 1038 AA.
AC Q7A3J7;

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DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Fnb protein.
GN Name=fnb; OrderedlocusNames=SA2291;
OS Staphylococcus aureus (strain N315).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=158879;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=21111952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2;
RX Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Lian J.-Q., Ito T.,
RA Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosooyama A.,
RA Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
RA Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
RA Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
RA Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
RT "Whole genome sequencing of methicillin-resistant Staphylococcus
RT aureus.";
RL Lancet 357:1225-1240(2001).
CC -!- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC an amide bond (By similarity).
EMBL; AP003137; BAB43594.1; -.
DR GO; GO:0009986; C:cell surface; IEA.
DR GO; GO:0005618; C:cell wall; IEA.
DR GO; GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:007155; P:cell adhesion; IEA.
DR InterPro; IPR008966; Adhes_bact.
DR InterPro; IPR004237; Fn_bind.
DR InterPro; IPR005877; Gpos_YsIRK.
DR InterPro; IPR001899; Gram_pos_anchor.
DR Pfam; PF02986; Fn_bind; 1.
DR Pfam; PF00746; Gram_pos_anchor; 1.
DR Pfam; PF04650; YsIRK_signal; 1.
DR TIGRFAMs; TIGR01167; LpxTG_anchor; 1.
DR TIGRFAMs; TIGR01168; YsIRK_signal; 1.
DR PROSITE; PS50847; GRAM_POS_ANCHORING; 1.
KW Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ SEQUENCE 1038 AA; 113618 MW; 666B6BF2BFBEB12 CRC64;

Query Match          91.2%; Score 52; DB 2; Length 1038;
Best Local Similarity 90.0%; Pred. No. 0.28;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HGONKGNOSF 10
   |||||
Db 778 HGONKGNOSF 787

RESULT 9
ID Q9AEP9 PRELIMINARY; PRT; 152 AA.
AC Q9AEP9;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Fibronectin-binding protein (Fragment).
GN Name=fnb;
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1280;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CMRSA-1;
RX MEDLINE=21246681; PubMed=11349044;
RX DOI=10.1128/IAI.69.6.3791-3799.2001;
RA Rice K., Huesca M., Vaz D., McGavin M.J.;
RT "Variance in fibronectin binding and fnb locus polymorphisms in
RT Staphylococcus aureus: identification of antigenic variation in a
RT fibronectin binding protein adhesin of the epidemic CMRSA-1 strain of
RT methicillin-resistant S. aureus.";

```

RL Infect. Immun. 69:3791-3799(2001).
 DR EMBL; AY029184; AAK31588.1; -.
 FT NON TER 1
 DT 01-OCT-2002 (TEMBLrel. 22, last sequence update)
 SQ SEQUENCE 152 AA; 17193 MW; CFA3913C2B11C025 CRC64;

Query Match 77.2%; Score 44; DB 2; Length 152;
 Best Local Similarity 88.9%; Pred. No. 1.3;
 Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 GONKGNQSF 10
 DB 38 GONKGNQSF 46

RESULT 10

Q6GDU5 PRELIMINARY; PRT; 965 AA.
 AC 06GDU5;
 DT 05-JUL-2004 (TEMBLrel. 27, Created)
 DT 05-JUL-2004 (TEMBLrel. 27, last sequence update)
 DT 05-JUL-2004 (TEMBLrel. 27, last annotation update)
 DE Fibronectin-binding protein.
 GN Name=fndA; OrderedLocNames=SA2580;
 OS Staphylococcus aureus (strain MRSA52).
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 OX NCBI_TaxID=282458;
 RN [1]

RP SEQUENCE FROM N.A.
 RA PubMed=15213324; DOI=10.1073/pnas.0402521101;
 RA Holden M.T.G., Fell E.J., Lindsay J.A., Peacock S.J., Day N.P.J.,
 RA Barltch M.C., Foster T.J., Moore C.E., Hurst L., Atkin R., Barron A.,
 RA Bason N., Bentley S.D., Chillingworth C., Chillingworth T.,
 RA Churcher C., Clark L., Court C., Cronin A., Doggett J., Dowd L.,
 RA Felwell T., Hance Z., Harris B., Hauser H., Holtroyd S., Jørgels K.,
 RA James K.D., Lennard N., Line A., Mayes R., Moule S., Mungall K.,
 RA Ormond D., Quail M.A., Rabinowitsch E., Rutherford K.M., Sanders M.,
 RA Sharp S., Simmonds M., Stevens K., Whitehead S., Barrett B.G.,
 RA Spratt B.G., Parkhill J.;
 RT "Complete genomes of two clinical Staphylococcus aureus strains:
 RT evidence for the rapid evolution of virulence and drug resistance.";
 RT Proc. Natl. Acad. Sci. U.S.A. 101:9786-9791(2004).
 CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
 CC an amide bond (By similarity).

DR EMBL; BX571856; CAG41560.1; -.
 DR GO; GO:0009986; C:cell surface; IEA.
 DR GO; GO:0009275; C:cell wall (senu Gram-positive Bacteria); IEA.
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0007155; P:cell adhesion; IEA.
 DR InterPro: IPR008966; Adhes bact.
 DR InterPro: IPR004237; Fn bind.
 DR InterPro: IPR005877; Gpos_YsIRK.
 DR InterPro: IPR001899; Gram_pos_anchor.
 DR Pfam; PF02986; Fn_bind. 1.
 DR Pfam; PF00746; Gram_pos_anchor. 1.
 DR Pfam; PF04650; YsIRK signal. 1.
 DR TIGRfams; TIGR01167; LPTXG anchor. 1.
 DR TIGRfams; TIGR01168; YsIRK signal. 1.
 DR PROSITE; PS50847; GRAM_POS_ANCHORING. 1.
 DR C011 wall; Complete proteome; Peptidoglycan-anchor.
 SQ SEQUENCE 965 AA; 105691 MW; 2982E132164D0551 CRC64;

Query Match 77.2%; Score 44; DB 2; Length 965;
 Best Local Similarity 88.9%; Pred. No. 10;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GONKGNQSF 10
 DB 748 GONKGNQSF 756

RESULT 11

Q8NUT7

ID Q8NUT7 PRELIMINARY; PRT; 1015 AA.
 AC Q8NUT7;
 DT 01-OCT-2002 (TEMBLrel. 22, Created)
 DT 01-OCT-2002 (TEMBLrel. 22, last sequence update)
 DT 01-OCT-2003 (TEMBLrel. 25, last annotation update)
 DE Fnb protein.
 GN Name=fnb; OrderedLocNames=MM2421;
 OS Staphylococcus aureus (strain MM2).
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 OX NCBI_TaxID=196620;
 RN [1]

RP SEQUENCE FROM N.A.
 RA STRAIN=MM2;
 RA MEDLINE=22040717; PubMed=12044378; DOI=10.1016/S0140-6736(02)08713-5;
 RA Baba T., Takeuchi F., Kuroda M., Tuzawa H., Aoki K.-I., Oguchi A.,
 RA Nagai Y., Iwama N., Asano K., Naim T., Kuroda H., Cui L.,
 RA Yamamoto K., Hiramoto K.;
 RT "Genome and virulence determinants of high virulence community-
 RT acquired MRSA";
 RT Lancet 359:1819-1827(2002).
 CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
 CC an amide bond (By similarity).

DR EMBL; AP004830; BAB96286.1; -.
 DR GO; GO:0009986; C:cell surface; IEA.
 DR GO; GO:0005618; C:cell wall; IEA.
 DR GO; GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0007155; P:cell adhesion; IEA.
 DR InterPro: IPR008966; Adhes bact.
 DR InterPro: IPR004237; Fn bind.
 DR InterPro: IPR005877; Gpos_YsIRK.
 DR InterPro: IPR001899; Gram_pos_anchor.
 DR Pfam; PF02986; Fn_bind. 1.
 DR Pfam; PF00746; Gram_pos_anchor. 1.
 DR Pfam; PF04650; YsIRK signal. 1.
 DR TIGRfams; TIGR01167; LPTXG anchor. 1.
 DR TIGRfams; TIGR01168; YsIRK signal. 1.
 DR PROSITE; PS50847; GRAM_POS_ANCHORING. 1.
 DR C011 wall; Complete proteome; Peptidoglycan-anchor.
 SQ SEQUENCE 1015 AA; 111145 MW; D0F9281BB64D4402 CRC64;

Query Match 77.2%; Score 44; DB 2; Length 1015;
 Best Local Similarity 88.9%; Pred. No. 11;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GONKGNQSF 10
 DB 746 GONKGNQSF 754

RESULT 12

Q6G6H3 PRELIMINARY; PRT; 1015 AA.

AC 06G6H3;
 DT 05-JUL-2004 (TEMBLrel. 27, Created)
 DT 05-JUL-2004 (TEMBLrel. 27, last sequence update)
 DT 05-JUL-2004 (TEMBLrel. 27, last annotation update)
 DE Fibronectin-binding protein.
 GN Name=fndA; OrderedLocNames=SA2388;
 OS Staphylococcus aureus (strain MSSA476).
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 OX NCBI_TaxID=282459;
 RN [1]

RP SEQUENCE FROM N.A.
 RA PubMed=15213324; DOI=10.1073/pnas.0402521101;
 RA Holden M.T.G., Fell E.J., Lindsay J.A., Peacock S.J., Day N.P.J.,
 RA Barltch M.C., Foster T.J., Moore C.E., Hurst L., Atkin R., Barron A.,
 RA Bason N., Bentley S.D., Chillingworth C., Chillingworth T.,
 RA Churcher C., Clark L., Court C., Cronin A., Doggett J., Dowd L.,
 RA Felwell T., Hance Z., Harris B., Hauser H., Holtroyd S., Jørgels K.,
 RA James K.D., Lennard N., Line A., Mayes R., Moule S., Mungall K.,
 RA Ormond D., Quail M.A., Rabinowitsch E., Rutherford K.M., Sanders M.,
 RA Sharp S., Simmonds M., Stevens K., Whitehead S., Barrett B.G.,

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RA Spratt B.G., Parkhill J.;
RT "Complete genomes of two clinical Staphylococcus aureus strains:
RL evidence for the rapid evolution of virulence and drug resistance.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:9786-9791(2004).
CC -1-SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC an amide bond (By similarity).
DR EMBL: BX571857; CAG44202.1; -.
DR GO: GO:0009986; C:cell surface; IEA.
DR GO: GO:0005618; C:cell wall; IEA.
DR GO: GO:0003275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO: GO:0016020; C:membrane; IEA.
DR GO: GO:0007155; P:cell adhesion; IEA.
DR InterPro: IPR008966; Adhes_bact.
DR InterPro: IPR004237; Fn_bind.
DR InterPro: IPR005877; Gpof_Ysirk.
DR InterPro: IPR001899; Gram_pos_anchor.
DR Pfam: PF02986; Fn_bind; 1.
DR Pfam: PF00746; Gram_pos_anchor; 1.
DR Pfam: PF04650; Ysirk_signal; 1.
DR TIGRFAMs: TIGR01167; Lpxng_anchor; 1.
DR TIGRFAMs: TIGR01168; Ysirk_signal; 1.
DR PROSITE: PS00847; GRAM_POS_ANCHORING; 1.
KW Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ SEQUENCE 1015 AA; 11145 MW; D0F9281BB64D4D2 CRC64;

Query Match 77.2%; Score 44; DB 2; Length 1015;
Best Local Similarity 88.9%; Pred. No. 11;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GONKGNQSF 10
DB 746 GONKGNQSF 754

RESULT 13
06A756 PRELIMINARY; PRT; 654 AA.
AC 06A756;
DT 25-OCT-2004 (TREMBlrel. 28, Created)
DT 25-OCT-2004 (TREMBlrel. 28, Last sequence update)
DT 25-OCT-2004 (TREMBlrel. 28, Last annotation update)
DE Ferrous iron transport protein B.
OS OrderedLocustNames=PPA1677;
OC Proionibacterium acnes.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Proionibacteriaceae; Proionibacteriaceae; Proionibacterium.
OX NCBI_TaxID=1747;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=KPA171202 / DSM 16379;
RX PubMed=15286373; DOI=10.1126/science.1100330;
RA Brueggemann H., Henne A., Hostet F., Liseegang H., Wierer A.,
RA Strittmatter A., Hufner S., Duerre P., Gottschalk G.;
RT "The complete genome sequence of Proionibacterium acnes, a commensal
RT of human skin.";
RL Science 305:671-673(2004).
DR EMBL: AE017283; AAT83409.1; -.
DR GO: GO:0016020; C:membrane; IEA.
DR GO: GO:0015093; F:ferrous iron transporter activity; IEA.
DR GO: GO:0005525; F:GTP binding; IEA.
DR GO: GO:0003700; F:transcription factor activity; IEA.
DR GO: GO:0015684; P:ferrous iron transport; IEA.
DR GO: GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro: IPR003373; Feob.
DR InterPro: IPR006073; GTP_OBG.
DR InterPro: IPR002197; HTH_Fib.
DR InterPro: IPR002917; MMR_HSR1.
DR Pfam: PF02421; Feob_N_1_1.
DR Pfam: PF01926; MMR_HSR1; 1.
DR PRINTS: PR00326; GTP_OBG.
DR PRINTS: PRO1590; HTH_FIS.
DR TIGRFAMs: TIGR00437; feob; 1.
KW Complete proteome.

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SQ SEQUENCE 654 AA; 70124 MW; 03B3E800913B0A5A CRC64;

Query Match 71.9%; Score 41; DB 2; Length 654;
Best Local Similarity 70.0%; Pred. No. 26;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 HGONKGNQSF 10
DB 584 HGONKGNQSF 593

RESULT 14
Q7MKL1 PRELIMINARY; PRT; 285 AA.
AC 07MKL1;
DT 01-MAR-2004 (TREMBlrel. 26, Created)
DT 01-MAR-2004 (TREMBlrel. 26, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE Probable transmembrane protein.
OS OrderedLocustNames=VVJ772;
OS Vibrio vulnificus (strain YJ016).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
OC Vibrionaceae; Vibrio.
OX NCBI_TaxID=196600;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=14656965; DOI=10.1101/gr.1295503;
RA Chen C.-Y., Wu K.-M., Chang Y.-C., Chang C.-H., Tsai H.-C.,
RA Liao T.-L., Liu Y.-M., Chen H.-J., Shen A.B.-T., Li J.-C., Su T.-L.,
RA Shao C.-P., Lee C.-T., Hor L.-I., Tsai S.-F.;
RT "Comparative genome analysis of Vibrio vulnificus, a marine
RT pathogen.";
RL Genome Res. 13:2577-2587(2003).
DR EMBL: AP005337; BAC94536.1; -.
DR GO: GO:0016021; C:integral to membrane; IEA.
DR GO: GO:0003677; F:DNA binding; IEA.
DR GO: GO:0003917; F:DNA topoisomerase type I activity; IEA.
DR GO: GO:0006265; P:DNA topological change; IEA.
DR GO: GO:0006268; P:DNA unwinding; IEA.
DR InterPro: IPR000380; DNA_topoisomerase.
DR InterPro: IPR007560; Mtr_cat.
DR Pfam: PF04471; Mtr_cat; 1.
DR Pfam: PF01396; zfc-C4_Topoisom; 1.
KW Complete proteome; Transmembrane.
SQ SEQUENCE 285 AA; 32103 MW; 051F9525370AC978 CRC64;

Query Match 70.2%; Score 40; DB 2; Length 285;
Best Local Similarity 77.8%; Pred. No. 16;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 GONKGNQSF 10
DB 260 GONKGNQSF 268

RESULT 15
Q6BGJ7 PRELIMINARY; PRT; 500 AA.
AC 06BGJ7;
DT 25-OCT-2004 (TREMBlrel. 28, Created)
DT 25-OCT-2004 (TREMBlrel. 28, Last sequence update)
DT 25-OCT-2004 (TREMBlrel. 28, Last annotation update)
DE Hypothetical protein.
OS OrderedLocustNames=PMB_06c;
OS Paramecium tetraurelia.
OS Eukaryota; Alveolata; Ciliophora; Oligohymenophorea; Peniculida;
OC Paramecium.
OX NCBI_TaxID=5888;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=stock d4-2;
RX PubMed=15296759; DOI=10.1016/j.cub.2004.07.029;
RA Zagulski M., Nowak J.K., Le Mouel A., Nowacki M., Migdalski A.,

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RA Gromadka R., Noel B., Blanc I., Deesen P., Wincker P., Keller A.M.,
RA Cohen J., Meyer B., Sperling L.;
RT "High Coding Density on the largest Paramecium tetraurelia Somatic
RT Chromosome.";
RL Curr. Biol. 14:1397-1404(2004).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Stock d4-2;
RA Nowak J.K., Migdalski A., Gromadka R., Zagulski M.;
RT "Paramecium megabase sequencing project.";
RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL, CR548612, CAH03203.1; -.
KW Hypothetical protein.
SQ SEQUENCE 500 AA; 56364 MW; DB4D7F90C86E79F0 CRC64;

Query Match 69.3%; Score 39.5; DB 2; Length 500;
Best Local Similarity 81.8%; Pred. No. 38;
Matches 9; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

Qy 1 HGON-KGNQSF 10
|||
Db 472 HGANKKGNQSF 482

Search completed: October 22, 2005, 08:00:53
Job time : 56.85 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 25, 2005, 20:21:18 ; Search time 63.2 Seconds
(without alignments)
61.196 Million cell updates/sec

Title: US-10-731-238-82

Perfect score: 53

Sequence: 1 ONKGNQSFEE 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:*
1: geneseqp1808:*
2: geneseqp1908:*
3: geneseqp2008:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	53	100.0	10	2 AAW65738	AAW65738 Fibronect
2	53	100.0	36	2 AAW65714	AAW65714 Fibronect
3	53	100.0	36	2 AAW65715	AAW65715 Peptide #
4	53	100.0	38	1 AAP80661	AAP80661 Protein w
5	53	100.0	38	1 AAP82117	AAP82117 Fibronect
6	53	100.0	38	2 AAW65664	AAW65664 Fibronect
7	53	100.0	38	2 AAW65705	AAW65705 Fibronect
8	53	100.0	38	2 AAW65663	AAW65663 Fibronect
9	53	100.0	38	2 AAW65704	AAW65704 Fibronect
10	53	100.0	134	2 AAY29087	AAY29087 S. aureus
11	53	100.0	139	2 AAW31556	AAW31556 Fibronect
12	53	100.0	1018	1 AAP82115	AAP82115 Fibronect
13	53	100.0	1018	4 AAU37245	AAU37245 Staphyloc
14	53	100.0	1018	4 AAU34301	AAU34301 Staphyloc
15	53	100.0	1018	6 ABJ18922	ABJ18922 Pathogen
16	53	100.0	1018	6 ABM72537	ABM72537 Staphyloc
17	53	100.0	1027	2 AAW89806	AAW89806 Staphyloc
18	48	90.6	10	2 AAW65719	AAW65719 Fibronect
19	48	90.6	30	4 AAB82164	AAB82164 Peptide f
20	48	90.6	30	7 ADC69221	ADC69221 Fibronect
21	48	90.6	31	7 ADC69222	ADC69222 Fibronect
22	48	90.6	38	1 AAP80660	AAP80660 Protein w
23	48	90.6	38	1 AAP82116	AAP82116 Fibronect
24	48	90.6	38	2 AAW65695	AAW65695 Fibronect
25	48	90.6	38	2 AAW65662	AAW65662 Fibronect

25	48	90.6	38	2 AAW65703	AAW65703 Fibronect
27	48	90.6	38	2 AAW65696	AAW65696 Fibronect
28	48	90.6	38	2 AAW65697	AAW65697 Fibronect
29	48	90.6	38	2 AAW65694	AAW65694 Fibronect
30	48	90.6	38	2 AAW65699	AAW65699 Fibronect
31	48	90.6	38	2 AAW65661	AAW65661 Fibronect
32	48	90.6	38	2 AAW65698	AAW65698 Fibronect
33	48	90.6	39	2 AAW65712	AAW65712 Fibronect
34	48	90.6	39	2 AAW65713	AAW65713 Fibronect
35	48	90.6	77	2 AAW88749	AAW88749 S. aureus
36	48	90.6	113	2 AAR90937	AAR90937 D3D4 poly
37	48	90.6	130	2 AAR58806	AAR58806 Fibronect
38	48	90.6	130	2 AAR58807	AAR58807 Fibronect
39	48	90.6	130	2 AAR91202	AAR91202 D1-D4 fib
40	48	90.6	130	2 AAR91201	AAR91201 D1-D4 fib
41	48	90.6	134	2 AAY29089	AAY29089 Cloned fl
42	48	90.6	134	2 AAY29088	AAY29088 S. aureus
43	48	90.6	162	2 AAR90942	AAR90942 D3D4 poly
44	48	90.6	164	2 AAR90938	AAR90938 D3D4 poly
45	48	90.6	174	2 AAR58808	AAR58808 Fbp fibro

ALIGNMENTS

RESULT 1
ID AAW65738 standard; peptide, 10 AA.
XX
AC AAW65738;
XX
DT 16-OCT-1998 (first entry)
XX
DE Fibronectin binding protein-derived peptide #82.
XX
DE microbial surface components recognising adhesive matrix molecule;
KM MRCRAM; fibronectin; fibronectin-binding protein; antibody; epitope;
KM antibiotic; bacterial infection; antibiotic-resistant strain.
XX
XX Synthetic.
OS Staphylococcus aureus.
XX
PN W09831389-A2.
XX
PD 23-JUL-1998.
XX
PF 21-JAN-1998; 98WO-US001222.
XX
PR 21-JAN-1997; 97US-0036139P.
XX
XX (TEXA) UNIV TEXAS A & M SYSTEM.
XX
PI Hoeoek M; Patti JM, House-Pompeo KL, Speziale P, Joh D;
PI McGavin MJ;
XX
DR WPI; 1998-413816/35.
XX
PT Antibody that binds to fibronectin-binding protein, preventing its
PT binding to fibronectin - used to treat or prevent bacterial infection,
PT especially by Staphylococci and Streptococci.
XX
XX Example 9, Page 110; 201p; English.
PS
XX The invention relates to antibodies that bind to a fibronectin-binding
XX domain of a fibronectin-binding protein, and inhibit binding of the
XX protein to fibronectin. Also claimed are: (1) isolated peptides of a
XX fibronectin-binding protein that do not bind to fibronectin; (2) fusion
XX protein containing at least one peptide of a fibronectin-binding protein
XX linked to a second amino acid sequence; (3) nucleic acid encoding the
XX isolated peptide of (1). Antibodies, the isolated peptides of (1) and the
XX nucleic acids are all useful for immunisation (active or passive) and (by
XX inhibiting binding of bacteria to fibronectin) for preventing or treating
XX infection in humans or other animals, particularly by staphylococci or

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CC streptococci, e.g. meningitis, otitis media, pneumonia, endocarditis,
CC mastitis in cattle, abortion in horses and many others. Since the
CC antibodies block binding of bacteria, they should be effective against
CC antibiotic-resistant strains, and may replace antibiotic therapy or
CC increase its effectiveness. Sequences AAW65719-41 and AAW65658 represent
CC peptides which were synthesised to span the D1 motif and the N-terminal
CC 18 amino acids of D2, with each peptide overlapping by eight amino acids
CC with the previous sequence
XX
SQ Sequence 10 AA;

Query Match          100.0%; Score 53; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0016;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ONKGNQSFEE 10
   |||||
   1 ONKGNQSFEE 10

Db

RESULT 2
AAW65714
ID AAW65714 standard; peptide; 36 AA.
XX
AC AAW65714;
XX
DT 16-OCT-1998 (first entry)
XX
DE Fibronectin binding protein-derived peptide #58.
XX
KM microbial surface components recognising adhesive matrix molecule;
KM MSCRAMM; fibronectin; fibronectin-binding protein; antibody; epitope;
KM antibiotic; bacterial infection; antibiotic-resistant strain.
XX
OS Synthetic.
OS Staphylococcus aureus.
XX
PN WO9831389-A2.
XX
PD 23-JUL-1998.
XX
PF 21-JAN-1998; 98WO-US001222.
XX
PR 21-JAN-1997; 97US-0036139P.
XX
PA (TEXA ) UNIV TEXAS A & M SYSTEM.
XX
PI Hoeoek M, Patti JM, House-Pompeo KL, Speziale P, Joh D;
PI McGavin MJ;
XX
DR WPI; 1998-413816/35.
XX
PT Antibody that binds to fibronectin-binding protein, preventing its
PT binding to fibronectin - used to treat or prevent bacterial infection,
PT especially by Staphylococci and Streptococci.
XX
PS Example 8; Page 104; 201pp; English.
XX
XX The invention relates to antibodies that bind to a fibronectin-binding
XX domain of a fibronectin-binding protein, and inhibit binding of the
XX protein to fibronectin. Also claimed are: (1) isolated peptides of a
XX fibronectin-binding protein that do not bind to fibronectin; (2) fusion
XX protein containing at least one peptide of a fibronectin-binding protein
XX linked to a second amino acid sequence; (3) nucleic acid encoding the
XX isolated peptide of (1). Antibodies, the isolated peptides of (1) and the
XX nucleic acids are all useful for immunisation (active or passive) and (by
XX inhibiting binding of bacteria to fibronectin) for preventing or treating
XX infection in humans or other animals, particularly by staphylococci or
XX streptococci, e.g. meningitis, otitis media, pneumonia, endocarditis,
XX mastitis in cattle, abortion in horses and many others. Since the
XX antibodies block binding of bacteria, they should be effective against
XX antibiotic-resistant strains, and may replace antibiotic therapy or
XX increase its effectiveness. The present sequence is shown in the
```

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CC specification
XX
SQ Sequence 36 AA;

Query Match          100.0%; Score 53; DB 2; Length 36;
Best Local Similarity 100.0%; Pred. No. 0.0067;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ONKGNQSFEE 10
   |||||
   1 ONKGNQSFEE 10

Db

RESULT 3
AAW65715
ID AAW65715 standard; peptide; 36 AA.
XX
AC AAW65715;
XX
DT 27-AUG-2003 (revised)
DT 16-OCT-1998 (first entry)
XX
DE Peptide #59.
XX
KM microbial surface components recognising adhesive matrix molecule;
KM MSCRAMM; fibronectin; fibronectin-binding protein; antibody; epitope;
KM antibiotic; bacterial infection; antibiotic-resistant strain.
XX
OS Synthetic.
OS Staphylococcus aureus.
XX
PN WO9831389-A2.
XX
PD 23-JUL-1998.
XX
PF 21-JAN-1998; 98WO-US001222.
XX
PR 21-JAN-1997; 97US-0036139P.
XX
PA (TEXA ) UNIV TEXAS A & M SYSTEM.
XX
PI Hoeoek M, Patti JM, House-Pompeo KL, Speziale P, Joh D;
PI McGavin MJ;
XX
DR WPI; 1998-413816/35.
XX
PT Antibody that binds to fibronectin-binding protein, preventing its
PT binding to fibronectin - used to treat or prevent bacterial infection,
PT especially by Staphylococci and Streptococci.
XX
PS Disclosure; Page 160; 201pp; English.
XX
XX The invention relates to antibodies that bind to a fibronectin-binding
XX domain of a fibronectin-binding protein, and inhibit binding of the
XX protein to fibronectin. Also claimed are: (1) isolated peptides of a
XX fibronectin-binding protein that do not bind to fibronectin; (2) fusion
XX protein containing at least one peptide of a fibronectin-binding protein
XX linked to a second amino acid sequence; (3) nucleic acid encoding the
XX isolated peptide of (1). Antibodies, the isolated peptides of (1) and the
XX nucleic acids are all useful for immunisation (active or passive) and (by
XX inhibiting binding of bacteria to fibronectin) for preventing or treating
XX infection in humans or other animals, particularly by staphylococci or
XX streptococci, e.g. meningitis, otitis media, pneumonia, endocarditis,
XX mastitis in cattle, abortion in horses and many others. Since the
XX antibodies block binding of bacteria, they should be effective against
XX antibiotic-resistant strains, and may replace antibiotic therapy or
XX increase its effectiveness. The present sequence is shown in the
XX specification. (Updated on 27-AUG-2003 to correct OS field.)
XX
SQ Sequence 36 AA;

Query Match          100.0%; Score 53; DB 2; Length 36;
Best Local Similarity 100.0%; Pred. No. 0.0067;
```

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QNKGNSFEE 10
 |||||
 DB 1 QNKGNSFEE 10

RESULT 4

AA080661 standard; protein; 38 AA.

AA080661;

25-MAR-2003 (revised)
 07-OCT-1990 (first entry)

Protein with fibronectin binding ability.

Hybrid DNA molecule; fibronectin binding; mastitis; ruminants;
 wound infection.

Staphylococcus aureus.

EP294349-A.

07-DEC-1988.

30-MAY-1988; 88EP-00850188.

01-JUN-1987; 87SE-00002272.

(ALFA) ALFA LAVAL AGRIC INT AB.

Lindberg MK, Signas LC, Madstrom TM, Froman G;

WPI; 1988-347978/49.

N-PSDB; AAN81098.

Hybrid DNA encoding Staphylococcus aureus fibronectin binding protein -
 useful for immunisation and topical application to prevent staphylococcal
 infections.

Claim 11; Page 12; 23pp; English.

The peptide has fibronectin binding ability. It is useful for immunising
 ruminants against staphylococcal mastitis, pref. when used at 0.5-5
 micrograms/kg, using 3 doses given at 1-3 week intervals; for topical
 application to prevent wound infection, using an isotonic saline soln. of
 concn. 25-250 micrograms/ml; and, when immobilised on a carrier, for
 diagnosing staphylococcal infections. (Updated on 25-MAR-2003 to correct
 PF field.) (Updated on 25-MAR-2003 to correct PA field.)

Sequence 38 AA:

Query Match 100.0%; Score 53; DB 1; Length 38;
 Best Local Similarity 100.0%; Pred. No. 0.0071;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QNKGNSFEE 10
 |||||
 DB 2 QNKGNSFEE 11

RESULT 5

AA082117 standard; protein; 38 AA.

AA082117;

25-MAR-2003 (revised)

05-JAN-1990 (first entry)

Fibronectin binding protein.

Fibronectin binding protein; S.aureus; immunisation; mastitis; ruminants;
 wound infection; diagnosis.

Staphylococcus aureus.

EP294349-A.

07-DEC-1988.

30-MAY-1988; 88EP-00850188.

01-JUN-1987; 87SE-00002272.

(ALFA) ALFA LAVAL AGRIC INT AB.

Lindberg MK, Signas LC, Madstrom TM, Froman G;

WPI; 1988-347978/49.

N-PSDB; AAN82055.

Hybrid DNA encoding Staphylococcus aureus fibronectin binding protein -
 useful for immunisation and topical application to prevent staphylococcal
 infections.

Claim 11; Page 12; 23pp; English.

The S.aureus fibronectin binding protein may be included in a hybrid
 protein. The protein may be used to immunise ruminants against
 staphylococcal mastitis, pref. when given at 0.5-5 microg/kg, using 3
 doses at 1-3 week intervals; and for topical applicn. to prevent wound
 infection, pref. using isotonic saline soln. of concn. 25-250 microg/mg.
 The DNA encoding the binding protein and the hybrid protein may be
 immobilised on a carrier and used to diagnose staphylococcal infections.
 (Updated on 25-MAR-2003 to correct PA field.)

Sequence 38 AA:

Query Match 100.0%; Score 53; DB 1; Length 38;
 Best Local Similarity 100.0%; Pred. No. 0.0071;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QNKGNSFEE 10
 |||||
 DB 2 QNKGNSFEE 11

RESULT 6

AA065664 standard; peptide; 38 AA.

AA065664;

16-OCT-1998 (first entry)

Fibronectin binding protein-derived peptide #8.

microbial surface components recognising adhesive matrix molecule;
 MSCRAMM; fibronectin; fibronectin-binding protein; antibody; epitope;
 antibiotic; bacterial infection; antibiotic-resistant strain.

Synthetic.

Staphylococcus aureus.

WO9831389-A2.

23-JUL-1998.

21-JAN-1998; 98WO-US001222.

21-JAN-1997; 97US-0036139P.

(TEXA) UNIV TEXAS A & M SYSTEM.


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XX Hoecek M, Patti JM, House-Pompeo KL, Speziale P, Joh D;
PI Mcgavin MJ;
DR WPI, 1998-413816/35.
XX
XX Antibody that binds to fibronectin-binding protein, preventing its
PT binding to fibronectin - used to treat or prevent bacterial infection,
PT especially by Staphylococci and Streptococci.
XX
XX Example 2; Page 92; 201pp; English.
XX
XX The invention relates to antibodies that bind to a fibronectin-binding
CC domain of a fibronectin-binding protein, and inhibit binding of the
CC protein to fibronectin. Also claimed are: (1) isolated peptides of a
CC fibronectin-binding protein that do not bind to fibronectin; (2) fusion
CC protein containing at least one peptide of a fibronectin-binding protein
CC linked to a second amino acid sequence; (3) nucleic acid encoding the
CC isolated peptide of (1). Antibodies, the isolated peptides of (1) and the
CC nucleic acids are all useful for immunisation (active or passive) and (by
CC inhibiting binding of bacteria to fibronectin) for preventing or treating
CC infection in humans or other animals, particularly by staphylococci or
CC streptococci, e.g. meningitis, otitis media, pneumonia, endocarditis,
CC mastitis in cattle, abortion in horses and many others. Since the
CC antibodies block binding of bacteria, they should be effective against
CC antibiotic-resistant strains, and may replace antibiotic therapy or
CC increase its effectiveness. Sequences AAM6559-68 represent synthetic
CC epitopes from the fibronectin binding domains DV and DI-D4 of the S.
CC aureus fnbA gene
XX
SQ Sequence 38 AA;

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Query Match          100.0%; Score 53; DB 2; Length 38;
Best Local Similarity 100.0%; Pred. NO. 0.0071;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 ONKGNOSFEE 10
   |||||
Db 1 ONKGNOSFEE 10

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RESULT 7
AAM65705
ID AAM65705 standard; peptide; 38 AA.
XX
XX AAM65705;
XX
XX 16-OCT-1998 (first entry)
XX
XX Fibronectin binding protein-derived peptide #49.
XX
XX microbial surface components recognising adhesive matrix molecule;
KW MSCRAMM; fibronectin; fibronectin-binding protein; antibody; epitope;
KW antibiotic; bacterial infection; antibiotic-resistant strain.
XX
XX Synthetic.
OS Staphylococcus aureus.
XX
XX WO9831389-A2.
XX
XX 23-JUL-1998.
XX
XX 21-JAN-1998; 98WO-US001222.
XX
XX 21-JAN-1997; 97US-0036139P.
XX
XX (TEXA ) UNIV TEXAS A & M SYSTEM.
XX
XX Hoecek M, Patti JM, House-Pompeo KL, Speziale P, Joh D;
PI Mcgavin MJ;
XX
XX WPI, 1998-413816/35.
XX

```

```

PT Antibody that binds to fibronectin-binding protein, preventing its
PT binding to fibronectin - used to treat or prevent bacterial infection,
PT especially by Staphylococci and Streptococci.
XX
XX Example 8; Page 102; 201pp; English.
XX
XX The invention relates to antibodies that bind to a fibronectin-binding
CC domain of a fibronectin-binding protein, and inhibit binding of the
CC protein to fibronectin. Also claimed are: (1) isolated peptides of a
CC fibronectin-binding protein that do not bind to fibronectin; (2) fusion
CC protein containing at least one peptide of a fibronectin-binding protein
CC linked to a second amino acid sequence; (3) nucleic acid encoding the
CC isolated peptide of (1). Antibodies, the isolated peptides of (1) and the
CC nucleic acids are all useful for immunisation (active or passive) and (by
CC inhibiting binding of bacteria to fibronectin) for preventing or treating
CC infection in humans or other animals, particularly by staphylococci or
CC streptococci, e.g. meningitis, otitis media, pneumonia, endocarditis,
CC mastitis in cattle, abortion in horses and many others. Since the
CC antibodies block binding of bacteria, they should be effective against
CC antibiotic-resistant strains, and may replace antibiotic therapy or
CC increase its effectiveness. Sequences AAM65701-706 represent a series of
CC synthetic peptides based on the D2 region of S. aureus fibronectin
CC binding protein A. They were synthesised to contain mutations
XX
SQ Sequence 38 AA;

```

```

Query Match          100.0%; Score 53; DB 2; Length 38;
Best Local Similarity 100.0%; Pred. NO. 0.0071;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 ONKGNOSFEE 10
   |||||
Db 1 ONKGNOSFEE 10

```

```

RESULT 8
AAM65663
ID AAM65663 standard; peptide; 38 AA.
XX
XX AAM65663;
XX
XX 16-OCT-1998 (first entry)
XX
XX Fibronectin binding protein-derived peptide #7.
XX
XX microbial surface components recognising adhesive matrix molecule;
KW MSCRAMM; fibronectin; fibronectin-binding protein; antibody; epitope;
KW antibiotic; bacterial infection; antibiotic-resistant strain.
XX
XX Synthetic.
OS Staphylococcus aureus.
XX
XX WO9831389-A2.
XX
XX 23-JUL-1998.
XX
XX 21-JAN-1998; 98WO-US001222.
XX
XX 21-JAN-1997; 97US-0036139P.
XX
XX (TEXA ) UNIV TEXAS A & M SYSTEM.
XX
XX Hoecek M, Patti JM, House-Pompeo KL, Speziale P, Joh D;
PI Mcgavin MJ;
XX
XX WPI, 1998-413816/35.
XX
XX Antibody that binds to fibronectin-binding protein, preventing its
PT binding to fibronectin - used to treat or prevent bacterial infection,
PT especially by Staphylococci and Streptococci.
XX
XX Example 2; Page 92; 201pp; English.
XX

```

CC The invention relates to antibodies that bind to a fibronectin-binding
 CC domain of a fibronectin-binding protein, and inhibit binding of the
 CC protein to fibronectin. Also claimed are: (1) isolated peptides of a
 CC fibronectin-binding protein that do not bind to fibronectin; (2) fusion
 CC protein containing at least one peptide of a fibronectin-binding protein
 CC linked to a second amino acid sequence; (3) nucleic acid encoding the
 CC isolated peptide of (1). Antibodies, the isolated peptides of (1) and the
 CC nucleic acids are all useful for immunisation (active or passive) and (by
 CC inhibiting binding of bacteria to fibronectin) for preventing or treating
 CC infection in humans or other animals, particularly by staphylococci or
 CC streptococci, e.g. meningitis, otitis media, pneumonia, endocarditis,
 CC mastitis in cattle, abortion in horses and many others. Since the
 CC antibodies block binding of bacteria, they should be effective against
 CC antibiotic-resistant strains, and may replace antibiotic therapy or
 CC increase its effectiveness. Sequences AAW65701-68 represent synthetic
 CC epitopes from the fibronectin binding domains DU and DI-D4 of the S.
 CC aureus fnba gene

XX Sequence 38 AA:

Query Match 100.0%; Score 53; DB 2; Length 38;
 Best Local Similarity 100.0%; Pred. No. 0.0071;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ONKGNQSFEE 10
 |||||
 DB 1 ONKGNQSFEE 10

RESULT 9
 AAW65704
 ID AAW65704 standard; peptide; 38 AA.

XX AAW65704;

XX 16-OCT-1998 (first entry)

XX Fibronectin binding protein-derived peptide #48.

XX microbial surface components recognising adhesive matrix molecule;

KW MSCRAMM; fibronectin; fibronectin-binding protein; antibody; epitope;

XX antibiotic; bacterial infection; antibiotic-resistant strain.

OS Synthetic.

XX Staphylococcus aureus.

XX WO9831389-A2.

XX 23-JUL-1998.

XX 21-JAN-1998; 98WO-US001222.

XX 21-JAN-1997; 97US-0036139P.

XX (TEXA) UNIV TEXAS A & M SYSTEM.

PI Hoeoek M, Patti JM, House-Pompeo KL, Speciale P, Joh D;

XX Mcgavin MJ;

XX WPI; 1998-413816/35.

XX Antibody that binds to fibronectin-binding protein, preventing its

XX binding to fibronectin - used to treat or prevent bacterial infection,

XX especially by Staphylococci and Streptococci.

XX Example 8; Page 102; 201pp; English.

CC isolated peptide of (1). Antibodies, the isolated peptides of (1) and the
 CC nucleic acids are all useful for immunisation (active or passive) and (by
 CC inhibiting binding of bacteria to fibronectin) for preventing or treating
 CC infection in humans or other animals, particularly by staphylococci or
 CC streptococci, e.g. meningitis, otitis media, pneumonia, endocarditis,
 CC mastitis in cattle, abortion in horses and many others. Since the
 CC antibodies block binding of bacteria, they should be effective against
 CC antibiotic-resistant strains, and may replace antibiotic therapy or
 CC increase its effectiveness. Sequences AAW65701-706 represent a series of
 CC synthetic peptides based on the D2 region of S. aureus fibronectin
 CC binding protein A. They were synthesised to contain mutations

XX Sequence 38 AA:

Query Match 100.0%; Score 53; DB 2; Length 38;
 Best Local Similarity 100.0%; Pred. No. 0.0071;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ONKGNQSFEE 10
 |||||
 DB 1 ONKGNQSFEE 10

RESULT 10
 AAY29087
 ID AAY29087 standard; protein; 134 AA.

XX AAY29087;

XX 28-SEP-1999 (first entry)

XX S. aureus fibronectin binding protein A (FnBA) binding domain.

XX Bovine herpes virus-2; BHV-2; cytokine; immune response; immunogen; IL;

KW interleukin; colony stimulating factor; CSF; interferon; IFN; TNF;

KW tumour necrosis factor; recombinant virus; vaccine; mucosal disease;

KW mastitis; breast cancer; stress-induced disease; binding domain; FnBA;

XX fibronectin binding protein.

OS Staphylococcus aureus.

XX WO9916892-A1.

XX 08-APR-1999.

XX 29-SEP-1998; 98WO-GB002927.

XX 29-SEP-1997; 97GB-00020633.

XX (UYBR-) UNIV BRISTOL.

PI Bradley AJ, Duffas WPB;

XX WPI; 1999-255101/21.

XX N-PSDB; AAX91504.

XX New bovine herpes virus-2 vectors.

XX Example 2; Fig 8A-B; 130pp; English.

XX The invention provides bovine herpes virus-2 (BHV-2) based vectors that

XX comprise at least one cytokine-encoding DNA sequence. The expression of

XX cytokines in mammals can up-regulate immune responses to the immunogens.

XX The cytokine is selected from interleukin (IL), colony stimulating

XX factors (CSF), interferons (IFN) and tumour necrosis factors (TNF). The

XX BHV-2 based vector or recombinant virus can be used as vaccines. They can

XX be used for preventing or treating a mucosal disease in a subject, e.g.

XX mastitis in cows or breast cancers in humans. They can also be used for

XX preventing or treating a stress-induced disease. The present sequence

XX represents the binding domain of a previously published S. aureus

XX fibronectin binding protein A (FnBA) sequence. The FnB binding domain

XX gene sequence FNBA, cloned for use in this invention has 97.8 percent

CC identity when compared to the previously published FNBA and FNBB gene
CC sequences

XX Sequence 134 AA;

Query Match 100.0%; Score 53; DB 2; Length 134;
Best Local Similarity 100.0%; Pred. No. 0.028;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ONKGNQSFEE 10
|||||

Db 40 ONKGNQSFEE 49

RESULT 11

AAW31556 standard; protein; 139 AA.

XX AAW31556;

AC 27-AUG-2003 (revised)

DT 25-MAR-2003 (revised)

DT 21-MAY-1998 (first entry)

XX Fibronectin-binding MSCRAMM derivative pQD.

XX Fibronectin; pQD; collagen binding protein; sepsis; infection;

XX microbial surface component recognising adhesive matrix molecule; MSCRAMM;

XX adhesin; vaccine; immunisation; diagnosis; therapy; mastitis.

XX Staphylococcus aureus.

XX Key Location/Qualifiers

FT Peptide 1..12

PN WO9743314-A2.

XX 20-NOV-1997.

PF 14-MAY-1997; 97WO-US008210.

PR 16-MAY-1996; 96US-0017678P.

XX (TEXA) UNIV TEXAS A & M SYSTEM.

PA (UABR-) UAB RES FOUND.

XX Hoeoek M, Patti JM, House-Pompeo K, Stanham N, Symersky J;

PI MPI; 1998-008801/01.

DR Antibody that interacts with collagen binding domain of Staphylococcal

XX cna gene product - useful to prevent bacterial sepsis in animal infected

XX with Staphylococcus aureus.

PS Disclosure; Page 91; 143pp; English.

XX This protein comprises Staphylococcus aureus fibronectin-binding

CC microbial surface component recognising adhesive matrix molecule (MSCRAMM)

CC derivative pQD, plus a vector-derived N-terminal peptide. The invention

CC relates to claimed nucleic acid sequences (see AAT93436-38) encoding S.

CC aureus collagen binding protein (CBP) epitopes M17, M31 and M55 (see

CC AAW31552-54) that confer protection against S. aureus infection. CBP

CC protein and antigenic epitopes are contemplated for use in the treatment

CC of pathological infections, especially to prevent bacterial adhesion to

CC collagen. The epitopes are also contemplated for use in the preparation

CC of vaccines and as carrier proteins in vaccine formulations, as well as

CC in the formulation of compositions for the prevention of S. aureus

CC infection. pCR33 and pQD (see AAW31556) were used to raise anti-MSCRAMM

CC polyclonal antibodies used in passive immunisation against bovine

CC mastitis. (Updated on 25-MAR-2003 to correct PI field.) (Updated on 27-

CC AUG-2003 to correct OS field.)

XX Sequence 139 AA;

Query Match 100.0%; Score 53; DB 2; Length 139;
Best Local Similarity 100.0%; Pred. No. 0.03;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ONKGNQSFEE 10
|||||

Db 54 ONKGNQSFEE 63

RESULT 12

AAW31556 standard; protein; 1018 AA.

XX AAW31556;

AC 25-MAR-2003 (revised)

DT 05-JAN-1990 (first entry)

XX Fibronectin binding protein.

XX Fibronectin binding protein; S.aureus; immunisation; mastitis; ruminants;

XX wound infection; diagnosis.

XX Staphylococcus aureus.

XX EP294349-A.

XX 30-MAY-1988; 88EP-00850188.

XX 01-JUN-1987; 87SE-00002272.

XX (ALFA) ALFA LAVAL AGRIC INT AB.

XX Lindberg MK, Signas LC, Wadstrom TM, Froman G;

XX MPI; 1988-347978/49.

XX P-PSDB; AAW31556.

XX Hybrid DNA encoding Staphylococcus aureus fibronectin binding protein -

XX useful for immunisation and topical application to prevent staphylococcal

XX infections.

XX Disclosure; Fig. 8A:1-8A:2; 23pp; English.

XX The S.aureus fibronectin binding protein may be included in a hybrid

CC protein. The protein may be used to immunise ruminants against

CC staphylococcal mastitis, pref. when given at 0.5-5 microg/kg, using 3

CC doses at 1-3 week intervals; and for topical applicn. to prevent wound

CC infection, pref. using isotonic saline soln. of concn. 25-250 microg/mg.

CC The DNA encoding the binding protein and the hybrid protein may be

CC immobilised on a carrier and used to diagnose staphylococcal infections.

CC (Updated on 25-MAR-2003 to correct PA field.)

XX Sequence 1018 AA;

OY 1 ONKGNQSFEE 10
|||||

Db 784 ONKGNQSFEE 793

RESULT 13

AAW31556 standard; protein; 1018 AA.

XX AAW31556;

AC AAW31556;

XX 14-FEB-2002 (first entry)
XX Staphylococcus aureus cellular proliferation protein #1415.
DE Staphylococcus aureus cellular proliferation protein; antibiotic;
XX Antisense; prokaryotic cellular proliferation protein; antibiotic;
XX Antibacterial; drug design.
XX Staphylococcus aureus.
XX WO200170955-A2.
XX PD 27-SEP-2001.
XX PF 21-MAR-2001; 2001WO-US009180.
XX PR 21-MAR-2000; 2000US-0191078P.
XX PR 23-MAY-2000; 2000US-0206848P.
XX PR 26-MAY-2000; 2000US-0207727P.
XX PR 23-OCT-2000; 2000US-0242578P.
XX PR 27-NOV-2000; 2000US-0253625P.
XX PR 22-DEC-2000; 2000US-0257931P.
XX PR 16-FEB-2001; 2001US-0269308P.
XX PA (ELIT-) ELITRA PHARM INC.
XX PI Haselbeck R, Ohlsen KL, Zyskind JW, Wall D, Trawick JD, Carr GJ;
XX PI Yamamoto RT, Xu HH;
XX DR WPI; 2001-611495/70.
XX DR N-PSDB; AAS55104.
XX PT New polynucleotides for the identification and development of
XX PT antibiotics, comprise sequences of antisense nucleic acids.
XX PS Example 3; SEQ ID NO 12838; 511pp; English.
XX XX The invention relates to antisense inhibitors of genes essential to
XX CC prokaryotic cellular proliferation, their use in identifying the genes,
XX CC their use in the discovery of novel antibiotics, the essential genes
XX CC themselves and the encoded proteins. The prokaryotes used are Escherichia
XX CC coli, Staphylococcus aureus, Salmonella typhi, Klebsiella pneumoniae,
XX CC Pseudomonas aeruginosa and Enterococcus faecalis. The invention is also
XX CC useful for the identification of potential new targets for antibiotic
XX CC development. The antisense nucleic acids can also be used to identify
XX CC proteins used in proliferation, to express these proteins, and to obtain
XX CC antibodies capable of binding to the expressed proteins. The proteins can
XX CC be used to screen compounds in rational drug discovery programmes. The
XX CC antisense nucleic acid sequence is also useful to screen for homologous
XX CC nucleic acids which are required for cell proliferation in a wide variety
XX CC of organisms. The present sequence represents an essential prokaryotic
XX CC cellular proliferation protein. Note: The sequence data for this patent
XX CC did not form part of the printed specification, but was obtained in
XX CC electronic format directly from WIPO at
XX CC ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 1018 AA;
XX
XX Query Match 100.0%; Score 53; DB 4; Length 1018;
XX Best Local Similarity 100.0%; Pred. No. 0.26;
XX Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DT 14-FEB-2002 (first entry)
XX Staphylococcus aureus cellular proliferation protein #577.
DE Staphylococcus aureus cellular proliferation protein; antibiotic;
XX Antisense; prokaryotic cellular proliferation protein; antibiotic;
XX Antibacterial; drug design.
XX Staphylococcus aureus.
XX WO200170955-A2.
XX PD 27-SEP-2001.
XX PF 21-MAR-2001; 2001WO-US009180.
XX PR 21-MAR-2000; 2000US-0191078P.
XX PR 23-MAY-2000; 2000US-0206848P.
XX PR 26-MAY-2000; 2000US-0207727P.
XX PR 23-OCT-2000; 2000US-0242578P.
XX PR 27-NOV-2000; 2000US-0253625P.
XX PR 22-DEC-2000; 2000US-0257931P.
XX PR 16-FEB-2001; 2001US-0269308P.
XX PA (ELIT-) ELITRA PHARM INC.
XX PI Haselbeck R, Ohlsen KL, Zyskind JW, Wall D, Trawick JD, Carr GJ;
XX PI Yamamoto RT, Xu HH;
XX DR WPI; 2001-611495/70.
XX DR N-PSDB; AAS52160.
XX PT New polynucleotides for the identification and development of
XX PT antibiotics, comprise sequences of antisense nucleic acids.
XX PS Example 3; SEQ ID NO 5797; 511pp; English.
XX XX The invention relates to antisense inhibitors of genes essential to
XX CC prokaryotic cellular proliferation, their use in identifying the genes,
XX CC their use in the discovery of novel antibiotics, the essential genes
XX CC themselves and the encoded proteins. The prokaryotes used are Escherichia
XX CC coli, Staphylococcus aureus, Salmonella typhi, Klebsiella pneumoniae,
XX CC Pseudomonas aeruginosa and Enterococcus faecalis. The invention is also
XX CC useful for the identification of potential new targets for antibiotic
XX CC development. The antisense nucleic acids can also be used to identify
XX CC proteins used in proliferation, to express these proteins, and to obtain
XX CC antibodies capable of binding to the expressed proteins. The proteins can
XX CC be used to screen compounds in rational drug discovery programmes. The
XX CC antisense nucleic acid sequence is also useful to screen for homologous
XX CC nucleic acids which are required for cell proliferation in a wide variety
XX CC of organisms. The present sequence represents an essential prokaryotic
XX CC cellular proliferation protein. Note: The sequence data for this patent
XX CC did not form part of the printed specification, but was obtained in
XX CC electronic format directly from WIPO at
XX CC ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 1018 AA;
XX
XX Query Match 100.0%; Score 53; DB 4; Length 1018;
XX Best Local Similarity 100.0%; Pred. No. 0.26;
XX Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 15
ABJ18922
ID ABJ18922 standard; protein; 1018 AA.
XX AC ABJ18922;
XX DT 06-MAR-2003 (first entry)

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XX Pathogen specific antigen related staphylococcal protein SEQ ID No 68.
DE
XX Antibacterial; virucide; fungicide; protozoacide; cytostatic; anti-HIV;
XX hyperimmune; serum-reactive; antigen; pathogen; tumour; allergen;
XX auto-immunity; vaccine; staphylococcal infection; antibody; cancer;
XX autoimmune disease; HIV; hepatitis.
XX Staphylococcus sp.
XX WO200259148-A2.
XX
XX 01-AUG-2002.
XX
XX 21-JAN-2002; 2002WO-EP000546.
XX
XX 26-JAN-2001; 2001AT-00000130.
XX
XX (CIST-) CISTEM BIOTECHNOLOGIES GMBH.
XX
XX Meinke A, Nagy E, Von Ahnen U, Klade C, Henics T, Zauner W,
XX Minb DB, Vytvytska O, Etz H, Dryla A, Weichart T, Hainer M,
XX Tempelmaier B;
XX
XX WPI; 2003-075410/07.
XX
XX Identifying, isolating and producing hyperimmune serum-reactive antigens
XX from a pathogen, for preparing vaccine or medicament for treating or
XX preventing e.g. staphylococcal infections, comprises providing antibody
XX preparation.
XX
XX Example 7; Page 157; 252pp; English.
XX
XX The invention relates to a novel method for identifying, isolating and
XX producing hyperimmune serum-reactive antigens from a pathogen, tumour,
XX allergen, a tissue or host prone to auto-immunity, where the antigens are
XX used in a vaccine, comprises providing antibody preparation from a plasma
XX pool of a type of animal, or individual sera with antibodies against the
XX specific pathogen, tumour, allergen, tissue or host prone to auto-
XX immunity. The hyperimmune serum-reactive antigens comprising any of the
XX 62 sequences of 53-2261 amino acids fully defined in the specification,
XX or their hyperimmune fragments are useful for the manufacture of a
XX pharmaceutical preparation, particularly a vaccine against staphylococcal
XX infections or colonisation against S. aureus or S. epidermidis. The
XX preparation of antibodies is useful for the manufacture of a medicament
XX for treating or preventing staphylococcal infections or colonisation
XX against S. aureus or S. epidermidis. The antibody preparations may also
XX be used for diagnostic and imaging purposes. Other conditions that can be
XX treated include cancer, autoimmune diseases or infections caused by viral
XX (e.g. HIV, hepatitis A, B or C), fungal or protozoan pathogens. This
XX sequence represents a staphylococcal protein relating to the method for
XX identifying and producing pathogen specific antigens of the invention
XX
XX Sequence 1018 AA;
SQ

```

```

Query Match 100.0%; Score 53; DB 6; Length 1018;
Best Local Similarity 100.0%; Pred. No. 0.26;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 QNKGNSFEE 10
| | | | | | | |
DB 764 QNKGNSFEE 793

```

Search completed: October 25, 2005, 20:58:48
Job time : 64.2 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 22, 2005, 05:46:56 ; Search time 17.3 Seconds
(without alignments)
43.150 Million cell updates/sec

Title: US-10-731-238-82
Perfect score: 53
Sequence: 1 ONKGNQSPFE 10

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-Processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents_AA:*

- 1: /cgn2_6/prodata/1/1aa/5A_COMB.pep.*
- 2: /cgn2_6/prodata/1/1aa/5B_COMB.pep.*
- 3: /cgn2_6/prodata/1/1aa/6A_COMB.pep.*
- 4: /cgn2_6/prodata/1/1aa/6B_COMB.pep.*
- 5: /cgn2_6/prodata/1/1aa/PCTUS_COMB.pep.*
- 6: /cgn2_6/prodata/1/1aa/backfile1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	53	100.0	10	4	US-09-010-317-82	Sequence 82, Appl
2	53	100.0	36	4	US-09-010-317-58	Sequence 58, Appl
3	53	100.0	36	4	US-09-010-317-59	Sequence 59, Appl
4	53	100.0	38	1	US-08-234-622A-3	Sequence 3, Appl
5	53	100.0	38	1	US-08-729-767-4	Sequence 4, Appl
6	53	100.0	38	4	US-09-010-317-7	Sequence 7, Appl
7	53	100.0	38	4	US-09-010-317-8	Sequence 8, Appl
8	53	100.0	38	4	US-09-010-317-48	Sequence 48, Appl
9	53	100.0	38	4	US-09-010-317-49	Sequence 49, Appl
10	53	100.0	114	1	US-08-259-000-3	Sequence 3, Appl
11	53	100.0	139	1	US-08-856-253-8	Sequence 8, Appl
12	53	100.0	1027	4	US-08-956-171E-5254	Sequence 5254, Ap
13	53	100.0	1027	4	US-08-781-986A-5254	Sequence 5254, Ap
14	48	90.6	10	4	US-09-010-317-63	Sequence 63, Appl
15	48	90.6	38	1	US-08-234-622A-2	Sequence 2, Appl
16	48	90.6	38	1	US-08-729-767-3	Sequence 3, Appl
17	48	90.6	38	4	US-09-010-317-5	Sequence 5, Appl
18	48	90.6	38	4	US-09-010-317-6	Sequence 6, Appl
19	48	90.6	38	4	US-09-010-317-38	Sequence 38, Appl
20	48	90.6	38	4	US-09-010-317-39	Sequence 39, Appl
21	48	90.6	38	4	US-09-010-317-40	Sequence 40, Appl
22	48	90.6	38	4	US-09-010-317-41	Sequence 41, Appl
23	48	90.6	38	4	US-09-010-317-42	Sequence 42, Appl
24	48	90.6	38	4	US-09-010-317-43	Sequence 43, Appl
25	48	90.6	38	4	US-09-010-317-47	Sequence 47, Appl
26	48	90.6	39	4	US-09-010-317-56	Sequence 56, Appl
27	48	90.6	39	4	US-09-010-317-57	Sequence 57, Appl

ALIGNMENTS

28	48	90.6	130	2	US-08-459-135A-7	Sequence 7, Appl
29	48	90.6	130	2	US-08-459-135A-8	Sequence 8, Appl
30	48	90.6	130	3	US-08-495-559-7	Sequence 7, Appl
31	48	90.6	130	3	US-08-495-559-8	Sequence 8, Appl
32	48	90.6	174	2	US-08-459-135A-10	Sequence 10, Appl
33	48	90.6	174	2	US-08-459-135A-13	Sequence 13, Appl
34	48	90.6	174	3	US-08-495-559-10	Sequence 10, Appl
35	48	90.6	174	3	US-08-495-559-13	Sequence 13, Appl
36	48	90.6	176	3	US-08-495-559-6	Sequence 6, Appl
37	48	90.6	178	2	US-08-459-135A-12	Sequence 12, Appl
38	48	90.6	178	2	US-08-495-559-12	Sequence 12, Appl
39	48	90.6	181	2	US-08-459-135A-6	Sequence 6, Appl
40	48	90.6	559	4	US-08-956-171E-5251	Sequence 5251, Ap
41	48	90.6	559	4	US-08-781-986A-5251	Sequence 5251, Ap
42	48	88.7	38	4	US-09-010-317-46	Sequence 46, Appl
43	45	84.9	686	4	US-09-653-839-8	Sequence 8, Appl
44	45	84.9	686	4	US-10-202-619-8	Sequence 8, Appl
45	45	84.9	702	4	US-09-653-839-6	Sequence 6, Appl

RESULT 1
US-09-010-317-82
; Sequence 82, Application US/09010317
; Patent No. 6685943
; GENERAL INFORMATION:
; APPLICANT: Hook, Magnus
; APPLICANT: Patti, Joseph M.
; APPLICANT: House-Pompeo, Karen L.
; APPLICANT: Speziale, Pietro
; APPLICANT: John, Danny
; APPLICANT: McGavin, Martin J.
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
; TITLE OF INVENTION: AND METHODS OF USE
; NUMBER OF SEQUENCES: 105
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: TX
; COUNTRY: USA
; ZIP: 77210-4433
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/010,317
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/036,139
; FILING DATE: 21-JAN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Hibler, David W.
; REGISTRATION NUMBER: 41,071
; REFERENCE/DOCKET NUMBER: TAMK:189
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 512-418-3000
; TELEFAX: 512-474-7577
; INFORMATION FOR SEQ ID NO: 82:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; US-09-010-317-82
Query Match 100.0%; Score 53; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0015;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ONKGNQSFEE 10
| | | | | | | | | |
Db 1 ONKGNQSFEE 10

RESULT 2
US-09-010-317-58
; Sequence 58, Application US/09010317
; Patent No. 6685943
; GENERAL INFORMATION:
; APPLICANT: Hook, Magnus
; APPLICANT: Patti, Joseph M.
; APPLICANT: House-Pompeo, Karen L.
; APPLICANT: Speziale, Pietro
; APPLICANT: Jch, Danny
; APPLICANT: McGavin, Martin J.
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
; TITLE OF INVENTION: AND METHODS OF USE
; NUMBER OF SEQUENCES: 105
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: TX
; COUNTRY: USA
; ZIP: 77210-4433
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/010.317
; FILING DATE:
; STRANDEDNESS:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/036,139
; FILING DATE: 21-JAN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Hibler, David W.
; REGISTRATION NUMBER: 41,071
; REFERENCE/DOCKET NUMBER: TANK:189
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 512-418-3000
; TELEFAX: 512-474-7577
; INFORMATION FOR SEQ ID NO: 58:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 36 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; US-09-010-317-58

Query Match 100.0%; Score 53; DB 4; Length 36;
Best Local Similarity 100.0%; Pred. No. 0.0056;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ONKGNQSFEE 10
| | | | | | | | | |
Db 1 ONKGNQSFEE 10

RESULT 3
US-09-010-317-59
; Sequence 59, Application US/09010317
; Patent No. 6685943
; GENERAL INFORMATION:
; APPLICANT: Hook, Magnus
; APPLICANT: Patti, Joseph M.
; APPLICANT: House-Pompeo, Karen L.
; APPLICANT: Speziale, Pietro

APPLICANT: Jch, Danny
APPLICANT: McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
TITLE OF INVENTION: AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/010.317
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TANK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 59:
SEQUENCE CHARACTERISTICS:
LENGTH: 36 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-09-010-317-59

Query Match 100.0%; Score 53; DB 4; Length 36;
Best Local Similarity 100.0%; Pred. No. 0.0056;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ONKGNQSFEE 10
| | | | | | | | | |
Db 1 ONKGNQSFEE 10

RESULT 4
US-08-234-622A-3
; Sequence 3, Application US/08234622A
; Patent No. 5440014
; GENERAL INFORMATION:
; APPLICANT: HOOK, Magnus
; APPLICANT: MCGAVIN, Martin
; APPLICANT: RAUCCI, Giuseppe
; TITLE OF INVENTION: A FIBRONECTIN BINDING PEPTIDE
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Doane, Swecker & Mathis
; STREET: P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/234,622A
; FILING DATE: 28-APR-1994

CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: SE 9002617-0
FILING DATE: 10-AUG-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/SE91/00534
FILING DATE: 09-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: Neult, Donna M
REGISTRATION NUMBER: 36,607
REFERENCE/DOCKET NUMBER: 012885-044
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-234-622A-3

Query Match 100.0%; Score 53; DB 1; Length 38;
Best Local Similarity 100.0%; Pred. No. 0.006;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ONKNGSFEE 10
DB 1 ONKNGSFEE 10

RESULT 5
US-08-729-767-4
Sequence 4, Application US/08729767
Patent No. 5770702
GENERAL INFORMATION:
APPLICANT: HOOK, Magnus
APPLICANT: LINDBERG, Martin Kjell
APPLICANT: SIGNAS, Lars Christer
APPLICANT: MADSTROM, Torkel Mikael
APPLICANT: FROMAN, Gunnar
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN AS WELL AS
TITLE OF INVENTION: ITS PREPARATION
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Burns, Doane, Swecker & Mathis, L.L.P.
STREET: P.O. Box 1404
CITY: Alexandria
STATE: Virginia
COUNTRY: United States
ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/729,767
FILING DATE: 07-OCT-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/259,000
FILING DATE: 13-JUN-1994
PRIOR APPLICATION DATA: US 08/007,817
FILING DATE: 22-JAN-1993
PRIOR APPLICATION DATA: US 07/201,028
FILING DATE: 01-JUN-1988
PRIOR APPLICATION DATA: SE 8702272-9
APPLICATION NUMBER: SE 8702272-9
FILING DATE: 01-JUN-1987

ATTORNEY/AGENT INFORMATION:
NAME: McGowan, Malcolm K.
REGISTRATION NUMBER: 39,300
REFERENCE/DOCKET NUMBER: 012899-036
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-729-767-4

Query Match 100.0%; Score 53; DB 1; Length 38;
Best Local Similarity 100.0%; Pred. No. 0.006;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ONKNGSFEE 10
DB 2 ONKNGSFEE 11

RESULT 6
US-09-010-317-7
Sequence 7, Application US/09010317
Patent No. 6685943
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
APPLICANT: Patti, Joseph M.
APPLICANT: House-Pompeo, Karen L.
APPLICANT: Speciale, Pietro
APPLICANT: Joh, Danny
APPLICANT: McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
TITLE OF INVENTION: AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA: US 60/036,139
APPLICATION NUMBER: 21-JAN-1997
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAMK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-010-317-7

Query Match 100.0%; Score 53; DB 4; Length 38;
 Best Local Similarity 100.0%; Pred. No. 0.006;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ONKGNQSFEE 10
 |||||
 DB 1 ONKGNQSFEE 10

RESULT 7
 US-09-010-317-8
 ; Sequence 8, Application US/09010317
 ; Patent No. 6685943

GENERAL INFORMATION:
 APPLICANT: Hook, Magnus
 APPLICANT: Patti, Joseph M.
 APPLICANT: House-Pompeo, Karen L.
 APPLICANT: Speziale, Pietro
 APPLICANT: Joh, Danny
 APPLICANT: McGavin, Martin J.
 TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
 TITLE OF INVENTION: AND METHODS OF USE
 NUMBER OF SEQUENCES: 105
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Arnold, White & Durkee
 STREET: P. O. Box 4433
 CITY: Houston
 STATE: TX
 COUNTRY: USA
 ZIP: 77210-4433
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/010,317
 FILING DATE:
 STRANDEDNESS:
 TOPOLOGY: linear
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 60/036,139
 FILING DATE: 21-JAN-1997
 ATTORNEY/AGENT INFORMATION:
 NAME: Hibler, David W.
 REGISTRATION NUMBER: 41,071
 REFERENCE/DOCKET NUMBER: TANK:189
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 512-418-3000
 TELEFAX: 512-474-7577
 INFORMATION FOR SEQ ID NO: 8:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 38 amino acids
 TYPE: amino acid
 STRANDEDNESS:
 TOPOLOGY: linear
 US-09-010-317-8

Query Match 100.0%; Score 53; DB 4; Length 38;
 Best Local Similarity 100.0%; Pred. No. 0.006;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ONKGNQSFEE 10
 |||||
 DB 1 ONKGNQSFEE 10

RESULT 8
 US-09-010-317-48
 ; Sequence 48, Application US/09010317
 ; Patent No. 6685943

GENERAL INFORMATION:
 APPLICANT: Hook, Magnus
 APPLICANT: Patti, Joseph M.

APPLICANT: House-Pompeo, Karen L.
 APPLICANT: Speziale, Pietro
 APPLICANT: Joh, Danny
 APPLICANT: McGavin, Martin J.
 TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
 TITLE OF INVENTION: AND METHODS OF USE
 NUMBER OF SEQUENCES: 105
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Arnold, White & Durkee
 STREET: P. O. Box 4433
 CITY: Houston
 STATE: TX
 COUNTRY: USA
 ZIP: 77210-4433

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/010,317
 FILING DATE:
 STRANDEDNESS:
 TOPOLOGY: linear

CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 60/036,139
 FILING DATE: 21-JAN-1997
 ATTORNEY/AGENT INFORMATION:
 NAME: Hibler, David W.
 REGISTRATION NUMBER: 41,071
 REFERENCE/DOCKET NUMBER: TANK:189
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 512-418-3000
 TELEFAX: 512-474-7577
 INFORMATION FOR SEQ ID NO: 48:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 38 amino acids
 TYPE: amino acid
 STRANDEDNESS:
 TOPOLOGY: linear
 US-09-010-317-48

Query Match 100.0%; Score 53; DB 4; Length 38;
 Best Local Similarity 100.0%; Pred. No. 0.006;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ONKGNQSFEE 10
 |||||
 DB 1 ONKGNQSFEE 10

RESULT 9
 US-09-010-317-49
 ; Sequence 49, Application US/09010317
 ; Patent No. 6685943

GENERAL INFORMATION:
 APPLICANT: Hook, Magnus
 APPLICANT: Patti, Joseph M.
 APPLICANT: House-Pompeo, Karen L.
 APPLICANT: Speziale, Pietro
 APPLICANT: Joh, Danny
 APPLICANT: McGavin, Martin J.
 TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
 TITLE OF INVENTION: AND METHODS OF USE
 NUMBER OF SEQUENCES: 105
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Arnold, White & Durkee
 STREET: P. O. Box 4433
 CITY: Houston
 STATE: TX
 COUNTRY: USA
 ZIP: 77210-4433

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TANK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 49:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-09-010-317-49

Query Match 100.0%; Score 53; DB 4; Length 38;
Best Local Similarity 100.0%; Pred. No. 0.006;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QNKGNSFEE 10
DB 1 QNKGNSFEE 10

RESULT 10
US-08-259-000-3
Sequence 3, Application US/08259000
Patent No. 5571514
GENERAL INFORMATION:
APPLICANT: HOOK, Magnus
APPLICANT: LINDBERG, Martin Kjell
APPLICANT: SIGMAS, Lars Christer
APPLICANT: MADSTROM, Torkel Mikael
APPLICANT: FROMAN, Gunnar
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN AS WELL AS
TITLE OF INVENTION: ITS PREPARATION
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Burns, Doane, Swecker & Mathis
STREET: P.O. Box 1404
CITY: Alexandria
STATE: Virginia
COUNTRY: United States
ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/259,000
FILING DATE: 13-JUN-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: SE 8702272-9
FILING DATE: 01-JUN-1987
ATTORNEY/AGENT INFORMATION:
NAME: Neuch, Donna M
REGISTRATION NUMBER: 36,607
REFERENCE/DOCKET NUMBER: 012885-062
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021

INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 114 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-259-000-3

Query Match 100.0%; Score 53; DB 1; Length 114;
Best Local Similarity 100.0%; Pred. No. 0.019;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QNKGNSFEE 10
DB 40 QNKGNSFEE 49

RESULT 11
US-08-856-253-8
Sequence 8, Application US/08856253
Patent No. 6288214
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
APPLICANT: Patti, Joseph M.
APPLICANT: House-Pompeo, Karen
APPLICANT: Stanam, Narayana
APPLICANT: Symersky, Jindrich
TITLE OF INVENTION: COLLAGEN BINDING PROTEIN COMPOSITIONS
TITLE OF INVENTION: AND METHODS OF USE
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: Texas
COUNTRY: U.S.
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/856,253
FILING DATE: Concurrently Herewith
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/017,678
FILING DATE: 16-MAY-1996
ATTORNEY/AGENT INFORMATION:
NAME: Kitchell, Barbara S.
REGISTRATION NUMBER: 33,928
REFERENCE/DOCKET NUMBER: TANK:193
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
TELEFAX: (512) 474-7577
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 139 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-08-856-253-8

Query Match 100.0%; Score 53; DB 3; Length 139;
Best Local Similarity 100.0%; Pred. No. 0.023;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QNKGNSFEE 10
DB 54 QNKGNSFEE 63

RESULT 12
US-08-956-171E-5254
Sequence 5254, Application US/08956171E
Patent No. 6593114
GENERAL INFORMATION:
APPLICANT: Charles Kunsch
GIL H. Choi
Patrick S. Dillon
Craig A. Rosen
Steven C. Barash
Michael R. Fannon
TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
NUMBER OF SEQUENCES: 5256
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COUNTRY: USA
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/956,171E
FILING DATE: 20-Oct-1997
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/009,861
FILING DATE: January 5, 1996
APPLICATION NUMBER: 08/781,986
FILING DATE: January 3, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Mark J. Hyman
REGISTRATION NUMBER: 46,789
REFERENCE/DOCKET NUMBER: PB248P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (240) 314-1224
TELEFAX: (301) 309-8439
INFORMATION FOR SEQ ID NO: 5254:
SEQUENCE CHARACTERISTICS:
LENGTH: 1027 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 5254:
US-08-956-171E-5254
Query Match 100.0%; Score 53; DB 4; Length 1027;
Best Local Similarity 100.0%; Pred. No. 0.18;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 QNKGNSFEE 10
DB 793 QNKGNSFEE 802
RESULT 13
US-08-781-986A-5254
Sequence 5254, Application US/08781986A
Patent No. 6737248
GENERAL INFORMATION:
APPLICANT: Charles Kunsch
TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
NUMBER OF SEQUENCES: 5255
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville

STATE: Maryland
COUNTRY: USA
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/781,986A
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Benson, Bob
REGISTRATION NUMBER: 30,446
REFERENCE/DOCKET NUMBER: PB248BP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 5254:
SEQUENCE CHARACTERISTICS:
LENGTH: 1027 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-781-986A-5254
Query Match 100.0%; Score 53; DB 4; Length 1027;
Best Local Similarity 100.0%; Pred. No. 0.18;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 QNKGNSFEE 10
DB 793 QNKGNSFEE 802
RESULT 14
US-09-010-317-63
Sequence 63, Application US/09010317
Patent No. 6685943
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
APPLICANT: Patti, Joseph M.
APPLICANT: House-Pompeo, Karen L.
APPLICANT: Speciale, Pietro
APPLICANT: Joh, Danny
APPLICANT: McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997

ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAMR:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 63:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-09-010-317-63

Query Match 90.6%; Score 48; DB 4; Length 10;
Best Local Similarity 90.0%; Pred. No. 0.012;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QNKGNSFEE 10
DB 1 QNKGNSFEE 10

RESULT 15
US-08-234-622A-2
Sequence 2, Application US/08234622A
Patent No. 5440014
GENERAL INFORMATION:
APPLICANT: HOOK, Magnus
APPLICANT: MCGAVIN, Martin
APPLICANT: RAUCCI, Giuseppe
TITLE OF INVENTION: A FIBRONECTIN BINDING PEPTIDE
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSER: Burns, Doane, Swecker & Mathis
STREET: P.O. Box 1404
CITY: Alexandria
STATE: Virginia
COUNTRY: United States
ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/234,622A
FILING DATE: 28-APR-1994
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: SE 9002617-0
FILING DATE: 10-AUG-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/SE91/00534
FILING DATE: 09-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: Meuth, Donna M
REGISTRATION NUMBER: 36,607
REFERENCE/DOCKET NUMBER: 012885-044
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-234-622A-2

Query Match 90.6%; Score 48; DB 1; Length 38;

Best Local Similarity 90.0%; Pred. No. 0.048;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QNKGNSFEE 10
DB 1 QNKGNSFEE 10

Search completed: October 22, 2005, 07:41:46
Job time : 17.35 secs

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OM protein - protein search, using sw model

Run on: October 22, 2005, 12:09:40 ; Search time 57.25 Seconds
(without alignments)
72.924 Million cell updates/sec

Title: US-10-731-238-82

Perfect score: 53

Sequence: 1 QKKGNSFEE 10

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Gapop 10.0 , Gapext 0.5

Searched: 1862951 segs, 417491010 residues

Total number of hits satisfying chosen parameters: 1862951

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	53	100.0	10	US-10-731-238-82	Sequence 82, Appl
2	53	100.0	36	US-10-731-238-58	Sequence 58, Appl
3	53	100.0	36	US-10-731-238-59	Sequence 59, Appl
4	53	100.0	38	US-10-731-238-7	Sequence 7, Appl
5	53	100.0	38	US-10-731-238-8	Sequence 8, Appl
6	53	100.0	38	US-10-731-238-48	Sequence 48, Appl
7	53	100.0	38	US-10-731-238-49	Sequence 49, Appl
8	53	100.0	139	US-09-813-820-8	Sequence 8, Appl
9	53	100.0	1018	US-09-815-242-5797	Sequence 5797, Ap
10	53	100.0	1018	US-09-815-242-12838	Sequence 12838, A
11	53	100.0	1018	US-10-470-048B-68	Sequence 68, Appl

12	53	100.0	1027	8	US-08-781-986A-5254	Sequence 5254, Ap
13	53	100.0	1027	15	US-10-329-624-5254	Sequence 5254, Ap
14	48	90.6	10	18	US-10-731-238-63	Sequence 63, Appl
15	48	90.6	30	14	US-10-287-821-1	Sequence 1, Appl
16	48	90.6	31	14	US-10-287-821-2	Sequence 2, Appl
17	48	90.6	38	18	US-10-731-238-5	Sequence 5, Appl
18	48	90.6	38	18	US-10-731-238-6	Sequence 6, Appl
19	48	90.6	38	18	US-10-731-238-38	Sequence 38, Appl
20	48	90.6	38	18	US-10-731-238-39	Sequence 39, Appl
21	48	90.6	38	18	US-10-731-238-40	Sequence 40, Appl
22	48	90.6	38	18	US-10-731-238-41	Sequence 41, Appl
23	48	90.6	38	18	US-10-731-238-42	Sequence 42, Appl
24	48	90.6	38	18	US-10-731-238-43	Sequence 43, Appl
25	48	90.6	38	18	US-10-731-238-47	Sequence 47, Appl
26	48	90.6	39	18	US-10-731-238-56	Sequence 56, Appl
27	48	90.6	39	18	US-10-731-238-57	Sequence 57, Appl
28	48	90.6	388	8	US-08-901-062-1	Sequence 1, Appl
29	48	90.6	559	8	US-08-781-986A-5251	Sequence 5251, Ap
30	48	90.6	559	15	US-10-329-624-5251	Sequence 5251, Ap
31	48	90.6	767	9	US-09-815-242-5899	Sequence 5899, Ap
32	48	90.6	767	9	US-09-815-242-13140	Sequence 13140, A
33	48	90.6	940	17	US-10-470-048B-424	Sequence 424, Ap
34	48	90.6	948	17	US-10-470-048B-69	Sequence 69, Appl
35	48	90.6	961	15	US-10-282-122A-43778	Sequence 43778, A
36	48	90.6	978	9	US-09-815-242-5456	Sequence 5456, Ap
37	48	90.6	1001	9	US-09-815-242-12686	Sequence 12686, A
38	48	90.6	1038	15	US-10-282-122A-43827	Sequence 43827, A
39	47	88.7	38	18	US-10-731-238-46	Sequence 46, Appl
40	45	84.9	686	16	US-10-760-709-8	Sequence 8, Appl
41	45	84.9	702	14	US-10-116-519-11	Sequence 11, Appl
42	45	84.9	702	15	US-10-390-585-9	Sequence 9, Appl
43	45	84.9	702	15	US-10-055-569A-39	Sequence 39, Appl
44	45	84.9	702	15	US-10-275-107-47	Sequence 47, Appl
45	45	84.9	702	16	US-10-760-709-6	Sequence 6, Appl

ALIGNMENTS

RESULT 1
US-10-731-238-82
Sequence 82, Appl
Publication No. US20050123552A1
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
Pattil, Joseph M.
House-Pompeo, Karen L.
Speziale, Pietro
Joh, Danny
McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/731.238
FILING DATE: 10-Dec-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/010.317
FILING DATE: 21-Jan-1998
APPLICATION NUMBER: US 60/036.139

```

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; FILING DATE: 21-JAN-1997
; ATTORNEY/AGENT INFORMATION:
;   NAME: Hibler, David W.
;   REGISTRATION NUMBER: 41,071
;   REFERENCE/DOCKET NUMBER: TAMK:189
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE: 512-418-3000
;     TELEFAX: 512-474-7577
; INFORMATION FOR SEQ ID NO: 82:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH: 10 amino acids
;     TYPE: amino acid
;     STRANDEDNESS: <Unknown>
;     TOPOLOGY: linear
;   SEQUENCE DESCRIPTION: SEQ ID NO: 82:
US-10-731-238-82

Query Match      100.0%; Score 53; DB 18; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0023;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 QNKGNSFEE 10
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Db      1 QNKGNSFEE 10

RESULT 2
US-10-731-238-58
; Sequence 58, Application US/10731238
; Publication No. US20050123552A1
; GENERAL INFORMATION:
;   APPLICANT: Hook, Magnus
;               Patti, Joseph M.
;               House-Pompeo, Karen L.
;               Speziale, Pietro
;               Joh, Danny
;               McGavin, Martin J.
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
; NUMBER OF SEQUENCES: 105
; CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Arnold, White & Durkee
;   STREET: P.O. Box 4433
;   CITY: Houston
;   STATE: TX
;   COUNTRY: USA
;   ZIP: 77210-4433
; COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/10/731,238
;   FILING DATE: 10-Dec-2003
;   CLASSIFICATION: <Unknown>
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER: US/09/010,317
;     FILING DATE: 21-Jan-1998
;     APPLICATION NUMBER: US 60/036,139
;     FILING DATE: 21-JAN-1997
;     ATTORNEY/AGENT INFORMATION:
;       NAME: Hibler, David W.
;       REGISTRATION NUMBER: 41,071
;       REFERENCE/DOCKET NUMBER: TAMK:189
;       TELECOMMUNICATION INFORMATION:
;         TELEPHONE: 512-418-3000
;         TELEFAX: 512-474-7577
; INFORMATION FOR SEQ ID NO: 58:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH: 36 amino acids
;     TYPE: amino acid
;     STRANDEDNESS: <Unknown>

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; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 58:
US-10-731-238-58

Query Match      100.0%; Score 53; DB 18; Length 36;
Best Local Similarity 100.0%; Pred. No. 0.0091;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 QNKGNSFEE 10
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Db      1 QNKGNSFEE 10

RESULT 3
US-10-731-238-59
; Sequence 59, Application US/10731238
; Publication No. US20050123552A1
; GENERAL INFORMATION:
;   APPLICANT: Hook, Magnus
;               Patti, Joseph M.
;               House-Pompeo, Karen L.
;               Speziale, Pietro
;               Joh, Danny
;               McGavin, Martin J.
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
; NUMBER OF SEQUENCES: 105
; CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Arnold, White & Durkee
;   STREET: P.O. Box 4433
;   CITY: Houston
;   STATE: TX
;   COUNTRY: USA
;   ZIP: 77210-4433
; COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/10/731,238
;   FILING DATE: 10-Dec-2003
;   CLASSIFICATION: <Unknown>
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER: US/09/010,317
;     FILING DATE: 21-Jan-1998
;     APPLICATION NUMBER: US 60/036,139
;     FILING DATE: 21-JAN-1997
;     ATTORNEY/AGENT INFORMATION:
;       NAME: Hibler, David W.
;       REGISTRATION NUMBER: 41,071
;       REFERENCE/DOCKET NUMBER: TAMK:189
;       TELECOMMUNICATION INFORMATION:
;         TELEPHONE: 512-418-3000
;         TELEFAX: 512-474-7577
; INFORMATION FOR SEQ ID NO: 59:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH: 36 amino acids
;     TYPE: amino acid
;     STRANDEDNESS: <Unknown>
;     TOPOLOGY: linear
;   SEQUENCE DESCRIPTION: SEQ ID NO: 59:
US-10-731-238-59

Query Match      100.0%; Score 53; DB 18; Length 36;
Best Local Similarity 100.0%; Pred. No. 0.0091;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 QNKGNSFEE 10
        |||||
Db      1 QNKGNSFEE 10

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RESULT 4
US-10-731-238-7
; Sequence 7, Application US/10731238
; Publication No. US20050123552A1
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
Patti, Joseph M.
House-Pompeo, Karen L.
Speziale, Pietro
John, Danny
McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/731,238
FILING DATE: 10-Dec-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE: 21-Jan-1998
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAMK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-10-731-238-7
Query Match 100.0%; Score 53; DB 18; Length 38;
Best Local Similarity 100.0%; Pred. No. 0.0096;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ONKNOSFEE 10
Db 1 ONKNOSFEE 10
RESULT 5
US-10-731-238-8
; Sequence 8, Application US/10731238
; Publication No. US20050123552A1
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
Patti, Joseph M.
House-Pompeo, Karen L.
Speziale, Pietro
John, Danny
McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
AND METHODS OF USE

NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/731,238
FILING DATE: 10-Dec-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE: 21-Jan-1998
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAMK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-10-731-238-8
Query Match 100.0%; Score 53; DB 18; Length 38;
Best Local Similarity 100.0%; Pred. No. 0.0096;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ONKNOSFEE 10
Db 1 ONKNOSFEE 10
RESULT 6
US-10-731-238-48
; Sequence 48, Application US/10731238
; Publication No. US20050123552A1
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
Patti, Joseph M.
House-Pompeo, Karen L.
Speziale, Pietro
John, Danny
McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30


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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/731,238
FILING DATE: 10-Dec-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE: 21-Jan-1998
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TANK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 48:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 48:
US-10-731-238-48

Query Match      100.0%; Score 53; DB 18; Length 38;
Best Local Similarity 100.0%; Pred. No. 0.0096;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0

Oy      1 ONKGNQSFEE 10
        |||||
        1 ONKGNQSFEE 10

RESULT 7
US-10-731-238-49
Sequence 49, Application US/10731238
Publication No. US20050123552A1
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
          Patti, Joseph M.
          House-Pompeo, Karen L.
          Speziale, Pietro
          Ohn, Danny
          McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
          AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSER: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/731,238
FILING DATE: 10-Dec-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE: 21-Jan-1998
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TANK:189

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1 TELECOMMUNICATION INFORMATION:
2 TELEPHONE: 512-418-3000
3 TELEFAX: 512-474-7577
4 INFORMATION FOR SEQ ID NO: 49:
5 SEQUENCE CHARACTERISTICS:
6 LENGTH: 38 amino acids
7 TYPE: amino acid
8 STRANDEDNESS: <Unknown>
9 TOPOLOGY: linear
10 SEQUENCE DESCRIPTION: SEQ ID NO: 49:
11
12 US-10-731-238-49
13
14 Query Match 100.0%; Score 53; DB 18; Length 38;
15 Best Local Similarity 100.0%; Pred. No. 0.0096;
16 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
17
18 QY 1 ONKNGSQSFEE 10
19 |||||
20 1 ONKNGSQSFEE 10
21
22 RESULT 8
23 US-09-813-820-8
24 Sequence 8, Application US/09813820
25 Patent No. US20020102262A1
26 GENERAL INFORMATION:
27 APPLICANT: Hook, Magnus
28 Patti, Joseph M.
29 House-Pompeo, Karen
30 Sthanam, Narayana
31 Symeraky, Jindrich
32 TITLE OF INVENTION: COLLAGEN BINDING PROTEIN COMPOSITIONS
33 AND METHODS OF USE
34
35 NUMBER OF SEQUENCES: 8
36 CORRESPONDENCE ADDRESS:
37 ADDRESSEE: Arnold, White & Dukee
38 STREET: P.O. Box 4433
39 CITY: Houston
40 STATE: Texas
41 COUNTRY: U.S.
42 ZIP: 77210
43
44 COMPUTER READABLE FORM:
45 MEDIUM TYPE: Floppy disk
46 OPERATING SYSTEM: PC-DOS/MS-DOS
47 SOFTWARE: Patentin Release #1.0, Version #1.30
48 CURRENT APPLICATION DATA:
49 APPLICATION NUMBER: US/09/813,820
50 FILING DATE: 22-Mar-2001
51 CLASSIFICATION: <Unknown>
52 PRIOR APPLICATION DATA:
53 APPLICATION NUMBER: 08/856,253
54 FILING DATE: <Unknown>
55 ATTORNEY/AGENT INFORMATION:
56 NAME: Kitchell, Barbara S.
57 REGISTRATION NUMBER: 33,928
58 REFERENCE/DOCKET NUMBER: TMWK:193
59 TELECOMMUNICATION INFORMATION:
60 TELEPHONE: (512) 418-3000
61 TELEFAX: (512) 474-7577
62 INFORMATION FOR SEQ ID NO: 8:
63 SEQUENCE CHARACTERISTICS:
64 LENGTH: 139 amino acids
65 TYPE: amino acid
66 STRANDEDNESS: <Unknown>
67 TOPOLOGY: linear
68 SEQUENCE DESCRIPTION: SEQ ID NO: 8:
69
70 US-09-813-820-8
71
72 Query Match 100.0%; Score 53; DB 9; Length 139;
73 Best Local Similarity 100.0%; Pred. No. 0.039;
74 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 QNKGNSFEE 10
|||||
Db 54 QNKGNSFEE 63

RESULT 9

US-09-815-242-5797
; Sequence 5797, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Karl L.
; APPLICANT: Zyckind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; FILE REFERENCE: ELITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5797
; LENGTH: 1018
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-09-815-242-5797

Query Match 100.0%; Score 53; DB 9; Length 1018;
Best Local Similarity 100.0%; Pred. No. 0.33; Mismatches 0; Indels 0; Gaps 0;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QNKGNSFEE 10
|||||
Db 784 QNKGNSFEE 793

RESULT 10

US-09-815-242-12838
; Sequence 12838, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Karl L.
; APPLICANT: Zyckind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; FILE REFERENCE: ELITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078

; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12838
; LENGTH: 1018
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-09-815-242-12838

Query Match 100.0%; Score 53; DB 9; Length 1018;
Best Local Similarity 100.0%; Pred. No. 0.33; Mismatches 0; Indels 0; Gaps 0;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QNKGNSFEE 10
|||||
Db 784 QNKGNSFEE 793

RESULT 11
US-10-470-048B-68
; Sequence 68, Application US/10470048B
; Publication No. US2005003744A1
; GENERAL INFORMATION:
; APPLICANT: MEINKE ET AL.
; TITLE OF INVENTION: A METHOD FOR IDENTIFICATION, ISOLATION AND PRODUCTION OF
; FILE REFERENCE: SONN.035US
; CURRENT APPLICATION NUMBER: US/10/470,048B
; PRIOR FILING DATE: 2003-07-25
; NUMBER OF SEQ ID NOS: 603
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 68
; LENGTH: 1018
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-10-470-048B-68

Query Match 100.0%; Score 53; DB 17; Length 1018;
Best Local Similarity 100.0%; Pred. No. 0.33; Mismatches 0; Indels 0; Gaps 0;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QNKGNSFEE 10
|||||
Db 784 QNKGNSFEE 793

RESULT 12
US-08-781-986A-5254
; Sequence 5254, Application US/08781986A
; Publication No. US20030054436A1
; GENERAL INFORMATION:
; APPLICANT: Charles Kunsch
; TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
; NUMBER OF SEQUENCES: 5255
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/781,986A
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Benson, Bob
REGISTRATION NUMBER: 30,446
REFERENCE/DOCKET NUMBER: PB248PP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 5254:
SEQUENCE CHARACTERISTICS:
LENGTH: 1027 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-781-986A-5254

Query Match 100.0%; Score 53; DB 8; Length 1027;
Best Local Similarity 100.0%; Pred. No. 0.33;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QNKGNSFEE 10
DB 793 QNKGNSFEE 802

RESULT 13

US-10-329-624-5254
Sequence 5254, Application US/10329624
Publication No. US20040043037A1
GENERAL INFORMATION:
APPLICANT: Charles Kunsch
Gil H. Choi
Patrick S. Dillon
Craig A. Rosen
Steven C. Barash
Michael R. Fannon
TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
NUMBER OF SEQUENCES: 5256
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COUNTRY: USA
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/329,624
FILING DATE: 27-Dec-2002
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/956,171
FILING DATE: October 20, 1997
APPLICATION NUMBER: 60/009,861
FILING DATE: January 5, 1996
APPLICATION NUMBER: 08/781,986
FILING DATE: January 3, 1997
ATTORNEY/AGENT INFORMATION:

NAME: Mark J. Hyman
REGISTRATION NUMBER: 46,789
REFERENCE/DOCKET NUMBER: PB248P1D1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (240) 314-1224
TELEFAX: (301) 309-8439
INFORMATION FOR SEQ ID NO: 5254:
SEQUENCE CHARACTERISTICS:
LENGTH: 1027 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 5254:
US-10-329-624-5254

Query Match 100.0%; Score 53; DB 15; Length 1027;
Best Local Similarity 100.0%; Pred. No. 0.33;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QNKGNSFEE 10
DB 793 QNKGNSFEE 802

RESULT 14

US-10-731-238-63
Sequence 63, Application US/10731238
Publication No. US20050123552A1
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
Patti, Joseph M.
House-Pompeo, Karen L.
Speziale, Pietro
Uhn, Danny
McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/731,238
FILING DATE: 10-Dec-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE: 21-Jan-1998
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-Jan-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TANK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 63:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear

SEQUENCE DESCRIPTION: SEQ ID NO: 63:
US-10-731-238-63

Query Match 90.6%; Score 48; DB 18; Length 10;
Best Local Similarity 90.0%; Pred. No. 0.021;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QNKGNSFEE 10
|||
Db 1 QNKGNSFEE 10

RESULT 15
US-10-287-821-1
; Sequence 1, Application US/10287821
; Publication No. US20030153022A1
; GENERAL INFORMATION:
; APPLICANT: PATTI, Joseph M.
; TITLE OF INVENTION: MONOCLONAL ANTIBODIES TO THE FIBRONECTIN BINDING PROTEIN. . .
; FILE REFERENCE: P07427US01/BAS
; CURRENT APPLICATION NUMBER: US/10/287,821
; CURRENT FILING DATE: 2002-11-05
; PRIOR APPLICATION NUMBER: 60/330,964
; PRIOR FILING DATE: 2001-11-05
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 30
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-10-287-821-1

Query Match 90.6%; Score 48; DB 14; Length 30;
Best Local Similarity 90.0%; Pred. No. 0.067;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QNKGNSFEE 10
|||
Db 2 QNKGNSFEE 11

Search completed: October 22, 2005, 12:39:49
Job time : 57.25 secs

Page Blank (uspo)

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 22, 2005, 06:10:10 ; Search time 11.45 Seconds
(without alignments)
84.032 Million cell updates/sec

Title: US-10-731-238-82

Perfect score: 53

Sequence: 1 ONKGNQSFEE 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	53	100.0	1018	2 A32192	fibronectin-binding
2	48	90.6	940	2 S19702	fibronectin-binding
3	48	90.6	961	2 G90053	hypothetical prote
4	48	90.6	1038	2 H90053	hypothetical prote
5	38	71.7	267	2 H86548	polymorphic outer
6	38	71.7	767	2 T41344	probable zinc-fing
7	37	69.8	182	2 JCI145	20K protein - Bac1
8	37	69.8	182	2 B32256	hypothetical 20K p
9	36	67.9	130	2 S64339	probable membrane
10	36	67.9	333	2 C84792	hypothetical prote
11	36	67.9	341	2 H71716	130 kD antigen pre
12	36	67.9	357	2 F83517	4-hydroxyphenylpyr
13	36	67.9	369	2 C82211	4-hydroxyphenylpyr
14	36	67.9	454	2 A70176	trigger factor (ti
15	35	66.0	218	2 J00181	replication protei
16	35	66.0	229	2 S49494	replication protei
17	35	66.0	441	2 E70461	pmbA protein - Agu
18	35	66.0	1062	2 F83335	RND multidrug effl
19	35	66.0	1062	2 T30830	hypothetical prote
20	35	66.0	1066	2 T18523	integrin alpha cha
21	34	64.2	210	2 A49180	glutathione transf
22	34	64.2	310	2 J10081	beta-lactamase (EC
23	34	64.2	475	2 H97062	glycerol-3-phospha
24	34	64.2	478	2 JCI1475	fatly-acyl-CoA red
25	34	64.2	543	2 A38093	transformation-sen
26	34	64.2	918	2 A55277	hexokinase (EC 2.7
27	34	64.2	967	2 T35125	ribonucleotide red
28	34	64.2	1082	2 H81982	hypothetical prote
29	34	64.2	2902	2 C71953	toxin-like outer m

30	33	62.3	79	2 G75155	hypothetical prote
31	33	62.3	149	2 T41481	very hypothetical
32	33	62.3	155	1 RN4XR6	DNA-directed RNA p
33	33	62.3	160	2 G95213	hypothetical prote
34	33	62.3	164	2 H98077	hypothetical prote
35	33	62.3	213	2 S26055	2-dehydro-3-deoxy-
36	33	62.3	246	2 T46392	hypothetical prote
37	33	62.3	358	2 S45911	hypothetical prote
38	33	62.3	432	2 T43476	hypothetical prote
39	33	62.3	509	2 D95053	transcription regu
40	33	62.3	571	2 A81797	hypothetical prote
41	33	62.3	591	2 S30145	ketol-acid reducto
42	33	62.3	591	2 T45681	ketol-acid reducto
43	33	62.3	917	2 S40178	isoleucine-tRNA 11
44	33	62.3	917	2 D89891	ile-tRNA synthetas
45	33	62.3	1028	2 AF3286	ATP-dependent DNA

ALIGNMENTS

RESULT 1
A32192
fibronectin-binding protein - Staphylococcus aureus
C/Species: Staphylococcus aureus
C/Date: 31-Jul-1989 #sequence_revision 31-Jul-1989 #ext_change 16-Feb-1997
C/Accession: A32192
R/Signaes, C.; Raucel, G.; Joansson, K.; Lindgren, P.E.; Anantharamaiah, G.M.; Hoeck, R.
Proc. Natl. Acad. Sci. U.S.A. 86, 699-703, 1989
A/Title: Nucleotide sequence of the gene for a fibronectin-binding protein from Staphyl
A/Reference number: A32192; PMID:8908998; PMID:2521391
A/Accession: A32192
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-1018 <Sig>
A/Cross-references: GB:J04151
C/Keywords: fibronectin binding

Query Match 100.0%; Score 53; DB 2; Length 1018;
Best Local Similarity 100.0%; Pred. No. 0.037;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ONKGNQSFEE 10
DB 784 ONKGNQSFEE 793

RESULT 2

S19702
fibronectin-binding protein B - Staphylococcus aureus
C/Species: Staphylococcus aureus
C/Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #ext_change 09-Jul-2004
C/Accession: S19702
R/Joenson, K.; Signaes, C.; Mueller, H.P.; Lindberg, M.
Eur. J. Biochem. 202, 1041-1048, 1991
A/Title: Two different genes encode fibronectin binding proteins in Staphylococcus aure
A/Reference number: S19702; PMID:92111475; PMID:1837286
A/Accession: S19702
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-940 <JOF>
A/Cross-references: UNIPROT:Q53682; EMBL:X62992; NID:949040; PIDD:CAA4726.1; PID:95815
C/Keywords: fibronectin binding

Query Match 90.6%; Score 48; DB 2; Length 940;
Best Local Similarity 90.0%; Pred. No. 0.33;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ONKGNQSFEE 10
DB 682 ONKGNQSFEE 691

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RESULT 3
G90053
Hypothetical protein fnbB [imported] - Staphylococcus aureus (strain N315)
C:Species: Staphylococcus aureus
C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C:Accession: G90053
R:Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguno, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.; C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hirataesu, K.
Lancet 357, 1225-1240, 2001
A:Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.
A:Reference number: A89758; PMID:21311952; PMID:11418146
A:Accession: G90053
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-961 <KUR>
A:Cross-references: UNIPROT:Q99RD3; GB:BA000018; PID:G13702452; PIDN:BA843593.1; GSPDB:G
A:Experimental source: strain N315
C:Genetics:
A:Gene: fnbB

Query Match          90.6%; Score 48; DB 2; Length 961;
Best Local Similarity 90.0%; Pred. No. 0.33;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QNKGNSFEF 10
DB 693 QNSGNSFEF 702

RESULT 4
H90053
Hypothetical protein fnb [imported] - Staphylococcus aureus (strain N315)
C:Species: Staphylococcus aureus
C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C:Accession: H90053
R:Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguno, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.; C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hirataesu, K.
Lancet 357, 1225-1240, 2001
A:Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.
A:Reference number: A89758; PMID:21311952; PMID:11418146
A:Accession: H90053
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1038 <KUR>
A:Cross-references: UNIPROT:Q99RD2; GB:BA000018; PID:G13702453; PIDN:BA843594.1; GSPDB:G
A:Experimental source: strain N315
C:Genetics:
A:Gene: fnbB

Query Match          90.6%; Score 48; DB 2; Length 1038;
Best Local Similarity 90.0%; Pred. No. 0.36;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QNKGNSFEF 10
DB 742 QNSGNSFEF 751

RESULT 5
H86548
Polymorphic outer membrane protein E family [imported] - Chlamydomonas pneumoniae (strain N315)
C:Species: Chlamydomonas pneumoniae
C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C:Accession: H86548
R:Shirai, M.; Hirakawa, H.; Kimoto, M.; Tabuchi, M.; Kishi, F.; Ouchi, K.; Shiba, T.; Inoue, R.; Kaito, C.; Sekimizu, K.; C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hirataesu, K.
Nucleic Acids Res. 28, 2311-2314, 2000
A:Title: Comparison of whole genome sequences of Chlamydomonas pneumoniae J138.
A:Reference number: A86491; PMID:20330349; PMID:10871362
A:Accession: H86548
A:Status: preliminary
A:Molecule type: DNA

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A:Residues: 1-267 <STO>
A:Cross-references: UNIPROT:Q9RB62; GB:BA000008; NID:G8978838; PIDN:BA838674.1; GSPDB:GN
A:Experimental source: strain J138
C:Genetics:
A:Gene: pmp_17.1

Query Match          71.7%; Score 38; DB 2; Length 267;
Best Local Similarity 77.8%; Pred. No. 7.8;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 QNKGNSFEF 9
DB 123 ENKGNLSFE 131

RESULT 6
T41344
probable zinc-finger protein - fission yeast (Schizosaccharomyces pombe)
C:Species: Schizosaccharomyces pombe
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C:Accession: T41344
R:Lyne, M.; Rajandream, M.A.; Barrell, B.G.; Volkert, G.
submitted to the EMBL Data Library, January 1999
A:Reference number: 221970
A:Accession: T41344
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-767 <LVN>
A:Cross-references: UNIPROT:Q94490; EMBL:AL035076; PIDN:CAA22655.1; GSPDB:GN000066; SPDB:
A:Experimental source: strain 972h-; cosmid c417
C:Genetics:
A:Gene: SPDB:SPCC417.09C
A:Map position: 1
A:Insertions: 116/2; 256/3; 453/2
F:112-148/Domain: GAL4 zinc binuclear cluster homology <GLA>

Query Match          71.7%; Score 38; DB 2; Length 767;
Best Local Similarity 66.7%; Pred. No. 24;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 2 NKGNSFEF 10
DB 256 NKGNSFEF 264

RESULT 7
JC1245
20K protein - Bacillus thuringiensis subsp. israelensis
C:Species: Bacillus thuringiensis subsp. israelensis
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
C:Accession: JC1245
R:Yoshida, H.; Yoshida, K.; Sen, K.; Sakai, H.; Komano, T.
Biotech. Biochem. 56, 1429-1433, 1992
A:Title: Effects of Bacillus thuringiensis var. israelensis 20-kDa protein on production
A:Reference number: JC1245; PMID:93043751; PMID:1368950
A:Accession: JC1245
A:Molecule type: DNA
A:Residues: 1-182 <YOS>
A:Cross-references: UNIPROT:Q53287; GB:S48751; NID:G260183; PIDN:AAC60419.1; PID:G260184
C:Comment: This protein stimulates the production of 130K protein and may be necessary for

Query Match          69.8%; Score 37; DB 2; Length 182;
Best Local Similarity 77.8%; Pred. No. 8.2;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 NKGNSFEF 10
DB 86 NKGNSFEF 94

RESULT 8
B32256
hypothetical 20K protein - Bacillus thuringiensis subsp. israelensis

```

C/Species: *Bacillus thuringiensis* subsp. *israelensis*
 C/Date: 12-Oct-1989 #sequence_revision 12-Oct-1989 #text_change 09-Jul-2004
 C/Accession: B32256
 R/Adams, L.F.; Vistic, J.E.; Whiteley, H.R.
 J. Bacteriol. 171, 521-530, 1989
 A/Title: A 20-kilodalton protein is required for efficient production of the *Bacillus thuringiensis* delta-endotoxin
 A/Reference number: A32256; MUID:89123065; PMID:2644205
 A/Accession: B32256
 A/Status: Preliminary
 A/Molecule type: DNA
 A/Residues: 1-182 <ADA>
 A/Cross-references: UNIPROT:Q45775; EMBL:M22860; NID:9143223; PTDN:AAA22612.1; PID:9143223

Query Match 69.8%; Score 37; DB 2; Length 182;
 Best Local Similarity 77.8%; Pred. No. 8.2;
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 NKGNSFE 10
 DB 86 NKGNSLSE 94

RESULT 9
 S64339
 Probable membrane protein YGR045C - Yeast (*Saccharomyces cerevisiae*)
 N/Alternate names: hypothetical protein G4309
 C/Species: *Saccharomyces cerevisiae*
 C/Date: 17-May-1996 #sequence_revision 17-May-1996 #text_change 09-Jul-2004
 C/Accession: S64339
 R/Stratton, K.D.; Rose, M.; Koetter, P.; Roehner, A.; Sehraam, I.; Hempel, S.
 submitted to the Protein Sequence Database, May 1996
 A/Reference number: S64335
 A/Accession: S64339
 A/Molecule type: DNA
 A/Residues: 1-120 <EMT>
 A/Cross-references: UNIPROT:P53223; EMBL:Z72830; NID:91323046; PID:91323047; GSPDB:GN000
 A/Experimental source: strain S288C
 C/Genetics:
 A/Genes: MIPS:YGR045C
 A/Cross-references: SGD:S0003277
 A/Map position: 7R
 C/Species: *Saccharomyces cerevisiae*
 C/Key words: transmembrane protein
 F:67-83/Domain: transmembrane #status predicted <TMM>

Query Match 67.9%; Score 36; DB 2; Length 120;
 Best Local Similarity 60.0%; Pred. No. 8.3;
 Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 QNKGNSFE 10
 DB 47 ENKGQSAFE 56

RESULT 10
 C84792
 Hypothetical protein At2g37400 [imported] - *Arabidopsis thaliana*
 C/Species: *Arabidopsis thaliana* (mouse-ear cress)
 C/Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
 C/Accession: C84792
 R/Lin, X.; Kaul, S.; Roundley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
 M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Vanhaken, S.E.; Umayam, L.; Tallon, L.;
 Neuge, D.; Nierman, W.C.; White, O.; Eissen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.
 Nature 402, 761-768, 1999
 A/Title: Sequence and analysis of chromosome 2 of the plant *Arabidopsis thaliana*.
 A/Reference number: A84420; MUID:20083487; PMID:10617197
 A/Accession: C84792
 A/Status: Preliminary
 A/Molecule type: DNA
 A/Residues: 1-333 <STO>
 A/Cross-references: UNIPROT:Q9ZUS6; GB:AE002093; NID:94056493; PTDN:AC98059.1; GSPDB:GN
 C/Genetics:
 A/Genes: At2g37400

A/Map position: 2

Query Match 67.9%; Score 36; DB 2; Length 333;
 Best Local Similarity 70.0%; Pred. No. 24;
 Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 QNKGNSFE 10
 DB 105 QSNGNVSFE 114

RESULT 11
 H71716
 190 kD antigen precursor (gca2) RP081 - *Rickettsia prowazekii*
 C/Species: *Rickettsia prowazekii*
 C/Date: 21-Nov-1998 #sequence_revision 21-Nov-1998 #text_change 09-Jul-2004
 C/Accession: H71716
 R/Andersson, S.G.E.; Zomorodipour, A.; Andersson, J.O.; Sichenitz-Ponten, T.; Alsmark, T.
 Nature 396, 133-140, 1998
 A/Title: The genome sequence of *Rickettsia prowazekii* and the origin of mitochondria.
 A/Reference number: A71630; MUID:99039499; PMID:9823893
 A/Accession: H71716
 A/Status: Preliminary; nucleic acid sequence not shown; translation not shown
 A/Molecule type: DNA
 A/Residues: 1-341 <AND>
 A/Cross-references: UNIPROT:Q9ZB66; GB:AJ235270; GB:AJ235269; NID:93860572; PTDN:CA145
 A/Experimental source: strain Madrid E
 C/Genetics:
 A/Genes: gca2; RP081

Query Match 67.9%; Score 36; DB 2; Length 341;
 Best Local Similarity 77.8%; Pred. No. 25;
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 QNKGNSFE 9
 DB 229 QKSNOSFE 237

RESULT 12
 F83537
 4-hydroxyphenylpyruvate dioxygenase PA0865 [imported] - *Pseudomonas aeruginosa* (strain
 C/Species: *Pseudomonas aeruginosa*
 C/Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 12-Jul-2004
 C/Accession: F83537
 R/Slover, C.K.; Pham, X.Q.; Ewin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.; B
 adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim
 ; Loy, S.; Olson, M.V.
 Nature 406, 959-964, 2000
 A/Title: Complete genome sequence of *Pseudomonas aeruginosa* PA01, an opportunistic path
 A/Reference number: A82950; MUID:20437337; PMID:10984043
 A/Accession: F83537
 A/Status: Preliminary
 A/Molecule type: DNA
 A/Residues: 1-357 <STO>
 A/Cross-references: UNIPROT:Q91576; GB:AE004521; GB:AE004091; NID:99946758; PTDN:AA042
 A/Experimental source: strain PA01
 C/Genetics:
 A/Genes: hpd; PA0865
 C/Species: *Pseudomonas aeruginosa*

Query Match 67.9%; Score 36; DB 2; Length 357;
 Best Local Similarity 70.0%; Pred. No. 26;
 Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 QNKGNSFE 10
 DB 328 QNKGNSFE 337

RESULT 13
 C82211
 4-hydroxyphenylpyruvate dioxygenase VC1344 [imported] - *Vibrio cholerae* (strain N16961

C/Species: *Vibrio cholerae*
 C/Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 12-Jul-2004
 C/Accession: C82211
 R/Heldelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwin, M.L.; Dodson, R.J.;
 Chardon, D.; Ermolaeva, M.D.; Vamathevan, J.; Baas, S.; Qin, H.; Dragol, I.; Sellers, F.
 L. R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
 Nature 406, 477-483, 2000
 A/Title: DNA Sequence of both chromosomes of the cholera pathogen *Vibrio cholerae*.
 A/Reference number: AB2035; NCID:20406833; PMID:10952301
 A/Accession: C82211
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-359 <HEI>
 A/Cross-references: UNIPROT:Q9RCH2; GB:AE004214; GB:AE003852; NID:g9655832; PIDN:AAF9450
 A/Experimental source: serogroup O1; strain N16961; biotype El Tor
 C/Genetics:
 A/Gene: VC1344
 A/Map position: 1
 C/Superfamily: 4-hydroxyphenylpyruvate_dioxygenase

Query Match 67.9%; Score 36; DB 2; Length 369;
 Best Local Similarity 70.0%; Pred. No. 27;
 Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 QNKGNSFEE 10
 DB 337 QKKGSGFGE 346

RESULT 14
 A70176
 trigger factor (tig) homolog - Lyme disease spirochete
 C/Species: *Borrelia burgdorferi* (Lyme disease spirochete)
 C/Date: 13-Feb-1998 #sequence_revision 13-Feb-1998 #text_change 09-Jul-2004
 C/Accession: A70176
 R/Fraser, C.M.; Castjens, S.; Huang, W.M.; Sutton, G.G.; Clayton, R.; Lathigra, R.; White
 son, D.; Peterson, J.; Kerlavage, A.R.; Quackenbush, J.; Salzberg, S.; Hanson, M.; Vugt,
 ; Bowman, C.; Garland, S.; Fujii, C.; Cotton, M.D.; Horst, K.; Roberts, K.; Hatch, B.
 Nature 390, 580-586, 1997
 A/Authors: Smith, H.O.; Venter, J.C.
 A/Title: Genomic sequence of a Lyme disease spirochete, *Borrelia burgdorferi*.
 A/Reference number: A70100; NCID:98065943; PMID:9403685
 A/Accession: A70176
 A/Status: preliminary; nucleic acid sequence not shown; translation not shown
 A/Molecule type: DNA
 A/Residues: 1-454 <RLS>
 A/Cross-references: UNIPROT:O51555; GB:AE001162; GB:AE000783; NID:g2688528; PIDN:AA06696
 A/Experimental source: strain B31
 C/Superfamily: PKBP-type peptidyl-prolyl cis-trans isomerase (trigger factor); BKBP-type

Query Match 67.9%; Score 36; DB 2; Length 454;
 Best Local Similarity 70.0%; Pred. No. 34;
 Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 QNKGNSFEE 10
 DB 331 QNKNMSLEB 340

RESULT 15
 JQ0181
 replication protein repB - *Lactobacillus plantarum*
 C/Species: *Lactobacillus plantarum*
 C/Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 09-Jul-2004
 C/Accession: JQ0181
 R/Bates, E.E.M.; Gilbert, H.J.
 Gene 85, 253-259, 1989
 A/Title: Characterization of a cryptic plasmid from *Lactobacillus plantarum*.
 A/Reference number: JQ0179; NCID:90152374; PMID:2695401
 A/Contents: plasmid pLB4, strain NCDO1088
 A/Accession: JQ0181
 A/Molecule type: DNA
 A/Residues: 1-218 <BAT>

A/Cross-references: UNIPROT:P20045; GB:M33531; NID:G149593; PIDN:AAA25254.1; PID:G149596
 C/Genetics:
 A/Gene: repB

Query Match 66.0%; Score 35; DB 2; Length 218;
 Best Local Similarity 75.0%; Pred. No. 25;
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 KGNOSFEE 10
 DB 80 KKNKSFEEQ 87

Search completed: October 22, 2005, 08:04:37
 Job time : 12.45 sec

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OM protein - protein search, using sw model

Run on: October 22, 2005, 06:06:36 ; Search time 55.85 Seconds
(without alignments)
91.688 Million cell updates/sec

Title: US-10-731-238-82
Perfect score: 53
Sequence: 1 QNKGQSFEE 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: UniProt_03.*
1: uniProt_sprot.*
2: uniProt_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	53	100.0	1018	1 FNBA_STAUA	P14738 staphylococ
2	48	90.6	152	2 Q9AEP9	Q9AEP9 staphylococ
3	48	90.6	940	2 Q51682	Q51682 staphylococ
4	48	90.6	943	2 Q8NUU8	Q8NUU8 staphylococ
5	48	90.6	957	2 Q6G6H4	Q6G6H4 staphylococ
6	48	90.6	961	2 Q93RD3	Q93RD3 staphylococ
7	48	90.6	961	2 Q7A3J8	Q7A3J8 staphylococ
8	48	90.6	965	2 Q6GDUS	Q6GDUS staphylococ
9	48	90.6	1015	2 Q8NUU7	Q8NUU7 staphylococ
10	48	90.6	1015	2 Q6G6H3	Q6G6H3 staphylococ
11	48	90.6	1038	2 Q93RD2	Q93RD2 staphylococ
12	48	90.6	1038	2 Q7A3J7	Q7A3J7 staphylococ
13	45	84.9	702	1 CANB_HUMAN	Q9UMG6 homo sapien
14	40	75.5	103	2 Q8PTY3	Q8PTY3 methanosarc
15	40	75.5	975	2 Q68CQ8	Q68CQ8 homo sapien
16	39	73.6	430	2 Q6DCK0	Q6DCK0 xenopus lae
17	39	73.6	543	2 Q8JHP9	Q8JHP9 xenopus lae
18	39	73.6	543	2 Q7ZMU1	Q7ZMU1 xenopus lae
19	39	73.6	1576	2 Q61RM6	Q61RM6 xenopus lae
20	38	71.7	250	2 Q7VVO6	Q7VVO6 chlamydia p
21	38	71.7	267	2 Q9RB62	Q9RB62 chlamydia p
22	38	71.7	486	2 Q8LDB8	Q8LDB8 arabidopsis
23	38	71.7	486	2 Q8H0X2	Q8H0X2 arabidopsis
24	38	71.7	767	2 Q94490	Q94490 echinosacch
25	37	69.8	177	2 Q6DDL3	Q6DDL3 xenopus lae
26	37	69.8	182	2 Q54775	Q54775 bacillus th
27	37	69.8	182	2 Q53287	Q53287 bacillus th
28	37	69.8	182	2 Q7AL75	Q7AL75 bacillus th
29	37	69.8	182	2 Q83ZNP	Q83ZNP bacillus th
30	37	69.8	182	2 Q83ZP0	Q83ZP0 bacillus th
31	37	69.8	182	2 Q83ZP1	Q83ZP1 bacillus th

ALIGNMENTS

RESULT 1	FNBA_STAUA	STANDARD;	PRT;	1018 AA.	
ID	FNBA_STAUA				
AC	P14738;				
DT	01-APR-1990 (Rel. 14, Created)				
DT	01-APR-1990 (Rel. 14, Last sequence update)				
DT	25-OCT-2004 (Rel. 45, Last annotation update)				
DE	Fibronectin-binding protein precursor (FNBP).				
GN	Name=fnba;				
OS	Staphylococcus aureus.				
OC	Bacteria; Firmicutes; Bacillales; Staphylococcus.				
OX	NCBI_TaxID=1280;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=NTC 8325-4;				
RX	MEDLINE=8909898; PubMed=2521391;				
RA	Signaes G., Raucel G., Joensson K., Lindgren P.-E.,				
RA	Anantharamiah G.M., Hoeck M., Lindberg M.;				
RT	"Nucleotide sequence of the gene for a fibronectin-binding protein				
RT	from Staphylococcus aureus: use of this peptide sequence in the				
RT	synthesis of biologically active peptides."				
RL	Proc. Natl. Acad. Sci. U.S.A. 86:1699-703(1989).				
CC	-1- FUNCTION: The ability of bacteria to bind fibronectin has been				
CC	proposed as a virulence factor enabling bacteria to colonize wound				
CC	tissues and blood clots. Binding of plasma fibronectin to the				
CC	bacterial surface might block adhesion receptors on S.aureus, thus				
CC	representing an important defense mechanism against tissue				
CC	invasion.				
CC	-1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by				
CC	an amide bond (Potential).				
CC	-----				
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration				
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -				
CC	the European Bioinformatics Institute. There are no restrictions on its				
CC	use by non-profit institutions as long as its content is in no way				
CC	modified and this statement is not removed. Usage by and for commercial				
CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/				
CC	or send an email to license@isb-sib.ch).				
CC	-----				
DR	EMBL: J04151; AAA26632.1; -				Q9RED4 bacillus th
DR	InterPro: IPR004237; Fm bind.				Q9SE66 bacillus th
DR	InterPro: IPR005877; GPos_XSIRK.				Q9SE67 bacillus th
DR	InterPro: IPR001899; Gram_pos_anchor.				Q9SE68 bacillus th
DR	Pfam: PF02986; Fm bind. 1.				Q9X702 bacillus th
DR	Pfam: PF00746; Gram_pos_anchor; 1.				Q8CRP6 staphylococ
DR	Pfam: PF04650; XSIRK signal; 1.				P53229 saccharomyc
DR	TIGRFAMS: TIGR01167; LPXG anchor; 1.				Q81932 arabidopsis
DR	TIGRFAMS: TIGR01166; XSIRK signal; 1.				Q9ZUS6 arabidopsis
DR	Cell adhesion; Cell wall; Peptidoglycan-anchor; Repeat; Signal;				Q9ZEB6 rickettsia
DR	Virulence.				Q53407 legionella
FT	SIGNAL	1	36		Q91576 pseudomonas
FT	CHAIN	37	985		Q629G1 burkholderi
FT	PROPEP	986	1018		
					Fibronectin-binding protein.
					Removed by sortase (Potential).

```

FT REPEAT 545 574 B-1.
FT REPEAT 575 604 B-2.
FT DOMAIN 745 878 4 X approximate tandem repeats,
  fibronectin-binding domain.
FT REPEAT 745 782 D-1.
FT REPEAT 783 820 D-2.
FT REPEAT 821 859 D-3.
FT REPEAT 860 878 D-4 (incomplete).
FT DOMAIN 879 948 5 X tandem repeats, Pro-rich (WR).
FT REPEAT 879 892 WR 1.
FT REPEAT 893 906 WR 2.
FT REPEAT 907 920 WR 3.
FT REPEAT 921 934 WR 4.
FT REPEAT 935 948 WR 5.
FT SITE 982 986 LpXTG sorting signal (Potential).
FT MOTIF 985 985 Pentaglycyl murein peptidoglycan amidated
  theonine (Potential).
SQ SEQUENCE 1018 AA; 111780 MW; 58175E020E81F1F CRC64;

Query Match 100.0%; Score 53; DB 1; Length 1018;
Best Local Similarity 100.0%; Pred. No. 0.17;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ONKNGSFEE 10
Db 784 ONKNGSFEE 793

RESULT 2
Q9AEP9 PRELIMINARY; PRT; 152 AA.
AC Q9AEP9;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Fibronectin-binding protein (Fragment).
GN Name=fnb;
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1280;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CMRSA-1;
RX MEDLINE=21246681; PubMed=11349044;
DOI=10.1128/IAI.69.6.3791-3799.2001;
RA Rice K., Huesca M., Vaz D., McGavin M.J.;
"Variance in fibronectin binding and fnb locus polymorphisms in
RT Staphylococcus aureus: identification of antigenic variation in a
RT fibronectin binding protein adhesin of the epidemic CMRSA-1 strain of
RT methicillin-resistant S. aureus.";
RL Infect. Immun. 69:3791-3799(2001).
DR EMBL; AY029184; AAK31588.1; -.
FT NON_TER 1 1
FT NON_TER 152 152
SQ SEQUENCE 152 AA; 17193 MW; CFA3913C2B11C025 CRC64;

Query Match 90.6%; Score 48; DB 2; Length 152;
Best Local Similarity 90.0%; Pred. No. 0.2;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ONKNGSFEE 10
Db 39 ONKNGSFEE 48

RESULT 3
Q53682 PRELIMINARY; PRT; 940 AA.
AC Q53682;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Fibronectin binding protein B.

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GN Name=fnbB;
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1280;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=8325-4;
RX MEDLINE=92111475; PubMed=1837266;
RA Jonsson K., Signas C., Muller H.P., Lindberg M.;
"Two different genes encode fibronectin binding proteins in
RT Staphylococcus aureus. The complete nucleotide sequence and
RT characterization of the second gene.";
RL Eur. J. Biochem. 202:1041-1048(1991).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
  an amide bond (By similarity).
DR EMBL; X62992; CAA44726.1; -.
DR PIR; S19702; S19702.
DR HSSP; Q53653; 1N67.
DR GO; GO:0009986; C:cell surface; IEA.
DR GO; GO:0005618; C:cell wall; IEA.
DR GO; GO:0002275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:007155; P:cell adhesion; IEA.
DR InterPro; IPR008966; Adhes_bact.
DR InterPro; IPR004237; Fn_bind.
DR InterPro; IPR005877; Gpos_YsIRK.
DR InterPro; IPR001899; Gram_pos_anchor.
DR Pfam; PF02986; Fn_bind; 2.
DR Pfam; PF00746; Gram_pos_anchor; 1.
DR Pfam; PF04650; YsIRK_signal; 1.
DR TIGRFAMs; TIGR01167; LpXTG_anchor; 1.
DR TIGRFAMs; TIGR01168; YsIRK_signal; 1.
DR PROSITE; PS50847; GRAM_POS_ANCHORING; 1.
KW Cell wall; Peptidoglycan-anchor.
SQ SEQUENCE 940 AA; 103555 MW; E35FBBCA907AE345 CRC64;

Query Match 90.6%; Score 48; DB 2; Length 940;
Best Local Similarity 90.0%; Pred. No. 1.6;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ONKNGSFEE 10
Db 682 ONKNGSFEE 691

RESULT 4
Q8NUU8 PRELIMINARY; PRT; 943 AA.
AC Q8NUU8;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE FnB protein.
GN Name=fnbB; OrderedLocusNames=MW2420;
OS Staphylococcus aureus (strain MW2).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=196620;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MW2;
RX MEDLINE=22040717; PubMed=12044378; DOI=10.1016/S0140-6736(02)08713-5;
RA Baba T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Oguchi A.,
RA Nagai Y., Iwana N., Asano K., Naito T., Kuroda H., Cui L.,
RA Yamamoto K., Hiramatsu K.;
"Genome and virulence determinants of high virulence community-
RT acquired MRSA.";
RL Lancet 359:1819-1827(2002).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
  an amide bond (By similarity).
DR EMBL; AP004830; BAB96285.1; -.
DR HSSP; Q53653; 1N67.
DR GO; GO:0009986; C:cell surface; IEA.
DR GO; GO:0005618; C:cell wall; IEA.

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DR GO; GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0007155; P:cell adhesion; IEA.
 DR InterPro: IPR008966; Adhes_bact.
 DR InterPro: IPR004237; Fn_bind.
 DR InterPro: IPR005877; Gpos_YsIRK.
 DR InterPro: IPR001899; Gram_pos_anchor.
 DR Pfam: PF02986; Fn_bind; 1.
 DR Pfam: PF02986; Gram_pos_anchor; 1.
 DR Pfam: PF04650; YsIRK_signal; 1.
 DR TIGRfams: TIGR01167; LPXTG_anchor; 1.
 DR TIGRfams: TIGR01168; YsIRK_signal; 1.
 DR PROSITE: PS50847; GRAM_POS_ANCHORING; 1.
 DR Cell wall; Complete proteome; Peptidoglycan-anchor.
 KW SEQUENCE 943 AA; 104537 MW; DA8A5F31947E1B6A CRC64;
 SQ

Query Match 90.6%; Score 48; DB 2; Length 943;
 Best Local Similarity 90.0%; Pred. No. 1.6;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QNKGNSFEE 10
 DB 689 QNKGNSFEE 698

RESULT 5
 Q6G6H4 PRELIMINARY; PRT; 957 AA.
 AC Q6G6H4;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DE Fibronectin-binding protein.
 GN Name=fndB: OrderedLocusNames=SA52387;
 OS Staphylococcus aureus (strain MSSA476).
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 OX NCBI_TaxID=282459;
 RX SEQUENCE FROM N.A.
 RP PubMed=15213324; DOI=10.1073/pnas.040251101;
 RA Holden M.T.G., Fell E.J., Lindsay J.A., Peacock S.J., Day N.P.J.,
 RA Enright M.C., Foster T.J., Moore C.E., Huret L., Atkin R., Barron A.,
 RA Baeson N., Bentley S.D., Chillingworth C., Chillingworth T.,
 RA Churcher C., Clark L., Corton C., Cronin A., Doggett J., Dowd L.,
 RA Felwell T., Hance Z., Harris B., Hauser H., Holtroyd S., Jagels K.,
 RA James K.D., Lennard N., Line A., Mayes R., Moule S., Mungall K.,
 RA Omond D., Quail M.A., Rabinowitch E., Rutherford K.M., Sanders M.,
 RA Sharp S., Simmonds M., Stevens K., Whitehead S., Barrett B.G.,
 RA Spratt B.G., Parkhill J.;
 RT "Complete genomes of two clinical Staphylococcus aureus strains:
 RT evidence for the rapid evolution of virulence and drug resistance.";
 RL Proc. Natl. Acad. Sci. U.S.A. 101:9786-9791(2004).
 CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
 CC an amide bond (By similarity).
 CC EMBL: BX571857; CAG44201.1;
 DR GO; GO:0009986; C:cell surface; IEA.
 DR GO; GO:0005618; C:cell wall; IEA.
 DR GO; GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0007155; P:cell adhesion; IEA.
 DR InterPro: IPR008966; Adhes_bact.
 DR InterPro: IPR004237; Fn_bind.
 DR InterPro: IPR005877; Gpos_YsIRK.
 DR InterPro: IPR001899; Gram_pos_anchor.
 DR Pfam: PF02986; Fn_bind; 1.
 DR Pfam: PF02986; Gram_pos_anchor; 1.
 DR Pfam: PF04650; YsIRK_signal; 1.
 DR TIGRfams: TIGR01167; LPXTG_anchor; 1.
 DR TIGRfams: TIGR01168; YsIRK_signal; 1.
 DR PROSITE: PS50847; GRAM_POS_ANCHORING; 1.
 KW Cell wall; Complete proteome; Peptidoglycan-anchor.
 SQ SEQUENCE 957 AA; 105980 MW; 28F8BA7FFDD3EAF CRC64;
 SQ

Query Match 90.6%; Score 48; DB 2; Length 957;
 Best Local Similarity 90.0%; Pred. No. 1.6;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QNKGNSFEE 10
 DB 689 QNKGNSFEE 698

RESULT 6
 Q99RD3 PRELIMINARY; PRT; 961 AA.
 ID Q99RD3;
 AC Q99RD3;
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Fibronectin-binding protein homolog.
 GN Name=fndB: OrderedLocusNames=SAV2502;
 OS Staphylococcus aureus (strain Mu50 / ATCC 700699).
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 OX NCBI_TaxID=158878;
 RX SEQUENCE FROM N.A.
 RP STRAIN=Mu50 / ATCC 700699;
 RC MEDLINE=21311952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2;
 RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
 RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Iian J.-O., Ito T.,
 RA Kanamori M., Matsunari H., Maruyama A., Murakami H., Hoshiyama A.,
 RA Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
 RA Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
 RA Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
 RA Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
 RT "Whole genome sequencing of methicillin-resistant Staphylococcus
 RT aureus.";
 RL Lancet 357:1225-1240(2001).
 CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
 CC an amide bond (By similarity).
 CC EMBL: AP003365; BAB58664.1;
 DR DR PIR: G90053; G90053.
 DR HSSP: Q53653; 1N67.
 DR GO; GO:0009986; C:cell surface; IEA.
 DR GO; GO:0005618; C:cell wall; IEA.
 DR GO; GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0007155; P:cell adhesion; IEA.
 DR InterPro: IPR008966; Adhes_bact.
 DR InterPro: IPR004237; Fn_bind.
 DR InterPro: IPR005877; Gpos_YsIRK.
 DR InterPro: IPR001899; Gram_pos_anchor.
 DR Pfam: PF02986; Fn_bind; 1.
 DR Pfam: PF02986; Gram_pos_anchor; 1.
 DR Pfam: PF04650; YsIRK_signal; 1.
 DR TIGRfams: TIGR01167; LPXTG_anchor; 1.
 DR TIGRfams: TIGR01168; YsIRK_signal; 1.
 DR PROSITE: PS50847; GRAM_POS_ANCHORING; 1.
 KW Cell wall; Complete proteome; Peptidoglycan-anchor.
 SQ SEQUENCE 961 AA; 106010 MW; 364940F884E4A4101 CRC64;
 SQ

Query Match 90.6%; Score 48; DB 2; Length 961;
 Best Local Similarity 90.0%; Pred. No. 1.6;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QNKGNSFEE 10
 DB 693 QNKGNSFEE 702

RESULT 7
 Q7A3J8 PRELIMINARY; PRT; 961 AA.
 ID Q7A3J8;
 AC Q7A3J8;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)

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DT 05-JUL-2004 (TrEMBLrel. 27, last annotation update)
DE FndB protein.
GN Name=fndB; OrderedLocustNames=SA2290;
OS Staphylococcus aureus (strain N315).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=158879;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21311952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2;
RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Iian J.-Q., Ito T.,
RA Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,
RA Mizutani-Uji Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
RA Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
RA Kanehisa M., Yamashita A., Ohnaka K., Furuya K., Yoshino C., Shida T.,
RA Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
RT "Whole genome sequencing of methicillin-resistant Staphylococcus
RT aureus";
RL Lancet 357:1225-1240(2001).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC an amide bond (By similarity).
DR EMBL; AP003137; BAB43593.1; -.
DR GO; GO:0009986; C:cell surface; IEA.
DR GO; GO:0005618; C:cell wall; IEA.
DR GO; GO:0009275; C:cell wall (sensus Gram-positive Bacteria); IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0007155; P:cell adhesion; IEA.
DR InterPro; IPR008966; Adhes_Dact.
DR InterPro; IPR004237; Fn_bind.
DR InterPro; IPR005877; GPos_YsIRK.
DR InterPro; IPR001899; Gram_pos_anchor.
DR Pfam; PF02986; Fn_bind; 1.
DR Pfam; PF00746; Gram_pos_anchor; 1.
DR Pfam; PF04650; YsIRK_signal; 1.
DR TIGRFAMs; TIGR01167; LPXTG_anchor; 1.
DR TIGRFAMs; TIGR01168; YsIRK_signal; 1.
DR PROSITE; PS50847; GRAM_POS_ANCHORING; 1.
KW Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ SEQUENCE 961 AA; 106010 MW; 364940F84E4A101 CRC64;

Query Match 90.6%; Score 48; DB 2; Length 961;
Best Local Similarity 90.0%; Pred. No. 1.6;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QNKGNSFEE 10
Db 693 QNKGNSFEE 702

RESULT 8
Q6GDUS PRELIMINARY; PRT; 965 AA.
ID Q6GDUS;
AC Q6GDUS;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Fibronectin-binding protein.
GN Name=fndA; OrderedLocustNames=SA2580;
OS Staphylococcus aureus (strain MRSA252).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=282458;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=15213324; DOI=10.1073/pnas.0402521101;
RA Hoiden M.T.G., Foster T.J., Moore C.E., Peacock S.J., Day N.P.J.,
RA Ehrlich M.C., Foster T.J., Moore C.E., Hurst L., Atkin R., Barron A.,
RA Bacon N., Bentley S.D., Chillingworth C., Chillingworth T.,
RA Churcher C., Clark L., Cotton C., Cronin A., Doggett J., Dowd L.,
RA Felwell T., Hance Z., Harris B., Hauser H., Holtroyd S., Jagsels K.,
RA James K.D., Lennard N., Line A., Mayes R., Moule S., Mungall K.,
RA Omond D., Quail M.A., Rabinowitch E., Rutherford K.M., Sanders M.,
RA Sharp S., Simmonds M., Stevens K., Whitehead S., Barrett B.G.,
RA Spratt B.G., Parkhill J.;

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RT "Complete genomes of two clinical Staphylococcus aureus strains:
RT evidence for the rapid evolution of virulence and drug resistance.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:9786-9791(2004)
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC an amide bond (By similarity).
DR EMBL; BX571856; CAG4560.1; -.
DR GO; GO:0009986; C:cell surface; IEA.
DR GO; GO:0009275; C:cell wall (sensus Gram-positive Bacteria); IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0007155; P:cell adhesion; IEA.
DR InterPro; IPR008966; Adhes_Dact.
DR InterPro; IPR004237; Fn_bind.
DR InterPro; IPR005877; GPos_YsIRK.
DR InterPro; IPR001899; Gram_pos_anchor.
DR Pfam; PF02986; Fn_bind; 1.
DR Pfam; PF00746; Gram_pos_anchor; 1.
DR Pfam; PF04650; YsIRK_signal; 1.
DR TIGRFAMs; TIGR01167; LPXTG_anchor; 1.
DR TIGRFAMs; TIGR01168; YsIRK_signal; 1.
DR PROSITE; PS50847; GRAM_POS_ANCHORING; 1.
KW Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ SEQUENCE 965 AA; 105691 MW; 2982B132164D0551 CRC64;

Query Match 90.6%; Score 48; DB 2; Length 965;
Best Local Similarity 90.0%; Pred. No. 1.6;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QNKGNSFEE 10
Db 749 QNKGNSFEE 758

RESULT 9
Q8NUU7 PRELIMINARY; PRT; 1015 AA.
ID Q8NUU7;
AC Q8NUU7;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE FndB protein.
GN Name=fndB; OrderedLocustNames=MM2421;
OS Staphylococcus aureus (strain MM2).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=196620;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=MM2;
RX MEDLINE=22040717; PubMed=12044378; DOI=10.1016/S0140-6736(02)08713-5;
RA Baba T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Oguchi A.,
RA Nagai Y., Iwano N., Asano K., Naimi T., Kuroda H., Cui L.,
RA Yamamoto K., Hiramatsu K.;
RT "Genome and virulence determinants of high virulence community-
RT acquired MRSA.";
RL Lancet 359:1819-1827(2002).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC an amide bond (By similarity).
DR EMBL; AP004830; BAB95286.1; -.
DR GO; GO:0009986; C:cell surface; IEA.
DR GO; GO:0005618; C:cell wall; IEA.
DR GO; GO:0009275; C:cell wall (sensus Gram-positive Bacteria); IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0007155; P:cell adhesion; IEA.
DR InterPro; IPR008966; Adhes_Dact.
DR InterPro; IPR004237; Fn_bind.
DR InterPro; IPR005877; GPos_YsIRK.
DR InterPro; IPR001899; Gram_pos_anchor.
DR Pfam; PF02986; Fn_bind; 1.
DR Pfam; PF00746; Gram_pos_anchor; 1.
DR Pfam; PF04650; YsIRK_signal; 1.
DR TIGRFAMs; TIGR01167; LPXTG_anchor; 1.
DR TIGRFAMs; TIGR01168; YsIRK_signal; 1.
DR PROSITE; PS50847; GRAM_POS_ANCHORING; 1.
KW Cell wall; Complete proteome; Peptidoglycan-anchor.

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SQ SEQUENCE 1015 AA; 111145 MW; DDP9281BB64D4D2 CRC64;
 Query Match 90.6%; Score 48; DB 2; Length 1015;
 Best Local Similarity 90.0%; Pred. No. 1.7;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QNKGNSFEE 10
 DB 747 QNKGNSFEE 756

RESULT 10
 Q6G6H3 PRELIMINARY; PRT; 1015 AA.
 AC Q6G6H3;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Fibronectin-binding protein.
 GN OrderedLocuNames=SA52338;
 OS Staphylococcus aureus (strain MSSA476).
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 NC NCB1_TaxID=282459;
 RX SEQUENCE FROM N.A.
 RP PubMed=1521324; DOI=10.1073/pnas.0402521101;
 RA Holden M.T.G., Fell E.J., Lindsay J.A., Peacock S.J., Day N.P.J.,
 RA Bright M.C., Foster T.J., Moore C.B., Hurst L., Atkin R., Barron A.,
 RA Bason N., Bentley S.D., Chillingworth C., Chillingworth T.,
 RA Churcher C., Clark L., Cotton C., Cronin A., Doggett J., Dowd L.,
 RA Feltham D., Hance Z., Harris B., Hauser H., Holtroyd S., Jagsels K.,
 RA James K.D., Lennard N., Line A., Mayes R., Mungall K.,
 RA Sharp S., Simmonds M., Stevens K., Whitehead S., Barrall B.G.,
 RA Spratt B.G., Parkhill J.,
 RT "Complete genomes of two clinical Staphylococcus aureus strains:
 RT evidence for the rapid evolution of virulence and drug resistance."
 RL Proc. Natl. Acad. Sci. U.S.A. 101:9786-9791(2004).
 CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
 CC an amide bond (by similarity).
 DR EMBL: BX571857; CAC44202.1;
 DR GO: GO:0009986; C:cell surface; IEA.
 DR GO: GO:0005618; C:cell wall; IEA.
 DR GO: GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
 DR GO: GO:0016020; C:membrane; IEA.
 DR GO: GO:007155; P:cell adhesion; IEA.
 DR InterPro: IPR008966; Adhes_bact.
 DR InterPro: IPR004237; Gpos_YsIRK.
 DR InterPro: IPR001899; Gram_pos_anchor.
 DR Pfam: PF02986; Fn_bind.1.
 DR Pfam: PF00746; Gram_pos_anchor.1.
 DR Pfam: PF04650; YsIRK_signal.1.
 DR TIGRFAMs: TIGR01167; LPTXG_anchor.1.
 DR TIGRFAMs: TIGR01168; YsIRK_signal.1.
 DR PROSITE: PSS0847; GRAM_POS_ANCHORING.1.
 KM Cell wall; Complete proteome; Peptidoglycan-anchor.
 SQ SEQUENCE 1015 AA; 111145 MW; DDP9281BB64D4D2 CRC64;

DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Fibronectin-binding protein homolog.
 GN Name=fnb; OrderedLocuNames=SAV2503;
 OS Staphylococcus aureus (strain Mu50 / ATCC 700699).
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 NC NCB1_TaxID=158878;
 RX SEQUENCE FROM N.A.
 RP STRAIN=Mu50 / ATCC 700699;
 RC MEDLINE=21311952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2;
 RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
 RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Iian J.-Q., Ito T.,
 RA Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,
 RA Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
 RA Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
 RA Kanehisa M., Yamashita N., Oshima K., Furuya K., Yoshino C., Shiba T.,
 RA Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.,
 RT "Whole genome sequencing of methicillin-resistant Staphylococcus
 RT aureus."
 RL Lancet 357:1225-1240(2001).
 CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
 CC an amide bond (by similarity).
 DR EMBL: AP003365; BAB58665.1;
 DR PIR: H90053; H90053.
 DR GO: GO:0009986; C:cell surface; IEA.
 DR GO: GO:0005618; C:cell wall; IEA.
 DR GO: GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
 DR GO: GO:0016020; C:membrane; IEA.
 DR GO: GO:007155; P:cell adhesion; IEA.
 DR InterPro: IPR008966; Adhes_bact.
 DR InterPro: IPR004237; Gpos_YsIRK.
 DR InterPro: IPR005877; Gpos_YsIRK.
 DR InterPro: IPR001899; Gram_pos_anchor.
 DR Pfam: PF02986; Fn_bind.1.
 DR Pfam: PF00746; Gram_pos_anchor.1.
 DR Pfam: PF04650; YsIRK_signal.1.
 DR TIGRFAMs: TIGR01167; LPTXG_anchor.1.
 DR TIGRFAMs: TIGR01168; YsIRK_signal.1.
 DR PROSITE: PSS0847; GRAM_POS_ANCHORING.1.
 KM Cell wall; Complete proteome; Peptidoglycan-anchor.
 SQ SEQUENCE 1038 AA; 113618 MW; 666BF6BF2BFEB12 CRC64;

Query Match 90.6%; Score 48; DB 2; Length 1038;
 Best Local Similarity 90.0%; Pred. No. 1.7;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QNKGNSFEE 10
 DB 742 QNKGNSFEE 751

RESULT 12
 Q7A3J7 PRELIMINARY; PRT; 1038 AA.
 AC Q7A3J7;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Fnb protein.
 GN Name=fnb; OrderedLocuNames=SA2291;
 OS Staphylococcus aureus (strain N315).
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 NC NCB1_TaxID=158879;
 RX SEQUENCE FROM N.A.
 RP MEDLINE=21311952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2;
 RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
 RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Iian J.-Q., Ito T.,
 RA Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,
 RA Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
 RA Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
 RA Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,

RA	Heterot.M., Ogasawara N., Hayashi R., Hiratsuki K.;
RT	"Whole genome sequencing of methicillin-resistant Staphylococcus
CC	aureus";
RL	Lancet 357:1225-1240(2001).
DR	-1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC	an amide bond (By similarity).
DR	EMBL: AP003137; BAB3594.1; -.
DR	GO: GO:0009986; C:cell surface; IEA.
DR	GO: GO:0005618; C:cell wall; IEA.
DR	GO: GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR	GO: GO:0016020; C:membrane; IEA.
DR	GO: GO:0007155; P:cell adhesion; IEA.
DR	InterPro: IPR008966; Adhes_bact.
DR	InterPro: IPR004237; Fn_bind
DR	InterPro: IPR005877; GPos_XSTRK.
DR	InterPro: IPR01899; Gram_pos_anchor.
DR	Pfam: PF00746; Gram_pos_anchor; 1.
DR	Pfam: PF04650; XSTRK_signal; 1.
DR	TIGRFAMs: TIGR01167; LPTXG_anchor; 1.
DR	TIGRFAMs: TIGR01168; XSTRK_signal; 1.
DR	PROSITE, PS50847; GRAM_POS_ANCHORING; 1.
KW	Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ	SEQUENCE 1038 AA; 113618 MW; 66BFBFB2BFEB12 CRC64;
OY	1 ONKGNSPFEI 10
Db	742 ONSGNOSFEE 751
Query Match	Beet Local Similarity 90.6%; Score 48; DB 2; Length 1038;
Matches	9; Conservative 0; Mismatches 1; Indels 0; Gaps
<hr/>	
RESULT 13	
ID	CANB_HUMAN STANDARD; PRT; 702 AA.
AC	Q5UOQ6; OSNARS; .
DT	16-OCT-2001 (Rel. 40, Created)
DT	16-OCT-2001 (Rel. 40, Last sequence update)
DE	25-OCT-2004 (Rel. 45, Last annotation update)
DE	Calpain 11 (EC 3.4.22.-) (Calcium-activated neutral proteinase 11)
DE	(CAMP 11)..
GN	Name=CAP11;
OS	Homo sapiens (Human).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX	NCLT_TaxID=9606;
RN	[1]
RP	SEQUENCE FROM N.A.
RP	MEBIJIN=9933989; PubMed=10409436; DOI=10.1006/geno.1999.5859;
RA	Dear T.N., Molter A., Boehm T.;
RT	"CAP11: a calpain with high mRNA levels in testis and located on
RT	chromosome 6.";
RL	Genomics 59:243-247(1999).
RN	[2]
RP	SEQUENCE FROM N.A.
RP	TISSUE=Brain;
RC	MEBIJIN=22388857; PubMed=12477932; DOI=10.1073/pnas.242603699;
RA	Strauberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA	Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuller G.D.,
RA	Aleschli S.F., Zeeberg B., Buelow K.H., Schaefer C.F., Bhat N.K.,
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heist F.,
RA	Dlachon L., Marusina K., Farmer A.A., Rubin G.W., Hong L.,
RA	Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA	Brownstein W.J., Usdin T.B., Tohyaki S., Carrinci P., Prange C.,
RA	Raha S.S., Loggellano N.A., Peters G.J., Adamson R.D., Mullaly S.J.,
RA	Boesk S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunnarste P.H.,
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Huliy S.W.,
RA	Villaiano D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA	Fahay J., Helton E., Kettelman M., Madan A., Rodriques S., Sanchez A.,
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

```

RT      "generation and initial analysis of more than 15,000 full-length human
RA      and mouse cDNA sequences.";
RA      Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)'.
RL      -1- FUNCTION: Calcium-regulated non-lysosomal thiol-protease which
CC      catalyze limited proteolysis of substrates involved in
CC      cytoskeletal remodeling and signal transduction.
CC      -1- CATALYTIC ACTIVITY: Broad endopeptidase specificity.
CC      -1- SUBUNIT: Heterodimer of a large (catalytic) and a small
CC      (regulatory) subunit.
CC      -1- TISSUE SPECIFICITY: Highest expression in testis.
CC      -1- SIMILARITY: Belongs to the peptidase C2 family.
CC      -1- SIMILARITY: Contains 1 calpain catalytic domain.
CC      -1- SIMILARITY: Contains 2 EF-hand calcium-binding domains.
CC      -----
CC      This SWISS-PROT entry is copyright. It is produced through a collaboration
CC      between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC      the European Bioinformatics Institute. There are no restrictions on its
CC      use by non-profit institutions as long as its content is in no way
CC      modified and this statement is not removed. Usage by and for commercial
CC      entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC      or send an email to license@isb-sib.ch).
CC      -----
DR      EMBL: AJ248832; CAB52137.1; -.
DR      EMBL: BC033733; AAH33733.1; -.
DR      HSSP: Q07009; IMDW.
DR      MEROPS: C02.013; -.
DR      Genew: HGNC:1478; CAPN11.
DR      MIM: 604822; -.
DR      GO: GO:0004198; F:calpain activity; TAS.
DR      GO: GO:0008233; F:peptidase activity; TAS.
DR      InterPro: IPR002048; EF-hand.
DR      InterPro: IPR010983; EF_Hand_Like.
DR      InterPro: IPR0010169; Pept_Cys_acsite.
DR      InterPro: IPR001300; Peptidase_C2.
DR      Pfam: PF01067; Calpain_III; 1.
DR      Pfam: PF00036; ehand; 2.
DR      Pfam: PF00648; Peptidase_C2; 1.
DR      PRINTS: PR00704; CALPAIN.
DR      SMART: SM00720; calpain_III; 1.
DR      SMART: SM00230; Cybpc; 1.
DR      SMART: SM0054; Efp; 2.
DR      PROSITE: PS50203; CALPAIN_CAT; 1.
DR      PROSITE: PS00018; EF_HAND; 2.
DR      PROSITE: PS00640; THIOL_PROTEASE_ASN_FALSE_NEG.
DR      PROSITE: PS00139; THIOL_PROTEASE_CYS; 1.
DR      PROSITE: PS00639; THIOL_PROTEASE_HIS_FALSE_NEG.
KW      Calcium-binding; Hydrolase; Multigene family; Thiol protease.
FT      DOMAIN 42 341 341
FT      DOMAIN 342 514 514
FT      DOMAIN 515 530 530
FT      DOMAIN 531 701 701
FT      CA_BIND 586 597 597
FT      CA_BIND 616 627 627
FT      DOMAIN 651 662 662
FT      DOMAIN 681 692 692
FT      ACT_SITE 102 102 102
FT      ACT_SITE 259 259 259
FT      ACT_SITE 283 283 283
FT      CONFLICT 404 404 404
SQ      SEQUENCE 702 AA; 80582 MW; 3A618682B9674FAE CRC64;
Query Match 84.9%; Score 45; DB 1; Length 702;
Best Local Similarity 90.0%; Pred. No. 4.4;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0.
OY      1 ONKGNOSFEE 10
DB      22 ONFGNOSFEE 31

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(ordn) yuajp eééé
The Doge Bank

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using SW model

Run on: October 25, 2005, 20:21:18 ; Search time 63.2 Seconds

(without alignments)
61.196 Million cell updates/sec

Title: US-10-731-238-83

Perfect score: 53

Sequence: 1 KGNQSFEDDT 10

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

1: Geneseq_16Dec04.*
2: geneseqp1960s.*
3: geneseqp1990s.*
4: geneseqp2000s.*
5: geneseqp2001s.*
6: geneseqp2002s.*
7: geneseqp2003as.*
8: geneseqp2003bs.*
9: geneseqp2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	53	100.0	10	2	AAW65739 Fibronec
2	53	100.0	36	2	AAW65714 Fibronec
3	53	100.0	36	2	AAW65715 Peptide #
4	53	100.0	38	1	AAW65715 Peptide #
5	53	100.0	38	1	AAW65715 Peptide #
6	53	100.0	38	1	AAW65715 Peptide #
7	53	100.0	38	1	AAW65715 Peptide #
8	53	100.0	38	1	AAW65715 Peptide #
9	53	100.0	38	1	AAW65715 Peptide #
10	53	100.0	38	1	AAW65715 Peptide #
11	53	100.0	38	1	AAW65715 Peptide #
12	53	100.0	38	1	AAW65715 Peptide #
13	53	100.0	38	1	AAW65715 Peptide #
14	53	100.0	38	1	AAW65715 Peptide #
15	53	100.0	38	1	AAW65715 Peptide #
16	53	100.0	38	1	AAW65715 Peptide #
17	53	100.0	38	1	AAW65715 Peptide #
18	53	100.0	38	1	AAW65715 Peptide #
19	53	100.0	38	1	AAW65715 Peptide #
20	53	100.0	38	1	AAW65715 Peptide #
21	53	100.0	38	1	AAW65715 Peptide #
22	53	100.0	38	1	AAW65715 Peptide #
23	53	100.0	38	1	AAW65715 Peptide #
24	53	100.0	38	1	AAW65715 Peptide #
25	53	100.0	38	1	AAW65715 Peptide #

26	48	90.6	38	2	AAW65699
27	48	90.6	38	2	AAW65661
28	48	90.6	38	2	AAW65698
29	48	90.6	39	2	AAW65712
30	48	90.6	39	2	AAW65713
31	48	90.6	77	2	AAW65749
32	48	90.6	113	2	AAW65937
33	48	90.6	110	2	AAW65805
34	48	90.6	110	2	AAW65807
35	48	90.6	130	2	AAW65807
36	48	90.6	130	2	AAW65807
37	48	90.6	134	2	AAW65807
38	48	90.6	134	2	AAW65807
39	48	90.6	162	2	AAW65807
40	48	90.6	164	2	AAW65807
41	48	90.6	174	2	AAW65807
42	48	90.6	174	2	AAW65807
43	48	90.6	181	2	AAW65807
44	48	90.6	181	2	AAW65807
45	48	90.6	559	2	AAW65807

ALIGNMENTS

RESULT 1
AAW65739
ID AAW65739 standard; peptide; 10 AA.
XX
XX AC AAW65739;
XX
XX 16-OCT-1998 (first entry)
XX
XX Fibronec binding protein-derived peptide #83.
XX
XX Microbial surface components recognising adhesive matrix molecule;
XX MSRAMM; fibronec; fibronec-binding protein; antibody; epitope;
XX antibiotic; bacterial infection; antibiotic-resistant strain.
XX
XX Synthetic.
XX Staphylococcus aureus.
XX
XX W09831389-A2.
XX
XX 23-JUL-1998.
XX
XX 21-JAN-1998; 98WO-US001222.
XX
XX 21-JAN-1997; 97US-0036139P.
XX
XX (TEXA) UNIV TEXAS A & M SYSTEM.
XX
XX Hoocek M, Patil JM, House-Pompeo KL, Speziale P, Joh D;
XX Mcgavin MJ;
XX WPI; 1998-413816/35.
XX
XX Antibody that binds to fibronec-binding protein, preventing its
XX binding to fibronec - used to treat or prevent bacterial infection,
XX especially by Staphylococci and Streptococci.
XX
XX Example 9; Page 110; 201P; English.
XX
XX The invention relates to antibodies that bind to a fibronec-binding
XX domain of a fibronec-binding protein, and inhibit binding of the
XX protein to a second amino acid sequence; (3) nucleic acid encoding the
XX protein containing at least one peptide of a fibronec-binding protein
XX linked to a second amino acid sequence; (4) isolated peptides of (1) and the
XX isolated peptide of (1). Antibodies, the isolated peptides of (1) and the
XX nucleic acids are all useful for immunisation (active or passive) and (by
XX inhibiting binding of bacteria to fibronec) for preventing or creating
XX infection in humans or other animals, particularly by staphylococci or

CC streptococci, e.g. meningitis, otitis media, pneumonia, endocarditis,
 CC mastitis in cattle, abortion in horses and many others. Since the
 CC antibodies block binding of bacteria, they should be effective against
 CC antibiotic-resistant strains, and may replace antibiotic therapy or
 CC increase its effectiveness. Sequences AAM65719-41 and AAM65658 represent
 CC peptides which were synthesised to span the D1 motif and the N-terminal
 CC 18 amino acids of D2, with each peptide overlapping by eight amino acids
 CC with the previous sequence
 CC
 CC
 SQ Sequence 10 AA;

Query Match 100.0%; Score 53; DB 2; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.0011;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 KGNOSFEEDT 10
 |||||
 Db 1 KGNOSFEEDT 10

RESULT 2
 ID AAM65714 standard; peptide; 36 AA.

AC AAM65714;
 DT 16-OCT-1998 (first entry)

DE Fibronectin binding protein-derived peptide #58.

KW microbial surface components recognising adhesive matrix molecule;
 KM MSCRAMM; fibronectin; fibronectin-binding protein; antibody; epitope;
 KW antibiotic; bacterial infection; antibiotic-resistant strain.

OS Synthetic.
 OS Staphylococcus aureus.

PN WO9831389-A2.

PD 23-JUL-1998.

PF 21-JAN-1998; 98WO-US001222.

PR 21-JAN-1997; 97US-0036139P.

PA (TEXA) UNIV TEXAS A & M SYSTEM.

PI Hoeoek M, Patti JM, House-Pompeo KL, Speciale P, Joh D;
 PI Megavlin MJ;

WP1; 1998-413816/35.

PT Antibody that binds to fibronectin-binding protein, preventing its
 binding to fibronectin - used to treat or prevent bacterial infection,
 PT especially by Staphylococci and Streptococci.

PS Example 8; Page 104; 201pp; English.

XX The invention relates to antibodies that bind to a fibronectin-binding
 CC domain of a fibronectin-binding protein, and inhibit binding of the
 CC protein to fibronectin. Also claimed are: (1) isolated peptides of a
 CC fibronectin-binding protein that do not bind to fibronectin; (2) fusion
 CC protein containing at least one peptide of a fibronectin-binding protein
 CC linked to a second amino acid sequence; (3) nucleic acid encoding the
 CC isolated peptide of (1). Antibodies, the isolated peptides of (1) and the
 CC nucleic acids are all useful for immunisation (active or passive) and (by
 CC inhibiting binding of bacteria to fibronectin) for preventing or treating
 CC infection in humans or other animals, particularly by staphylococci or
 CC streptococci, e.g. meningitis, otitis media, pneumonia, endocarditis,
 CC mastitis in cattle, abortion in horses and many others. Since the
 CC antibodies block binding of bacteria, they should be effective against
 CC antibiotic-resistant strains, and may replace antibiotic therapy or
 CC increase its effectiveness. The present sequence is shown in the

CC specification
 XX Sequence 36 AA;
 SQ

Query Match 100.0%; Score 53; DB 2; Length 36;
 Best Local Similarity 100.0%; Pred. No. 0.0049;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 KGNOSFEEDT 10
 |||||
 Db 3 KGNOSFEEDT 12

RESULT 3
 ID AAM65715 standard; peptide; 36 AA.

AC AAM65715;

DT 27-AUG-2003 (revised)
 DT 16-OCT-1998 (first entry)

DE Peptide #59.

KW microbial surface components recognising adhesive matrix molecule;
 KM MSCRAMM; fibronectin; fibronectin-binding protein; antibody; epitope;
 KW antibiotic; bacterial infection; antibiotic-resistant strain.

OS Synthetic.
 OS Staphylococcus aureus.

PN WO9831389-A2.

PD 23-JUL-1998.

PF 21-JAN-1998; 98WO-US001222.

PR 21-JAN-1997; 97US-0036139P.

PA (TEXA) UNIV TEXAS A & M SYSTEM.

PI Hoeoek M, Patti JM, House-Pompeo KL, Speciale P, Joh D;
 PI Megavlin MJ;

WP1; 1998-413816/35.

PT Antibody that binds to fibronectin-binding protein, preventing its
 binding to fibronectin - used to treat or prevent bacterial infection,
 PT especially by Staphylococci and Streptococci.

PS Disclosure; Page 160; 201pp; English.

XX The invention relates to antibodies that bind to a fibronectin-binding
 CC domain of a fibronectin-binding protein, and inhibit binding of the
 CC protein to fibronectin. Also claimed are: (1) isolated peptides of a
 CC fibronectin-binding protein that do not bind to fibronectin; (2) fusion
 CC protein containing at least one peptide of a fibronectin-binding protein
 CC linked to a second amino acid sequence; (3) nucleic acid encoding the
 CC isolated peptide of (1). Antibodies, the isolated peptides of (1) and the
 CC nucleic acids are all useful for immunisation (active or passive) and (by
 CC inhibiting binding of bacteria to fibronectin) for preventing or treating
 CC infection in humans or other animals, particularly by staphylococci or
 CC streptococci, e.g. meningitis, otitis media, pneumonia, endocarditis,
 CC mastitis in cattle, abortion in horses and many others. Since the
 CC antibodies block binding of bacteria, they should be effective against
 CC antibiotic-resistant strains, and may replace antibiotic therapy or
 CC increase its effectiveness. The present sequence is shown in the
 CC specification. (Updated on 27-AUG-2003 to correct OS field.)

XX Sequence 36 AA;

Query Match 100.0%; Score 53; DB 2; Length 36;
 Best Local Similarity 100.0%; Pred. No. 0.0049;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KGNQSFEDT 10
 |||||
 DB 3 KGNQSFEDT 12

RESULT 4

AAp80661
 ID AAp80661 standard; protein; 38 AA.

AC AAp80661;

DT 25-MAR-2003 (revised)
 DT 07-OCT-1990 (first entry)

DE Protein with fibronectin binding ability.

XX Hybrid DNA molecule; fibronectin binding; mastitis; ruminants;
 KW wound infection.

XX Staphylococcus aureus.

PN EP294349-A.

PD 07-DEC-1988.

PF 30-MAY-1988; 88EP-00850188.

PR 01-JUN-1987; 87SE-00002272.

PA (ALFA) ALFA LAVAL AGRIC INT AB.

PI Lindberg MK, Signas LC, Wadstrom TM, Froman G;

DR WPI; 1988-347978/49.

DR N-PSDB; AAN81098.

PT Hybrid DNA encoding Staphylococcus aureus fibronectin binding protein -
 useful for immunisation and topical application to prevent staphylococcal
 PT infections.

PS Claim 11; Page 12; 23pp; English.

XX The peptide has fibronectin binding ability. It is useful for immunising
 CC ruminants against staphylococcal mastitis, pref. when used at 0.5-5
 CC micrograms/kg, using 3 doses given at 1-3 week intervals; for topical
 CC application to prevent wound infection, using an isotonic saline soln. of
 CC concn. 25-250 micrograms/ml; and, when immobilised on a carrier, for
 CC diagnosing staphylococcal infections. (Updated on 25-MAR-2003 to correct
 CC PF field.) (Updated on 25-MAR-2003 to correct PA field.)

XX Sequence 38 AA;

Query Match 100.0%; Score 53; DB 1; Length 38;
 Best Local Similarity 100.0%; Pred. No. 0.0053;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KGNQSFEDT 10
 |||||
 DB 4 KGNQSFEDT 13

RESULT 5

AAp82117
 ID AAp82117 standard; protein; 38 AA.

AC AAp82117;

DT 25-MAR-2003 (revised)
 DT 05-JAN-1990 (first entry)

DE Fibronectin binding protein.

XX Fibronectin binding protein; S.aureus; immunisation; mastitis; ruminants;
 KW wound infection; diagnosis.

XX Staphylococcus aureus.

PN EP294349-A.

PD 07-DEC-1988.

PF 30-MAY-1988; 88EP-00850188.

PR 01-JUN-1987; 87SE-00002272.

PA (ALFA) ALFA LAVAL AGRIC INT AB.

PI Lindberg MK, Signas LC, Wadstrom TM, Froman G;

DR WPI; 1988-347978/49.

DR N-PSDB; AAN82055.

PT Hybrid DNA encoding Staphylococcus aureus fibronectin binding protein -
 useful for immunisation and topical application to prevent staphylococcal
 PT infections.

PS Claim 11; Page 12; 23pp; English.

XX The S.aureus fibronectin binding protein may be included in a hybrid
 CC protein. The protein may be used to immunise ruminants against
 CC staphylococcal mastitis, pref. when given at 0.5-5 microg/kg, using 3
 CC doses at 1-3 week intervals; and for topical applicn. to prevent wound
 CC infection, pref. using isotonic saline soln. of concn. 25-250 microg/mg.
 CC The DNA encoding the binding protein and the hybrid protein may be
 CC immobilised on a carrier and used to diagnose staphylococcal infections.
 CC (Updated on 25-MAR-2003 to correct PA field.)

XX Sequence 38 AA;

Query Match 100.0%; Score 53; DB 1; Length 38;
 Best Local Similarity 100.0%; Pred. No. 0.0053;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KGNQSFEDT 10
 |||||
 DB 4 KGNQSFEDT 13

RESULT 6

AAW65664
 ID AAW65664 standard; peptide; 38 AA.

AC AAW65664;

DT 16-OCT-1998 (first entry)

DE Fibronectin binding protein-derived peptide #8.

XX microbial surface components recognising adhesive matrix molecule;
 KW MSCRAMM; fibronectin; fibronectin-binding protein; antibody; epitope;
 KW antibiotic; bacterial infection; antibiotic-resistant strain.

OS Synthetic.

OS Staphylococcus aureus.

PN MO9831389-A2.

PD 23-JUL-1998.

PF 21-JAN-1998; 98WO-US001222.
 PR 21-JAN-1997; 97US-0036139P.

PA (TEXA) UNIV TEXAS A & M SYSTEM.

```

XX  Hoeoek M,  Patci JM,  House-Pompeo KL,  Speziale P,  Joh D;
PI  McGavin MJ;
XX
XX  WPI; 1998-413816/35.
DR
XX  Antibody that binds to fibronectin-binding protein, preventing its
PT  binding to fibronectin - used to treat or prevent bacterial infection,
PT  especially by Staphylococci and Streptococci.
XX
XX  Example 2; Page 92; 201pp; English.
XX
XX  The invention relates to antibodies that bind to a fibronectin-binding
CC  domain of a fibronectin-binding protein, and inhibit binding of the
CC  protein to fibronectin. Also claimed are: (1) isolated peptides of a
CC  fibronectin-binding protein that do not bind to fibronectin; (2) fusion
CC  protein containing at least one peptide of a fibronectin-binding protein
CC  linked to a second amino acid sequence; (3) nucleic acid encoding the
CC  isolated peptide of (1). Antibodies, the isolated peptides of (1) and the
CC  nucleic acids are all useful for immunisation (active or passive) and (by
CC  inhibiting binding of bacteria to fibronectin) for preventing or treating
CC  infection in humans or other animals, particularly by staphylococci or
CC  streptococci, e.g. meningitis, otitis media, pneumonia, endocarditis,
CC  mastitis in cattle, abortion in horses and many others. Since the
CC  antibodies block binding of bacteria, they should be effective against
CC  antibiotic-resistant strains, and may replace antibiotic therapy or
CC  increase its effectiveness. Sequences AAM65659-68 represent synthetic
CC  epitopes from the fibronectin binding domains DU and D1-D4 of the S.
CC  aureus fnda gene
XX
XX  Sequence 38 AA:
SQ
XX
XX  Query Match          100.0%; Score 53; DB 2; Length 38;
XX  Best Local Similarity 100.0%; Pred. No. 0.0053;
XX  Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX  1 KGNOSFEEDT 10
XX  |||||
XX  3 KGNOSFEEDT 12
XX
XX  RESULT 7
XX  ID AAM65705 standard; peptide; 38 AA.
XX  AC AAM65705;
XX  DT 16-OCT-1998 (first entry)
XX
XX  DE Fibronectin binding protein-derived peptide #49.
XX
XX  KM microbial surface components recognising adhesive matrix molecule;
XX  MSCRAMM; fibronectin; fibronectin-binding protein; antibody; epitope;
XX  KM antibiotic; bacterial infection; antibiotic-resistant strain.
XX
XX  OS Synthetic.
XX  OS Staphylococcus aureus.
XX
XX  WO9831389-A2.
XX  PN 23-JUL-1998.
XX  PD 23-JUL-1998.
XX  PF 21-JAN-1998; 98WO-US001222.
XX  PR 21-JAN-1997; 97US-0036139P.
XX
XX  (TEXA ) UNIV TEXAS A & M SYSTEM.
XX
XX  Hoeoek M, Patci JM, House-Pompeo KL, Speziale P, Joh D;
PI  McGavin MJ;
XX  WPI; 1998-413816/35.
XX

```

```

PT  Antibody that binds to fibronectin-binding protein, preventing its
PT  binding to fibronectin - used to treat or prevent bacterial infection,
PT  especially by Staphylococci and Streptococci.
XX
XX  Example 8; Page 102; 201pp; English.
XX
XX  The invention relates to antibodies that bind to a fibronectin-binding
CC  domain of a fibronectin-binding protein, and inhibit binding of the
CC  protein to fibronectin. Also claimed are: (1) isolated peptides of a
CC  fibronectin-binding protein that do not bind to fibronectin; (2) fusion
CC  protein containing at least one peptide of a fibronectin-binding protein
CC  linked to a second amino acid sequence; (3) nucleic acid encoding the
CC  isolated peptide of (1). Antibodies, the isolated peptides of (1) and the
CC  nucleic acids are all useful for immunisation (active or passive) and (by
CC  inhibiting binding of bacteria to fibronectin) for preventing or treating
CC  infection in humans or other animals, particularly by staphylococci or
CC  streptococci, e.g. meningitis, otitis media, pneumonia, endocarditis,
CC  mastitis in cattle, abortion in horses and many others. Since the
CC  antibodies block binding of bacteria, they should be effective against
CC  antibiotic-resistant strains, and may replace antibiotic therapy or
CC  increase its effectiveness. Sequences AAM65701-706 represent a series of
CC  synthetic peptides based on the D2 region of S. aureus fibronectin
CC  binding protein A. They were synthesised to contain mutations
XX
XX  Sequence 38 AA:
SQ
XX
XX  Query Match          100.0%; Score 53; DB 2; Length 38;
XX  Best Local Similarity 100.0%; Pred. No. 0.0053;
XX  Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX  1 KGNOSFEEDT 10
XX  |||||
XX  3 KGNOSFEEDT 12
XX
XX  RESULT 8
XX  ID AAM65663 standard; peptide; 38 AA.
XX  AC AAM65663;
XX  DT 16-OCT-1998 (first entry)
XX
XX  DE Fibronectin binding protein-derived peptide #7.
XX
XX  KM microbial surface components recognising adhesive matrix molecule;
XX  MSCRAMM; fibronectin; fibronectin-binding protein; antibody; epitope;
XX  KM antibiotic; bacterial infection; antibiotic-resistant strain.
XX
XX  OS Synthetic.
XX  OS Staphylococcus aureus.
XX
XX  WO9831389-A2.
XX  PN 23-JUL-1998.
XX  PD 23-JUL-1998.
XX  PF 21-JAN-1998; 98WO-US001222.
XX  PR 21-JAN-1997; 97US-0036139P.
XX
XX  (TEXA ) UNIV TEXAS A & M SYSTEM.
XX
XX  Hoeoek M, Patci JM, House-Pompeo KL, Speziale P, Joh D;
PI  McGavin MJ;
XX  WPI; 1998-413816/35.
XX
XX  Antibody that binds to fibronectin-binding protein, preventing its
PT  binding to fibronectin - used to treat or prevent bacterial infection,
PT  especially by Staphylococci and Streptococci.
XX
XX  Example 2; Page 92; 201pp; English.
XX

```

CC The invention relates to antibodies that bind to a fibronectin-binding
 CC domain of a fibronectin-binding protein, and inhibit binding of the
 CC protein to fibronectin. Also claimed are: (1) isolated peptides of a
 CC fibronectin-binding protein that do not bind to fibronectin; (2) fusion
 CC protein containing at least one peptide of a fibronectin-binding protein
 CC linked to a second amino acid sequence; (3) nucleic acid encoding the
 CC isolated peptide of (1). Antibodies, the isolated peptides of (1) and the
 CC nucleic acids are all useful for immunisation (active or passive) and (by
 CC inhibiting binding of bacteria to fibronectin) for preventing or treating
 CC infection in humans or other animals, particularly by staphylococci or
 CC streptococci, e.g. meningitis, otitis media, pneumonia, endocarditis,
 CC mastitis in cattle, abortion in horses and many others. Since the
 CC antibodies block binding of bacteria, they should be effective against
 CC antibiotic-resistant strains, and may replace antibiotic therapy or
 CC increase its effectiveness. Sequences AAW5659-68 represent synthetic
 CC epitopes from the fibronectin binding domains DU and D1-D4 of the S.
 CC aureus fnbA gene

XX Sequence 38 AA;

Query Match 100.0%; Score 53; DB 2; Length 36;
 Best Local Similarity 100.0%; Pred. No. 0.0053;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KGNOSFEEDT 10
 |||||
 DB 3 KGNOSFEEDT 12

RESULT 9
 AAY29087
 ID AAY29087 standard; protein; 134 AA.

AC AAY29087;

XX 28-SEP-1999 (first entry)

DT S. aureus fibronectin binding protein A (FnBA) binding domain.

XX Bovine herpes virus-2; BHV-2; cytokine; immune response; immunogen; IL;

KM interleukin; colony stimulating factor; CSF; interferon; IFN; TNF;

KM tumour necrosis factor; recombinant virus; vaccine; mucosal disease;

KM mastitis; breast cancer; stress-induced disease; binding domain; FnBA;

KM fibronectin binding protein.

XX Staphylococcus aureus.

OS W09916892-A1.

XX 08-APR-1999.

PD 29-SEP-1998; 98WO-GB002927.

XX 29-SEP-1997; 97GB-00020633.

PR (UYBR-) UNIV BRISTOL.

XX Bradley AJ, Duffas WP;

XX WPI; 1999-255101/21.

DR N-PSDB; AAX91504.

XX New bovine herpes virus-2 vectors.

PT Example 2; Fig 8A-B; 130pp; English.

XX The invention provides bovine herpes virus-2 (BHV-2) based vectors that
 CC comprise at least one cytokine-encoding DNA sequence. The expression of
 CC cytokines in mammals can up-regulate immune responses to the immunogens.
 CC The cytokine is selected from interleukins (IL), colony stimulating
 CC factors (CSF), interferons (IFN) and tumour necrosis factors (TNF). The
 CC BHV-2 based vector or recombinant virus can be used as vaccines. They can
 CC be used for preventing or treating a mucosal disease in a subject, e.g.

CC ruminants, cattle, sheep, goats, dogs, cats, horses, or man, particularly
 CC mastitis in cows or breast cancers in humans. They can also be used for
 CC preventing or treating a stress-induced disease. The present sequence
 CC represents the binding domain of a previously published S. aureus
 CC fibronectin binding protein A (FnBA) sequence. The FnB binding domain
 CC gene sequence FNBA1, cloned for use in this invention has 97.8 percent
 CC identity when compared to the previously published FnBA and FnBB gene
 CC sequences

XX Sequence 134 AA;

Query Match 100.0%; Score 53; DB 2; Length 134;
 Best Local Similarity 100.0%; Pred. No. 0.023;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KGNOSFEEDT 10
 |||||
 DB 42 KGNOSFEEDT 51

RESULT 10
 AAW31556
 ID AAW31556 standard; protein; 139 AA.

AC AAW31556;

XX 27-AUG-2003 (revised)

DT 25-MAR-2003 (revised)

DT 21-MAY-1998 (first entry)

XX Fibronectin-binding MSCRAMM derivative pOD.

KM Fibronectin; pOD; collagen binding protein; sepsis; infection;

KM microbial surface component recognising adhesive matrix molecule; MSCRAMM;

KM adhesin; vaccine; immunisation; diagnosis; therapy; mastitis.

XX Staphylococcus aureus.

OS W09743314-A2.

XX 20-NOV-1997.

PD 14-MAY-1997; 97WO-US008210.

XX 16-MAY-1996; 96US-0017678P.

PR (TEXA) UNIV TEXAS A & M SYSTEM.

XX (UABR-) UAB RES FOUND.

XX Hoecek M, Patti JM, House-Pompeo K, Sthanam N, Symersky J;

XX WPI; 1998-008801/01.

XX Antibody that interacts with collagen binding domain of Staphylococcal

XX gene product - useful to prevent bacterial sepsis in animal infected

XX with Staphylococcus aureus.

XX Disclousure; Page 91; 143pp; English.

XX This protein comprises Staphylococcus aureus fibronectin-binding
 CC microbial surface component recognising adhesive matrix molecule (MSCRAMM)
 CC derivative pOD, plus a vector-derived N-terminal peptide. The invention
 CC relates to claimed nucleic acid sequences (see AAT93436-38) encoding S.
 CC aureus collagen binding protein (CBP) epitopes M17, M31 and M55 (see
 CC AAW31552-54) that confer protection against S. aureus infection. CBP
 CC protein and antigenic epitopes are contemplated for use in the treatment
 CC of pathological infections, especially to prevent bacterial adhesion to
 CC collagen. The epitopes are also contemplated for use in the preparation
 CC of vaccines and as carrier proteins in vaccine formulations, as well as

CC in the formulation of compositions for the prevention of *S. aureus*
 CC infection. pCF33 and pQD (see AAW31556) were used to raise anti-MSCRAMM
 CC polyclonal antibodies used in passive immunisation against bovine
 CC mastitis. (Updated on 25-MAR-2003 to correct PI field.) (Updated on 27-
 CC AUG-2003 to correct OS field.)

XX
 SQ Sequence 139 AA;

Query Match 100.0%; Score 53; DB 2; Length 139;
 Best Local Similarity 100.0%; Pred. No. 0.024;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KGNOSFEEDT 10
 |||||
 Db 56 KGNOSFEEDT 65

RESULT 11

AAp82115
 ID AAP82115 standard; protein; 1018 AA.

XX AAP82115;
 AC 25-MAR-2003 (revised)
 DT 05-JUN-1990 (first entry)
 XX
 DE Fibronectin binding protein.
 DE Fibronectin binding protein; *S. aureus*; immunisation; mastitis; ruminants;
 KM Fibronectin binding protein; *S. aureus*; immunisation; mastitis; ruminants;
 KM wound infection; diagnosis.
 XX
 OS Staphylococcus aureus.
 XX
 PN EP294349-A.
 PD 07-DEC-1988.
 PF 30-MAY-1988; 88EP-00850188.
 PR 01-JUN-1987; 87SE-00002272.
 XX
 PA (ALFA) ALFA LAVAL AGRIC INT AB.

XX Lindberg MK, Signas LC, Wadstrom TM, Froman G;
 XX
 DR P-PSDB; AAP82115.
 XX
 PT Hybrid DNA encoding Staphylococcus aureus fibronectin binding protein -
 PT useful for immunisation and topical application to prevent staphylococcal
 PT infections.
 XX
 PS Disclosure; Fig. 8A:1-8A:2; 23pp; English.

CC The *S. aureus* fibronectin binding protein may be included in a hybrid
 CC protein. The protein may be used to immunise ruminants against
 CC staphylococcal mastitis, pref. when given at 0.5-5 microg/Kg, using 3
 CC doses at 1-3 week intervals; and for topical applicn. to prevent wound
 CC infection, pref. using isotonic saline soln. of concn. 25-250 microg/mg.
 CC The DNA encoding the binding protein and the hybrid protein may be
 CC immobilised on a carrier and used to diagnose staphylococcal infections.
 CC (Updated on 25-MAR-2003 to correct PA field.)
 CC
 XX

SQ Sequence 1018 AA;

Query Match 100.0%; Score 53; DB 1; Length 1018;
 Best Local Similarity 100.0%; Pred. No. 0.24;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KGNOSFEEDT 10
 |||||
 Db 786 KGNOSFEEDT 795

RESULT 12

AAU37245
 ID AAU37245 standard; protein; 1018 AA.

XX AAU37245;
 AC 14-FEB-2002 (first entry)
 DT
 XX Staphylococcus aureus cellular proliferation protein #1415.
 DE
 XX Antisense; prokaryotic cellular proliferation protein; antibiotic;
 XX antibacterial; drug design.
 KM
 XX Staphylococcus aureus.
 OS
 PN WO200170955-A2.
 PD 27-SEP-2001.
 XX
 PF 21-MAR-2001; 2001WO-US009180.
 XX
 PR 21-MAR-2000; 2000US-0191078P.
 PR 23-MAY-2000; 2000US-0206848P.
 PR 26-MAY-2000; 2000US-0207127P.
 PR 23-OCT-2000; 2000US-0242578P.
 PR 27-NOV-2000; 2000US-0253625P.
 PR 22-DEC-2000; 2000US-0257931P.
 PR 16-FEB-2001; 2001US-0269308P.
 XX
 PA (ELIT-) ELITRA PHARM INC.
 XX
 PI Haselbeck R, Ohlsen KL, Zyskind JM, Wall D, Trawick JD, Carr GJ;
 PI Yamamoto RT, Xu HH;
 XX
 DR N-PSDB; AAS55104.
 XX
 PT New polymucleotides for the identification and development of
 PT antibiotics, comprise sequences of antisense nucleic acids.
 XX
 PS Example 3; SEQ ID NO 12838; 51pp; English.

CC The invention relates to antisense inhibitors of genes essential to
 CC prokaryotic cellular proliferation, their use in identifying the genes,
 CC their use in the discovery of novel antibiotics, the essential genes
 CC themselves and the encoded proteins. The prokaryotes used are *Escherichia*
 CC coli, *Staphylococcus aureus*, *Salmonella typhi*, *Klebsiella pneumoniae*,
 CC *Pseudomonas aeruginosa* and *Enterococcus faecalis*. The invention is also
 CC useful for the identification of potential new targets for antibiotic
 CC development. The antisense nucleic acids can also be used to identify
 CC proteins used in proliferation, to express these proteins, and to obtain
 CC antibodies capable of binding to the expressed proteins. The proteins can
 CC be used to screen compounds in rational drug discovery programmes. The
 CC antisense nucleic acid sequence is also useful to screen for homologous
 CC nucleic acids which are required for cell proliferation in a wide variety
 CC of organisms. The present sequence represents an essential prokaryotic
 CC cellular proliferation protein. Note: The sequence data for this patent
 CC did not form part of the printed specification, but was obtained in
 CC electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 CC
 XX

SQ Sequence 1018 AA;

Query Match 100.0%; Score 53; DB 4; Length 1018;
 Best Local Similarity 100.0%; Pred. No. 0.24;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KGNOSFEEDT 10
 |||||
 Db 786 KGNOSFEEDT 795

RESULT 13

AAU34301 standard; protein; 1018 AA.

AAU34301;

14-FEB-2002 (first entry)

Staphylococcus aureus cellular proliferation protein #577.

Antisense: prokaryotic cellular proliferation protein; antibiotic;

antibacterial; drug design.

Staphylococcus aureus.

MO200170955-A2.

27-SEP-2001.

21-MAR-2001; 2001WO-US009180.

21-MAR-2000; 2000US-0191078P.

23-MAY-2000; 2000US-0206848P.

26-MAY-2000; 2000US-0207272P.

23-OCT-2000; 2000US-0242578P.

27-NOV-2000; 2000US-0253625P.

22-DEC-2000; 2000US-0257931P.

16-FEB-2001; 2001US-0269308P.

WPI: 2001-611495/70.

N-PSDB; AAS52160.

New polynucleotides for the identification and development of

antibiotics, comprise sequences of antisense nucleic acids.

Example 3; SEQ ID NO 5797; 511pp; English.

The invention relates to antisense inhibitors of genes essential to

prokaryotic cellular proliferation, their use in identifying the genes,

their use in the discovery of novel antibiotics, the essential genes

themselves and the encoded proteins. The prokaryotes used are *Escherichia**coli*, *Staphylococcus aureus*, *Salmonella typhi*, *Klebsiella pneumoniae*,*Pseudomonas aeruginosa* and *Enterococcus faecalis*. The invention is also

useful for the identification of potential new targets for antibiotic

development. The antisense nucleic acids can also be used to identify

antibodies capable of binding to the expressed proteins. The proteins can

be used to screen compounds in rational drug discovery programmes. The

antisense nucleic acid sequence is also useful to screen for homologous

nucleic acids which are required for cell proliferation in a wide variety

of organisms. The present sequence represents an essential prokaryotic

cellular proliferation protein. Note: The sequence data for this patent

did not form part of the printed specification, but was obtained in

electronic format directly from WIPO at

ftp.wipo.int/pub/published_pct_sequences

ABU18922

ABU18922 standard; protein; 1018 AA.

ABU18922;

06-MAR-2003 (first entry)

Pathogen specific antigen related staphylococcal protein SEQ ID No 68.

Antibacterial; virucide; fungicide; protozoacide; cytostatic; anti-HIV;

hyperimmune; serum-reactive; antigen; pathogen; tumour; allergen;

auto-immunity; vaccine; staphylococcal infection; antibody; cancer;

autoimmune disease; HIV; hepatitis.

Staphylococcus sp.

MO200259148-A2.

01-AUG-2002.

21-JAN-2002; 2002WO-EP000546.

26-JAN-2001; 2001AT-00000130.

(CIST-) CISTEM BIOTECHNOLOGIES GMBH.

Weinke A, Nagy E, Von Ahnen U, Klade C, Henies T, Zauner W;

Muh DB, Vycvyska O, Ecz H, Dryla A, Weichart T, Hafner M;

Temelmaier B;

WPI: 2003-075410/07.

Identifying, isolating and producing hyperimmune serum-reactive antigens

from a pathogen, for preparing vaccine or medicament for treating or

preventing e.g. staphylococcal infections, comprises providing antibody

preparation.

Example 7; Page 157; 252pp; English.

The invention relates to a novel method for identifying, isolating and

producing hyperimmune serum-reactive antigens from a pathogen, tumour,

allergen, a tissue or host prone to auto-immunity, where the antigens are

used in a vaccine, comprises providing antibody preparation from a plasma

pool of a type of animal, or individual sera with antibodies against the

specific pathogen, tumour, allergen, tissue or host prone to auto-

immunity. The hyperimmune serum-reactive antigens comprising any of the

62 sequences of 53-2261 amino acids fully defined in the specification,

or their hyperimmune fragments are useful for the manufacture of a

pharmaceutical preparation, particularly a vaccine against staphylococcal

infections or colonisation against *S. aureus* or *S. epidermidis*. The

preparation of antibodies is useful for the manufacture of a medicament

for treating or preventing staphylococcal infections or colonisation

against *S. aureus* or *S. epidermidis*. The antibody preparations may also

be used for diagnostic and imaging purposes. Other conditions that can be

treated include cancer, autoimmune diseases or infections caused by viral

ABU18922

ABU18922 standard; protein; 1018 AA.

ABU18922;

06-MAR-2003 (first entry)

Pathogen specific antigen related staphylococcal protein SEQ ID No 68.

Antibacterial; virucide; fungicide; protozoacide; cytostatic; anti-HIV;

hyperimmune; serum-reactive; antigen; pathogen; tumour; allergen;

auto-immunity; vaccine; staphylococcal infection; antibody; cancer;

autoimmune disease; HIV; hepatitis.

Staphylococcus sp.

MO200259148-A2.

01-AUG-2002.

21-JAN-2002; 2002WO-EP000546.

26-JAN-2001; 2001AT-00000130.

(CIST-) CISTEM BIOTECHNOLOGIES GMBH.

Weinke A, Nagy E, Von Ahnen U, Klade C, Henies T, Zauner W;

Muh DB, Vycvyska O, Ecz H, Dryla A, Weichart T, Hafner M;

Temelmaier B;

WPI: 2003-075410/07.

Identifying, isolating and producing hyperimmune serum-reactive antigens

from a pathogen, for preparing vaccine or medicament for treating or

preventing e.g. staphylococcal infections, comprises providing antibody

preparation.

Example 7; Page 157; 252pp; English.

The invention relates to a novel method for identifying, isolating and

producing hyperimmune serum-reactive antigens from a pathogen, tumour,

allergen, a tissue or host prone to auto-immunity, where the antigens are

used in a vaccine, comprises providing antibody preparation from a plasma

pool of a type of animal, or individual sera with antibodies against the

specific pathogen, tumour, allergen, tissue or host prone to auto-

immunity. The hyperimmune serum-reactive antigens comprising any of the

62 sequences of 53-2261 amino acids fully defined in the specification,

or their hyperimmune fragments are useful for the manufacture of a

pharmaceutical preparation, particularly a vaccine against staphylococcal

infections or colonisation against *S. aureus* or *S. epidermidis*. The

preparation of antibodies is useful for the manufacture of a medicament

for treating or preventing staphylococcal infections or colonisation

against *S. aureus* or *S. epidermidis*. The antibody preparations may also

be used for diagnostic and imaging purposes. Other conditions that can be

treated include cancer, autoimmune diseases or infections caused by viral


```

XX ABM72537;
AC 20-NOV-2003 (first entry)
XX DT
XX DE Staphylococcus aureus protein #1777.
XX DE
XX DE Antibacterial; vaccine; gene therapy; infection; sepsis; diagnosis;
XX KM enzymatic assay; antibiotic target.
XX OS Staphylococcus aureus.
XX PN W0200294868-A2.
XX PD 28-NOV-2002.
XX PF 27-MAR-2002; 2002MO-IB002637.
XX PR 27-MAR-2001; 2001GB-00007661.
XX PA (CHIR-) CHIRON SPA.
XX PI Masignani V, Mora M, Scarselli M;
XX DR MPI; 2003-120786/11.
XX DR N-PSDB; ACF74097.
XX PT New Staphylococcus aureus protein, useful as a vaccine for treating or
XX PT preventing Staphylococcal infection, specifically an infection caused by
XX PT S. aureus, e.g. sepsis.
XX PS Claim 1; SEQ ID NO 3554; 49pp; English.
XX CC The invention relates to novel genes and encoded proteins from
XX CC Staphylococcus aureus. A composition comprising the S. aureus protein, a
XX CC nucleic acid encoding the protein, or an antibody to the protein, is
XX CC useful as a pharmaceutical, particularly as a vaccine for treating or
XX CC preventing infection due to Staphylococcus bacteria, specifically an
XX CC infection caused by S. aureus. The composition is particularly useful for
XX CC treating or preventing sepsis in a patient. The composition can also be
XX CC used for diagnostics. The protein is also used in an assay for enzymatic
XX CC studies and as a target for antibiotics. This sequence represents one of
XX CC the novel S. aureus proteins of the invention
XX SQ Sequence 1018 AA;

Query Match 100.0%; Score 53; DB 6; Length 1018;
Best Local Similarity 100.0%; Pred. NO. 0.24;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KGNOSFEEDT 10
   |||||
Db 786 KGNOSFEEDT 795

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Search completed: October 25, 2005, 20:58:48
 Job time : 63.2 secs

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OM protein - protein search, using sw model

Run on: October 22, 2005, 05:46:56 ; Search time 17.3 Seconds
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43.150 Million cell updates/sec

Title: US-10-731-238-83

Perfect score: 53

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Maximum Match 100%

Listing first 45 summaries

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- 6: /cgn2_6/ptodata/1/1aa/backfile1.dep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	53	100.0	10	4	US-09-010-317-83 Sequence 83, Appl
2	53	100.0	36	4	US-09-010-317-58 Sequence 58, Appl
3	53	100.0	36	4	US-09-010-317-59 Sequence 59, Appl
4	53	100.0	38	1	US-08-234-622A-3 Sequence 3, Appl
5	53	100.0	38	1	US-08-729-767-4 Sequence 4, Appl
6	53	100.0	38	4	US-09-010-317-7 Sequence 7, Appl
7	53	100.0	38	4	US-09-010-317-8 Sequence 8, Appl
8	53	100.0	38	4	US-09-010-317-49 Sequence 49, Appl
9	53	100.0	114	1	US-08-259-000-3 Sequence 3, Appl
10	53	100.0	129	3	US-08-856-253-8 Sequence 8, Appl
11	53	100.0	1027	4	US-08-956-171E-5254 Sequence 5254, Ap
12	53	100.0	1027	4	US-08-781-986A-5254 Sequence 5254, Ap
13	48	90.6	10	4	US-09-010-317-64 Sequence 64, Appl
14	48	90.6	38	1	US-08-234-622A-2 Sequence 2, Appl
15	48	90.6	38	1	US-08-729-767-3 Sequence 3, Appl
16	48	90.6	38	4	US-09-010-317-5 Sequence 5, Appl
17	48	90.6	38	4	US-09-010-317-6 Sequence 6, Appl
18	48	90.6	38	4	US-09-010-317-40 Sequence 40, Appl
19	48	90.6	38	4	US-09-010-317-41 Sequence 41, Appl
20	48	90.6	38	4	US-09-010-317-42 Sequence 42, Appl
21	48	90.6	38	4	US-09-010-317-43 Sequence 43, Appl
22	48	90.6	39	4	US-09-010-317-56 Sequence 56, Appl
23	48	90.6	39	4	US-09-010-317-57 Sequence 57, Appl
24	48	90.6	130	2	US-08-459-135A-7 Sequence 7, Appl
25	48	90.6	130	2	US-08-459-135A-8 Sequence 8, Appl
26	48	90.6	130	3	US-08-495-559-7 Sequence 7, Appl
27	48	90.6	130	3	US-08-495-559-8 Sequence 8, Appl

28	48	90.6	174	2	US-08-459-135A-10 Sequence 10, Appl
29	48	90.6	174	2	US-08-459-135A-13 Sequence 13, Appl
30	48	90.6	174	3	US-08-495-559-10 Sequence 10, Appl
31	48	90.6	174	3	US-08-495-559-13 Sequence 13, Appl
32	48	90.6	176	3	US-08-495-559-6 Sequence 6, Appl
33	48	90.6	178	2	US-08-459-135A-12 Sequence 12, Appl
34	48	90.6	178	3	US-08-495-559-12 Sequence 12, Appl
35	48	90.6	181	2	US-08-459-135A-6 Sequence 6, Appl
36	48	90.6	559	4	US-08-956-171E-5251 Sequence 5251, Ap
37	48	90.6	559	4	US-08-781-986A-5251 Sequence 5251, Ap
38	47	88.7	38	4	US-09-010-317-46 Sequence 46, Appl
39	47	88.7	38	4	US-09-010-317-47 Sequence 47, Appl
40	46	86.8	38	4	US-09-010-317-48 Sequence 48, Appl
41	43	81.1	38	4	US-09-010-317-39 Sequence 39, Appl
42	43	81.1	38	4	US-09-010-317-45 Sequence 45, Appl
43	42	79.2	10	4	US-09-010-317-65 Sequence 65, Appl
44	42	79.2	10	4	US-09-010-317-82 Sequence 82, Appl
45	42	79.2	10	4	US-09-010-317-84 Sequence 84, Appl

ALIGNMENTS

RESULT 1
US-09-010-317-83
Sequence 83, Application US/09010317
Patent No. 6685943
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
APPLICANT: Patti, Joseph M.
APPLICANT: House-Pompeo, Karen L.
APPLICANT: Speziale, Pietro
APPLICANT: Jon, Danny
APPLICANT: McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
TITLE OF INVENTION: AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hidler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAMK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-5000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 83:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-09-010-317-83
Query Match 100.0%; Score 53; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.00027;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KGNOSFEEDT 10
| | | | | | | | | |
Db 1 KGNOSFEEDT 10

RESULT 2

US-09-010-317-58

; Sequence 58, Application US/09010317

; Patent No. 6685943

; GENERAL INFORMATION:

; APPLICANT: Hook, Magnus

; APPLICANT: Patci, Joseph M.

; APPLICANT: House-Pompeo, Karen L.

; APPLICANT: Speziale, Pietro

; APPLICANT: John, Danny

; APPLICANT: McGavin, Martin J.

; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS

; TITLE OF INVENTION: AND METHODS OF USE

; NUMBER OF SEQUENCES: 105

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Arnold, White & Durkee

; STREET: P.O. Box 4433

; CITY: Houston

; STATE: TX

; COUNTRY: USA

; ZIP: 77210-4433

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/010,317

; FILING DATE:

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 60/036,139

; FILING DATE: 21-JAN-1997

; ATTORNEY/AGENT INFORMATION:

; NAME: Hibler, David W.

; REGISTRATION NUMBER: 41,071

; REFERENCE/DOCKET NUMBER: TANK:189

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 512-418-3000

; TELEFAX: 512-474-7577

; INFORMATION FOR SEQ ID NO: 58:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 36 amino acids

; TYPE: amino acid

; STRANDEDNESS:

; TOPOLOGY: linear

US-09-010-317-58

Query Match 100.0%; Score 53; DB 4; Length 36;
Best Local Similarity 100.0%; Pred. No. 0.0012;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KGNOSFEEDT 10
| | | | | | | | | |
Db 3 KGNOSFEEDT 12

RESULT 3

US-09-010-317-59

; Sequence 59, Application US/09010317

; Patent No. 6685943

; GENERAL INFORMATION:

; APPLICANT: Hook, Magnus

; APPLICANT: Patci, Joseph M.

; APPLICANT: House-Pompeo, Karen L.

; APPLICANT: Speziale, Pietro

APPLICANT: John, Danny
APPLICANT: McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
TITLE OF INVENTION: AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/010,317

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 60/036,139

FILING DATE: 21-JAN-1997

ATTORNEY/AGENT INFORMATION:

NAME: Hibler, David W.

REGISTRATION NUMBER: 41,071

REFERENCE/DOCKET NUMBER: TANK:189

TELECOMMUNICATION INFORMATION:

TELEPHONE: 512-418-3000

TELEFAX: 512-474-7577

INFORMATION FOR SEQ ID NO: 59:

SEQUENCE CHARACTERISTICS:

LENGTH: 36 amino acids

TYPE: amino acid

STRANDEDNESS:

TOPOLOGY: linear

US-09-010-317-59

Query Match 100.0%; Score 53; DB 4; Length 36;
Best Local Similarity 100.0%; Pred. No. 0.0012;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KGNOSFEEDT 10
| | | | | | | | | |
Db 3 KGNOSFEEDT 12

RESULT 4

US-08-234-622A-3

; Sequence 3, Application US/08234622A

; Patent No. 5440014

; GENERAL INFORMATION:

; APPLICANT: HOOK, Magnus

; APPLICANT: MCGAVIN, Martin

; APPLICANT: RAUCCI, Giuseppe

; TITLE OF INVENTION: A FIBRONECTIN BINDING PEPTIDE

; NUMBER OF SEQUENCES: 4

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Burns, Doane, Swecker & Mathis

; STREET: P.O. Box 1404

; CITY: Alexandria

; STATE: Virginia

; COUNTRY: United States

; ZIP: 22313-1404

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/234,622A

; FILING DATE: 28-APR-1994

CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: SE 9002617-0
FILING DATE: 10-AUG-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/SE91/00534
FILING DATE: 09-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: Meuth, Donna M
REGISTRATION NUMBER: 36,607
REFERENCE/DOCKET NUMBER: 012885-044
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-234-622A-3

Query Match 100.0%; Score 53; DB 1; Length 38;
Best Local Similarity 100.0%; Pred. No. 0.0013;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KGNOSFEEDT 10
Db 3 KGNOSFEEDT 12

RESULT 5
US-08-729-767-4
Sequence 4, Application US/08729767
Patent No. 5770702
GENERAL INFORMATION:
APPLICANT: HOOK, Magnus
APPLICANT: LINDBERG, Martin Kjell
APPLICANT: SIGNAS, Lars Christer
APPLICANT: WADSTROM, Torkel Mikael
APPLICANT: FROMAN, Gunnar
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN AS WELL AS
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Burns, Doane, Swecker & Mathis, L.L.P.
STREET: P.O. Box 1404
CITY: Alexandria
STATE: Virginia
COUNTRY: United States
ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/729,767
FILING DATE: 07-OCT-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/259,000
FILING DATE: 13-JUN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/007,817
FILING DATE: 22-JAN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/201,028
FILING DATE: 01-JUN-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: SE 8702272-9
FILING DATE: 01-JUN-1987

ATTORNEY/AGENT INFORMATION:
NAME: McGowan, Malcolm K.
REGISTRATION NUMBER: 39,300
REFERENCE/DOCKET NUMBER: 012889-036
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-729-767-4

Query Match 100.0%; Score 53; DB 1; Length 38;
Best Local Similarity 100.0%; Pred. No. 0.0013;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KGNOSFEEDT 10
Db 4 KGNOSFEEDT 13

RESULT 6
US-09-010-317-7
Sequence 7, Application US/09010317
Patent No. 6685943
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
APPLICANT: Patti, Joseph M.
APPLICANT: House-Pompeo, Karen L.
APPLICANT: Speziale, Pietro
APPLICANT: Joh, Danny
APPLICANT: McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAMK-189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-474-7577
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-09-010-317-7

Query Match 100.0%; Score 53; DB 4; Length 38;
Best Local Similarity 100.0%; Pred. No. 0.0013;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KGNOSFEEDT 10
Db 3 KGNOSFEEDT 12

RESULT 7

US-09-010-317-8
Sequence 8, Application US/09010317
Patent No. 6685943
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
APPLICANT: Patti, Joseph M.
APPLICANT: House-Pompeo, Karen L.
APPLICANT: Speziale, Pietro
APPLICANT: John, Danny
APPLICANT: McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
TITLE OF INVENTION: AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TBMK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-09-010-317-8

Query Match 100.0%; Score 53; DB 4; Length 38;
Best Local Similarity 100.0%; Pred. No. 0.0013;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KGNOSFEEDT 10
Db 3 KGNOSFEEDT 12

RESULT 8

US-09-010-317-49
Sequence 49, Application US/09010317
Patent No. 6685943
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
APPLICANT: Patti, Joseph M.

APPLICANT: House-Pompeo, Karen L.
APPLICANT: Speziale, Pietro
APPLICANT: John, Danny
APPLICANT: McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
TITLE OF INVENTION: AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TBMK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 49:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-09-010-317-49

Query Match 100.0%; Score 53; DB 4; Length 38;
Best Local Similarity 100.0%; Pred. No. 0.0013;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KGNOSFEEDT 10
Db 3 KGNOSFEEDT 12

RESULT 9
US-08-259-000-3
Sequence 3, Application US/08259000
Patent No. 5571514
GENERAL INFORMATION:
APPLICANT: HOOK, Magnus
APPLICANT: LINDBERG, Martin Kjell
APPLICANT: SIGNAS, Lars Christer
APPLICANT: WADSTROM, Torkel Mikael
APPLICANT: FROWAN, Gunnar
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN AS WELL AS
ITS PREPARATION
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Burns, Doane, Swecker & Mathis
STREET: P.O. Box 1404
CITY: Alexandria
STATE: Virginia
COUNTRY: United States
ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/259,000
FILING DATE: 13-JUN-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: SE 8702272-9
FILING DATE: 01-JUN-1987
ATTORNEY/AGENT INFORMATION:
NAME: Meuth, Donna M
REGISTRATION NUMBER: 36,607
REFERENCE/DOCKET NUMBER: 012885-062
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 114 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-259-000-3

Query Match 100.0%; Score 53; DB 1; Length 114;
Best Local Similarity 100.0%; Pred. No. 0.0045;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KGNOSFEEDT 10
|||||
Db 42 KGNOSFEEDT 51

RESULT 10
US-08-856-253-8
Sequence 8, Application US/08856253
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
APPLICANT: Patti, Joseph M.
APPLICANT: House-Pompeo, Karen
APPLICANT: Shanam, Narayana
APPLICANT: Symersky, Jindrich
TITLE OF INVENTION: COLLAGEN BINDING PROTEIN COMPOSITIONS
TITLE OF INVENTION: AND METHODS OF USE
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P. O. Box 4433
CITY: Houston
STATE: Texas
COUNTRY: U.S.
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/856,253
FILING DATE: Concurrently Herewith
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/017,678
FILING DATE: 16-MAY-1996
ATTORNEY/AGENT INFORMATION:
NAME: Kitchell, Barbara S.
REGISTRATION NUMBER: 33,928
REFERENCE/DOCKET NUMBER: TANK:193
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
TELEFAX: (512) 474-7577

INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 139 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-08-856-253-8

Query Match 100.0%; Score 53; DB 3; Length 139;
Best Local Similarity 100.0%; Pred. No. 0.0057;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KGNOSFEEDT 10
|||||
Db 56 KGNOSFEEDT 65

RESULT 11
US-08-956-171E-5254
Sequence 5254, Application US/08956171E
Patent No. 6593114
GENERAL INFORMATION:
APPLICANT: Charles Kunsch
Gil H. Choi
Patrick S. Dillon
Craig A. Rosen
Steven C. Barash
Michael R. Fannon
TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
NUMBER OF SEQUENCES: 5256
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COUNTRY: USA
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/956,171E
FILING DATE: 20-Oct-1997
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/009,861
FILING DATE: January 5, 1996
APPLICATION NUMBER: 08/781,986
FILING DATE: January 3, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Mark J. Hyman
REGISTRATION NUMBER: 46,789
REFERENCE/DOCKET NUMBER: PB248P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (240) 314-1224
TELEFAX: (301) 309-8439
INFORMATION FOR SEQ ID NO: 5254:
SEQUENCE CHARACTERISTICS:
LENGTH: 1027 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 5254:
US-08-956-171E-5254

Query Match 100.0%; Score 53; DB 4; Length 1027;
Best Local Similarity 100.0%; Pred. No. 0.058;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KGNOSFEEDT 10

Db |||||
795 KGNOSFEEDT 804

RESULT 12
US-08-781-986A-5254
Sequence 5254, Application US/08781986A
Patent No. 6737248
GENERAL INFORMATION:
APPLICANT: Charles Kunach
TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
NUMBER OF SEQUENCES: 5255
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COUNTRY: USA
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/781,986A
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Benson, Bob
REGISTRATION NUMBER: 30,446
REFERENCE/DOCKET NUMBER: PB248BP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 5254:
SEQUENCE CHARACTERISTICS:
LENGTH: 1027 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-781-986A-5254

Query Match 100.0%; Score 53; DB 4; Length 1027;
Best Local Similarity 100.0%; Pred. No. 0.058;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KGNOSFEEDT 10
|||
Db 795 KGNOSFEEDT 804

RESULT 13
US-09-010-317-64
Sequence 64, Application US/09010317
Patent No. 6685943
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
APPLICANT: Patti, Joseph M.
APPLICANT: House-Pompeo, Karen L.
APPLICANT: Speziale, Pietro
APPLICANT: Joh, Danny
APPLICANT: McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433

CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hilder, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAMK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-474-7577
TELEFAX: 512-474-3000
INFORMATION FOR SEQ ID NO: 64:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-09-010-317-64

Query Match 90.6%; Score 48; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0026;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GGNOSFEEDT 10
|||
Db 2 GGNOSFEEDT 10

RESULT 14
US-08-234-622A-2
Sequence 2, Application US/08234622A
Patent No. 5440014
GENERAL INFORMATION:
APPLICANT: HOOK, Magnus
APPLICANT: MCGAVIN, Martin
APPLICANT: RAUCCI, Giuseppe
TITLE OF INVENTION: A FIBRONECTIN BINDING PEPTIDE
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Burns, Doane, Swecker & Mathis
STREET: P.O. Box 1404
CITY: Alexandria
STATE: Virginia
COUNTRY: United States
ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/234,622A
FILING DATE: 28-APR-1994
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: SE 9002617-0
FILING DATE: 10-AUG-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/SE91/00534
FILING DATE: 09-AUG-1991
ATTORNEY/AGENT INFORMATION:

NAME: Meuth, Donna M
REGISTRATION NUMBER: 36,607
REFERENCE/DOCKET NUMBER: 012885-044
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-234-622A-2

Query Match 90.6%; Score 48; DB 1; Length 38;
Best Local Similarity 100.0%; Pred. No. 0.012;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GNOSFEEDT 10
Db 4 GNOSFEEDT 12

RESULT 15
US-08-729-767-3
Sequence 3, Application US/08729767
Patent No. 5770702
GENERAL INFORMATION:
APPLICANT: HOOK, Magnus
APPLICANT: LINDBERG, Martin Kjell
APPLICANT: SIGNAS, Lars Christler
APPLICANT: WADSTROM, Torkel Mikael
APPLICANT: ROMAN, Gunnar
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN AS WELL AS
NUMBER OF INVENTION: ITS PREPARATION
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Burns, Doane, Swecker & Mathis, L.L.P.
STREET: P.O. Box 1404
CITY: Alexandria
STATE: Virginia
COUNTRY: United States
ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/729,767
FILING DATE: 07-OCT-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/259,000
FILING DATE: 13-JUN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/007,817
FILING DATE: 22-JAN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/201,028
FILING DATE: 01-JUN-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: SE 8702272-9
FILING DATE: 01-JUN-1987
ATTORNEY/AGENT INFORMATION:
NAME: McGowan, Malcolm K.
REGISTRATION NUMBER: 39,300
REFERENCE/DOCKET NUMBER: 012889-036
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-729-767-3

Query Match 90.6%; Score 48; DB 1; Length 38;
Best Local Similarity 100.0%; Pred. No. 0.012;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GNOSFEEDT 10
Db 5 GNOSFEEDT 13

Search completed: October 22, 2005, 07:41:46
Job time : 17.35 secs

Chicago Blank (uspo)

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OM protein - protein search, using sw model

Run on: October 22, 2005, 12:09:40 ; Search time 57.25 Seconds
(without alignments)
72.924 Million cell updates/sec

Title: US-10-731-238-83

Perfect score: 53

Sequence: 1 KGNQSFEDT 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1862951 seqs, 417491010 residues

Total number of hits satisfying chosen parameters: 1862951

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA:*

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10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep.*
11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep.*
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19: /cgn2_6/ptodata/2/pubpaa/US11A_PUBCOMB.pep.*
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22: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	53	100.0	10	US-10-731-238-83	Sequence 83, Appl
2	53	100.0	36	US-10-731-238-58	Sequence 58, Appl
3	53	100.0	36	US-10-731-238-59	Sequence 59, Appl
4	53	100.0	38	US-10-731-238-7	Sequence 7, Appl
5	53	100.0	38	US-10-731-238-8	Sequence 8, Appl
6	53	100.0	38	US-10-731-238-9	Sequence 9, Appl
7	53	100.0	139	US-09-813-820-8	Sequence 49, Appl
8	53	100.0	1018	US-09-815-242-5797	Sequence 8, Appl
9	53	100.0	1018	US-09-815-242-5797	Sequence 5797, A
10	53	100.0	1018	US-10-470-0468-68	Sequence 12838, A
11	53	100.0	1027	US-08-781-986A-5254	Sequence 68, Appl

12	53	100.0	1027	US-10-329-624-5254	Sequence 5254, Ap
13	48	90.6	30	US-10-731-238-64	Sequence 64, Appl
14	48	90.6	30	US-10-287-821-1	Sequence 1, Appl
15	48	90.6	31	US-10-287-821-2	Sequence 2, Appl
16	48	90.6	38	US-10-731-238-5	Sequence 5, Appl
17	48	90.6	38	US-10-731-238-6	Sequence 6, Appl
18	48	90.6	38	US-10-731-238-40	Sequence 40, Appl
19	48	90.6	38	US-10-731-238-41	Sequence 41, Appl
20	48	90.6	38	US-10-731-238-42	Sequence 42, Appl
21	48	90.6	38	US-10-731-238-43	Sequence 43, Appl
22	48	90.6	39	US-10-731-238-56	Sequence 56, Appl
23	48	90.6	39	US-10-731-238-57	Sequence 57, Appl
24	48	90.6	388	US-08-901-062-1	Sequence 1, Appl
25	48	90.6	555	US-08-781-986A-5251	Sequence 5251, Ap
26	48	90.6	555	US-10-329-624-5251	Sequence 5251, Ap
27	48	90.6	767	US-09-815-242-5899	Sequence 5899, Ap
28	48	90.6	940	US-09-815-242-13140	Sequence 13140, A
29	48	90.6	948	US-10-470-0468-424	Sequence 424, Ap
30	48	90.6	948	US-10-470-0468-69	Sequence 69, Appl
31	48	90.6	961	US-10-282-122A-43778	Sequence 43778, A
32	48	90.6	978	US-09-815-242-5455	Sequence 5455, Ap
33	48	90.6	1001	US-09-815-242-12686	Sequence 12686, A
34	48	90.6	1038	US-10-282-122A-43827	Sequence 43827, A
35	47	88.7	38	US-10-731-238-46	Sequence 46, Appl
36	47	88.7	38	US-10-731-238-47	Sequence 47, Appl
37	46	86.8	38	US-10-731-238-48	Sequence 48, Appl
38	46	86.8	38	US-10-731-238-39	Sequence 39, Appl
39	43	81.1	38	US-10-731-238-45	Sequence 45, Appl
40	42	79.2	10	US-10-731-238-65	Sequence 65, Appl
41	42	79.2	10	US-10-731-238-82	Sequence 82, Appl
42	42	79.2	10	US-10-731-238-84	Sequence 84, Appl
43	42	79.2	38	US-10-731-238-36	Sequence 36, Appl
44	42	79.2	38	US-10-731-238-37	Sequence 37, Appl
45	41	77.4	38	US-10-731-238-38	Sequence 38, Appl

ALIGNMENTS

RESULT 1
US-10-731-238-83
Sequence 83, Application US/10731238
Publication No. US20050123552A1
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
Patl, Joseph M.
House-Pompeo, Karen L.
Speziale, Pietro
Joh, Danny
McGavin, Martin J
TITLE OF INVENTION: FIBROBLAST BINDING PROTEIN COMPOSITIONS
AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/731,238
FILING DATE: 10-Dec-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE: 21-Jan-1998
APPLICATION NUMBER: US 60/036,139

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; FILING DATE: 21-JAN-1997
; ATTORNEY/AGENT INFORMATION:
;   NAME: Hibler, David W.
;   REGISTRATION NUMBER: 41,071
;   REFERENCE/DOCKET NUMBER: TAMK:189
; TELECOMMUNICATION INFORMATION:
;   TELEPHONE: 512-418-3000
;   TELEFAX: 512-474-7577
; INFORMATION FOR SEQ ID NO: 83:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH: 10 amino acids
;     TYPE: amino acid
;     STRANDEDNESS: <Unknown>
;     TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 83:
US-10-731-238-83

Query Match      100.0%; Score 53; DB 18; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0026;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KGNQSFEDT 10
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Db      1 KGNQSFEDT 10

RESULT 2
US-10-731-238-58
; Sequence 58, Application US/10731238
; Publication No. US20050123552A1
; GENERAL INFORMATION:
;   APPLICANT: Hook, Magnus
;               Patli, Joseph M.
;               House-Pompeo, Karen L.
;               Speziale, Pietro
;               Joh, Danny
;               McGavin, Martin J.
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
; AND METHODS OF USE
; NUMBER OF SEQUENCES: 105
; CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Arnold, White & Durkee
;   STREET: P.O. Box 4433
;   CITY: Houston
;   STATE: TX
;   COUNTRY: USA
;   ZIP: 77210-4433
; COMPUTER READABLE FORM:
;   MEDIUM TYPE: floppy disk
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/10/731,238
;   FILING DATE: 10-Dec-2003
;   CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US/09/010,317
;   FILING DATE: 21-Jan-1998
;   APPLICATION NUMBER: US 60/036,139
;   FILING DATE: 21-JAN-1997
; ATTORNEY/AGENT INFORMATION:
;   NAME: Hibler, David W.
;   REGISTRATION NUMBER: 41,071
;   REFERENCE/DOCKET NUMBER: TAMK:189
; TELECOMMUNICATION INFORMATION:
;   TELEPHONE: 512-418-3000
;   TELEFAX: 512-474-7577
; INFORMATION FOR SEQ ID NO: 58:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH: 36 amino acids
;     TYPE: amino acid
;     STRANDEDNESS: <Unknown>
;     TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 58:
US-10-731-238-58

Query Match      100.0%; Score 53; DB 18; Length 36;
Best Local Similarity 100.0%; Pred. No. 0.01;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KGNQSFEDT 10
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Db      3 KGNQSFEDT 12
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; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 58:
US-10-731-238-58

Query Match      100.0%; Score 53; DB 18; Length 36;
Best Local Similarity 100.0%; Pred. No. 0.01;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KGNQSFEDT 10
        |||||
Db      3 KGNQSFEDT 12

RESULT 3
US-10-731-238-59
; Sequence 59, Application US/10731238
; Publication No. US20050123552A1
; GENERAL INFORMATION:
;   APPLICANT: Hook, Magnus
;               Patli, Joseph M.
;               House-Pompeo, Karen L.
;               Speziale, Pietro
;               Joh, Danny
;               McGavin, Martin J.
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
; AND METHODS OF USE
; NUMBER OF SEQUENCES: 105
; CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Arnold, White & Durkee
;   STREET: P.O. Box 4433
;   CITY: Houston
;   STATE: TX
;   COUNTRY: USA
;   ZIP: 77210-4433
; COMPUTER READABLE FORM:
;   MEDIUM TYPE: floppy disk
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/10/731,238
;   FILING DATE: 10-Dec-2003
;   CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US/09/010,317
;   FILING DATE: 21-Jan-1998
;   APPLICATION NUMBER: US 60/036,139
;   FILING DATE: 21-JAN-1997
; ATTORNEY/AGENT INFORMATION:
;   NAME: Hibler, David W.
;   REGISTRATION NUMBER: 41,071
;   REFERENCE/DOCKET NUMBER: TAMK:189
; TELECOMMUNICATION INFORMATION:
;   TELEPHONE: 512-418-3000
;   TELEFAX: 512-474-7577
; INFORMATION FOR SEQ ID NO: 59:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH: 36 amino acids
;     TYPE: amino acid
;     STRANDEDNESS: <Unknown>
;     TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 59:
US-10-731-238-59

Query Match      100.0%; Score 53; DB 18; Length 36;
Best Local Similarity 100.0%; Pred. No. 0.01;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KGNQSFEDT 10
        |||||
Db      3 KGNQSFEDT 12
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RESULT 4
US-10-731-238-7
; Sequence 7, Application US/10731238
; Publication No. US20050123552A1
; GENERAL INFORMATION:
; APPLICANT: Hook, Magnus
; Patti, Joseph M.
; House-Pompeo, Karen L.
; Speziale, Pietro
; Joh, Danny
; McGavin, Martin J.
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
; AND METHODS OF USE
; NUMBER OF SEQUENCES: 105
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: TX
; COUNTRY: USA
; ZIP: 77210-4433
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/731,238
; FILING DATE: 10-Dec-2003
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/010,317
; FILING DATE: 21-Jan-1998
; APPLICATION NUMBER: US 60/036,139
; FILING DATE: 21-JAN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Hibler, David W.
; REGISTRATION NUMBER: 41,071
; REFERENCE/DOCKET NUMBER: TANK:189
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 512-418-3000
; TELEFAX: 512-474-7577
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 38 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-10-731-238-7
Query Match 100.0%; Score 53; DB 18; Length 38;
Best Local Similarity 100.0%; Pred. No. 0.011;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 KGNOSFEEDT 10
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Db 3 KGNOSFEEDT 12
RESULT 5
US-10-731-238-8
; Sequence 8, Application US/10731238
; Publication No. US20050123552A1
; GENERAL INFORMATION:
; APPLICANT: Hook, Magnus
; Patti, Joseph M.
; House-Pompeo, Karen L.
; Speziale, Pietro
; Joh, Danny
; McGavin, Martin J.
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
; AND METHODS OF USE

NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/731,238
FILING DATE: 10-Dec-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE: 21-Jan-1998
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TANK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-10-731-238-8
Query Match 100.0%; Score 53; DB 18; Length 38;
Best Local Similarity 100.0%; Pred. No. 0.011;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 KGNOSFEEDT 10
| | | | | | | | | |
Db 3 KGNOSFEEDT 12
RESULT 6
US-10-731-238-49
; Sequence 49, Application US/10731238
; Publication No. US20050123552A1
; GENERAL INFORMATION:
; APPLICANT: Hook, Magnus
; Patti, Joseph M.
; House-Pompeo, Karen L.
; Speziale, Pietro
; Joh, Danny
; McGavin, Martin J.
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
; AND METHODS OF USE
; NUMBER OF SEQUENCES: 105
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: TX
; COUNTRY: USA
; ZIP: 77210-4433
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30

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; INFORMATION FOR SEQ ID NO: 8:
;
; SEQUENCE CHARACTERISTICS:
;     LENGTH: 139 amino acids
;     TYPE: amino acid
;     STRANDEDNESS: <Unknown>
;     TOPOLOGY: linear
;
; SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-09-813-820-8

Query Match          100.0%; Score 53; DB 9; Length 139;
Best Local Similarity 100.0%; Pred. No. 0.046;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KGNOSFEEDT 10
      |||||
Db      56 KGNOSFEEDT 65

RESULT 8
US-09-815-242-5797
; Sequence 5797, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Karl L.
; APPLICANT: Zykind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; FILE REFERENCE: ELITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5797
; LENGTH: 1018
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-09-815-242-5797

Query Match          100.0%; Score 53; DB 9; Length 1018;
Best Local Similarity 100.0%; Pred. No. 0.4;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KGNOSFEEDT 10
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Db      786 KGNOSFEEDT 795

RESULT 9
US-09-815-242-12838
; Sequence 12838, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert

```

APPLICANT: Ohlsen, Kari L.
APPLICANT: Zykkind, Judith W.
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John D.
APPLICANT: Carr, Grant J.
APPLICANT: Yamamoto, Robert T.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in
FILE REFERENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 12838
LENGTH: 1018
TYPE: PRT
ORGANISM: Staphylococcus aureus
US-09-815-242-12838

Query Match 100.0%; Score 53; DB 9; Length 1018;
Best Local Similarity 100.0%; Pred. No. 0.4;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KGNOSFEEDT 10
|||||
Db 786 KGNOSFEEDT 795

RESULT 10
US-10-470-048B-68
Sequence 68, Application US/10470048B
Publication No. US2005003744A1
GENERAL INFORMATION:
APPLICANT: MEINKE ET AL.
TITLE OF INVENTION: A METHOD FOR IDENTIFICATION, ISOLATION AND PRODUCTION OF
FILE REFERENCE: SONN-03US
CURRENT APPLICATION NUMBER: US/10/470,048B
CURRENT FILING DATE: 2003-07-25
NUMBER OF SEQ ID NOS: 603
SOFTWARE: PatentIn version 3.1
SEQ ID NO 68
LENGTH: 1018
TYPE: PRT
ORGANISM: Staphylococcus aureus
US-10-470-048B-68

Query Match 100.0%; Score 53; DB 17; Length 1018;
Best Local Similarity 100.0%; Pred. No. 0.4;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KGNOSFEEDT 10
|||||
Db 786 KGNOSFEEDT 795

RESULT 11
US-08-781-986A-5254

Sequence 5254, Application US/08781986A
Publication No. US2003005436A1
GENERAL INFORMATION:
APPLICANT: Charles Kunach
TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
NUMBER OF SEQUENCES: 5255
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COUNTRY: USA
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/781,986A
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Benson, Bob
REGISTRATION NUMBER: 30,446
REFERENCE/DOCKET NUMBER: PB248BP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 5254:
SEQUENCE CHARACTERISTICS:
LENGTH: 1027 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-781-986A-5254

Query Match 100.0%; Score 53; DB 8; Length 1027;
Best Local Similarity 100.0%; Pred. No. 0.41;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KGNOSFEEDT 10
|||||
Db 795 KGNOSFEEDT 804

RESULT 12
US-10-329-624-5254
Sequence 5254, Application US/10329624
Publication No. US20040043037A1
GENERAL INFORMATION:
APPLICANT: Charles Kunach
Gail H. Choi
Patrick S. Dillon
Craig A. Rosen
Steven C. Barash
Michael R. Fannon
TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
NUMBER OF SEQUENCES: 5256
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COUNTRY: USA
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4mb storage
COMPUTER: HP Vectra 486/33

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OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
  APPLICATION NUMBER: US/10/329,624
  FILING DATE: 27-Dec-2002
PRIOR APPLICATION DATA:
  APPLICATION NUMBER: 08/956,171
  FILING DATE: October 20, 1997
  APPLICATION NUMBER: 60/009,861
  FILING DATE: January 5, 1996
  APPLICATION NUMBER: 08/781,986
  FILING DATE: January 3, 1997
ATTORNEY/AGENT INFORMATION:
  NAME: Mark J. Hyman
  REGISTRATION NUMBER: 46,789
  REFERENCE/DOCKET NUMBER: PB248PD1
TELECOMMUNICATION INFORMATION:
  TELEPHONE: (240) 314-1224
  TELEFAX: (301) 309-8439
INFORMATION FOR SEQ ID NO: 5254:
SEQUENCE CHARACTERISTICS:
  LENGTH: 1027 amino acids
  TYPE: amino acid
  STRANDEDNESS: single
  TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 5254:
US-10-329-624-5254

Query Match      100.0%; Score 53; DB 15; Length 1027;
Best Local Similarity 100.0%; Pred. No. 0.41;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  KGNOSFEEDT 10
      |||||
Db      795  KGNOSFEEDT 804

RESULT 13
US-10-731-238-64
Sequence 64, Application US/10731238
Publication No. US20050123552A1
GENERAL INFORMATION:
  APPLICANT: Hook, Magnus
  Patti, Joseph M.
  House-Pompeo, Karen L.
  Speciale, Pietro
  Joh, Danny
  McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
  ADDRESSEE: Arnold, White & Durkee
  STREET: P. O. Box 4433
  CITY: Houston
  STATE: TX
  COUNTRY: USA
  ZIP: 77210-4433
COMPUTER READABLE FORM:
  MEDIUM TYPE: floppy disk
  COMPUTER: IBM PC compatible
  OPERATING SYSTEM: PC-DOS/MS-DOS
  SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
  APPLICATION NUMBER: US/10/731,238
  FILING DATE: 10-Dec-2003
  CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
  APPLICATION NUMBER: US/09/010,317
  FILING DATE: 21-Jan-1998
  APPLICATION NUMBER: US 60/036,139
  FILING DATE: 21-JAN-1997
```

```
ATTORNEY/AGENT INFORMATION:
  NAME: Hibler, David W.
  REGISTRATION NUMBER: 41,071
  REFERENCE/DOCKET NUMBER: TBMK.189
TELECOMMUNICATION INFORMATION:
  TELEPHONE: 512-418-3000
  TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 64:
SEQUENCE CHARACTERISTICS:
  LENGTH: 10 amino acids
  TYPE: amino acid
  STRANDEDNESS: <Unknown>
  TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 64:
US-10-731-238-64

Query Match      90.6%; Score 48; DB 18; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.023;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2  GGNOSFEEDT 10
      |||||
Db      2  GGNOSFEEDT 10

RESULT 14
US-10-287-821-1
Sequence 1, Application US/10287821
Publication No. US20030153022A1
GENERAL INFORMATION:
  APPLICANT: Patti, Joseph M.
TITLE OF INVENTION: MONOCLONAL ANTIBODIES TO THE FIBRONECTIN BINDING PROTEIN.
FILE REFERENCE: P07427U501/BAS
CURRENT APPLICATION NUMBER: US/10/287,821
CURRENT FILING DATE: 2002-11-05
PRIOR APPLICATION NUMBER: 60/330,964
PRIOR FILING DATE: 2001-11-05
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PatentIn version 3.1
SEQ ID NO 1
LENGTH: 30
TYPE: PRT
ORGANISM: Staphylococcus aureus
US-10-287-821-1

Query Match      90.6%; Score 48; DB 14; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.076;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2  GGNOSFEEDT 10
      |||||
Db      5  GGNOSFEEDT 13

RESULT 15
US-10-287-821-2
Sequence 2, Application US/10287821
Publication No. US20030153022A1
GENERAL INFORMATION:
  APPLICANT: Patti, Joseph M.
TITLE OF INVENTION: MONOCLONAL ANTIBODIES TO THE FIBRONECTIN BINDING PROTEIN.
FILE REFERENCE: P07427U501/BAS
CURRENT APPLICATION NUMBER: US/10/287,821
CURRENT FILING DATE: 2002-11-05
PRIOR APPLICATION NUMBER: 60/330,964
PRIOR FILING DATE: 2001-11-05
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PatentIn version 3.1
SEQ ID NO 2
LENGTH: 31
TYPE: PRT
ORGANISM: Staphylococcus aureus
US-10-287-821-2
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Query Match	90.6%	Score 48	DB 14	Length 31
Best Local Similarity	100.0%	Pred. No. 0.079		
Matches	9	Conservative 0	Mismatches 0	Indels 0
				Gaps 0

QY 2 GNQSFEDT 10
|||||||

Db 6 GNQSFEDT 14

Search completed: October 22, 2005, 12:39:50
Job time : 58.25 secs

The Page Bank (asp19)

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 22, 2005, 06:10:10 ; Search time 11.45 Seconds
(without alignments)
84.032 Million cell updates/sec

Title: US-10-731-238-83

Perfect score: 53

Sequence: 1 KGNQSFEDT 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

PIR-79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	53	100.0	1018	2	A32192 fibronectin-binding protein B - Staphylococcus aureus
2	48	90.6	940	2	S19702 fibronectin-binding protein B - Staphylococcus aureus
3	48	90.6	961	2	G90053 fibronectin-binding protein B - Staphylococcus aureus
4	48	90.6	1038	2	H90053 fibronectin-binding protein B - Staphylococcus aureus
5	39	73.6	499	2	A30151 fibronectin-binding protein B - Staphylococcus aureus
6	37	69.8	429	2	G64649 fibronectin-binding protein B - Staphylococcus aureus
7	36	67.9	323	2	D68847 fibronectin-binding protein B - Staphylococcus aureus
8	36	67.9	461	2	S23420 fibronectin-binding protein B - Staphylococcus aureus
9	35	66.0	72	2	C86714 fibronectin-binding protein B - Staphylococcus aureus
10	35	66.0	167	2	S37843 fibronectin-binding protein B - Staphylococcus aureus
11	35	66.0	218	2	JQ0181 fibronectin-binding protein B - Staphylococcus aureus
12	35	66.0	229	2	S49494 fibronectin-binding protein B - Staphylococcus aureus
13	35	66.0	263	2	T38351 fibronectin-binding protein B - Staphylococcus aureus
14	35	66.0	374	2	T20481 fibronectin-binding protein B - Staphylococcus aureus
15	35	66.0	441	1	E70461 fibronectin-binding protein B - Staphylococcus aureus
16	35	66.0	480	2	T50511 fibronectin-binding protein B - Staphylococcus aureus
17	35	66.0	509	2	D95053 fibronectin-binding protein B - Staphylococcus aureus
18	35	66.0	530	2	B86326 fibronectin-binding protein B - Staphylococcus aureus
19	35	66.0	848	2	T28055 fibronectin-binding protein B - Staphylococcus aureus
20	35	66.0	967	2	T35125 fibronectin-binding protein B - Staphylococcus aureus
21	34	64.2	165	2	T52114 fibronectin-binding protein B - Staphylococcus aureus
22	34	64.2	339	2	F85098 fibronectin-binding protein B - Staphylococcus aureus
23	34	64.2	429	2	G71937 fibronectin-binding protein B - Staphylococcus aureus
24	34	64.2	452	2	I49542 fibronectin-binding protein B - Staphylococcus aureus
25	34	64.2	475	2	H97062 fibronectin-binding protein B - Staphylococcus aureus
26	34	64.2	478	2	JC1475 fibronectin-binding protein B - Staphylococcus aureus
27	34	64.2	526	2	C84993 fibronectin-binding protein B - Staphylococcus aureus
28	34	64.2	526	2	D96977 fibronectin-binding protein B - Staphylococcus aureus
29	34	64.2	531	2	H81928 fibronectin-binding protein B - Staphylococcus aureus

30	34	64.2	531	2	F81176 fibronectin-binding protein B - Staphylococcus aureus
31	34	64.2	538	2	D75381 fibronectin-binding protein B - Staphylococcus aureus
32	34	64.2	540	2	AC2353 fibronectin-binding protein B - Staphylococcus aureus
33	34	64.2	547	2	S77410 fibronectin-binding protein B - Staphylococcus aureus
34	34	64.2	1351	2	S44665 fibronectin-binding protein B - Staphylococcus aureus
35	34	64.2	1376	2	F83711 fibronectin-binding protein B - Staphylococcus aureus
36	34	64.2	2529	2	B64635 fibronectin-binding protein B - Staphylococcus aureus
37	33	62.3	79	2	G75155 fibronectin-binding protein B - Staphylococcus aureus
38	33	62.3	170	2	I49055 fibronectin-binding protein B - Staphylococcus aureus
39	33	62.3	176	2	I67435 fibronectin-binding protein B - Staphylococcus aureus
40	33	62.3	297	1	NBRT fibronectin-binding protein B - Staphylococcus aureus
41	33	62.3	361	2	AF1593 fibronectin-binding protein B - Staphylococcus aureus
42	33	62.3	412	2	AG1922 fibronectin-binding protein B - Staphylococcus aureus
43	33	62.3	416	2	S39684 fibronectin-binding protein B - Staphylococcus aureus
44	33	62.3	457	2	T26642 fibronectin-binding protein B - Staphylococcus aureus
45	33	62.3	507	2	T10753 fibronectin-binding protein B - Staphylococcus aureus

ALIGNMENTS

RESULT 1

A32192 fibronectin-binding protein B - Staphylococcus aureus
C:Species: Staphylococcus aureus
C:Date: 31-Jul-1989 #sequence_revision 31-Jul-1989 #text_change 16-Feb-1997
C:Accession: A32192
R:Signaas, C.; Raucel, G.; Joensson, K.; Lindgren, P.E.; Anantharamiah, G.M.; Hoecek, Proc. Natl. Acad. Sci. U.S.A. 86, 699-703, 1989
A:Title: Nucleotide sequence of the gene for a fibronectin-binding protein from Staphylococcus aureus
A:Reference number: A32192; MUID:69098998; PMID:2521391
A:Accession: A32192
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1018 <SIG>
A:Cross-references: GB:J04151
C:Keywords: fibronectin binding

Query Match 100.0%; Score 53; DB 2; Length 1018;
Best Local Similarity 100.0%; Pred. No. 0.04;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KGNQSFEDT 10
DB 786 KGNQSFEDT 795

RESULT 2

S19702 fibronectin-binding protein B - Staphylococcus aureus
C:Species: Staphylococcus aureus
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
R:Joensson, K.; Signaas, C.; Mueller, H.P.; Lindberg, M. Eur. J. Biochem. 202, 1041-1048, 1991
A:Title: Two different genes encode fibronectin binding proteins in Staphylococcus aureus
A:Reference number: S19702; MUID:9211475; PMID:1837266
A:Accession: S19702
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-940 <JOB>
A:Cross-references: NIDPROT:053682; EMBL:X62992; NID:949040; PIDN:CAA44726.1; PID:95815
C:Keywords: fibronectin binding

Query Match 90.6%; Score 48; DB 2; Length 940;
Best Local Similarity 100.0%; Pred. No. 0.35;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GNSQSFEDT 10
DB 685 GNSQSFEDT 693

```
RESULT 3
G90053
hypothetical protein fnbA [imported] - Staphylococcus aureus (strain N315)
C:Species: Staphylococcus aureus
C>Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C:Accession: G90053
R:Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Ogura, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.;
C:Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
A:Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.
A:Reference number: A89758; MUID:21311952; PMID:11418146
A:Accession: G90053
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-961 <KIR>
A:Cross-references: UNIPROT:Q99RD3; GB:BA000018; PID:g13702452; PIDN:BA845593.1; GSPDB:C
A:Experimental source: strain N315
C:Genetics:
A:Gene: fnbA

Query Match          90.6%; Score 48; DB 2; Length 961;
Best Local Similarity 100.0%; Pred. No. 0.36;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GNGSFEDT 10
Db 696 GNGSFEDT 704

RESULT 4
H90053
hypothetical protein fnb [imported] - Staphylococcus aureus (strain N315)
C:Species: Staphylococcus aureus
C>Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C:Accession: H90053
R:Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Ogura, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.;
C:Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
A:Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.
A:Reference number: A89758; MUID:21311952; PMID:11418146
A:Accession: H90053
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1038 <KIR>
A:Cross-references: UNIPROT:Q99RD2; GB:BA000018; PID:g13702453; PIDN:BA845594.1; GSPDB:C
A:Experimental source: strain N315
C:Genetics:
A:Gene: fnbA

Query Match          90.6%; Score 48; DB 2; Length 1038;
Best Local Similarity 100.0%; Pred. No. 0.39;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GNGSFEDT 10
Db 745 GNGSFEDT 753

RESULT 5
A30151
dihydrolypamidase dehydrogenase (EC 1.8.1.4) precursor - yeast (Saccharomyces cerevisiae)
N:Alternate names: protein YFL018C
C:Species: Saccharomyces cerevisiae
C>Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 09-Jul-2004
C:Accession: A30151; A46562; S48323; S56236; S62295
R:Browning, K.S.; Uhlinger, D.J.; Reed, L.J.
Proc. Natl. Acad. Sci. U.S.A. 85, 1831-1834, 1988
A:Title: Nucleotide sequence for yeast dihydrolypamidase dehydrogenase.
A:Reference number: A30151; MUID:88158087; PMID:3279419
A:Accession: A30151
A:Molecule type: mRNA

A:Residues: 1-499 <BRO>
A:Cross-references: UNIPROT:P09624; EMBL:J03645; NID:g171389; PIDN:AAA34565.1; PID:g1713
A>Note: part of this sequence was confirmed by protein sequencing
R:Rosa, J.; Reid, G.A.; Dawes, I.W.
J. Gen. Microbiol. 134, 1131-1139, 1988
A:Title: The nucleotide sequence of the LPD1 gene encoding lipamidase dehydrogenase in S.
A:Reference number: A46562; MUID:89067880; PMID:3058861
A:Accession: A46562
A:Molecule type: DNA
A:Residues: 1-499 <ROS>
A:Cross-references: GB:M20880; NID:g171847; PIDN:AA863974.1; PID:g171848
R:Churcher, C.
Submitted to the EMBL Data Library, September 1994
A:Reference number: S48310
A:Accession: S48323
A:Molecule type: DNA
A:Residues: 1-499 <CHU>
A:Cross-references: EMBL:Z46255; NID:g559925; PIDN:CAA86354.1; PID:g559939; MIPS:YFL018
R:Murakami, Y.; Naitou, M.; Hagiwara, H.; Shibata, T.; Ozawa, M.; Sasanuma, S.I.; Sasam
Submitted to the EMBL Data Library, May 1995
A:Description: Analysis of the nucleotide sequence of chromosome VI from Saccharomyces c
A:Reference number: S56186
A:Accession: S56236
A:Molecule type: DNA
A:Residues: 1-499 <MUR>
A:Cross-references: EMBL:D50617; NID:g836685; PIDN:BA09220.1; PID:g836736; MIPS:YFL018
R:Murakami, Y.
Submitted to the EMBL Data Library, December 1994
A:Reference number: S62230
A:Accession: S62295
A:Molecule type: DNA
A:Residues: 1-499 <MUR>
A:Cross-references: EMBL:D44596; NID:g1100783; PIDN:BA07999.1; PID:g1100786
C:Genetics:
A:Gene: SGD:LPD1
A:Cross-references: SGD:S0001876; MIPS:YFL018C
A:Map position: 6L
A:Genome: nuclear
C:Superfamily: dihydrolypamidase dehydrogenase; dihydrolypamidase dehydrogenase homology
C:Keywords: FAD; flavoprotein; liponamide; mitochondrion; #status experimental <TMP>
F:1-21/Domain: transit peptide (mitochondrion) #status experimental <TMP>
F:22-499/Product: dihydrolypamidase dehydrogenase #status experimental <TMP>
F:28-56/Region: beta-alpha-beta FAD nucleotide-binding fold
F:30-485/Domain: dihydrolypamidase dehydrogenase homology <DLD>
F:265-334/Region: beta-alpha-beta NAD nucleotide-binding fold
F:65-70/Disulfide bonds: redox-active #status predicted

Query Match          73.6%; Score 39; DB 2; Length 499;
Best Local Similarity 70.0%; Pred. No. 10;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 KNGSFEDT 10
Db 136 KNGSFEDT 145

RESULT 6
G64649
hypothetical protein HP1039 - Helicobacter pylori (strain 26695)
C:Species: Helicobacter pylori
C>Date: 09-Aug-1997 #sequence_revision 09-Aug-1997 #text_change 09-Jul-2004
C:Accession: G64649
R:Tomb, J.F.; White, O.; Karlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.D.
Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khalak, H.G.; Glodok, A.; McKen-
son, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Wathey, L.
Nature 388, 359-347, 1997
A:Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser, C
A:Title: The complete genome sequence of the gastric pathogen Helicobacter pylori.
A:Reference number: A64520; MUID:97394467; PMID:9252185
A:Accession: G64649
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
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A:Residues: 1-429 <TOM>
 A:Cross-references: UNIPROT:O25682; GB:AE000611; GB:AE000511; NID:92314173; PIDN:AAD0808
 C:Genetics:
 A:Start codon: GTG

Query Match 69.8%; Score 37; DB 2; Length 429;
 Best Local Similarity 100.0%; Pred. No. 22;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 NOSPEED 9
 DB 270 NOSPEED 276

RESULT 7

biothin-lactate-CoA-carboxylase) ligase (EC 6.3.4.15) [imported] - Lactococcus lactis subsp. *N/A*
 N/Alternate names: bifunctional protein BifA
 C/Species: Lactococcus lactis subsp. *Lactis*
 C/Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 09-Jul-2004
 C/Accession: D86847
 R/Bolotin, A.; Mincker, P.; Manger, S.; Jallion, O.; Malarme, K.; Weissenbach, J.; Ehrlich
 Genome Res. 11, 731-753, 2001
 A>Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis ssp
 A/Reference number: A86625; MUID:21235186; PMID:11337471
 A/Accession: D86847
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-523 <STO>
 A:Cross-references: UNIPROT:Q9CE06; GB:AE005176; PID:912724804; PIDN:AAK05878.1; GSPDB:C
 A:Experimental source: strain IL1403
 C:Genetics:
 A:Gene: bifa1
 C:Keywords: ligase

Query Match 67.9%; Score 36; DB 2; Length 323;
 Best Local Similarity 66.7%; Pred. No. 25;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 GNSPEED 10
 DB 62 GNSLEDEDT 70

RESULT 8

S23420
 Problematic subtilisin-like protease (EC 3.4.21.-) eplp - Staphylococcus epidermidis
 N/Alternate names: lantibiotic epidermin biosynthesis protein eplp
 C/Species: Staphylococcus epidermidis
 C/Date: 22-Nov-1993 #sequence_revision 01-Dec-1995 #text_change 09-Jul-2004
 C/Accession: S23420
 R/Schnell, N.; Engelske, G.; Augustin, J.; Rosenstein, R.; Ungermann, V.; Goetz, F.; Entl
 Eur. J. Biochem. 204, 57-68, 1992
 A>Title: Analysis of genes involved in the biosynthesis of lantibiotic epidermin.
 A/Reference number: S23413; MUID:92155237; PMID:1740156
 A/Accession: S23420
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-461 <SCH>
 A:Cross-references: UNIPROT:P30199; EMBL:X62386; NID:946964; PIDN:CAA44257.1; PID:946971
 C:Keywords: hydrolase; serine proteinase

Query Match 67.9%; Score 36; DB 2; Length 461;
 Best Local Similarity 75.0%; Pred. No. 37;
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 GNSPEED 9
 DB 189 GNSFEED 190

RESULT 9

C86714

hypothetical protein yhcC [imported] - Lactococcus lactis subsp. *Lactis* (strain IL1403)
 C/Species: Lactococcus lactis subsp. *Lactis*
 C/Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 09-Jul-2004
 C/Accession: C86714
 R/Bolotin, A.; Mincker, P.; Manger, S.; Jallion, O.; Malarme, K.; Weissenbach, J.; Ehrlich
 Genome Res. 11, 731-753, 2001
 A>Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis ssp
 A/Reference number: A86625; MUID:21235186; PMID:11337471
 A/Accession: C86714
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-72 <STO>
 A:Cross-references: UNIPROT:Q9CHL4; GB:AE005176; PID:912723627; PIDN:AAK04813.1; GSPDB:C
 A:Experimental source: strain IL1403
 C:Genetics:
 A:Gene: yhcC

Query Match 66.0%; Score 35; DB 2; Length 72;
 Best Local Similarity 75.0%; Pred. No. 7.9;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 GNSPEED 9
 DB 14 GNSFEED 21

RESULT 10

S37843
 glutathione peroxidase homolog YKL026C - yeast (Saccharomyces cerevisiae)
 C/Species: Saccharomyces cerevisiae
 C/Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 09-Jul-2004
 C/Accession: S37843
 R/Rieger, M.
 submitted to the Protein Sequence Database, March 1994
 A/Reference number: S37832
 A/Accession: S37843
 A:Molecule type: DNA
 A:Residues: 1-167 <RIB>
 A:Cross-references: UNIPROT:P36014; EMBL:Z28026; NID:9486022; PIDN:CAA1861.1; PID:9486
 A:Experimental source: strain S288C
 C:Genetics:
 A:Gene: SGD:GPX1; MIPS:YKL026C
 A:Cross-references: SGD:S0001509
 A:Map position: 11L
 C:Superfamily: glutathione peroxidase

Query Match 66.0%; Score 35; DB 2; Length 167;
 Best Local Similarity 75.0%; Pred. No. 20;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 GNSPEED 9
 DB 68 GNSFEED 75

RESULT 11

J00181
 replication protein reph - Lactobacillus plantarum
 C/Species: Lactobacillus plantarum
 C/Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 09-Jul-2004
 C/Accession: J00181
 R/Bates, E.E.M.; Gilbert, H.J.
 Gene 85, 253-258, 1989
 A>Title: Characterization of a cryptic plasmid from Lactobacillus plantarum.
 A/Reference number: J00179; MUID:90152374; PMID:2695401
 A:Contents: Plasmid pLB4, strain NCD01088
 A/Accession: J00181
 A:Molecule type: DNA
 A:Residues: 1-218 <BAT>
 A:Cross-references: UNIPROT:P20045; GB:M33531; NID:9149593; PIDN:AAA25254.1; PID:914959

A:Gene: reph

Query Match 66.0%; Score 35; DB 2; Length 218;
Best Local Similarity 75.0%; Pred. No. 26;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 KGNOSFEE 8
|||:|:
DB 80 KGNKSFEQ 87

RESULT 12

S49494
replication protein repB - Lactobacillus fermentum
N:Alternate names: repB protein
C:Species: Lactobacillus fermentum
C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004
C:Accession: S49494
R:Allyoshin, V.V.; Yomantas, Y.; Torban, E.; Tarakanov, B.V.; Livshits, V.A.
Submitted to the EMBL Data Library, September 1993
A:Reference number: S49493
A:Accession: S49494
A:Molecule type: DNA
A:Residues: 1-229 <ALY>
A:Cross-references: UNIPROT:Q48551; EMBL:X74860; NID:G559460; PIDN:CAA52853.1; PID:G5594
A:Experimental source: ATCC 9338
C:Genetics:
A:Gene: repB

Query Match 66.0%; Score 35; DB 2; Length 229;
Best Local Similarity 75.0%; Pred. No. 28;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 KGNOSFEE 8
|||:|:
DB 80 KGNKSFEQ 87

RESULT 13

T38351
ribosomal protein mrp4, mitochondrial - fission yeast (Schizosaccharomyces pombe)
C:Species: Schizosaccharomyces pombe
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C:Accession: T38351
R:Murphy, L.; Harris, D.; Barrell, B.G.; Rajandream, M.A.; Wood, V.
Submitted to the EMBL Data Library, August 1995
A:Reference number: 221787
A:Accession: T38351
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-263 <MUR>
A:Cross-references: UNIPROT:Q13970; EMBL:Z98601; PIDN:CA11267.1; GSPDB:GN00066; SPDB:SH
A:Experimental source: strain 972h-; cosmid C24C9
C:Genetics:
A:Gene: SPDB:SPAC24C9.10C
A:Map position: 1
A:Genome: nuclear
C:Superfamily: Escherichia coli ribosomal protein S2
C:Keywords: mitochondrial

Query Match 66.0%; Score 35; DB 2; Length 263;
Best Local Similarity 66.7%; Pred. No. 32;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 KGNOSFEED 9
|||:|:
DB 249 KANQAFEXD 257

RESULT 14

T20481
hypothetical protein F01G10.9 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T20481

R:Hembry, C.
Submitted to the EMBL Data Library, October 1996
A:Reference number: 219280
A:Accession: T20481

A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-374 <MIL>
A:Cross-references: UNIPROT:Q1767; EMBL:281055; PIDN:CAB02897.1; GSPDB:GN00022; CBSP:FC
A:Experimental source: clone F01G10
C:Genetics:
A:Gene: CBSP:F01G10.9
A:Map position: 4
A:Insertions: 43/2; 75/3; 153/2; 196/1

Query Match 66.0%; Score 35; DB 2; Length 374;
Best Local Similarity 77.8%; Pred. No. 47;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 KGNOSFEED 9
|||:|:
DB 153 KGNQDNED 161

RESULT 15

E70461
pmbA protein - Aquifex aeolicus
C:Species: Aquifex aeolicus
C:Date: 29-Jan-1999 #sequence_revision 29-Jan-1999 #text_change 09-Jul-2004
C:Accession: E70461
R:Deckert, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.; O
V.
Nature 392, 353-358, 1998
A:Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.
A:Reference number: A70300; MUID:98196666; PMID:9537320
A:Accession: E70461
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-441 <AQF>
A:Cross-references: UNIPROT:Q67719; GB:AE000761; NID:G2984149; PIDN:AACT07693.1; PID:G29
A:Experimental source: strain VF5
C:Genetics:
A:Gene: pmbA
C:Superfamily: Escherichia coli pmbA protein

Query Match 66.0%; Score 35; DB 1; Length 441;
Best Local Similarity 87.5%; Pred. No. 56;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KGNOSFEE 8
|||:|:
DB 345 KGNISFEE 352

Search completed: October 22, 2005, 08:04:38
Job time : 12.45 secs

GenCore version 5.1.6
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OM protein - protein search, using SW model

Run on: October 22, 2005, 06:06:36 ; Search time 55.85 Seconds

(without alignments)
91.688 Million cell updates/sec

Title: US-10-731-238-83
Perfect score: 53
Sequence: 1 KGNQSFEDRT 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_03.*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	53	100.0	1018	1	FNBA STAAU
2	48	90.6	152	2	Q9AEP9
3	48	90.6	940	2	Q53682
4	48	90.6	943	2	Q8NNU8
5	48	90.6	957	2	Q6G6H4
6	48	90.6	961	2	Q99RD3
7	48	90.6	961	2	Q7A3J8
8	48	90.6	965	2	Q6GDU5
9	48	90.6	1015	2	Q8NNU7
10	48	90.6	1015	2	Q6G6H3
11	48	90.6	1038	2	Q99RD2
12	48	90.6	1038	2	Q7A3J7
13	39	73.6	347	2	Q8MYE6
14	39	73.6	499	1	DLDH YEAST
15	38	71.7	486	2	Q8LDH8
16	38	71.7	486	2	Q8H0X2
17	38	71.7	789	2	Q6SR79
18	37	69.8	367	2	Q8S0V7
19	37	69.8	384	2	Q8LH13
20	37	69.8	429	2	Q9XSH1
21	37	69.8	429	2	Q25682
22	37	69.8	493	2	Q9GR04
23	37	69.8	702	1	CANB HUMAN
24	36	67.9	125	1	LMIP MOUSE
25	36	67.9	169	2	Q8LHX4
26	36	67.9	323	2	Q9CE06
27	36	67.9	377	2	Q67U18
28	36	67.9	461	1	EPSP STABP
29	36	67.9	489	1	Q6AZI2
30	36	67.9	500	1	SYE_LACDE
31	36	67.9	697	2	Q8TQ09

32	35	67.9	724	2	Q961W7	Q961W7 drosophila
33	35	67.9	724	2	Q9V846	Q9V846 drosophila
34	36	67.9	826	2	Q8T4G5	Q8T4G5 drosophila
35	36	67.9	831	2	Q7Q1M2	Q7Q1M2 anopheles g
36	36	67.9	946	2	Q8B0H5	Q8B0H5 mus musculus
37	36	67.9	975	2	Q6BC08	Q6BC08 homo sapien
38	36	67.9	1067	2	Q84QV5	Q84QV5 oryza sativ
39	36	67.9	1638	2	Q869R3	Q869R3 dictyostell
40	35	66.0	72	2	Q9CHL4	Q9CHL4 lactococcus
41	35	66.0	79	2	Q9A188	Q9A188 streptococ
42	35	66.0	125	1	LMIP HUMAN	LMIP HUMAN
43	35	66.0	157	1	Q82YP2	Q82YP2 enterococu
44	35	66.0	167	1	GPX1 YEAST	GPX1 YEAST
45	35	66.0	213	2	Q939P2	Q939P2 saccharomyc
						Q939P2 lactococcus

ALIGNMENTS

RESULT 1
FNBA STAAU STANDARD; PRT; 1018 AA.
ID FNBA STAAU
AC P14738;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Fibronectin-binding protein precursor (FNBP).
GN Name=fnba;
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1280;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NTCC 8325-4;
RX MEDLINE=89098998; PubMed=2521391;
RA Sinaas C., Raucel G., Joensen K., Lindgren P.-E.,
RA Anantharamaiah G.M., Hoeck M., Lindberg M.;
RT "Nucleotide sequence of the gene for a fibronectin-binding protein
RT from Staphylococcus aureus: use of this peptide sequence in the
RT synthesis of biologically active peptides."
RL Proc. Natl. Acad. Sci. U.S.A. 86:699-703(1989).
CC -I- FUNCTION: The ability of bacteria to bind fibronectin has been
CC proposed as a virulence factor enabling bacteria to colonize wound
CC tissues and blood clots. Binding of plasma fibronectin to the
CC bacterial surface might block adhesion receptors on S.aureus, thus
CC representing an important defense mechanism against tissue
CC invasion.
CC -I- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC an amide bond (Potential).
CC -----
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CC or send an email to license@ebi.ac.uk).
CC -----
CC EMBL: J04151; AAA26632.1; -;
DR InterPro: IPR004237; Fn_bind.
DR InterPro: IPR005877; Gpos_YSTRK.
DR InterPro: IPR001899; Gram_pos_anchor.
DR Pfam: PF002986; Fn_bind. 1.
DR Pfam: PF00746; Gram_pos_anchor. 1.
DR Pfam: PF04650; YSTRK_signal. 1.
DR TIGRfam: TIGR01167; LPXTG_anchor. 1.
DR TIGRfam: TIGR01168; YSTRK_signal. 1.
DR PROSITE: PS08477; GRAM_POS_ANCHORING. 1.
DR Cell adhesion; Cell wall; Peptidoglycan-anchor; Repeat; Signal;
DR Virulence.
KW SIGNAL.
FT CHAIN 37 985 Fibronectin-binding protein.
FT PROPEP 986 1018 Removed by sortase (Potential).
FT

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FT REPEAT 545 574 B-1.
FT REPEAT 575 604 B-2.
FT DOMAIN 745 878 4 X approximate tandem repeats,
  fibronectin-binding domain.
FT REPEAT 745 782 D-1.
FT REPEAT 783 820 D-2.
FT REPEAT 821 859 D-3.
FT REPEAT 860 878 D-4 (incomplete).
FT DOMAIN 879 948 5 X tandem repeats, Pro-rich (WR).
FT REPEAT 879 892 WR 1.
FT REPEAT 893 906 WR 2.
FT REPEAT 907 920 WR 3.
FT REPEAT 921 934 WR 4.
FT REPEAT 935 948 WR 5.
FT SITE 982 986 LPXG sorting signal (Potential).
FT MOD_RES 985 985 Pentaglycyl murein peptidoglycan amidated
  threonine (Potential).
SQ SEQUENCE 1018 AA, 111780 MW, 581758020E81F1F CRC64;

Query Match 100.0%; Score 53; DB 1; Length 1018;
Best Local Similarity 100.0%; Pred. No. 0.19;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KGNOSFEEDT 10
Db 786 KGNOSFEEDT 795

RESULT 2
Q9AEP9 PRELIMINARY; PRT; 152 AA.
ID Q9AEP9
AC Q9AEP9;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Fibronectin-binding protein (Fragment).
OS Name=fnb;
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1280;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CMRSA-1;
RX MEDLINE=21246681; PubMed=11349044;
RX DOI=10.1128/JAI.69.6.3791-3799.2001;
RA Rice K., Huesca M., Vaz D., McGavin M.J.;
RT "Variance in fibronectin binding and fnb locus polymorphisms in
  Staphylococcus aureus: identification of antigenic variation in a
  fibronectin binding protein adhesin of the epidemic CMRSA-1 strain of
  RT methicillin-resistant S. aureus."
RT Infect. Immun. 69:3791-3799(2001).
DR EMBL; AY029184; AAK31588.1; -.
FT NON_TER 1 1
FT SEQUENCE 152 152
SQ SEQUENCE 152 AA, 17193 MW, CFA3913C2B11C025 CRC64;

Query Match 90.6%; Score 48; DB 2; Length 152;
Best Local Similarity 100.0%; Pred. No. 0.23;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GGNOSFEEDT 10
Db 4 GGNOSFEEDT 12

RESULT 3
Q53682 PRELIMINARY; PRT; 940 AA.
ID Q53682
AC Q53682;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Fibronectin binding protein B.

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GN Name=fnbB;
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1280;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=8325-4;
RX MEDLINE=92111475; PubMed=1837266;
RX Jonsson K., Signas C., Muller H.P., Lindberg M.;
RT "Two different genes encode fibronectin binding proteins in
  Staphylococcus aureus. The complete nucleotide sequence and
  RT characterization of the second gene."
RT Eur. J. Biochem. 202:1041-1048(1991).
CC CC
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
  an amide bond (By similarity).
DR EMBL; X62992; CAA44726.1; -.
DR PIR; S19702; S19702.
DR HSSP; Q53653; 1N67.
DR GO; GO:0009986; C:cell surface; IEA.
DR GO; GO:0005618; C:cell wall; IEA.
DR GO; GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0007155; P:cell adhesion; IEA.
DR InterPro; IPR008966; Adhes_bact.
DR InterPro; IPR004237; Fn_bind.
DR InterPro; IPR005877; Gpos_YsIRK.
DR InterPro; IPR001899; Gram_pos_anchor.
DR Pfam; PF02986; Fn_bind_2.
DR Pfam; PF00746; Gram_pos_anchor_1.
DR Pfam; PF04650; YsIRK_signal_1.
DR TIGRfam; TIGR01167; LPXG_anchor_1.
DR TIGRfam; TIGR01168; YsIRK_signal_1.
DR PROSITE; PS50847; GRAM_POS_ANCHORING; 1.
DR Cell wall; Peptidoglycan-anchor.
SQ SEQUENCE 940 AA, 103555 MW, E35FBBCA907AE345 CRC64;

Query Match 90.6%; Score 48; DB 2; Length 940;
Best Local Similarity 100.0%; Pred. No. 1.8;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GGNOSFEEDT 10
Db 685 GGNOSFEEDT 693

RESULT 4
Q8NU8 PRELIMINARY; PRT; 943 AA.
ID Q8NU8
AC Q8NU8;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE FnbB protein.
OS Name=fnbB; Ordered locus names=MM2420;
OS Staphylococcus aureus (strain MM2).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=196620;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MM2;
RX MEDLINE=22040717; PubMed=12044378; DOI=10.1016/S0140-6736(02)08713-5;
RX Baba T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Oguchi A.,
RX Nagai Y., Iwama N., Amano K., Naimi T., Kuroda H., Cui L.,
RX Yamamoto K., Hiramatsu K.;
RT "Genome and virulence determinants of high virulence community-
  RT acquired MRSA."
RT Lancet 359:1819-1827(2002).
CC CC
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
  an amide bond (By similarity).
DR EMBL; AP004830; BAB96285.1; -.
DR HSSP; Q53653; 1N67.
DR GO; GO:0009986; C:cell surface; IEA.
DR GO; GO:0005618; C:cell wall; IEA.

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DR GO; GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0007155; P:cell adhesion; IEA.
DR InterPro; IPR008966; Adhes_bact.
DR InterPro; IPR004237; Fn_bind.
DR InterPro; IPR005877; Gpos_YsIRK.
DR InterPro; IPR001899; Gram_pos_anchor.
DR Pfam; PF02986; Fn_bind; 1.
DR Pfam; PF00746; Gram_pos_anchor; 1.
DR Pfam; PF04650; YsIRK_signal; 1.
DR TIGRFAMs; TIGR01167; LPXTG_anchor; 1.
DR TIGRFAMs; TIGR01168; YsIRK_signal; 1.
DR PROSITE; PS50847; GRAM_POS_ANCHORING; 1.
DR Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ SEQUENCE 943 AA; 104537 MW; DABA5F31947E1B6A CRC64;

Query Match          90.6%; Score 48; DB 2; Length 943;
Best Local Similarity 100.0%; Pred. No. 1.8;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY 2 GNOSFEEDT 10
DB 692 GNOSFEEDT 700

RESULT 5
ID Q6G6H4 PRELIMINARY; PRT; 957 AA.
AC Q6G6H4
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Fibronectin-binding protein.
GN Name=fnbB; OrderedLocustNames=SA52387;
OS Staphylococcus aureus (strain MSSA476).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=282459;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=15213324; DOI=10.1073/pnas.0402521101;
RA Holden M.T.G., Fell E.J., Lindsay J.A., Peacock S.J., Day N.P.J.,
RA Enright M.C., Foster T.J., Moore C.E., Hurst L., Atkin R., Barron A.,
RA Baeson N., Bentley S.D., Chillingworth C., Chillingworth T.,
RA Churcher C., Clark L., Corton C., Cronin H., Doggett J., Dowd L.,
RA Fellwell T., Hance Z., Harris B., Hauser H., Hoggard S., Jagsels K.,
RA James K.D., Lennard N., Line A., Mayes R., Moule S., Mungall K.,
RA Ormond D., Quail M.A., Rabinowitch E., Rutherford K.M., Sanders M.,
RA Sharp S., Simmonds M., Stevens K., Whitehead S., Barrett B.G.,
RA Spratt B.G., Parkhill J.;
RT "Complete genomes of two clinical Staphylococcus aureus strains:
RT evidence for the rapid evolution of virulence and drug resistance.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:9786-9791(2004).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC an amide bond (By similarity).
CC EMBL; BX571857; CAG44201.1; -.
DR GO; GO:0009986; C:cell surface; IEA.
DR GO; GO:0005618; C:cell wall; IEA.
DR GO; GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0007155; P:cell adhesion; IEA.
DR InterPro; IPR008966; Adhes_bact.
DR InterPro; IPR004237; Fn_bind.
DR InterPro; IPR005877; Gpos_YsIRK.
DR InterPro; IPR001899; Gram_pos_anchor.
DR Pfam; PF02986; Fn_bind; 1.
DR Pfam; PF00746; Gram_pos_anchor; 1.
DR Pfam; PF04650; YsIRK_signal; 1.
DR TIGRFAMs; TIGR01167; LPXTG_anchor; 1.
DR TIGRFAMs; TIGR01168; YsIRK_signal; 1.
DR PROSITE; PS50847; GRAM_POS_ANCHORING; 1.
DR Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ SEQUENCE 957 AA; 105380 MW; 28F8BA7FFD3EAF CRC64;

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Query Match          90.6%; Score 48; DB 2; Length 957;
Best Local Similarity 100.0%; Pred. No. 1.8;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY 2 GNOSFEEDT 10
DB 692 GNOSFEEDT 700

RESULT 6
ID Q99RD3 PRELIMINARY; PRT; 961 AA.
AC Q99RD3
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Fibronectin-binding protein homolog.
GN Name=fnbB; OrderedLocustNames=SAV2502;
OS Staphylococcus aureus (strain Mu50 / ATCC 700699).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=158878;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=Mu50 / ATCC 700699;
RC MEDLINE=21311952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2;
RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Itoh T.,
RA Kanamori M., Matsunaru H., Maruyama A., Murakami H., Hoshiyama A.,
RA Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kato C.,
RA Sekimizu K., Hiraoka H., Kuhara S., Goto S., Yabuzaki J.,
RA Kanehisa M., Yanaishita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
RA Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
RT "Whole genome sequencing of methicillin-resistant Staphylococcus
RT aureus.";
RL Lancet 357:1225-1240(2001).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC an amide bond (By similarity).
CC EMBL; AF003365; BAB58664.1; -.
DR PIR; G90053; G90053.
DR HSSP; Q53653; IN67.
DR GO; GO:0009986; C:cell surface; IEA.
DR GO; GO:0005618; C:cell wall; IEA.
DR GO; GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0007155; P:cell adhesion; IEA.
DR InterPro; IPR008966; Adhes_bact.
DR InterPro; IPR004237; Fn_bind.
DR InterPro; IPR005877; Gpos_YsIRK.
DR InterPro; IPR001899; Gram_pos_anchor.
DR Pfam; PF02986; Fn_bind; 1.
DR Pfam; PF00746; Gram_pos_anchor; 1.
DR Pfam; PF04650; YsIRK_signal; 1.
DR TIGRFAMs; TIGR01167; LPXTG_anchor; 1.
DR TIGRFAMs; TIGR01168; YsIRK_signal; 1.
DR PROSITE; PS50847; GRAM_POS_ANCHORING; 1.
DR Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ SEQUENCE 961 AA; 106010 MW; 364940F84E44101 CRC64;

Query Match          90.6%; Score 48; DB 2; Length 961;
Best Local Similarity 100.0%; Pred. No. 1.8;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY 2 GNOSFEEDT 10
DB 696 GNOSFEEDT 704

RESULT 7
ID Q7A3J8 PRELIMINARY; PRT; 961 AA.
AC Q7A3J8
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)

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DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE FdbB protein.
 GN Name=fdbB; OrderedLocNames=SA2290;
 OS Staphylococcus aureus (strain N315).
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 ON NCBI_TaxID=158879;
 RX MEDLINE=1511952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2;
 RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
 Cui L., Oguchi A., Aoki K.-I., Nagai Y., Iian J.-Q., Ito T.,
 Kanamori M., Matsunaru H., Maruyama A., Murakami H., Hosoyama A.,
 Mizutani-U. Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
 Sekimizu K., Hiraoka H., Kuhara S., Goto S., Yabuzaki J.,
 Kanehisa M., Yamaoka A., Oshima K., Furuya K., Yoshino C., Shiba T.,
 Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.,
 "Whole genome sequencing of methicillin-resistant Staphylococcus
 aureus."
 RT Lancel 357:1225-1240(2001).
 CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
 an amide bond (By similarity).
 DR EMBL: AP003137; BAB43593.1; -.
 DR GO: GO:0009986; C:cell surface; IEA.
 DR GO: GO:0005618; C:cell wall; IEA.
 DR GO: GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
 DR GO: GO:0016020; C:membrane; IEA.
 DR GO: GO:0007155; P:cell adhesion; IEA.
 DR InterPro: IPR008966; Adhes_bact.
 DR InterPro: IPR004237; Fn_bind.
 DR InterPro: IPR005877; Gpos_YsIRK.
 DR InterPro: IPR001899; Gram_pos_anchor.
 DR Pfam: PF02986; Fn_bind; 1.
 DR Pfam: PF00746; Gram_pos_anchor; 1.
 DR TIGRFAMs: TIGR01167; LPXTG_anchor; 1.
 DR TIGRFAMs: TIGR01168; YsIRK_signal; 1.
 DR PROSITE: PS50847; GRAM_POS_ANCHORING; 1.
 KM Cell wall; Complete proteome; Peptidoglycan-anchor.
 SQ SEQUENCE 961 AA; 106010 MW; 364940F84EBA4101 CRC64;

 Query Match 90.6%; Score 48; DB 2; Length 961;
 Best Local Similarity 100.0%; Pred. No. 1.8;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 QY 2 GNOSFEEDT 10
 Db 696 GNOSFEEDT 704

 RESULT 8
 ID 06GDUS PRELIMINARY; PRT; 965 AA.
 AC 06GDUS;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Fibronecin-binding protein.
 GN Name=fdbA; OrderedLocNames=SA2580;
 OS Staphylococcus aureus (strain MRSA252).
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 ON NCBI_TaxID=282458;
 RX MEDLINE=1521324; DOI=10.1073/pnas.040251101;
 RA Holden M.T.G., Feil E.J., Lindsay J.A., Peacock S.J., Day N.P.J.,
 Ehrlich M.C., Foster T.J., Moore C.E., Hurst L., Atkin R., Barron A.,
 Bason N., Bentley S.D., Chillingworth C., Chillingworth T.,
 Churcher C., Clark L., Corton C., Cronin A., Doggett J., Dowd L.,
 Felwell T., Hance Z., Harris B., Hauser H., Holtroyd S., Jagers K.,
 James K.D., Lennard N., Line A., Mayes R., Moule S., Mungall K.,
 Omond D., Quail M.A., Rabinowicz E., Rutherford K.M., Sanders M.,
 Sharp S., Simmonds M., Stevens K., Whitehead S., Barrell B.G.,
 Spratt B.G., Parkhill J.;

RT "Complete genomes of two clinical Staphylococcus aureus strains:
 evidence for the rapid evolution of virulence and drug resistance."
 RT Proc. Natl. Acad. Sci. U.S.A. 101:9786-9791(2004).
 CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
 an amide bond (By similarity).
 DR EMBL: BX571856; CAG41560.1; -.
 DR GO: GO:0009986; C:cell surface; IEA.
 DR GO: GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
 DR GO: GO:0016020; C:membrane; IEA.
 DR GO: GO:0007155; P:cell adhesion; IEA.
 DR InterPro: IPR008966; Adhes_bact.
 DR InterPro: IPR004237; Fn_bind.
 DR InterPro: IPR005877; Gpos_YsIRK.
 DR InterPro: IPR001899; Gram_pos_anchor.
 DR Pfam: PF02986; Fn_bind; 1.
 DR Pfam: PF00746; Gram_pos_anchor; 1.
 DR TIGRFAMs: TIGR01167; LPXTG_anchor; 1.
 DR TIGRFAMs: TIGR01168; YsIRK_signal; 1.
 DR PROSITE: PS50847; GRAM_POS_ANCHORING; 1.
 KM Cell wall; Complete proteome; Peptidoglycan-anchor.
 SQ SEQUENCE 965 AA; 105691 MW; 2982E132164D0551 CRC64;

 Query Match 90.6%; Score 48; DB 2; Length 965;
 Best Local Similarity 100.0%; Pred. No. 1.8;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 QY 2 GNOSFEEDT 10
 Db 752 GNOSFEEDT 760

 RESULT 9
 ID 08NUU7 PRELIMINARY; PRT; 1015 AA.
 AC 08NUU7;
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Fdb protein.
 GN Name=fdb; OrderedLocNames=MM2421;
 OS Staphylococcus aureus (strain MM2).
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 ON NCBI_TaxID=196620;
 RX MEDLINE=22040717; PubMed=12044378; DOI=10.1016/S0140-6736(02)08713-5;
 RA Baba T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Oguchi A.,
 Nagai Y., Iwano N., Asano K., Naito T., Kuroda H., Cui L.,
 Yamamoto K., Hiramatsu K.,
 "Genome and virulence determinants of high virulence community-
 acquired MRSA."
 RT Lancel 359:1819-1827(2002).
 CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
 an amide bond (By similarity).
 DR EMBL: AP004830; BAB96286.1; -.
 DR GO: GO:0009986; C:cell surface; IEA.
 DR GO: GO:0005618; C:cell wall; IEA.
 DR GO: GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
 DR GO: GO:0016020; C:membrane; IEA.
 DR GO: GO:0007155; P:cell adhesion; IEA.
 DR InterPro: IPR008966; Adhes_bact.
 DR InterPro: IPR004237; Gpos_YsIRK.
 DR InterPro: IPR001899; Gram_pos_anchor.
 DR Pfam: PF02986; Fn_bind; 1.
 DR Pfam: PF00746; Gram_pos_anchor; 1.
 DR TIGRFAMs: TIGR01167; LPXTG_anchor; 1.
 DR TIGRFAMs: TIGR01168; YsIRK_signal; 1.
 DR PROSITE: PS50847; GRAM_POS_ANCHORING; 1.
 KM Cell wall; Complete proteome; Peptidoglycan-anchor.

SQ SEQUENCE 1015 AA; 111145 MW; DOF9291BB64D44D2 CRC64;
 Query Match 90.6%; Score 48; DB 2; Length 1015;
 Best Local Similarity 100.0%; Pred. No. 1.9;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 GNOSFEEDT 10
 |||||
 DB 750 GNOSFEEDT 758
 |||||
 RESULT 10
 Q6G6H3 PRELIMINARY; PRT; 1015 AA.
 ID 06G6H3
 AC 06G6H3;
 DT 05-JUL-2004 (TREMBlrel. 27, Created)
 DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
 DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
 DE Fibronectin-binding protein.
 GN OrderedlocusNames=SA5238;
 OS Staphylococcus aureus (strain MSSA476).
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 NCBI_TaxID=282459;
 RX SEQUENCE FROM N.A.
 RP PubMed=15213324; DOI=10.1073/pnae.0402521101;
 RA Holden M.T.G., Fell E.J., Lindsey J.A., Peacock S.J., Day N.P.J.,
 RA Enright M.C., Foster T.J., Moore C.E., Hurst L., Atkin R., Barron A.,
 RA Baon N., Bentley S.D., Chillingworth C., Chillingworth T.,
 RA Churcher C., Clark L., Corton C., Cronin A., Doggett J., Doud L.,
 RA Fellwell T., Hance Z., Harris B., Hauser H., Holtroyd S., Jagels K.,
 RA James K.D., Lennard N., Line A., Mayes R., Moule S., Mungall K.,
 RA Omond D., Quail M.A., Rabinowitch B., Rutherford K.M., Sanders M.,
 RA Sharp S., Simmonds M., Stevens K., Whitehead S., Barrell B.G.,
 RA Spratt B.G., Parkhill J.;
 RT "Complete genomes of two clinical Staphylococcus aureus strains:
 RL evidence for the rapid evolution of virulence and drug resistance.";
 RT Proc. Natl. Acad. Sci. U.S.A. 101:9786-9791(2004).
 CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
 an amide bond (By similarity).
 CC EMBL; BX571857; CAG44202.1; -.
 DR GO; GO:0009986; C:cell surface; IEA.
 DR GO; GO:0005618; C:cell wall; IEA.
 DR GO; GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0007155; P:cell adhesion; IEA.
 DR InterPro; IPR008966; Adhes_Bact.
 DR InterPro; IPR004237; Fn_bind.
 DR InterPro; IPR005877; Gpos_YsIRK.
 DR InterPro; IPR01899; Gram_pos_anchor.
 DR Pfam; PF02986; Fn_bind; 1.
 DR Pfam; PF00746; Gram_pos_anchor; 1.
 DR Pfam; PF04650; YsIRK_signal; 1.
 DR TIGRFAMs; TIGR01167; LpxTG_anchor; 1.
 DR TIGRFAMs; TIGR01168; YsIRK_signal; 1.
 DR PROSITE; PS50847; GRAM_POS_ANCHORING; 1.
 KW Cell wall, Complete proteome; Peptidoglycan-anchor.
 SQ SEQUENCE 1015 AA; 111145 MW; DOF9281BB64D44D2 CRC64;
 Query Match 90.6%; Score 48; DB 2; Length 1015;
 Best Local Similarity 100.0%; Pred. No. 1.9;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 GNOSFEEDT 10
 |||||
 DB 750 GNOSFEEDT 758
 |||||
 RESULT 11
 Q99RD2 PRELIMINARY; PRT; 1038 AA.
 ID 099RD2;
 AC 099RD2;
 DT 01-JUN-2001 (TREMBlrel. 17, Created)

DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
 DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
 DE Fibronectin-binding protein homolog.
 GN Name=fnb; OrderedlocusNames=SAV2503;
 OS Staphylococcus aureus (strain Mu50 / ATCC 700699).
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 NCBI_TaxID=158878;
 RX SEQUENCE FROM N.A.
 RP STRAIN=Mu50 / ATCC 700699;
 RX MEDLINE=21311952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2;
 RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
 RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Iian J.-O., Ito T.,
 RA Kanamori M., Matsunaru H., Maruyama A., Murakami H., Hoshiyama A.,
 RA Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
 RA Sekimizu K., Hiraoka H., Kuhara S., Goto S., Yabuzaki J.,
 RA Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
 RA Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
 RT "Whole genome sequencing of methicillin-resistant Staphylococcus
 RT aureus.";
 RL Lancet 357:1225-1240(2001).
 CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
 an amide bond (By similarity).
 CC EMBL; AP003365; BAB58665.1; -.
 DR PIR; H90053; H90053.
 DR GO; GO:0009986; C:cell surface; IEA.
 DR GO; GO:0005618; C:cell wall; IEA.
 DR GO; GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0007155; P:cell adhesion; IEA.
 DR InterPro; IPR008966; Adhes_bact.
 DR InterPro; IPR004237; Fn_bind.
 DR InterPro; IPR005877; Gpos_YsIRK.
 DR InterPro; IPR01899; Gram_pos_anchor.
 DR Pfam; PF02986; Fn_bind; 1.
 DR Pfam; PF00746; Gram_pos_anchor; 1.
 DR Pfam; PF04650; YsIRK_signal; 1.
 DR TIGRFAMs; TIGR01167; LpxTG_anchor; 1.
 DR TIGRFAMs; TIGR01168; YsIRK_signal; 1.
 DR PROSITE; PS50847; GRAM_POS_ANCHORING; 1.
 KW Cell wall, Complete proteome; Peptidoglycan-anchor.
 SQ SEQUENCE 1038 AA; 113618 MW; 666BF6BF2FBFB12 CRC64;
 Query Match 90.6%; Score 48; DB 2; Length 1038;
 Best Local Similarity 100.0%; Pred. No. 2;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 GNOSFEEDT 10
 |||||
 DB 745 GNOSFEEDT 753
 |||||
 RESULT 12
 Q7A3J7 PRELIMINARY; PRT; 1038 AA.
 ID 07A3J7;
 AC 07A3J7;
 DT 05-JUL-2004 (TREMBlrel. 27, Created)
 DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
 DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
 DE Fnb protein.
 GN Name=fnb; OrderedlocusNames=SA2291;
 OS Staphylococcus aureus (strain N315).
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 NCBI_TaxID=158879;
 RX SEQUENCE FROM N.A.
 RP MEDLINE=21311952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2;
 RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
 RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Iian J.-O., Ito T.,
 RA Kanamori M., Matsunaru H., Maruyama A., Murakami H., Hoshiyama A.,
 RA Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
 RA Sekimizu K., Hiraoka H., Kuhara S., Goto S., Yabuzaki J.,
 RA Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,

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Db                254 GDSCFEEDT 262

RESULT 14
ID      DLDH_YEAST      STANDARD;      PRT;      499 AA.
AC      P09624;
DT      01-MAR-1989 (Rel. 10, Created)
DT      01-MAR-1989 (Rel. 10, Last sequence update)
DT      25-OCT-2004 (Rel. 45, Last annotation update)
DE      Dihydroliipooyl dehydrogenase, mitochondrial precursor (EC 1.8.1.4)
DE      (Dihydroliipoamide dehydrogenase).
GN      Name=LPDI; Synonyms=DHLPI; OrderedLocNames=YFL018C;
OS      Saccharomyces cerevisiae (Baker's yeast).
OC      Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC      Saccharomycetales; Saccharomycetaceae; Saccharomyces.
CX      NCBI_TaxID=4932;
RN      [1]
RP      SEQUENCE FROM N.A.
RX      MEDLINE=88158087; Pubmed=3279419;
RA      Browning K.S., Uhlinger D.J., Reed L.J.;
RT      "Nucleotide sequence for yeast dihydroliipoamide dehydrogenase.";
RT      Proc. Natl. Acad. Sci. U.S.A. 85:1831-1834(1988).
RN      [2]
RP      SEQUENCE FROM N.A.
RX      MEDLINE=89067880; Pubmed=3058861;
RA      Roes J., Reid G.A., Dawes I.W.;
RT      "The nucleotide sequence of the LPDI gene encoding liipoamide
RT      dehydrogenase in Saccharomyces cerevisiae: comparison between
RT      eukaryotic and prokaryotic sequences for related enzymes and
RT      identification of potential upstream control sites.";
RT      J. Gen. Microbiol. 134:1131-1139(1988).
RN      [3]
RP      SEQUENCE FROM N.A.
RX      STRAIN=S288c / AB972;
RX      MEDLINE=95400292; Pubmed=7670463;
RA      Murakami Y., Naitou M., Hagiwara H., Shibata T., Ozawa M.,
RA      Sasaanna S.-I., Sasaanna M., Tsuchiya Y., Soeda E., Yokoyama K.,
RA      Yamazaki M.-H., Tashiro H., Eki T.;
RT      "Analysis of the nucleotide sequence of chromosome VI from
RT      Saccharomyces cerevisiae.";
RT      Nat. Genet. 10:261-268(1995).
RN      [4]
RP      SEQUENCE FROM N.A.
RX      STRAIN=S288c / AB972;
RA      Barrell B.G., Churcher C., Rajandream M.A.;
RA      Submitted (SEP-1994) to the EMBL/GenBank/DBJ databases.
RN      [5]
RP      X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS).
RX      Pubmed=9538259;
RA      Toyoda T., Suzuki K., Sekiguchi T., Reed L.J., Takenaka A.;
RT      "Crystal structure of eucaryotic E3, liipoamide dehydrogenase from
RT      yeast.";
RT      J. Biochem. 123:668-674(1998).
RN      [6]
RP      FUNCTION: Liipoamide dehydrogenase is a component of the alpha-
RP      ketoacid dehydrogenase complexes.
RN      [7]
RP      CATALYTIC ACTIVITY: Protein N(6)-(dihydroliipoyl)lysine + NAD(+) =
RP      protein N(6)-(liipoyl)lysine + NADH.
RN      [8]
RP      COFACTOR: Binds 1 FAD per subunit (By similarity).
RN      [9]
RP      SUBUNIT: Homodimer.
RN      [10]
RP      SUBCELLULAR LOCATION: Mitochondrial matrix.
RN      [11]
RP      MISCELLANEOUS: The active site is a redox-active disulfide bond.
RN      [12]
RP      SIMILARITY: Belongs to the class-I pyridine nucleotide-disulfide
RP      oxidoreductase family.
CC      This SWISS-PROT entry is copyright. It is produced through a collaboration
CC      between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC      the European Bioinformatics Institute. There are no restrictions on its
CC      use by non-profit institutions as long as its content is in no way
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CC      or send an email to license@ebi.ac.uk).
CC      -----

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DR EMBL; J03645; AAA34565.1; -.
 DR EMBL; M20880; AAB63974.1; -.
 DR EMBL; D50617; BAA09220.1; -.
 DR EMBL; Z46255; CAAB6354.1; -.
 DR PIR; A30151; A30151.
 DR PDB; 1JEH; X-ray; A/B=22-499.
 DR InAcC; P09624; -.
 DR Germonline; 140137; -.
 DR SCD; S000001876; LPD1.
 DR GO; GO:0042645; C:mitochondrial nucleoid; IDA.
 DR GO; GO:0004148; F:dihydrolipoyl dehydrogenase activity; IDA.
 DR GO; GO:0006546; P:glycine catabolism; IMP.
 DR GO; GO:0006550; P:isoleucine catabolism; IMP.
 DR GO; GO:0006564; P:L-serine biosynthesis; IMP.
 DR GO; GO:0006552; P:leucine catabolism; IMP.
 DR GO; GO:0006574; P:valine catabolism; IMP.
 DR InterPro; IPR001327; FAD pyr redox.
 DR InterPro; IPR000815; Hg_reductase.
 DR InterPro; IPR006258; Lipamide_dh.
 DR InterPro; IPR001100; Pyr_redox.
 DR InterPro; IPR004099; Pyr_redox_dim.
 DR Pfam; PF000070; Pyr_redox; 1.
 DR Pfam; PF02852; Pyr_redox_dim; 1.
 DR PRINTS; PR00368; FADPNR.
 DR PRINTS; PR00945; HGRD7ASE.
 DR PRINTS; PR00411; NDRD7ASE1.
 DR ProDom; PD000139; FAD_pyr_redox; 1.
 DR TIGRfam; TIGR01350; lipamide DH; 1.
 DR PROSITE; PS00076; PYRIDINE REDOX_1; 1.
 DR 3D-structure; FAD; Flavoprotein; Mitochondrion; NAD; Oxidoreductase;
 Redox-active center; Transit peptide.
 FT TRANSIT 1 21 Mitochondrion.
 FT CHAIN 22 499 Dihydrolipoyl dehydrogenase.
 FT NP_BIND 65 65 FAD (ADP part) (By similarity).
 FT DISULFID 66 70 Redox-active.
 FT ACT_SITE 478 478 Proton acceptor.
 FT STRAND 23 23
 FT STRAND 26 32
 FT STRAND 36 47
 FT HELIX 48 49
 FT TURN 52 56
 FT STRAND 63 68
 FT HELIX 70 88
 FT HELIX 89 94
 FT TURN 95 103
 FT STRAND 105 129
 FT HELIX 130 131
 FT TURN 133 136
 FT STRAND 138 143
 FT STRAND 144 145
 FT TURN 146 150
 FT STRAND 156 157
 FT TURN 158 158
 FT STRAND 163 172
 FT STRAND 176 178
 FT STRAND 182 183
 FT TURN 188 190
 FT TURN 194 198
 FT HELIX 194 198
 FT STRAND 206 210
 FT HELIX 214 226
 FT TURN 227 227
 FT STRAND 229 234
 FT STRAND 241 242
 FT TURN 245 257
 FT HELIX 258 259
 FT TURN 260 264
 FT STRAND 265 265
 FT TURN 266 274
 FT STRAND 275 278
 FT TURN 279 286
 FT STRAND 292 297
 FT STRAND 299 302
 FT STRAND 306 308

FT TURN 311 313
 FT HELIX 315 318
 FT TURN 319 319
 FT STRAND 322 322
 FT TURN 324 325
 FT STRAND 328 328
 FT TURN 332 333
 FT STRAND 335 335
 FT TURN 339 340
 FT STRAND 341 343
 FT HELIX 345 347
 FT HELIX 354 370
 FT TURN 377 378
 FT STRAND 382 384
 FT STRAND 389 394
 FT TURN 397 402
 FT HELIX 403 404
 FT TURN 407 413
 FT STRAND 414 415
 FT TURN 418 422
 FT HELIX 423 424
 FT TURN 429 435
 FT STRAND 436 438
 FT TURN 440 448
 FT STRAND 449 450
 FT TURN 451 464
 FT HELIX 465 465
 FT TURN 467 467
 FT STRAND 468 472
 FT HELIX 473 473
 FT TURN 481 482
 FT HELIX 483 493
 SQ SEQUENCE 499 AA; 54010 MW; 986A370F2E079DBC CRC64;
 Query Match 73.6%; Score 39; DB 1; Length 499;
 Best Local Similarity 70.0%; Pred. No. 53;
 Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 Oy 1 KGNOSFEDET 10
 Db 136 KGNOSFEDET 145
 RESULT 15
 OBLDH8 PRELIMINARY; PRT; 486 AA.
 AC OBLDH8;
 DT 01-OCT-2002 (TREMblrel. 22, Created)
 DT 01-OCT-2002 (TREMblrel. 22, last sequence update)
 DT 01-MAR-2004 (TREMblrel. 26, last annotation update)
 DE Hypothetical protein.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
 OC NCBI_TaxID=3702;
 OX [1]
 RP SEQUENCE FROM N.A.
 RP MEDLINE=22088475; PubMed=12093376;
 RA Haas B.J., Volfovsky N., Town C.D., Troupkan M., Alexandrov N.,
 RA Feldmann K.A., Flavell R.B., White O., Salzberg S.L.;
 RT "Full-length messenger RNA sequences greatly improve genome
 RT annotation.";
 RL Genome Biol. 3:RESEARCH0029-RESEARCH0029 (2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RP Broyer V., Troupkan M., Alexandrov N., Lu Y.-P., Flavell R.,
 RA Feldmann K.,
 RL Submitted (Mar-2002) to the EMBL/GenBank/DBJ databases.
 CC -I SIMILARITY: Contains 1 RING-type zinc finger.
 DR EMBL; AY085998; AAM63208.1; -.
 DR HSSP; P31948; IELW.
 DR GO; GO:0000151; C:ubiquitin ligase complex; IEA.

DR GO: GO:0004176; F:ATP-dependent peptidase activity; IEA.
DR GO: GO:0004842; F:ubiquitin-protein ligase activity; IEA.
DR GO: GO:0008270; F:zinc ion binding; IEA.
DR GO: GO:0006510; P:ATP-dependent proteolysis; IEA.
DR GO: GO:0016567; P:protein ubiquitination; IEA.
DR InterPro: IPR003111; Pept_S16_N.
DR InterPro: IPR008941; TPR-like.
DR InterPro: IPR001841; Znf_ring.
DR Pfam: PF02190; LON; 1.
DR Pfam: PF00097; zf-C3HC4; 1.
DR SMART: SM00184; RING; 1.
DR PROSITE: PS00518; ZF_RING_1; 1.
DR PROSITE: PS50089; ZF_RING_2; 1.
KM Hypothetical protein; Metal-binding; Zinc; Zinc-finger.
SQ SEQUENCE 486 AA; 55434 MW; 996389FEB377AC6 CRC64;

Query Match 71.7%; Score 38; DB 2; Length 486;
Best Local Similarity 87.5%; Pred. No. 82;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KGNOSFEE 8
Db 45 KGNOSFKE 52

Search completed: October 22, 2005, 08:00:56
Job time : 56.85 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using SW model

Run on: October 25, 2005, 20:21:18 ; Search time 63.2 Seconds
(without alignments)
61.196 Million cell updates/sec

Title: US-10-731-238-84
Perfect score: 52
Sequence: 1 NQSFEBPTK 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:*

- 1: geneseqp1980s:*
- 2: geneseqp1990s:*
- 3: geneseqp2000s:*
- 4: geneseqp2001s:*
- 5: geneseqp2002s:*
- 6: geneseqp2003as:*
- 7: geneseqp2003bs:*
- 8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	52	100.0	10	2	AAW65740 Fibronec
2	52	100.0	30	4	AAW65740 Fibronec
3	52	100.0	30	7	AAW65740 Fibronec
4	52	100.0	31	7	AAW65740 Fibronec
5	52	100.0	36	2	AAW65714 Fibronec
6	52	100.0	36	2	AAW65714 Fibronec
7	52	100.0	38	1	AAW65715 Fibronec
8	52	100.0	38	1	AAW65715 Fibronec
9	52	100.0	38	2	AAW65715 Fibronec
10	52	100.0	38	2	AAW65715 Fibronec
11	52	100.0	38	2	AAW65715 Fibronec
12	52	100.0	38	2	AAW65715 Fibronec
13	52	100.0	134	2	AAW65715 Fibronec
14	52	100.0	139	2	AAW65715 Fibronec
15	52	100.0	559	2	AAW65715 Fibronec
16	52	100.0	767	4	AAW65715 Fibronec
17	52	100.0	767	4	AAW65715 Fibronec
18	52	100.0	940	6	AAW65715 Fibronec
19	52	100.0	940	6	AAW65715 Fibronec
20	52	100.0	948	6	AAW65715 Fibronec
21	52	100.0	948	6	AAW65715 Fibronec
22	52	100.0	948	6	AAW65715 Fibronec
23	52	100.0	978	4	AAW65715 Fibronec
24	52	100.0	1001	4	AAW65715 Fibronec
25	52	100.0	1018	1	AAW65715 Fibronec

26	52	100.0	1018	4	AAU37245 Staphyloc
27	52	100.0	1018	4	AAU37245 Staphyloc
28	52	100.0	1018	6	ABU18922 Pathogen
29	52	100.0	1018	6	ABU18922 Pathogen
30	52	100.0	1027	2	AAW65721 Fibronec
31	48	92.3	10	2	AAW65721 Fibronec
32	48	92.3	38	1	AAW65721 Fibronec
33	48	92.3	38	1	AAW65721 Fibronec
34	48	92.3	38	2	AAW65721 Fibronec
35	48	92.3	38	2	AAW65721 Fibronec
36	48	92.3	38	2	AAW65721 Fibronec
37	48	92.3	38	2	AAW65721 Fibronec
38	48	92.3	39	2	AAW65713 Fibronec
39	48	92.3	39	2	AAW65713 Fibronec
40	48	92.3	130	2	AAW65713 Fibronec
41	48	92.3	130	2	AAW65713 Fibronec
42	48	92.3	130	2	AAW65713 Fibronec
43	48	92.3	130	2	AAW65713 Fibronec
44	48	92.3	134	2	AAW65713 Fibronec
45	48	92.3	174	2	AAW65713 Fibronec

ALIGNMENTS

RESULT 1
ID AAW65740 standard; peptide; 10 AA.

XX AAW65740;

XX 16-OCT-1998 (first entry)

XX Fibronecin binding protein-derived peptide #84.

XX microbial surface components recognising adhesive matrix molecule;

XX MGRAM; fibronecin; fibronecin-binding protein; antibody; epitope;

XX antibiotic; bacterial infection; antibiotic-resistant strain.

XX Synthetic.

XX Staphylococcus aureus.

XX WO9831389-A2.

XX 23-JUL-1998.

XX 21-JAN-1998; 98WO-US001222.

XX 21-JAN-1997; 97US-0036139P.

XX (TEXA) UNIV TEXAS A & M SYSTEM.

XX Hooeek M, Patil JM, House-Pompeo KL, Speziale P, Joh D;

XX Mcgavin M;

XX WPI; 1998-413816/35.

XX Example 9; Page 110; 201P; English.

XX The invention relates to antibodies that bind to a fibronecin-binding

XX domain of a fibronecin-binding protein, and inhibit binding of the

XX protein to fibronecin. Also claimed are: (1) isolated peptides of a

XX fibronecin-binding protein that do not bind to fibronecin; (2) fusion

XX protein containing at least one peptide of a fibronecin-binding protein

XX linked to a second amino acid sequence; (3) nucleic acid encoding the

XX isolated peptide of (1). Antibodies, the isolated peptides of (1) and the

XX nucleic acids are all useful for immunisation (active or passive) and (by

XX inhibiting binding of bacteria to fibronecin) for preventing or treating

XX infection in humans or other animals, particularly by staphylococci or

CC streptococci, e.g. meningitis, otitis media, pneumonia, endocarditis,
CC mastitis in cattle, abortion in horses and many others. Since the
CC antibodies block binding of bacteria, they should be effective against
CC antibiotic-resistant strains, and may replace antibiotic therapy or
CC increase its effectiveness. Sequences AAM65719-41 and AAM65658 represent
CC peptides which were synthesized to span the D1 motif and the N-terminal
CC 18 amino acids of D2, with each peptide overlapping by eight amino acids
CC with the previous sequence
XX

SQ Sequence 10 AA;

Query Match 100.0%; Score 52; DB 2; Length 10;

Best Local Similarity 100.0%; Pred. No. 0.0071; Mismatches 0; Indels 0; Gaps 0;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 NOSFEEDTEK 10
DB 1 NOSFEEDTEK 10

RESULT 2

AAB82164 standard; peptide; 30 AA.

ID AAB82164;

AC AAB82164;

XX 20-JUL-2001 (first entry)

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DB 6 NOSFEEDTEK 15
RESULT 3
ID ADC69221 standard; peptide; 30 AA.

AC ADC69221;

XX 18-DEC-2003 (first entry)

XX Fibronectin binding protein B (FnBPB) D2 peptide.

XX Fibronectin binding protein A; FnBPB; fibronectin binding protein B;
XX FnBPB; antibody; staphylococcal infection; D2 peptide; fibronectin;
XX antibacterial; immunostimulant.

XX Staphylococcus aureus.

XX US2003153022-A1.

XX 14-AUG-2003.

XX 05-NOV-2002; 2002US-00287821.

XX 05-NOV-2001; 2001US-0330964P.

XX (PAT/) PATRI J M.

XX (PAT/) PATRI P.

XX (HAL/) HALU A.

XX (DOMA/) DOMANSKI P.

XX (SYRI/) SYRIBEYS P.

XX (HUTC/) HUTCHINS J T.

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DB 6 NOSFEEDTEK 15
RESULT 4
ID ADC69222 standard; peptide; 31 AA.

AC ADC69222;

XX 18-DEC-2003 (first entry)

XX Fibronectin binding protein B (FnBPB) modified D2 peptide.

XX Fibronectin binding protein B (FnBPB) modified D2 peptide.

XX Staphylococcus aureus.

XX US2003153022-A1.

XX 14-AUG-2003.

XX 05-NOV-2002; 2002US-00287821.

XX 05-NOV-2001; 2001US-0330964P.

XX (PAT/) PATRI J M.

XX (PAT/) PATRI P.

XX (HAL/) HALU A.

XX (DOMA/) DOMANSKI P.

XX (SYRI/) SYRIBEYS P.

XX (HUTC/) HUTCHINS J T.

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DB 6 NOSFEEDTEK 15
RESULT 4
ID ADC69222 standard; peptide; 31 AA.

AC ADC69222;

XX 18-DEC-2003 (first entry)

XX Fibronectin binding protein B (FnBPB) modified D2 peptide.

XX Fibronectin binding protein B (FnBPB) modified D2 peptide.

XX Staphylococcus aureus.

XX US2003153022-A1.

XX 14-AUG-2003.

XX 05-NOV-2002; 2002US-00287821.

XX 05-NOV-2001; 2001US-0330964P.

XX (PAT/) PATRI J M.

XX (PAT/) PATRI P.

XX (HAL/) HALU A.

XX (DOMA/) DOMANSKI P.

XX (SYRI/) SYRIBEYS P.

XX (HUTC/) HUTCHINS J T.

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DB 6 NOSFEEDTEK 15
RESULT 4
ID ADC69222 standard; peptide; 31 AA.

AC ADC69222;

XX 18-DEC-2003 (first entry)

XX Fibronectin binding protein B (FnBPB) modified D2 peptide.

XX Fibronectin binding protein B (FnBPB) modified D2 peptide.

XX Staphylococcus aureus.

XX US2003153022-A1.

XX 14-AUG-2003.

XX 05-NOV-2002; 2002US-00287821.

XX 05-NOV-2001; 2001US-0330964P.

XX (PAT/) PATRI J M.

XX (PAT/) PATRI P.

XX (HAL/) HALU A.

XX (DOMA/) DOMANSKI P.

XX (SYRI/) SYRIBEYS P.

XX (HUTC/) HUTCHINS J T.

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DB 6 NOSFEEDTEK 15
RESULT 4
ID ADC69222 standard; peptide; 31 AA.

AC ADC69222;

XX 18-DEC-2003 (first entry)

XX Fibronectin binding protein B (FnBPB) modified D2 peptide.

XX Fibronectin binding protein B (FnBPB) modified D2 peptide.

XX Staphylococcus aureus.

XX US2003153022-A1.

XX 14-AUG-2003.

XX 05-NOV-2002; 2002US-00287821.

XX 05-NOV-2001; 2001US-0330964P.

XX (PAT/) PATRI J M.

XX (PAT/) PATRI P.

XX (HAL/) HALU A.

XX (DOMA/) DOMANSKI P.

XX (SYRI/) SYRIBEYS P.

XX (HUTC/) HUTCHINS J T.

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DB 6 NOSFEEDTEK 15
RESULT 4
ID ADC69222 standard; peptide; 31 AA.

AC ADC69222;

XX 18-DEC-2003 (first entry)

XX Fibronectin binding protein B (FnBPB) modified D2 peptide.

XX Fibronectin binding protein B (FnBPB) modified D2 peptide.

XX Staphylococcus aureus.

XX US2003153022-A1.

XX 14-AUG-2003.

XX 05-NOV-2002; 2002US-00287821.

XX 05-NOV-2001; 2001US-0330964P.

XX (PAT/) PATRI J M.

XX (PAT/) PATRI P.

XX (HAL/) HALU A.

XX (DOMA/) DOMANSKI P.

XX (SYRI/) SYRIBEYS P.

XX (HUTC/) HUTCHINS J T.

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DB 6 NOSFEEDTEK 15
RESULT 4
ID ADC69222 standard; peptide; 31 AA.

AC ADC69222;

XX 18-DEC-2003 (first entry)

XX Fibronectin binding protein B (FnBPB) modified D2 peptide.

XX Fibronectin binding protein B (FnBPB) modified D2 peptide.

XX Staphylococcus aureus.

XX US2003153022-A1.

XX 14-AUG-2003.

XX 05-NOV-2002; 2002US-00287821.

XX 05-NOV-2001; 2001US-0330964P.

XX (PAT/) PATRI J M.

XX (PAT/) PATRI P.

XX (HAL/) HALU A.

XX (DOMA/) DOMANSKI P.

XX (SYRI/) SYRIBEYS P.

XX (HUTC/) HUTCHINS J T.

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DB 6 NOSFEEDTEK 15
RESULT 4
ID ADC69222 standard; peptide; 31 AA.

AC ADC69222;

XX 18-DEC-2003 (first entry)

XX Fibronectin binding protein B (FnBPB) modified D2 peptide.

XX Fibronectin binding protein B (FnBPB) modified D2 peptide.

XX Staphylococcus aureus.

XX US2003153022-A1.

XX 14-AUG-2003.

XX 05-NOV-2002; 2002US-00287821.

XX 05-NOV-2001; 2001US-0330964P.

XX (PAT/) PATRI J M.

XX (PAT/) PATRI P.

XX (HAL/) HALU A.

XX (DOMA/) DOMANSKI P.

XX (SYRI/) SYRIBEYS P.

XX (HUTC/) HUTCHINS J T.

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DB 6 NOSFEEDTEK 15
RESULT 4
ID ADC69222 standard; peptide; 31 AA.

AC ADC69222;

XX 18-DEC-2003 (first entry)

XX Fibronectin binding protein B (FnBPB) modified D2 peptide.

XX Fibronectin binding protein B (FnBPB) modified D2 peptide.

XX Staphylococcus aureus.

XX US2003153022-A1.

XX 14-AUG-2003.

XX 05-NOV-2002; 2002US-00287821.

XX 05-NOV-2001; 2001US-0330964P.

XX (PAT/) PATRI J M.

XX (PAT/) PATRI P.

XX (HAL/) HALU A.

XX (DOMA/) DOMANSKI P.

XX (SYRI/) SYRIBEYS P.

XX (HUTC/) HUTCHINS J T.

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XX Fibronection binding protein A; FnbpA; fibronection binding protein B;
 KM FnbpB; antibody; staphylococcal infection; D2 peptide; fibronection;
 KW antibacterial; immunostimulant.
 XX
 OS Synthetic.
 OS Staphylococcus aureus.
 XX
 PN US2003153022-A1.
 XX
 PD 14-AUG-2003.
 XX
 PF 05-NOV-2002; 2002US-00287821.
 XX
 PR 05-NOV-2001; 2001US-0330964P.
 XX
 PA (PATTI/) PATTI J M.
 PA (PATEL/) PATEL P.
 PA (HALL/) HALL A.
 PA (DOMA/) DOMANSKI P.
 PA (SYRI/) SYRIBEYS P.
 PA (HUTC/) HUTCHINS J T.
 XX
 PI Patti JM, Patel P, Hall A, Domanski P, Syribeys P, Hutchins JT;
 XX
 DR WPI; 2003-801749/75.
 XX
 PT Monoclonal antibody for treating or preventing staphylococcal infections
 PT binds specified fibronection binding protein from Staphylococcus aureus.
 XX
 PS Claim 10; SEQ ID NO 2; 12pp; English.
 XX
 CC The invention relates to a new monoclonal antibody that binds fibronection
 CC binding proteins from Staphylococcus aureus, including fibronection
 CC binding protein A (FnbpA) and fibronection binding protein B (FnbpB). The
 CC antibody is useful in treating, preventing or diagnosing staphylococcal
 CC infections in a human or animal. The antibody is capable of recognising
 CC Staphylococcus aureus with high affinity. It also inhibits binding of
 CC staphylococcal bacteria to fibronection. This sequence represents a
 CC modified FnbpB D2 peptide of the invention.
 CC
 XX Sequence 31 AA;
 SQ
 Query Match 100.0%; Score 52; DB 7; Length 31;
 Best Local Similarity 100.0%; Pred. No. 0.025;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NOSFEEDTEK 10
 DB |||||
 7 NOSFEEDTEK 16

RESULT 5
 ID AAM65714 standard; peptide; 36 AA.
 XX
 AC AAM65714;
 XX
 DT 16-OCT-1998 (first entry)
 XX
 DE Fibronection binding protein-derived peptide #58.
 XX
 KM microbial surface components recognising adhesive matrix molecule;
 KM MSCRAM; fibronection; fibronection-binding protein; antibody; epitope;
 KM antibiotic; bacterial infection; antibiotic-resistant strain.
 XX
 OS Synthetic.
 OS Staphylococcus aureus.
 XX
 PN WO9831389-A2.
 XX
 PD 23-JUL-1998.

PF 21-JAN-1998; 98WO-US001222.
 XX
 XX 21-JAN-1997; 97US-0036139P.
 XX
 PA (TEXA) UNIV TEXAS A & M SYSTEM.
 XX
 PI Hoeoek M, Patti JM, House-Pompeo KL, Speziale P, Joh D;
 PI McGavin MJ;
 XX
 DR WPI; 1998-413816/35.
 XX
 PT Antibody that binds to fibronection-binding protein, preventing its
 PT binding to fibronection - used to treat or prevent bacterial infection,
 PT especially by Staphylococci and Streptococci.
 XX
 PS Example 8; Page 104; 201pp; English.
 XX
 CC The invention relates to antibodies that bind to a fibronection-binding
 CC domain of a fibronection-binding protein, and inhibit binding of the
 CC protein to fibronection. Also claimed are: (1) isolated peptides of a
 CC fibronection-binding protein that do not bind to fibronection; (2) fusion
 CC protein containing at least one peptide of a fibronection-binding protein
 CC linked to a second amino acid sequence; (3) nucleic acid encoding the
 CC isolated peptide of (1). Antibodies, the isolated peptides of (1) and (by
 CC nucleic acids are all useful for immunisation (active or passive) and (by
 CC inhibiting binding of bacteria to fibronection) for preventing or treating
 CC infection in humans or other animals, particularly by staphylococci or
 CC streptococci, e.g. meningitis, otitis media, pneumonia, endocarditis,
 CC mastitis in cattle, abortion in horses and many others. Since the
 CC antibodies block binding of bacteria, they should be effective against
 CC antibiotic-resistant strains, and may replace antibiotic therapy or
 CC increase its effectiveness. The present sequence is shown in the
 CC specification
 XX
 SQ Sequence 36 AA;
 XX
 Query Match 100.0%; Score 52; DB 2; Length 36;
 Best Local Similarity 100.0%; Pred. No. 0.03;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NOSFEEDTEK 10
 DB |||||
 5 NOSFEEDTEK 14

RESULT 6
 ID AAM65715 standard; peptide; 36 AA.
 XX
 AC AAM65715;
 XX
 DT 27-AUG-2003 (revised)
 DT 16-OCT-1998 (first entry)
 XX
 DE Peptide #59.
 XX
 KM microbial surface components recognising adhesive matrix molecule;
 KM MSCRAM; fibronection; fibronection-binding protein; antibody; epitope;
 KM antibiotic; bacterial infection; antibiotic-resistant strain.
 XX
 OS Synthetic.
 OS Staphylococcus aureus.
 XX
 PN WO9831389-A2.
 XX
 PD 23-JUL-1998.
 XX
 PF 21-JAN-1998; 98WO-US001222.
 XX
 PR 21-JAN-1997; 97US-0036139P.
 XX
 PA (TEXA) UNIV TEXAS A & M SYSTEM.

PI Hoeoek M, Patti JM, House-Pompeo KL, Speziale P, Joh D;
 PI McGavin MJ;
 DR WPI; 1998-413816/35.
 XX
 XX
 PT Antibody that binds to fibronectin-binding protein, preventing its
 binding to fibronectin - used to treat or prevent bacterial infection,
 PT especially by Staphylococci and Streptococci.
 XX
 PS Disclosure; Page 160; 201pp; English.
 XX
 CC The invention relates to antibodies that bind to a fibronectin-binding
 CC domain of a fibronectin-binding protein, and inhibit binding of the
 CC protein to fibronectin. Also claimed are: (1) isolated peptides of a
 CC fibronectin-binding protein that do not bind to fibronectin; (2) fusion
 CC protein containing at least one peptide of a fibronectin-binding protein
 CC linked to a second amino acid sequence; (3) nucleic acid encoding the
 CC isolated peptide of (1). Antibodies, the isolated peptides of (1) and the
 CC nucleic acids are all useful for immunisation (active or passive) and (by
 CC inhibiting binding of bacteria to fibronectin) for preventing or treating
 CC infection in humans or other animals, particularly by staphylococci or
 CC streptococci, e.g. meningitis, otitis media, pneumonia, endocarditis,
 CC mastitis in cattle, abortion in horses and many others. Since the
 CC antibodies block binding of bacteria, they should be effective against
 CC antibiotic-resistant strains, and may replace antibiotic therapy or
 CC increase its effectiveness. The present sequence is shown in the
 CC specification. (Updated on 27-AUG-2003 to correct OS field.)
 XX
 SQ Sequence 36 AA;
 QY
 DB 1 NOSFEEDTEK 10
 5 NOSFEEDTEK 14
 RESULT 7
 AAP80661
 ID AAP80661 standard; protein; 38 AA.
 XX
 AC AAP80661;
 XX
 DT 25-MAR-2003 (revised)
 DT 07-OCT-1990 (first entry)
 XX
 DE Protein with fibronectin binding ability.
 XX
 KM Hybrid DNA molecule; fibronectin binding; mastitis; ruminants;
 KM wound infection.
 XX
 OS Staphylococcus aureus.
 OS
 XX
 PN BP294349-A.
 PD
 PD 07-DEC-1988.
 PF 30-MAY-1988; 88EP-00850188.
 PR 01-JUN-1987; 87SE-00002272.
 XX
 PA (ALFA) ALFA LAVAL AGRIC INT AB.
 XX
 PI Lindberg MK, Signas LC, Wadstrom TM, Froman G;
 DR WPI; 1988-347978/49.
 DR N-PSDB; AAN81098.
 XX
 PT Hybrid DNA encoding Staphylococcus aureus fibronectin binding protein -
 PT useful for immunisation and topical application to prevent staphylococcal
 PT infections.

XX
 XX Claim 11; Page 12; 23pp; English.
 XX
 CC The peptide has fibronectin binding ability. It is useful for immunising
 CC ruminants against staphylococcal mastitis, pref. when used at 0.5-5
 CC micrograms/kg, using 3 doses given at 1-3 week intervals; for topical
 CC application to prevent wound infection, using an isotonic saline soln. of
 CC concn. 25-250 micrograms/ml; and, when immobilised on a carrier, for
 CC diagnosing staphylococcal infections. (Updated on 25-MAR-2003 to correct
 CC PF field.) (Updated on 25-MAR-2003 to correct PA field.)
 XX
 SQ Sequence 38 AA;
 QY
 DB 1 NOSFEEDTEK 10
 6 NOSFEEDTEK 15
 RESULT 8
 AAP82117
 ID AAP82117 standard; protein; 38 AA.
 XX
 AC AAP82117;
 XX
 DT 25-MAR-2003 (revised)
 DT 05-JAN-1990 (first entry)
 XX
 DE Fibronectin binding protein.
 XX
 KM Fibronectin binding protein; S. aureus; immunisation; mastitis; ruminants;
 KM wound infection; diagnosis.
 XX
 OS Staphylococcus aureus.
 OS
 XX
 PN BP294349-A.
 PD
 PD 07-DEC-1988.
 PF 30-MAY-1988; 88EP-00850188.
 PR 01-JUN-1987; 87SE-00002272.
 XX
 PA (ALFA) ALFA LAVAL AGRIC INT AB.
 XX
 PI Lindberg MK, Signas LC, Wadstrom TM, Froman G;
 DR WPI; 1988-347978/49.
 DR N-PSDB; AAN82055.
 XX
 PT Hybrid DNA encoding Staphylococcus aureus fibronectin binding protein -
 PT useful for immunisation and topical application to prevent staphylococcal
 PT infections.
 XX
 PS Claim 11; Page 12; 23pp; English.
 XX
 CC The S aureus fibronectin binding protein may be included in a hybrid
 CC protein. The protein may be used to immunise ruminants against
 CC staphylococcal mastitis, pref. when given at 0.5-5 microg/kg, using 3
 CC doses at 1-3 week intervals; and for topical application to prevent wound
 CC infection, pref. using isotonic saline soln. of concn. 25-250 microg/mg.
 CC The DNA encoding the binding protein and the hybrid protein may be
 CC immobilised on a carrier and used to diagnose staphylococcal infections.
 CC (Updated on 25-MAR-2003 to correct PA field.)
 XX
 SQ Sequence 38 AA;
 QY
 DB 1 NOSFEEDTEK 10
 6 NOSFEEDTEK 15
 RESULT 8
 AAP82117
 ID AAP82117 standard; protein; 38 AA.
 XX
 AC AAP82117;
 XX
 DT 25-MAR-2003 (revised)
 DT 05-JAN-1990 (first entry)
 XX
 DE Fibronectin binding protein.
 XX
 KM Fibronectin binding protein; S. aureus; immunisation; mastitis; ruminants;
 KM wound infection; diagnosis.
 XX
 OS Staphylococcus aureus.
 OS
 XX
 PN BP294349-A.
 PD
 PD 07-DEC-1988.
 PF 30-MAY-1988; 88EP-00850188.
 PR 01-JUN-1987; 87SE-00002272.
 XX
 PA (ALFA) ALFA LAVAL AGRIC INT AB.
 XX
 PI Lindberg MK, Signas LC, Wadstrom TM, Froman G;
 DR WPI; 1988-347978/49.
 DR N-PSDB; AAN82055.
 XX
 PT Hybrid DNA encoding Staphylococcus aureus fibronectin binding protein -
 PT useful for immunisation and topical application to prevent staphylococcal
 PT infections.
 XX
 PS Claim 11; Page 12; 23pp; English.
 XX
 CC The S aureus fibronectin binding protein may be included in a hybrid
 CC protein. The protein may be used to immunise ruminants against
 CC staphylococcal mastitis, pref. when given at 0.5-5 microg/kg, using 3
 CC doses at 1-3 week intervals; and for topical application to prevent wound
 CC infection, pref. using isotonic saline soln. of concn. 25-250 microg/mg.
 CC The DNA encoding the binding protein and the hybrid protein may be
 CC immobilised on a carrier and used to diagnose staphylococcal infections.
 CC (Updated on 25-MAR-2003 to correct PA field.)
 XX
 SQ Sequence 38 AA;
 QY
 DB 1 NOSFEEDTEK 10
 6 NOSFEEDTEK 15
 RESULT 8
 AAP82117
 ID AAP82117 standard; protein; 38 AA.
 XX
 AC AAP82117;
 XX
 DT 25-MAR-2003 (revised)
 DT 05-JAN-1990 (first entry)
 XX
 DE Fibronectin binding protein.
 XX
 KM Fibronectin binding protein; S. aureus; immunisation; mastitis; ruminants;
 KM wound infection; diagnosis.
 XX
 OS Staphylococcus aureus.
 OS
 XX
 PN BP294349-A.
 PD
 PD 07-DEC-1988.
 PF 30-MAY-1988; 88EP-00850188.
 PR 01-JUN-1987; 87SE-00002272.
 XX
 PA (ALFA) ALFA LAVAL AGRIC INT AB.
 XX
 PI Lindberg MK, Signas LC, Wadstrom TM, Froman G;
 DR WPI; 1988-347978/49.
 DR N-PSDB; AAN82055.
 XX
 PT Hybrid DNA encoding Staphylococcus aureus fibronectin binding protein -
 PT useful for immunisation and topical application to prevent staphylococcal
 PT infections.
 XX
 PS Claim 11; Page 12; 23pp; English.
 XX
 CC The S aureus fibronectin binding protein may be included in a hybrid
 CC protein. The protein may be used to immunise ruminants against
 CC staphylococcal mastitis, pref. when given at 0.5-5 microg/kg, using 3
 CC doses at 1-3 week intervals; and for topical application to prevent wound
 CC infection, pref. using isotonic saline soln. of concn. 25-250 microg/mg.
 CC The DNA encoding the binding protein and the hybrid protein may be
 CC immobilised on a carrier and used to diagnose staphylococcal infections.
 CC (Updated on 25-MAR-2003 to correct PA field.)
 XX
 SQ Sequence 38 AA;
 QY
 DB 1 NOSFEEDTEK 10
 6 NOSFEEDTEK 15
 RESULT 8
 AAP82117
 ID AAP82117 standard; protein; 38 AA.
 XX
 AC AAP82117;
 XX
 DT 25-MAR-2003 (revised)
 DT 05-JAN-1990 (first entry)
 XX
 DE Fibronectin binding protein.
 XX
 KM Fibronectin binding protein; S. aureus; immunisation; mastitis; ruminants;
 KM wound infection; diagnosis.
 XX
 OS Staphylococcus aureus.
 OS
 XX
 PN BP294349-A.
 PD
 PD 07-DEC-1988.
 PF 30-MAY-1988; 88EP-00850188.
 PR 01-JUN-1987; 87SE-00002272.
 XX
 PA (ALFA) ALFA LAVAL AGRIC INT AB.
 XX
 PI Lindberg MK, Signas LC, Wadstrom TM, Froman G;
 DR WPI; 1988-347978/49.
 DR N-PSDB; AAN82055.
 XX
 PT Hybrid DNA encoding Staphylococcus aureus fibronectin binding protein -
 PT useful for immunisation and topical application to prevent staphylococcal
 PT infections.
 XX
 PS Claim 11; Page 12; 23pp; English.
 XX
 CC The S aureus fibronectin binding protein may be included in a hybrid
 CC protein. The protein may be used to immunise ruminants against
 CC staphylococcal mastitis, pref. when given at 0.5-5 microg/kg, using 3
 CC doses at 1-3 week intervals; and for topical application to prevent wound
 CC infection, pref. using isotonic saline soln. of concn. 25-250 microg/mg.
 CC The DNA encoding the binding protein and the hybrid protein may be
 CC immobilised on a carrier and used to diagnose staphylococcal infections.
 CC (Updated on 25-MAR-2003 to correct PA field.)
 XX
 SQ Sequence 38 AA;
 QY
 DB 1 NOSFEEDTEK 10
 6 NOSFEEDTEK 15
 RESULT 8
 AAP82117
 ID AAP82117 standard; protein; 38 AA.
 XX
 AC AAP82117;
 XX
 DT 25-MAR-2003 (revised)
 DT 05-JAN-1990 (first entry)
 XX
 DE Fibronectin binding protein.
 XX
 KM Fibronectin binding protein; S. aureus; immunisation; mastitis; ruminants;
 KM wound infection; diagnosis.
 XX
 OS Staphylococcus aureus.
 OS
 XX
 PN BP294349-A.
 PD
 PD 07-DEC-1988.
 PF 30-MAY-1988; 88EP-00850188.
 PR 01-JUN-1987; 87SE-00002272.
 XX
 PA (ALFA) ALFA LAVAL AGRIC INT AB.
 XX
 PI Lindberg MK, Signas LC, Wadstrom TM, Froman G;
 DR WPI; 1988-347978/49.
 DR N-PSDB; AAN82055.
 XX
 PT Hybrid DNA encoding Staphylococcus aureus fibronectin binding protein -
 PT useful for immunisation and topical application to prevent staphylococcal
 PT infections.

QY 1 NOSFEEDTEK 10
 |||||
 DB 6 NOSFEEDTEK 15

RESULT 9
 AAM65664 ID AAM65664 standard; peptide; 38 AA.

XX AAM65664;
 AC
 XX

DT 16-OCT-1998 (first entry)

DE Fibronectin binding protein-derived peptide #8.

XX microbial surface components recognising adhesive matrix molecule;
 KM MSCRAMM; fibronectin; fibronectin-binding protein; antibody; epitope;
 KM antibiotic; bacterial infection; antibiotic-resistant strain.

XX Synthetic.
 OS Staphylococcus aureus.

PN WC98J3389-A2.

XX 23-JUL-1998.

XX 21-JAN-1998; 98MO-US001222.

XX 21-JAN-1997; 97US-0036139P.

XX (TEXA) UNIV TEXAS A & M SYSTEM.

PI Hoesek M, Patti JM, House-Pompeo KL, Speziale P, Joh D;
 PI McGavin MJ;

DR WPI; 1998-413816/35.

XX Antibody that binds to fibronectin-binding protein, preventing its
 PT binding to fibronectin - used to treat or prevent bacterial infection,
 PT especially by Staphylococci and Streptococci.

PS Example 2; Page 92; 201pp; English.

XX The invention relates to antibodies that bind to a fibronectin-binding
 CC domain of a fibronectin-binding protein, and inhibit binding of the
 CC protein to fibronectin. Also claimed are: (1) isolated peptides of a
 CC fibronectin-binding protein that do not bind to fibronectin; (2) fusion
 CC protein containing at least one peptide of a fibronectin-binding protein
 CC linked to a second amino acid sequence; (3) nucleic acid encoding the
 CC isolated peptide of (1). Antibodies, the isolated peptides of (1) and the
 CC nucleic acids are all useful for immunisation (active or passive) and (by
 CC inhibiting binding of bacteria to fibronectin) for preventing or treating
 CC infection in humans or other animals, particularly by staphylococci or
 CC streptococci, e.g. meningitis, otitis media, pneumonia, endocarditis,
 CC mastitis in cattle, abortion in horses and many others. Since the
 CC antibodies block binding of bacteria, they should be effective against
 CC antibiotic-resistant strains, and may replace antibiotic therapy or
 CC increase its effectiveness. Sequences AAM65659-68 represent synthetic
 CC epitopes from the fibronectin binding domains DU and DI-D4 of the S.
 CC aureus fnda gene

XX Sequence 38 AA;

Query Match 100.0%; Score 52; DB 2; Length 38;
 Best Local Similarity 100.0%; Pred. No. 0.032;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NOSFEEDTEK 10
 |||||
 DB 5 NOSFEEDTEK 14

RESULT 10
 AAM65705 ID AAM65705 standard; peptide; 38 AA.

XX AAM65705;
 AC
 XX

DT 16-OCT-1998 (first entry)

DE Fibronectin binding protein-derived peptide #49.

XX microbial surface components recognising adhesive matrix molecule;
 KM MSCRAMM; fibronectin; fibronectin-binding protein; antibody; epitope;
 KM antibiotic; bacterial infection; antibiotic-resistant strain.

XX Synthetic.
 OS Staphylococcus aureus.

PN WC98J3389-A2.

XX 23-JUL-1998.

XX 21-JAN-1998; 98MO-US001222.

XX 21-JAN-1997; 97US-0036139P.

XX (TEXA) UNIV TEXAS A & M SYSTEM.

PI Hoesek M, Patti JM, House-Pompeo KL, Speziale P, Joh D;
 PI McGavin MJ;

DR WPI; 1998-413816/35.

XX Antibody that binds to fibronectin-binding protein, preventing its
 PT binding to fibronectin - used to treat or prevent bacterial infection,
 PT especially by Staphylococci and Streptococci.

PS Example 8; Page 102; 201pp; English.

XX The invention relates to antibodies that bind to a fibronectin-binding
 CC domain of a fibronectin-binding protein, and inhibit binding of the
 CC protein to fibronectin. Also claimed are: (1) isolated peptides of a
 CC fibronectin-binding protein that do not bind to fibronectin; (2) fusion
 CC protein containing at least one peptide of a fibronectin-binding protein
 CC linked to a second amino acid sequence; (3) nucleic acid encoding the
 CC isolated peptide of (1). Antibodies, the isolated peptides of (1) and the
 CC nucleic acids are all useful for immunisation (active or passive) and (by
 CC inhibiting binding of bacteria to fibronectin) for preventing or treating
 CC infection in humans or other animals, particularly by staphylococci or
 CC streptococci, e.g. meningitis, otitis media, pneumonia, endocarditis,
 CC mastitis in cattle, abortion in horses and many others. Since the
 CC antibodies block binding of bacteria, they should be effective against
 CC antibiotic-resistant strains, and may replace antibiotic therapy or
 CC increase its effectiveness. Sequences AAM65701-706 represent a series of
 CC synthetic peptides based on the D2 region of S. aureus fibronectin
 CC binding protein A. They were synthesised to contain mutations

XX Sequence 38 AA;

Query Match 100.0%; Score 52; DB 2; Length 38;
 Best Local Similarity 100.0%; Pred. No. 0.032;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NOSFEEDTEK 10
 |||||
 DB 5 NOSFEEDTEK 14

RESULT 11
 AAM65663 ID AAM65663 standard; peptide; 38 AA.

XX AAM65663;
 AC

XX		KM	tumour necrosis factor; recombinant virus; vaccine; mucosal disease;
XX		XV	mastitis; breast cancer; stress-induced disease; binding domain; FnBb; fibronectin binding protein.
OS		XX	Staphylococcus aureus.
XX		PN	WO916892-A1.
PN		PD	08-APR-1999.
PP		XP	29-SEP-1998; 98MO-GBO02927.
PR		XX	29-SEP-1997; 97GB-00020633.
PA	(UYBR-) UNIV BRISTOL.	PI	Bradley AJ, Duffas WPJ; WPI; 1999-255101/21. DR N-PSDB; AAX91505.
PT	New bovine herpes virus-2 vectors.	PS	Example 2; Fig 8A-B; 130pp; English.
CC	The invention provides bovine herpes virus-2 (BHV-2) based vectors that comprise at least one cytokine-encoding DNA sequence. The expression of cytokines in mammals can up-regulate immune responses to the immunogens. The cytokine is selected from interleukins (IL), colony stimulating factors (CSF), interferons (IFN) and tumour necrosis factors (TNF). The BHV-2 based vector or recombinant virus can be used as vaccines. They can be used for preventing or treating a mucosal disease in a subject, e.g., ruminants, cattle, sheep, goats, cats, horses, or man, particularly masticitis in cows or breast cancers in humans. They can also be used for preventing or treating a stress-induced disease. The present sequence represents the binding domain of a previously published S. aureus fibronectin binding protein B (Fnbb) sequence. The Fnb binding domain gene sequence FNBBab, cloned for use in this invention has 97.8 percent identity when compared to the previously published FNba and Fnbb gene sequences	SQ	Sequence 134 AA: Query Match 100.0%; Score 52; DB 2; Length 134; Best Local Similarity 100.0%; Pred. No. 0.13; Indels 0; Matches 10; Conservative 0; Mismatches 0; Gaps 0; OY 1 NOSFEEDTEK 10 Db 44 NOSFEEDTEK 53 RESULT 13 CD AAY29087 AC AAY29087 standard; protein; 134 AA. XX AAY29087; DT 28-SEP-1999 (first entry) DE S. aureus fibronectin binding protein A (FnBa) binding domain. XX Bovine herpes virus-2; BHV-2; cytokine; immune response; immunogen; IL; KW interleukin; colony stimulating factor; CSF; interferon; IFN; TNF; KW tumour necrosis factor; recombinant virus; vaccine; mucosal disease; KW mastitis; breast cancer; stress-induced disease; binding domain; FnBa, fibronectin binding protein. XX Staphylococcus aureus. OS Staphylococcus aureus. PM WO916892-A1. DD 08-APR-1999.

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XX PF 29-SEP-1998; 98MO-GB002927.
XX XX 29-SEP-1997; 97GB-00020633.
XX PA (UYBR-) UNIV BRISTOL.
XX PI Bradley AJ, Duffae WPH;
XX DR WPI; 1999-255101/21.
XX DR N-PSDB; AAX91504.
XX PT New bovine herpes virus-2 vectors.
XX PS Example 2; Fig 8A-B; 130pp; English.
XX CC The invention provides bovine herpes virus-2 (BHV-2) based vectors that
XX CC comprise at least one cytokine-encoding DNA sequence. The expression of
XX CC cytokines in mammals can up-regulate immune responses to the immunogens.
XX CC The cytokine is selected from interleukins (IL), colony stimulating
XX CC factors (CSF), interferons (IFN) and tumour necrosis factors (TNF). The
XX CC BHV-2 based vector or recombinant virus can be used as vaccines. They can
XX CC be used for preventing or treating a mucosal disease in a subject, e.g.
XX CC ruminants, cattle, sheep, goats, cats, horses, or man, particularly
XX CC mastitis in cows or breast cancers in humans. They can also be used for
XX CC preventing or treating a stress-induced disease. The present sequence
XX CC represents the binding domain of a previously published S. aureus
XX CC fibronectin binding protein A (FnBA) sequence. The FnB binding domain
XX CC gene sequence FnBAB, cloned for use in this invention has 97.8 percent
XX CC identity when compared to the previously published FnBA and FnBB gene
XX CC sequences
XX SQ Sequence 134 AA;

Query Match 100.0%; Score 52; DB 2; Length 134;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NOSFEEDTEK 10
DB 44 NOSFEEDTEK 53

RESULT 14
AAW31556
ID AAW31556 standard; protein; 139 AA.
XX AC AAW31556;
XX DT 27-AUG-2003 (revised)
XX DT 25-MAR-2003 (revised)
XX DT 21-MAY-1998 (first entry)
XX DE Fibronectin-binding MSCRAMM derivative POD.
XX KW Fibronectin; POD; collagen binding protein; sepsis; infection;
XX KW microbial surface component recognising adhesive matrix molecule; MSCRAMM;
XX KW adhesin; vaccine; immunisation; diagnosis; therapy; mastitis.
XX OS Staphylococcus aureus.
XX PF Key Location/Qualifiers
XX FT Peptide 1..12
XX FT /note= "vector pGB30-derived peptide"
XX PN WO9743314-A2.
XX PD 20-NOV-1997.
XX PF 14-MAY-1997; 97WO-US008210.
XX PR 16-MAY-1996; 96US-0017678P.
XX XX

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PA (TEXA ) UNIV TEXAS A & M SYSTEM.
PA (UABR-) UAB RES FOUND.
XX PI Hoeek M, Patti JM, House-Pompeo K, Sthanam N, Symersky J;
XX DR WPI; 1998-008801/01.
XX XX
XX PT Antibody that interacts with collagen binding domain of Staphylococcal
XX PT cna gene product - useful to prevent bacterial sepsis in animal infected
XX PT with Staphylococcus aureus.
XX PS Disclosure; Page 91; 143pp; English.
XX CC This protein comprises Staphylococcus aureus fibronectin-binding
XX CC microbial surface component recognising adhesive matrix molecule (MSCRAMM)
XX CC derivative POD, plus a vector-derived N-terminal peptide. The invention
XX CC relates to claimed nucleic acid sequences (see AAT93436-38) encoding S.
XX CC aureus collagen binding protein (CBP) epitopes M17, M31 and M55 (see
XX CC AAW31552-54) that confer protection against S. aureus infection. CBP
XX CC protein and antigenic epitopes are contemplated for use in the treatment
XX CC of pathological infections, especially to prevent bacterial adhesion to
XX CC collagen. The epitopes are also contemplated for use in the preparation
XX CC of vaccines and as carrier proteins in vaccine formulations, as well as
XX CC in the formulation of compositions for the prevention of S. aureus
XX CC infection. PCR3 and POD (see AAW31556) were used to raise anti-MSCRAMM
XX CC polyclonal antibodies used in passive immunisation against bovine
XX CC mastitis. (Updated on 25-MAR-2003 to correct PI field.) (Updated on 27-
XX CC AUG-2003 to correct OS field.)
XX SQ Sequence 139 AA;

Query Match 100.0%; Score 52; DB 2; Length 139;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NOSFEEDTEK 10
DB 58 NOSFEEDTEK 67

RESULT 15
AAW89803
ID AAW89803 standard; protein; 559 AA.
XX AC AAW89803;
XX DT 16-MAR-1999 (first entry)
XX DE Staphylococcus aureus protein SEQ ID #5251.
XX KW Computer readable medium; vaccine; S. aureus infection; immunodetection;
XX KW cellulitis; eyelid infection; food poisoning; osteomyelitis; therapy;
XX KW skin infection; surgical wound infection; scalded skin syndrome;
XX KW toxic shock syndrome.
XX OS Staphylococcus aureus.
XX PF EP786519-A2.
XX PN 30-JUL-1997.
XX PF 07-JAN-1997; 97EP-00100117.
XX PR 05-JAN-1996; 96US-0009861P.
XX PA (HUMA-) HUMAN GENOME SCI INC.
XX PI Kunsch CA, Choi GH, Barash SC, Dillon PJ, Fannon MR, Rosen CA;
XX DR WPI; 1997-374922/35.
XX PT Polynucleotide(s) and proteins derived from Staphylococcus aureus -
XX PT stored on computer readable medium and used in the production of anti-

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PT S. aureus vaccines.

XX
PS Claim 23; Page 3259-3261; 3271pp; English.

CC This sequence represents a Staphylococcus aureus protein sequence of the
CC invention. The DNA sequences encoding the S. aureus proteins are recorded
CC on a computer readable medium, preferably selected from a floppy or hard
CC disk, random access memory (RAM), read-only memory (ROM) or CD-ROM.
CC Homology searches using the S. aureus DNA sequences allows putative
CC functions to be assigned so that protein-encoding or regulatory regions
CC of commercial, therapeutic or industrial importance can be obtained.
CC Specifically, sequences which are likely to encode antigens have been
CC identified and these polypeptides can be used in a vaccine composition
CC against S. aureus infection. The polypeptides can also be used in a kit
CC for the immunodetection of S. aureus in a sample. S. aureus is implicated
CC in numerous human diseases, including cellulitis, eyelid infections, food
CC poisoning, osteomyelitis, skin and surgical wound infections, scalded
CC skin syndrome, toxic shock syndrome, etc. Organisms transformed with the
CC DNA sequences can be used for recombinant production of the polypeptides.
CC The new DNA sequences (and their fragments) are useful as primers or
CC probes for isolating homologues of any of the 5191 S. aureus DNA sequences
CC contained on the computer readable medium

XX
SQ Sequence 559 AA;

Query Match 100.0%; Score 52; DB 2; Length 559;

Best Local Similarity 100.0%; Pred. No. 0.63;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NOSFEEDTEK 10
|||||

Db 343 NOSFEEDTEK 352

Search completed: October 25, 2005, 20:58:48
Job time : 63.2 secs

(qdsn) yuqig elba q:q1

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OM protein - protein search, using sw model

Run on: October 22, 2005, 05:46:56 ; Search time 17.3 Seconds
(without alignments)
43.150 Million cell updates/sec

Title: US-10-731-238-84

Perfect score: 52

Sequence: 1 NOSFEEDTEK 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

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6: /cgn2_6/ptodata/1/1aa/backfltest1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match length	ID	Description
1	52	100.0	10 4 US-09-010-317-84	Sequence 84, Appl
2	52	100.0	36 4 US-09-010-317-58	Sequence 58, Appl
3	52	100.0	36 4 US-09-010-317-59	Sequence 59, Appl
4	52	100.0	38 1 US-08-234-622A-3	Sequence 3, Appl
5	52	100.0	38 1 US-08-729-767-4	Sequence 4, Appl
6	52	100.0	38 4 US-09-010-317-7	Sequence 7, Appl
7	52	100.0	38 4 US-09-010-317-8	Sequence 8, Appl
8	52	100.0	38 4 US-09-010-317-49	Sequence 49, Appl
9	52	100.0	114 1 US-08-259-000-3	Sequence 3, Appl
10	52	100.0	139 3 US-08-856-253-8	Sequence 8, Appl
11	52	100.0	559 4 US-08-956-171E-5251	Sequence 5251, Ap
12	52	100.0	559 4 US-08-781-986A-5251	Sequence 5251, Ap
13	52	100.0	1027 4 US-08-956-171E-5254	Sequence 5254, Ap
14	52	100.0	1027 4 US-08-781-986A-5254	Sequence 5254, Ap
15	48	92.3	10 4 US-09-010-317-65	Sequence 65, Appl
16	48	92.3	38 1 US-08-234-622A-2	Sequence 2, Appl
17	48	92.3	38 1 US-08-729-767-3	Sequence 3, Appl
18	48	92.3	38 4 US-09-010-317-5	Sequence 5, Appl
19	48	92.3	38 4 US-09-010-317-6	Sequence 6, Appl
20	48	92.3	38 4 US-09-010-317-42	Sequence 42, Appl
21	48	92.3	38 4 US-09-010-317-43	Sequence 43, Appl
22	48	92.3	39 4 US-09-010-317-56	Sequence 56, Appl
23	48	92.3	39 4 US-09-010-317-57	Sequence 57, Appl
24	48	92.3	130 2 US-08-459-135A-7	Sequence 7, Appl
25	48	92.3	130 2 US-08-459-135A-8	Sequence 8, Appl
26	48	92.3	130 3 US-08-495-559-7	Sequence 7, Appl
27	48	92.3	130 3 US-08-495-559-8	Sequence 8, Appl

28	48	92.3	174 2 US-08-459-135A-10	Sequence 10, Appl
29	48	92.3	174 2 US-08-459-135A-13	Sequence 13, Appl
30	48	92.3	174 3 US-08-495-559-10	Sequence 10, Appl
31	48	92.3	174 3 US-08-495-559-13	Sequence 13, Appl
32	48	92.3	176 2 US-08-495-559-6	Sequence 6, Appl
33	48	92.3	178 2 US-08-459-135A-12	Sequence 12, Appl
34	48	92.3	181 2 US-08-459-559-12	Sequence 12, Appl
35	48	92.3	181 2 US-08-459-135A-6	Sequence 6, Appl
36	47	90.4	38 4 US-09-010-317-41	Sequence 41, Appl
37	46	88.5	38 4 US-09-010-317-46	Sequence 46, Appl
38	46	88.5	38 4 US-09-010-317-47	Sequence 47, Appl
39	45	86.5	38 4 US-09-010-317-48	Sequence 48, Appl
40	42	80.8	10 4 US-09-010-317-64	Sequence 64, Appl
41	42	80.8	10 4 US-09-010-317-83	Sequence 83, Appl
42	42	80.8	38 4 US-09-010-317-36	Sequence 36, Appl
43	42	80.8	38 4 US-09-010-317-37	Sequence 37, Appl
44	42	80.8	38 4 US-09-010-317-39	Sequence 39, Appl
45	42	80.8	38 4 US-09-010-317-40	Sequence 40, Appl

ALIGNMENTS

RESULT 1
US-09-010-317-84
Sequence 84, Application US/09010317
Patent No. 6685943
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
APPLICANT: Patti, Joseph M.
APPLICANT: House-Pompeo, Karen L.
APPLICANT: Speziale, Pietro
APPLICANT: John, Danny
APPLICANT: McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
TITLE OF INVENTION: AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/010.317
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibley, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAMK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO.: 84:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-09-010-317-84
Query Match 100.0%; Score 52; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0023;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 NOSFEEDTEK 10
Db 1 NOSFEEDTEK 10

RESULT 2

US-09-010-317-58
Sequence 58, Application US/09010317
Patent No. 6685943
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
APPLICANT: Patti, Joseph M.
APPLICANT: House-Pompeo, Karen L.
APPLICANT: Speziale, Pietro
APPLICANT: Joh, Danny
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
TITLE OF INVENTION: AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAMK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 58:
SEQUENCE CHARACTERISTICS:
LENGTH: 36 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-09-010-317-58

Query Match 100.0%; Score 52; DB 4; Length 36;
Best Local Similarity 100.0%; Pred. No. 0.0091;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NOSFEEDTEK 10
Db 5 NOSFEEDTEK 14

RESULT 3

US-09-010-317-59
Sequence 59, Application US/09010317
Patent No. 6685943
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
APPLICANT: Patti, Joseph M.
APPLICANT: House-Pompeo, Karen L.
APPLICANT: Speziale, Pietro

APPLICANT: Joh, Danny
APPLICANT: McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
TITLE OF INVENTION: AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAMK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 59:
SEQUENCE CHARACTERISTICS:
LENGTH: 36 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-09-010-317-59

Query Match 100.0%; Score 52; DB 4; Length 36;
Best Local Similarity 100.0%; Pred. No. 0.0091;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NOSFEEDTEK 10
Db 5 NOSFEEDTEK 14

RESULT 4

US-08-234-622A-3
Sequence 3, Application US/08234622A
Patent No. 5440014
GENERAL INFORMATION:
APPLICANT: HOOK, Magnus
APPLICANT: MCGAVIN, Martin
APPLICANT: RAUCCI, Giuseppe
TITLE OF INVENTION: A FIBRONECTIN BINDING PEPTIDE
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Burns, Doane, Swecker & Mathis
STREET: P.O. Box 1404
CITY: Alexandria
STATE: Virginia
COUNTRY: United States
ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/234,622A
FILING DATE: 28-APR-1994

CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: SE 9002617-0
FILING DATE: 10-AUG-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/SE91/00534
FILING DATE: 09-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: Meuth, Donna M
REGISTRATION NUMBER: 36,607
REFERENCE/DOCKET NUMBER: 012885-044
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-6620
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-234-622A-3

Query Match 100.0%; Score 52; DB 1; Length 38;
Best Local Similarity 100.0%; Pred. No. 0.0097;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NOSFEEDTEK 10
Db 5 NOSFEEDTEK 14

RESULT 5
US-08-729-767-4
Sequence 4, Application US/08729767
Patent No. 5770702
GENERAL INFORMATION:
APPLICANT: HOOK, Magnus
APPLICANT: LINDBERG, Martin Kjell
APPLICANT: SIGNS, Lars Christer
APPLICANT: MADSTROM, Torkel Mikael
APPLICANT: FROMAN, Gunnar
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN AS WELL AS
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Burns, Doane, Swecker & Mathis, L.L.P.
STREET: P. O. Box 1404
CITY: Alexandria
STATE: Virginia
COUNTRY: United States
ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/729,767
FILING DATE: 07-OCT-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/259,000
FILING DATE: 13-JUN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/007,817
FILING DATE: 22-JAN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/201,028
FILING DATE: 01-JUN-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: SE 8702272-9
FILING DATE: 01-JUN-1987

ATTORNEY/AGENT INFORMATION:
NAME: McGowan, Malcolm K.
REGISTRATION NUMBER: 39,300
REFERENCE/DOCKET NUMBER: 012889-036
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-729-767-4

Query Match 100.0%; Score 52; DB 1; Length 38;
Best Local Similarity 100.0%; Pred. No. 0.0097;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NOSFEEDTEK 10
Db 6 NOSFEEDTEK 15

RESULT 6
US-09-010-317-7
Sequence 7, Application US/09010317
Patent No. 6685943
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
APPLICANT: Patli, Joseph M.
APPLICANT: House-Pompeo, Karen L.
APPLICANT: Speziale, Pietro
APPLICANT: Joh, Danny
APPLICANT: McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P. O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hihler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAWK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-09-010-317-7

Query Match 100.0%; Score 52; DB 4; Length 38;
Best Local Similarity 100.0%; Pred. No. 0.0097;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NOSFEEDTEK 10
Db 5 NOSFEEDTEK 14

RESULT 7

US-09-010-317-8
; Sequence 8, Application US/09010317
; Patent No. 6685943
; GENERAL INFORMATION:
; APPLICANT: Hook, Magnus
; APPLICANT: Patti, Joseph M.
; APPLICANT: House-Pompeo, Karen L.
; APPLICANT: Speziale, Pietro
; APPLICANT: Joh, Danny
; APPLICANT: McGavin, Martin J.
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
; TITLE OF INVENTION: AND METHODS OF USE
; NUMBER OF SEQUENCES: 105
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: TX
; COUNTRY: USA
; ZIP: 77210-4433
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/010,317
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/036,139
; FILING DATE: 21-JAN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Hibler, David W.
; REGISTRATION NUMBER: 41,071
; REFERENCE/DOCKET NUMBER: TLMK:189
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 512-418-3000
; TELEFAX: 512-474-7577
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 38 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
US-09-010-317-8

Query Match 100.0%; Score 52; DB 4; Length 38;
Best Local Similarity 100.0%; Pred. No. 0.0097;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NOSFEEDTEK 10
Db 5 NOSFEEDTEK 14

RESULT 8

US-09-010-317-49
; Sequence 49, Application US/09010317
; Patent No. 6685943
; GENERAL INFORMATION:
; APPLICANT: Hook, Magnus
; APPLICANT: Patti, Joseph M.

; APPLICANT: House-Pompeo, Karen L.
; APPLICANT: Speziale, Pietro
; APPLICANT: Joh, Danny
; APPLICANT: McGavin, Martin J.
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
; TITLE OF INVENTION: AND METHODS OF USE
; NUMBER OF SEQUENCES: 105
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: TX
; COUNTRY: USA
; ZIP: 77210-4433
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/010,317
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/036,139
; FILING DATE: 21-JAN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Hibler, David W.
; REGISTRATION NUMBER: 41,071
; REFERENCE/DOCKET NUMBER: TLMK:189
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 512-418-3000
; TELEFAX: 512-474-7577
; INFORMATION FOR SEQ ID NO: 49:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 38 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
US-09-010-317-49

Query Match 100.0%; Score 52; DB 4; Length 38;
Best Local Similarity 100.0%; Pred. No. 0.0097;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NOSFEEDTEK 10
Db 5 NOSFEEDTEK 14

RESULT 9

US-08-259-000-3
; Sequence 3, Application US/08259000
; Patent No. 5571514
; GENERAL INFORMATION:
; APPLICANT: HOOK, Magnus
; APPLICANT: LINDBERG, Martin Kjell
; APPLICANT: SIGNAS, Lars Christer
; APPLICANT: MADSTROM, Torkel Mikael
; APPLICANT: FROMAN, Gunnar
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN AS WELL AS
; TITLE OF INVENTION: ITS PREPARATION
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Doane, Swecker & Mathis
; STREET: P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; SOFTWARE: IBM PC compatible

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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/259,000
FILING DATE: 13-JUN-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: SE 8702272-9
FILING DATE: 01-JUN-1987
ATTORNEY/AGENT INFORMATION:
NAME: Meluch, Donna M
REGISTRATION NUMBER: 36,607
REFERENCE/DOCKET NUMBER: 012895-062
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 114 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-259-000-3

Query Match      100.0%; Score 52; DB 1; Length 114;
Best Local Similarity 100.0%; Pred. No. 0.031;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 NOSFEEDTEK 10
DB      44 NOSFEEDTEK 53

RESULT 10
US-08-856-253-8
Sequence 8, Application US/08856253
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
APPLICANT: Patti, Joseph M.
APPLICANT: House-Pompeo, Karen
APPLICANT: Shanam, Narayana
APPLICANT: Symersky, Jindrich
TITLE OF INVENTION: COLLAGEN BINDING PROTEIN COMPOSITIONS
TITLE OF INVENTION: AND METHODS OF USE
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSES: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: Texas
COUNTRY: U.S.
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/856,253
FILING DATE: Concurrently Herewith
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/017,678
FILING DATE: 16-MAY-1996
ATTORNEY/AGENT INFORMATION:
NAME: Kitchell, Barbara S.
REGISTRATION NUMBER: 33,928
REFERENCE/DOCKET NUMBER: TANK:193
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
TELEFAX: (512) 474-7577
```

```
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 139 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-08-856-253-8

Query Match      100.0%; Score 52; DB 3; Length 139;
Best Local Similarity 100.0%; Pred. No. 0.038;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 NOSFEEDTEK 10
DB      58 NOSFEEDTEK 67

RESULT 11
US-08-956-171E-5251
Sequence 5251, Application US/08956171E
GENERAL INFORMATION:
APPLICANT: Charles Kunsch
APPLICANT: Gil H. Choi
APPLICANT: Patrick S. Dillon
APPLICANT: Craig A. Rosen
APPLICANT: Steven C. Barash
APPLICANT: Michael R. Fannon
TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
NUMBER OF SEQUENCES: 5256
CORRESPONDENCE ADDRESS:
ADDRESSES: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COUNTRY: USA
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/956,171E
FILING DATE: 20-Oct-1997
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/009,861
FILING DATE: January 5, 1996
APPLICATION NUMBER: 08/781,986
FILING DATE: January 3, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Mark J. Hyman
REGISTRATION NUMBER: 46,789
REFERENCE/DOCKET NUMBER: PB248P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (240) 314-1224
TELEFAX: (301) 309-8439
INFORMATION FOR SEQ ID NO: 5251:
SEQUENCE CHARACTERISTICS:
LENGTH: 559 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 5251:
US-08-956-171E-5251

Query Match      100.0%; Score 52; DB 4; Length 559;
Best Local Similarity 100.0%; Pred. No. 0.17;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 NOSFEEDTEK 10
```

Db |||||
343 NOSFEEDTEK 352

RESULT 12
US-08-781-986A-5251
; Sequence 5251, Application US/08781986A
; Patent No. 6737248
; GENERAL INFORMATION:
; APPLICANT: Charles Kunsch
; TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
; NUMBER OF SEQUENCES: 5255
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4mb storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/781,986A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Benson, Bob
; REGISTRATION NUMBER: 30,446
; REFERENCE/DOCKET NUMBER: PB248PP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 5251:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 559 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-781-986A-5251

Query Match 100.0%; Score 52; DB 4; Length 559;
Best Local Similarity 100.0%; Pred. No. 0.17;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NOSFEEDTEK 10
Db 343 NOSFEEDTEK 352

RESULT 13
US-08-956-171E-5254
; Sequence 5254, Application US/08956171E
; Patent No. 6593114
; GENERAL INFORMATION:
; APPLICANT: Charles Kunsch
; Gil H. Choi
; Patrick S. Dillon
; Craig A. Rosen
; Steven C. Barash
; Michael R. Pannou
; TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
; NUMBER OF SEQUENCES: 5256
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville

STATE: Maryland
COUNTRY: USA
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/956,171E
FILING DATE: 20-Oct-1997
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/009,861
FILING DATE: January 5, 1996
APPLICATION NUMBER: 08/781,986
FILING DATE: January 3, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Mark J. Hyman
REGISTRATION NUMBER: 46,789
REFERENCE/DOCKET NUMBER: PB248P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (240) 314-1224
TELEFAX: (301) 309-8439
INFORMATION FOR SEQ ID NO: 5254:
SEQUENCE CHARACTERISTICS:
LENGTH: 1027 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 5254:
US-08-956-171E-5254

Query Match 100.0%; Score 52; DB 4; Length 1027;
Best Local Similarity 100.0%; Pred. No. 0.32;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NOSFEEDTEK 10
Db 797 NOSFEEDTEK 806

RESULT 14
US-08-781-986A-5254
; Sequence 5254, Application US/08781986A
; Patent No. 6737248
; GENERAL INFORMATION:
; APPLICANT: Charles Kunsch
; TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
; NUMBER OF SEQUENCES: 5255
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4mb storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/781,986A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Benson, Bob
; REGISTRATION NUMBER: 30,446

REFERENCE/DOCKET NUMBER: PB248PP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 5254:
SEQUENCE CHARACTERISTICS:
LENGTH: 1027 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-781-986A-5254

Query Match 100.0%; Score 52; DB 4; Length 1027;
Best Local Similarity 100.0%; Pred. No. 0.32;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NOSFEEDTEK 10
Db 797 NOSFEEDTEK 806

RESULT 15

US-09-010-317-65
Sequence 65, Application US/09010317
Patent No. 6685943
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
APPLICANT: Patti, Joseph M.
APPLICANT: House-Pompeo, Karen, L.
APPLICANT: Speziale, Pietro
APPLICANT: Joh, Danny
APPLICANT: McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
NUMBER OF SEQUENCES: 105
TITLE OF INVENTION: AND METHODS OF USE
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hblber, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TANK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 65:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-09-010-317-65

Query Match 92.3%; Score 48; DB 4; Length 10;
Best Local Similarity 90.0%; Pred. No. 0.012;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 NOSFEEDTEK 10
Db 1 NOSFEEDTEK 10

Search completed: October 22, 2005, 07:41:47
Job time : 18.35 secs

510
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 22, 2005, 12:09:40 ; Search time 57.25 Seconds
(without alignments)
72.924 Million cell updates/sec

Title: US-10-731-238-84
Perfect score: 52
Sequence: 1 NQSFEDTEK 10

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 1862951 seqs, 417491010 residues

Total number of hits satisfying chosen parameters: 1862951

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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20: /cgn2_6/prodata/2/pubppa/US11_NEW PUB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	52	100.0	10	US-10-731-238-84	Sequence 84, Appl
2	52	100.0	30	US-10-287-821-1	Sequence 1, Appl
3	52	100.0	31	US-10-287-821-2	Sequence 2, Appl
4	52	100.0	36	US-10-731-238-58	Sequence 58, Appl
5	52	100.0	36	US-10-731-238-59	Sequence 59, Appl
6	52	100.0	38	US-10-731-238-7	Sequence 7, Appl
7	52	100.0	38	US-10-731-238-8	Sequence 8, Appl
8	52	100.0	38	US-10-731-238-49	Sequence 49, Appl
9	52	100.0	139	US-09-813-820-8	Sequence 8, Appl
10	52	100.0	388	US-08-901-062-1	Sequence 1, Appl
11	52	100.0	559	US-08-781-986A-5251	Sequence 5251, Ap

12	52	100.0	559	US-10-329-624-5251	Sequence 5251, Ap
13	52	100.0	767	US-09-815-242-5899	Sequence 5899, Ap
14	52	100.0	767	US-09-815-242-13140	Sequence 13140, A
15	52	100.0	940	US-10-470-048B-424	Sequence 424, App
16	52	100.0	948	US-10-470-048B-69	Sequence 69, Appl
17	52	100.0	978	US-09-815-242-5456	Sequence 5456, Ap
18	52	100.0	1001	US-09-815-242-12686	Sequence 12686, A
19	52	100.0	1018	US-09-815-242-5797	Sequence 5797, Ap
20	52	100.0	1018	US-09-815-242-12838	Sequence 12838, A
21	52	100.0	1027	US-10-470-048B-68	Sequence 68, Appl
22	52	100.0	1027	US-08-781-986A-5254	Sequence 5254, Ap
23	52	100.0	1027	US-10-329-624-5254	Sequence 5254, Ap
24	48	92.3	1027	US-10-731-238-65	Sequence 5, Appl
25	48	92.3	38	US-10-731-238-5	Sequence 6, Appl
26	48	92.3	38	US-10-731-238-6	Sequence 42, Appl
27	48	92.3	38	US-10-731-238-42	Sequence 43, Appl
28	48	92.3	38	US-10-731-238-43	Sequence 56, Appl
29	48	92.3	39	US-10-731-238-56	Sequence 57, Appl
30	48	92.3	39	US-10-731-238-57	Sequence 43778, A
31	48	92.3	961	US-10-282-122A-43778	Sequence 43827, A
32	48	92.3	1028	US-10-282-122A-43827	Sequence 41, Appl
33	47	90.4	38	US-10-731-238-41	Sequence 46, Appl
34	46	88.5	38	US-10-731-238-46	Sequence 47, Appl
35	46	88.5	38	US-10-731-238-47	Sequence 48, Appl
36	45	86.5	38	US-10-731-238-64	Sequence 64, Appl
37	42	80.8	10	US-10-731-238-64	Sequence 83, Appl
38	42	80.8	18	US-10-731-238-83	Sequence 36, Appl
39	42	80.8	38	US-10-731-238-36	Sequence 37, Appl
40	42	80.8	38	US-10-731-238-37	Sequence 39, Appl
41	42	80.8	38	US-10-731-238-39	Sequence 40, Appl
42	42	80.8	38	US-10-731-238-40	Sequence 45, Appl
43	42	80.8	38	US-10-731-238-45	Sequence 85, Appl
44	41	78.8	10	US-10-731-238-85	Sequence 62, Appl
45	41	78.8	12	US-10-731-238-62	

ALIGNMENTS

RESULT 1
US-10-731-238-84
; Sequence 84, Application US/10731238
; Publication No. US0050123552A1
; GENERAL INFORMATION:
; APPLICANT: Hook, Magnus
; Patli, Joseph M.
; House-Pompeo, Karen L.
; Speziale, Pietro
; John, Danny
; McGavin, Martin J.
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
; AND METHODS OF USE
; NUMBER OF SEQUENCES: 105
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: TX
; COUNTRY: USA
; ZIP: 77210-4433
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/731, 238
; FILING DATE: 10-Dec-2003
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/010, 317
; FILING DATE: 21-Jan-1998
; APPLICATION NUMBER: US 60/036, 139

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; FILING DATE: 21-JAN-1997
; ATTORNEY/AGENT INFORMATION:
;   NAME: Hibler, David W.
;   REGISTRATION NUMBER: 41,071
;   REFERENCE/DOCKET NUMBER: TMMK:189
; TELECOMMUNICATION INFORMATION:
;   TELEPHONE: 512-418-3000
;   TELEFAX: 512-474-7577
; INFORMATION FOR SEQ ID NO: 84:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH: 10 amino acids
;     TYPE: amino acid
;     STRANDEDNESS: <Unknown>
;     TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 84:
US-10-731-238-84

Query Match          100.0%; Score 52; DB 18; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.015;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NOSFEEDTEK 10
Db 1 NOSFEEDTEK 10

RESULT 2
US-10-287-821-1
; Sequence 1, Application US/10287821
; Publication No. US20030153022A1
; GENERAL INFORMATION:
; APPLICANT: PATTI, Joseph M.
; TITLE OF INVENTION: MONOCLONAL ANTIBODIES TO THE FIBRONECTIN BINDING PROTEIN.
; FILE REFERENCE: P07427US01/BAS
; CURRENT APPLICATION NUMBER: US/10/287,821
; PRIOR FILING DATE: 2002-11-05
; PRIOR APPLICATION NUMBER: 60/330,964
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 30
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-10-287-821-1

Query Match          100.0%; Score 52; DB 14; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.047;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NOSFEEDTEK 10
Db 6 NOSFEEDTEK 15

RESULT 3
US-10-287-821-2
; Sequence 2, Application US/10287821
; Publication No. US20030153022A1
; GENERAL INFORMATION:
; APPLICANT: PATTI, Joseph M.
; TITLE OF INVENTION: MONOCLONAL ANTIBODIES TO THE FIBRONECTIN BINDING PROTEIN.
; FILE REFERENCE: P07427US01/BAS
; CURRENT APPLICATION NUMBER: US/10/287,821
; PRIOR FILING DATE: 2002-11-05
; PRIOR APPLICATION NUMBER: 60/330,964
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 31
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
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US-10-287-821-2

Query Match          100.0%; Score 52; DB 14; Length 31;
Best Local Similarity 100.0%; Pred. No. 0.049;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NOSFEEDTEK 10
Db 7 NOSFEEDTEK 16

RESULT 4
US-10-731-238-58
; Sequence 58, Application US/10731238
; Publication No. US20050123552A1
; GENERAL INFORMATION:
; APPLICANT: Hook, Magnus
;   Patti, Joseph M.
;   House-Pompeo, Karen L.
;   Speziale, Pietro
;   Joh, Danny
;   McGavin, Martin J.
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
; AND METHODS OF USE
; NUMBER OF SEQUENCES: 105
; CORRESPONDENCE ADDRESSES:
; ADDRESSER: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: TX
; COUNTRY: USA
; ZIP: 77210-4433
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/731,238
; FILING DATE: 10-Dec-2003
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/010,317
; FILING DATE: 21-Jan-1998
; APPLICATION NUMBER: US 60/036,139
; FILING DATE: 21-JAN-1997
; ATTORNEY/AGENT INFORMATION:
;   NAME: Hibler, David W.
;   REGISTRATION NUMBER: 41,071
;   REFERENCE/DOCKET NUMBER: TMMK:189
; TELECOMMUNICATION INFORMATION:
;   TELEPHONE: 512-418-3000
;   TELEFAX: 512-474-7577
; INFORMATION FOR SEQ ID NO: 58:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH: 36 amino acids
;     TYPE: amino acid
;     STRANDEDNESS: <Unknown>
;     TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 58:
US-10-731-238-58

Query Match          100.0%; Score 52; DB 18; Length 36;
Best Local Similarity 100.0%; Pred. No. 0.058;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NOSFEEDTEK 10
Db 5 NOSFEEDTEK 14

RESULT 5
US-10-731-238-59
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Sequence 59, Application US/10731238
Publication No. US20050123552A1
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
Patti, Joseph M.
House-Pompeo, Karen L.
Speziale, Pietro
Joh, Danny
McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/731,238
FILING DATE: 10-Dec-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE: 21-Jan-1998
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAWK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 59:
SEQUENCE CHARACTERISTICS:
LENGTH: 36 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 59:
US-10-731-238-59
Query Match 100.0%; Score 52; DB 18; Length 36;
Best Local Similarity 100.0%; Pred. No. 0.058;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 NOSFEEDTEK 10
|||||
Db 5 NOSFEEDTEK 14
RESULT 6
US-10-731-238-7
Sequence 7, Application US/10731238
Publication No. US20050123552A1
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
Patti, Joseph M.
House-Pompeo, Karen L.
Speziale, Pietro
Joh, Danny
McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
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ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/731,238
FILING DATE: 10-Dec-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE: 21-Jan-1998
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAWK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-10-731-238-7
Query Match 100.0%; Score 52; DB 18; Length 38;
Best Local Similarity 100.0%; Pred. No. 0.061;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 NOSFEEDTEK 10
|||||
Db 5 NOSFEEDTEK 14
RESULT 7
US-10-731-238-8
Sequence 8, Application US/10731238
Publication No. US20050123552A1
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
Patti, Joseph M.
House-Pompeo, Karen L.
Speziale, Pietro
Joh, Danny
McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/731,238
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FILED DATE: 10-Dec-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE: 21-Jan-1998
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-Jan-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-10-731-238-8

Query Match 100.0%; Score 52; DB 18; Length 38;
Best Local Similarity 100.0%; Pred. No. 0.061;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NOSFEEDTEK 10
DB 5 NOSFEEDTEK 14

RESULT 8
US-10-731-238-49
Sequence 49; Application US/10731238
Publication No. US20050123552A1
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
Pactl, Joseph M.
House-Pompeo, Karen L.
Speziale, Pietro
John, Danny
McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/731,238
FILING DATE: 10-Dec-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE: 21-Jan-1998
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-Jan-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000

TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 49:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 49:
US-10-731-238-49

Query Match 100.0%; Score 52; DB 18; Length 38;
Best Local Similarity 100.0%; Pred. No. 0.061;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NOSFEEDTEK 10
DB 5 NOSFEEDTEK 14

RESULT 9
US-09-813-820-8
Sequence 8; Application US/09813820
Patent No. US20020102262A1
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
Pactl, Joseph M.
House-Pompeo, Karen
Sthanam, Narayana
Symerky, Jindrich
TITLE OF INVENTION: COLLAGEN BINDING PROTEIN COMPOSITIONS
AND METHODS OF USE
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: Texas
COUNTRY: U.S.
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/813,820
FILING DATE: 22-Mar-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/856,253
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Kitchell, Barbara S.
REGISTRATION NUMBER: 33,928
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
TELEFAX: (512) 474-7577
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 139 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-09-813-820-8

Query Match 100.0%; Score 52; DB 9; Length 139;
Best Local Similarity 100.0%; Pred. No. 0.24;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NOSFEEDTEK 10
DB 5 NOSFEEDTEK 14

Db 58 NOSFEEDTEK 67

RESULT 10

US-08-901-062-1

Sequence 1, Application US/08901062

Publication No. US20020025324A1

GENERAL INFORMATION:

APPLICANT: SEALS, JONATHAN R.

TITLE OF INVENTION: RECOMBINANT BIVALENT BACTERIAL VACCINE

TITLE OF INVENTION: FOR THE PREVENTION OF MASTITIS

NUMBER OF SEQUENCES: 2

CORRESPONDENCE ADDRESS:

ADDRESSEE: HALB AND DORR LLP

STREET: 60 State Street

CITY: Boston

STATE: MA

COUNTRY: United States Of America

ZIP: 02109

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/901,062

FILING DATE: 25-JUL-1997

CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:

NAME: Baker, Hollie L.

REGISTRATION NUMBER: 31,321

REFERENCE/DOCKET NUMBER: 106941.153

TELECOMMUNICATION INFORMATION:

TELEPHONE: (617) 526-6000

TELEFAX: (617) 526-5000

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 388 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

HYPOTHETICAL: NO

ANTI-SENSE: NO

US-08-901-062-1

Query Match 100.0%; Score 52; DB 8; Length 388;

Best Local Similarity 100.0%; Pred. No. 0.73;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NOSFEEDTEK 10

Db 307 NOSFEEDTEK 316

RESULT 11

US-08-781-986A-5251

Sequence 5251, Application US/08781986A

Publication No. US20030054436A1

GENERAL INFORMATION:

APPLICANT: Charles Kunach

TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences

NUMBER OF SEQUENCES: 5255

CORRESPONDENCE ADDRESS:

ADDRESSEE: Human Genome Sciences, Inc.

STREET: 9410 Key West Avenue

CITY: Rockville

STATE: Maryland

COUNTRY: USA

ZIP: 20850

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.50 inch, 1.4mb storage

COMPUTER: HP Vectra 486/33

OPERATING SYSTEM: MSDOS version 6.2

SOFTWARE: ASCII Text

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/781,986A

FILING DATE:

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Benson, Bob

REGISTRATION NUMBER: 30,446

REFERENCE/DOCKET NUMBER: PB248PP

TELECOMMUNICATION INFORMATION:

TELEPHONE: (301) 309-8504

TELEFAX: (301) 309-8512

INFORMATION FOR SEQ ID NO: 5251:

SEQUENCE CHARACTERISTICS:

LENGTH: 559 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-781-986A-5251

Query Match 100.0%; Score 52; DB 8; Length 559;

Best Local Similarity 100.0%; Pred. No. 1.1;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NOSFEEDTEK 10

Db 343 NOSFEEDTEK 352

RESULT 12

US-10-329-624-5251

Sequence 5251, Application US/10329624

Publication No. US20040045037A1

GENERAL INFORMATION:

APPLICANT: Charles Kunach

Gil H. Choi

Patrick S. Dillon

Craig A. Rosen

Steven C. Barash

Michael R. Fannon

TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences

NUMBER OF SEQUENCES: 5256

CORRESPONDENCE ADDRESS:

ADDRESSEE: Human Genome Sciences, Inc.

STREET: 9410 Key West Avenue

CITY: Rockville

STATE: Maryland

COUNTRY: USA

ZIP: 20850

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.50 inch, 1.4mb storage

COMPUTER: HP Vectra 486/33

OPERATING SYSTEM: MSDOS version 6.2

SOFTWARE: ASCII Text

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/329,624

FILING DATE: 27-Dec-2002

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/956,171

FILING DATE: October 20, 1997

APPLICATION NUMBER: 60/009,861

FILING DATE: January 5, 1996

APPLICATION NUMBER: 08/781,986

FILING DATE: January 3, 1997

ATTORNEY/AGENT INFORMATION:

NAME: Mark J. Hyman

REGISTRATION NUMBER: 46,789

REFERENCE/DOCKET NUMBER: PB248P1D1

```
TELECOMMUNICATION INFORMATION:
TELEPHONE: (240) 314-11224
TELEFAX: (301) 309-8439
INFORMATION FOR SEQ ID NO: 5251:
SEQUENCE CHARACTERISTICS:
LENGTH: 559 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 5251:
US-10-329-624-5251
```

```
Query Match          100.0%; Score 52; DB 15; Length 559;
Best Local Similarity 100.0%; Pred. No. 1.1;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
QY      1 NOSFEEDTEK 10
        |||||
Db       343 NOSFEEDTEK 352
```

```
RESULT 13
US-09-815-242-5899
Sequence 5899, Application US/09815242
Patent No. US20020061569A1
GENERAL INFORMATION:
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Karl L.
APPLICANT: Zyskind, Judith W.
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John D.
APPLICANT: Carr, Grant J.
APPLICANT: Yamamoto, Robert T.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in
FILE REFERENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 5899
LENGTH: 767
TYPE: PRT
ORGANISM: Staphylococcus aureus
US-09-815-242-5899
```

```
Query Match          100.0%; Score 52; DB 9; Length 767;
Best Local Similarity 100.0%; Pred. No. 1.5;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 NOSFEEDTEK 10
        |||||
Db       724 NOSFEEDTEK 733
```

```
RESULT 14
US-09-815-242-13140
```

```
Sequence 13140, Application US/09815242
Patent No. US20020061569A1
GENERAL INFORMATION:
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Karl L.
APPLICANT: Zyskind, Judith W.
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John D.
APPLICANT: Carr, Grant J.
APPLICANT: Yamamoto, Robert T.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in
FILE REFERENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 13140
LENGTH: 767
TYPE: PRT
ORGANISM: Staphylococcus aureus
US-09-815-242-13140
```

```
Query Match          100.0%; Score 52; DB 9; Length 767;
Best Local Similarity 100.0%; Pred. No. 1.5;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 NOSFEEDTEK 10
        |||||
Db       724 NOSFEEDTEK 733
```

```
RESULT 15
US-10-470-048B-424
Sequence 424, Application US/10470048B
Publication No. US2005003744A1
GENERAL INFORMATION:
APPLICANT: MEINKE ET AL.
TITLE OF INVENTION: A METHOD FOR IDENTIFICATION, ISOLATION AND PRODUCTION OF
FILE REFERENCE: SONN.035US
CURRENT APPLICATION NUMBER: US/10/470,048B
CURRENT FILING DATE: 2003-07-25
NUMBER OF SEQ ID NOS: 603
SOFTWARE: PatentIn version 3.1
SEQ ID NO 424
LENGTH: 940
TYPE: PRT
ORGANISM: Staphylococcus aureus
US-10-470-048B-424
```

```
Query Match          100.0%; Score 52; DB 17; Length 940;
Best Local Similarity 100.0%; Pred. No. 1.9;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 NOSFEEDTEK 10
        |||||
Db       724 NOSFEEDTEK 733
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Wed Oct 26 15:03:09 2005

us-10-731-238-84.rapb

Page 7

Search completed: October 22, 2005, 12:39:50
Job time : 57.25 secs

This Page Blank (uspto)

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 22, 2005, 06:10:10 ; Search time 11.45 Seconds

(without alignments)
84.032 Million cell updates/sec

Title: US-10-731-238-84

Perfect score: 52

Sequence: 1 NQSFEDPTK 10

Scoring table: BIOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR 79:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	52	100.0	940 2 S19702	fibronectin-binding protein B - Staphylococcus aureus
2	52	100.0	1018 2 A32192	fibronectin-binding protein B - Staphylococcus aureus
3	48	92.3	961 2 G90053	hypothetical prote
4	48	92.3	1038 2 H90053	hypothetical prote
5	39	75.0	429 2 G64642	hypothetical prote
6	38	73.1	457 2 T26642	hypothetical prote
7	37	71.2	705 2 S54521	probable membrane
8	37	71.2	5255 2 T31677	bactera-like protein
9	36	69.2	324 2 B96742	hypothetical prote
10	36	69.2	429 2 G71937	canavalin - jack b
11	36	69.2	445 2 JQ2264	canavalin - sword
12	36	69.2	445 2 S00281	ALG2 protein precu
13	36	69.2	503 2 S64069	1-phosphatidylinos
14	36	69.2	1093 2 T18275	conserved hypotet
15	35	67.3	288 2 G90556	hypothetical prote
16	35	67.3	319 2 E70091	transcription regu
17	35	67.3	321 2 T22961	conserved hypotet
18	35	67.3	509 2 D95053	hypothetical prote
19	35	67.3	521 2 B69222	hypothetical prote
20	35	67.3	648 2 T20358	hypothetical prote
21	35	67.3	670 2 T06742	hypothetical prote
22	35	67.3	943 2 T33795	hypothetical prote
23	35	67.3	1052 2 T37133	hypothetical prote
24	34	65.4	219 2 F71710	hypothetical prote
25	34	65.4	222 2 G97704	hypothetical prote
26	34	65.4	382 2 A82173	probable ABC trans
27	34	65.4	685 2 T40162	transketolase - fi
28	34	65.4	1152 2 S20106	hypothetical prote
29	34	65.4	1514 2 S70099	hypothetical prote

30	34	65.4	2168 2 D88131	protein F10G7.10 (
31	33	63.5	144 1 JQ0088	phosphotransferase
32	33	63.5	159 2 AG1796	hypothetical prote
33	33	63.5	167 2 S37843	glutathione peroxi
34	33	63.5	170 2 I49055	bcl-x short - mous
35	33	63.5	176 2 I67435	gene bcl-xshort pr
36	33	63.5	349 2 D69856	conserved hypotet
37	33	63.5	539 2 T02508	hypothetical prote
38	33	63.5	633 2 T05883	ATP-dependent heli
39	33	63.5	665 2 AG1117	transketolase homo
40	33	63.5	665 2 A11477	transketolase homo
41	33	63.5	756 2 S43085	DNA mismatch repai
42	33	63.5	799 2 C86287	F9L1.24 protein -
43	33	63.5	944 2 G86720	translation initia
44	33	63.5	1066 2 S72479	Nuc-2 protein - Ne
45	33	63.5	1259 2 T32901	hypothetical prote

ALIGNMENTS

RESULT 1

S19702

fibronectin-binding protein B - Staphylococcus aureus

C:Species: Staphylococcus aureus

C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004

C:Accession: S19702

R:Joensson, K.; Signaes, C.; Mueller, H.P.; Lindberg, M.

Eur. J. Biochem. 202, 1041-1048, 1991

A:Title: Two different genes encode fibronectin binding proteins in Staphylococcus aure

A:Reference number: S19702; MUID:92111475; PMID:1837266

A:Accession: S19702

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-940 <JOB>

A:Cross-references: UNIPROT:Q53682; EMBL:X62992; NID:G49040; PIDN:CAA44726.1; PID:G5815

C:Keywords: fibronectin binding

Query Match

Best Local Similarity 100.0%; Score 52; DB 2; Length 940;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NQSFEDPTK 10

DB 724 NQSFEDPTK 733

RESULT 2

A32192

fibronectin-binding protein - Staphylococcus aureus

C:Species: Staphylococcus aureus

C:Date: 31-Jul-1989 #sequence_revision 31-Jul-1989 #text_change 16-Feb-1997

C:Accession: A32192

R:Signaes, C.; Raucel, G.; Joensson, K.; Lindgren, P.E.; Anantharamiah, G.M.; Hoecek,

Proc. Natl. Acad. Sci. U.S.A. 86, 699-703, 1989

A:Title: Nucleotide sequence of the gene for a fibronectin-binding protein from Staphyl

A:Reference number: A32192; MUID:89098998; PMID:2521391

A:Accession: A32192

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-1018 <SIG>

A:Cross-references: GB:J04151

C:Keywords: fibronectin binding

Query Match

Best Local Similarity 100.0%; Score 52; DB 2; Length 1018;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NQSFEDPTK 10

DB 788 NQSFEDPTK 797

```
RESULT 3
G90053
hypothetical protein fnbB [imported] - Staphylococcus aureus (strain N315)
C/Species: Staphylococcus aureus
C/Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C/Accession: G90053
R/Kuroda, M.; Ohba, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.;
Lancet 357, 1225-1240, 2001
A/Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.
A/Reference number: A89758; PMID:21311952; PMID:11418146
A/Accession: G90053
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-961 <KUR>
A/Cross-references: UNIPROT:Q99RD3; GB:BA000018; PID:g13702452; PIDN:BAB43593.1; GSPDB:G
A/Experimental source: strain N315
C/Genetics:
A/Gene: fnbB

Query Match          92.3%; Score 48; DB 2; Length 961;
Best Local Similarity 90.0%; Pred. No. 0.79;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 NOSFEEDTEK 10
Db 697 NOSFEEDTEE 706

RESULT 4
H90053
hypothetical protein fnb [imported] - Staphylococcus aureus (strain N315)
C/Species: Staphylococcus aureus
C/Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C/Accession: H90053
R/Kuroda, M.; Ohba, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.;
C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
A/Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.
A/Reference number: A89758; PMID:21311952; PMID:11418146
A/Accession: H90053
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-1038 <KUR>
A/Cross-references: UNIPROT:Q99RD2; GB:BA000018; PID:g13702453; PIDN:BAB43594.1; GSPDB:G
A/Experimental source: strain N315
C/Genetics:
A/Gene: fnbB

Query Match          92.3%; Score 48; DB 2; Length 1038;
Best Local Similarity 90.0%; Pred. No. 0.86;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 NOSFEEDTEK 10
Db 746 NOSFEEDTEE 755

RESULT 5
G64649
hypothetical protein HP1039 - Helicobacter pylori (strain 26695)
C/Species: Helicobacter pylori
C/Date: 09-Aug-1997 #sequence_revision 09-Aug-1997 #text_change 09-Jul-2004
C/Accession: G64649
R/Tomb, J.F.; White, O.; Kesteven, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.D.;
Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khaliq, H.G.; Glodek, A.; McKenna,
son, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Wathey, L.;
Nature 388, 539-547, 1997
A/Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser, C.;
A/Title: The complete genome sequence of the gastric pathogen Helicobacter pylori.
A/Reference number: A64520; PMID:97394467; PMID:9252185

A/Accession: G64649
A/Status: preliminary; nucleic acid sequence not shown; translation not shown
A/Molecule type: DNA
A/Residues: 1-429 <TOM>
A/Cross-references: UNIPROT:Q25682; GB:AE000611; GB:AE000511; NID:g2314173; PIDN:AMD080
C/Genetics:
A/Start codon: GTG

Query Match          75.0%; Score 39; DB 2; Length 429;
Best Local Similarity 70.0%; Pred. No. 16;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 NOSFEEDTEK 10
Db 270 NOSFEEDLKR 279

RESULT 6
T26642
hypothetical protein Y37D8A.22 - Caenorhabditis elegans
C/Species: Caenorhabditis elegans
C/Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C/Accession: T26642
R/Bartlow, K.
submitted to the EMBL Data Library, October 1998
A/Reference number: Z20247
A/Accession: T26642
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-457 <WIL>
A/Cross-references: UNIPROT:Q9XWU8; EMBL:AL032626; PIDN:CAA21543.1; CESP:Y37D8A.22
A/Experimental source: clone Y37D8A
C/Genetics:
A/Gene: CESP:Y37D8A.22
A/Introns: 59/3; 220/2; 363/3; 385/3; 418/3

Query Match          73.1%; Score 38; DB 2; Length 457;
Best Local Similarity 70.0%; Pred. No. 25;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 NOSFEEDTEK 10
Db 425 NOSFEEDTEE 434

RESULT 7
S54521
probable membrane protein YMR163c - yeast (Saccharomyces cerevisiae)
N/Alternate names: hypothetical protein YM6520.12c
C/Species: Saccharomyces cerevisiae
C/Date: 08-Jul-1995 #sequence_revision 01-Sep-1995 #text_change 09-Jul-2004
C/Accession: S54521; S54608
R/Hunt, S.; Bowman, S.
submitted to the EMBL Data Library, May 1995
A/Reference number: S54510
A/Accession: S54521
A/Molecule type: DNA
A/Residues: 1-705 <HUN>
A/Cross-references: UNIPROT:Q03824; GB:Z49705; EMBL:Z49700; NID:g825556; PID:g825568; E
A/Experimental source: strain AB972
C/Genetics:
A/Gene: MIPS:YMR163c
A/Cross-references: SGD:S0004773
A/Map position: 13R
C/Superfamily: Saccharomyces cerevisiae probable membrane protein YMR163c
C/Keywords: transmembrane protein
F/215-231/Domain: transmembrane #status predicted <TM1>
F/415-431/Domain: transmembrane #status predicted <TM2>

Query Match          71.2%; Score 37; DB 2; Length 705;
Best Local Similarity 71.8%; Pred. No. 62;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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Qy 1 NOSFEEDTE 9
Db 569 NOSFEEDTE 577

RESULT 8

TJ1677
bactlactacin synthetase 1 - Bacillus licheniformis
C:Species: Bacillus licheniformis
C:Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
C:Accession: TJ1677
R:Kornz, D.; Klenz, A.; Schorgendorfer, K.; Marthiel, M.A.
Chem. Biol. 4, 927-937, 1997
A:Title: The bactlactacin biosynthesis operon of Bacillus licheniformis ATCC 10716: molecu
A:Reference number: 221058; MUID:98089193; PMID:9427658
A:Accession: TJ1677
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-5255 <KON>
A:Cross-references: UNIPROT:O68006; EMBL:AF007865; NID:G4464275; PID:G2982194; PIDN:AACQ
C:Genetics:
A:Gene: bach
C:Keywords: carrier protein
F:83-524/Domain: acetate-CoA ligase homology <ACLI>
F:542-610/Domain: acyl carrier protein homology <ACP1>
F:1134-1561/Domain: acetate-CoA ligase homology <ACLI2>
F:1583-1651/Domain: acyl carrier protein homology <ACP2>
F:2171-2601/Domain: acetate-CoA ligase homology <ACLI3>
F:2619-2687/Domain: acyl carrier protein homology <ACP3>
F:3195-3642/Domain: acetate-CoA ligase homology <ACLI4>
F:3662-3729/Domain: acyl carrier protein homology <ACP4>
F:4712-5151/Domain: acetate-CoA ligase homology <ACLI5>
F:5169-5237/Domain: acyl carrier protein homology <ACP5>

Query Match 71.2%; Score 37; DB 2; Length 5255;
Best Local Similarity 70.0%; Pred. No. 5.3e+02;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NOSFEEDTEK 10
Db 4157 NOSFEEDTEK 4166

RESULT 9
B96742
NAM-like protein, 48543-50167 [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C:Accession: B96742
R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
Chin, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luoro, J.S.; Maiti, R.; Marziani,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A:Authors: Salberg, S.L.; Schwartz, J.R.; Shim, P.; Southwick, A.M.; Sun, H.; Tallon,
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A:Reference number: A86141; MUID:21016719; PMID:11130712
A:Accession: B96742
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-324 <STO>
A:Cross-references: UNIPROT:Q9C8W9; GB:AE005173; NID:G6578918; PIDN:AAF4310.1; GSPDB:GN
A:Gene: F17M19.8
A:Map position: 1

Query Match 69.2%; Score 36; DB 2; Length 324;
Best Local Similarity 60.0%; Pred. No. 41;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NOSFEEDTEK 10
Db 251 NESFEDEEEK 260

RESULT 10

G71997
hypothetical protein jhp0385 - Helicobacter pylori (strain J99)
C:Species: Helicobacter pylori
A:Variety: strain J99
C:Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 09-Jul-2004
C:Accession: G71997
R:Alm, R.A.; Ling, L.S.L.; Moir, D.T.; King, B.L.; Brown, E.D.; Doig, P.C.; Smith, D.R.
; Ives, C.; Gibson, R.; Merberg, D.; Mills, S.D.; Jiang, Q.; Taylor, D.E.; Vovis, G.F.;
Nature 397, 176-180, 1999
A:Title: Genomic sequence comparison of two unrelated isolates of the human gastric pat
A:Reference number: A71800; MUID:99120557; PMID:99233682
A:Accession: G71997
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-429 <ARN>
A:Cross-references: UNIPROT:Q9ZM38; GB:AE001473; GB:AE001439; NID:G4154910; PIDN:AAD059
A:Experimental source: strain J99
C:Genetics:
A:Gene: jhp0385

Query Match 69.2%; Score 36; DB 2; Length 429;
Best Local Similarity 60.0%; Pred. No. 56;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NOSFEEDTEK 10
Db 265 NQFEEDLKR 274

RESULT 11
J02264
canavalin - jack bean
C:Species: Canavalia ensiformis (jack bean)
C:Date: 28-Aug-1985 #sequence_revision 07-Oct-1994 #text_change 09-Jul-2004
C:Accession: J02264; S19137
R:Ng, J.D.; Ko, T.P.; McPherson, A.
Plant Physiol. 101, 713-728, 1993
A:Title: Cloning, expression, and crystallization of jack bean (Canavalia ensiformis) c
A:Reference number: J02264; MUID:94143475; PMID:8310055
A:Accession: J02264
A:Molecule type: mRNA
A:Residues: 1-445 <NGJ1>
A:Cross-references: UNIPROT:P50477; GB:X59467; GB:S76871; NID:G17976; PIDN:CAA42075.1;
A:Experimental source: seed
R:Ng, J.D.; Stinchcombe, T.; Ko, T.P.; Alexander, E.; McPherson, A.
Plant Mol. Biol. 18, 147-149, 1992
A:Title: PCR cloning of the full-length cDNA for the seed protein canavalin from the ja
A:Reference number: S19137; MUID:92119225; PMID:1731967
A:Accession: S19137
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-445 <NGJ2>
A:Cross-references: EMBL:X59467; NID:G17976; PIDN:CAA42075.1; PID:G17977
C:Superfamily: glycinin
C:Keywords: storage protein

Query Match 69.2%; Score 36; DB 2; Length 445;
Best Local Similarity 77.8%; Pred. No. 58;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 OSFEEDTEK 10
Db 71 QRFNEDTEK 79

RESULT 12
S00281

Canavalia - sword bean
C:Species: Canavalia gladiata (sword bean)
C:Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 09-Jul-2004
C:Accession: S00281; S04598
R:Yamachi, D.; Nakamura, K.; Asahi, T.; Minamikawa, T.
Eur. J. Biochem. 170, 515-520, 1988
A:Title: cDNAs for canavalia and canavalia A from Canavalia gladiata seeds. Nucleotide
S.
A:Reference number: S00281; MUID:88111636; PMID:3338449
A:Accession: S00281
A:Molecule type: mRNA
A:Residues: 1-445 <YAM>
A:Cross-references: UNIPROT:P10562; EMBL:X06733; NID:G18003; PIDN:CAA29910.1; PID:G18004
R:Takei, Y.; Yamachi, D.; Minamikawa, T.
Nucleic Acids Res. 17, 4381, 1989
A:Title: Nucleotide sequence of the canavalia gene from Canavalia gladiata seeds.
A:Reference number: S04598; MUID:88296493; PMID:2740227
A:Accession: S04598
A:Molecule type: DNA
A:Residues: 1-160, 'K', 162-445 <TAK>
A:Cross-references: EMBL:X15076; NID:G18006; PIDN:CAA33172.1; PID:G18007
C:Genetics:
A:Introns: 115/1, 173/3; 200/3; 290/3; 381/1
C:Superfamily: glycinnin
C:Keywords: seed

Query Match 69.2%; Score 36; DB 2; Length 445;
Best Local Similarity 77.8%; Pred. No. 58;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 QSFEDTEK 10
DB 71 QRFNEDTEK 79

RESULT 13
S64069
ALG2 protein precursor - yeast (Saccharomyces cerevisiae)
N:Alternate names: protein G3409; protein YGL065C
C:Species: Saccharomyces cerevisiae
C:Date: 17-May-1996 #sequence_revision 17-May-1996 #text_change 09-Jul-2004
C:Accession: S64069; S64072; S59763
R:Feuerhahn, M.; Potier, S.; Souciet, J.L.
Submitted to the Protein Sequence Database, May 1996
A:Reference number: S64069
A:Accession: S64069
A:Molecule type: DNA
A:Residues: 1-503 <FRU>
A:Cross-references: UNIPROT:P43636; EMBL:Z72587; NID:G1322571; PIDN:CAA96768.1; PID:e243
A:Experimental source: strain S288C
R:Rieger, M.; Mueller-Auer, S.; Breckner, M.; Schaefer, M.
Submitted to the Protein Sequence Database, May 1996
A:Reference number: S64071
A:Accession: S64071
A:Molecule type: DNA
A:Residues: 1-503 <RIB>
A:Cross-references: EMBL:Z72587; NID:G1322571; PIDN:CAA96768.1; PID:e243955; PID:G132257
A:Experimental source: strain S288C
R:Jackson, B.J.; Kukuruzinska, M.A.; Robbins, P.
Glycobiology 3, 357-364, 1993
A:Title: Biosynthesis of asparagine-linked oligosaccharides in Saccharomyces cerevisiae:
A:Reference number: S59763; MUID:94003656; PMID:8400550
A:Accession: S59763
A:Molecule type: DNA
A:Residues: 1-7, 'S', 9-226, 'NG', 239-301, 'A', 303-456, 'I', 458-469, 'S', 484-486, 'PLU', 490, 'YV'
A:Cross-references: EMBL:X87947; NID:9871530; PIDN:CAA61199.1; PID:9871531
C:Genetics:
A:Gene: SGD:ALG2
A:Cross-references: SGD:S0003033; MIPS:YGL065C
A:Map position: 7L
F:1-21/Domain: signal sequence #status predicted <SIG>
F:22-503/Product: ALG2 protein #status predicted <MAT>

Query Match 69.2%; Score 36; DB 2; Length 503;
Best Local Similarity 77.8%; Pred. No. 66;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 QSFEDTEK 10
DB 424 QSFENVEK 432

RESULT 14
T18275
1-phosphatidylinositol 3-kinase (EC 2.7.1.137) 4 - blime mold (Dictyostellium discoideum)
C:Species: Dictyostellium discoideum
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T18275
R:Zhou, K.; Takegawa, K.; Emr, S.D.; Firtel, R.A.
Mol. Cell Biol. 15, 5645-5656, 1995
A:Title: A phosphatidylinositol (PI) kinase gene family in Dictyostellium discoideum. Bt.
A:Reference number: Z06411
A:Accession: T18275
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-1093 <ZHO>
A:Cross-references: UNIPROT:P54677; EMBL:U23479; NID:G733527; PID:G733528; PIDN:AAA8572
C:Genetics:
A:Note: PIK4
C:Keywords: phosphotransferase

Query Match 69.2%; Score 36; DB 2; Length 1093;
Best Local Similarity 77.8%; Pred. No. 1,5e+02;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 QSFEDTEK 10
DB 94 QAFEDGEEK 102

RESULT 15
G90556
conserved hypothetical protein MYPU_3590 [imported] - Mycoplasma pulmonis (strain UAB C)
C:Species: Mycoplasma pulmonis
C:Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 09-Jul-2004
C:Accession: G90556
R:Chamaud, I.; Heilig, R.; Ferris, S.; Barbe, V.; Samson, D.; Galisson, F.; Moszer, I.
Nucleic Acids Res. 29, 2145-2153, 2001
A:Title: The complete genome sequence of the murine respiratory pathogen Mycoplasma pul.
A:Reference number: A99512; MUID:21267165; PMID:11353084
A:Accession: G90556
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-288 <KUR>
A:Cross-references: UNIPROT:Q980K2; GB:AL445566; PID:G14089773; PIDN:CAC133532.1; GSPDB:
A:Experimental source: strain UAB CTIP
C:Genetics:
A:Gene: MYPU_3590
A:Genetic code: SGC3

Query Match 67.3%; Score 35; DB 2; Length 288;
Best Local Similarity 60.0%; Pred. No. 56;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 NOSFEDTEK 10
DB 134 NOSFDELKK 143

Search completed: October 22, 2005, 08:04:38
Job time : 11.45 secs

GenCore version 5.1.6
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OM protein - protein search, using SW model

Run on: October 22, 2005, 06:06:36 ; Search time 55.85 Seconds
(without alignments)

91.688 Million cell updates/sec

Title: US-10-731-238-84
Perfect score: 52
Sequence: 1 NOSFEEDTEK 10

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: UniProt_03.*
1: uniprot_sprot.*
2: uniprot_tramb.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	52	100.0	152	2	Q9AEP9
2	52	100.0	940	2	Q53682
3	52	100.0	1015	2	Q8NUU7
4	52	100.0	1015	2	Q6G6H3
5	52	100.0	1018	1	FNBA_STAU
6	48	92.3	943	2	Q8NUU8
7	48	92.3	957	2	Q6G6H4
8	48	92.3	961	2	Q99RD3
9	48	92.3	961	2	Q7A3J8
10	48	92.3	965	2	Q6GDU5
11	48	92.3	1038	2	Q99RD2
12	48	92.3	1038	2	Q7A3J7
13	40	76.9	679	1	FTSH_BACPF
14	39	75.0	429	2	Q9KSH1
15	39	75.0	429	2	Q25682
16	39	75.0	551	2	Q8L1B3
17	39	75.0	1638	2	Q869R3
18	38	73.1	458	2	Q9XWU8
19	37	71.2	199	2	Q6PPA3
20	37	71.2	502	2	Q8NFC6
21	37	71.2	705	1	YMA7_YEAST
22	37	71.2	806	2	Q9W8T5
23	37	71.2	5255	1	BACA_BACLI
24	36	69.2	123	2	Q6DKA6
25	36	69.2	197	2	Q6BUN3
26	36	69.2	208	2	Q72RT6
27	36	69.2	208	2	Q8F3W5
28	36	69.2	324	2	Q9C8W9
29	36	69.2	324	2	Q7YZS1
30	36	69.2	429	2	Q9ZM38
31	36	69.2	445	1	CANA_CANEN

32	36	69.2	445	1	CANA_CANGL	P10562 canavalia g
33	36	69.2	473	2	Q9DSG5	Q9d5G5 mus musculu
34	36	69.2	485	2	Q9V9N1	Q9v9N1 drosophila
35	36	69.2	503	1	ALG2_YEAST	P43636 saccharomyc
36	36	69.2	753	2	Q6H899	Q6h899 oryza sativ
37	36	69.2	925	2	Q7RA33	Q7r433 giardia lam
38	36	69.2	946	2	Q8BUH5	Q8buh5 mus musculu
39	36	69.2	975	2	Q68C08	Q68c08 homo sapien
40	36	69.2	1093	1	P14K_DICDI	P54677 dictyosteli
41	35	67.3	136	2	Q8MQ89	Q8mq89 caenorhabdi
42	35	67.3	260	2	Q6VU49	Q6vu49 manduca sex
43	35	67.3	288	1	Y359_MYCPU	Q98GK2 mycoplasma
44	35	67.3	303	2	Q7RRM4	Q7rew4 plasmodium
45	35	67.3	303	2	Q9XUM3	Q9xum3 caenorhabdi

ALIGNMENTS

RESULT 1

ID	Q9AEP9	PRELIMINARY;	PRT;	152 AA.
AC	Q9AEP9;			
DT	01-JUN-2001 (TRENBLREL, 17, Created)			
DT	01-JUN-2001 (TRENBLREL, 17, Last sequence update)			
DT	01-DEC-2001 (TRENBLREL, 19, Last annotation update)			
DE	Fibronectin-binding protein (Fragment).			
GN	Name=fnb;			
OS	Staphylococcus aureus.			
OC	Bacteria; Firmicutes; Bacillales; Staphylococcus.			
OK	NCBI_TaxID=1280;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=CMRSA-1;			
RX	MEDLINE=21246681; PubMed=11349044;			
RX	DOI=10.1128/IAI.69.6.3791-3799.2001;			
RA	Rice K., Huesca M., Var D., McGavin M.J.;			
RT	"Variance in fibronectin binding and fnb locus polymorphisms in			
RT	Staphylococcus aureus: identification of antigenic variation in a			
RT	fibronectin binding protein adhesin of the epidemic CMRSA-1 strain of			
RL	methicillin-resistant S. aureus."			
RU	Infect. Immun. 69:3791-3799(2001).			
DR	EMBL; AY029184; AAK31586.1; -.			
FT	NON_TER	1		
FT	NON_TER	152		
SQ	SEQUENCE	152 AA;	17193 MW;	CFA3913C2B11C025 CRC64;
Query Match				
Best Local Similarity 100.0%; Score 52; DB 2; Length 152;				
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;				
QY	1 NOSFEEDTEK 10			
DB	81 NOSFEEDTEK 90			
RESULT 2				
ID	Q53682	PRELIMINARY;	PRT;	940 AA.
AC	Q53682;			
DT	01-NOV-1996 (TRENBLREL, 01, Created)			
DT	01-NOV-1996 (TRENBLREL, 01, Last sequence update)			
DT	01-MAR-2004 (TRENBLREL, 26, Last annotation update)			
DE	Fibronectin binding protein B.			
GN	Name=fnbB;			
OS	Staphylococcus aureus.			
OC	Bacteria; Firmicutes; Bacillales; Staphylococcus.			
OX	NCBI_TaxID=1280;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=8325-4;			
RX	MEDLINE=92111475; PubMed=1837266;			
RA	Jonsson K., Sigmas C., Muller H.P., Lindberg M.;			

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RT      "Two different genes encode fibronectin binding proteins in
RT      Staphylococcus aureus. The complete nucleotide sequence and
RT      characterization of the second gene."
RT      Eur. J. Biochem 202;1041-1048 (1991).
CC      -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC      an amide bond (By similarity).
DR      EMBL; X62992; CAA44726.1; -.
DR      PIR; S19702; S19702.
DR      HSSP; Q53653; 1N67.
DR      GO; GO:0009986; C:cell surface; IEA.
DR      GO; GO:0005618; C:cell wall; IEA.
DR      GO; GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR      GO; GO:0016020; C:membrane; IEA.
DR      GO; GO:0007155; P:cell adhesion; IEA.
DR      InterPro; IPR008966; Adhes_bact.
DR      InterPro; IPR004237; Fn_bind.
DR      InterPro; IPR005877; Gpos_YsIRK.
DR      InterPro; IPR01899; Gram_pos_anchor.
DR      Pfam; PF02986; Fn_bind_2.
DR      Pfam; PF04650; Gram_pos_anchor; 1.
DR      TIGRFAMs; TIGR01167; LPXTG_anchor; 1.
DR      TIGRFAMs; TIGR01166; YsIRK_signal; 1.
DR      PROSITE; PS50847; GRAM_POS_ANCHORING; 1.
DR      Cell wall; peptidoglycan-anchor.
SQ      SEQUENCE 940 AA; 103555 MW; E35FBBCA907AE345 CRC64;

Query Match 100.0%; Score 52; DB 2; Length 940;
Best Local Similarity 100.0%; Pred. No. 0.89;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 NOSFEEDTEK 10
Db      724 NOSFEEDTEK 733

RESULT 3
Q8NUU7 PRELIMINARY; PRT; 1015 AA.
AC      Q8NUU7
DT      01-OCT-2002 (TrEMBLrel. 22, Created)
DT      01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT      01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE      Fnb protein.
GN      Name=fnb; OrderedLocustNames=MM2421;
OS      Staphylococcus aureus (strain MM2).
OC      Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX      NCBI_TaxID=196620;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN=MM2;
RX      MEDLINE=22040717; PubMed=12044378; DOI=10.1016/S0140-6736(02)08713-5;
RA      Baba T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-i., Oguchi A.,
RA      Nagai Y., Iwama N., Asano K., Naito T., Kuroda H., Cui L.,
RA      Yamamoto K., Hiramatsu K.;
RT      "genome and virulence determinants of high virulence community-
RT      acquired MRSA."
RL      Lancet 359:1819-1827 (2002).
CC      -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC      an amide bond (By similarity).
DR      EMBL; AP004830; BAB96286.1; -.
DR      GO; GO:0009986; C:cell surface; IEA.
DR      GO; GO:0005618; C:cell wall; IEA.
DR      GO; GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR      GO; GO:0016020; C:membrane; IEA.
DR      GO; GO:0007155; P:cell adhesion; IEA.
DR      InterPro; IPR008966; Adhes_bact.
DR      InterPro; IPR004237; Fn_bind.
DR      InterPro; IPR005877; Gpos_YsIRK.
DR      InterPro; IPR01899; Gram_pos_anchor.
DR      Pfam; PF02986; Fn_bind_1.
DR      Pfam; PF00746; Gram_pos_anchor; 1.
DR      Pfam; PF04650; YsIRK_signal; 1.

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DR      TIGRFAMs; TIGR01167; LPXTG_anchor; 1.
DR      TIGRFAMs; TIGR01168; YsIRK_signal; 1.
DR      PROSITE; PS50847; GRAM_POS_ANCHORING; 1.
DR      Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ      SEQUENCE 1015 AA; 111145 MW; D0F9281BB64D44D2 CRC64;

Query Match 100.0%; Score 52; DB 2; Length 1015;
Best Local Similarity 100.0%; Pred. No. 0.97;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 NOSFEEDTEK 10
Db      789 NOSFEEDTEK 798

RESULT 4
O6G6H3 PRELIMINARY; PRT; 1015 AA.
AC      O6G6H3
DT      05-JUL-2004 (TrEMBLrel. 27, Created)
DT      05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT      05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE      Fibronectin-binding protein.
GN      OrderedLocustNames=SA52388;
OS      Staphylococcus aureus (strain MSSA476).
OC      Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX      NCBI_TaxID=282459;
RN      [1]
RP      SEQUENCE FROM N.A.
RX      PubMed=1521324; DOI=10.1073/pnas.0402521101;
RA      Holden M.T.G., Fell E.J., Lindsay J.A., Peacock S.J., Day N.P.J.,
RA      Enright M.C., Foster T.J., Moore C.E., Hurst L., Atkin R., Barton A.,
RA      Bason N., Bentley S.D., Chillingworth C., Chillingworth T.,
RA      Churcher C., Clark L., Corton C., Cronin A., Doggett J., Dowd L.,
RA      Felwell T., Hance Z., Harris B., Hauser H., Holtroyd S., Jagels K.,
RA      James K.D., Lennard N., Line A., Mayes R., Moule S., Mungall K.,
RA      Ormond D., Quail M.A., Rabinowitch E., Rutherford K.M., Sanders M.,
RA      Sharp S., Simmonds M., Stevens K., Whitehead S., Barrett B.G.,
RA      Spratt B.G., Parkhill J.;
RT      "Complete genomes of two clinical Staphylococcus aureus strains:
RT      evidence for the rapid evolution of virulence and drug resistance."
RL      Proc. Natl. Acad. Sci. U.S.A. 101:9786-9791 (2004).
CC      -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC      an amide bond (By similarity).
DR      EMBL; BX571857; CAG44202.1; -.
DR      GO; GO:0009986; C:cell surface; IEA.
DR      GO; GO:0005618; C:cell wall; IEA.
DR      GO; GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR      GO; GO:0016020; C:membrane; IEA.
DR      GO; GO:0007155; P:cell adhesion; IEA.
DR      InterPro; IPR008966; Adhes_bact.
DR      InterPro; IPR004237; Fn_bind.
DR      InterPro; IPR005877; Gpos_YsIRK.
DR      InterPro; IPR01899; Gram_pos_anchor.
DR      Pfam; PF02986; Fn_bind_1.
DR      Pfam; PF00746; Gram_pos_anchor; 1.
DR      Pfam; PF04650; YsIRK_signal; 1.
DR      TIGRFAMs; TIGR01167; LPXTG_anchor; 1.
DR      TIGRFAMs; TIGR01168; YsIRK_signal; 1.
DR      PROSITE; PS50847; GRAM_POS_ANCHORING; 1.
DR      Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ      SEQUENCE 1015 AA; 111145 MW; D0F9281BB64D44D2 CRC64;

Query Match 100.0%; Score 52; DB 2; Length 1015;
Best Local Similarity 100.0%; Pred. No. 0.97;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 NOSFEEDTEK 10
Db      789 NOSFEEDTEK 798

RESULT 5

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FNBA STAAU STANDARD; PRT; 1018 AA.
ID FNBA STAAU STANDARD; PRT; 1018 AA.
AC P14738;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Fibronectin-binding protein precursor (FNBP).
GN Name=fnba;
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
NCBI_TaxID=1280;
OX NCBI_TaxID=1280;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NCITC 8325-4;
RX MEDLINE=89098998; PubMed=2521391;
RA Signaes C., Raucsi G., Joensen K., Lindgren P.-E.,
RA Mantharimaiah G.M., Hoeck M., Lindberg M.;
RA "Nucleotide sequence of the gene for a fibronectin-binding protein
RT from Staphylococcus aureus: use of this peptide sequence in the
RT synthesis of biologically active peptides.";
RL Proc. Natl. Acad. Sci. U.S.A. 86:699-703(1989).
CC -1- FUNCTION: The ability of bacteria to bind fibronectin has been
CC proposed as a virulence factor enabling bacteria to colonize wound
CC tissues and blood clots. Binding of plasma fibronectin to the
CC bacterial surface might block adhesion receptors on S.aureus, thus
CC representing an important defense mechanism against tissue
CC invasion.
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC an amide bond (potential).
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (see <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; J04151; AAA26632.1; -.
DR InterPro; IPR004237; Fp_bind.
DR InterPro; IPR005877; Gpos_YsIRK.
DR InterPro; IPR01899; Gram_pos_anchor.
DR Pfam; PF02986; Fp_bind; 1.
DR Pfam; PF00746; Gram_pos_anchor; 1.
DR TIGRFAMs; TIGR01167; LpxTG_anchor; 1.
DR TIGRFAMs; TIGR01168; YsIRK_signal; 1.
DR TIGRFAMs; TIGR01168; YsIRK_signal; 1.
DR PROSITE; PS50847; GRAM_POS_ANCHORING; 1.
KW Cell adhesion; Cell wall; Peptidoglycan-anchor; Repeat; signal;
KW Virulence.
FT SIGNAL 1 36
FT CHAIN 37 985
FT PROPEP 986 1018
FT REPEAT 545 574
FT REPEAT 575 604
FT DOMAIN 745 878
FT REPEAT 745 782
FT REPEAT 783 820
FT REPEAT 821 859
FT REPEAT 860 878
FT DOMAIN 879 948
FT REPEAT 879 892
FT REPEAT 893 906
FT REPEAT 907 920
FT REPEAT 921 934
FT REPEAT 935 948
FT SITE 982 986
FT MOD_RES 985 985
FT SEQUENCE 1018 AA; 111780 MW; 58175E0020E81F CRC64;
Query Match 100.0%; Score 52; DB 1; Length 1018;

Best Local Similarity 100.0%; Pred. No. 0.97;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 NOSFEEDTEK 10
Db 788 NOSFEEDTEK 797
RESULT 6
Q8NU8 PRELIMINARY; PRT; 943 AA.
ID Q8NU8
AC Q8NU8;
DT 01-OCT-2002 (TReMBLrel. 22, Created)
DT 01-OCT-2002 (TReMBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE FnbB protein.
GN Name=fnbB; OrderedLocNames=MM2420;
OS Staphylococcus aureus (strain MM2).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
NCBI_TaxID=196620;
OX NCBI_TaxID=196620;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MM2;
RX MEDLINE=22040717; PubMed=12044378; DOI=10.1016/S0140-6736(02)08713-5;
RA Baba T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Oguchi A.,
RA Nagai Y., Ikema N., Amano K., Naito T., Kuroda H., Cui L.,
RA Yamamoto K., Hiratake K.;
RT "Genome and virulence determinants of high virulence community-
RT acquired MRSA.";
RL Lancet 359:1819-1827(2002).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC an amide bond (by similarity).
CC EMBL; AP004830; BAB96285.1; -.
DR HSSP; Q53653; IN67.
DR GO; GO:0009986; C:cell surface; IEA.
DR GO; GO:0005618; C:cell wall; IEA.
DR GO; GO:0009275; C:cell wall (aerobic Gram-positive Bacteria); IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0007155; P:cell adhesion; IEA.
DR InterPro; IPR008966; Adhes_bact.
DR InterPro; IPR004237; Fp_bind.
DR InterPro; IPR005877; Gpos_YsIRK.
DR InterPro; IPR01899; Gram_pos_anchor.
DR Pfam; PF02986; Fp_bind; 1.
DR Pfam; PF00746; Gram_pos_anchor; 1.
DR Pfam; PF04650; YsIRK_signal; 1.
DR TIGRFAMs; TIGR01167; LpxTG_anchor; 1.
DR TIGRFAMs; TIGR01168; YsIRK_signal; 1.
DR PROSITE; PS50847; GRAM_POS_ANCHORING; 1.
KW Cell wall; Complete proteome; Peptidoglycan-anchor.
KW SEQUENCE 943 AA; 104537 MW; DA8A5F31947E1B6A CRC64;
Query Match 92.3%; Score 48; DB 2; Length 943;
Best Local Similarity 90.0%; Pred. No. 4.9;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 1 NOSFEEDTEK 10
Db 693 NOSFEEDTEK 702
RESULT 7
Q6G6H4 PRELIMINARY; PRT; 957 AA.
ID Q6G6H4
AC Q6G6H4;
DT 05-JUL-2004 (TReMBLrel. 27, Created)
DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TReMBLrel. 27, Last annotation update)
DE Fibronectin-binding protein.
GN Name=fnbB; OrderedLocNames=SAS2387;
OS Staphylococcus aureus (strain MSSA476).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
NCBI_TaxID=282459;

```

RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=1521324; DOI=10.1073/pnas.0402521101;
RA Holden M.T.G., Fell E.J., Lindsay J.A., Peacock S.J., Day N.P.J.,
RA Berridge M.C., Foster T.J., Moore C.E., Hurst L., Atkin R., Barron A.,
RA Bason N., Bentley S.D., Chillingworth C., Chillingworth T.,
RA Churcher C., Clark L., Corton C., Cronin A., Doggett J., Dowd L.,
RA Felwell T., Hance Z., Harris B., Hauser H., Holtroyd S., Jagsis K.,
RA James K.D., Lennard N., Line A., Mayes R., Moule S., Mungall K.,
RA Omond D., Quail M.A., Rabinowitch E., Rutherford K.M., Sanders M.,
RA Sharp S., Simmonds M., Stevens K., Whitehead S., Barrell B.G.,
RA Spratt B.G., Parkhill J.;
RT "Complete genomes of two clinical Staphylococcus aureus strains:
RT evidence for the rapid evolution of virulence and drug resistance.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:9786-9791(2004).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC an amide bond (By similarity).
DR EMBL; BX571857; CAG4201.1; -.
DR GO; GO:0009986; C:cell surface; IEA.
DR GO; GO:0005618; C:cell wall; IEA.
DR GO; GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0007155; P:cell adhesion; IEA.
DR InterPro; IPR008966; Adhes_bact.
DR InterPro; IPR004237; Fn_bind.
DR InterPro; IPR005877; Gpos_YsIRK.
DR InterPro; IPR001899; Gram_pos_anchor.
DR Pfam; PF02986; Fn_bind_1.
DR Pfam; PF00746; Gram_pos_anchor; 1.
DR Pfam; PF04650; YsIRK_signal; 1.
DR TIGRFAMs; TIGR01167; LPXTG_anchor; 1.
DR TIGRFAMs; TIGR01168; YsIRK_signal; 1.
DR PROSITE; PS50847; GRAM_POS_ANCHORING; 1.
KW Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ SEQUENCE 957 AA; 105980 MW; 28FEB87FDD33AF CRC64;

Query Match 92.3%; Score 48; DB 2; Length 957;
Best Local Similarity 90.0%; Pred. No. 5;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 NOSFEEDTEK 10
Db 693 NOSFEEDTEK 702

RESULT 8
Q99RD3 PRELIMINARY; PRT; 961 AA.
ID Q99RD3
AC Q99RD3;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Fibronectin-binding protein homolog.
GN Name=fnbB; OrderedLocustNames=SAV2502;
OS Staphylococcus aureus (strain Mu50 / ATCC 700699).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=158878;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=MU50 / ATCC 700699;
RX MEDLINE=21311952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2;
RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Iian J.-O., Ito T.,
RA Kanamori M., Matsunaru H., Maruyama A., Murakami H., Hosoyama A.,
RA Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
RA Sekimizu K., Hiraoka H., Kuhara S., Goto S., Yabuzaki J.,
RA Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
RA Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
RT "Whole genome sequencing of methicillin-resistant Staphylococcus
RT aureus.";
RL Lancet 357:1225-1240(2001).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC an amide bond (By similarity).
DR EMBL; AP003137; BAB43593.1; -.
DR GO; GO:0009986; C:cell surface; IEA.
DR GO; GO:0005618; C:cell wall; IEA.
DR GO; GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0007155; P:cell adhesion; IEA.
DR InterPro; IPR008966; Adhes_bact.
DR InterPro; IPR004237; Fn_bind.
DR InterPro; IPR005877; Gpos_YsIRK.
DR InterPro; IPR001899; Gram_pos_anchor.
DR Pfam; PF02986; Fn_bind_1.
DR Pfam; PF00746; Gram_pos_anchor; 1.
DR Pfam; PF04650; YsIRK_signal; 1.
DR TIGRFAMs; TIGR01167; LPXTG_anchor; 1.
DR TIGRFAMs; TIGR01168; YsIRK_signal; 1.
DR PROSITE; PS50847; GRAM_POS_ANCHORING; 1.

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DR EMBL; AP003365; BAB58664.1; -.
DR PIR; G90053; G90053.
DR HSSP; OS3653; 1N67.
DR GO; GO:0009986; C:cell surface; IEA.
DR GO; GO:0005618; C:cell wall; IEA.
DR GO; GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0007155; P:cell adhesion; IEA.
DR InterPro; IPR008966; Adhes_bact.
DR InterPro; IPR004237; Fn_bind.
DR InterPro; IPR005877; Gpos_YsIRK.
DR InterPro; IPR001899; Gram_pos_anchor.
DR Pfam; PF02986; Fn_bind_1.
DR Pfam; PF00746; Gram_pos_anchor; 1.
DR Pfam; PF04650; YsIRK_signal; 1.
DR TIGRFAMs; TIGR01167; LPXTG_anchor; 1.
DR TIGRFAMs; TIGR01168; YsIRK_signal; 1.
DR PROSITE; PS50847; GRAM_POS_ANCHORING; 1.
KW Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ SEQUENCE 961 AA; 106010 MW; 364940F84EA4101 CRC64;

Query Match 92.3%; Score 48; DB 2; Length 961;
Best Local Similarity 90.0%; Pred. No. 5;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 NOSFEEDTEK 10
Db 697 NOSFEEDTEK 706

RESULT 9
Q7A3J8 PRELIMINARY; PRT; 961 AA.
ID Q7A3J8
AC Q7A3J8;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE FnbB protein.
GN Name=fnbB; OrderedLocustNames=SA2290;
OS Staphylococcus aureus (strain N15).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=158879;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21311952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2;
RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Iian J.-O., Ito T.,
RA Kanamori M., Matsunaru H., Maruyama A., Murakami H., Hosoyama A.,
RA Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
RA Sekimizu K., Hiraoka H., Kuhara S., Goto S., Yabuzaki J.,
RA Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
RA Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
RT "Whole genome sequencing of methicillin-resistant Staphylococcus
RT aureus.";
RL Lancet 357:1225-1240(2001).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC an amide bond (By similarity).
DR EMBL; AP003137; BAB43593.1; -.
DR GO; GO:0009986; C:cell surface; IEA.
DR GO; GO:0005618; C:cell wall; IEA.
DR GO; GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0007155; P:cell adhesion; IEA.
DR InterPro; IPR008966; Adhes_bact.
DR InterPro; IPR004237; Fn_bind.
DR InterPro; IPR005877; Gpos_YsIRK.
DR InterPro; IPR001899; Gram_pos_anchor.
DR Pfam; PF02986; Fn_bind_1.
DR Pfam; PF00746; Gram_pos_anchor; 1.
DR Pfam; PF04650; YsIRK_signal; 1.
DR TIGRFAMs; TIGR01167; LPXTG_anchor; 1.
DR TIGRFAMs; TIGR01168; YsIRK_signal; 1.
DR PROSITE; PS50847; GRAM_POS_ANCHORING; 1.

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KM Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ SEQUENCE 961 AA; 106010 MW; 364940F884EA4101 CRC64;
Query Match 92.3%; Score 48; DB 2; Length 961;
Best Local Similarity 90.0%; Pred. No. 5;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 NOSFEEDTEK 10
Db 697 NOSFEEDTEE 706
RESULT 10
06GDU5 PRELIMINARY; PRT; 965 AA.
ID 06GDU5
AC 06GDU5
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE Fibronectin-binding protein.
GN Name=fnbA; OrderedLocuNames=SA2580;
OS Staphylococcus aureus (strain MRSA252).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=282458;
RN PIR; H90053; H90053.
RP SEQUENCE FROM N.A.
RX Holden M.T.G., Peil E.J., Lindsey J.A., Peacock S.J., Day N.P.J.,
Enlight M.C., Foster T.J., Moore C.E., Hurst L., Atkin R., Barron A.,
Baeson N., Bentley S.D., Chillingworth C., Chillingworth T.,
Churcher C., Clark L., Cotton C., Cronin A., Doggett J., Dowd L.,
Fellwell T., Hance Z., Harris B., Hauser H., Holtroyd S., Jagsle K.,
James K.D., Lennard N., Line A., Mayes R., Moule S., Mungall K.,
Ormond D., Quail M.A., Rabinowitsch E., Rutherford K.M., Sanders M.,
Sharp S., Simmonds M., Stevens K., Whitehead S., Barrall B.G.,
Spratt B.G., Parthill J.;
RT "Complete genomes of two clinical Staphylococcus aureus strains:
evidence for the rapid evolution of virulence and drug resistance";
Proc. Natl. Acad. Sci. U.S.A. 101:9786-9791(2004).
RL -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
an amide bond (By similarity).
CC EMBL; BX571856; CAG41560.1; -.
DR GO; GO:0009986; C:cell surface; IEA.
DR GO; GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0007155; P:cell adhesion; IEA.
DR InterPro; IPR008966; Adhes_Bact.
DR InterPro; IPR004237; Fn_bind.
DR InterPro; IPR005877; Gpos_YsIRK.
DR InterPro; IPR001899; Gram_pos_anchor.
DR Pfam; PF02986; Fn_bind; 1.
DR Pfam; PF00746; Gram_pos_anchor; 1.
DR Pfam; PF04650; YsIRK_signal; 1.
DR TIGRFAMs; TIGR01167; LpxTG_anchor; 1.
DR TIGRFAMs; TIGR01168; YsIRK_signal; 1.
DR PROSITE; PS50847; GRAM_POS_ANCHORING; 1.
KW Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ SEQUENCE 965 AA; 105591 MW; 2982E1321640551 CRC64;

Query Match 92.3%; Score 48; DB 2; Length 965;
Best Local Similarity 90.0%; Pred. No. 5;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 NOSFEEDTEK 10
Db 753 NOSFEEDTEE 762
RESULT 11
099RD2 PRELIMINARY; PRT; 1038 AA.
AC 099RD2
DT 01-JUN-2001 (TREMBlrel. 17, Created)

DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE Fibronectin-binding protein homolog.
GN Name=fnb; OrderedLocuNames=SAV2503;
OS Staphylococcus aureus (strain Mu50 / ATCC 700699).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=158878;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Mu50 / ATCC 700699;
RX MEDLINE=21311952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2;
RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
Cui L., Oguchi A., Aoki K.-I., Nagai Y., Iian J.-O., Ito T.,
Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,
Mizutani U.Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
RA Sekimizu K., Hirakawa H., Kihara S., Goto S., Yabuzaki J.,
RA Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
Hattori M., Ogasawara N., Hayashi H., Hiratake K.;
RT "Whole genome sequencing of methicillin-resistant Staphylococcus
aureus";
RT Lancet 357:1225-1240(2001).
RL -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
an amide bond (By similarity).
CC EMBL; AP003365; BAB58665.1; -.
DR PIR; H90053; H90053.
DR GO; GO:0009986; C:cell surface; IEA.
DR GO; GO:0005618; C:cell wall; IEA.
DR GO; GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0007155; P:cell adhesion; IEA.
DR InterPro; IPR008966; Adhes_bact.
DR InterPro; IPR004237; Fn_bind.
DR InterPro; IPR005877; Gpos_YsIRK.
DR InterPro; IPR001899; Gram_pos_anchor.
DR Pfam; PF02986; Fn_bind; 1.
DR Pfam; PF00746; Gram_pos_anchor; 1.
DR Pfam; PF04650; YsIRK_signal; 1.
DR TIGRFAMs; TIGR01167; LpxTG_anchor; 1.
DR TIGRFAMs; TIGR01168; YsIRK_signal; 1.
DR PROSITE; PS50847; GRAM_POS_ANCHORING; 1.
KW Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ SEQUENCE 1038 AA; 113618 MW; 666BF6F2FBE12 CRC64;

Query Match 92.3%; Score 48; DB 2; Length 1038;
Best Local Similarity 90.0%; Pred. No. 5.5;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 NOSFEEDTEK 10
Db 746 NOSFEEDTEE 755

RESULT 12
07A3J7 PRELIMINARY; PRT; 1038 AA.
AC 07A3J7
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE Fnb protein.
GN Name=fnb; OrderedLocuNames=SA2291;
OS Staphylococcus aureus (strain N315).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=158879;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21311952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2;
RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
Cui L., Oguchi A., Aoki K.-I., Nagai Y., Iian J.-O., Ito T.,
Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,
Mizutani U.Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
RA Sekimizu K., Hirakawa H., Kihara S., Goto S., Yabuzaki J.,
RA Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,

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RA Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
RT "Whole genome sequencing of methicillin-resistant Staphylococcus
RT aureus."
CC Lancelot 357:1225-1240(2001).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC an amide bond (By similarity).
CC EMBL; AP003137; BAB43594.1; -.
CC DR GO: GO:0009986; C:cell surface; IEA.
CC DR GO: GO:0005518; C:cell wall; IEA.
CC DR GO: GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
CC DR GO: GO:0016020; C:membrane; IEA.
CC DR GO: GO:0007155; P:cell adhesion; IEA.
CC DR InterPro: IPR008966; Adhes_bact.
CC DR InterPro: IPR004237; Fn_bind.
CC DR InterPro: IPR005877; Gpos_YSRK.
CC DR InterPro: IPR001899; Gram_pos_anchor.
CC DR Pfam; PF02986; Fn_bind_1.
CC DR Pfam; PF00746; Gram_pos_anchor_1.
CC DR Pfam; PF04650; YSRK_signal_1.
CC DR TIGRPFAMs; TIGR01167; LPXTG_anchor_1.
CC DR TIGRPFAMs; TIGR01168; YSRK_signal_1.
CC DR PROSITE; PS50847; GRAM_POS_ANCHORING_1.
CC Cell wall; Complete proteome; Peptidoglycan-anchor.
CC KW SEQUENCE 1038 AA; 113618 MW; 666BF6BF2FBEB12 CRC64;
SQ
Query Match 92.3%; Score 48; DB 2; Length 1038;
Best Local Similarity 90.0%; Pred. No. 5.5;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 NOSFEEDTEK 10
Db 746 NOSFEEDTEE 755

RESULT 13
FTSH_BACPF STANDARD; PRT; 679 AA.
ID FTSH_BACPF
AC P94304;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Cell division protein ftsh homolog (EC 3.4.24.-).
GN Name=ftsh;
OS Bacillus pseudofirmus.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=79885;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=OF4;
RX MEDLINE=98343927; PubMed=9680333;
RA Ito M., Cooperberg B., Kurlwich T.A.;
RT "Diverse genes of alkaliphilic Bacillus firmus OF4 that complement K+-
RT uptake-deficient Escherichia coli include an ftsh homologue."
RL Extremophiles 1:22-28(1997).
CC -1- FUNCTION: Seems to act as an ATP-dependent zinc metallopeptidase
CC (By similarity).
CC -1- COFACTOR: Binds 1 zinc ion (Potential).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- SIMILARITY: In the N-terminal section; belongs to the AAA ATPase
CC family.
CC -1- SIMILARITY: In the C-terminal section; belongs to the peptidase
CC M41 family.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
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CC entities requires a license agreement (See http://www.ebi.ac.uk/announcement/
CC or send an email to license@ebi.ac.uk).
CC
CC EMBL; U61844; AAB41679.1; -.
CC DR HSSP; P28691; ILV7.

```

```

DR MEROPS; M41.009; -.
DR InterPro; IPR003593; AAA_ATPase.
DR InterPro; IPR003959; AAA_ATPase_cent.
DR InterPro; IPR003960; AAA_sub.
DR InterPro; IPR005936; Pept_M41_Fth.
DR InterPro; IPR000642; Peptidase_M41.
DR Pfam; PF00004; AAA_1.
DR Pfam; PF06480; Fth_ext_1.
DR Pfam; PF01434; Peptidase_M41_1.
DR SMART; SM00382; AAA; 1.
DR TIGRPFAMs; TIGR01241; Fth_fam; 1.
DR PROSITE; PS00674; AAA_1.
KW ATP-binding; Cell division; Hydrolyase; Metalloprotease; Transmembrane;
KW Zinc.
FT DOMAIN 1 6 Cytoplasmic (Potential).
FT TRANSMEM 7 27 Potential.
FT DOMAIN 28 114 Extracellular (Potential).
FT TRANSMEM 115 135 Potential.
FT DOMAIN 136 679 Cytoplasmic (Potential).
FT NF_BIND 206 213 ATP (Potential).
FT METAL 428 428 Zinc (catalytic) (By similarity).
FT ACT_SITE 429 429 By similarity.
FT METAL 432 432 Zinc (catalytic) (By similarity).
SQ SEQUENCE 679 AA; 75429 MW; B7209B4930DF964 CRC64;

QY 1 NOSFEEDTEK 10
Db 668 NRSFEDTINK 677

Query Match 76.9%; Score 40; DB 1; Length 679;
Best Local Similarity 70.0%; Pred. No. 1e+02;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 NOSFEEDTEK 10
Db 270 NOSFEEDLKR 279

RESULT 14
Q9XSH1 PRELIMINARY; PRT; 429 AA.
ID Q9XSH1
AC Q9XSH1;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein.
OS Helicobacter pylori (Campylobacter pylori).
OC Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;
OC Helicobacteraceae; Helicobacter.
OX NCBI_TaxID=210;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 43504;
RX MEDLINE=99214098; PubMed=10198012;
RA McGee D.J., May C.A., Garner R.M., Himpel J.M., Mobley H.L.T.;
RT "Isolation of Helicobacter pylori genes that modulate urease
RT activity."
RL J. Bacteriol. 181:2477-2484(1999).
DR EMBL; AF125197; AAD27687.1; -.
DR InterPro; IPR001865; Ribosomal_S2.
DR InterPro; IPR007016; Wzy_C.
DR Pfam; PF04932; Wzy_C_1.
DR PROSITE; PS00962; RIBOSOMAL_S2_1; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 429 AA; 49457 MW; D8BDDC2B6FE2C3C CRC64;

Query Match 75.0%; Score 39; DB 2; Length 429;
Best Local Similarity 70.0%; Pred. No. 97;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 NOSFEEDTEK 10
Db 270 NOSFEEDLKR 279

RESULT 15
Q2S682

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ID 025682      PRELIMINARY;      PRT;      429 AA.
AC 025682;
DT 01-JAN-1998 (TREMBlrel. 05, Created)
DT 01-JAN-1998 (TREMBlrel. 05, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE Hypothetical protein HP1039.
GN OrderedLocustNames=HP1039;
OS Helicobacter pylori (Campylobacter pylori).
OC Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;
OC Helicobacteraceae; Helicobacter.
OX NCBI_TaxID=210;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=26695 / ATCC 700392;
RX MEDLINE=97394467; PubMed=9252185; DOI=10.1038/41483;
RA Tomb J.-F., White O., Kervavage A.R., Clayton R.A., Sutton G.G.,
RA Fleischmann R.D., Ketchum K.A., Klenk H.-P., Gill S.R.,
RA Dougherty B.A., Nelson K.E., Quackenbush J., Zhou L., Kirkness E.F.,
RA Peterson S.N., Loftus B.J., Richardson D.L., Dodson R.J., Khalak H.G.,
RA Glodek A., McKenney K., Fitzgerald L.M., Lee N., Adams M.D.,
RA Hickey E.K., Berg D.E., Gocayne J.D., Utterback T.R., Peterson J.D.,
RA Kelley J.M., Cotton M.D., Meldman J.F., Fujii C., Bowman C.,
RA Wachtel L., Wallin E., Hayes W.S., Borodovsky M., Karp P.D.,
RA Smith H.O., Frazer C.M., Venter J.C.;
RT "The complete genome sequence of the gastric pathogen Helicobacter
RT pylori."
RL Nature 388:539-547(1997).
DR EMBL; AB000611; AAD08086.1; -.
DR PIR; G64649; G64649.
DR TIGR; HP1039; -.
DR InterPro; IPR001865; Ribosomal_S2.
DR InterPro; IPR007016; Wzy_C.
DR Pfam; PF04932; Wzy_C.1.
DR PROSITE; PS00962; RIBOSOMAL_S2_1; UNKNOWN_1.
KW Complete proteome; Hypothetical protein.
SQ
SEQUENCE 429 AA; 49404 MW; 34921792532903E4 CRC64;

```

```

Query Match 75.0%; Score 39; DB 2; Length 429;
Best Local Similarity 70.0%; Pred. No. 97;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

```

```

QY 1 NQSFEDTER 10
   |||||
   :
Db 270 NQSFEDLKR 279

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Search completed: October 22, 2005, 08:00:57
 Job time : 56.85 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 25, 2005, 20:58:51 ; Search time 69.7126 Seconds
(without alignments)
55.479 Million cell updates/sec

Title: US-10-731-238-85
Perfect score: 52
Sequence: 1 SFEDTEKDK 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:*

- 1: geneseqp1980s:*
- 2: geneseqp1990s:*
- 3: geneseqp2000s:*
- 4: geneseqp2001s:*
- 5: geneseqp2002s:*
- 6: geneseqp2003as:*
- 7: geneseqp2003bs:*
- 8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	52	100.0	10	2	AAW65741 Fibronec
2	52	100.0	12	2	AAW65718 Fibronec
3	52	100.0	30	4	AAH82164 Peptide f
4	52	100.0	30	7	ADC69221 Peptide f
5	52	100.0	31	7	ADC69222 Fibronec
6	52	100.0	36	2	AAW65714 Fibronec
7	52	100.0	36	2	AAW65715 Peptide #
8	52	100.0	38	1	AAH80661 Fibronec
9	52	100.0	38	1	AAH82117 Fibronec
10	52	100.0	38	2	AAW65664 Fibronec
11	52	100.0	38	2	AAW65705 Fibronec
12	52	100.0	38	2	AAW65663 Fibronec
13	52	100.0	77	2	AAH88749 S. aureus
14	52	100.0	113	2	AAH90937 D3D4 poly
15	52	100.0	130	2	AAH58806 Fibronec
16	52	100.0	130	2	AAH58807 Fibronec
17	52	100.0	130	2	AAH91502 Fibronec
18	52	100.0	134	2	AAH91501 Fibronec
19	52	100.0	134	2	AAH29088 S. aureus
20	52	100.0	134	2	AAH29087 S. aureus
21	52	100.0	139	2	AAW31556 Fibronec
22	52	100.0	162	2	AAH90942 D3D4 poly
23	52	100.0	164	2	AAH90938 D3D4 poly
24	52	100.0	174	2	AAH58808 Fbp fibro
25	52	100.0	174	2	AAH91203 D1-D4 fib

26	52	100.0	181	2	AAH58805 Fibronec
27	52	100.0	181	2	AAH91200 D1-D4 fib
28	52	100.0	559	2	AAH58803 Stephyloc
29	52	100.0	767	4	AAU34403 Stephyloc
30	52	100.0	767	4	AAU37547 Stephyloc
31	52	100.0	940	2	AAH07070 Fibronec
32	52	100.0	940	6	ABJ19111 Patchogen
33	52	100.0	948	6	ADA89470 Stephyloc
34	52	100.0	948	6	ABJ18923 Patchogen
35	52	100.0	948	6	ABM72536 Stephyloc
36	52	100.0	948	6	ABM72536 Stephyloc
37	52	100.0	1001	4	AAU37093 Stephyloc
38	52	100.0	1001	4	AAH82115 Fibronec
39	52	100.0	1018	4	AAU37245 Stephyloc
40	52	100.0	1018	4	AAU34301 Stephyloc
41	52	100.0	1018	6	ABJ18922 Patchogen
42	52	100.0	1018	6	ABM72537 Stephyloc
43	52	100.0	1027	2	AAH58806 Stephyloc
44	52	100.0	1038	6	ABU15903 Protein e
45	48	92.3	10	2	AAW65722 Fibronec

ALIGNMENTS

RESULT 1
AAW65741
ID AAW65741 standard; peptide; 10 AA.

XX AC AAW65741;

XX DT 16-OCT-1998 (first entry)

XX DE Fibronecctin binding protein-derived peptide #85.

XX KM Microbial surface components recognising adhesive matrix molecule;

KM MGRAMM; fibronecctin, fibronecctin-binding protein; antibody; epitope;

KM KMBRMM; bacterial infection; antibiotic-resistant strain.

XX OS Synthetic.

XX OS Staphylococcus aureus.

XX PM W09831389-A2.

XX PD 23-JUL-1998.

XX PF 21-JAN-1998; 98WO-US001222.

XX PR 21-JAN-1997; 97US-0036139P.

XX PT (TEXA) UNIV TEXAS A & M SYSTEM.

XX PI Hooeek M, Patti JM, House-Pompeo KL, Speziale P, Joh D; Mcgavin MJ;

XX DR WPI; 1998-413816/35.

XX PT Antibody that binds to fibronecctin-binding protein, preventing its binding to fibronecctin - used to treat or prevent bacterial infection, especially by Staphylococci and Streptococci.

PS Example 9; Page 110; 201pp; English.

The invention relates to antibodies that bind to a fibronecctin-binding domain of a fibronecctin-binding protein, and inhibit binding of the protein to fibronecctin. Also claimed are: (1) isolated peptides of a fibronecctin-binding protein that do not bind to fibronecctin; (2) fusion protein containing at least one peptide of a fibronecctin-binding protein linked to a second amino acid sequence; (3) nucleic acid encoding the isolated peptide of (1). Antibodies, the isolated peptides of (1) and the nucleic acids are all useful for immunisation (active or passive) and (by inhibiting binding of bacteria to fibronecctin) for preventing or treating infection in humans or other animals, particularly by staphylococci or

CC streptococci, e.g. meningitis, otitis media, pneumonia, endocarditis,
 CC mastitis in cattle, abortion in horses and many others. Since the
 CC antibodies block binding of bacteria, they should be effective against
 CC antibiotic-resistant strains, and may replace antibiotic therapy or
 CC increase its effectiveness. Sequences AAW65719-41 and AAW65658 represent
 CC peptides which were synthesised to span the D1 motif and the N-terminal
 CC 18 amino acids of D2, with each peptide overlapping by eight amino acids
 CC with the previous sequence
 CC
 XX
 SQ Sequence 10 AA;

Query Match 100.0%; Score 52; DB 2; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.011;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SPEEDTEKDK 10
 |||||
 DB 1 SPEEDTEKDK 10

RESULT 2

AAW65718
 ID AAW65718 standard; peptide; 12 AA.

AC AAW65718;
 XX

DT 16-OCT-1998 (first entry)

DE Fibronectin binding protein-derived peptide #62.

XX microbial surface components recognising adhesive matrix molecule;
 KM MSCRAMM; fibronectin; fibronectin-binding protein; antibody; epitope;
 KM antibiotic; bacterial infection; antibiotic-resistant strain.

XX Synthetic.

OS Staphylococcus aureus.

PN WO9831389-A2.

PD 23-JUL-1998.

PF 21-JAN-1998; 98WO-US001222.

XX 21-JAN-1997; 97US-0036139P.

XX (TEXA) UNIV TEXAS A & M SYSTEM.

PA Hoeoek M, Patti JM, House-Pompeo KL, Speziale P, Joh D;
 PI McGavin MJ;

DR WPI; 1998-413816/35.

PT Antibody that binds to fibronectin-binding protein, preventing its
 binding to fibronectin - used to treat or prevent bacterial infection,
 PT especially by Staphylococci and Streptococci.

XX Example 9; Page 109; 201pp; English.

CC The invention relates to antibodies that bind to a fibronectin-binding
 CC domain of a fibronectin-binding protein, and inhibit binding of the
 CC protein to fibronectin. Also claimed are: (1) isolated peptides of a
 CC fibronectin-binding protein that do not bind to fibronectin; (2) fusion
 CC protein containing at least one peptide of a fibronectin-binding protein
 CC linked to a second amino acid sequence; (3) nucleic acid encoding the
 CC isolated peptide of (1). Antibodies, the isolated peptides of (1) and the
 CC nucleic acids are all useful for immunisation (active or passive) and (by
 CC inhibiting binding of bacteria to fibronectin) for preventing or treating
 CC infection in humans or other animals, particularly by staphylococci or
 CC streptococci, e.g. meningitis, otitis media, pneumonia, endocarditis,
 CC mastitis in cattle, abortion in horses and many others. Since the
 CC antibodies block binding of bacteria, they should be effective against
 CC antibiotic-resistant strains, and may replace antibiotic therapy or
 CC increase its effectiveness. The present sequence is shown in the

CC specification
 XX
 SQ Sequence 12 AA;

Query Match 100.0%; Score 52; DB 2; Length 12;
 Best Local Similarity 100.0%; Pred. No. 0.013;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SPEEDTEKDK 10
 |||||
 DB 1 SPEEDTEKDK 10

RESULT 3

AAAB82164
 ID AAB82164 standard; peptide; 30 AA.

AC AAB82164;
 XX

DT 20-JUL-2001 (first entry)

DE Peptide fragment of fibronectin-binding protein, FnBP.

XX Antibacterial; antiallergic; cytostatic; TH1 immune response inducer;
 KM vaccine; infectious disease; allergy; cancer;

KM fibronectin-binding protein; FnBP.

XX Staphylococcus aureus.

PN WO200126682-A2.

XX 19-APR-2001.

PF 13-OCT-2000; 2000WO-US028443.

PR 14-OCT-1999; 99GB-00024351.

XX (DOWC) DOW CHEM CO.

PI Brennan F;

DR WPI; 2001-281838/29.

XX Increasing the level of TH1-type responses to molecules, used to treat
 PT infectious diseases, allergies and cancer, comprises conjugating the
 PT molecule to a plant virus.

PS Disclosure; Page 56; 89pp; English.

CC The present invention relates to a method for increasing the level of a
 CC TH1-type immune response to a molecule. The method comprising conjugating
 CC the molecule to a heterologous peptide expressed by a plant virus, and
 CC administering the conjugate to an animal. The method is useful for
 CC treating infectious diseases, allergies and cancer, by administering
 CC appropriate antigens conjugated to a plant virus. The present sequence is
 CC a peptide fragment of the fibronectin-binding protein, FnBP, of
 CC Staphylococcus aureus. This peptide was used to generate a chimeric virus
 CC particle of cowpea mosaic virus (CPMV) for use in the present invention
 CC

SQ Sequence 30 AA;

Query Match 100.0%; Score 52; DB 4; Length 30;
 Best Local Similarity 100.0%; Pred. No. 0.035;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SPEEDTEKDK 10
 |||||
 DB 8 SPEEDTEKDK 17

RESULT 4

ADCC9221
 ID ADC69221 standard; peptide; 30 AA.

```

XX AC ADC69221;
XX DT 18-DEC-2003 (first entry)
XX DE Fibronectin binding protein B (FnbpB) D2 peptide.
XX KM Fibronectin binding protein A; FnbpA; fibronectin binding protein B;
XX KW FnbpB; antibody; staphylococcal infection; D2 peptide; fibronectin;
XX KB antibacterial; immunostimulant.
XX OS Staphylococcus aureus.
XX PN US2003153022-A1.
XX PD 14-AUG-2003.
XX PF 05-NOV-2002; 2002US-00287821.
XX PR 05-NOV-2001; 2001US-0330964P.
XX PA (PATI/) PATTI J M.
XX PA (PATE/) PATEL P.
XX PA (HAL/) HALL A.
XX PA (DOMA/) DOMANSKI P.
XX PA (SYRI/) SYRIBES P.
XX PA (HUTC/) HUTCHINS J T.
XX PI Patti JM, Patel P, Hall A, Domaneki P, Syribes P, Hutchins JT;
XX DR WPI; 2003-801749/75.
XX PT Monoclonal antibody for treating or preventing staphylococcal infections
XX PT binds specified fibronectin binding protein from Staphylococcus aureus.
XX PS Claim 10; SEQ ID NO 1; 12pp; English.
XX CC The invention relates to a new monoclonal antibody that binds fibronectin
XX CC binding proteins from Staphylococcus aureus, including fibronectin
XX CC binding protein A (FnbpA) and fibronectin binding protein B (FnbpB). The
XX CC antibody is useful in treating, preventing or diagnosing staphylococcal
XX CC infections in a human or animal. The antibody is capable of recognising
XX CC Staphylococcus aureus with high affinity. It also inhibits binding of
XX CC staphylococcal bacteria to fibronectin. This sequence represents an FnbpB
XX CC D2 peptide of the invention.
XX SQ Sequence 30 AA;

Query Match 100.0%; Score 52; DB 7; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.035;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 SPEEDTEKDK 10
    |||||
    8 SPEEDTEKDK 17

DB 8 SPEEDTEKDK 17

RESULT 5
ADC69222
ID ADC69222 standard; peptide; 31 AA.
XX AC ADC69222;
XX DT 18-DEC-2003 (first entry)
XX DE Fibronectin binding protein B (FnbpB) modified D2 peptide.
XX KM Fibronectin binding protein A; FnbpA; fibronectin binding protein B;
XX KW FnbpB; antibody; staphylococcal infection; D2 peptide; fibronectin;
XX KB antibacterial; immunostimulant.
XX OS Synthetic.
XX PN Staphylococcus aureus.

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XX PN US2003153022-A1.
XX PD 14-AUG-2003.
XX PF 05-NOV-2002; 2002US-00287821.
XX PR 05-NOV-2001; 2001US-0330964P.
XX PA (PATI/) PATTI J M.
XX PA (PATE/) PATEL P.
XX PA (HAL/) HALL A.
XX PA (DOMA/) DOMANSKI P.
XX PA (SYRI/) SYRIBES P.
XX PA (HUTC/) HUTCHINS J T.
XX PI Patti JM, Patel P, Hall A, Domaneki P, Syribes P, Hutchins JT;
XX DR WPI; 2003-801749/75.
XX PT Monoclonal antibody for treating or preventing staphylococcal infections
XX PT binds specified fibronectin binding protein from Staphylococcus aureus.
XX PS Claim 10; SEQ ID NO 2; 12pp; English.
XX CC The invention relates to a new monoclonal antibody that binds fibronectin
XX CC binding proteins from Staphylococcus aureus, including fibronectin
XX CC binding protein A (FnbpA) and fibronectin binding protein B (FnbpB). The
XX CC antibody is useful in treating, preventing or diagnosing staphylococcal
XX CC infections in a human or animal. The antibody is capable of recognising
XX CC Staphylococcus aureus with high affinity. It also inhibits binding of
XX CC staphylococcal bacteria to fibronectin. This sequence represents a
XX CC modified FnbpB D2 peptide of the invention.
XX SQ Sequence 31 AA;

Query Match 100.0%; Score 52; DB 7; Length 31;
Best Local Similarity 100.0%; Pred. No. 0.036;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 SPEEDTEKDK 10
    |||||
    9 SPEEDTEKDK 18

DB 9 SPEEDTEKDK 18

RESULT 6
AAW65714
ID AAW65714 standard; peptide; 36 AA.
XX AC AAW65714;
XX DT 16-OCT-1998 (first entry)
XX DE Fibronectin binding protein-derived peptide #58.
XX KM microbial surface components recognising adhesive matrix molecule;
XX KW MSCRAMM; fibronectin; fibronectin-binding protein; antibody; epitope;
XX KB antibiotic; bacterial infection; antibiotic-resistant strain.
XX OS Synthetic.
XX PN Staphylococcus aureus.
XX WO9831389-A2.
XX PD 23-JUL-1998.
XX PF 21-JAN-1998; 98WO-US001222.
XX PR 21-JAN-1997; 97US-0036139P.
XX PA (TEXA ) UNIV TEXAS A & M SYSTEM.
XX PI Hoeoek M, Patti JM, House-Pompeo KL, Speziale P, Joh D;

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P1 Mcgavln MJ;
 XX WPI; 1998-413816/35.
 DR
 PT Antibody that binds to fibronectin-binding protein, preventing its
 binding to fibronectin - used to treat or prevent bacterial infection,
 PT especially by *Staphylococci* and *Streptococci*.
 XX
 PS Example 8; page 104; 201pp; English.
 XX
 CC The invention relates to antibodies that bind to a fibronectin-binding
 CC domain of a fibronectin-binding protein, and inhibit binding of the
 CC protein to fibronectin. Also claimed are: (1) isolated peptides of a
 CC fibronectin-binding protein that do not bind to fibronectin; (2) fusion
 CC protein containing at least one peptide of a fibronectin-binding protein
 CC linked to a second amino acid sequence; (3) nucleic acid encoding the
 CC isolated peptide of (1). Antibodies, the isolated peptides of (1) and the
 CC nucleic acids are all useful for immunisation (active or passive) and (by
 CC inhibitory binding of bacteria to fibronectin) for preventing or treating
 CC infection in humans or other animals, particularly by *staphylococci* or
 CC streptococci, e.g. meningitis, otitis media, pneumonia, endocarditis,
 CC mastitis in cattle, abortion in horses and many others. Since the
 CC antibodies block binding of bacteria, they should be effective against
 CC antibiotic-resistant strains, and may replace antibiotic therapy or
 CC increase its effectiveness. The present sequence is shown in the
 CC specification
 CC
 SO Sequence 36 AA;
 QY
 Query Match 100.0%; Score 52; DB 2; Length 36;
 Best Local Similarity 100.0%; Pred. No. 0.043;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0.
 DQ 1 SPEEDTERKD 10
 |||||
 7 SPEEDTERKDK 16
 DB
 RESULT 7
 AAM65715
 AAM65715 standard; peptide; 36 AA.
 AC AAM65715;
 XX
 DT 27-AUG-2003 (revised)
 DT 16-OCT-1998 (first entry)
 XX
 DE Peptide #59.
 XX
 KW microbial surface components recognising adhesive matrix molecule;
 KW MSCRAMM; fibronectin; fibronectin-binding protein; antibody; epitope;
 KW antibiotic; bacterial infection; antibiotic-resistant strain.
 XX
 OS Synthetic.
 OS *Staphylococcus aureus*.
 XX
 PN MO3831389-A2.
 PD
 XX 23-JUL-1998.
 PF
 XX 21-JAN-1998; 98WO-US001222.
 PR 21-JAN-1997; 97US-0036139P.
 PA (TEXA) UNIV TEXAS A & M SYSTEM.
 XX
 PI Hooeok M, Patti JM, House-Pompeo KL, Speziale P, Joh D;
 PI Mcgavln MJ;
 DR WPI; 1998-413816/35.
 PT Antibody that binds to fibronectin-binding protein, preventing its
 binding to fibronectin - used to treat or prevent bacterial infection,
 PT

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PT especially by Staphylococci and Streptococci.
XX Disclosure; Page 160; 20pp; English.
XX
XX The invention relates to antibodies that bind to a fibronectin-binding
CC domain of a fibronectin-binding protein, and inhibit binding of the
CC protein to fibronectin. Also claimed are: (1) isolated peptides of a
CC fibronectin-binding protein that do not bind to fibronectin; (2) fusion
CC protein containing at least one peptide of a fibronectin-binding protein
CC linked to a second amino acid sequence; (3) nucleic acid encoding the
CC isolated peptide of (1). Antibodies, the isolated peptides of (1) and the
CC nucleic acids are all useful for immunisation (active or passive) and (by
CC inhibiting binding of bacteria to fibronectin) for preventing or treating
CC infection in humans or other animals, particularly by staphylococci or
CC streptococci, e.g. meningitis, otitis media, pneumonia, endocarditis,
CC mastitis in cattle, abortion in horses and many others. Since the
CC antibodies block binding of bacteria, they should be effective against
CC antibiotic-resistant strains, and may replace antibiotic therapy or
CC increase its effectiveness. The present sequence is shown in the
CC specification. (Updated on 27-AUG-2003 to correct OS field.)
XX
XX Sequence 36 AA;
XX
XX Query Match 100.0%; Score 52; DB 2; Length 36;
XX Best Local Similarity 100.0%; Pred. No. 0.043;
XX Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0
XX
XX 1 SPEEDTEKDK 10
XX |||||
XX 7 SPEEDTEKDK 16
XX
XX RESULT 8
XX ID AAB80661
XX AAB80661 standard; protein; 38 AA.
XX
XX AAB80661;
XX
XX 25-MAR-2003 (revised)
XX DT 07-OCT-1990 (first entry)
XX
XX Protein with fibronectin binding ability.
XX
XX Hybrid DNA molecule; fibronectin binding; mastitis; ruminants;
XX wound infection.
XX
XX Staphylococcus aureus.
XX
XX EP294349-A.
XX
XX 07-DEC-1988.
XX
XX 30-MAY-1988; 88EP-00850188.
XX
XX 01-JUN-1987; 87SE-00002272.
XX
XX (ALFA ) ALFA LAVAL AGRIC INT AB.
XX
XX Lindberg MK, Signaes LC, Wadstrom TW, Froman G;
XX
XX WPI; 1988-347978/49.
XX
XX N-PSDB; AAN81098.
XX
XX Hybrid DNA encoding Staphylococcus aureus fibronectin binding protein -
XX useful for immunisation and topical application to prevent staphylococcal
XX infections.
XX
XX Claim 11; Page 12; 23pp; English.
XX
XX The peptide has fibronectin binding ability. It is useful for immunising
XX ruminants against staphylococcal mastitis, pref. when used at 0.5-5
XX micrograms/kg, using 3 doses given at 1-3 week intervals; for topical
XX application to prevent wound infection, using an isotonic saline soln. of

```

CC concn. 25-250 micrograms/ml; and, when immobilised on a carrier, for
 CC diagnosing staphylococcal infections. (Updated on 25-MAR-2003 to correct
 CC PF field.) (Updated on 25-MAR-2003 to correct PA field.)
 XX

SQL Sequence 38 AA;

Query Match 100.0%; Score 52; DB 1; Length 38;
 Best Local Similarity 100.0%; Pred. No. 0.045;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SPEEDTEKDK 10
 |||||
 DB 8 SPEEDTEKDK 17

RESULT 9

AA82117
 ID AAP82117 standard; protein; 38 AA.

XX AAP82117;

AC 25-MAR-2003 (revised)
 XX 05-JAN-1990 (first entry)

DT Fibronectin binding protein.
 XX

XX Fibronectin binding protein; S.aureus; immunisation; mastitis; ruminants;
 KM wound infection; diagnosis.

XX Staphylococcus aureus.

XX EP294349-A.

XX 07-DEC-1988.

XX 30-MAY-1988; 88EP-00850188.

XX 01-JUN-1987; 87SE-00002272.

XX (ALFA) ALFA LAVVL AGRIC INT AB.

XX Lindberg MK, Signas LC, Wadstrom TM, Froman G;
 DR WPI: 1988-347978/49.

XX N-PSDB; AAN82055.

XX Hybrid DNA encoding Staphylococcus aureus fibronectin binding protein -
 PT useful for immunisation and topical application to prevent staphylococcal
 PT infections.

XX Claim 11; Page 12; 23pp; English.

XX The S.aureus fibronectin binding protein may be included in a hybrid
 CC protein. The protein may be used to immunise ruminants against
 CC staphylococcal mastitis, pref. when given at 0.5-5 microg/kg, using 3
 CC doses at 1-3 week intervals; and for topical applicn. to prevent wound
 CC infection, pref. using isotonic saline soln. of concn. 25-250 microg/mg.
 CC The DNA encoding the binding protein and the hybrid protein may be
 CC immobilised on a carrier and used to diagnose staphylococcal infections.
 CC (Updated on 25-MAR-2003 to correct PA field.)
 XX

SQL Sequence 38 AA;

Query Match 100.0%; Score 52; DB 1; Length 38;
 Best Local Similarity 100.0%; Pred. No. 0.045;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SPEEDTEKDK 10
 |||||
 DB 8 SPEEDTEKDK 17

RESULT 10

AAW65664
 ID AAW65664 standard; peptide; 38 AA.

XX AAW65664;

XX 16-OCT-1998 (first entry)

XX Fibronectin binding protein-derived peptide #8.

XX microbial surface components recognising adhesive matrix molecule;
 KM MSCRAMM; fibronectin; fibronectin-binding protein; antibody; epitope;
 KM antibiotic; bacterial infection; antibiotic-resistant strain.

XX Synthetic.

OS Staphylococcus aureus.

XX WO9831389-A2.

XX 23-JUL-1998.

XX 21-JAN-1998; 98WO-US001222.

XX 21-JAN-1997; 97US-0036139P.

XX (TEXA) UNIV TEXAS A & M SYSTEM.

XX Hoeoek M, Patti JM, House-Pompeo KL, Speziale P, Joh D;
 PI McGavin MJ;

XX WPI: 1998-413816/35.

XX Antibody that binds to fibronectin-binding protein, preventing its
 PT binding to fibronectin - used to treat or prevent bacterial infection,
 PT especially by Staphylococci and Streptococci.

XX Example 2; Page 92; 201pp; English.

XX The invention relates to antibodies that bind to a fibronectin-binding
 CC domain of a fibronectin-binding protein, and inhibit binding of the
 CC protein to fibronectin. Also claimed are: (1) isolated peptides of a
 CC fibronectin-binding protein that do not bind to fibronectin; (2) fusion
 CC protein containing at least one peptide of a fibronectin-binding protein
 CC linked to a second amino acid sequence; (3) nucleic acid encoding the
 CC isolated peptide of (1). Antibodies, the isolated peptides of (1) and the
 CC nucleic acids are all useful for immunisation (active or passive) and (by
 CC inhibiting binding of bacteria to fibronectin) for preventing or treating
 CC infection in humans or other animals, particularly by staphylococci or
 CC streptococci, e.g. meningitis, otitis media, pneumonia, endocarditis,
 CC mastitis in cattle, abortion in horses and many others. Since the
 CC antibodies block binding of bacteria, they should be effective against
 CC antibiotic-resistant strains, and may replace antibiotic therapy or
 CC increase its effectiveness. Sequences AAW65659-68 represent synthetic
 CC epitopes from the fibronectin binding domains DU and DI-D4 of the S.
 CC aureus fnbA gene
 XX

SQL Sequence 38 AA;

Query Match 100.0%; Score 52; DB 2; Length 38;
 Best Local Similarity 100.0%; Pred. No. 0.045;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SPEEDTEKDK 10
 |||||
 DB 7 SPEEDTEKDK 16

RESULT 11

AAW65705
 ID AAW65705 standard; peptide; 38 AA.

XX AAW65705;

XX 16-OCT-1998 (first entry)

```

XX Fibronectin binding protein-derived peptide #49.
DE
XX microbial surface components recognising adhesive matrix molecule;
XX MSCRAMM; fibronectin; fibronectin-binding protein; antibody; epitope;
KM antibiotic; bacterial infection; antibiotic-resistant strain.
XX
OS Synthetic.
OS Staphylococcus aureus.
XX
XX WO9831389-A2.
XX
XX 23-JUL-1998.
XX
XX 21-JAN-1998; 98WO-US001222.
XX
XX 21-JAN-1997; 97US-0036139P.
XX
XX (TEXA ) UNIV TEXAS A & M SYSTEM.
XX
XX Hoeoek M, Patli JM, House-Pompeo KL, Speziale P, Joh D;
XX McGavin MJ;
XX WPI; 1998-413816/35.
XX
XX Antibody that binds to fibronectin-binding protein, preventing its
XX binding to fibronectin - used to treat or prevent bacterial infection,
XX especially by Staphylococci and Streptococci.
XX
XX Example 8, Page 102; 201pp; English.
XX
XX The invention relates to antibodies that bind to a fibronectin-binding
XX domain of a fibronectin-binding protein, and inhibit binding of the
XX protein to fibronectin. Also claimed are: (1) isolated peptides of a
XX fibronectin-binding protein that do not bind to fibronectin; (2) fusion
XX protein containing at least one peptide of a fibronectin-binding protein
XX linked to a second amino acid sequence; (3) nucleic acid encoding the
XX isolated peptide of (1). Antibodies, the isolated peptides of (1) and the
XX nucleic acids are all useful for immunisation (active or passive) and (by
XX inhibiting binding of bacteria to fibronectin) for preventing or treating
XX infection in humans or other animals, particularly by staphylococci or
XX streptococci, e.g. meningitis, otitis media, pneumonia, endocarditis,
XX mastitis in cattle, abortion in horses and many others. Since the
XX antibodies block binding of bacteria, they should be effective against
XX antibiotic-resistant strains, and may replace antibiotic therapy or
XX increase its effectiveness. Sequences AAM65701-706 represent a series of
XX synthetic peptides based on the D2 region of S. aureus fibronectin
XX binding protein A. They were synthesised to contain mutations
XX
XX Sequence 38 AA:
SQ
Query Match 100.0%; Score 52; DB 2; Length 38;
Best Local Similarity 100.0%; Pred. No. 0.045;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 SPEEDTEKDK 10
Db 7 SPEEDTEKDK 16
RESULT 12
AAM65663
ID AAM65663 standard; peptide; 38 AA.
XX
XX AAM65663;
AC
XX
XX 16-OCT-1998 (first entry)
XX
XX Fibronectin binding protein-derived peptide #7.
DE
XX microbial surface components recognising adhesive matrix molecule;
KM MSCRAMM; fibronectin; fibronectin-binding protein; antibody; epitope;
KM antibiotic; bacterial infection; antibiotic-resistant strain.

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XX
OS Synthetic.
OS Staphylococcus aureus.
XX
XX WO9831389-A2.
XX
XX 23-JUL-1998.
XX
XX 21-JAN-1998; 98WO-US001222.
XX
XX 21-JAN-1997; 97US-0036139P.
XX
XX (TEXA ) UNIV TEXAS A & M SYSTEM.
XX
XX Hoeoek M, Patli JM, House-Pompeo KL, Speziale P, Joh D;
XX McGavin MJ;
XX WPI; 1998-413816/35.
XX
XX Antibody that binds to fibronectin-binding protein, preventing its
XX binding to fibronectin - used to treat or prevent bacterial infection,
XX especially by Staphylococci and Streptococci.
XX
XX Example 2; Page 92; 201pp; English.
XX
XX The invention relates to antibodies that bind to a fibronectin-binding
XX domain of a fibronectin-binding protein, and inhibit binding of the
XX protein to fibronectin. Also claimed are: (1) isolated peptides of a
XX fibronectin-binding protein that do not bind to fibronectin; (2) fusion
XX protein containing at least one peptide of a fibronectin-binding protein
XX linked to a second amino acid sequence; (3) nucleic acid encoding the
XX isolated peptide of (1). Antibodies, the isolated peptides of (1) and the
XX nucleic acids are all useful for immunisation (active or passive) and (by
XX inhibiting binding of bacteria to fibronectin) for preventing or treating
XX infection in humans or other animals, particularly by staphylococci or
XX streptococci, e.g. meningitis, otitis media, pneumonia, endocarditis,
XX mastitis in cattle, abortion in horses and many others. Since the
XX antibodies block binding of bacteria, they should be effective against
XX antibiotic-resistant strains, and may replace antibiotic therapy or
XX increase its effectiveness. Sequences AAM6559-68 represent synthetic
XX epitopes from the fibronectin binding domains DV and DI-D4 of the S.
XX aureus fbnA gene
XX
XX Sequence 38 AA:
SQ
Query Match 100.0%; Score 52; DB 2; Length 38;
Best Local Similarity 100.0%; Pred. No. 0.045;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 SPEEDTEKDK 10
Db 7 SPEEDTEKDK 16
RESULT 13
AAR8749
ID AAR8749 standard; protein; 77 AA.
XX
XX AAR8749;
AC
XX
XX 24-SEP-1996 (first entry)
XX
XX S. aureus fibronectin binding protein D2D3 polypeptide.
DE
XX Fibronectin binding protein; D2D3; prevention; adhesion; bacteria;
KM gram positive; extra-cellular matrix protein; in-dwelling device;
KM catheter; wound; D2D3; oral pathogen; oral cavity; J2385; NCIMB 40532.
XX
XX Staphylococcus aureus.
XX
XX WO9604380-A1.
XX
XX 15-FEB-1996.

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XX PF 28-JUL-1995; 95WO-EP003039.
XX XX
PR 05-AUG-1994; 94GB-00015901.
XX PA (SMIK ) SMITHKLIN BEECHAM PLC.
XX PI Critchley IA, Dodd I, Barnett P, Mosakowska DEI;
XX DR WPI; 1996-129396/13.
XX DR N-PSDB; AAT12582.
XX PT Staphylococcus aureus fibronectin binding protein D2D3 polypeptide -
XX PT useful for combatting infection at wound sites, surgical implants, etc.
XX PT and as antiadherent agent in oral hygiene.
XX PS Claim 5; Page 26; 38pp; English.
XX CC The present sequence is the S. aureus fibronectin binding protein
XX CC polypeptide D2D3, which can be used to prevent adhesion of (e.g. gram
XX CC positive) bacteria, to extra-cellular matrix proteins on in-dwelling
XX CC devices, e.g. catheters or in wounds. D2D3 can also be used to prevent
XX CC oral pathogens from binding to extra-cellular matrix proteins, in the
XX CC oral cavity. D2D3 was found to be effective at inhibiting S. aureus 8325-
XX CC 4, and 120 adhesion to fibronectin coated PMMA coverslips, at a min.
XX CC adhesion inhibitor concn. of 10 microg/ml. D2D3 was derived from the D2
XX CC and D3 regions of the S. aureus J2385 (NCIMB 40532) fibronectin binding
XX CC protein
XX SQ Sequence 77 AA;

Query Match 100.0%; Score 52; DB 2; Length 77;
Best Local Similarity 100.0%; Pred. No. 0.099;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SPEEDTERKX 10
DB 8 SPEEDTERKX 17

RESULT 14
AAR90937
ID AAR90937 standard; peptide; 113 AA.
XX AC AAR90937;
XX DT 23-SEP-1996 (first entry)
XX DE D3D4 polypeptide #1.
XX KW Fibronectin binding protein; Fbp; S. aureus J2385; monoclonal antibody;
XX KW infection; surgical implant; antiadherent agent; hygiene; adhesion;
XX KW extracellular matrix protein; oral pathogen; oral cavity.
XX OS Staphylococcus aureus.
XX FH Key Location/Qualifiers
FH FT 1..21 Region /note="D1 region fragment"
FH FT 22..59 Region /note="D2 region"
FH FT 60..98 Region /note="D3 region"
FH FT 99..113 Region /note="D4 region"
FH FT Misc-difference 113 /note="D4 region"
FH FT /note="P113T"
XX WO9604381-A1.
XX PD 15-FEB-1996.
XX PF 28-JUL-1995; 95WO-EP003040.

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XX PR 05-AUG-1994; 94GB-00015900.
XX XX
XX PA (SMIK ) SMITHKLIN BEECHAM PLC.
XX PI Critchley IA, Dodd I, Barnett P, Mcbay DL;
XX DR WPI; 1996-129397/13.
XX PT Polypeptide(s) derived from Staphylococcus aureus fibronectin binding
XX PT protein - inhibit binding of bacteria to extracellular matrix proteins,
XX PT for combatting infection at the site of wounds and surgical implants, and
XX PT in oral hygiene.
XX PS Claim 6; Page 24; 35pp; English.
XX CC AAR90937-R90942 represent D3D4 polypeptides. These sequences correspond
XX CC to fragments of the Staphylococcus aureus fibronectin binding protein
XX CC (Fbp). This sequence corresponds to residues 18-130 of S. aureus J2385
XX CC Fbp, and also contains the D2 region, and a portion of the D1 region.
XX CC These sequences, and monoclonal antibodies against them can be used to
XX CC combat infection at the site of wounds, surgical implants and other in-
XX CC dwelling devices (such as catheters), and as antiadherent agents in oral
XX CC hygiene. They can also be used in the manufacture of a medicament for the
XX CC prevention of adhesion of bacteria to extracellular matrix proteins
XX CC present on in-dwelling devices or in wounds, or of oral pathogens to
XX CC similar proteins on surfaces in the oral cavity
XX SQ Sequence 113 AA;

Query Match 100.0%; Score 52; DB 2; Length 113;
Best Local Similarity 100.0%; Pred. No. 0.15;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SPEEDTERKX 10
DB 29 SPEEDTERKX 38

RESULT 15
AAR58806
ID AAR58806 standard; protein; 130 AA.
XX AC AAR58806;
XX DT 25-MAR-2003 (revised)
XX DT 30-MAR-1995 (first entry)
XX DE Fibronectin binding domain D1-D4(709-838(P838T)).
XX KW Fibronectin binding protein; Fbp; fibronectin binding domain;
XX KW monoclonal antibody; Mab; adhesion; Gram-positive bacterium; bacteremia;
XX KW Escherichia coli.
XX OS Staphylococcus aureus.
XX FH Key Location/Qualifiers
FH FT 1..18327-A1.
FH FT 18-AUG-1994.
FH FT 04-FEB-1994; 94WO-GB000215.
FH FT 05-FEB-1993; 93GB-00002289.
FH FT 20-OCT-1993; 93GB-00021592.
XX PA (SMIK ) SMITHKLIN BEECHAM PLC.
XX PI Burnham MKR, Chopra I, Critchley IA, Knowles DJC;
XX DR WPI; 1994-279748/34.
XX PT Fibronectin binding protein and monoclonal antibodies specific for Fbp -
XX PT useful to prevent adherence of Gram-positive bacteria to indwelling

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PT devices or wounds.

PS Disclosure; Page 30; 40pp; English.

CC Polypeptides corresponding to residues G709-1886 plus P19YPT, G709-
CC P838 (P838T) and G709-P838 (AA958605-07, respectively) of *S. aureus* J2395
CC (NCIMB 40532). Pop type A fibronectin binding domain D1-D4 region
CC (AA958608) were expressed in *E. coli* BL21 (DE4) and used to raise Mabs
CC specific for Fbp. (Updated on 25-MAR-2003 to correct PN field.)

SQ Sequence 130 AA;

Sequence 130 AA;

Query Match	Score 52;	DB 2;	Length 130;
	100.0%		

Best Local Similarity 100.0%; Pred. NO. 0.18;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SPEEDTEKDK 10

Db 46 SPEEDTEK 55

Search completed: October 25, 2005, 21:29:08
Job time : 71.7126 secs

Job time : 71.7126 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 22, 2005, 07:41:53 ; Search time 17.2989 Seconds
(without alignments)
43.153 Million cell updates/sec

Title: US-10-731-238-85

Sequence: 1 SPEDTEKDK 10

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database:

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2: /cgn2_6/ptodata/1/1aa/5B.COMB.pep:*
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4: /cgn2_6/ptodata/1/1aa/6B.COMB.pep:*
5: /cgn2_6/ptodata/1/1aa/PCTUS.COMB.pep:*
6: /cgn2_6/ptodata/1/1aa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	52	100.0	10	4	US-09-010-317-85
2	52	100.0	12	4	US-09-010-317-62
3	52	100.0	36	4	US-09-010-317-58
4	52	100.0	36	4	US-09-010-317-59
5	52	100.0	38	1	US-08-234-622A-3
6	52	100.0	38	1	US-08-729-767-4
7	52	100.0	38	4	US-09-010-317-7
8	52	100.0	38	4	US-09-010-317-8
9	52	100.0	38	4	US-09-010-317-49
10	52	100.0	114	1	US-08-259-000-3
11	52	100.0	130	2	US-08-459-135A-7
12	52	100.0	130	2	US-08-459-135A-8
13	52	100.0	130	3	US-08-495-559-7
14	52	100.0	130	3	US-08-495-559-8
15	52	100.0	139	3	US-08-856-253-8
16	52	100.0	174	2	US-08-459-135A-10
17	52	100.0	174	2	US-08-459-135A-13
18	52	100.0	174	2	US-08-495-559-10
19	52	100.0	174	3	US-08-495-559-13
20	52	100.0	176	3	US-08-495-559-6
21	52	100.0	178	3	US-08-459-135A-12
22	52	100.0	181	2	US-08-459-135A-6
23	52	100.0	559	4	US-08-956-171E-5251
24	52	100.0	559	4	US-08-781-986A-5251
25	52	100.0	1027	4	US-08-956-171E-5254
26	52	100.0	1027	4	US-08-781-986A-5254
27	52	100.0	1027	4	US-08-781-986A-5254

28	48	92.3	10	4	US-09-010-317-66	Sequence 66, Appl
29	48	92.3	14	4	US-09-010-317-105	Sequence 105, App
30	48	92.3	38	1	US-08-234-622A-2	Sequence 2, Appl1
31	48	92.3	38	1	US-08-729-767-3	Sequence 3, Appl1
32	48	92.3	38	4	US-09-010-317-5	Sequence 5, Appl1
33	48	92.3	38	4	US-09-010-317-6	Sequence 6, Appl1
34	48	92.3	38	4	US-09-010-317-43	Sequence 43, Appl1
35	48	92.3	39	4	US-09-010-317-56	Sequence 56, Appl
36	48	92.3	39	4	US-09-010-317-57	Sequence 57, Appl
37	46	88.5	38	4	US-09-010-317-41	Sequence 41, Appl
38	46	88.5	38	4	US-09-010-317-46	Sequence 46, Appl
39	46	88.5	38	4	US-09-010-317-47	Sequence 47, Appl
40	45	86.5	38	4	US-09-010-317-48	Sequence 48, Appl
41	42	80.8	10	4	US-09-010-317-2	Sequence 2, Appl1
42	42	80.8	38	4	US-09-010-317-36	Sequence 36, Appl
43	42	80.8	38	4	US-09-010-317-37	Sequence 37, Appl
44	42	80.8	38	4	US-09-010-317-39	Sequence 39, Appl
45	42	80.8	38	4	US-09-010-317-40	Sequence 40, Appl

ALIGNMENTS

RESULT 1
US-09-010-317-85
Sequence 85, Application US/09010317
Patent No. 6685943
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
APPLICANT: Patl, Joseph M.
APPLICANT: House-Pompeo, Karen L.
APPLICANT: Speziale, Pietro
APPLICANT: Joh, Danny
APPLICANT: McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
TITLE OF INVENTION: AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/010.317
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAMK.189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 85:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-09-010-317-85
Query Match 100.0%; Score 52; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0051;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 SPEEDTEKDK 10
Db 1 SPEEDTEKDK 10

RESULT 2

US-09-010-317-62
; Sequence 62, Application US/09010317
; Patent No. 6685943
; GENERAL INFORMATION:
; APPLICANT: Hook, Magnus
; APPLICANT: Patti, Joseph M.
; APPLICANT: House-Pompeo, Karen L.
; APPLICANT: Speziale, Pietro
; APPLICANT: Joh, Danny
; APPLICANT: McGavin, Martin J.
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
; TITLE OF INVENTION: AND METHODS OF USE
; NUMBER OF SEQUENCES: 105
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: TX
; COUNTRY: USA
; ZIP: 77210-4433
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/010,317
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/036,139
; FILING DATE: 21-JAN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Hibler, David W.
; REGISTRATION NUMBER: 41,071
; REFERENCE/DOCKET NUMBER: TAMK:189
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 512-418-3000
; TELEFAX: 512-474-7577
; INFORMATION FOR SEQ ID NO: 62:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
US-09-010-317-62

Query Match 100.0%; Score 52; DB 4; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.0062;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SPEEDTEKDK 10
Db 1 SPEEDTEKDK 10

RESULT 3

US-09-010-317-58
; Sequence 58, Application US/09010317
; Patent No. 6685943
; GENERAL INFORMATION:
; APPLICANT: Hook, Magnus
; APPLICANT: Patti, Joseph M.
; APPLICANT: House-Pompeo, Karen L.
; APPLICANT: Speziale, Pietro

; APPLICANT: Joh, Danny
; APPLICANT: McGavin, Martin J.
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
; TITLE OF INVENTION: AND METHODS OF USE
; NUMBER OF SEQUENCES: 105
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: TX
; COUNTRY: USA
; ZIP: 77210-4433
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/010,317
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/036,139
; FILING DATE: 21-JAN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Hibler, David W.
; REGISTRATION NUMBER: 41,071
; REFERENCE/DOCKET NUMBER: TAMK:189
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 512-418-3000
; TELEFAX: 512-474-7577
; INFORMATION FOR SEQ ID NO: 58:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 36 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
US-09-010-317-58

Query Match 100.0%; Score 52; DB 4; Length 36;
Best Local Similarity 100.0%; Pred. No. 0.019;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SPEEDTEKDK 10
Db 7 SPEEDTEKDK 16

RESULT 4

US-09-010-317-59
; Sequence 59, Application US/09010317
; Patent No. 6685943
; GENERAL INFORMATION:
; APPLICANT: Hook, Magnus
; APPLICANT: Patti, Joseph M.
; APPLICANT: House-Pompeo, Karen L.
; APPLICANT: Speziale, Pietro
; APPLICANT: Joh, Danny
; APPLICANT: McGavin, Martin J.
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
; TITLE OF INVENTION: AND METHODS OF USE
; NUMBER OF SEQUENCES: 105
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: TX
; COUNTRY: USA
; ZIP: 77210-4433
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/010,317
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/036,139
; FILING DATE: 21-JAN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Hibler, David W.
; REGISTRATION NUMBER: 41,071
; REFERENCE/DOCKET NUMBER: TAMK:189
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 512-418-3000
; TELEFAX: 512-474-7577
; INFORMATION FOR SEQ ID NO: 59:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 36 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
US-09-010-317-59

SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 59:
SEQUENCE CHARACTERISTICS:
LENGTH: 36 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-09-010-317-59

Query Match 100.0%; Score 52; DB 4; Length 36;
Best Local Similarity 100.0%; Pred. No. 0.019;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SPEEDTERDK 10
Db 7 SPEEDTERDK 16

RESULT 5
US-08-234-622A-3
Sequence 3, Application US/08234622A
Patent No. 5440014
GENERAL INFORMATION:
APPLICANT: HOOK, Magnus
APPLICANT: MCGAVIN, Martin
APPLICANT: RAUCCI, Giuseppe
TITLE OF INVENTION: A FIBRONECTIN BINDING PEPTIDE
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Burns, Doane, Swecker & Mathis
STREET: P.O. Box 1404
CITY: Alexandria
STATE: Virginia
COUNTRY: United States
ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/234,622A
FILING DATE: 28-APR-1994
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: SE 9002617-0
FILING DATE: 10-AUG-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/SE91/00534
FILING DATE: 09-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: Neuth, Donna M
REGISTRATION NUMBER: 36,607
REFERENCE/DOCKET NUMBER: 012885-044
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:

LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-234-622A-3

Query Match 100.0%; Score 52; DB 1; Length 38;
Best Local Similarity 100.0%; Pred. No. 0.02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SPEEDTERDK 10
Db 7 SPEEDTERDK 16

RESULT 6
US-08-729-767-4
Sequence 4, Application US/08729767
Patent No. 5770702
GENERAL INFORMATION:
APPLICANT: HOOK, Magnus
APPLICANT: LINDBERG, Martin Kjell
APPLICANT: SIGNAS, Lars Christer
APPLICANT: WADSTROM, Torkel Mikael
APPLICANT: FROMAN, Gunnar
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN AS WELL AS
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Burns, Doane, Swecker & Mathis, L.L.P.
STREET: P.O. Box 1404
CITY: Alexandria
STATE: Virginia
COUNTRY: United States
ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/729,767
FILING DATE: 07-OCT-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/259,000
FILING DATE: 13-JUN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/007,817
FILING DATE: 22-JAN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/201,028
FILING DATE: 01-JUN-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: SE 8702272-9
FILING DATE: 01-JUN-1987
ATTORNEY/AGENT INFORMATION:
NAME: McGowan, Malcolm K.
REGISTRATION NUMBER: 39,300
REFERENCE/DOCKET NUMBER: 012889-036
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-729-767-4

Query Match 100.0%; Score 52; DB 1; Length 38;
Best Local Similarity 100.0%; Pred. No. 0.02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SPEEDTEKDK 10
Db 8 SPEEDTEKDK 17

RESULT 7

US-09-010-317-7
; Sequence 7, Application US/09010317
; Patent No. 6685943
; GENERAL INFORMATION:
; APPLICANT: Hook, Magnus
; APPLICANT: Patti, Joseph M.
; APPLICANT: House-Pompeo, Karen L.
; APPLICANT: Speziale, Pietro
; APPLICANT: Joh, Danny
; APPLICANT: McGavin, Martin J.
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
; TITLE OF INVENTION: AND METHODS OF USE
; NUMBER OF SEQUENCES: 105
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: TX
; COUNTRY: USA
; ZIP: 77210-4433
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/010,317
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/036,139
; FILING DATE: 21-JAN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Hibler, David W.
; REGISTRATION NUMBER: 41,071
; REFERENCE/DOCKET NUMBER: TAMK:189
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 512-418-3000
; TELEFAX: 512-474-7577
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 38 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
US-09-010-317-7

Query Match 100.0%; Score 52; DB 4; Length 38;
Best Local Similarity 100.0%; Pred. No. 0.02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SPEEDTEKDK 10
Db 7 SPEEDTEKDK 16

RESULT 8

US-09-010-317-8
; Sequence 8, Application US/09010317
; Patent No. 6685943
; GENERAL INFORMATION:
; APPLICANT: Hook, Magnus
; APPLICANT: Patti, Joseph M.

; APPLICANT: House-Pompeo, Karen L.
; APPLICANT: Speziale, Pietro
; APPLICANT: Joh, Danny
; APPLICANT: McGavin, Martin J.
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
; TITLE OF INVENTION: AND METHODS OF USE
; NUMBER OF SEQUENCES: 105
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: TX
; COUNTRY: USA
; ZIP: 77210-4433
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/010,317
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/036,139
; FILING DATE: 21-JAN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Hibler, David W.
; REGISTRATION NUMBER: 41,071
; REFERENCE/DOCKET NUMBER: TAMK:189
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 512-418-3000
; TELEFAX: 512-474-7577
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 38 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
US-09-010-317-8

Query Match 100.0%; Score 52; DB 4; Length 38;
Best Local Similarity 100.0%; Pred. No. 0.02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SPEEDTEKDK 10
Db 7 SPEEDTEKDK 16

RESULT 9

US-09-010-317-49
; Sequence 49, Application US/09010317
; Patent No. 6685943
; GENERAL INFORMATION:
; APPLICANT: Hook, Magnus
; APPLICANT: Patti, Joseph M.
; APPLICANT: House-Pompeo, Karen L.
; APPLICANT: Speziale, Pietro
; APPLICANT: Joh, Danny
; APPLICANT: McGavin, Martin J.
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
; TITLE OF INVENTION: AND METHODS OF USE
; NUMBER OF SEQUENCES: 105
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: TX
; COUNTRY: USA
; ZIP: 77210-4433
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/010.317
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/036.139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAMK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 49:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-09-010-317-49

Query Match 100.0%; Score 52; DB 4; Length 38;
Best Local Similarity 100.0%; Pred. No. 0.02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SPEEDTEKDK 10
Db 7 SPEEDTEKDK 16

RESULT 10
US-08-259-000-3
Sequence 3, Application US/08259000
Patent No. 5571514
GENERAL INFORMATION:
APPLICANT: HOOK, Magnus
APPLICANT: LINDBERG, Martin Kjell
APPLICANT: SIGNAS, Lars Christer
APPLICANT: WADSTROM, Torke Mikael
APPLICANT: FROMAN, Gunnar
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN AS WELL AS
TITLE OF INVENTION: ITS PREPARATION
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSER: Burns, Doane, Swecker & Mathis
STREET: P. O. Box 1404
CITY: Alexandria
STATE: Virginia
COUNTRY: United States
ZIP: 2213-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/259.000
FILING DATE: 13-JUN-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: SE 8702272-9
FILING DATE: 01-JUN-1987
ATTORNEY/AGENT INFORMATION:
NAME: Meuth, Donna M
REGISTRATION NUMBER: 36,607
REFERENCE/DOCKET NUMBER: 012885-062
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021

INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 114 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-259-000-3

Query Match 100.0%; Score 52; DB 1; Length 114;
Best Local Similarity 100.0%; Pred. No. 0.063;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SPEEDTEKDK 10
Db 46 SPEEDTEKDK 55

RESULT 11
US-08-459-135A-7
Sequence 7, Application US/08459135A
Patent No. 5955078
GENERAL INFORMATION:
APPLICANT: BURHAM, Martin Karl Russel
APPLICANT: CHOPRA, Ian
APPLICANT: CRITCHLEY, Ian Alfred
APPLICANT: KNOWLES, David Justin Charles
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN: MONOCLONAL ANTIBODY AND THEIR US
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSER: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
STATE: PA
COUNTRY: U.S.A.
ZIP: 19406-0939
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: Fastseq, Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/459.135A
FILING DATE: 02-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB/94/00215
FILING DATE: 04-Feb-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Gimm, Edward R
REGISTRATION NUMBER: 38,891
REFERENCE/DOCKET NUMBER: P30591C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-4478
TELEFAX: 610-270-5090
TELEX:
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 130 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-459-135A-7

Query Match 100.0%; Score 52; DB 2; Length 130;
Best Local Similarity 100.0%; Pred. No. 0.072;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SPEEDTEKDK 10
Db 46 SPEEDTEKDK 55

RESULT 12

US-08-459-135A-8

Sequence 8, Application US/08459135A

Patent No. 5953078

GENERAL INFORMATION:

APPLICANT: BURHAM, Martin Karl Russel

APPLICANT: CHOPRA, Ian

APPLICANT: CRITCHLEY, Ian Alfred

APPLICANT: KNOWLES, David Justin Charles

TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN: MONOCLONAL ANTIBODY AND THEIR USE

NUMBER OF SEQUENCES: 15

CORRESPONDENCE ADDRESS:

ADDRESS: SmithKline Beecham Corporation

STREET: 709 Swedeland Road

CITY: King of Prussia

STATE: PA

COUNTRY: U.S.A.

ZIP: 19406-0939

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FastSeq, Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/459,135A

FILING DATE: 02-JUN-1995

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/GB/94/00215

FILING DATE: 04-Feb-1994

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Gimml, Edward R

REGISTRATION NUMBER: 38,891

REFERENCE/DOCKET NUMBER: P30591C2

TELECOMMUNICATION INFORMATION:

TELEPHONE: 610-270-4478

TELEFAX: 610-270-5090

TELEX:

INFORMATION FOR SEQ ID NO: 8:

SEQUENCE CHARACTERISTICS:

LENGTH: 130 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-459-135A-8

Query Match 100.0%; Score 52; DB 2; Length 130;

Best Local Similarity 100.0%; Pred. No. 0.072;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SPEEDTEKDK 10

Db 46 SPEEDTEKDK 55

RESULT 13

US-08-495-559-7

Sequence 7, Application US/08495559A

Patent No. 6054572

GENERAL INFORMATION:

APPLICANT: BURHAM, Martin Karl Russel

APPLICANT: CHOPRA, Ian

APPLICANT: CRITCHLEY, Ian Alfred

APPLICANT: KNOWLES, David Justin Charles

TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN: MONOCLONAL

FILE REFERENCE: P30591

CURRENT APPLICATION NUMBER: US/08/495,559A

EARLIER FILING DATE: 1995-08-03

EARLIER APPLICATION NUMBER: GB 9302289.5

EARLIER FILING DATE: 1993-02-05

EARLIER APPLICATION NUMBER: GB 9321592.9

EARLIER FILING DATE: 1993-10-20

NUMBER OF SEQ ID NOS: 13

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 7

LENGTH: 130

TYPE: PRT

ORGANISM: Staphylococcus aureus

US-08-495-559-7

Query Match 100.0%; Score 52; DB 3; Length 130;

Best Local Similarity 100.0%; Pred. No. 0.072;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SPEEDTEKDK 10

Db 46 SPEEDTEKDK 55

RESULT 14

US-08-495-559-8

Sequence 8, Application US/08495559A

Patent No. 6054572

GENERAL INFORMATION:

APPLICANT: BURHAM, Martin Karl Russel

APPLICANT: CHOPRA, Ian

APPLICANT: CRITCHLEY, Ian Alfred

APPLICANT: KNOWLES, David Justin Charles

TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN: MONOCLONAL

FILE REFERENCE: P30591

CURRENT APPLICATION NUMBER: US/08/495,559A

CURRENT FILING DATE: 1995-08-03

EARLIER APPLICATION NUMBER: GB 9302289.5

EARLIER FILING DATE: 1993-02-05

EARLIER APPLICATION NUMBER: GB 9321592.9

EARLIER FILING DATE: 1993-10-20

NUMBER OF SEQ ID NOS: 13

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 8

LENGTH: 130

TYPE: PRT

ORGANISM: Staphylococcus aureus

US-08-495-559-8

Query Match 100.0%; Score 52; DB 3; Length 130;

Best Local Similarity 100.0%; Pred. No. 0.072;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SPEEDTEKDK 10

Db 46 SPEEDTEKDK 55

RESULT 15

US-08-856-253-8

Sequence 8, Application US/08856253

Patent No. 6288214

GENERAL INFORMATION:

APPLICANT: Hook, Magnus

APPLICANT: Patti, Joseph M.

APPLICANT: House-Pompeo, Karen

APPLICANT: Sthanam, Narayana

APPLICANT: Symersky, Jindrich

TITLE OF INVENTION: COLLAGEN BINDING PROTEIN COMPOSITIONS

NUMBER OF SEQUENCES: 8

CORRESPONDENCE ADDRESS:

ADDRESS: Arnold, White & Durkee

STREET: P.O. Box 4433

CITY: Houston

STATE: Texas

COUNTRY: U.S.

```
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/856,253
FILING DATE: Concurrently Herewith
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/017,678
FILING DATE: 16-MAY-1996
ATTORNEY/AGENT INFORMATION:
NAME: Kitchell, Barbara S.
REGISTRATION NUMBER: 33,928
REFERENCE/DOCKET NUMBER: TMMK:193
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
TELEFAX: (512) 474-7577
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 139 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-08-856-253-8

Query Match 100.0%; Score 52; DB 3; Length 139;
Best Local Similarity 100.0%; Pred. No. 0.077;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SPEEDTEKDK 10
   |||||
Db 60 SPEEDTEKDK 69
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Search completed: October 22, 2005, 09:35:42
Job time : 18.2989 secs

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OM protein - protein search, using SW model

Run on: October 22, 2005, 12:39:57 ; Search time 56.1494 Seconds
(without alignments)
74.354 Million cell updates/sec

Title: US-10-731-238-85
Perfect score: 52
Sequence: 1 SFREDTEKDK 10

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1862951 seqs, 417491010 residues
Total number of hits satisfying chosen parameters: 1862951

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications_AA:*

- 1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
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- 7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
- 8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
- 9: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep.*
- 10: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
- 12: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep.*
- 13: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep.*
- 14: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep.*
- 15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pep.*
- 17: /cgn2_6/ptodata/2/pubpaa/US10F_PUBCOMB.pep.*
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- 20: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep.*
- 21: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
- 22: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	52	100.0	10	US-10-731-238-85	Sequence 85, Appl
2	52	100.0	12	US-10-731-238-62	Sequence 62, Appl
3	52	100.0	30	US-10-287-821-1	Sequence 1, Appl
4	52	100.0	31	US-10-287-821-2	Sequence 2, Appl
5	52	100.0	36	US-10-731-238-58	Sequence 58, Appl
6	52	100.0	36	US-10-731-238-59	Sequence 59, Appl
7	52	100.0	38	US-10-731-238-7	Sequence 7, Appl
8	52	100.0	38	US-10-731-238-8	Sequence 8, Appl
9	52	100.0	38	US-10-731-238-49	Sequence 49, Appl
10	52	100.0	139	US-09-813-820-8	Sequence 8, Appl
11	52	100.0	388	US-08-901-062-1	Sequence 1, Appl

12	52	100.0	559	8	US-08-781-986A-5251	Sequence 5251, Ap
13	52	100.0	559	15	US-10-329-624-5251	Sequence 5251, Ap
14	52	100.0	767	9	US-09-815-242-5899	Sequence 5899, Ap
15	52	100.0	767	9	US-09-815-242-13140	Sequence 13140, A
16	52	100.0	948	17	US-10-470-048B-424	Sequence 424, Appl
17	52	100.0	948	17	US-10-470-048B-69	Sequence 69, Appl
18	52	100.0	978	9	US-09-815-242-5456	Sequence 5456, Ap
19	52	100.0	1001	9	US-09-815-242-12686	Sequence 12686, A
20	52	100.0	1018	9	US-09-815-242-5797	Sequence 5797, Ap
21	52	100.0	1018	9	US-09-815-242-12838	Sequence 12838, A
22	52	100.0	1018	9	US-09-815-242-12838	Sequence 68, Appl
23	52	100.0	1027	8	US-08-781-986A-5254	Sequence 5254, Ap
24	52	100.0	1027	15	US-10-329-624-5254	Sequence 5254, Ap
25	52	100.0	1038	15	US-10-282-122A-43827	Sequence 43827, A
26	48	92.3	10	18	US-10-731-238-66	Sequence 66, Appl
27	48	92.3	14	18	US-10-731-238-105	Sequence 105, App
28	48	92.3	38	18	US-10-731-238-5	Sequence 5, Appl1
29	48	92.3	38	18	US-10-731-238-6	Sequence 6, Appl1
30	48	92.3	38	18	US-10-731-238-43	Sequence 43, Appl
31	48	92.3	39	18	US-10-731-238-56	Sequence 56, Appl
32	48	92.3	39	18	US-10-731-238-57	Sequence 57, Appl
33	48	92.3	961	15	US-10-282-122A-43778	Sequence 43778, A
34	46	88.5	38	18	US-10-731-238-41	Sequence 41, Appl
35	46	88.5	38	18	US-10-731-238-46	Sequence 46, Appl
36	46	88.5	38	18	US-10-731-238-47	Sequence 47, Appl
37	45	86.5	38	18	US-10-731-238-48	Sequence 48, Appl
38	42	80.8	10	18	US-10-731-238-2	Sequence 2, Appl1
39	42	80.8	38	18	US-10-731-238-36	Sequence 36, Appl
40	42	80.8	38	18	US-10-731-238-37	Sequence 37, Appl
41	42	80.8	38	18	US-10-731-238-39	Sequence 39, Appl
42	42	80.8	38	18	US-10-731-238-40	Sequence 40, Appl
43	42	80.8	38	18	US-10-731-238-45	Sequence 45, Appl
44	41	78.8	10	18	US-10-731-238-84	Sequence 84, Appl
45	41	78.8	38	18	US-10-731-238-38	Sequence 38, Appl

ALIGNMENTS

RESULT 1
US-10-731-238-85
Sequence 85, Application US/10731238
Publication No. US2005012552A1
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
Patel, Joseph M.
House-Pompeo, Karen L.
Speziale, Pietro
Joh, Danny
McGavin, Martin J.
TITLE OF INVENTION: FIBROBLAST BINDING PROTEIN COMPOSITIONS
AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESS: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/731, 238
FILING DATE: 10-Dec-2003
CLASSIFICATION: <unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/010, 317
FILING DATE: 21-Jan-1998
APPLICATION NUMBER: US 60/036, 139

```
/
/ FILING DATE: 21-JAN-1997
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Hibler, David W.
/ REGISTRATION NUMBER: 41,071
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 512-418-3000
/ TELEFAX: 512-474-7577
/ INFORMATION FOR SEQ ID NO: 85:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 10 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: <Unknown>
/ TOPOLOGY: linear
/
/ SEQUENCE DESCRIPTION: SEQ ID NO: 85:
US-10-731-238-85

Query Match      100.0%; Score 52; DB 18; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.054;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 SPEEDTEKDK 10
Db      1 SPEEDTEKDK 10

RESULT 2
US-10-731-238-62
/ Sequence 62, Application US/10731238
/ Publication No. US20050123552A1
/ GENERAL INFORMATION:
/ APPLICANT: Hook, Magnus
/          Patti, Joseph M.
/          House-Pompeo, Karen L.
/          Speziale, Pietro
/          John, Danny
/          McGavin, Martin J.
/ TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
/ AND METHODS OF USE
/ NUMBER OF SEQUENCES: 105
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Arnold, White & Durkee
/ STREET: P.O. Box 4433
/ CITY: Houston
/ STATE: TX
/ COUNTRY: USA
/ ZIP: 77210-4433
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/10/731,238
/ FILING DATE: 10-Dec-2003
/ CLASSIFICATION: <Unknown>
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US/09/010,317
/ FILING DATE: 21-Jan-1998
/ APPLICATION NUMBER: US 60/036,139
/ FILING DATE: 21-JAN-1997
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Hibler, David W.
/ REGISTRATION NUMBER: 41,071
/ REFERENCE/DOCKET NUMBER: TAMK.189
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 512-418-3000
/ TELEFAX: 512-474-7577
/ INFORMATION FOR SEQ ID NO: 62:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 12 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: <Unknown>
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/
/ TOPOLOGY: linear
/ SEQUENCE DESCRIPTION: SEQ ID NO: 62:
US-10-731-238-62

Query Match      100.0%; Score 52; DB 18; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.065;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 SPEEDTEKDK 10
Db      1 SPEEDTEKDK 10

RESULT 3
US-10-287-821-1
/ Sequence 1, Application US/10287821
/ Publication No. US20030153022A1
/ GENERAL INFORMATION:
/ APPLICANT: PATTI, Joseph M.
/ TITLE OF INVENTION: MONOCLONAL ANTIBODIES TO THE FIBRONECTIN BINDING PROTEIN. . .
/ FILE REFERENCE: P07427US01/BAS
/ CURRENT APPLICATION NUMBER: US/10/287,821
/ CURRENT FILING DATE: 2002-11-05
/ PRIOR APPLICATION NUMBER: 60/330,964
/ PRIOR FILING DATE: 2001-11-05
/ NUMBER OF SEQ ID NOS: 2
/ SOFTWARE: Patentin version 3.1
/ SEQ ID NO 1
/ LENGTH: 30
/ TYPE: PRT
/ ORGANISM: Staphylococcus aureus
US-10-287-821-1

Query Match      100.0%; Score 52; DB 14; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.17;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 SPEEDTEKDK 10
Db      8 SPEEDTEKDK 17

RESULT 4
US-10-287-821-2
/ Sequence 2, Application US/10287821
/ Publication No. US20030153022A1
/ GENERAL INFORMATION:
/ APPLICANT: PATTI, Joseph M.
/ TITLE OF INVENTION: MONOCLONAL ANTIBODIES TO THE FIBRONECTIN BINDING PROTEIN. . .
/ FILE REFERENCE: P07427US01/BAS
/ CURRENT APPLICATION NUMBER: US/10/287,821
/ CURRENT FILING DATE: 2002-11-05
/ PRIOR APPLICATION NUMBER: 60/330,964
/ PRIOR FILING DATE: 2001-11-05
/ NUMBER OF SEQ ID NOS: 2
/ SOFTWARE: Patentin version 3.1
/ SEQ ID NO 2
/ LENGTH: 31
/ TYPE: PRT
/ ORGANISM: Staphylococcus aureus
US-10-287-821-2

Query Match      100.0%; Score 52; DB 14; Length 31;
Best Local Similarity 100.0%; Pred. No. 0.17;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 SPEEDTEKDK 10
Db      9 SPEEDTEKDK 18

RESULT 5
US-10-731-238-58
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```
; Sequence 58, Application US/10731238
; Publication No. US20050123552A1
; GENERAL INFORMATION:
; APPLICANT: Hook, Magnus
;             Patti, Joseph M.
;             House-Pompeo, Karen L.
;             Speziale, Pietro
;             Joh, Danny
;             McGavin, Martin J.
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
; AND METHODS OF USE
; NUMBER OF SEQUENCES: 105
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: TX
; COUNTRY: USA
; ZIP: 77210-4433
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/731,238
; FILING DATE: 10-Dec-2003
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/010,317
; FILING DATE: 21-Jan-1998
; APPLICATION NUMBER: US 60/036,139
; FILING DATE: 21-JAN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Hibler, David W.
; REGISTRATION NUMBER: 41,071
; REFERENCE/DOCKET NUMBER: TANK:189
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 512-418-3000
; TELEFAX: 512-474-7577
; INFORMATION FOR SEQ ID NO: 58:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 36 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 58:
US-10-731-238-58
Query Match      100.0%; Score 52; DB 18; Length 36;
Best Local Similarity 100.0%; Pred. No. 0.2;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 SPEEDTERKD 10
       |||||||
Db      7 SPEEDTERKD 16

RESULT 6
US-10-731-238-59
; Sequence 59, Application US/10731238
; Publication No. US20050123552A1
; GENERAL INFORMATION:
; APPLICANT: Hook, Magnus
;             Patti, Joseph M.
;             House-Pompeo, Karen L.
;             Speziale, Pietro
;             Joh, Danny
;             McGavin, Martin J.
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
; AND METHODS OF USE
; NUMBER OF SEQUENCES: 105
; CORRESPONDENCE ADDRESS:
```

```
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/731,238
FILING DATE: 10-Dec-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE: 21-Jan-1998
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TANK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 59:
SEQUENCE CHARACTERISTICS:
LENGTH: 36 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 59:
US-10-731-238-59
Query Match      100.0%; Score 52; DB 18; Length 36;
Best Local Similarity 100.0%; Pred. No. 0.2;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 SPEEDTERKD 10
       |||||||
Db      7 SPEEDTERKD 16

RESULT 7
US-10-731-238-7
; Sequence 7, Application US/10731238
; Publication No. US20050123552A1
; GENERAL INFORMATION:
; APPLICANT: Hook, Magnus
;             Patti, Joseph M.
;             House-Pompeo, Karen L.
;             Speziale, Pietro
;             Joh, Danny
;             McGavin, Martin J.
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
; AND METHODS OF USE
; NUMBER OF SEQUENCES: 105
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: TX
; COUNTRY: USA
; ZIP: 77210-4433
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/731,238
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FILING DATE: 10-Dec-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE: 21-Jan-1998
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-Jan-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-10-731-238-7
Query Match 100.0%; Score 52; DB 18; Length 38;
Best Local Similarity 100.0%; Pred. No. 0.22;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 SPEEDTEKDK 10
DB 7 SPEEDTEKDK 16
RESULT 8
US-10-731-238-8
Sequence 8, Application US/10731238
Publication No. US20050123552A1
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
Patti, Joseph M.
House-Pompeo, Karen L.
Speziale, Pietro
John, Danny
McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/731,238
FILING DATE: 10-Dec-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE: 21-Jan-1998
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-Jan-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000

TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-10-731-238-8
Query Match 100.0%; Score 52; DB 18; Length 38;
Best Local Similarity 100.0%; Pred. No. 0.22;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 SPEEDTEKDK 10
DB 7 SPEEDTEKDK 16
RESULT 9
US-10-731-238-49
Sequence 49, Application US/10731238
Publication No. US20050123552A1
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
Patti, Joseph M.
House-Pompeo, Karen L.
Speziale, Pietro
John, Danny
McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/731,238
FILING DATE: 10-Dec-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE: 21-Jan-1998
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-Jan-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 49:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 49:
US-10-731-238-49
Query Match 100.0%; Score 52; DB 18; Length 38;
Best Local Similarity 100.0%; Pred. No. 0.22;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 SPEEDTEKDK 10
| | | | |
Db 7 SPEEDTEKDK 16

RESULT 10
US-09-813-820-8
Sequence 8, Application US/09813820
Patent No. US2002010262A1
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
Patti, Joseph M.
House-Pompeo, Karen
Sharnam, Narayana
Symerky, Jindrich
TITLE OF INVENTION: COLLAGEN BINDING PROTEIN COMPOSITIONS
AND METHODS OF USE
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESS: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: Texas
COUNTRY: U.S.
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/813,820
FILING DATE: 22-Mar-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/856,253
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Kitchell, Barbara S.
REGISTRATION NUMBER: 33,928
REFERENCE/DOCKET NUMBER: TANK:193
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
TELEFAX: (512) 474-7577
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 139 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-09-813-820-8
Query Match 100.0%; Score 52; DB 9; Length 139;
Best Local Similarity 100.0%; Pred. No. 0.84;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 SPEEDTEKDK 10
| | | | |
Db 60 SPEEDTEKDK 69
RESULT 11
US-08-901-062-1
Sequence 1, Application US/08901062
Publication No. US20020025324A1
GENERAL INFORMATION:
APPLICANT: SEALS, JONATHAN R.
TITLE OF INVENTION: RECOMBINANT BIVALENT BACTERIAL VACCINE
TITLE OF INVENTION: FOR THE PREVENTION OF MASTITIS
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:

ADDRESS: HALE AND DORR LLP
STREET: 60 State Street
CITY: Boston
STATE: MA
COUNTRY: United States of America
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/901,062
FILING DATE: 25-JUL-1997
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Baker, Hollie L.
REGISTRATION NUMBER: 31,321
REFERENCE/DOCKET NUMBER: 106941.153
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 526-6000
TELEFAX: (617) 526-5000
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 388 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-901-062-1
Query Match 100.0%; Score 52; DB 8; Length 388;
Best Local Similarity 100.0%; Pred. No. 2.4;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 SPEEDTEKDK 10
| | | | |
Db 309 SPEEDTEKDK 318
RESULT 12
US-08-781-986A-5251
Sequence 5251, Application US/08781986A
Publication No. US20030054436A1
GENERAL INFORMATION:
APPLICANT: Charles Kunach
TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
NUMBER OF SEQUENCES: 5255
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COUNTRY: USA
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/781,986A
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Benson, Bob
REGISTRATION NUMBER: 30,446
REFERENCE/DOCKET NUMBER: PB248PP

TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 5251:
SEQUENCE CHARACTERISTICS:
LENGTH: 559 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-781-986A-5251

Query Match 100.0%; Score 52; DB 8; Length 559;
Best Local Similarity 100.0%; Pred. No. 3.6;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SPEEDTEKDK 10
Db 345 SPEEDTEKDK 354

RESULT 13
US-10-329-624-5251
Sequence 5251, Application US/10329624
Publication No. US20040043037A1
GENERAL INFORMATION:
APPLICANT: Gil H. Choi
Patrick S. Dillon
Craig A. Rosen
Steven C. Barash
Michael R. Fannon
TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
NUMBER OF SEQUENCES: 5256
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COUNTRY: USA
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/329,624
FILING DATE: 27-Dec-2002
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/956,171
FILING DATE: October 20, 1997
APPLICATION NUMBER: 60/009,861
FILING DATE: January 5, 1996
APPLICATION NUMBER: 08/781,986
FILING DATE: January 3, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Mark J. Hyman
REGISTRATION NUMBER: 46,789
REFERENCE/DOCKET NUMBER: PB248P1D1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (240) 314-1224
TELEFAX: (301) 309-8439
INFORMATION FOR SEQ ID NO: 5251:
SEQUENCE CHARACTERISTICS:
LENGTH: 559 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 5251:
US-10-329-624-5251

Query Match 100.0%; Score 52; DB 15; Length 559;
Best Local Similarity 100.0%; Pred. No. 3.6;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SPEEDTEKDK 10
Db 345 SPEEDTEKDK 354

RESULT 14
US-09-815-242-5899
Sequence 5899, Application US/09815242
Patent No. US20020061569A1
GENERAL INFORMATION:
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Karl L.
APPLICANT: Zyskind, Judith W.
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John D.
APPLICANT: Carr, Grant J.
APPLICANT: Yamamoto, Robert T.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 5899
LENGTH: 767
TYPE: PRT
ORGANISM: Staphylococcus aureus
US-09-815-242-5899

Query Match 100.0%; Score 52; DB 9; Length 767;
Best Local Similarity 100.0%; Pred. No. 5;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SPEEDTEKDK 10
Db 726 SPEEDTEKDK 735

RESULT 15
US-09-815-242-13140
Sequence 13140, Application US/09815242
Patent No. US20020061569A1
GENERAL INFORMATION:
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Karl L.
APPLICANT: Zyskind, Judith W.
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John D.
APPLICANT: Carr, Grant J.
APPLICANT: Yamamoto, Robert T.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: Prokaryotes

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; FILE REFERENCE: ELITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815.242
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 13140
; LENGTH: 767
; TYPE: prf
; ORGANISM: Staphylococcus aureus
; US-09-815-242-13140
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Query Match      100.0%; Score 52; DB 9; Length 767;
Best Local Similarity 100.0%; Pred. No. 5;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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OY      1 SPEEDTEKDK 10
        |||||
Db      726 SPEEDTEKDK 735
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Search completed: October 22, 2005, 12:56:22
Job time : 57.1494 secs

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GenCore version 5.1.6
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OM protein - protein search, using SW model

Run on: October 22, 2005, 08:04:46 ; Search time 11.6092 Seconds
(without alignments)
82.880 Million cell updates/sec

Title: US-10-731-238-85
Perfect score: 52
Sequence: 1 SPEEDTEKDK 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_79:.*
1: pir1:.*
2: pir2:.*
3: pir3:.*
4: pir4:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	52	100.0	940	2	S19702 fibronectin-binding
2	52	100.0	1018	2	A32192 fibronectin-binding
3	52	100.0	1038	2	H30053 hypothetical prote
4	48	92.3	961	2	G90053 hypothetical prote
5	38	73.1	1259	2	T32901 hypothetical prote
6	37	71.2	296	2	T20726 hypothetical prote
7	37	71.2	591	2	C64220 propionyl-CoA carb
8	37	71.2	602	2	T42401 ubiquitin thioleat
9	37	71.2	771	2	T13618 hypothetical prote
10	37	71.2	928	2	S50578 hypothetical prote
11	36	69.2	325	2	T18283 hypothetical prote
12	36	69.2	419	2	T18450 hypothetical prote
13	36	69.2	438	2	T37786 probable RNA-bind
14	36	69.2	467	2	AG0771 probable two-compo
15	36	69.2	555	2	A56560 zinc finger protei
16	36	69.2	659	2	T00128 hypothetical 76.4k
17	35	67.3	376	2	A56480 N-acetylglucosamin
18	35	67.3	447	2	G75201 probable beta-lact
19	35	67.3	502	2	T14286 embryogenic callus
20	35	67.3	626	1	NBHUA platelet glycoprot
21	35	67.3	681	2	F68295 acetyl-CoA synthet
22	35	67.3	1875	2	S38173 myosin-like protei
23	34	65.4	183	1	TPCH15 troponin I, fast s
24	34	65.4	193	2	A23569 troponin I, fast s
25	34	65.4	397	2	AC2110 hypothetical prote
26	34	65.4	457	2	C90207 seryl-CRNA synthet
27	34	65.4	653	2	T15665 hypothetical prote
28	34	65.4	717	2	T2816 hypothetical prote
29	34	65.4	734	2	B42680 nucleolus-cytoplas

30	34	65.4	752	2	S64750 probable ATP-depen
31	34	65.4	782	2	T43277 host cell factor 1
32	34	65.4	969	2	T27997 hypothetical prote
33	34	65.4	1074	2	T01906 hypothetical prote
34	34	65.4	1129	2	T25635 hypothetical prote
35	34	65.4	1175	2	T25634 hypothetical prote
36	34	65.4	1245	2	D71613 GAF domain protein
37	34	65.4	4869	2	S66572 ryanodine receptor
38	33	63.5	115	2	B72355 hypothetical prote
39	33	63.5	185	2	F97991 tm5252, relaxase,
40	33	63.5	328	2	T00547 hypothetical prote
41	33	63.5	335	2	A54458 Gi progression neg
42	33	63.5	339	2	C84653 hypothetical prote
43	33	63.5	342	2	T43667 ubiquitin fusion d
44	33	63.5	349	2	D69856 conserved hypothet
45	33	63.5	367	2	H70519 probable acea pro

ALIGNMENTS

RESULT 1

S19702 fibronectin-binding protein B - Staphylococcus aureus
C:Species: Staphylococcus aureus
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
C:Accession: S19702
R:Joensson, K.; Signaes, C.; Mueller, H.P.; Lindberg, M.
Eur. J. Biochem. 202, 1041-1048, 1991
A:Title: Two different genes encode fibronectin binding proteins in Staphylococcus aure
A:Reference number: S19702; MUID:92111475; PMID:1837266
A:Accession: S19702
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-940 <JOB>
A:Cross-references: UNIPROT:Q53682; EMBL:X62992; NID:q49040; PIDN:CAA44726.1; PID:G5811
C:Keywords: fibronectin binding

Query Match 100.0%; Score 52; DB 2; Length 940;
Best Local Similarity 100.0%; Pred. No. 0.36;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SPEEDTEKDK 10
DB 726 SPEEDTEKDK 735

RESULT 2

A32192 fibronectin-binding protein - Staphylococcus aureus
C:Species: Staphylococcus aureus
C:Date: 31-Jul-1989 #sequence_revision 31-Jul-1989 #text_change 16-Feb-1997
C:Accession: A32192
R:Signaes, C.; Raucsi, G.; Joensson, K.; Lindgren, P.E.; Anantharamiah, G.M.; Hoeoek,
Proc. Natl. Acad. Sci. U.S.A. 86, 699-703, 1989
A:Title: Nucleotide sequence of the gene for a fibronectin-binding protein from Staphy
A:Reference number: A32192; MUID:89098998; PMID:2521391
A:Accession: A32192
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1018 <SIG>
A:Cross-references: GB:U04151
C:Keywords: fibronectin binding

Query Match 100.0%; Score 52; DB 2; Length 1018;
Best Local Similarity 100.0%; Pred. No. 0.4;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SPEEDTEKDK 10
DB 790 SPEEDTEKDK 799

```

RESULT 3
H90053
hypothetical protein fnb [imported] - Staphylococcus aureus (strain N315)
C/Species: Staphylococcus aureus
C/Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C/Accession: H90053
R/Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Ogud
ma, A.; Mitutani, U.; Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.;
C.; Shibata, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
A/Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.
A/Reference number: A89758; MUID:21311952; PMID:11418146
A/Accession: H90053
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-1038 <KIR>
A/Cross-references: UNIPROT:Q99RD2; GB:BA000018; PID:g13702453; PIDN:BAB43594.1; GSPDB:G
A/Experimental source: strain N315
C/Genetics:
A/Gene: fnb

Query Match          100.0%; Score 52; DB 2; Length 1038;
Best Local Similarity 100.0%; Pred. No. 0.4;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SPEEDTEKDK 10
Db 786 SPEEDTEKDK 795

RESULT 4
G90053
hypothetical protein fnb [imported] - Staphylococcus aureus (strain N315)
C/Species: Staphylococcus aureus
C/Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C/Accession: G90053
R/Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Ogud
ma, A.; Mitutani, U.; Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.;
C.; Shibata, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
A/Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.
A/Reference number: A89758; MUID:21311952; PMID:11418146
A/Accession: G90053
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-961 <KIR>
A/Cross-references: UNIPROT:Q99RD3; GB:BA000018; PID:g13702452; PIDN:BAB43593.1; GSPDB:G
A/Experimental source: strain N315
C/Genetics:
A/Gene: fnb

Query Match          92.3%; Score 48; DB 2; Length 961;
Best Local Similarity 90.0%; Pred. No. 1.9;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SPEEDTEKDK 10
Db 699 SPEEDTEKDK 708

RESULT 5
T32901
hypothetical protein C42C1.4 - Caenorhabditis elegans
C/Species: Caenorhabditis elegans
C/Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
C/Accession: T32901
R/Murray, J.; Rohlfing, T.; Davidson, S.
submitted to the EMBL Data Library, January 1998
A/Description: The sequence of C. elegans cosmid C42C1.
A/Reference number: Z21243
A/Accession: T32901
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA

A/Residues: 1-1259 <MUR>
A/Cross-references: UNIPROT:Q44971; EMBL:AF043695; PIDN:AAB97546.1; GSPDB:GN00019; CESP
A/Experimental source: strain Bristol N2; clone C42C1
C/Genetics:
A/Gene: CESP:C42C1.4
A/Map position: 1
A/Intons: 32/3; 84/1; 163/3; 330/3; 633/3; 747/3; 889/3; 1046/1; 1131/2; 1158/3; 1200/5

Query Match          73.1%; Score 38; DB 2; Length 1259;
Best Local Similarity 77.8%; Pred. No. 1.4e+02;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 FEEDTEKDK 10
Db 1083 FEEDTEKDK 1091

RESULT 6
T20726
hypothetical protein F10G8.7 - Caenorhabditis elegans
C/Species: Caenorhabditis elegans
C/Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C/Accession: T20726
R/Basham, V.
submitted to the EMBL Data Library, September 1996
A/Reference number: Z19315
A/Accession: T20726
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-296 <WIL>
A/Cross-references: UNIPROT:Q93456; EMBL:Z80216; PIDN:CAB02283.1; GSPDB:GN00019; CESP:F1
A/Experimental source: clone F10G8
C/Genetics:
A/Gene: CESP:F10G8.7
A/Map position: 1
A/Intons: 53/1; 129/3; 153/3; 187/3; 209/2; 249/2

Query Match          71.2%; Score 37; DB 2; Length 296;
Best Local Similarity 87.5%; Pred. No. 45;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 FEEDTEKDK 9
Db 52 FEEDTEKDK 59

RESULT 7
C84220
proplyl-CoA carboxylase homolog [imported] - Halobacterium sp. NRC-1
C/Species: Halobacterium sp. NRC-1
C/Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
C/Accession: C84220
R/Ne, W.V.; Kennedy, S.P.; Mahairis, G.G.; Bergquist, B.; Pan, M.; Shukla, H.D.; Laeky,
; Leithauer, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Jabl
; Jung, K.H.; Alam, M.; Freitas, T.
Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000
A/Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ehardt, H.; Lowe, T.M.; L
A/Title: Genome sequence of Halobacterium species NRC-1.
A/Reference number: A84160; MUID:20504483; PMID:11016950
A/Accession: C84220
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-591 <STO>
A/Cross-references: UNIPROT:Q9HRN1; GB:AE004437; NID:g10580213; PIDN:AAJ19127.1; GSPDB:
C/Genetics:
A/Gene: yngE
C/Superfamily: propyl-CoA carboxylase beta chain

Query Match          71.2%; Score 37; DB 2; Length 591;
Best Local Similarity 70.0%; Pred. No. 93;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 SPEEDTEKDK 10

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Db 573 SFYEDVERKDR 582

RESULT 8

T12401
ubiquitin thiolesterase homolog - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C:Accession: T12401
R:Waterston, R.
submitted to the EMBL Data Library, June 1999
A:Reference number: Z22153
A:Accession: T12401
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-602 <MAT>
A:Cross-references: UNIPROT:O44787; EMBL:AF040640; PIDN:ADJ4652.1
C:Genetics:
A:introns: 30/1; 56/2; 78/3; 109/3; 144/2; 175/3; 239/3; 272/3; 377/2; 458/3; 552/3
A:Note: F0901.1

Query Match 71.2%; Score 37; DB 2; Length 602;
Best Local Similarity 70.0%; Pred. No. 95;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 SFEDTEKDK 10
DB 17 STQEDSEKDK 26

RESULT 9

T13618
hypothetical protein 8D8.4 - fruit fly (Drosophila melanogaster)
C:Species: Drosophila melanogaster
C:Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 09-Jul-2004
C:Accession: T13618
R:Papadogiannakis, G.; Spanos, L.; Cox, S.; Siden-Kiamos, I.; Louis, C.
submitted to the EMBL Data Library, April 1999
A:Description: Sequencing the distal X chromosome of Drosophila melanogaster.
A:Reference number: Z17695
A:Accession: T13618
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-771 <PAP>
A:Cross-references: UNIPROT:O46307; EMBL:AL022018; NID:el273253; PID:el254565; PIDN:CAAL
C:Genetics:
A:Cross-references: FLYBase:FBgn0024367
A:Note: EG:8D8.4

Query Match 71.2%; Score 37; DB 2; Length 771;
Best Local Similarity 70.0%; Pred. No. 12e+02;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 SFEDTEKDK 10
DB 367 SPEEDTPSDE 376

RESULT 10

S50578
hypothetical protein YER075c - yeast (Saccharomyces cerevisiae)
C:Species: Saccharomyces cerevisiae
C:Date: 28-May-1993 #sequence_revision 24-Feb-1995 #text_change 09-Jul-2004
C:Accession: S50578
R:Dietrich, F.S.
submitted to the EMBL Data Library, December 1994
A:Description: The sequence of S. cerevisiae lambda clone 3612 and cosmid 9747.
A:Reference number: S50438
A:Accession: S50578
A:Molecule type: DNA
A:Residues: 1-928 <DIR>
A:Cross-references: UNIPROT:P40048; EMBL:U18814; NID:g603309; PIDN:AB64614.1; PID:g6033

C:Genetics:
A:Gene: SGD:PTP3
A:Cross-references: SGD:S0000877; MIPS:YER075C
A:Map position: 5R

C:Keywords: phosphoprotein
P:527-867/Domain: protein-tyrosine-phosphatase homology <PTP>
F:804/Active site: Cys (phosphocysteine intermediate) #status predicted
F:810/Binding site: substrate phosphate (Arg) #status predicted

Query Match 71.2%; Score 37; DB 2; Length 928;
Best Local Similarity 70.0%; Pred. No. 1.5e+02;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 SFEDTEKDK 10
DB 380 SLERDTNMDK 389

RESULT 11

T18283
hypothetical protein G5 - slime mold (Dictyostelium discoideum)
C:Species: Dictyostelium discoideum
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T18283
R:Rieben Jr., W.K.; Gonzalez, C.M.; Gonzalez, S.T.; Pilkington, K.J.; Kiyosawa, H.; Hug
Genetics 148, 1117-1125, 1998
A:Title: Dictyostelium discoideum nuclear plasmid dpgs is a chimera related to the Ddpl
A:Reference number: Z14684; MUID:98198836; PMID:9539429
A:Accession: T18283
A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA
A:Residues: 1-325 <RIB>
A:Cross-references: UNIPROT:O44016; EMBL:U00796; NID:g2702254; PID:g2702258; PIDN:AACTE
C:Genetics:
A:introns: 85/1

Query Match 69.2%; Score 36; DB 2; Length 325;
Best Local Similarity 87.5%; Pred. No. 75;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 EEDTEKDK 10
DB 227 EEDKEDK 234

RESULT 12

T18450
hypothetical protein C0570C - malaria parasite (Plasmodium falciparum)
C:Species: Plasmodium falciparum
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T18450
R:Lawson, D.; Bowman, S.; Barrett, B.
submitted to the EMBL Data Library, November 1998
A:Reference number: Z18937
A:Accession: T18450
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-419 <LAW>
A:Cross-references: UNIPROT:O77337; EMBL:AL008970; NID:el407852; PIDN:CAAL5592.1
C:Genetics:
A:Map position: 3
A:introns: 15/3; 169/1
A:Note: C0570C

Query Match 69.2%; Score 36; DB 2; Length 419;
Best Local Similarity 87.5%; Pred. No. 98;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 EEDTEKDK 10
DB 347 EEDKEDK 354

RESULT 13

T37786
 Probable RNA-binding protein - fission yeast (*Schizosaccharomyces pombe*)
 C:Species: *Schizosaccharomyces pombe*
 C>Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
 C/Accession: T37786
 R/Oliver, K.; Harris, D.; Barrell, B.G.; Rajandream, M.A.; Wood, V.
 Submitted to the EMBL Data Library, September 1995
 A:Reference number: 221746
 A/Accession: T37786
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: DNA
 A/Residues: 1-438 <OL1>
 A/Cross-references: UNIPROT:Q13741; EMBL:Z98529; PDB:CAH1047.1; GSPDB:GN00066; SPDB:SH
 C/Experimental source: strain 972h-; cosmid c16E8
 C/Genetics:
 A/Gene: SPDB:SPAC16B8.06c
 A/Map position: 1
 A/Introns: 36/3

Query Match 69.2%; Score 36; DB 2; Length 438;
 Best Local Similarity 87.5%; Pred. No. 1e+02;
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 EEDTEKDK 10
 ||| |||
 Db 109 EEDTEKDK 116

RESULT 14

AG0771
 Probable two-component system sensor kinase (EC 2.7.3.-) [imported] - *Salmonella enterica*
 C/Species: *Salmonella enterica* subsp. *enterica* serovar Typhi
 A/Note: this species has also been called *Salmonella typhi*
 C/Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
 R/Parikh, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, T.; Connor, P.; Cronin, A.; Davies, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, S.; Moule, S.; O'Gaora, P.
 Nature 413, 848-852, 2001
 A/Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.;
 A/Title: Complete genome sequence of a multiple drug resistant *Salmonella enterica* serov.
 A/Reference number: AB0502; MUID:21534947; PMID:11677608
 A/Accession: AG0771
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-467 <PAR>
 A/Cross-references: GB:AL513382; PDB:CAD02493.1; PDB:G16503357; GSPDB:GN00176
 C/Genetics:
 A/Gene: STY2343
 C/Keywords: phosphotransferase

Query Match 69.2%; Score 36; DB 2; Length 467;
 Best Local Similarity 60.0%; Pred. No. 1.1e+02;
 Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 SPEEDTEKDK 10
 ||| |||
 Db 84 SPEEDTEKDK 93

RESULT 15

A56560
 zinc finger protein/transferase Zfp-38 - mouse
 C/Species: *Mus musculus* (house mouse)
 C/Date: 21-Jul-1995 #sequence_revision 28-Jul-1995 #text_change 09-Jul-2004
 C/Accession: A56560; C48827
 R/Chowdhury, K.; Goulding, M.; Walther, C.; Imai, K.; Pickencher, H.
 Mech. Dev. 39, 129-142, 1992
 A/Title: The ubiquitous transferase Zfp-38 is upregulated during spermatogenesis with
 A/Reference number: A56560; MUID:93183757; PMID:1264028
 A/Accession: A56560
 A/Molecule type: mRNA

A/Residues: 1-555 <CHO>
 A/Cross-references: UNIPROT:Q07231; GB:X63747; NID:G55476; PDB:CAA45280.1; PID:G55477
 A/Experimental source: embryo
 A/Note: sequence extracted from NCBI backbone (NCBI:126596, NCBI:126599)
 R/Noce, T.; Fujiwara, Y.; Sezaki, M.; Fujimoto, H.; Higashinakagawa, T.
 Dev. Biol. 153, 356-367, 1992
 A/Title: Expression of a mouse zinc finger protein gene in both spermatocytes and oocyte
 A/Reference number: A48827; MUID:93012481; PMID:1397691
 A/Accession: C48827
 A/Molecule type: mRNA
 A/Residues: 1-192, 'T', 194-494, 'E', 496-506, 'F', 508-509, 'S', 511-555 <NOC>
 A/Cross-references: EMBL:D10630; NID:G220640; PDB:BA01480.1; PID:G220641
 A/Experimental source: spermatogenic cells; clone CTfins1
 A/Note: sequence extracted from NCBI backbone (NCBI:114773)
 C/Genetics:
 A/Gene: Zfp-38
 A/Map position: 5
 C/Superfamily: zinc finger protein ZFP-36; LIM metal-binding repeat homology
 C/Keywords: spermatogenesis; transcription regulation; zinc finger

Query Match 69.2%; Score 36; DB 2; Length 555;
 Best Local Similarity 87.5%; Pred. No. 1.3e+02;
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 EEDTEKDK 10
 ||| |||
 Db 28 EEDTEKDK 35

Search completed: October 22, 2005, 09:55:37
 Job time : 13.6092 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 22, 2005, 08:01:06 ; Search time 56.2069 Seconds
(without alignments)
91.106 Million cell updates/sec

Title: US-10-731-238-85
Perfect score: 52
Sequence: 1 SFEEDTEKDK 10

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: uniprot_sprotc:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Length	DB	ID	Description
1	52	100.0	152	2	Q9AEP9	Q9AEP9 staphylococ
2	52	100.0	940	2	Q53682	Q53682 staphylococ
3	52	100.0	943	2	Q8NUU8	Q8NUU8 staphylococ
4	52	100.0	957	2	Q6G6H4	Q6G6H4 staphylococ
5	52	100.0	1015	2	Q8NUU7	Q8NUU7 staphylococ
6	52	100.0	1015	2	Q6G6H3	Q6G6H3 staphylococ
7	52	100.0	1018	1	FNBA STAAU	P14738 staphylococ
8	52	100.0	1038	2	Q99RD2	Q99RD2 staphylococ
9	52	100.0	1038	2	Q7A3J7	Q7A3J7 staphylococ
10	48	92.3	961	2	Q99RD3	Q99RD3 staphylococ
11	48	92.3	961	2	Q7A3J8	Q7A3J8 staphylococ
12	48	92.3	965	2	Q6GDU5	Q6GDU5 staphylococ
13	39	75.0	502	2	Q8NFC6	Q8NFC6 homo sapien
14	38	73.1	132	2	Q975R5	Q975R5 sulfolobus
15	38	73.1	173	2	Q9W308	Q9W308 drosophila
16	38	73.1	319	2	Q6TE07	Q6TE07 cryzias lat
17	38	73.1	319	2	Q67ER0	Q67ER0 xenopus lae
18	38	73.1	450	2	Q6C655	Q6C655 yarrowia li
19	38	73.1	912	2	Q759E8	Q759E8 ashbya gos
20	38	73.1	1102	2	Q8A7W6	Q8A7W6 bacteroides
21	38	73.1	1259	2	Q44971	Q44971 caenorhabdi
22	37	71.2	148	2	Q884N2	Q884N2 streptococci
23	37	71.2	215	2	Q6FQW8	Q6FQW8 candida gla
24	37	71.2	314	2	Q7PLP2	Q7PLP2 drosophila
25	37	71.2	328	2	Q67ER3	Q67ER3 gallus gall
26	37	71.2	591	2	Q9HRN1	Q9HRN1 halobacteri
27	37	71.2	602	2	Q44787	Q44787 caenorhabdi
28	37	71.2	771	2	Q46307	Q46307 drosophila
29	37	71.2	785	2	Q8MR29	Q8MR29 drosophila
30	37	71.2	876	2	Q7ZMU7	Q7ZMU7 xenopus lae
31	37	71.2	928	1	PTP3_YEAST	P40048 saccharomyc

32	37	71.2	955	2	Q6DE79	Q6DE79 xenopus lae
33	37	71.2	1302	1	GPBS_DROME	061366 drosophila
34	36	69.2	145	2	Q95B19	Q95B19 digitaria s
35	36	69.2	146	2	Q95B12	Q95B12 digitaria x
36	36	69.2	150	2	Q95B17	Q95B17 digitaria i
37	36	69.2	170	2	Q95B10	Q95B10 digitaria c
38	36	69.2	179	2	Q6H1B9	Q6H1B9 human adeno
39	36	69.2	197	2	Q23872	Q23872 dictyosteli
40	36	69.2	249	2	Q89817	Q89817 clostridium
41	36	69.2	265	2	Q70E89	Q70E89 methanospira
42	36	69.2	302	2	Q6MQF6	Q6MQF6 bdellovibri
43	36	69.2	322	1	Z18L_HUMAN	Q812P6 homo sapien
44	36	69.2	325	2	Q44016	Q44016 dictyosteli
45	36	69.2	438	1	YDR6_SCHPO	013741 sechiobasach

ALIGNMENTS

RESULT 1

Q9AEP9 PRELIMINARY; PRT; 152 AA.
ID Q9AEP9:
AC Q9AEP9: 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Fibronectin-binding protein (Fragment).
GN Name=fnb;
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1280;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CMRSA-1;
RX DOI=10.1128/IAI.69.6.3791-3799.2001;
RA Rice K., Huebner M., Vaz D., McGavin M.J.;
RT "Variance in fibronectin binding and fnb locus polymorphisms in a
RT Staphylococcus aureus: identification of antigenic variation in a
RT fibronectin binding protein adhesin of the epidemic CMRSA-1 strain of
RT methicillin-resistant S. aureus.";
RL Infect. Immun. 69:3791-3799 (2001).
DR EMBL; AY029184; AAK31588.1; ..
FT NON_TER 1
FT NON_TER 152
SQ SEQUENCE 152 AA; 17193 MW; CFA3913C2B11C025 CRC64;

Query Match 100.0%; Score 52; DB 2; Length 152;
Best Local Similarity 100.0%; Pred. NO. 0.5; Mismatches 0; Indels 0; Gaps 0;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SFEEDTEKDK 10
Db 45 SFEEDTEKDK 54

RESULT 2

Q53682 PRELIMINARY; PRT; 940 AA.
ID Q53682:
AC Q53682: 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Fibronectin binding protein B.
GN Name=fnbB;
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1280;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=8325-4;
RX MEDLINE=92111475; PubMed=1837266;
RA Jonsson K., Signas C., Muller H.P., Lindberg M.;

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RT      "Two different genes encode fibronectin binding proteins in
RT      Staphylococcus aureus. The complete nucleotide sequence and
RT      characterization of the second gene.";
RL      Eur. J. Biochem. 202:1041-1048(1991).
CC      -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC      an amide bond (by similarity).
DR      EMBL; X62992; CAA44726.1; -.
DR      PIR; S19702; S19702.
DR      HSSP; O53653; IN67.
DR      GO; GO:0009986; C:cell surface; IEA.
DR      GO; GO:0005618; C:cell wall; IEA.
DR      GO; GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR      GO; GO:0016020; C:membrane; IEA.
DR      GO; GO:0071155; P:cell adhesion; IEA.
DR      InterPro; IPR008966; Adhes_bact.
DR      InterPro; IPR004237; Fn_bind.
DR      InterPro; IPR005877; Gpos_YSIIRK.
DR      InterPro; IPR001899; Gram_pos_anchor.
DR      Pfam; PF02986; Fn_bind; 1.
DR      Pfam; PF00746; Gram_pos_anchor; 1.
DR      Pfam; PF04650; YSIIRK_signal; 1.
DR      TIGRFAMs; TIGR01167; LpxTG_anchor; 1.
DR      TIGRFAMs; TIGR01168; YSIIRK_signal; 1.
DR      PROSITE; PS50847; GRAM_POS_ANCHORING; 1.
SQ      Cell wall, peptidoglycan-anchor.
SQ      SEQUENCE   940 AA;  103555 MW;  E35FBBCA907AE345 CRC64;

Query Match          100.0%; Score 52; DB 2; Length 940;
Best Local Similarity 100.0%; Pred. No. 3.3;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      1 SPEEDTEKDK 10
Db      726 SPEEDTEKDK 735

RESULT 3
Q8NU08 PRELIMINARY; PRT; 943 AA.
ID      Q8NU08
AC      Q8NU08;
DT      01-OCT-2002 (TREMBlrel. 22, Created)
DT      01-OCT-2002 (TREMBlrel. 22, Last sequence update)
DT      01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE      FmbB protein.
DE      Name=fmbB; OrderedLocuNames=MM2420;
OS      Staphylococcus aureus (strain MM2).
OC      Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX      NCBI_TaxID=196620;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN=MM2;
RX      MEDLINE=22040717; PubMed=12044378; DOI=10.1016/S0140-6736(02)08713-5;
RA      Baba T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Oguchi A.,
RA      Nagai Y., Iwama N., Asano K., Naito T., Kuroda H., Cui L.,
RA      Yamamoto K., Hizamatsu K.;
RT      "Genome and virulence determinants of high virulence community-
RT      acquired MRSA.";
RL      Lancet 359:1819-1827(2002).
RL      -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC      an amide bond (by similarity).
CC      EMBL; AP004830; BAB96285.1; -.
DR      HSSP; O53653; IN67.
DR      GO; GO:0009986; C:cell surface; IEA.
DR      GO; GO:0005618; C:cell wall; IEA.
DR      GO; GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR      GO; GO:0016020; C:membrane; IEA.
DR      GO; GO:0071155; P:cell adhesion; IEA.
DR      InterPro; IPR008966; Adhes_bact.
DR      InterPro; IPR004237; Fn_bind.
DR      InterPro; IPR005877; Gpos_YSIIRK.
DR      InterPro; IPR001899; Gram_pos_anchor.
DR      Pfam; PF02986; Fn_bind; 1.
DR      Pfam; PF00746; Gram_pos_anchor; 1.

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DR	Pfam; PF04650; YSIRK_signal; 1.
DR	TIGRFAMs; TIGR01167; LPXTG_anchor; 1.
DR	TIGRFAMs; TIGR01168; YSIRK_signal; 1.
DR	PROSITE; PS50847; GRAM_POS_ANCHORING; 1.
KM	Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ	SEQUENCE 943 AA; 104537 MW; DA6A5F31947E1B6A CRC64;
Query Match	100.0%; Score 52; DB 2; Length 943;
Best Local Similarity	100.0%; Pred. No. 3.3;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
OY	1 SPEEDTEKDK 10
Db	733 SPEEDTEKDK 742
RESULT 4	
O6G6H4	PRELIMINARY; PRT; 957 AA.
AC	O6G6H4;
DT	05-JUL-2004 (TREMBlrel_27, Created)
DT	05-JUL-2004 (TREMBlrel_27, Last sequence update)
DT	05-JUL-2004 (TREMBlrel_27, Last annotation update)
DE	Fibroectin-binding protein.
CN	Name=fnb3; OrderedLocusNames=SAS2387;
OS	Staphylococcus aureus (strain MSSA476).
OC	Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX	NCBI_TaxID=282459;
RN	[1]
RP	SEQUENCE FROM N.A.
RX	Pubmed:15213324; DOI=10.1073/pnas.0402521101; Holden M.T.G., Fell E.J., Lindsay J.A., Peacock S.J., Day N.P.J., Enright M.C., Foster T.J., Moore C.E., Hurst L., Atkin R., Barron A., Baeson N., Bentley S.D., Chillingworth C., Chillingworth T., Churcher C., Clark L., Corton C., Cronin A., Doggett J., Dowd L., Feltwell T., Hance Z., Harris B., Hauser H., Holtroyd S., Jagels K., James K.D., Lennard N., Lane A., Mayes R., Moule S., Mungall K., Ra Ommond D., Quail M.A., Rabinowitch E., Rutherford K.M., Sanders M., Sharp S., Simmonds M., Stevens K., Whitehead S., Barrell B.G., Spratt B.G., Parkhill J.; RT "Complete genomes of two clinical <i>Staphylococcus aureus</i> strains: evidence for the rapid evolution of virulence and drug resistance."; Proc. Natl. Acad. Sci. U.S.A. 101:9786-9791(2004). CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by an amide bond (By similarity). CC EMBL; BX51857; CA644201.1;-. DR GO; GO:0009986; C:cell surface; IEA. DR GO; GO:0005618; C:cell wall; IEA. DR GO; GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA. DR GO; GO:0016020; C:membrane; IEA. DR GO; GO:0007155; P:cell adhesion; IEA. DR InterPro; IPR008966; Adhes_bact. DR InterPro; IPR004237; Fn_bind. DR InterPro; IPR005877; Opos_YSIRK. DR InterPro; IPR001899; Gram_pos_anchor. DR Pfam; PF02986; Fn_bind; 1. DR Pfam; PF00746; Gram_pos_anchor; 1. DR TIGRFAMs; TIGR01167; LPXTG_signal; 1. DR TIGRFAMs; TIGR01168; YSIRK_signal; 1. DR PROSITE; PS50847; GRAM_POS_ANCHORING; 1. KM Cell wall; Complete proteome; Peptidoglycan-anchor. SQ SEQUENCE 957 AA; 105980 MW; 28FBAB7FFD3EAF CRC64;
Query March	100.0%; Score 52; DB 2; Length 957;
Best Local Similarity	100.0%; Pred. No. 3.3;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
OY	1 SPEEDTEKDK 10
Db	733 SPEEDTEKDK 742

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RESULT 5
Q8NUU7 PRELIMINARY; PRT; 1015 AA.
AC Q8NUU7;
DT 01-OCT-2002 (TREMBLrel. 22, Created)
DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Pub protein.
GN Name=fnb; OrderedLocNames=WM2421;
OS Staphylococcus aureus (strain WM2).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=196620;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MM2;
RX MEDLINE=22040717; PubMed=12044378; DOI=10.1016/S0140-6736(02)08713-5;
RA Baba T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Oguni A.,
RA Nagai Y., Iwama N., Asano K., Naito T., Kuroda H., Cui L.,
RA Yamamoto K., Hiramatsu K.;
RT "Genome and virulence determinants of high virulence community-
acquired MRSA.";
RL Lancet 359:1819-1827 (2002).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
an amide bond (By similarity).
DR EMBL; AP004830; BAB96286.1; -.
DR GO; GO:0009986; C:cell surface; IEA.
DR GO; GO:0005618; C:cell wall; IEA.
DR GO; GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0007155; P:cell adhesion; IEA.
DR InterPro; IPR008966; Adhes_bact.
DR InterPro; IPR004237; Fn_bind.
DR InterPro; IPR005877; Gpos_YsIRK.
DR InterPro; IPR001899; Gram_pos_anchor.
DR Pfam; PF02986; Fn_bind; 1.
DR Pfam; PF00746; Gram_pos_anchor; 1.
DR Pfam; PF04650; YsIRK_signal; 1.
DR TIGRfams; TIGR01167; LpxTG_anchor; 1.
DR TIGRfams; TIGR01168; YsIRK_signal; 1.
DR PROSITE; PS50847; GRAM_POS_ANCHORING; 1.
KW Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ SEQUENCE 1015 AA; 11115 MW; D0F9281BB64D4D2 CRC64;

Query Match 100.0%; Score 52; DB 2; Length 1015;
Best Local Similarity 100.0%; Pred. No. 3.6;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SPEEDTEKDK 10
DB 791 SPEEDTEKDK 800

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RA Ormond D., Quail M.A., Rabbintowitch E., Rutherford K.M., Sanders M.,
RA Sharp S., Simmonds M., Stevens K., Whitehead S., Barrell B.G.,
RA Spratt B.G., Parkhill J.;
RT "Complete genomes of two clinical Staphylococcus aureus strains:
RT evidence for the rapid evolution of virulence and drug resistance.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:9786-9791 (2004).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
an amide bond (By similarity).
DR EMBL; BX571857; CAG44202.1; -.
DR GO; GO:0009986; C:cell surface; IEA.
DR GO; GO:0005618; C:cell wall; IEA.
DR GO; GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0007155; P:cell adhesion; IEA.
DR InterPro; IPR008966; Adhes_bact.
DR InterPro; IPR004237; Fn_bind.
DR InterPro; IPR005877; Gpos_YsIRK.
DR InterPro; IPR001899; Gram_pos_anchor.
DR Pfam; PF02986; Fn_bind; 1.
DR Pfam; PF00746; Gram_pos_anchor; 1.
DR Pfam; PF04650; YsIRK_signal; 1.
DR TIGRfams; TIGR01167; LpxTG_anchor; 1.
DR TIGRfams; TIGR01168; YsIRK_signal; 1.
DR PROSITE; PS50847; GRAM_POS_ANCHORING; 1.
KW Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ SEQUENCE 1015 AA; 11115 MW; D0F9281BB64D4D2 CRC64;

Query Match 100.0%; Score 52; DB 2; Length 1015;
Best Local Similarity 100.0%; Pred. No. 3.6;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SPEEDTEKDK 10
DB 791 SPEEDTEKDK 800

RESULT 7
FNA STRAU STANDARD; PRT; 1018 AA.
ID FNA STRAU
AC F14738;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Fibronectin-binding protein precursor (FNBp).
GN Name=FNBp;
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1280;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NCTC 8325-4;
RX MEDLINE=89098998; PubMed=2521391;
RA Signaes C., Raucel G., Joensson K., Lindberg M.;
RA Anantharamaiah G.M., Hoeck M., Lindberg M.;
RT "Nucleotide sequence of the gene for a fibronectin-binding protein
RT from Staphylococcus aureus: use of this peptide sequence in the
RT synthesis of biologically active peptides.";
RL Proc. Natl. Acad. Sci. U.S.A. 86:699-703 (1989).
CC -1- FUNCTION: The ability of bacteria to bind fibronectin has been
CC proposed as a virulence factor enabling bacteria to colonize wound
CC tissues and blood clots. Binding of plasma fibronectin to the
CC bacterial surface might block adhesion receptors on S.aureus, thus
CC representing an important defense mechanism against tissue
CC invasion.
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC an amide bond (Potential).
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (see http://www.isb-sb.ch/announce/)

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CC or send an email to license@lsb.slb.ch).
CC -----
DR EMBL: J04151; AAA5632.1; -.
DR InterPro: IPR004237; Fn_bind.
DR InterPro: IPR005877; Gpoa_YsIRK.
DR InterPro: IPR001899; Gram_pos_anchor.
DR Pfam: PF02986; Fn_bind.1.
DR Pfam: PF00746; Gram_pos_anchor.1.
DR Pfam: PF04650; YsIRK_signal.1.
DR TIGRFAMs: TIGR01167; LPXTG_anchor.1.
DR TIGRFAMs: TIGR01168; YsIRK_signal.1.
DR TIGRFAMs: TIGR01167; LPXTG_anchor.1.
DR PROSITE: PSS0847; GRAM_POS_ANCHORING.1.
DR Cell adhesion; Cell wall; Peptidoglycan-anchor; Repeat; Signal;
KM virulence.
FT CHAIN 1 36
FT PROPEP 37 985 Fibronectin-binding protein.
FT REPEAT 986 1018 Removed by sortase (Potential).
FT REPEAT 545 574 B-1.
FT REPEAT 575 604 B-2.
FT DOMAIN 745 878 4 X approximate tandem repeats,
Fibronectin-binding domain.
FT REPEAT 745 782 D-1.
FT REPEAT 783 820 D-2.
FT REPEAT 821 859 D-3.
FT REPEAT 860 878 D-4 (incomplete).
FT DOMAIN 879 948 5 X tandem repeats, Pro-rich (WR).
FT REPEAT 879 892 WR.1.
FT REPEAT 893 906 WR.2.
FT REPEAT 907 920 WR.3.
FT REPEAT 921 934 WR.4.
FT REPEAT 935 948 WR.5.
FT SITE 982 986 LPXTG sorting signal (Potential).
FT MOD_RES 985 985 Pentaglycyl murein peptidoglycan amidated
threonine (Potential)
SQ SEQUENCE 1018 AA; 111780 MW; 58175E0020BE81F1F CRC64;

Query Match 100.0%; Score 52; DB 1; Length 1018;
Best Local Similarity 100.0%; Pred. No. 3.6;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SPEEDTEKDK 10
Db 790 SPEEDTEKDK 799

RESULT 8
Q99RD2 PRELIMINARY; PRT; 1038 AA.
ID Q99RD2
AC Q99RD2;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Fibronectin-binding protein homolog.
GN Name=fnb; OrderedLocustNames=SAV2503;
OS Staphylococcus aureus (strain Mu50 / ATCC 700699).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=158878;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MU50 / ATCC 700699;
RX MEDLINE=21311952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2;
RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
Cui L., Oguchi A., Aoki K.-I., Nagai Y., Iian J.-Q., Ito T.,
Kanamori M., Matsunaru H., Maruyama A., Murakami H., Hosoyama A.,
Mizutani U. Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
Kanehisa M., Yamashita A., Ohlma K., Furuya K., Yoshino C., Shiba T.,
Hattori M., Ogasawara N., Hayaishi H., Hiramatsu K.;
RT "Whole genome sequencing of methicillin-resistant Staphylococcus
aureus."
RL Lancet 357:1225-1240(2001).
CC -!- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
an amide bond (By similarity).
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DR EMBL: AP003365; BAB58665.1; -.
DR PIR: H90053; H90053.
DR GO: GO:0009986; C:cell surface; IEA.
DR GO: GO:0005618; C:cell wall; IEA.
DR GO: GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO: GO:0016020; C:membrane; IEA.
DR GO: GO:0007155; P:cell adhesion; IEA.
DR InterPro: IPR008966; Adhes_Bact.
DR InterPro: IPR004237; Fn_bind.
DR InterPro: IPR001899; Gpoa_YsIRK.
DR Pfam: PF02986; Fn_bind.1.
DR Pfam: PF00746; Gram_pos_anchor.1.
DR Pfam: PF04650; YsIRK_signal.1.
DR TIGRFAMs: TIGR01167; LPXTG_anchor.1.
DR TIGRFAMs: TIGR01168; YsIRK_signal.1.
DR PROSITE: PSS0847; GRAM_POS_ANCHORING.1.
KM Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ SEQUENCE 1038 AA; 113618 MW; 666BF6BF2BFEBB12 CRC64;

Query Match 100.0%; Score 52; DB 2; Length 1038;
Best Local Similarity 100.0%; Pred. No. 3.6;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SPEEDTEKDK 10
Db 786 SPEEDTEKDK 795

RESULT 9
Q7A3J7 PRELIMINARY; PRT; 1038 AA.
ID Q7A3J7
AC Q7A3J7;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Fnb protein.
GN Name=fnb; OrderedLocustNames=SA2291;
OS Staphylococcus aureus (strain N315).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=158879;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21311952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2;
RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
Cui L., Oguchi A., Aoki K.-I., Nagai Y., Iian J.-Q., Ito T.,
Kanamori M., Matsunaru H., Maruyama A., Murakami H., Hosoyama A.,
Mizutani U. Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
Kanehisa M., Yamashita A., Ohlma K., Furuya K., Yoshino C., Shiba T.,
Hattori M., Ogasawara N., Hayaishi H., Hiramatsu K.;
RT "Whole genome sequencing of methicillin-resistant Staphylococcus
aureus."
RL Lancet 357:1225-1240(2001).
CC -!- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
an amide bond (By similarity).
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SQ SEQUENCE 1038 AA; 113618 MW; 666BFBFB2BFBEB12 CRC64;
 Query Match 100.0%; Score 52; DB 2; Length 1038;
 Best Local Similarity 100.0%; Pred. No. 3.6;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 SPEEDTEKDK 10
 Db 786 SPEEDTEKDK 795
 RESULT 10
 ID Q99RD3 PRELIMINARY; PRT; 961 AA.
 AC Q99RD3;
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Fibronectin-binding protein homolog.
 GN Name=fnb; OrderedLocuNames=SAV2502; ATCC 700699.
 OS Staphylococcus aureus (strain Mu50 / ATCC 700699).
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 NC NCBI_TaxID=158878;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC SRRALN=Mu50 / ATCC 700699;
 RX MEDLINE=21311952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2;
 RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
 RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Iian J.-O., Ito T.,
 RA Kanamori M., Matsunaru H., Maruyama A., Murakami H., Hoshoyama A.,
 RA Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
 RA Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
 RA Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
 RA Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
 RT "Whole genome sequencing of methicillin-resistant Staphylococcus
 aureus."
 RL Lancet 357:1225-1240(2001).
 CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
 an amide bond (By similarity).
 DR EMBL; AP003365; BAB58664.1; -.
 DR PIR; G90053; G90053.
 DR HSSP; Q53653; IM67.
 DR GO; GO:0009986; C:cell surface; IEA.
 DR GO; GO:0005618; C:cell wall; IEA.
 DR GO; GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0007155; P:cell adhesion; IEA.
 DR InterPro; IPR008966; Adhes_bact.
 DR InterPro; IPR004237; Fn_bind.
 DR InterPro; IPR005877; Gpos_YsIRK.
 DR InterPro; IPR001899; Gram_pos_anchor.
 DR Pfam; PF02986; Fn_bind; 1.
 DR Pfam; PF00746; Gram_pos_anchor; 1.
 DR Pfam; PF04650; YsIRK_signal; 1.
 DR TIGRFAMs; TIGR01167; LpXTG_anchor; 1.
 DR TIGRFAMs; TIGR01168; YsIRK_signal; 1.
 DR PROSITE; PS50847; GRAM_POS_ANCHORING; 1.
 KM Cell wall; Complete proteome; Peptidoglycan-anchor.
 SQ SEQUENCE 961 AA; 106010 MW; 364940F884EA4101 CRC64;
 Query Match 92.3%; Score 48; DB 2; Length 961;
 Best Local Similarity 90.0%; Pred. No. 16;
 Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 SPEEDTEKDK 10
 Db 699 SPEEDTEKDK 708
 RESULT 11
 ID Q7A3J8 PRELIMINARY; PRT; 961 AA.
 AC Q7A3J8;

DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE FnbB protein.
 GN Name=fnb; OrderedLocuNames=SA2290;
 OS Staphylococcus aureus (strain N315).
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 NC NCBI_TaxID=158879;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21311952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2;
 RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
 RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Iian J.-O., Ito T.,
 RA Kanamori M., Matsunaru H., Maruyama A., Murakami H., Hoshoyama A.,
 RA Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
 RA Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
 RA Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
 RA Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
 RT "Whole genome sequencing of methicillin-resistant Staphylococcus
 aureus."
 RL Lancet 357:1225-1240(2001).
 CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
 an amide bond (By similarity).
 DR EMBL; AP003337; BAB43593.1; -.
 DR GO; GO:0009986; C:cell surface; IEA.
 DR GO; GO:0005618; C:cell wall; IEA.
 DR GO; GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0007155; P:cell adhesion; IEA.
 DR InterPro; IPR008966; Adhes_bact.
 DR InterPro; IPR004237; Fn_bind.
 DR InterPro; IPR005877; Gpos_YsIRK.
 DR InterPro; IPR001899; Gram_pos_anchor.
 DR Pfam; PF02986; Fn_bind; 1.
 DR Pfam; PF00746; Gram_pos_anchor; 1.
 DR Pfam; PF04650; YsIRK_signal; 1.
 DR TIGRFAMs; TIGR01167; LpXTG_anchor; 1.
 DR TIGRFAMs; TIGR01168; YsIRK_signal; 1.
 DR PROSITE; PS50847; GRAM_POS_ANCHORING; 1.
 KM Cell wall; Complete proteome; Peptidoglycan-anchor.
 SQ SEQUENCE 961 AA; 106010 MW; 364940F884EA4101 CRC64;
 Query Match 92.3%; Score 48; DB 2; Length 961;
 Best Local Similarity 90.0%; Pred. No. 16;
 Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 SPEEDTEKDK 10
 Db 699 SPEEDTEKDK 708
 RESULT 12
 ID Q6GDUS PRELIMINARY; PRT; 965 AA.
 AC Q6GDUS;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Fibronectin-binding protein.
 GN Name=fnbA; OrderedLocuNames=SA2580;
 OS Staphylococcus aureus (strain MRSA252).
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 NC NCBI_TaxID=282458;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX PubMed=15213324; DOI=10.1073/pnas.0402521101;
 RA Holden M.T.G., Peil E.J., Lindsey J.A., Peacock S.J., Day N.P.J.,
 RA Enright M.C., Foster T.J., Moore C.E., Huret L., Atkin R., Barron A.,
 RA Baeson N., Bentley S.D., Chillingworth C., Chillingworth T.,
 RA Churcher C., Clark L., Cotton C., Cronin A., Doggett J., Dowd L.,
 RA Feltham T., Hance Z., Harris B., Hauser H., Holtroyd S., Jagsels K.,
 RA James K.D., Leonard N., Line A., Mayes R., Mungall K.,
 RA Ormond D., Quail M.A., Rabinowitch E., Rutherford K.M., Sanders M.,

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RA Sharp S., Simmonds M., Stevens K., Whitehead S., Barrell B.G.,
RA Spratt B.G., Parkhill J.;
RT "Complete genomes of two clinical Staphylococcus aureus strains:
RT evidence for the rapid evolution of virulence and drug resistance.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:9786-9791(2004).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC an amide bond (By similarity).
EMBL: BX571856; CAC41560.1; -.
DR GO: GO:0009986; C:cell surface; IEA.
DR GO: GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO: GO:0016020; C:membrane; IEA.
DR GO: GO:0007155; P:cell adhesion; IEA.
DR InterPro: IPR004966; Adhes_bact.
DR InterPro: IPR004237; Fn_bind.
DR InterPro: IPR005877; Gpos_YsIRK.
DR InterPro: IPR001899; Gram_pos_anchor.
DR Pfam: PF02986; Fn_bind; 1.
DR Pfam: PF00746; Gram_pos_anchor; 1.
DR Pfam: PF04650; YsIRK_signal; 1.
DR TIGRPFAMs: TIGR01167; LPXTG_anchor; 1.
DR TIGRPFAMs: TIGR01168; YsIRK_signal; 1.
DR PROSITE: PSS0847; GRAM_POS_ANCHORING; 1.
KW Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ SEQUENCE 965 AA; 105691 MW; 2982E13164D0551 CRC64;

Query Match 92.3%; Score 48; DB 2; Length 965;
Best Local Similarity 90.0%; Pred. No. 16;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SPEEDTEKD 10
Db 755 SPEEDTEKD 764

RESULT 13
Q8NFC6 PRELIMINARY; PRT; 502 AA.
ID Q8NFC6;
AC Q8NFC6;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Ovary;
RA Guo J.H., Yu L.;
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF28529; AAM94279.1; -.
KW Hypothetical protein.
SQ SEQUENCE 502 AA; 55115 MW; C77D17CCA720FA04 CRC64;

Query Match 75.0%; Score 39; DB 2; Length 502;
Best Local Similarity 77.8%; Pred. No. 2,7e+02;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 SPEEDTEKD 9
Db 418 SPEEDTEKD 426

RESULT 14
Q975RS PRELIMINARY; PRT; 132 AA.
ID Q975RS;
AC Q975RS;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Hypothetical protein ST0356.
OrderedLocNames=ST0356;

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OS Sulfolobus tokodaii.
OC Archaea; Crenarchaeota; Thermoprotei; Sulfolobales; Sulfolobaceae;
OC Sulfolobus.
OX NCBI_TaxID=111955;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=JCM 10545 / 7;
RX MEDLINE=21456156; PubMed=11572479;
RA Kawarabayashi Y., Hino Y., Horikawa H., Jin-no K., Takahashi M.,
RA Sekine M., Baba S.-I., Ankael A., Kosugi H., Hosoyama A., Fukui S.,
RA Nagai Y., Nishijima K., Otsuka R., Nakazawa H., Kato Y.,
RA Yoshizawa T., Tanaka T., Kudoh Y., Yamazaki J., Kuehida N., Oguchi A.,
RA Aoki K.-I., Masuda S., Yanagishi M., Nishimura M., Yamagishi A.,
RA Oshima T., Kikuchi H.;
RT "Complete genome sequence of an aerobic thermophilic
RT Crenarchaeon, Sulfolobus tokodaii strain7.";
RL DNA Res. 8:123-140(2001).
DR EMBL: AF00982; BAB6535.1; -.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 132 AA; 15598 MW; 64BB76F39B3E6180 CRC64;

Query Match 73.1%; Score 38; DB 2; Length 132;
Best Local Similarity 77.8%; Pred. No. 1e+02;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 SPEEDTEKD 9
Db 108 SPEEDTEKD 116

RESULT 15
Q9W308 PRELIMINARY; PRT; 173 AA.
ID Q9W308;
AC Q9W308;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DE CG9689-PA (GH05731p).
GN ORFNames=CG9689;
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;
RA Adams M.D., Celisner S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sulten G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.H., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter B.G., Helt G., Neilson C.R., Gaber G.L.,
RA Abri1 J.F., Agbayani A., An H.J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.W., Basu A., Bayendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Bertman B.P., Bhandari D., Bolshakov S.,
RA Borokova D., Botchan M.R., Bouck J., Brokstein P., Brotlier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablo B., Delcher A., Deng Z., Meyers A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Fertiera S., Fleischmann W.,
RA Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.H., Iobegam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kenson J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Laske P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Moberg C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Paclet J.M.,

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RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svirskaas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.Y., Wassarman D.A., Weinstein G.M., Weissbach J.,
 RA Williams S.M., Woodruff, Worley K.C., Wu D., Yang S., Yao Q.A., Ye J.,
 RA Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of *Drosophila melanogaster*.";
 RL Science 287:2185-2195(2000).
 RN [2]
 RN SEQUENCE FROM N.A.
 RP MEDLINE=22426065; PubMed=12537568;
 RA Ceiniker S.E., Wheeler D.A., Krommiller B., Carlson J.W., Halpern A.,
 RA Patel S., Adams M., Champe M., Dugan S.P., Friese E., Hodgson A.,
 RA George R.A., Hoskins R.A., Laverly T., Muzny D.M., Nelson C.R.,
 RA Pacleb J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,
 RA Svirskaas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,
 RA Weinstein G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.;
 RT "Finishing a whole-genome shotgun. Release 3 of the *Drosophila*
 RT *melanogaster* euchromatic genome sequence.";
 RL Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
 RN [3]
 RN SEQUENCE FROM N.A.
 RP MEDLINE=22426070; PubMed=12537573;
 RA Kaminiker J.S., Bergman C.M., Krommiller B., Carlson J., Svirskaas R.,
 RA Patel S., Friese E., Wheeler D.A., Lewis S.E., Rubin G.M.,
 RA Ashburner M., Ceiniker S.E.;
 RT "The transposable elements of the *Drosophila melanogaster* euchromatin:
 RT a genomics perspective.";
 RL Genome Biol. 3:RESEARCH0084-RESEARCH0084(2002).
 RN [4]
 RN SEQUENCE FROM N.A.
 RP MEDLINE=22426069; PubMed=12537572;
 RA Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
 RA Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,
 RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,
 RA Betencourt B.R., Ceiniker S.E., de Grey A.D., Drysdale R.A.,
 RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
 RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
 RA Lewis S.E.;
 RT "Annotation of the *Drosophila melanogaster* euchromatic genome: a
 RT systematic review.";
 RL Genome Biol. 3:RESEARCH0083-RESEARCH0083(2002).
 RN [5]
 RN SEQUENCE FROM N.A.
 RP SEQUENCE FROM N.A.
 RG FlyBase;
 RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
 RN [6]
 RN SEQUENCE FROM N.A.
 RG FlyBase;
 RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
 RN [7]
 RN SEQUENCE FROM N.A.
 RC STRAIN-Berkeley;
 RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
 RA Champe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Friese E.,
 RA George R., Gonzalez M., Guarin H., Krommiller B., Li P., Liao G.,
 RA Miranda A., Mungall C.J., Nunco J., Pacleb J., Paragas V., Park S.,
 RA Patel S., Phouanavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
 RA Ceiniker S.;
 RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AE003448; AA046529.1; -;
 DR EMBL; AY094677; AA011030.1; -;
 DR FlyBase; FBgn0030159; CG9689.
 SQ SEQUENCE 173 AA; 18990 MW; C5625913758437B3 CRC64;

Query Match 73.1%; Score 38; DB 2; Length 173;
 Best Local Similarity 77.8%; Pred. No. 1.3e+02;
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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 DB 107 FEKDXEKX 115
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OM protein - protein search, using bw model

Run on: October 25, 2005, 20:58:51 ; Search time 69.7126 Seconds
(without alignments)
55.479 Million cell updates/sec

Title: US-10-731-238-88
Perfect score: 53
Sequence: 1 FNKXTRIEE 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:*

- 1: Geneseqp1980s:*
- 2: Geneseqp1990s:*
- 3: Geneseqp2000s:*
- 4: Geneseqp2001s:*
- 5: Geneseqp2002s:*
- 6: Geneseqp2003as:*
- 7: Geneseqp2003bs:*
- 8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	53	100.0	10	AAW65744
2	53	100.0	37	AAW65744 Fibronect
3	53	100.0	37	AAW65744 Fibronect
4	53	100.0	38	AAW65744 Fibronect
5	53	100.0	77	AAW65744 Fibronect
6	53	100.0	113	AAW65744 Fibronect
7	53	100.0	124	AAW65744 Fibronect
8	53	100.0	128	AAW65744 Fibronect
9	53	100.0	130	AAW65744 Fibronect
10	53	100.0	130	AAW65744 Fibronect
11	53	100.0	130	AAW65744 Fibronect
12	53	100.0	134	AAW65744 Fibronect
13	53	100.0	134	AAW65744 Fibronect
14	53	100.0	134	AAW65744 Fibronect
15	53	100.0	134	AAW65744 Fibronect
16	53	100.0	139	AAW65744 Fibronect
17	53	100.0	162	AAW65744 Fibronect
18	53	100.0	164	AAW65744 Fibronect
19	53	100.0	174	AAW65744 Fibronect
20	53	100.0	174	AAW65744 Fibronect
21	53	100.0	181	AAW65744 Fibronect
22	53	100.0	181	AAW65744 Fibronect
23	53	100.0	559	AAW65744 Fibronect
24	53	100.0	540	AAW65744 Fibronect
25	53	100.0	940	AAW65744 Fibronect

26	53	100.0	948	6	ADA89470
27	53	100.0	948	6	ABJ18923
28	53	100.0	948	6	ABW72536
29	53	100.0	1018	1	AAW62115
30	53	100.0	1018	4	AAU37245
31	53	100.0	1018	4	AAU34301
32	53	100.0	1018	6	ABJ18922
33	53	100.0	1018	6	ABW72537
34	53	100.0	1027	2	AAW69806
35	48	90.6	961	6	ABU15854
36	48	90.6	978	4	AAU33960
37	48	90.6	1001	4	AAU37093
38	48	90.6	1038	6	ABU15903
39	45	84.9	767	4	AAU34403
40	45	84.9	767	4	AAU37547
41	41	77.4	10	2	AAW65745
42	41	77.4	52	8	ABO57274
43	41	77.4	225	8	ADE84609
44	41	77.4	429	2	AAU32953
45	41	77.4	429	8	ADE84607

ALIGNMENTS

RESULT 1
AAW65744 standard; peptide; 10 AA.

AAW65744:

16-OCT-1998 (first entry)

Fibronectin binding protein-derived peptide #8.

microbial surface components recognising adhesive matrix molecule;
MSCRAMM; fibronectin; fibronectin-binding protein; antibody; epitope;
antibiotic; bacterial infection; antibiotic-resistant strain.

Synthetic.

Staphylococcus aureus.

23-JUL-1998.

21-JAN-1997; 97US-0036139P.

21-JAN-1998; 98WO-US001222.

21-JAN-1997; 97US-0036139P.

(TEXAS) UNIV TEXAS A & M SYSTEM.

Hoeck M, Patti JM, House-Pompeo KL, Speziale P, Joh D;

McGarvin MJ;

WPI; 1998-413816/35.

Antibody that binds to fibronectin-binding protein, preventing its

binding to fibronectin - used to treat or prevent bacterial infection,

especially by Staphylococci and Streptococci.

Example 9; Page 11; 201pp; English.

The invention relates to antibodies that bind to a fibronectin-binding domain of a fibronectin-binding protein, and inhibit binding of the protein to fibronectin. Also claimed are: (1) isolated peptides of a fibronectin-binding protein that do not bind to fibronectin; (2) fusion protein containing at least one peptide of a fibronectin-binding protein linked to a second amino acid sequence; (3) nucleic acid encoding the isolated peptide of (1). Antibodies, the isolated peptides of (1) and the nucleic acids are all useful for immunisation (active or passive) and (b) inhibiting binding of bacteria to fibronectin for preventing or treating infection in humans or other animals, particularly by staphylococci or

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CC streptococci, e.g. meningitis, otitis media, pneumonia, endocarditis,
CC mastitis in cattle, abortion in horses and many others. Since the
CC antibodies block binding of bacteria, they should be effective against
CC antibiotic-resistant strains, and may replace antibiotic therapy or
CC increase its effectiveness. Sequences AAM65744-58 represent peptides
CC which were synthesised to span the D3 motif of S. aureus fibronectin
CC binding protein A
CC
XX
SQ Sequence 10 AA;
Query Match 100.0%; Score 53; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0057;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 FNKHTETIEE 10
   |||||
   1 FNKHTETIEE 10
Db
RESULT 2
AAP82118
ID AAP82118 standard; protein; 37 AA.
XX
AC AAP82118;
XX
DT 25-MAR-2003 (revised)
DT 05-JAN-1990 (first entry)
XX
DE Fibronectin binding protein.
XX
KM Fibronectin binding protein; S.aureus; immunisation; mastitis; ruminants;
KM wound infection; diagnosis.
XX
OS Staphylococcus aureus.
XX
PN EP294349-A.
XX
PD 07-DEC-1988.
XX
PF 30-MAY-1988; 88EP-00850188.
XX
PR 01-JUN-1987; 87SE-00002272.
XX
PA (ALFA ) ALFA LAVAL AGRIC INT AB.
XX
PI Lindberg MK, Signas LC, Madstrom TM, Froman G;
XX
DR WPI; 1988-347978/49.
DR N-PSDB; AAN82056.
XX
PT Hybrid DNA encoding Staphylococcus aureus fibronectin binding protein -
PT useful for immunisation and topical application to prevent staphylococcal
PT infections.
XX
PS Claim 11; Page 12; 23pp; English.
XX
CC The S.aureus fibronectin binding protein may be included in a hybrid
CC protein. The protein may be used to immunise ruminants against
CC staphylococcal mastitis, pref. when given at 0.5-5 microg/kg, using 3
CC doses at 1-3 week intervals; and for topical applicn. to prevent wound
CC infection, pref. using isotonic saline soln. of concn. 25-250 microg/mg.
CC The DNA encoding the binding protein and the hybrid protein may be
CC immobilised on a carrier and used to diagnose staphylococcal infections.
CC (Updated on 25-MAR-2003 to correct PA field.)
XX
SQ Sequence 37 AA;
Query Match 100.0%; Score 53; DB 1; Length 37;
Best Local Similarity 100.0%; Pred. No. 0.022;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 FNKHTETIEE 10
   |||||
   1 FNKHTETIEE 10

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Db 2 FNKHTETIEE 11
RESULT 3
AAB91958
ID AAB91958 standard; peptide; 37 AA.
XX
AC AAB91958;
XX
DT 22-JUN-2001 (first entry)
XX
DE Fibronectin fragment and fibrin related peptide SEQ ID NO.1134.
XX
KM Protection; endogenous therapeutic peptide; peptidase; conjugation;
KM blood component; modification; succinimidy1; maleimido group; amino;
KM hydroxyl; thiol; hormone; growth factor; neurotransmitter.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200069900-A2.
XX
PD 23-NOV-2000.
XX
PF 17-MAY-2000; 2000WO-US013576.
XX
PR 17-MAY-1999; 99US-0134406P.
PR 10-SEP-1999; 99US-0153406P.
PR 15-OCT-1999; 99US-0159783P.
XX
PA (CONU-) CONJUCHEM INC.
XX
PI Bridon DP, Ezrin AM, Milner PG, Holmes DL, Thibaudau K;
XX
DR WPI; 2001-112059/12.
XX
PT Modifying and attaching therapeutic peptides to albumin prevents
PT peptidase degradation, useful for increasing length of in vivo activity.
XX
PS Disclosure; Page 566; 733pp; English.
XX
CC The present invention describes a modified therapeutic peptide (I)
CC comprising a therapeutically active amino acid region (III) and a
CC reactive group (II) (e.g. succinimidy1 and maleimido groups) attached to
CC a less therapeutically active amino acid region (IV), which covalently
CC bonds with amino/hydroxyl/thiol groups on blood components to form a
CC peptidase stabilised therapeutic peptide composed of 3-50 amino acids.
CC (I) are useful for modifying therapeutic peptides e.g. hormones, growth
CC factors and neurotransmitters, to protect them from peptidase activity in
CC vivo for the treatment of various disorders. Endogenous therapeutic
CC peptides are not suitable as drug candidates as they require frequent
CC administration due to rapid degradation by peptidases in the body.
CC Modifying and attaching therapeutic peptides to albumin prevents or
CC reduces the action of peptidases to increase length of activity (half
CC life) and specificity as bonding to large molecules decreases.
CC Intracellular uptake and interference with physiological processes.
CC AAB90829 to AAB92441 represent peptides which can be used in the
CC exemplification of the present invention
XX
SQ Sequence 37 AA;
Query Match 100.0%; Score 53; DB 4; Length 37;
Best Local Similarity 100.0%; Pred. No. 0.022;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 FNKHTETIEE 10
   |||||
   1 FNKHTETIEE 10
Db 1 FNKHTETIEE 10
RESULT 4
AAP80662
ID AAP80662 standard; protein; 38 AA.

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XX AC AAF80662;
XX XX 25-MAR-2003 (revised)
DT 07-OCT-1990 (first entry)
XX DE Protein with fibronectin binding ability.
XX XX Hybrid DNA molecule; fibronectin binding; mastitis; ruminants;
KW wound infection.
XX OS Staphylococcus aureus.
XX PN EP294349-A.
XX PD 07-DEC-1988.
XX PF 30-MAY-1988; 88EP-00850188.
XX PR 01-JUN-1987; 87SE-00002272.
XX PA (ALFA ) ALFA LAVAL AGRIC INT AB.
XX PI Lindberg MK, Signas LC, Wadstrom TM, Froman G;
DR WPI, 1988-347978/49.
DR N-PSDB; AAN81099.
XX PT Hybrid DNA encoding Staphylococcus aureus fibronectin binding protein -
PT useful for immunisation and topical application to prevent staphylococcal
PT infections.
XX PS Claim 11; Page 12; 23pp; English.
XX XX The peptide has fibronectin binding ability. It is useful for immunising
CC ruminants against staphylococcal mastitis, pret. when used at 0.5-5
CC micrograms/kg, using 3 doses given at 1-3 week intervals; for topical
CC application to prevent wound infection, using an isotonic saline soln. of
CC concn. 25-250 micrograms/ml; and, when immobilised on a carrier, for
CC diagnosing staphylococcal infections. (Updated on 25-MAR-2003 to correct
CC PF field.) (Updated on 25-MAR-2003 to correct PA field.)
XX SQ Sequence 38 AA;
Query Match 100.0%; Score 53; DB 1; Length 38;
Best Local Similarity 100.0%; Pred. No. 0.023; 0; Indels 0; Gaps 0;
Matches 10; Conservative 0; Mismatches 0;
QY 1 FNKHTETIEE 10
DB 2 FNKHTETIEE 11
RESULT 5
AAR8749
ID AAR8749 standard; protein; 77 AA.
XX AAR8749;
XX 24-SEP-1996 (first entry)
XX DE S. aureus fibronectin binding protein D2D3 polypeptide.
XX KW Fibronectin binding protein; D2D3; prevention; adhesion; bacteria;
KW gram positive; extra-cellular matrix protein; in-dwelling device;
KW catheter; wound; D2D3; oral pathogen; oral cavity; J2385; NCIMB 40532.
XX OS Staphylococcus aureus.
XX PN WO9604380-A1.
XX PD 15-FEB-1996.

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PF 28-JUL-1995; 95WO-EP003039.
XX 05-AUG-1994; 94GB-00015901.
XX (SMIK ) SMITHKLINE BEECHAM PLC.
XX PI Critchley IA, Dodd I, Barnett P, Mosakowska DEI;
XX WPI, 1996-129396/13.
DR N-PSDB; AAT12582.
XX PT Staphylococcus aureus fibronectin binding protein D2D3 polypeptide -
PT useful for combatting infection at wound sites, surgical implants, etc.
PT and as adherent agent in oral hygiene.
XX PS Claim 5; Page 26; 38pp; English.
XX XX The present sequence is the S. aureus fibronectin binding protein
CC polypeptide D2D3, which can be used to prevent adhesion of (e.g. gram
CC positive) bacteria, to extra-cellular matrix proteins on in-dwelling
CC devices, e.g. catheters or in wounds. D2D3 can also be used to prevent
CC oral pathogens from binding to extra-cellular matrix proteins, in the
CC oral cavity. D2D3 was found to be effective at inhibiting S. aureus 8325-
CC 4, and 120 adhesion to fibronectin coated PMMA coverlips, at a min.
CC adhesion inhibitor concn. of 10 microg/ml. D2D3 was derived from the D2
CC and D3 regions of the S. aureus J2385 (NCIMB 40532) fibronectin binding
CC protein
XX SQ Sequence 77 AA;
Query Match 100.0%; Score 53; DB 2; Length 77;
Best Local Similarity 100.0%; Pred. No. 0.048; 0; Indels 0; Gaps 0;
Matches 10; Conservative 0; Mismatches 0;
QY 1 FNKHTETIEE 10
DB 40 FNKHTETIEE 49
RESULT 6
AAR90937
ID AAR90937 standard; peptide; 113 AA.
XX AAR90937;
XX 23-SEP-1996 (first entry)
XX DE D3D4 polypeptide #1.
XX KW Fibronectin binding protein; Fbp; S. aureus J2385; monoclonal antibody;
KW infection; surgical implant; antiadherent agent; hygiene; adhesion;
KW extracellular matrix protein; oral pathogen; oral cavity.
XX OS Staphylococcus aureus.
XX FH Key Location/Qualifiers
FH FT 1..21
FH FT /note= "D1 region fragment"
FH FT 22..59
FH FT /note= "D2 region"
FH FT 60..98
FH FT /note= "D3 region"
FH FT 99..113
FH FT /note= "D4 region"
FH FT Misc-difference 113
FH FT /note= "P113T"
XX PN WO9604381-A1.
XX PD 15-FEB-1996.
XX PF 28-JUL-1995; 95WO-EP003040.

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PR	05-AUG-1994;	94GB--00015900.
XX	(SMIK) SMITHKLINE BEECHAM PLC.	
PA	Critchley IA, Dodd I, Barnett P, Mcbay DL;	
P1	WP1, 1996-129397/13.	
DR		
XX		
XX		
PT	Polypeptide(s) derived from Staphylococcus aureus fibronectin binding	
PT	protein - inhibit binding of bacteria to extracellular matrix proteins,	
PT	for combating infection at the site of wounds and surgical implants, and	
PS	in oral hygiene.	
PS	Claim 6; Page 24; 35pp; English.	
XX		
CC	AA09037-R0942 represent D3D4 polypeptides. These sequences correspond	
CC	to fragments of the Staphylococcus aureus fibronectin binding protein	
CC	(Fbp). This sequence corresponds to residues 18-130 of S. aureus J2385	
CC	Fbp, and also contains the D2 region, and a portion of the D1 region.	
CC	These sequences, and monoclonal antibodies against them can be used to	
CC	combat infection at the site of wounds, surgical implants and other in-	
CC	dwelling devices (such as catheters), and as antiadherent agents in oral	
CC	hygiene. They can also be used in the manufacture of a medicament for the	
CC	prevention of adhesion of bacteria to extracellular matrix proteins	
CC	present on in-dwelling devices or in wounds, or of oral pathogens to	
CC	similar proteins on surfaces in the oral cavity	
SQ	Sequence 113 AA;	
Query March	100.0%; Score 53; DB 2; Length 113;	
Best Local Similarity	100.0%; Pred. NO. 0.072;	
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
QY	1 FNKHTETIEE 10 61 FNKHTETIEE 70	
Db		
RESULT 7		
AA030940		
ID	AA030940 standard; peptide; 124 AA.	
XX		
AC	AA030940;	
XX		
DT	23-SEP-1996 (first entry)	
XX		
DE	D3D4 polypeptide #4.	
KM	Fibronectin binding protein; Fbp; S. aureus J2385; monoclonal antibody;	
KW	Infection; surgical implant; antiadherent agent; hygiene; adhesion;	
XX	extracellular matrix protein; oral pathogen; oral cavity.	
OS	Staphylococcus aureus.	
XX		
XX		
FH	Key	Location/Qualifiers
FT	Region	1..19
FT	/note= "D2 region fragment"	20..58
FT	Region	/note= "D3 region"
FT	Region	59..62
FT	/note= "D4 region"	63..124
FT	Region	/note= "WRI region"
XX		
PN	WO9604381-A1.	
XX		
PD	15-FEB-1996.	
PF	28-JUL-1995;	95WO-EP003040.
PR	05-AUG-1994;	94GB--00015900.
XX		
PA	(SMIK) SMITHKLINE BEECHAM PLC.	

XX	Critchley IA, Dodd I, Barnett P, Mcbey DL;
PI	
XX	WP1: 1996-129397/13.
DR	
XX	Polypeptide(s) derived from Staphylococcus aureus fibronectin binding
PT	protein - inhibit binding of bacteria to extracellular matrix proteins,
PT	for combating infection at the site of wounds and surgical implants, and
PT	in oral hygiene.
PS	
XX	Claim 6; Page 24; 35pp; English.
CC	
CC	AA90937-R90942 represent D3D4 polypeptides. These sequences correspond
CC	to fragments of the Staphylococcus aureus fibronectin binding protein
CC	(Fbp). This sequence corresponds to residues 58-181 of S.aureus J2385
CC	Fbp, and also contains a portion of the D2 region, and a portion of the
CC	wall region 1 (WR1). These sequences, and monoclonal antibodies against
CC	them can be used to combat infection at the site of wounds, surgical
CC	implants and other in-dwelling devices (such as catheters), and as
CC	antidherent agents in oral hygiene. They can also be used in the
CC	manufacture of a medicament for the prevention of adhesion of bacteria to
CC	extracellular matrix proteins present on in-dwelling devices or in
CC	wounds, or of oral pathogens to similar proteins on surfaces in the oral
CC	cavity
XX	
SQ	Sequence 124 AA;
	Query Match 100.0%; Score 53; DB 2; Length 124;
	Best Local Similarity 100.0%; Pred. No. 0.079;
	Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY	1 FNKATETIEE 10 21 FNKATETIEE 30
Db	
	RESULT 8
AA90941	
ID	AA90941 standard; peptide: 128 AA.
XX	
AC	AA90941;
XX	
DT	23-SEP-1996 (first entry)
XX	
DE	D3D4 polypeptide #5.
XX	
KW	Fibronectin binding protein; Fbp; S.aureus J2385; monoclonal antibody;
KW	infection; surgical implant; antiadherent agent; hygiene; adhesion;
KW	extracellular matrix protein; oral pathogen; oral cavity.
XX	
OS	Staphylococcus aureus.
XX	
FH	
FT	Key Location/Qualifiers
FT	1..23
FT	/note= "D2 region"
FT	24..62
FT	/note= "D3 region"
FT	63..77
FT	/note= "D4 region"
FT	78..128
FT	/note= "WR1 region"
XX	
PN	W09604381-A1.
XX	
PD	15-FEB-1996.
XX	
PF	28-JUL-1995; 95WO-EP003040.
XX	
PR	05-AUG-1994; 94GB-00015900.
XX	
PA	(SMIK) SMITHKLINE BEECHAM PLC.
PI	Critchley IA, Dodd I, Barnett P, Mcbey DL;

XX WPI; 1996-129397/13.
 XX Polypeptide(s) derived from *Staphylococcus aureus* fibronectin binding
 PT protein- inhibit binding of bacteria to extracellular matrix proteins,
 PT for combating infection at the site of wounds and surgical implants, and
 PT in oral hygiene.
 XX Claim 6; Page 24; 35pp; English.
 XX
 CC AAR90937-R90942 represent D3d4 polypeptides. These sequences correspond
 CC to fragments of the *Staphylococcus aureus* fibronectin binding protein
 CC (Fbp). This sequence corresponds to residues 54-181 of *S. aureus* J2385
 CC Fbp, and also contains the D2 region, and a portion of the wall region 1
 CC (WR1). These sequences, and monoclonal antibodies against them can be
 CC used to combat infection at the site of wounds, surgical implants and
 CC other in-dwelling devices (such as catheters), and as antiadherent agents
 CC in oral hygiene. They can also be used in the manufacture of a medicament
 CC for the prevention of adhesion of bacteria to extracellular matrix
 CC proteins present on in-dwelling devices or in wounds, or of oral
 CC pathogens to similar proteins on surfaces in the oral cavity
 CC
 SQ Sequence 128 AA;
 Query Match 100.0%; Score 53; DB 2; Length 128;
 Best Local Similarity 100.0%; Pred. No. 0.082;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 FNKHTETIEE 10
 |||||
 Db 25 FNKHTETIEE 34
 RESULT 9
 AAR58806
 ID AAR58806 standard; protein; 130 AA.
 XX
 AC AAR58806;
 XX
 DT 25-MAR-2003 (revised)
 DT 30-MAR-1995 (first entry)
 XX
 DE Fibronectin binding domain D1-D4(709-838(P838T)).
 XX
 KW Fibronectin binding protein; Fbp; fibronectin binding domain;
 KW monoclonal antibody; Mab; adhesion; Gram-positive bacterium; bacteremia;
 KW *Escherichia coli*.
 XX
 OS *Staphylococcus aureus*.
 XX
 PN WO9418327-A1.
 XX
 PD 18-AUG-1994.
 XX
 PF 04-FEB-1994; 94WO-GB000215.
 XX
 PR 05-FEB-1993; 93GB-00002289.
 PR 20-OCT-1993; 93GB-00021592.
 XX
 PA (SMIK) SMITHKLINE BEECHAM PLC.
 XX
 PI Burnham MKR, Chopra I, Critchley IA, Knowles DJC;
 XX WPI; 1994-279748/34.
 DR
 XX
 PT Fibronectin binding protein and monoclonal antibodies specific for Fbp -
 PT useful to prevent adherence of Gram-positive bacteria to indwelling
 PT devices or wounds.
 XX
 PS Disclosure; Page 30; 40pp; English.
 CC Polypeptides corresponding to residues G709-T886 plus PPIVPT, G709-
 CC P838(P838T) and G709-P838 (AAR58805-07, respectively) of *S. aureus* J2385
 CC P838(P838T) and G709-P838 (AAR58805-07, respectively) of *S. aureus* J2385

CC (NCIMB 40532) Fbp type A fibronectin binding domain D1-D4 region
 CC (AAR58808) were expressed in *E. coli* BL21(DE4) and used to raise MAb
 CC specific for Fbp. (Updated on 25-MAR-2003 to correct PN field.)
 XX
 SQ Sequence 130 AA;
 Query Match 100.0%; Score 53; DB 2; Length 130;
 Best Local Similarity 100.0%; Pred. No. 0.083;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 FNKHTETIEE 10
 |||||
 Db 78 FNKHTETIEE 87
 RESULT 10
 AAR58807
 ID AAR58807 standard; protein; 130 AA.
 XX
 AC AAR58807;
 XX
 DT 25-MAR-2003 (revised)
 DT 30-MAR-1995 (first entry)
 XX
 DE Fibronectin binding domain D1-D4(709-838).
 XX
 KW Fibronectin binding protein; Fbp; fibronectin binding domain;
 KW monoclonal antibody; Mab; adhesion; Gram-positive bacterium; bacteremia;
 KW *Escherichia coli*.
 XX
 OS *Staphylococcus aureus*.
 XX
 PN WO9418327-A1.
 XX
 PD 18-AUG-1994.
 XX
 PF 04-FEB-1994; 94WO-GB000215.
 XX
 PR 05-FEB-1993; 93GB-00002289.
 PR 20-OCT-1993; 93GB-00021592.
 XX
 PA (SMIK) SMITHKLINE BEECHAM PLC.
 XX
 PI Burnham MKR, Chopra I, Critchley IA, Knowles DJC;
 XX WPI; 1994-279748/34.
 DR
 XX
 PT Fibronectin binding protein and monoclonal antibodies specific for Fbp -
 PT useful to prevent adherence of Gram-positive bacteria to indwelling
 PT devices or wounds.
 XX
 PS Disclosure; Page 30; 40pp; English.
 CC Polypeptides corresponding to residues G709-T886 plus PPIVPT, G709-
 CC P838(P838T) and G709-P838 (AAR58805-07, respectively) of *S. aureus* J2385
 CC (NCIMB 40532) Fbp type A fibronectin binding domain D1-D4 region
 CC (AAR58808) were expressed in *E. coli* BL21(DE4) and used to raise MAb
 CC specific for Fbp. (Updated on 25-MAR-2003 to correct PN field.)
 XX
 SQ Sequence 130 AA;
 Query Match 100.0%; Score 53; DB 2; Length 130;
 Best Local Similarity 100.0%; Pred. No. 0.083;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 FNKHTETIEE 10
 |||||
 Db 78 FNKHTETIEE 87
 RESULT 11
 AAR91202
 ID AAR91202 standard; peptide; 130 AA.

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XX AC AAR91202;
XX DT 13-NOV-1996 (first entry)
XX DE D1-D4 fibronectin binding domains.
XX KM Fibronectin; oral hygiene; gingivitis; gum disease; adhesion;
XX KM periodontitis; oral pathogen; caries; calculus; candidiasis; oral surgery;
XX KM tissue regeneration; irrigation; toothpaste; dentifrice; mouthwash;
XX KM lozenge.
XX OS Staphylococcus aureus.
XX PN WO9604003-A1.
XX PD 15-FEB-1996.
XX PF 18-JUL-1995; 95WO-EP002825.
XX PR 05-AUG-1994; 94GB-00015902.
XX PS (SMIK ) SMITHKLINE BEECHAM PLC.
XX PI Barnett P, Critchley IA, Dodd I;
XX DR WPI; 1996-129122/13.
XX PT Prevention of adherence of oral pathogens in the oral cavity, partic.
XX PT tooth surfaces - by application of a fibronectin binding protein or
XX PT polypeptide or a monoclonal antibody or fragment against it.
XX PS Claim 5; Page 32; 41pp; English.
XX CC Adherence of oral pathogens, particularly to tooth surfaces, can be
XX CC prevented by application of a fibronectin binding protein or polypeptide.
XX CC The fibronectin binding protein or polypeptide is useful in the
XX CC manufacture of oral hygiene compositions, eg. toothpaste, liquid
XX CC dentifrice, mouthwash or lozenge. They are useful to prevent the plaque-
XX CC related development of carious lesions, gingivitis, calculus or
XX CC periodontal disease and to combat oral cavity infections, e.g.
XX CC candidiasis. They may also be useful in oral surgery e.g. in guided
XX CC tissue regeneration procedures to prevent subsequent bacterial infection,
XX CC and for irrigation of periodontal pockets. This sequence corresponds to
XX CC amino acids 709-838 of the D1-D4 fibronectin binding domain of
XX CC Staphylococcus aureus
XX SQ Sequence 130 AA;
XX
Query Match 100.0%; Score 53; DB 2; Length 130;
Best Local Similarity 100.0%; Pred. No. 0.083;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 FNKHTETIEE 10
DB 78 FNKHTETIEE 87
RESULT 12
ID AAR91201 standard; peptide; 130 AA.
XX AAR91201;
XX AC AAR91201;
XX DT 13-NOV-1996 (first entry)
XX DE D1-D4 fibronectin binding domains.
XX KM Fibronectin; oral hygiene; gingivitis; gum disease; adhesion;
XX KM periodontitis; oral pathogen; caries; calculus; candidiasis; oral surgery;
XX KM tissue regeneration; irrigation; toothpaste; dentifrice; mouthwash;
XX KM lozenge.

```

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OS Staphylococcus aureus.
XX PN WO9604003-A1.
XX PD 15-FEB-1996.
XX PF 18-JUL-1995; 95WO-EP002825.
XX PR 05-AUG-1994; 94GB-00015902.
XX PS (SMIK ) SMITHKLINE BEECHAM PLC.
XX PI Barnett P, Critchley IA, Dodd I;
XX DR WPI; 1996-129122/13.
XX PT Prevention of adherence of oral pathogens in the oral cavity, partic.
XX PT tooth surfaces - by application of a fibronectin binding protein or
XX PT polypeptide or a monoclonal antibody or fragment against it.
XX PS Claim 5; Page 31-32; 41pp; English.
XX CC Adherence of oral pathogens, particularly to tooth surfaces, can be
XX CC prevented by application of a fibronectin binding protein or polypeptide.
XX CC The fibronectin binding protein or polypeptide is useful in the
XX CC manufacture of oral hygiene compositions, eg. toothpaste, liquid
XX CC dentifrice, mouthwash or lozenge. They are useful to prevent the plaque-
XX CC related development of carious lesions, gingivitis, calculus or
XX CC periodontal disease and to combat oral cavity infections, e.g.
XX CC candidiasis. They may also be useful in oral surgery e.g. in guided
XX CC tissue regeneration procedures to prevent subsequent bacterial infection,
XX CC and for irrigation of periodontal pockets. This sequence corresponds to
XX CC amino acids 709-838 of the D1-D4 fibronectin binding domain of
XX CC Staphylococcus aureus with a P838T substitution
XX SQ Sequence 130 AA;
XX
Query Match 100.0%; Score 53; DB 2; Length 130;
Best Local Similarity 100.0%; Pred. No. 0.083;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 FNKHTETIEE 10
DB 78 FNKHTETIEE 87
RESULT 13
ID AAY29089 standard; protein; 134 AA.
XX AAY29089;
XX AC AAY29089;
XX DT 28-SEP-1999 (first entry)
XX DE Cloned fibronectin binding protein binding domain (FnBAB) sequence.
XX KM Bovine herpes virus-2; BHV-2; cytokine; immune response; immunogen; IL;
XX KM interleukin; colony stimulating factor; CSF; interferon; IFN; TNF;
XX KM tumour necrosis factor; recombinant virus; vaccine; mucosal disease;
XX KM mastitis; breast cancer; stress-induced disease; binding domain; FnBAB;
XX KM fibronectin binding protein.
XX OS Staphylococcus aureus.
XX PN WO9916892-A1.
XX PD 08-APR-1999.
XX PF 29-SEP-1998; 98WO-GB002927.
XX PR 29-SEP-1997; 97GB-00020633.
XX PA (UYBR-) UNIV BRISTOL.

```

CC The invention provides bovine herpes virus-2 (BHV-2) based vectors that
CC comprise at least one cytokine-encoding DNA sequence. The expression of
CC cytokines in mammals can up-regulate immune responses to the immunogens.
CC The cytokine is selected from interleukins (IL), colony stimulating
CC factors (CSF), interferons (IFN) and tumour necrosis factors (TNF). The
CC BHV-2 based vector or recombinant virus can be used as vaccine. They can
CC be used for preventing or treating a mucosal disease in a subject, e.g.,
CC ruminants, cattle, sheep, goats, dogs, cats, horses, or man, particularly
CC mastitis in cows or breast cancers in humans. They can also be used for
CC preventing or treating a stress-induced disease. The present sequence
CC represents the binding domain of a previously published *S. aureus*
CC fibronectin binding protein B (FnBb) sequence. The FnB binding domain
CC gene sequence FNBBb, cloned for use in this invention has 97.8 percent
CC identity when compared to the previously published FNbA and FnBb gene
CC sequences

XX
SQ Sequence 134 AA;

Query Match 100.0%; Score 53; DB 2; Length 134;
Best Local Similarity 100.0%; Pred. No. 0.086;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FNKHTETLEE 10
|||||
Db 78 FNKHTETLEE 87

CC	RESULT 15
CC	AA129087
ID	AA129087 standard; protein, 134 AA.
XX	
AC	AA129087;
XX	
DT	28-SEP-1999 (first entry)
DE	
XX	S. aureus fibronectin binding protein A (FnBA) binding domain.
XX	
KW	Bovine herpes virus-2; BHV-2; cytokine; immune response; immunogen; IL;
KW	interleukin; colony stimulating factor; CSF; interferon; IFN; TNF;
KW	tumour necrosis factor; recombinant virus; vaccine; mucosal disease;
KW	mastitis; breast cancer; stress-induced disease; binding domain; FnBA;
OS	fibronectin binding protein.
XX	
XX	Staphylococcus aureus.
PN	MO9916892-A1.
XX	
PD	08-APR-1999.
XX	
PF	29-SEP-1998; 98WO-GB002927.
XX	
PR	29-SEP-1997; 97GB-00020633.
XX	
PA	(UYBR-) UNIV BRISTOL.
XX	
PI	Bradley AJ, Duffas WPB;
XX	
DR	WPI: 1999-255101/21.
DR	N-PSDB; AAX91504.
XX	
PT	New bovine herpes virus-2 vectors.
XX	
PS	Example 2; Fig 8A-B; 130BP; English.
XX	
CC	The invention provides bovine herpes virus-2 (BHV-2) based vectors that
CC	comprise at least one cytokine-encoding DNA sequence. The expression of
CC	cytokines in mammals can up-regulate immune responses to the immunogen.
CC	The cytokine is selected from interleukins (IL), colony stimulating
CC	factors (CSF), interferons (IFN) and tumour necrosis factors (TNF). The
CC	BHV-2 based vector or recombinant virus can be used as vaccines. They can
CC	be used for preventing or treating a mucosal disease in a subject, e.g.
CC	ruminants, cattle, sheep, goats, cats, horses, or man, particularly
CC	mastitis in cows or breast cancers in humans. They can also be used for

CC preventing or treating a stress-induced disease. The present sequence
CC represents the binding domain of a previously published S. aureus
CC fibronectin binding protein A (FnBA) sequence. The FnB binding domain
CC gene sequence FNBA6, cloned for use in this invention has 97.8 percent
CC identity when compared to the previously published FnBA and FnB5 gene
CC sequences
XX

SO Sequence 134 AA;

Query Match 100.0%; Score 53; DB 2; Length 134;
Best Local Similarity 100.0%; Pred. NO. 0.086;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FNKATEIIEE 10
Db 78 FNKATEIIEE 87

Search completed: October 25, 2005, 21:29:09
Job time : 70.7126 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 22, 2005, 07:41:53 ; Search time 17.2989 Seconds
(without alignments)
43.153 Million cell updates/sec

Title: US-10-731-238-88

Percent score: 53

Sequence: 1 FNNKTEIIEE 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents AA: *
1: /cgn2_6/ptodata/1/1aa/5A.COMB.pep: *
2: /cgn2_6/ptodata/1/1aa/5B.COMB.pep: *
3: /cgn2_6/ptodata/1/1aa/6A.COMB.pep: *
4: /cgn2_6/ptodata/1/1aa/6B.COMB.pep: *
5: /cgn2_6/ptodata/1/1aa/PCITUS.COMB.pep: *
6: /cgn2_6/ptodata/1/1aa/backfile1.pep: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	53	100.0	10	4	US-09-010-317-88
2	53	100.0	37	1	US-08-234-622A-4
3	53	100.0	38	1	US-08-729-767-5
4	53	100.0	114	1	US-08-259-000-3
5	53	100.0	130	2	US-08-459-135A-7
6	53	100.0	130	2	US-08-459-135A-8
7	53	100.0	130	3	US-08-495-559-7
8	53	100.0	130	3	US-08-495-559-8
9	53	100.0	139	3	US-08-856-253-8
10	53	100.0	174	2	US-08-459-135A-10
11	53	100.0	174	2	US-08-459-135A-13
12	53	100.0	174	3	US-08-495-559-10
13	53	100.0	174	3	US-08-495-559-13
14	53	100.0	176	3	US-08-495-559-6
15	53	100.0	178	2	US-08-459-135A-12
16	53	100.0	178	2	US-08-495-559-12
17	53	100.0	181	2	US-08-459-135A-6
18	53	100.0	559	4	US-08-956-171E-5251
19	53	100.0	559	4	US-08-781-986A-5251
20	53	100.0	1027	4	US-08-956-171E-5254
21	53	100.0	1027	4	US-08-781-986A-5254
22	41	77.4	10	4	US-09-010-317-89
23	41	77.4	225	2	US-09-074-512-3
24	41	77.4	429	2	US-09-074-512-1
25	36	67.9	142	4	US-09-270-767-37074
26	36	67.9	142	4	US-09-270-767-52291
27	36	67.9	448	4	US-09-583-110-4489

28	36	67.9	615	3	US-09-134-001C-3284	Sequence 3284, Ap
29	36	67.9	1972	4	US-08-875-435B-4	Sequence 4, Appl
30	35	66.0	197	4	US-09-248-796A-23752	Sequence 23752, A
31	35	66.0	506	4	US-09-252-991A-27119	Sequence 27119, A
32	35	66.0	565	4	US-09-248-796A-15341	Sequence 15341, A
33	34	64.2	65	4	US-09-248-796A-24462	Sequence 24462, A
34	34	64.2	89	4	US-09-270-767-57719	Sequence 57719, A
35	34	64.2	131	4	US-09-107-433-4637	Sequence 4637, Ap
36	34	64.2	166	4	US-09-248-796A-22103	Sequence 22103, A
37	34	64.2	253	4	US-09-270-767-42427	Sequence 42427, A
38	34	64.2	273	4	US-09-107-433-4284	Sequence 4284, Ap
39	34	64.2	275	4	US-09-583-110-3006	Sequence 3006, Ap
40	34	64.2	311	4	US-09-248-796A-14776	Sequence 14776, A
41	34	64.2	335	4	US-09-583-110-3726	Sequence 3726, Ap
42	34	64.2	399	4	US-09-270-767-48048	Sequence 48048, A
43	34	64.2	403	4	US-09-248-796A-14239	Sequence 14239, A
44	34	64.2	519	4	US-09-248-796A-18734	Sequence 18734, A
45	34	64.2	530	4	US-09-861-451A-18	Sequence 18, Appl

ALIGNMENTS

RESULT 1
US-09-010-317-88
Sequence 88, Application US/09010317
Patent No. 6685943
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
APPLICANT: Patti, Joseph M.
APPLICANT: House-Pompeo, Karen L.
APPLICANT: Speziale, Pietro
APPLICANT: John, Danny
APPLICANT: McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
TITLE OF INVENTION: AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/010.317
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hieber, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAMK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 88:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-09-010-317-88
Query Match 100.0%; Score 53; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0017;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 FNNKTEIIIEE 10
Db 1 FNNKTEIIIEE 10

RESULT 2

US-08-234-622A-4
; Sequence 4, Application US/08234622A
; Patent No. 5440014
; GENERAL INFORMATION:
; APPLICANT: HOOK, Magnus
; APPLICANT: MCGAVIN, Martin
; APPLICANT: RAUCCI, Giuseppe
; TITLE OF INVENTION: A FIBRONECTIN BINDING PEPTIDE
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Doane, Swecker & Mathis
; STREET: P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/234,622A
; FILING DATE: 28-APR-1994
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Meuth, Donna M
; REGISTRATION NUMBER: 36,607
; REFERENCE/DOCKET NUMBER: 012885-044
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 37 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-234-622A-4

Query Match 100.0%; Score 53; DB 1; Length 37;
Best Local Similarity 100.0%; Pred. No. 0.0062;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FNNKTEIIIEE 10
Db 1 FNNKTEIIIEE 10

RESULT 3

US-08-729-767-5
; Sequence 5, Application US/08729767
; Patent No. 5770702
; GENERAL INFORMATION:
; APPLICANT: HOOK, Magnus
; APPLICANT: LINDBERG, Martin Kjell
; APPLICANT: SIGNAS, Lars Christer
; APPLICANT: WADSTROM, Torkei Mikael

APPLICANT: FROMAN, Gunnar
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN AS WELL AS
; TITLE OF INVENTION: ITS PREPARATION
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Doane, Swecker & Mathis, L.L.P.
; STREET: P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/729,767
; FILING DATE: 07-OCT-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/259,000
; FILING DATE: 13-JUN-1994
; PRIOR APPLICATION DATA: US 08/007,817
; FILING DATE: 22-JAN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/201,028
; FILING DATE: 01-JUN-1988
; PRIOR APPLICATION DATA: SE 8702272-9
; APPLICATION NUMBER: 01-JUN-1987
; FILING DATE: 01-JUN-1987
; ATTORNEY/AGENT INFORMATION:
; NAME: McGowan, Malcolm K.
; REGISTRATION NUMBER: 39,300
; REFERENCE/DOCKET NUMBER: 012889-036
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 38 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-729-767-5

Query Match 100.0%; Score 53; DB 1; Length 38;
Best Local Similarity 100.0%; Pred. No. 0.0063;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FNNKTEIIIEE 10
Db 2 FNNKTEIIIEE 11

RESULT 4

US-08-259-000-3
; Sequence 3, Application US/08259000
; Patent No. 5571514
; GENERAL INFORMATION:
; APPLICANT: HOOK, Magnus
; APPLICANT: LINDBERG, Martin Kjell
; APPLICANT: SIGNAS, Lars Christer
; APPLICANT: WADSTROM, Torkei Mikael
; APPLICANT: FROMAN, Gunnar
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN AS WELL AS
; TITLE OF INVENTION: ITS PREPARATION
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Doane, Swecker & Mathis
; STREET: P.O. Box 1404

CITY: Alexandria
STATE: Virginia
COUNTRY: United States
ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/259,000
FILING DATE: 13-JUN-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: SE 8702272-9
FILING DATE: 01-JUN-1987
ATTORNEY/AGENT INFORMATION:
NAME: Meuth, Donna M
REGISTRATION NUMBER: 36,607
REFERENCE/DOCKET NUMBER: 012885-062
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 114 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-259-000-3

Query Match 100.0%; Score 53; DB 1; Length 114;
Best Local Similarity 100.0%; Pred. No. 0.019;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 FNKHTETIEE 10
|||||
78 FNKHTETIEE 87

Db

RESULT 5
US-08-459-135A-7
Sequence 7, Application US/08459135A
Patent No. 5955078
GENERAL INFORMATION:
APPLICANT: BURNHAM, Martin Karl Russel
APPLICANT: CHOPRA, Ian
APPLICANT: CRITCHLEY, Ian Alfred
APPLICANT: KNOWLES, David Justin Charles
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN: MONOCLONAL ANTIBODY AND THEIR US
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSER: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
STATE: PA
COUNTRY: U.S.A.
ZIP: 19406-0939
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: Fastseq, Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/459,135A
FILING DATE: 02-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB/94/00215
FILING DATE: 04-Feb-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:

NAME: Gimml, Edward R
REGISTRATION NUMBER: 38,891
REFERENCE/DOCKET NUMBER: P30591C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-4478
TELEFAX: 610-270-5090
TELEX:
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 130 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-459-135A-7

Query Match 100.0%; Score 53; DB 2; Length 130;
Best Local Similarity 100.0%; Pred. No. 0.022;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 FNKHTETIEE 10
|||||
78 FNKHTETIEE 87

Db

RESULT 6
US-08-459-135A-8
Sequence 8, Application US/08459135A
Patent No. 5955078
GENERAL INFORMATION:
APPLICANT: BURNHAM, Martin Karl Russel
APPLICANT: CHOPRA, Ian
APPLICANT: CRITCHLEY, Ian Alfred
APPLICANT: KNOWLES, David Justin Charles
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN: MONOCLONAL ANTIBODY AND THEIR US
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSER: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
STATE: PA
COUNTRY: U.S.A.
ZIP: 19406-0939
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: Fastseq, Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/459,135A
FILING DATE: 02-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB/94/00215
FILING DATE: 04-Feb-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Gimml, Edward R
REGISTRATION NUMBER: 38,891
REFERENCE/DOCKET NUMBER: P30591C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-4478
TELEFAX: 610-270-5090
TELEX:
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 130 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-459-135A-8

Query Match 100.0%; Score 53; DB 2; Length 130;
Best Local Similarity 100.0%; Pred. No. 0.022;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FNNKTEIIIE 10
Db 78 FNNKTEIIIE 87

RESULT 7

US-08-495-559-7
Sequence 7, Application US/08495559A
Patent No. 6034572
GENERAL INFORMATION:
APPLICANT: BURHAM, Martin Karl Russel
APPLICANT: CHOPRA, Ian
APPLICANT: CRITCHLEY, Ian Alfred
APPLICANT: KNOWLES, David Justin Charles
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN: MONOCLONAL
FILE REFERENCE: P30591
CURRENT APPLICATION NUMBER: US/08/495,559A
EARLIER FILING DATE: 1995-08-03
EARLIER APPLICATION NUMBER: GB 9302289.5
EARLIER FILING DATE: 1993-02-05
EARLIER APPLICATION NUMBER: GB 9321592.9
EARLIER FILING DATE: 1993-10-20
NUMBER OF SEQ ID NOS: 13
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 7
LENGTH: 130
TYPE: PRT
ORGANISM: Staphylococcus aureus
US-08-495-559-7

Query Match 100.0%; Score 53; DB 3; Length 130;

Best Local Similarity 100.0%; Pred. No. 0.022; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FNNKTEIIIE 10
Db 78 FNNKTEIIIE 87

RESULT 8

US-08-495-559-8
Sequence 8, Application US/08495559A
Patent No. 6034572
GENERAL INFORMATION:
APPLICANT: BURHAM, Martin Karl Russel
APPLICANT: CHOPRA, Ian
APPLICANT: CRITCHLEY, Ian Alfred
APPLICANT: KNOWLES, David Justin Charles
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN: MONOCLONAL
FILE REFERENCE: P30591
CURRENT APPLICATION NUMBER: US/08/495,559A
EARLIER FILING DATE: 1995-08-03
EARLIER APPLICATION NUMBER: GB 9302289.5
EARLIER FILING DATE: 1993-02-05
EARLIER APPLICATION NUMBER: GB 9321592.9
EARLIER FILING DATE: 1993-10-20
NUMBER OF SEQ ID NOS: 13
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 8
LENGTH: 130
TYPE: PRT
ORGANISM: Staphylococcus aureus
US-08-495-559-8

Query Match 100.0%; Score 53; DB 3; Length 130;

Best Local Similarity 100.0%; Pred. No. 0.022; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FNNKTEIIIE 10

Db 78 FNNKTEIIIE 87

RESULT 9

US-08-856-253-8
Sequence 8, Application US/08856253
Patent No. 6288214
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
APPLICANT: Patti, Joseph M.
APPLICANT: House-Pompeo, Karen
APPLICANT: Stnam, Narayana
APPLICANT: Symersky, Jindrich
TITLE OF INVENTION: COLLAGEN BINDING PROTEIN COMPOSITIONS
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESS: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: Texas
COUNTRY: U.S.
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/856,253
FILING DATE: Concurrently Herewith
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/017,678
FILING DATE: 16-MAY-1996
ATTORNEY/AGENT INFORMATION:
NAME: Kitchell, Barbara S.
REGISTRATION NUMBER: 33,928
REFERENCE/DOCKET NUMBER: TAMK:193
TELEPHONE: (512) 418-3000
TELEFAX: (512) 474-7577
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 139 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-08-856-253-8

Query Match 100.0%; Score 53; DB 3; Length 139;

Best Local Similarity 100.0%; Pred. No. 0.023; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FNNKTEIIIE 10
Db 92 FNNKTEIIIE 101

RESULT 10

US-08-459-135A-10
Sequence 10, Application US/08459135A
Patent No. 595078
GENERAL INFORMATION:
APPLICANT: BURHAM, Martin Karl Russel
APPLICANT: CHOPRA, Ian
APPLICANT: CRITCHLEY, Ian Alfred
APPLICANT: KNOWLES, David Justin Charles
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN: MONOCLONAL ANTIBODY AND THEIR US
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESS: SmithKline Beecham Corporation

STREET: 709 Swedeland Road
CITY: King of Prussia
STATE: PA
COUNTRY: U.S.A.
ZIP: 19406-0939
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
OPERATING SYSTEM: DOS
SOFTWARE: Fastseq, Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/459,135A
FILING DATE: 02-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB/94/00215
FILING DATE: 04-Feb-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Gimmil, Edward R
REGISTRATION NUMBER: 38,891
REFERENCE/DOCKET NUMBER: P30591C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-4478
TELEFAX: 610-270-5090
TELEX:
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 174 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: Protein
US-08-459-135A-10

Query Match 100.0%; Score 53; DB 2; Length 174;
Best Local Similarity 100.0%; Pred. No. 0.029;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 FNKHTETIEE 10
|||||||
Db 78 FNKHTETIEE 87

RESULT 11
US-08-459-135A-13
Sequence 13, Application US/08459135A
Patent No. 5955078
GENERAL INFORMATION:
APPLICANT: BURHAM, Martin Karl Russel
APPLICANT: CHOPRA, Ian
APPLICANT: CRITCHLEY, Ian Alfred
APPLICANT: KNOWLES, David Justin Charles
TITLE OF INVENTION: FIBROBLAST BINDING PROTEIN: MONOCLONAL ANTIBODY AND THEIR USE
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESSES:
ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
STATE: PA
COUNTRY: U.S.A.
ZIP: 19406-0939
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
OPERATING SYSTEM: DOS
SOFTWARE: Fastseq, Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/459,135A
FILING DATE: 02-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB/94/00215
FILING DATE: 04-Feb-1994

CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Gimmil, Edward R
REGISTRATION NUMBER: 38,891
REFERENCE/DOCKET NUMBER: P30591C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-4478
TELEFAX: 610-270-5090
TELEX:
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 174 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-459-135A-13

Query Match 100.0%; Score 53; DB 2; Length 174;
Best Local Similarity 100.0%; Pred. No. 0.029;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 FNKHTETIEE 10
|||||||
Db 78 FNKHTETIEE 87

RESULT 12
US-08-495-559-10
Sequence 10, Application US/08495559A
Patent No. 6054572
GENERAL INFORMATION:
APPLICANT: BURHAM, Martin Karl Russel
APPLICANT: CHOPRA, Ian
APPLICANT: CRITCHLEY, Ian Alfred
APPLICANT: KNOWLES, David Justin Charles
TITLE OF INVENTION: FIBROBLAST BINDING PROTEIN: MONOCLONAL
TITLE OF INVENTION: ANTIBODY AND THEIR USE IN PREVENTING BACTERIAL ADHESION
FILE REFERENCE: P30591
CURRENT APPLICATION NUMBER: US/08/495,559A
CURRENT FILING DATE: 1995-08-03
EARLIER APPLICATION NUMBER: GB 9302289.5
EARLIER FILING DATE: 1993-02-05
EARLIER APPLICATION NUMBER: GB 9321592.9
EARLIER FILING DATE: 1993-10-20
NUMBER OF SEQ ID NOS: 13
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 10
LENGTH: 174
TYPE: PRT
ORGANISM: Staphylococcus aureus
US-08-495-559-10

Query Match 100.0%; Score 53; DB 3; Length 174;
Best Local Similarity 100.0%; Pred. No. 0.029;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 FNKHTETIEE 10
|||||||
Db 78 FNKHTETIEE 87

RESULT 13
US-08-495-559-13
Sequence 13, Application US/08495559A
Patent No. 6054572
GENERAL INFORMATION:
APPLICANT: BURHAM, Martin Karl Russel
APPLICANT: CHOPRA, Ian
APPLICANT: CRITCHLEY, Ian Alfred
APPLICANT: KNOWLES, David Justin Charles
TITLE OF INVENTION: FIBROBLAST BINDING PROTEIN: MONOCLONAL
TITLE OF INVENTION: ANTIBODY AND THEIR USE IN PREVENTING BACTERIAL ADHESION

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; FILE REFERENCE: P30591
; CURRENT APPLICATION NUMBER: US/08/495,559A
; CURRENT FILING DATE: 1995-08-03
; EARLIER APPLICATION NUMBER: GB 9302289.5
; EARLIER FILING DATE: 1993-02-05
; EARLIER APPLICATION NUMBER: GB 9321592.9
; EARLIER FILING DATE: 1993-10-20
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 13
; LENGTH: 174
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
; US-08-495-559-13

Query Match          100.0%; Score 53; DB 3; Length 174;
Best Local Similarity 100.0%; Pred. No. 0.029;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 FNNKTEIIIE 10
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Db      78 FNNKTEIIIE 87

RESULT 14
US-08-495-559-6
; Sequence 6, Application US/08495559A
; Patent No. 6054572
; GENERAL INFORMATION:
; APPLICANT: BURHAM, Martin Karl Russel
; APPLICANT: CHOPRA, Ian
; APPLICANT: CRITCHLEY, Ian Alfred
; APPLICANT: KNOWLES, David Justin Charles
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN: MONOCLONAL
; TITLE OF INVENTION: ANTIBODY AND THEIR USE IN PREVENTING BACTERIAL ADHESION
; FILE REFERENCE: P30591
; CURRENT APPLICATION NUMBER: US/08/495,559A
; CURRENT FILING DATE: 1995-08-03
; EARLIER APPLICATION NUMBER: GB 9302289.5
; EARLIER FILING DATE: 1993-02-05
; EARLIER APPLICATION NUMBER: GB 9321592.9
; EARLIER FILING DATE: 1993-10-20
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 176
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
; US-08-495-559-6

Query Match          100.0%; Score 53; DB 3; Length 176;
Best Local Similarity 100.0%; Pred. No. 0.03;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 FNNKTEIIIE 10
        |||||
Db      78 FNNKTEIIIE 87

RESULT 15
US-08-459-135A-12
; Sequence 12, Application US/08459135A
; Patent No. 5955078
; GENERAL INFORMATION:
; APPLICANT: BURHAM, Martin Karl Russel
; APPLICANT: CHOPRA, Ian
; APPLICANT: CRITCHLEY, Ian Alfred
; APPLICANT: KNOWLES, David Justin Charles
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN: MONOCLONAL ANTIBODY AND THEIR USE
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: SmithKline Beecham Corporation
; STREET: 709 Swedeland Road
```

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; CITY: King of Prussia
; STATE: PA
; COUNTRY: U.S.A.
; ZIP: 19406-0939
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq, Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/459,135A
; FILING DATE: 02-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB/94/00215
; FILING DATE: 04-Feb-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Glimm, Edward R
; REGISTRATION NUMBER: 38,891
; REFERENCE/DOCKET NUMBER: P30591C2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-270-4478
; TELEFAX: 610-270-5090
; TELEX:
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 178 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Protein
; US-08-459-135A-12

Query Match          100.0%; Score 53; DB 2; Length 178;
Best Local Similarity 100.0%; Pred. No. 0.03;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 FNNKTEIIIE 10
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Db      78 FNNKTEIIIE 87

Search completed: October 22, 2005, 09:35:42
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 22, 2005, 12:39:57 ; Search time 56.1494 Seconds
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74.354 Million cell updates/sec

Title: US-10-731-238-88
Perfect score: 53
Sequence: 1 FNKHTERIEE 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1862951 seqs, 417491010 residues
Total number of hits satisfying chosen parameters: 1862951

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA:*

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- 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
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- 7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
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- 9: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep.*
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- 12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
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- 19: /cgn2_6/ptodata/2/pubpaa/US11_PUBCOMB.pep.*
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- 21: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
- 22: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	53	100.0	10	18	US-10-731-238-88
2	53	100.0	37	20	US-11-066-697-1134
3	53	100.0	139	9	US-09-813-820-8
4	53	100.0	388	8	US-08-901-062-1
5	53	100.0	559	15	US-10-329-624-5251
6	53	100.0	559	15	US-10-329-624-5251
7	53	100.0	940	17	US-10-470-048B-424
8	53	100.0	948	17	US-10-470-048B-69
9	53	100.0	1018	9	US-09-815-242-5797
10	53	100.0	1018	9	US-09-815-242-12838
11	53	100.0	1018	17	US-10-470-048B-68

12	53	100.0	1027	8	US-08-781-986A-5254	Sequence 5254, Ap
13	53	100.0	1027	15	US-10-329-624-5254	Sequence 5254, Ap
14	48	90.6	961	15	US-10-282-122A-43778	Sequence 43778, A
15	48	90.6	978	9	US-09-815-242-5456	Sequence 5456, A
16	48	90.6	1001	9	US-09-815-242-12686	Sequence 12686, A
17	48	90.6	1038	15	US-10-282-122A-43827	Sequence 43827, A
18	45	84.9	767	9	US-09-815-242-5899	Sequence 5899, A
19	45	84.9	767	9	US-09-815-242-13140	Sequence 13140, A
20	41	77.4	10	18	US-10-731-238-89	Sequence 89, Appl
21	41	77.4	52	14	US-10-029-386-30908	Sequence 30908, A
22	41	77.4	225	14	US-10-309-379-3	Sequence 3, Appl1
23	41	77.4	429	14	US-10-309-379-1	Sequence 1, Appl1
24	41	77.4	875	15	US-10-363-616-397	Sequence 397, App
25	40	75.5	176	16	US-10-437-963-201469	Sequence 167370, A
26	39	73.6	219	16	US-10-437-963-167370	Sequence 6938, Ap
27	38	71.7	256	17	US-10-732-923-8938	Sequence 67021, A
28	38	71.7	334	15	US-10-282-122A-67021	Sequence 7519, Ap
29	38	71.7	1171	14	US-10-032-585-7519	Sequence 7128, Ap
30	37	69.8	243	16	US-10-739-930-7128	Sequence 23, Appl
31	37	69.8	310	16	US-10-471-115-23	Sequence 2007, Ap
32	37	69.8	535	13	US-10-087-192-2007	Sequence 20, Appl
33	37	69.8	561	16	US-10-471-115-20	Sequence 2496, Ap
34	37	69.8	612	15	US-10-094-749-2496	Sequence 2010, Ap
35	37	69.8	617	13	US-10-087-192-2010	Sequence 1524, Ap
36	37	69.8	939	15	US-10-292-798-1524	Sequence 1868, Ap
37	37	69.8	1068	14	US-10-017-161-1868	Sequence 516, App
38	36	67.9	430	10	US-09-882-227-516	Sequence 8285, Ap
39	36	67.9	437	15	US-10-335-977-8285	Sequence 8286, Ap
40	36	67.9	440	15	US-10-335-977-8286	Sequence 74024, A
41	36	67.9	448	15	US-10-282-122A-74024	Sequence 2632, Ap
42	36	67.9	448	17	US-10-472-928-2632	Sequence 6415, Ap
43	36	67.9	615	18	US-10-724-97A-6415	Sequence 1221, Ap
44	36	67.9	939	20	US-11-097-143-1221	Sequence 343179, A
45	36	67.9	1053	16	US-10-425-115-343179	

ALIGNMENTS

RESULT 1
US-10-731-238-88
; Sequence 88, Application US/10731238
; Publication No. US20050123552A1
; GENERAL INFORMATION:
; APPLICANT: Hook, Magnus
; Patli, Joseph M.
; House-Pompeo, Karen L.
; Speziale, Pietro
; John, Danny
; McGavin, Martin J.
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
; AND METHODS OF USE
; NUMBER OF SEQUENCES: 105
; CORRESPONDENCE ADDRESSES:
; ADDRESSER: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: TX
; COUNTRY: USA
; ZIP: 77210-4433
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/731,238
; FILING DATE: 10-Dec-2003
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/010,317
; FILING DATE: 21-Jan-1998
; APPLICATION NUMBER: US 60/036,139

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: FILING DATE: 21-JAN-1997
: ATTORNEY/AGENT INFORMATION:
:   NAME: Hibler, David W.
:   REGISTRATION NUMBER: 41,071
:   REFERENCE/DOCKET NUMBER: TANK:189
: TELECOMMUNICATION INFORMATION:
:   TELEPHONE: 512-418-3000
:   TELEFAX: 512-474-7577
: INFORMATION FOR SEQ ID NO: 88:
:   SEQUENCE CHARACTERISTICS:
:     LENGTH: 10 amino acids
:     TYPE: amino acid
:     STRANDEDNESS: <Unknown>
:     TOPOLOGY: linear
: SEQUENCE DESCRIPTION: SEQ ID NO: 88:
US-10-731-238-88

Query Match      100.0%; Score 53; DB 18; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0073;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 FNNKHTETIEE 10
DB      1 FNNKHTETIEE 10

RESULT 2
US-11-066-697-1134
: Sequence 1134, Application US/11066697
: Publication No. US20050187159A1
: GENERAL INFORMATION:
:   APPLICANT: Bridon, Dominique P.
:   APPLICANT: Ezrin, Alan M.
:   APPLICANT: Milner, Peter G.
:   APPLICANT: Holmes, Darren L.
:   APPLICANT: Thibaudau, Karen
: TITLE OF INVENTION: PROTECTION OF ENDOGENOUS THERAPEUTIC PEPTIDES FROM
: TITLE OF INVENTION: PEPTIDASE ACTIVITY THROUGH CONJUGATION TO BLOOD
: FILE REFERENCE: 500862002301
: CURRENT APPLICATION NUMBER: US/11/066,697
: CURRENT FILING DATE: 2005-02-25
: PRIOR APPLICATION NUMBER: 09/657,276
: PRIOR FILING DATE: 2000-09-07
: PRIOR APPLICATION NUMBER: 60/153,406
: PRIOR FILING DATE: 1999-09-10
: PRIOR APPLICATION NUMBER: 60/159,783
: PRIOR FILING DATE: 1999-10-15
: NUMBER OF SEQ ID NOS: 1617
: SOFTWARE: PatentIn Ver. 2.1
: SEQ ID NO 1134
: LENGTH: 37
: TYPE: PRT
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: Description of Artificial Sequence: Synthetic
: OTHER INFORMATION: Peptide
US-11-066-697-1134

Query Match      100.0%; Score 53; DB 20; Length 37;
Best Local Similarity 100.0%; Pred. No. 0.029;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 FNNKHTETIEE 10
DB      1 FNNKHTETIEE 10

RESULT 3
US-09-813-820-8
: Sequence 8, Application US/09813820
: Patent No. US20020102262A1
: GENERAL INFORMATION:
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: APPLICANT: Hook, Magnus
:   Patti, Joseph M.
:   House-Pompeo, Karen
:   Sthanam, Narayana
:   Symercky, Jindrich
: TITLE OF INVENTION: COLLAGEN BINDING PROTEIN COMPOSITIONS
:   AND METHODS OF USE
: NUMBER OF SEQUENCES: 8
: CORRESPONDENCE ADDRESS:
:   ADDRESSEE: Arnold, White & Durkee
:   STREET: P.O. Box 4433
:   CITY: Houston
:   STATE: Texas
:   COUNTRY: U.S.
: ZIP: 77210
: COMPUTER READABLE FORM:
:   MEDIUM TYPE: Floppy disk
:   COMPUTER: IBM PC compatible
:   OPERATING SYSTEM: PC-DOS/MS-DOS
:   SOFTWARE: PatentIn Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
:   APPLICATION NUMBER: US/09/813,820
:   FILING DATE: 22-Mar-2001
: CLASSIFICATION: <Unknown>
: PRIOR APPLICATION DATA:
:   APPLICATION NUMBER: 08/856,253
:   FILING DATE: <Unknown>
: ATTORNEY/AGENT INFORMATION:
:   NAME: Kitchell, Barbara S.
:   REGISTRATION NUMBER: 33,928
:   REFERENCE/DOCKET NUMBER: TANK:193
: TELECOMMUNICATION INFORMATION:
:   TELEPHONE: (512) 418-3000
:   TELEFAX: (512) 474-7577
: INFORMATION FOR SEQ ID NO: 8:
:   SEQUENCE CHARACTERISTICS:
:     LENGTH: 139 amino acids
:     TYPE: amino acid
:     STRANDEDNESS: <Unknown>
:     TOPOLOGY: linear
: SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-09-813-820-8

Query Match      100.0%; Score 53; DB 9; Length 139;
Best Local Similarity 100.0%; Pred. No. 0.11;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 FNNKHTETIEE 10
DB      92 FNNKHTETIEE 101

RESULT 4
US-08-901-062-1
: Sequence 1, Application US/08901062
: Publication No. US20020025324A1
: GENERAL INFORMATION:
:   APPLICANT: SEALS, JONATHAN R.
:   TITLE OF INVENTION: RECOMBINANT BIVALENT BACTERIAL VACCINE
:   TITLE OF INVENTION: FOR THE PREVENTION OF MASTITIS
: NUMBER OF SEQUENCES: 2
: CORRESPONDENCE ADDRESS:
:   ADDRESSEE: HALE AND DORR LLP
:   STREET: 60 State Street
:   CITY: Boston
:   STATE: MA
:   COUNTRY: United States Of America
: ZIP: 02109
: COMPUTER READABLE FORM:
:   MEDIUM TYPE: Floppy disk
:   COMPUTER: IBM PC compatible
:   OPERATING SYSTEM: PC-DOS/MS-DOS
:   SOFTWARE: PatentIn Release #1.0, Version #1.30
```

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/901.062
FILING DATE: 25-JUL-1997
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Baker, Hollie L.
REGISTRATION NUMBER: 31,321
REFERENCE/DOCKET NUMBER: 106941.153
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 526-6000
TELEFAX: (617) 526-5000
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 388 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-901-062-1

Query Match 100.0%; Score 53; DB 8; Length 388;
Best Local Similarity 100.0%; Pred. No. 0.34; Indels 0; Gaps 0;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 1 FNNKTEIIIEE 10
|||||||
Db 341 FNNKTEIIIEE 350

RESULT 5
US-08-781-986A-5251
Sequence 5251, Application US/08781986A
Publication No. US20030054436A1
GENERAL INFORMATION:
APPLICANT: Charles Kunesh
TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
NUMBER OF SEQUENCES: 5255
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COUNTRY: USA
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/781,986A
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Bengson, Bob
REGISTRATION NUMBER: 30,446
REFERENCE/DOCKET NUMBER: PB248PP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 5251:
SEQUENCE CHARACTERISTICS:
LENGTH: 559 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-781-986A-5251

Query Match 100.0%; Score 53; DB 8; Length 559;
Best Local Similarity 100.0%; Pred. No. 0.49; Indels 0; Gaps 0;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 1 FNNKTEIIIEE 10
|||||||
Db 377 FNNKTEIIIEE 386

RESULT 6
US-10-329-624-5251
Sequence 5251, Application US/10329624
Publication No. US20040043037A1
GENERAL INFORMATION:
APPLICANT: Charles Kunesh
Gil H. Choi
Patrick S. Dillon
Craig A. Rosen
Steven C. Barash
Michael R. Fannon
TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
NUMBER OF SEQUENCES: 5256
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COUNTRY: USA
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/329,624
FILING DATE: 27-Dec-2002
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/956,171
FILING DATE: October 20, 1997
APPLICATION NUMBER: 60/009,861
FILING DATE: January 5, 1996
APPLICATION NUMBER: 08/781,986
FILING DATE: January 3, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Mark J. Hyman
REGISTRATION NUMBER: 46,789
REFERENCE/DOCKET NUMBER: PB248P1D1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (240) 314-1224
TELEFAX: (301) 309-8439
INFORMATION FOR SEQ ID NO: 5251:
SEQUENCE CHARACTERISTICS:
LENGTH: 559 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 5251:
US-10-329-624-5251

Query Match 100.0%; Score 53; DB 15; Length 559;
Best Local Similarity 100.0%; Pred. No. 0.49; Indels 0; Gaps 0;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 1 FNNKTEIIIEE 10
|||||||
Db 377 FNNKTEIIIEE 386

RESULT 7
US-10-470-048B-424

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; Sequence 424, Application US/10470048B
; Publication No. US20050037444A1
; GENERAL INFORMATION:
; APPLICANT: MEINKE ET AL.
; TITLE OF INVENTION: A METHOD FOR IDENTIFICATION, ISOLATION AND PRODUCTION OF
; FILE REFERENCE: SONN:03505
; CURRENT APPLICATION NUMBER: US/10/470,048B
; CURRENT FILING DATE: 2003-07-25
; NUMBER OF SEQ ID NOS: 603
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 424
; LENGTH: 940
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-10-470-048B-424

Query Match          100.0%; Score 53; DB 17; Length 940;
Best Local Similarity 100.0%; Pred. No. 0.85;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 FNNKTEIIIE 10
Db      758 FNNKTEIIIE 767

RESULT 8
US-10-470-048B-69
; Sequence 69, Application US/10470048B
; Publication No. US20050037444A1
; GENERAL INFORMATION:
; APPLICANT: MEINKE ET AL.
; TITLE OF INVENTION: A METHOD FOR IDENTIFICATION, ISOLATION AND PRODUCTION OF
; FILE REFERENCE: SONN:03505
; CURRENT APPLICATION NUMBER: US/10/470,048B
; CURRENT FILING DATE: 2003-07-25
; NUMBER OF SEQ ID NOS: 603
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 69
; LENGTH: 948
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-10-470-048B-69

Query Match          100.0%; Score 53; DB 17; Length 948;
Best Local Similarity 100.0%; Pred. No. 0.86;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 FNNKTEIIIE 10
Db      766 FNNKTEIIIE 775

RESULT 9
US-09-815-242-5797
; Sequence 5797, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haeselbeck, Robert
; APPLICANT: Ohlsen, Kari L.
; APPLICANT: Zyekind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; FILE REFERENCE: ELITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
```

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; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 1410
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5797
; LENGTH: 1018
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-09-815-242-5797

Query Match          100.0%; Score 53; DB 9; Length 1018;
Best Local Similarity 100.0%; Pred. No. 0.92;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 FNNKTEIIIE 10
Db      822 FNNKTEIIIE 831

RESULT 10
US-09-815-242-12838
; Sequence 12838, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haeselbeck, Robert
; APPLICANT: Ohlsen, Kari L.
; APPLICANT: Zyekind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; FILE REFERENCE: ELITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 1410
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12838
; LENGTH: 1018
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-09-815-242-12838
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QY 1 FNNKTEIIIEE 10
|||||
Db 822 FNNKTEIIIEE 831

RESULT 11
US-10-470-048B-68
; Sequence 68, Application US/10470048B
; Publication No. US20050037444A1
; GENERAL INFORMATION:
; APPLICANT: MEINKE ET AL.
; TITLE OF INVENTION: A METHOD FOR IDENTIFICATION, ISOLATION AND PRODUCTION OF
; FILE REFERENCE: SOMN:035US
; CURRENT APPLICATION NUMBER: US/10/470,048B
; CURRENT FILING DATE: 2003-07-25
; NUMBER OF SEQ ID NOS: 603
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 68
; LENGTH: 1018
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-10-470-048B-68

Query Match 100.0%; Score 53; DB 17; Length 1018;
Best Local Similarity 100.0%; Pred. No. 0.92;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FNNKTEIIIEE 10
|||||
Db 822 FNNKTEIIIEE 831

RESULT 12
US-08-781-986A-5254
; Sequence 5254, Application US/08781986A
; Publication No. US20030054436A1
; GENERAL INFORMATION:
; APPLICANT: Charles Kunsch
; TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
; NUMBER OF SEQUENCES: 5255
; CORRESPONDENCE ADDRESS:
; ADDRESS: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4mb storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/781,986A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION NUMBER:
; ATTORNEY/AGENT INFORMATION:
; NAME: Benson, Bob
; REGISTRATION NUMBER: 30,446
; REFERENCE/DOCKET NUMBER: PB248PP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 5254:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1027 amino acids
; TYPE: amino acid
; STRANDEDNESS: single

; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-781-986A-5254

Query Match 100.0%; Score 53; DB 8; Length 1027;
Best Local Similarity 100.0%; Pred. No. 0.93;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FNNKTEIIIEE 10
|||||
Db 831 FNNKTEIIIEE 840

RESULT 13
US-10-329-624-5254
; Sequence 5254, Application US/10329624
; Publication No. US20040043037A1
; GENERAL INFORMATION:
; APPLICANT: Charles Kunsch
; GIL H. Choi
; Patrick S. Dillon
; Craig A. Rosen
; Steven C. Barash
; Michael R. Fannon
; TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
; NUMBER OF SEQUENCES: 5256
; CORRESPONDENCE ADDRESS:
; ADDRESS: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4mb storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/329,624
; FILING DATE: 27-Dec-2002
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/956,171
; FILING DATE: October 20, 1997
; APPLICATION NUMBER: 60/009,861
; FILING DATE: January 5, 1996
; APPLICATION NUMBER: 08/781,986
; FILING DATE: January 3, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Mark J. Hyman
; REGISTRATION NUMBER: 46,789
; REFERENCE/DOCKET NUMBER: PB248P1D1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (240) 314-1224
; TELEFAX: (301) 309-8439
; INFORMATION FOR SEQ ID NO: 5254:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1027 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 5254:

US-10-329-624-5254

Query Match 100.0%; Score 53; DB 15; Length 1027;
Best Local Similarity 100.0%; Pred. No. 0.93;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FNNKTEIIIEE 10
|||||
Db 831 FNNKTEIIIEE 840


```

RESULT 14
US-10-282-122A-43778
; Sequence 43778, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyekind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282.122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 43778
; LENGTH: 961
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-10-282-122A-43778

Query Match          90.6%; Score 48; DB 15; Length 961;
Best Local Similarity 90.0%; Pred. No. 6.9;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 FNNKTEIIIEE 10
      |||||
Db      769 FNNKNEIIIEE 778

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; TITLE OF INVENTION: Identification of Essential Genes in
; PROKARYOTES
; FILE REFERENCE: ELITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5456
; LENGTH: 978
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-09-815-242-5456

Query Match          90.6%; Score 48; DB 9; Length 978;
Best Local Similarity 90.0%; Pred. No. 7;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 FNNKTEIIIEE 10
      |||||
Db      800 FNNKNEIIIEE 809

Search completed: October 22, 2005, 12:56:23
Job time : 57.1494 secs

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GenCore version 5.1.6
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OM protein - protein search, using SW model

Run on: October 22, 2005, 08:04:46 ; Search time 11.6092 Seconds
(without alignments)
82.880 Million cell updates/sec

Title: US-10-731-238-88
Perfect score: 53
Sequence: 1 FNKHTETIEE 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	53	100.0	940	2	S19702 fibronectin-binding protein - Staphylococcus aureus
2	53	100.0	1018	2	A32192 fibronectin-binding protein - Staphylococcus aureus
3	48	90.6	961	2	G90053 hypothetical prote
4	48	90.6	1038	2	H90053 hypothetical prote
5	41	77.4	791	2	T12455 isopropylmalate dehydrogenase
6	38	71.7	448	2	G97019 von Willebrand factor
7	36	67.9	55	2	T03337 gene 630 protein -
8	36	67.9	414	2	P80323 hypothetical prote
9	36	67.9	424	2	T24935 conserved hypotetic
10	36	67.9	437	1	E64553 hypothetical prote
11	36	67.9	437	2	E71953 NADP-specific glut
12	36	67.9	448	2	H95151 glutamate dehydrog
13	36	67.9	448	2	D98019 clathrin-associated
14	36	67.9	700	2	S57020 myosin heavy chain
15	36	67.9	1972	1	A41604 hypothetical prote
16	35	66.0	176	2	T32618 hypothetical prote
17	35	66.0	505	2	T19770 methylmalonyl-CoA
18	35	66.0	653	2	E84206 ribonucleoside-tri
19	35	66.0	712	2	AC0419 ribonucleoside-tri
20	35	66.0	788	2	G81294 hypothetical prote
21	35	66.0	824	2	AB2829 DNA helicase II
22	35	66.0	827	2	H97606 probable DNA helic
23	35	66.0	1588	2	T38660 probable transcrip
24	35	66.0	3144	2	S64791 VP33 protein - ye
25	34	64.2	70	2	G97804 hypothetical prote
26	34	64.2	275	2	B95215 exodeoxyribonuclea
27	34	64.2	275	2	A32301 exodeoxyribonuclea
28	34	64.2	275	2	B98079 exodeoxyribonuclea
29	34	64.2	288	2	A99305 hypothetical prote

30	34	64.2	329	2	T28412	ORF MSV251 hypothe
31	34	64.2	335	2	D95119	iron-compound ABC
32	34	64.2	335	2	H97988	hypothetical prote
33	34	64.2	360	2	F96902	aspartate-semialde
34	34	64.2	392	2	T40624	probable class V p
35	34	64.2	416	1	ITSH	alpha-1-antitrypsin
36	34	64.2	442	2	C81370	probable thiophene
37	34	64.2	524	2	G90109	T-complex protein
38	34	64.2	574	2	C83725	endo-beta-1,4-gluc
39	34	64.2	579	1	A55369	lysine 3-monooxy
40	34	64.2	1086	1	B46335	HIV-1 retroprotein
41	34	64.2	1233	1	G71612	novel serine/threo
42	34	64.2	1670	2	T06754	DNA-directed RNA p
43	33	62.3	122	2	AF2228	hypothetical prote
44	33	62.3	127	2	AB0684	hypothetical prote
45	33	62.3	142	2	E84934	50S ribosomal prot

ALIGNMENTS

RESULT 1

S19702 fibronectin-binding protein B - Staphylococcus aureus
C:Species: Staphylococcus aureus
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
C:Accession: S19702
R:Joensson, K.; Signaes, C.; Mueller, H.P.; Lindberg, M.
Eur. J. Biochem. 202, 1041-1048, 1991
A:Title: Two different genes encode fibronectin binding proteins in Staphylococcus aureus
A:Reference number: S19702; MUID:92111475; PMID:1837266
A:Accession: S19702
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-940 <JOB>
A:Cross-references: UNIPROT:Q53682; EMBL:X62992; NID:949040; PIDN:CAA44726.1; PID:G5815
C:Keywords: fibronectin binding

Query Match 100.0%; Score 53; DB 2; Length 940;
Best Local Similarity 100.0%; Pred. No. 0.064;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FNKHTETIEE 10
Db 758 FNKHTETIEE 767

RESULT 2

A32192 fibronectin-binding protein - Staphylococcus aureus
C:Species: Staphylococcus aureus
C:Date: 31-Jul-1989 #sequence_revision 31-Jul-1989 #text_change 16-Feb-1997
C:Accession: A32192
R:Signaes, C.; Raucel, G.; Joensson, K.; Lindgren, P.E.; Anantharamiah, G.M.; Hoecek, Proc. Natl. Acad. Sci. U.S.A. 86, 699-703, 1989
A:Title: Nucleotide sequence of the gene for a fibronectin-binding protein from Staphylococcus aureus
A:Reference number: A32192; MUID:89098998; PMID:2521391
A:Accession: A32192
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1018 <SIG>
A:Cross-references: GB:U04151
C:Keywords: fibronectin binding

Query Match 100.0%; Score 53; DB 2; Length 1018;
Best Local Similarity 100.0%; Pred. No. 0.07;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FNKHTETIEE 10
Db 822 FNKHTETIEE 831

```
RESULT 3
G90053
hypothetical protein fnbB [imported] - Staphylococcus aureus (strain N315)
C/Species: Staphylococcus aureus
C/Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C/Accession: G90053
R/Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguc
ma, A.; Mitutani, H.; Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.;
C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
A/Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.
A/Reference number: A89758; MUID:21311952; PMID:11418146
A/Accession: G90053
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-961 <KUR>
A/Cross-references: UNIPROT:Q99RD3; GB:BA000018; PID:g13702452; PIDN:BA043593.1; GSPDB:
A/Experimental source: strain N315
C/Genetics:
A/Gene: fnbB

Query Match          90.6%; Score 48; DB 2; Length 961;
Best Local Similarity 90.0%; Pred. No. 0.59; 1; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 FNKATEIIEE 10
    |||||
Db 769 FNKKNIEIEE 778

RESULT 4
H90053
hypothetical protein fnb [imported] - Staphylococcus aureus (strain N315)
C/Species: Staphylococcus aureus
C/Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C/Accession: H90053
R/Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguc
ma, A.; Mitutani, H.; Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.;
C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
A/Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.
A/Reference number: A89758; MUID:21311952; PMID:11418146
A/Accession: H90053
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-1038 <KUR>
A/Cross-references: UNIPROT:Q99RD2; GB:BA000018; PID:g13702453; PIDN:BA043594.1; GSPDB:
A/Experimental source: strain N315
C/Genetics:
A/Gene: fnb

Query Match          90.6%; Score 48; DB 2; Length 1038;
Best Local Similarity 90.0%; Pred. No. 0.65; 1; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 FNKATEIIEE 10
    |||||
Db 818 FNKKNIEIEE 827

RESULT 5
T12455
hypothetical protein DKFZP564H2023.1 - human (fragments)
C/Species: Homo sapiens (man)
C/Date: 23-Jul-1999 #sequence_revision 23-Jul-1999 #text_change 09-Jul-2004
C/Accession: T12455
R/Wambut, R.; Heubner, D.; Mewes, H.W.; Gaasenhuber, J.; Wiemann, S.
submitted to the Protein Sequence Database, June 1999
A/Reference number: Z17524
A/Accession: T12455
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-562;563-791 <WAM>
```

```
A/Cross-references: UNIPROT:Q9Y4S4; EMBL:AL096723
A/Experimental source: fetal brain; clone DKFZP564H2023
A/Note: the cDNA sequence contains a -1 frameshift near codon 562
C/Genetics:
A/Note: DKFZP564H2023.1

Query Match          77.4%; Score 41; DB 2; Length 791;
Best Local Similarity 80.0%; Pred. No. 10;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 FNKATEIIEE 10
    |||||
Db 648 FNKAEKIEE 657

RESULT 6
G97019
isopropylmalate synthase [imported] - Clostridium acetobutylicum
C/Species: Clostridium acetobutylicum
C/Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 09-Jul-2004
C/Accession: G97019
R/Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee,
J.; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.
J. Bacteriol. 183, 4823-4838, 2001
A/Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Cl.
A/Reference number: A96900; MUID:21359325; PMID:21359325
A/Accession: G97019
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1448 <KUR>
A/Cross-references: UNIPROT:Q97KX9; GB:AE001437; PIDN:AAK78946.1; PID:g15023876; GSPDB:
A/Experimental source: Clostridium acetobutylicum ATCC824
C/Genetics:
A/Gene: CAC0970

Query Match          71.7%; Score 38; DB 2; Length 448;
Best Local Similarity 60.0%; Pred. No. 21;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 FNKATEIIEE 10
    |||||
Db 155 YNKYEIVIEE 164

RESULT 7
T03337
gene e30 protein - Lactococcus phage b1170
C/Species: Lactococcus phage b1170
C/Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 09-Jul-2004
C/Accession: T03337
R/Cruetz-Le Coq, A.M.; Cesselin, B.; Commissaire, J.; Anba, J.; Kyriakidis, S.; Chopin,
submitted to the EMBL Data Library, June 1997
A/Description: Sequence and organization of the lactococcal isometric b1170 phage geno
A/Reference number: Z14903
A/Accession: T03337
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-55 <CRU>
A/Cross-references: UNIPROT:O80130; EMBL:AF009630; NID:g3282260; PIDN:AAC27209.1; PID:9
C/Genetics:
A/Gene: e30

Query Match          67.9%; Score 36; DB 2; Length 55;
Best Local Similarity 100.0%; Pred. No. 5;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 KATEIIEE 9
    |||||
Db 46 KATEIIEE 52

RESULT 8
PS0323
```

von Willebrand factor - pig (fragment)
 A:Species: Sus scrofa domestica (domestic pig)
 C:Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-Jul-2004
 C:Accession: P50323
 R:Bahnak, B.R.; Lavergne, J.M.; Perrelet, V.; Kerbiriou-Nabias, D.; Meyer, D.
 Biochem. Biophys. Res. Commun. 182, 561-568, 1992
 A:Title: Comparison of the primary structure of the functional domains of human and porc
 A:Reference number: P50323; MUID:92134270; PMID:1370885
 A:Accession: P50323
 A:Molecule type: mRNA
 A:Residues: 1-414 <BAH>
 A:Cross-references: UNIPROT:Q28904
 A>Note: The authors translated the codon CAG for residue 120 as Glu, TAC for residue 344
 C:Comment: This protein is a complex multimeric glycoprotein which has a critical functi
 C:Superfamily: von Willebrand factor; von Willebrand factor type A repeat homology; von
 C:Keywords: collagen binding; heparin binding
 F:36-204/Domain: von Willebrand factor type A repeat homology <VWA1>
 F:36-197/Region: heparin binding #status predicted
 F:63-77,93-107,153-167/Region: botrocetin binding #status predicted
 F:66-142/Region: collagen binding #status predicted
 F:93-108/Region: sulfatide binding #status predicted
 F:256-414/Domain: von Willebrand factor type A repeat homology <VWA2>
 F:33-219/Disulfide bonds: #status predicted

Query Match 67.9%; Score 36; DB 2; Length 414;
 Best Local Similarity 60.0%; Pred. No. 46;
 Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 FNKHTETIEE 10
 DB 274 FNKSTFVEE 283

RESULT 9
 T24935
 hypothetical protein T15D6.4 - Caenorhabditis elegans
 C:Species: Caenorhabditis elegans
 C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
 C:Accession: T24935
 R:Dobson, R.
 submitted to the EMBL Data Library, November 1996
 A:Reference number: Z19956
 A:Accession: T24935
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-424 <WLU>
 A:Cross-references: UNIPROT:O02320; EMBL:Z83125; PIDN:CAB05626.1; GSPDB:GN00019; CESP:TL
 A:Experimental source: clone T15D6
 C:Genetics:
 A:Gene: CESP:T15D6.4
 A:Map position: 1
 A:Introns: 27/1; 74/1; 195/2; 219/2; 258/2; 289/3; 372/3

Query Match 67.9%; Score 36; DB 2; Length 424;
 Best Local Similarity 60.0%; Pred. No. 47;
 Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 FNKHTETIEE 10
 DB 124 FOKNTLEEE 133

RESULT 10
 B64553
 conserved hypothetical ATP-binding protein HPO269 - Helicobacter pylori (strain 26695)
 C:Species: Helicobacter pylori
 C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
 C:Accession: B64553
 R:Tomb, J.F.; White, O.; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.D.
 Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khalak, H.G.; Glodek, A.; McKenna
 son, J.D.; Kelley, J.M.; Cotton, M.D.; Weisman, J.M.; Fujii, C.; Bowman, C.; Matthey, L.
 Nature 388, 539-547, 1997
 A:Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Frazer, C.

A:Title: The complete genome sequence of the gastric pathogen Helicobacter pylori.
 A:Reference number: A64520; MUID:97394467; PMID:9252185
 A:Accession: B64553
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-437 <TOM>
 A:Cross-references: UNIPROT:P56131; GB:AE000546; GB:AE000511; NID:92313363; PIDN:AA073
 C:Genetics:
 A:Start codon: TTG
 C:Superfamily: conserved hypothetical protein b0835

Query Match 67.9%; Score 36; DB 1; Length 437;
 Best Local Similarity 66.7%; Pred. No. 49;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 NKHTETIEE 10
 DB 359 NRKHTLEEE 367

RESULT 11
 E71953
 hypothetical protein jhp0254 - Helicobacter pylori (strain J99)
 C:Species: Helicobacter pylori
 A:Variety: strain J99
 C:Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 09-Jul-2004
 C:Accession: E71953
 R:Alm, R.A.; Ling, L.S.L.; Moir, D.T.; King, B.L.; Brown, E.D.; Doig, P.C.; Smith, D.R
 Ives, C.; Gibson, R.; Merberg, D.; Mills, S.D.; Jiang, Q.; Taylor, D.E.; Vovis, G.F.,
 Nature 397, 176-180, 1999
 A:Title: Genomic sequence comparison of two unrelated isolates of the human gastric pat
 A:Reference number: A71800; MUID:99120557; PMID:9923682
 A:Accession: E71953
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-437 <ARM>
 A:Cross-references: UNIPROT:Q9ZNG6; GB:AE001463; GB:AE001439; NID:94154775; PIDN:AA05C
 A:Experimental source: strain J99
 C:Genetics:
 A:Gene: jhp0254
 C:Superfamily: conserved hypothetical protein b0835

Query Match 67.9%; Score 36; DB 2; Length 437;
 Best Local Similarity 66.7%; Pred. No. 49;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 NKHTETIEE 10
 DB 359 NRKHTLEEE 367

RESULT 12
 H95151
 NADP-specific glutamate dehydrogenase [imported] - Streptococcus pneumoniae (strain T1
 C:Species: Streptococcus pneumoniae
 C:Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 09-Jul-2004
 C:Accession: H95151
 R:Retcelin, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Hei
 on, J.D.; Unayam, L.A.; White, O.; Salberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapfel,
 neon, T.; Hickey, E.K.; Holt, I.E.
 Science 293, 498-506, 2001
 A:Authors: Loftus, B.O.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrisio
 A:Title: Complete Genome Sequence of a virulent isolate of Streptococcus pneumoniae.
 A:Reference number: A95000; MUID:21357209; PMID:11463916
 A:Accession: H95151
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-448 <KUM>
 A:Cross-references: UNIPROT:Q97GB4; GB:AE005672; PIDN:AAK75409.1; PID:944972791; GSPDB
 A:Experimental source: strain T1GR4
 C:Genetics:
 A:Gene: SPI306
 C:Superfamily: glutamate dehydrogenase (NAD(P)+)

Query Match 67.9%; Score 36; DB 2; Length 448;
 Best Local Similarity 70.0%; Pred. No. 50;
 Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FNNKTEIIIEE 10
 |||
 Db 40 FEKKPEYIEE 49

RESULT 13

D98019
 glutamate dehydrogenase (NADP) (EC 1.4.1.4) [imported] - Streptococcus pneumoniae (strain
 C/Species: Streptococcus pneumoniae
 C/Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 09-Jul-2004
 C/Accession: D98019
 R/Hoskins, J.A.; Alborn Jr., W.; Arnold, J.; Blaszcak, L.; Burgett, S.; Dehoff, B.S.; F
 e, R.; LeBlanc, D.J.; Lee, L.N.; Lefkowitz, E.J.; Lu, J.; Matsushima, P.; McAnren, S.; M
 y, P.; Sun, P.M.; Winkler, M.E.
 J. Bacteriol. 183, 5709-5717, 2001
 A/Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, S.R.;
 A/Title: Genome of the Bacterium Streptococcus pneumoniae Strain R6.
 A/Reference number: A97872; MUID:21429245; PMID:11544234
 A/Accession: D98019
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-448 <KUR>
 A/Cross-references: UNIPROT:Q8DBG0; GB:AE007317; PIDN:AAK9984.1; PID:G15458813; GSPDB:C
 C/Genetics:
 A/Gene: gdhA
 C/Superfamily: glutamate dehydrogenase (NAD(P)+)
 C/Keywords: oxidoreductase

Query Match 67.9%; Score 36; DB 2; Length 448;
 Best Local Similarity 70.0%; Pred. No. 50;
 Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FNNKTEIIIEE 10
 |||
 Db 40 FEKKPEYIEE 49

RESULT 14

S57020
 clathrin-associated protein complex beta chain homolog YAP80 - Yeast (Saccharomyces cere
 N/Alternate names: beta-adaptin; protein J1422; protein YXR005W
 C/Species: Saccharomyces cerevisiae
 C/Date: 08-Jul-1995 #sequence_revision 08-Sep-1995 #text_change 09-Jul-2004
 C/Accession: S57020; S55193; S12934
 R/de Haan, M.; Grivell, L.A.; Smits, P.H.M.
 Submitted to the Protein Sequence Database, September 1995
 A/Reference number: S56771

A/Accession: S57020
 A/Molecule type: DNA
 A/Residues: 1-700 <ZAG>
 A/Cross-references: UNIPROT:P27351; EMBL:Z49505; NID:G1015627; PIDN:CAA89527.1; PID:G101
 R/de Haan, M.; Smits, P.H.M.; Grivell, L.A.
 Submitted to the EMBL Data Library, May 1995
 A/Reference number: S55183

A/Accession: S55193
 A/Molecule type: DNA
 A/Residues: 'NAK', 53-700 <DEH>
 A/Cross-references: EMBL:X87611; NID:G854567; PIDN:CAA60927.1; PID:G854578
 R/Kirchhausen, T.

Mol. Cell. Biol. 10, 6089-6090, 1990
 A/Title: Identification of a putative yeast homolog of the mammalian beta chains of the
 A/Reference number: S12934; MUID:91042546; PMID:2122239
 A/Accession: S12934
 A/Status: nucleic acid sequence not shown

A/Molecule type: DNA
 A/Residues: 1-54, 'L', 56-483, 'N', 485-503, 'N', 505-520, 'T', 522-628, 'I', 630-700 <KIR>
 A/Cross-references: EMBL:M64998; NID:G173201; PIDN:AAA55226.1; PID:G173202
 C/Genetics:

A/Gene: SGD:APL1; YAP80
 A/Cross-references: MIPS:YXR005W; SGD:S0003765
 A/Map position: 10R

Query Match 67.9%; Score 36; DB 2; Length 700;
 Best Local Similarity 62.5%; Pred. No. 82;
 Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 3 KNTETIEE 10
 |||
 Db 443 KNTETVQE 450

RESULT 15

A41604
 myosin heavy chain, smooth muscle, long splice form - rabbit
 N/Contains: myosin ATPase (EC 3.6.4.1)
 C/Species: Oryctolagus cuniculus (domestic rabbit)
 C/Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 19-Apr-2002
 C/Accession: A41604; A33501
 R/Babji, P.; Kelly, C.; Periasamy, M.
 Proc. Natl. Acad. Sci. U.S.A. 88, 10676-10680, 1991
 A/Title: Characterization of a mammalian smooth muscle myosin heavy-chain gene: complet
 A/Reference number: A41604; MUID:92073350; PMID:1961735

A/Accession: A41604
 A/Molecule type: mRNA
 A/Residues: 1-1972 <BAB>
 A/Cross-references: GB:M77812
 R/Nagai, R.; Kuro-o, M.; Babji, P.; Periasamy, M.
 J. Biol. Chem. 264, 9734-9737, 1989
 A/Title: Identification of two types of smooth muscle myosin heavy chain isoforms by cD
 A/Reference number: A33501; MUID:8925535; PMID:2722872

A/Accession: A33501
 A/Molecule type: mRNA
 A/Residues: 1455-1972 <NAG>
 A/Cross-references: GB:J04833; NID:G165519; PIDN:AAA11407.1; PID:G165520
 A/Experimental source: smooth muscle
 A/Note: examination by Southern blotting for the regions of difference between this iso
 active splicing
 C/Superfamily: myosin heavy chain; myosin motor domain homology
 C/Keywords: actin binding; alternative splicing; ATP; coiled coil; hydrolyase; methylase
 F/88-771/Domain: myosin motor domain homology <MMOT>
 F/178-185/Region: nucleotide-binding motif A (P-loop)
 F/559-572/Region: actin binding #status predicted
 F/633-647/Region: actin binding #status predicted
 F/844-1938/Domain: coiled coil #status predicted <COI>
 F/844-1284/Region: S2
 F/1285-1972/Region: light meromyosin
 F/1339-1972/Domain: carboxyl-terminal <CBT>
 F/159/Modified site: N6,N6,N6-trimethyllysine (Lys) #status predicted
 F/184/Binding site: ATP (Lys) #status predicted
 F/701,711/Active site: Cys #status predicted

Query Match 67.9%; Score 36; DB 1; Length 1972;
 Best Local Similarity 62.5%; Pred. No. 2.6e+02;
 Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 3 KNTETIEE 10
 |||
 Db 1200 KNTETVQE 1207

Search completed: October 22, 2005, 09:55:38
 Job time: 12.6092 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 22, 2005, 08:01:06 ; Search time 56.2069 Seconds
(without alignments)
91.106 Million cell updates/sec

Title: US-10-731-238-88
Perfect score: 53
Sequence: 1 FNKHTETIEE 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues
Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_03:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	53	100.0	152 2 Q9AEP9	Q9AEP9 staphylococ
2	53	100.0	940 2 Q53682	Q53682 staphylococ
3	53	100.0	943 2 Q8NUU8	Q8NUU8 staphylococ
4	53	100.0	957 2 Q6G6H4	Q6G6H4 staphylococ
5	53	100.0	1015 2 Q8NUU7	Q8NUU7 staphylococ
6	53	100.0	1015 2 Q6G6H3	Q6G6H3 staphylococ
7	53	100.0	1018 1 FNBA_STPAU	Q99RD3 staphylococ
8	48	90.6	961 2 Q7A3J8	Q7A3J8 staphylococ
9	48	90.6	961 2 Q6GDU5	Q6GDU5 staphylococ
10	48	90.6	965 2 Q99RD2	Q99RD2 staphylococ
11	48	90.6	1038 2 Q7A3J7	Q7A3J7 staphylococ
12	48	90.6	1038 2 Q7A3J7	Q7A3J7 staphylococ
13	41	77.4	226 2 Q724Y3	Q724Y3 homo sapien
14	41	77.4	290 1 ARS2_CRIGR	Q60436 cricetus
15	41	77.4	422 2 Q8VBE6	Q8VBE6 mus musculu
16	41	77.4	788 2 Q8TDO5	Q8TDO5 homo sapien
17	41	77.4	791 2 Q9Y4S4	Q9Y4S4 homo sapien
18	41	77.4	812 2 Q6NT74	Q6NT74 homo sapien
19	41	77.4	844 2 Q6INH5	Q6INH5 xenopus lae
20	41	77.4	875 1 ARS2_MOUSE	Q99MT6 mus musculu
21	41	77.4	876 1 ARS2_HUMAN	Q9KBP5 homo sapien
22	40	75.5	175 2 Q9O8G9	Q9O8G9 myxoma viru
23	40	75.5	184 2 Q8OSR5	Q8OSR5 undentified
24	40	75.5	563 2 Q894M7	Q894M7 clostridium
25	40	75.5	987 2 Q7PKJ9	Q7PKJ9 anopheles g
26	40	75.5	1762 2 Q94DC2	Q94DC2 oryza sativ
27	39	73.6	289 2 Q9EMF8	Q9EMF8 amesacta moo
28	39	73.6	372 2 Q6SP84	Q6SP84 small rumin
29	39	73.6	372 2 Q6SP86	Q6SP86 small rumin
30	39	73.6	587 2 Q7RJT2	Q7RJT2 plasmodium
31	39	73.6	609 2 Q812K8	Q812K8 plasmodium

32	38	71.7	206	2	Q7XIM4	Q7XIM4 leptocitri
33	38	71.7	316	2	Q6MTI9	Q6MTI9 mycoplasma
34	38	71.7	334	1	PURR_PASMU	Q8G88 pasteurilla
35	38	71.7	377	2	Q8GT57	Q8GT57 cucurbita m
36	38	71.7	448	2	Q97KE9	Q97KE9 clostridium
37	38	71.7	499	2	Q6RIAT	Q6RIAT brachydanio
38	37.5	70.8	211	2	Q6FMD5	Q6FMD5 candida gla
39	37	69.8	246	2	Q87R06	Q87R06 vibrio para
40	37	69.8	612	1	COG8_HUMAN	Q9GMS5 homo sapien
41	37	69.8	640	1	COG8_MOUSE	Q9JIA2 mus musculu
42	37	69.8	640	2	Q8BFW5	Q8BFW5 m mus muscu
43	37	69.8	709	2	Q6FI54	Q6FI54 mesoplasma
44	37	69.8	775	2	P88981	P88981 murid herpe
45	37	69.8	909	2	Q814V7	Q814V7 plasmodium

ALIGNMENTS

```

RESULT 1
Q9AEP9 PRELIMINARY; PRT; 152 AA.
AC Q9AEP9;
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Fibronectin-binding protein (fragment).
GN Name=fnb;
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1280;
RN (1)
RP SEQUENCE FROM N.A.
RX STRAIN=CMRSA-1;
RX MEDLINE=21246681; PubMed=11349044;
RX DOI=10.1128/IAI.69.6.3791-3799.2001;
RA Rice K., Huesca M., Vaz D., McGavin M.J.;
RA "Variance in fibronectin binding and fnb locus polymorphisms in
RT Staphylococcus aureus: identification of antigenic variation in a
RT fibronectin binding protein adhesin of the epidemic CMRSA-1 strain of
RT methicillin-resistant S. aureus.";
RL Infect. Immun. 69:3791-3799 (2001).
DR EMBL, AY029184; AAK31586.1; -.
FT NON_TER
FT NON_TER
SQ SEQUENCE 152 AA; 17193 MW; CFA3913C2B11C025 CRC64;

Query Match 100.0%; Score 53; DB 2; Length 152;
Best Local Similarity 100.0%; Pred. No. 0.07; Mismatches 0; Gaps 0;
Matches 10; Conservative 0; Indels 0;

QY 1 FNKHTETIEE 10
DB 115 FNKHTETIEE 124

RESULT 2
Q53682 PRELIMINARY; PRT; 940 AA.
AC Q53682;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Fibronectin binding protein B.
GN Name=fnbB;
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1280;
RN (1)
RP SEQUENCE FROM N.A.
RX STRAIN=8325-4;
RX MEDLINE=92111475; PubMed=1837266;
RX Jonsson K., Signas C., Muller H.P., Lindberg M.;

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RT "Two different genes encode fibronectin binding proteins in
RT Staphylococcus aureus. The complete nucleotide sequence and
RT characterization of the second gene."
RL Eur. J. Biochem. 202:1041-1048 (1991).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC an amide bond (By similarity).
DR EMBL: X62992; CAA44726.1; -.
DR PIR: S19702; S19702.
DR HSSP: Q53653; IN67.
DR GO: GO:0009986; C:cell surface; IEA.
DR GO: GO:0005618; C:cell wall; IEA.
DR GO: GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO: GO:0016020; C:membrane; IEA.
DR GO: GO:0007155; P:cell adhesion; IEA.
DR InterPro: IPR008966; Adhes_bact.
DR InterPro: IPR004237; Fn_bind.
DR InterPro: IPR005877; Gpos_Ysirk.
DR Pfam: PF02986; Fn_bind; 2.
DR TIGRFAMs: TIGR01167; LPXTG_anchor; 1.
DR TIGRFAMs: TIGR01168; Ysirk_signal; 1.
DR PROSITE: PS50847; GRAM_POS_ANCHORING; 1.
DR Cell wall; Peptidoglycan-anchor.
SQ SEQUENCE 940 AA; 10355 MW; E35FBBCA907AE345 CRC64;

Query Match 100.0%; Score 53; DB 2; Length 940;
Best Local Similarity 100.0%; Pred. No. 0.47;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FNKGTETIEE 10
Db 758 FNKGTETIEE 767

RESULT 3
Q8NTU8 PRELIMINARY; PRT; 943 AA.
ID Q8NTU8;
AC Q8NTU8;
DT 01-OCT-2002 (TReMBLrel. 22, Created)
DT 01-OCT-2002 (TReMBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE FndB protein.
GN Name=fndB; OrderedLocuNames=MM2420;
OS Staphylococcus aureus (strain MM2).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=196620;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MM2;
RX MEDLINE=22040717; PubMed=12044378; DOI=10.1016/S0140-6736(02)08713-5;
RA Baba T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Oguchi A.,
RA Nagai Y., Iwama N., Asano K., Naito T., Kuroda H., Cui L.,
RA Yamamoto K., Hiramatsu K.;
RT "Genome and virulence determinants of high virulence community-
RT acquired MRSA."
RL Lancet 359:1819-1827 (2002).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC an amide bond (By similarity).
DR EMBL: AF004830; BAB96285.1; -.
DR HSSP: Q53653; IN67.
DR GO: GO:0009986; C:cell surface; IEA.
DR GO: GO:0005618; C:cell wall; IEA.
DR GO: GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO: GO:0016020; C:membrane; IEA.
DR GO: GO:0007155; P:cell adhesion; IEA.
DR InterPro: IPR008966; Adhes_bact.
DR InterPro: IPR004237; Fn_bind.
DR InterPro: IPR005877; Gpos_Ysirk.
DR Pfam: PF02986; Fn_bind; 1.
DR Cell wall; Peptidoglycan-anchor.
DR Pfam: PF00746; Gram_pos_anchor; 1.
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DR Pfam: PF04650; Ysirk_signal; 1.
DR TIGRFAMs: TIGR01167; LPXTG_anchor; 1.
DR TIGRFAMs: TIGR01168; Ysirk_signal; 1.
DR PROSITE: PS50847; GRAM_POS_ANCHORING; 1.
DR Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ SEQUENCE 943 AA; 104537 MW; DA0A5F3197E1B6A CRC64;

Query Match 100.0%; Score 53; DB 2; Length 943;
Best Local Similarity 100.0%; Pred. No. 0.47;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FNKGTETIEE 10
Db 765 FNKGTETIEE 774

RESULT 4
Q6G6H4 PRELIMINARY; PRT; 957 AA.
ID Q6G6H4;
AC Q6G6H4;
DT 05-JUL-2004 (TReMBLrel. 27, Created)
DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TReMBLrel. 27, Last annotation update)
DE Fibronectin-binding protein.
GN Name=fndB; OrderedLocuNames=SAS2387;
OS Staphylococcus aureus (strain MSSA476).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=282459;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=15213324; DOI=10.1073/pnas.0402521101;
RA Holden M.T.G., Fell E.J., Lindsey J.A., Peacock S.J., Day N.P.J.,
RA Enright M.C., Foster T.J., Moore C.E., Hurst L., Atkin R., Barron A.,
RA Bason N., Bentley S.D., Chillingworth C., Chillingworth T.,
RA Churcher C., Clark L., Cotton C., Cronin A., Doggett J., Dowd L.,
RA Felwell T., Hance Z., Harris B., Hauser H., Holtroyd S., Jagels K.,
RA James K.D., Lennard N., Line A., Mayes R., Moul S., Mungall K.,
RA Ormond D., Quail M.A., Rabinowitsch E., Rutherford K.M., Sanders M.,
RA Sharp S., Simmonds M., Stevens K., Whitehead S., Barrett B.G.,
RA Spratt B.G., Parkhill J.;
RT "Complete genomes of two clinical Staphylococcus aureus strains:
RT evidence for the rapid evolution of virulence and drug resistance."
RL Proc. Natl. Acad. Sci. U.S.A. 101:9786-9791 (2004).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC an amide bond (By similarity).
DR EMBL: BX571857; CAG44201.1; -.
DR GO: GO:0009986; C:cell surface; IEA.
DR GO: GO:0005618; C:cell wall; IEA.
DR GO: GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO: GO:0016020; C:membrane; IEA.
DR GO: GO:0007155; P:cell adhesion; IEA.
DR InterPro: IPR008966; Adhes_bact.
DR InterPro: IPR004237; Fn_bind.
DR InterPro: IPR005877; Gpos_Ysirk.
DR InterPro: IPR001899; Gram_pos_anchor.
DR Pfam: PF02986; Fn_bind; 1.
DR Pfam: PF00746; Gram_pos_anchor; 1.
DR TIGRFAMs: TIGR01167; LPXTG_anchor; 1.
DR TIGRFAMs: TIGR01168; Ysirk_signal; 1.
DR PROSITE: PS50847; GRAM_POS_ANCHORING; 1.
DR Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ SEQUENCE 957 AA; 105980 MW; 28F8BA7FDFD3EAF CRC64;

Query Match 100.0%; Score 53; DB 2; Length 957;
Best Local Similarity 100.0%; Pred. No. 0.48;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FNKGTETIEE 10
Db 765 FNKGTETIEE 774
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RESULT 5
08NU7       PRELIMINARY;      PRT; 1015 AA.
ID 08NU7
AC 08NU7
DT 01-OCT-2002 (TREMBlrel. 22, Created)
DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Fnb protein.
GN Name=fnb; OrderedLocNames=NM2421;
OS Staphylococcus aureus (strain MM2).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
CX NCBI_TaxID=196620;
RN [1]
RP SEQUENCE FROM N.A.
RC STAIN=MM2;
RX MEDLINE=22040717; PubMed=12044378; DOI=10.1016/S0140-6736(02)08713-5;
RA Baba T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Oguchi A.,
RA Nagai Y., Iwama N., Asano K., Naito T., Kuroda H., Cui L.,
RA Yamamoto K., Hiramatsu K.;
RT "Genome and virulence determinants of high virulence community-
acquired MRSA.";
RL Lancet 359:1819-1827(2002).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
an amide bond (By similarity).
DR EMBL; AP004830; BAB96286.1; -.
DR GO; GO:0009986; C:cell surface; IEA.
DR GO; GO:0005618; C:cell wall; IEA.
DR GO; GO:0009227; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0009275; P:cell adhesion; IEA.
DR InterPro; IPR008966; Adhes_bact.
DR InterPro; IPR004237; Fb_bind.
DR InterPro; IPR005877; Gpos_YsIRK.
DR InterPro; IPR001899; Gram_pos_anchor.
DR Pfam; PF02986; Fb_bind; 1.
DR Pfam; PF00746; Gram_pos_anchor; 1.
DR Pfam; PF04650; YsIRK_signal; 1.
DR TIGRFAMs; TIGR01167; LPXTG_anchor; 1.
DR TIGRFAMs; TIGR01168; YsIRK_signal; 1.
DR PROSITE; PS50847; GRAM_POS_ANCHORING; 1.
KM Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ SEQUENCE 1015 AA; 11145 MW; D0F9281B864D4D2 CRC64;

Query Match      100.0%; Score 53; DB 2; Length 1015;
Best Local Similarity 100.0%; Pred. No. 0.51;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FNKHTETIEE 10
DB 823 FNKHTETIEE 832

RESULT 6
06G6H3       PRELIMINARY;      PRT; 1015 AA.
ID 06G6H3
AC 06G6H3
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE Fibronectin-binding protein.
GN OrderedLocNames=SA52388;
OS Staphylococcus aureus (strain MSSA476).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
CX NCBI_TaxID=282459;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=15213324; DOI=10.1073/pnas.0402521101;
RA Holden M.T.G., Fell E.J., Lindsay J.A., Peacock S.D., Day N.P.J.,
RA Knight M.C., Foster T.J., Moore C.E., Hurst L., Actin R., Barron A.,
RA Bason N., Bentley S.D., Chillingworth C., Chillingworth T.,
RA Churcher C., Clark L., Cotton C., Cronin A., Doggett J., Dowd L.,
RA Felwell T., Hance Z., Harris B., Hauser H., Holtroyd S., Jagsis K.,
RA James K.D., Lennard N., Line A., Mayes R., Moule S., Mungall K.,

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RA Ormond D., Quail M.A., Rabinowitch E., Rutherford K.M., Sanders M.,
RA Sharp S., Simmonds M., Stevens K., Whitehead S., Barrell B.G.,
RA Spratt B.G., Parkhill J.;
RT "Complete genomes of two clinical Staphylococcus aureus strains:
RT evidence for the rapid evolution of virulence and drug resistance.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:9786-9791(2004).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
an amide bond (By similarity).
DR EMBL; BX571857; CAG44202.1; -.
DR GO; GO:0009986; C:cell surface; IEA.
DR GO; GO:0005618; C:cell wall; IEA.
DR GO; GO:0009227; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0007155; P:cell adhesion; IEA.
DR InterPro; IPR008966; Adhes_bact.
DR InterPro; IPR004237; Fb_bind.
DR InterPro; IPR005877; Gpos_YsIRK.
DR InterPro; IPR001899; Gram_pos_anchor.
DR Pfam; PF02986; Fb_bind; 1.
DR Pfam; PF00746; Gram_pos_anchor; 1.
DR Pfam; PF04650; YsIRK_signal; 1.
DR TIGRFAMs; TIGR01167; LPXTG_anchor; 1.
DR TIGRFAMs; TIGR01168; YsIRK_signal; 1.
DR PROSITE; PS50847; GRAM_POS_ANCHORING; 1.
KM Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ SEQUENCE 1015 AA; 11145 MW; D0F9281B864D4D2 CRC64;

Query Match      100.0%; Score 53; DB 2; Length 1015;
Best Local Similarity 100.0%; Pred. No. 0.51;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FNKHTETIEE 10
DB 823 FNKHTETIEE 832

RESULT 7
FNBA STAU     STANDARD;      PRT; 1018 AA.
ID FNBA STAU
AC P14738;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Fibronectin-binding protein precursor (FNBP).
GN Name=fnbA;
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
CX NCBI_TaxID=1280;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NCCT 8325-4; PubMed=2521391;
RX MEDLINE=89098998; PubMed=2521391;
RA Signaes C., Raucel G., Joensson K., Lindgren P.-E.,
RA Anantharamiah G.M., Hoeeok M., Lindberg M.;
RT "Nucleotide sequence of the gene for a fibronectin-binding protein
RT from Staphylococcus aureus: use of this peptide sequence in the
RT synthesis of biologically active peptides.";
RL Proc. Natl. Acad. Sci. U.S.A. 86:699-703(1989).
CC -1- FUNCTION: The ability of bacteria to bind fibronectin has been
CC proposed as a virulence factor enabling bacteria to colonize wound
CC tissues and blood clots. Binding of plasma fibronectin to the
CC bacterial surface might block adhesion receptors on S.aureus, thus
CC representing an important defense mechanism against tissue
CC invasion.
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC an amide bond (potential).
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation-
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CC or send an email to license@lsb-sib.ch).
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CC EMBL: J04151; AAA26632.1; -.
DR InterPro: IPR004237; Fn_bind.
DR InterPro: IPR005877; GpoS_Ysirk.
DR InterPro: IPR001899; Gram_pos_anchor.
DR Pfam: PF02986; Fn_bind_1.
DR Pfam: PF00746; Gram_pos_anchor; 1.
DR Pfam: PF04650; Ysirk_signal; 1.
DR TIGRfams: TIGR01167; LpXg_anchor; 1.
DR TIGRfams: TIGR01168; Ysirk_signal; 1.
DR PROSITE: PSS0847; GRAM_POS_ANCHORING; 1.
DR Cell adhesion; Cell wall; Peptidoglycan-anchor; Repeat; Signal;
KM Cell wall; Peptidoglycan-anchor; Repeat; Signal;
FT SIGNAL 1 36
FT CHAIN 37 985
FT PROPEP 986 1018
FT REPEAT 545 574
FT REPEAT 575 604
FT DOMAIN 745 878
FT REPEAT 745 782
FT REPEAT 783 820
FT REPEAT 821 859
FT REPEAT 860 878
FT DOMAIN 879 948
FT REPEAT 879 892
FT REPEAT 893 906
FT REPEAT 907 920
FT REPEAT 921 934
FT REPEAT 935 948
FT SITE 982 986
FT MOD_RSS 985 985
SQ SEQUENCE 1018 AA; 111780 MW; 58175E0020E81F1F CRC64;

Query Match
Best Local Similarity 100.0%; Score 53; DB 1; Length 1018;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FNKHTETIEE 10
DB 822 FNKHTETIEE 831

RESULT 8
Q99RD3 PRELIMINARY; PRT; 961 AA.
ID Q99RD3
AC Q99RD3;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Fibronectin-binding protein homolog.
GN Name=fnb3; OrderedLocustNames=SAV2502.
OS Staphylococcus aureus (strain Mu50 / ATCC 700699).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxId=158878;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Mu50 / ATCC 700699;
RX MEDLINE=21311952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2;
RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Iian J.-O., Ito T.,
RA Kanamori M., Matsunaru H., Maruyama A., Murakami H., Hosoyama A.,
RA Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
RA Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
RA Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
RA Hattori M., Ogasawara N., Hayaishi H., Hirataesu K.;
RT "Whole genome sequencing of methicillin-resistant Staphylococcus
RT aureus."
RL Lancet 357:1225-1240(2001).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
an amide bond (By similarity).
```

```
DR EMBL: AP003365; BAB58664.1; -.
DR PIR: G90053; G90053.
DR HSSP: OS3653; 1N67.
DR GO: GO:0009986; C:cell surface; IEA.
DR GO: GO:0005618; C:cell wall; IEA.
DR GO: GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO: GO:0016020; C:membrane; IEA.
DR GO: GO:0007155; P:cell adhesion; IEA.
DR InterPro: IPR008966; Adhes_bact.
DR InterPro: IPR004237; Fn_bind.
DR InterPro: IPR005877; GpoS_Ysirk.
DR InterPro: IPR001899; Gram_pos_anchor.
DR Pfam: PF02986; Fn_bind_1.
DR Pfam: PF00746; Gram_pos_anchor; 1.
DR Pfam: PF04650; Ysirk_signal; 1.
DR TIGRfams: TIGR01167; LpXg_anchor; 1.
DR TIGRfams: TIGR01168; Ysirk_signal; 1.
DR PROSITE: PSS0847; GRAM_POS_ANCHORING; 1.
DR Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ SEQUENCE 961 AA; 106010 MW; 364940F884EA4101 CRC64;

Query Match
Best Local Similarity 90.6%; Score 48; DB 2; Length 961;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 FNKHTETIEE 10
DB 769 FNKHTETIEE 778

RESULT 9
Q7A3J8 PRELIMINARY; PRT; 961 AA.
ID Q7A3J8
AC Q7A3J8;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE FnbB protein.
GN Name=fnb3; OrderedLocustNames=SA2290.
OS Staphylococcus aureus (strain N115).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxId=158879;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21311952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2;
RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Iian J.-O., Ito T.,
RA Kanamori M., Matsunaru H., Maruyama A., Murakami H., Hosoyama A.,
RA Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
RA Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
RA Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
RA Hattori M., Ogasawara N., Hayaishi H., Hirataesu K.;
RT "Whole genome sequencing of methicillin-resistant Staphylococcus
RT aureus."
RL Lancet 357:1225-1240(2001).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
an amide bond (By similarity).
EMBL: AP003137; BAB43593.1; -.
DR GO: GO:0009986; C:cell surface; IEA.
DR GO: GO:0005618; C:cell wall; IEA.
DR GO: GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO: GO:0016020; C:membrane; IEA.
DR GO: GO:0007155; P:cell adhesion; IEA.
DR InterPro: IPR008966; Adhes_bact.
DR InterPro: IPR004237; Fn_bind.
DR InterPro: IPR005877; GpoS_Ysirk.
DR InterPro: IPR001899; Gram_pos_anchor.
DR Pfam: PF02986; Fn_bind_1.
DR Pfam: PF00746; Gram_pos_anchor; 1.
DR Pfam: PF04650; Ysirk_signal; 1.
DR TIGRfams: TIGR01167; LpXg_anchor; 1.
DR TIGRfams: TIGR01168; Ysirk_signal; 1.
DR PROSITE: PSS0847; GRAM_POS_ANCHORING; 1.
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KM Cell wall; Complete proteome; Peptidoglycan-anchor.
 SQ SEQUENCE 961 AA; 106010 MW; 364940F884EA4101 CRC64;
 Query Match 90.6%; Score 48; DB 2; Length 961;
 Best Local Similarity 90.0%; Pred. No. 4.2;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 FNKATETITEE 10
 |||||
 Db 769 FNKATETITEE 778

RESULT 10
 O6GDUS PRELIMINARY; PRT; 965 AA.
 ID O6GDUS
 AC O6GDUS; 05-JUL-2004 (TREMBlrel. 27, Created)
 DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
 DE Fibronectin-binding protein.
 GN Name=fnba; OrderedlocusNames=SA2580;
 OS Staphylococcus aureus (strain MRSA252).
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 OX NCBI_TaxID=282458;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX Holden M.T.G., Feil E.J., Lindsay J.A., Peacock S.J., Day N.P.J.,
 Enright M.C., Foster T.J., Moore C.E., Hurst L., Atkin R., Barron A.,
 Baeson N., Bentley S.D., Chillingworth C., Chillingworth T.,
 Churcher C., Clark L., Corton C., Cronin A., Doggett J., Dowd L.,
 Fellwell T., Lennard Z., Harris B., Hauser H., Holroyd S., Jagels K.,
 James K.D., Leonard N., Line A., Mayes R., Moule S., Mungall K.,
 Ormond D., Quail M.A., Rabinowitch E., Rutherford K.M., Sanders M.,
 Sharp S., Simmonds M., Stevens K., Whitehead S., Barrall B.G.,
 Spratt B.G., Partridge L.;
 RT "Complete genomes of two clinical Staphylococcus aureus strains:
 evidence for the rapid evolution of virulence and drug resistance";
 RL Proc. Natl. Acad. Sci. U.S.A. 101:9786-9791(2004).
 CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
 an amide bond (By similarity).
 DR EMBL; BX571856; CAG41560.1; -;
 DR GO; GO:0009986; C:cell surface; IEA.
 DR GO; GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0007155; P:cell adhesion; IEA.
 DR InterPro; IPR008966; Adhes_Bact.
 DR InterPro; IPR004237; Fn_bind.
 DR InterPro; IPR001899; Gram_pos_anchor.
 DR Pfam; PF02986; Fn_bind; 1.
 DR Pfam; PF00746; Gram_pos_anchor; 1.
 DR Pfam; PF04650; YSIRK_signal; 1.
 DR TIGRFAMs; TIGR01167; LpxTG_anchor; 1.
 DR TIGRFAMs; TIGR01168; YSIRK_signal; 1.
 DR PROSITE; PS50847; GRAM_POS_ANCHORING; 1.
 KW Cell wall; Complete proteome; Peptidoglycan-anchor.
 SQ SEQUENCE 965 AA; 105691 MW; 2982E332164D0551 CRC64;

Query Match 90.6%; Score 48; DB 2; Length 965;
 Best Local Similarity 90.0%; Pred. No. 4.2;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 FNKATETITEE 10
 |||||
 Db 787 FNKATETITEE 796

RESULT 11
 O99RD2 PRELIMINARY; PRT; 1038 AA.
 ID O99RD2
 AC O99RD2; 01-JUN-2001 (TREMBlrel. 17, Created)

DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
 DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
 DE Fibronectin-binding protein homolog.
 GN Name=fnb; OrderedlocusNames=SAV2503;
 OS Staphylococcus aureus (strain Mu50 / ATCC 700699).
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 OX NCBI_TaxID=158878;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Mu50 / ATCC 700699;
 RX MEDLINE=21311952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2;
 RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
 Cui L., Oguchi A., Aoki K.-I., Nagai Y., Iino T.,
 Kanamori M., Matsunaru H., Maruyama A., Murakami H., Hosoyama A.,
 Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
 Sekimizu K., Hirakawa H., Kihara S., Goto S., Yabuzaki J.,
 Kanehisa M., Yamashta A., Oshima K., Furuya K., Yoshino C., Shiba T.,
 Hattori M., Ogasawara N., Hayashi H., Hiratake K.;
 RT "Whole genome sequencing of methicillin-resistant Staphylococcus
 aureus";
 RL Lancet 357:1225-1240(2001).
 CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
 an amide bond (By similarity).
 DR EMBL; AP003365; BAB58665.1; -;
 DR PIR; H90053; H90053.
 DR GO; GO:0009986; C:cell surface; IEA.
 DR GO; GO:0005618; C:cell wall; IEA.
 DR GO; GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0007155; P:cell adhesion; IEA.
 DR InterPro; IPR008966; Adhes_Bact.
 DR InterPro; IPR004237; Fn_bind.
 DR InterPro; IPR005877; Gpos_YSIRK.
 DR InterPro; IPR001899; Gram_pos_anchor.
 DR Pfam; PF02986; Fn_bind; 1.
 DR Pfam; PF00746; Gram_pos_anchor; 1.
 DR Pfam; PF04650; YSIRK_signal; 1.
 DR TIGRFAMs; TIGR01167; LpxTG_anchor; 1.
 DR TIGRFAMs; TIGR01168; YSIRK_signal; 1.
 DR PROSITE; PS50847; GRAM_POS_ANCHORING; 1.
 KW Cell wall; Complete proteome; Peptidoglycan-anchor.
 SQ SEQUENCE 1038 AA; 113618 MW; 666BF6F28FBE12 CRC64;

Query Match 90.6%; Score 48; DB 2; Length 1038;
 Best Local Similarity 90.0%; Pred. No. 4.5;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 FNKATETITEE 10
 |||||
 Db 818 FNKATETITEE 827

RESULT 12
 O7A3J7 PRELIMINARY; PRT; 1038 AA.
 ID O7A3J7
 AC O7A3J7; 05-JUL-2004 (TREMBlrel. 27, Created)
 DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
 DE Fnb protein.
 GN Name=fnb; OrderedlocusNames=SA2291;
 OS Staphylococcus aureus (strain N315).
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 OX NCBI_TaxID=158879;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21311952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2;
 RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
 Cui L., Oguchi A., Aoki K.-I., Nagai Y., Iino T.,
 Kanamori M., Matsunaru H., Maruyama A., Murakami H., Hosoyama A.,
 Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
 Sekimizu K., Hirakawa H., Kihara S., Goto S., Yabuzaki J.,
 Kanehisa M., Yamashta A., Oshima K., Furuya K., Yoshino C., Shiba T.,

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RA Hactori M., Ogaawara N., Hayashi H., Hiramatsu K.;
RT "Whole genome sequencing of methicillin-resistant Staphylococcus
RT aureus."
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC an amide bond (By similarity).
CC EMBL: AP003137; BAB43594.1; -.
DR GO: GO:0009986; C:cell surface; IEA.
DR GO: GO:0005618; C:cell wall; IEA.
DR GO: GO:0009275; C:cell wall (senu Gram-positive Bacteria); IEA.
DR GO: GO:0016020; C:membrane; IEA.
DR GO: GO:0007155; P:cell adhesion; IEA.
DR InterPro: IPR008966; Adhes_bact.
DR InterPro: IPR004237; Fn_bind.
DR InterPro: IPR008199; Gram_pos_anchor.
DR Pfam: PF02986; Fn_bind; 1.
DR Pfam: PF00746; Gram_pos_anchor; 1.
DR Pfam: PF04650; YSIRK_signal; 1.
DR TIGRFAMs: TIGR01167; LpxTG_anchor; 1.
DR TIGRFAMs: TIGR01168; YSIRK_signal; 1.
DR PROSITE: PS50847; GRAM_POS_ANCHORING; 1.
KW Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ SEQUENCE 1038 AA; 113618 MW; 666BFBFBFBEB12 CRC64;

Query Match 90.6%; Score 48; DB 2; Length 1038;
Best Local Similarity 90.0%; Pred. No. 4.5;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 FNKHTETIEE 10
Db 818 FNKKNETIEE 827

RESULT 13
Q724Y3 PRELIMINARY; PRT; 226 AA.
ID Q724Y3
AC Q724Y3;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Argenite-resistance protein ARS2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Fu Q., Yu L., Yang J., Mao N.H., Chen S.Y., Zhao S.Y.;
RA Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
RL EMBL: AF112994; AAP97227.1; -.
DR InterPro: IPR007042; ARS2.
DR Pfam: PF04959; ARS2; 1.
SQ SEQUENCE 226 AA; 25514 MW; A47AB75A019D1C4 CRC64;

Query Match 77.4%; Score 41; DB 2; Length 226;
Best Local Similarity 80.0%; Pred. No. 19;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 FNKHTETIEE 10
Db 98 FNKKAETIEE 107

RESULT 14
ARS2_CRIGR STANDARD; PRT; 290 AA.
ID ARS2_CRIGR
AC Q60436;
DT 15-JUL-1999 (Rel. 38, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Argenite-resistance protein 2 (Fragment).
Name=ARS2; Synonyms=ARS2;

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OS Cricetus griseus (Chinese hamster).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
OC Cricetus.
OX NCBI_TaxID=10029;
RN [1]
RP SEQUENCE FROM N.A.
RA TISSUE=lung;
RX MEDLINE=99167000; PubMed=10069470; DOI=10.1093/carcin/20.2.311;
RA Rosman T.G., Wang Z.;
RT "Expression cloning for arsenite-resistance resulted in isolation of
RT tumor-suppressor Iau cDNA: possible involvement of the ubiquitin
RT system in arsenic carcinogenesis."
RL Carcinogenesis 20:311-316(1999).
CC -1- FUNCTION: Confers arsenite resistance.
CC -1- SIMILARITY: Belongs to the ARS2 family.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: U41500; AAA63777.1; ALT_INIT.
DR InterPro: IPR007042; ARS2.
DR Pfam: PF04959; ARS2; 1.
FT NON_TER 1
SQ SEQUENCE 290 AA; 33001 MW; 848F1BD2E024BF99 CRC64;

Query Match 77.4%; Score 41; DB 1; Length 290;
Best Local Similarity 80.0%; Pred. No. 24;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 FNKHTETIEE 10
Db 162 FNKKAETIEE 171

RESULT 15
Q8VEE6 PRELIMINARY; PRT; 422 AA.
ID Q8VEE6
AC Q8VEE6;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Ars2-pending protein.
DE Name=Ars2;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=FVB/N; TISSUE=Nammary tumor. C3;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klapper R.D., Collins F.S., Wagner L., Shenmen C.M., Bhat N.K.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Uedin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Locuelli N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Vallalón D.K., Wuzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smalins D.E., Schmeich A., Schein J.B.,

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RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=FVB/N; TISSUE=Mammary tumor. C3;
RA Strauberg R.;
RL Submitted (DEC-2001) to the EMBL/Genbank/DBJ databases.
DR EMBL; BC019117; AAH19117.1; -
DR MGD; MGI:1933527; Arsg2.
DR GO; GO:0046885; P:response to arsenate; TAS.
DR Pfam; PF04959; ARS2; 1.
SQ SEQUENCE 422 AA; 47928 MW; 069B8C94BC4AF64 CRC64;
Query Match 77.4%; Score 41; DB 2; Length 422;
Best Local Similarity 80.0%; Pred. No. 36;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Oy 1 FNKHTETIEE 10
||| |
Db 286 FNKHTAKTIEE 295

Search completed: October 22, 2005, 09:52:11
Job time : 58.2069 secs

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OM protein - protein search, using sw model

Run on: October 25, 2005, 20:58:51 ; Search time 69.7126 Seconds
(without alignments)
55.479 Million cell updates/sec

Title: US-10-731-238-89
Perfect score: 52
Sequence: 1 KHTELLIEDT 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:*

- 1: Geneseqp1980s:*
- 2: Geneseqp1990s:*
- 3: Geneseqp2000s:*
- 4: Geneseqp2001s:*
- 5: Geneseqp2002s:*
- 6: Geneseqp2003as:*
- 7: Geneseqp2003bs:*
- 8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	52	100.0	10 2 AAW65745	AAW65745 Fibronect
2	52	100.0	37 1 AAP82118	AAP82118 Fibronect
3	52	100.0	37 4 AAB91958	AAB91958 Fibronect
4	52	100.0	38 1 AAP80662	AAP80662 Protein w
5	52	100.0	77 2 AAR88749	AAR88749 S. aureus
6	52	100.0	113 2 AAR90937	AAR90937 D3D4 poly
7	52	100.0	124 2 AAR90940	AAR90940 D3D4 poly
8	52	100.0	128 2 AAR90941	AAR90941 D3D4 poly
9	52	100.0	130 2 AAR58806	AAR58806 Fibronect
10	52	100.0	130 2 AAR58807	AAR58807 Fibronect
11	52	100.0	130 2 AAR91202	AAR91202 D1-D4 fib
12	52	100.0	130 2 AAR91201	AAR91201 D1-D4 fib
13	52	100.0	134 2 AAY29089	AAY29089 Cloned f1
14	52	100.0	134 2 AAY29088	AAY29088 S. aureus
15	52	100.0	134 2 AAY29087	AAY29087 S. aureus
16	52	100.0	139 2 AAW31556	AAW31556 Fibronect
17	52	100.0	162 2 AAR90942	AAR90942 D3D4 poly
18	52	100.0	164 2 AAR90938	AAR90938 D3D4 poly
19	52	100.0	174 2 AAR58808	AAR58808 Fbp fibro
20	52	100.0	174 2 AAR91203	AAR91203 D1-D4 fib
21	52	100.0	181 2 AAR58805	AAR58805 Fibronect
22	52	100.0	181 2 AAR91200	AAR91200 D1-D4 fib
23	52	100.0	559 2 AAW89803	AAW89803 Staphyloc
24	52	100.0	940 2 AAR07070	AAR07070 Fibronect
25	52	100.0	940 6 ABJ19111	ABJ19111 Pathogen

26 52 100.0 948 6 ADA89470
27 52 100.0 948 6 ABJ18923
28 52 100.0 948 6 ABM72536
29 52 100.0 1018 1 AAP82115
30 52 100.0 1018 4 AAU37245
31 52 100.0 1018 4 AAU34301
32 52 100.0 1018 6 ABJ18922
33 52 100.0 1018 6 ABM72537
34 52 100.0 1027 2 AAW89806
35 47 90.4 101 2 AAR90939
36 47 90.4 961 6 ABU15854
37 47 90.4 978 4 AAU33960
38 47 90.4 1001 4 AAU37093
39 47 90.4 1038 6 ABU15903
40 41 78.8 10 2 AAW65744
41 39 75.0 10 2 AAW65746
42 39 75.0 1670 5 ABB92708
43 38 73.1 708 8 ADN07103
44 37 71.2 57 3 AAG44340
45 37 71.2 63 3 AAG28420

ALIGNMENTS

RESULT 1
AAW65745
ID AAW65745 standard; peptide; 10 AA.

XX AC AAW65745;

XX DT 16-OCT-1998 (first entry)

XX DE Fibronectin binding protein-derived peptide #89.

XX KM microbial surface components recognising adhesive matrix molecule;

XX KM MSCRAMM; fibronectin; fibronectin-binding protein; antibody; epitope;

XX KM antibiotic; bacterial infection; antibiotic-resistant strain.

XX OS Synthetic.

XX OS Staphylococcus aureus.

XX FN W09831389-A2.

XX PD 23-JUL-1998.

XX PF 21-JAN-1998; 98WO-US001222.

XX PR 21-JAN-1997; 97US-0036139P.

XX PA (TEXAS) UNIV TEXAS A & M SYSTEM.

XX PI Hoocek M, Patti JM, House-Pompeo KL, Speziale P, Joh D;

XX PI McGeavin MJ;

XX PS WPI, 1998-413816/35.

XX CC Example 9; Page 111; 201pp; English.

XX CC The invention relates to antibodies that bind to a fibronectin-binding

XX CC domain of a fibronectin-binding protein, and inhibit binding of the

XX CC protein to fibronectin. Also claimed are: (1) isolated peptides of a

XX CC fibronectin-binding protein that do not bind to fibronectin; (2) fusion

XX CC protein containing at least one peptide of a fibronectin-binding protein

XX CC linked to a second amino acid sequence; (3) nucleic acid encoding the

XX CC isolated peptide of (1). Antibodies, the isolated peptides of (1) and the

XX CC nucleic acids are all useful for immunisation (active or passive) and (by

XX CC inhibiting binding of bacteria to fibronectin) for preventing or treating

XX CC infection in humans or other animals, particularly by staphylococci or

CC streptococci, e.g. meningitis, otitis media, pneumonia, endocarditis,
CC mastitis in cattle, abortion in horses and many others. Since the
CC antibodies block binding of bacteria, they should be effective against
CC antibiotic-resistant strains, and may replace antibiotic therapy or
CC increase its effectiveness. Sequences AAB65744-58 represent peptides
CC which were synthesised to span the D3 motif of S. aureus fibronectin
CC binding protein A
XX
SQ Sequence 10 AA;

Query Match 100.0%; Score 52; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0081;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KHTIIIEDT 10
| | | | | | | | | |
Db 1 KHTIIIEDT 10

RESULT 2
AAB82118
ID AAB82118 standard; protein; 37 AA.
XX
AC AAB82118;
XX
DT 25-MAR-2003 (revised)
DT 05-JAN-1990 (first entry)
XX
DE Fibronectin binding protein.
XX
KM Fibronectin binding protein; S.aureus; immunisation; mastitis; ruminants;
KM wound infection; diagnosis.
XX
OS Staphylococcus aureus.
XX
PN EP294349-A.
XX
PD 07-DEC-1988.
XX
PF 30-MAY-1988; 88EP-00850188.
XX
PR 01-JUN-1987; 87SE-00002272.
XX
PA (ALFA) ALFA LAVAL AGRIC INT AB.
XX
PI Lindberg MK, Signae LC, Wadstrom TM, Froman G;
XX WPI; 1988-347978/49.
DR N-PSDB; AAN82056.
XX
PT Hybrid DNA encoding Staphylococcus aureus fibronectin binding protein -
PT useful for immunisation and topical application to prevent staphylococcal
PT infections.
XX
PS Claim 11; Page 12; 23pp; English.
XX
CC The S.aureus fibronectin binding protein may be included in a hybrid
CC protein. The protein may be used to immunise ruminants against
CC staphylococcal mastitis, pref. when given at 0.5-5 microg/kg, using 3
CC doses at 1-3 week intervals; and for topical applicn. to prevent wound
CC infection, pref. using isotonic saline soln. of concn. 25-250 microg/mg.
CC The DNA encoding the binding protein and the hybrid protein may be
CC immobilised on a carrier and used to diagnose staphylococcal infections.
CC (Updated on 25-MAR-2003 to correct PA field.)
XX
SQ Sequence 37 AA;

Query Match 100.0%; Score 52; DB 1; Length 37;
Best Local Similarity 100.0%; Pred. No. 0.032;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KHTIIIEDT 10
| | | | | | | | | |
Db 1 KHTIIIEDT 10

Db 4 KHTIIIEDT 13

RESULT 3
AAB91958
ID AAB91958 standard; peptide; 37 AA.
XX
AC AAB91958;
XX
DT 22-JUN-2001 (first entry)
XX
DE Fibronectin fragment and fibrin related peptide SEQ ID NO:1134.
XX
KM Protection; endogenous therapeutic peptide; peptidase; conjugation;
KM blood component; modification; succinimidyl; maleimido group; amino;
KM hydroxyl; thiol; hormone; growth factor; neurotransmitter.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200069900-A2.
XX
PD 23-NOV-2000.
XX
PF 17-MAY-2000; 2000WO-US013576.
XX
PR 17-MAY-1999; 99US-0134406P.
PR 10-SEP-1999; 99US-0153406P.
PR 15-OCT-1999; 99US-0159783P.
XX
PA (CONJ-) CONJUCHEM INC.
XX
PI Bridon DP, Ezrin AM, Milner PG, Holmes DL, Thibaudau K;
XX WPI; 2001-112059/12.
XX
PT Modifying and attaching therapeutic peptides to albumin prevents
PT peptidase degradation, useful for increasing length of in vivo activity.
XX
PS Disclosure; Page 566; 733pp; English.
XX
CC The present invention describes a modified therapeutic peptide (I)
CC comprising a therapeutically active amino acid region (III) and a
CC reactive group (II) (e.g. succinimidyl and maleimido groups) attached to
CC a less therapeutically active amino acid region (IV), which covalently
CC bonds with amino/hydroxyl/thiol groups on blood components to form a
CC peptidase stabilised therapeutic peptide composed of 3-50 amino acids.
CC (I) are useful for modifying therapeutic peptides e.g. hormones, growth
CC factors and neurotransmitters, to protect them from peptidase activity in
CC vivo for the treatment of various disorders. Endogenous therapeutic
CC peptides are not suitable as drug candidates as they require frequent
CC administration due to rapid degradation by peptidases in the body.
CC Modifying and attaching therapeutic peptides to albumin prevents or
CC reduces the action of peptidases to increase length of activity (half
CC life) and specificity as bonding to large molecules decreases
CC intracellular uptake and interference with physiological processes.
CC AAB90829 to AAB82441 represent peptides which can be used in the
CC exemplification of the present invention
XX
SQ Sequence 37 AA;

Query Match 100.0%; Score 52; DB 4; Length 37;
Best Local Similarity 100.0%; Pred. No. 0.032;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KHTIIIEDT 10
| | | | | | | | | |
Db 3 KHTIIIEDT 12

RESULT 4
AAB80662
ID AAB80662 standard; protein; 38 AA.

```

XX AAP80662;
AC 25-MAR-2003 (revised)
XX 07-OCT-1990 (first entry)
DT
DE Protein with fibronectin binding ability.
XX
XX Hybrid DNA molecule; fibronectin binding; mastitis; ruminants;
KW wound infection.
XX
XX Staphylococcus aureus.
OS
XX EP294349-A.
XX
XX 07-DEC-1988.
XX
XX 30-MAY-1988; 88EP-00850188.
XX
XX 01-JUN-1987; 87SE-00002272.
XX
XX (ALFA ) ALFA LAVALL AGRIC INT AB.
XX
XX Lindberg MK, Signae LC, Wadstrom TM, Froman G;
PI WPI; 1988-347978/49.
XX
XX N-PSDB; AAN81099.
XX
XX Hybrid DNA encoding Staphylococcus aureus fibronectin binding protein -
PT useful for immunisation and topical application to prevent staphylococcal
PT infections.
XX
XX Claim 11; Page 12; 23pp; English.
XX
XX The peptide has fibronectin binding ability. It is useful for immunising
XX ruminants against staphylococcal mastitis, pref. when used at 0.5-5
XX micrograms/kg, using 3 doses given at 1-3 week intervals; for topical
XX application to prevent wound infection, using an isotonic saline soln. of
XX concn. 25-250 micrograms/ml; and, when immobilised on a carrier, for
XX diagnosing staphylococcal infections. (Updated on 25-MAR-2003 to correct
XX PF field.) (Updated on 25-MAR-2003 to correct PA field.)
XX
XX Sequence 38 AA:
SQ
Query Match 100.0%; Score 52; DB 1; Length 38;
Best Local Similarity 100.0%; Pred. No. 0.033;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 KHTETIEEDT 10
    |||||
    4 KHTETIEEDT 13
DB
RESULT 5
AAR8749
ID AAR8749 standard; protein; 77 AA.
XX
XX AAR8749;
AC
XX
XX 24-SEP-1996 (first entry)
XX
XX S. aureus fibronectin binding protein D2D3 polypeptide.
DE
XX
XX Fibronectin binding protein; D2D3; prevention; adhesion; bacteria;
KW gram positive; extra-cellular matrix protein; in-dwelling device;
KW catheter; wound; D2D3; oral pathogen; oral cavity; NCIMB 40532.
XX
XX Staphylococcus aureus.
OS
XX
XX WO9604380-A1.
XX
XX 15-FEB-1996.
XX

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```

PF 28-JUL-1995; 95WO-EP003039.
XX
XX 05-AUG-1994; 94GB-00015901.
XX
XX (SMIK ) SMITHKLINE BEECHAM PLC.
XX
XX Critchley IA, Dodd I, Barnett P, Mossakowska DEI;
PI WPI; 1996-129396/13.
XX
XX N-PSDB; AAT12582.
XX
XX Staphylococcus aureus fibronectin binding protein D2D3 polypeptide -
PT useful for combatting infection at wound sites, surgical implants, etc.
PT and as adherent agent in oral hygiene.
XX
XX Claim 5; Page 26; 38pp; English.
XX
XX The present sequence is the S. aureus fibronectin binding protein
XX polypeptide D2D3, which can be used to prevent adhesion of (e.g. gram
XX positive) bacteria, to extra-cellular matrix proteins on in-dwelling
XX devices, e.g. catheters or in wounds. D2D3 can also be used to prevent
XX oral pathogens from binding to extra-cellular matrix proteins, in the
XX oral cavity. D2D3 was found to be effective at inhibiting S. aureus 8325-
XX 4, and 120 adhesion to fibronectin coated PMMA coverslips, at a min.
XX adhesion inhibitor concn. of 10 microg/ml. D2D3 was derived from the D2
XX and D3 regions of the S. aureus J2385 (NCIMB 40532) fibronectin binding
XX protein
XX
XX Sequence 77 AA:
SQ
Query Match 100.0%; Score 52; DB 2; Length 77;
Best Local Similarity 100.0%; Pred. No. 0.07;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 KHTETIEEDT 10
    |||||
    42 KHTETIEEDT 51
DB
RESULT 6
AAR90937
ID AAR90937 standard; peptide; 113 AA.
XX
XX AAR90937;
AC
XX
XX 23-SEP-1996 (first entry)
XX
XX D3D4 polypeptide #1.
DE
XX
XX Fibronectin binding protein; Fbp; S. aureus J2385; monoclonal antibody;
KW infection; surgical implant; antiadherent agent; hygiene; adhesion;
KW extracellular matrix protein; oral pathogen; oral cavity.
XX
XX Staphylococcus aureus.
OS
XX
XX Key Location/Qualifiers
FH 1..21
FT Region /note= "D1 region fragment"
FT 22..59
FT Region /note= "D2 region"
FT 60..98
FT Region /note= "D3 region"
FT 99..113
FT Region /note= "D4 region"
FT Misc-difference 113
FT /note= "P113T"
XX
XX WO9604381-A1.
XX
XX 15-FEB-1996.
XX
XX 28-JUL-1995; 95WO-EP003040.
XX

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```
PR 05-AUG-1994; 94GB-00015900.
XX
XX (SMIK ) SMITHKLINE BEECHAM PLC.
PA
PI Critchley IA, Dodd I, Barnett P, Mcbay DL;
XX WPI; 1996-129397/13.
XX
PT Polypeptide(s) derived from Staphylococcus aureus fibronectin binding
PT protein - inhibit binding of bacteria to extracellular matrix proteins,
PT for combating infection at the site of wounds and surgical implants, and
PT in oral hygiene.
XX
XX Claim 6; Page 24; 35pp; English.
PS
XX
XX AAR90937-R90942 represent D3D4 polypeptides. These sequences correspond
CC to fragments of the Staphylococcus aureus fibronectin binding protein
CC (Fbp). This sequence corresponds to residues 18-130 of S.aureus J2385
CC Fbp, and also contains the D2 region, and a portion of the D1 region.
CC These sequences, and monoclonal antibodies against them can be used to
CC combat infection at the site of wounds, surgical implants and other in-
CC dwelling devices (such as catheters), and as antiadherent agents in oral
CC hygiene. They can also be used in the manufacture of a medicament for the
CC prevention of adhesion of bacteria to extracellular matrix proteins
CC present on in-dwelling devices or in wounds, or of oral pathogens to
CC similar proteins on surfaces in the oral cavity
XX
SQ Sequence 113 AA;
XX
Query Match 100.0%; Score 52; DB 2; Length 113;
Best Local Similarity 100.0%; Pred. No. 0.1;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 KHTETIEEDT 10
DB 63 KHTETIEEDT 72
| | | | | | | |
| | | | | | | |

RESULT 7
AAR90940
ID AAR90940 standard; peptide; 124 AA.
XX
XX AAR90940;
AC
XX
XX 23-SEP-1996 (first entry)
DT
XX
XX D3D4 polypeptide #4.
DE
XX
XX Fibronectin binding protein; Fbp; S.aureus J2385; monoclonal antibody;
KW infection; surgical implant; antiadherent agent; hygiene; adhesion;
KM extracellular matrix protein; oral pathogen; oral cavity.
XX
XX Staphylococcus aureus.
OS
XX
XX Key Location/Qualifiers
FH 1..19
FT Region /note= "D2 region fragment"
FT 20..58
FT Region /note= "D3 region"
FT 59..62
FT Region /note= "D4 region"
FT 63..124
FT /note= "WRI region"
XX
XX WO9604381-A1.
XX
XX 15-FEB-1996.
PD
XX
XX 28-JUL-1995; 95WO-EP003040.
PF
XX
XX 05-AUG-1994; 94GB-00015900.
PR
XX (SMIK ) SMITHKLINE BEECHAM PLC.
PA
XX
```

```
XX
XX Critchley IA, Dodd I, Barnett P, Mcbay DL;
PI WPI; 1996-129397/13.
XX
XX Polypeptide(s) derived from Staphylococcus aureus fibronectin binding
PT protein - inhibit binding of bacteria to extracellular matrix proteins,
PT for combating infection at the site of wounds and surgical implants, and
PT in oral hygiene.
XX
XX Claim 6; Page 24; 35pp; English.
PS
XX
XX AAR90937-R90942 represent D3D4 polypeptides. These sequences correspond
CC to fragments of the Staphylococcus aureus fibronectin binding protein
CC (Fbp). This sequence corresponds to residues 58-181 of S.aureus J2385
CC Fbp, and also contains a portion of the D2 region, and a portion of the
CC wall region 1 (WRI). These sequences, and monoclonal antibodies against
CC them can be used to combat infection at the site of wounds, surgical
CC implants and other in-dwelling devices (such as catheters), and as
CC antiadherent agents in oral hygiene. They can also be used in the
CC manufacture of a medicament for the prevention of adhesion of bacteria to
CC extracellular matrix proteins present on in-dwelling devices or in
CC wounds, or of oral pathogens to similar proteins on surfaces in the oral
CC cavity
XX
SQ Sequence 124 AA;
XX
Query Match 100.0%; Score 52; DB 2; Length 124;
Best Local Similarity 100.0%; Pred. No. 0.11;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 KHTETIEEDT 10
DB 23 KHTETIEEDT 32
| | | | | | | |
| | | | | | | |

RESULT 8
AAR90941
ID AAR90941 standard; peptide; 128 AA.
XX
XX AAR90941;
AC
XX
XX 23-SEP-1996 (first entry)
DT
XX
XX D3D4 polypeptide #5.
DE
XX
XX Fibronectin binding protein; Fbp; S.aureus J2385; monoclonal antibody;
KW infection; surgical implant; antiadherent agent; hygiene; adhesion;
KM extracellular matrix protein; oral pathogen; oral cavity.
XX
XX Staphylococcus aureus.
OS
XX
XX Key Location/Qualifiers
FH 1..23
FT Region /note= "D2 region"
FT 24..62
FT Region /note= "D3 region"
FT 63..77
FT Region /note= "D4 region"
FT 78..128
FT /note= "WRI region"
XX
XX WO9604381-A1.
XX
XX 15-FEB-1996.
PD
XX
XX 28-JUL-1995; 95WO-EP003040.
PF
XX
XX 05-AUG-1994; 94GB-00015900.
PR
XX (SMIK ) SMITHKLINE BEECHAM PLC.
PA
XX Critchley IA, Dodd I, Barnett P, Mcbay DL;
XX
```

XX
DR WPI; 1996-129397/13.
XX
PT Polypeptide(s) derived from *Staphylococcus aureus* fibronectin binding
PT protein - inhibit binding of bacteria to extracellular matrix proteins,
PT for combating infection at the site of wounds and surgical implants, and
PT in oral hygiene.
XX
PS Claim 6; Page 24; 35pp; English.
XX
CC AAR90937-R90942 represent D3D4 polypeptides. These sequences correspond
CC to fragments of the *Staphylococcus aureus* fibronectin binding protein
CC (Fbp). This sequence corresponds to residues 54-181 of *S. aureus* J2385
CC (Fbp), and also contains the D2 region, and a portion of the wall region 1
CC (WRI). These sequences, and monoclonal antibodies against them can be
CC used to combat infection at the site of wounds, surgical implants and
CC other in-dwelling devices (such as catheters), and as antiadherent agents
CC in oral hygiene. They can also be used in the manufacture of a medicament
CC for the prevention of adhesion of bacteria to extracellular matrix
CC proteins present on in-dwelling devices or in wounds, or of oral
CC pathogens to similar proteins on surfaces in the oral cavity
XX
SQ Sequence 128 AA;
XX
Query Match 100.0%; Score 52; DB 2; Length 128;
Best Local Similarity 100.0%; Pred. No. 0.12;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 1 KHTETIEEDT 10
Db 27 KHTETIEEDT 36
XX
RESULT 9
AAR58806
ID AAR58806 standard; protein; 130 AA.
XX
AC AAR58806;
XX
DT 25-MAR-2003 (revised)
DT 30-MAR-1995 (first entry)
XX
DE Fibronectin binding domain D1-D4(709-838(P838T)).
XX
KM Fibronectin binding protein; Fbp; fibronectin binding domain;
KM monoclonal antibody; Mab; adhesion; Gram-positive bacterium; bacteremia;
KM *Escherichia coli*.
XX
OS *Staphylococcus aureus*.
XX
PN WO9418327-A1.
XX
PD 18-AUG-1994.
XX
PF 04-FEB-1994; 94WO-GB000215.
XX
PR 05-FEB-1993; 93GB-00002289.
PR 20-OCT-1993; 93GB-00021592.
XX
PA (SMIK) SMITHKLINE BEECHAM PLC.
XX
PI Burnham MKR, Chopra I, Critchley IA, Knowles DJC;
XX
DR WPI; 1994-279748/34.
XX
PT Fibronectin binding protein and monoclonal antibodies specific for Fbp -
PT useful to prevent adherence of Gram-positive bacteria to indwelling
PT devices or wounds.
XX
PS Disclosure; Page 30; 40pp; English.
XX
CC Polypeptides corresponding to residues G709-T886 plus PPIVPT, G709-
CC P838(P838T) and G709-P838 (AAR58805-07, respectively) of *S. aureus* J2385
CC P838(P838T) and G709-P838 (AAR58805-07, respectively) of *S. aureus* J2385

CC (NCIMB 40532) Fbp type A fibronectin binding domain D1-D4 region
CC (AAR58808) were expressed in *E. coli* BL21(DE4) and used to raise Mabs
CC specific for Fbp. (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ Sequence 130 AA;
XX
Query Match 100.0%; Score 52; DB 2; Length 130;
Best Local Similarity 100.0%; Pred. No. 0.12;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 1 KHTETIEEDT 10
Db 80 KHTETIEEDT 89
XX
RESULT 10
AAR58807
ID AAR58807 standard; protein; 130 AA.
XX
AC AAR58807;
XX
DT 25-MAR-2003 (revised)
DT 30-MAR-1995 (first entry)
XX
DE Fibronectin binding domain D1-D4(709-838).
XX
KM Fibronectin binding protein; Fbp; fibronectin binding domain;
KM monoclonal antibody; Mab; adhesion; Gram-positive bacterium; bacteremia;
KM *Escherichia coli*.
XX
OS *Staphylococcus aureus*.
XX
PN WO9418327-A1.
XX
PD 18-AUG-1994.
XX
PF 04-FEB-1994; 94WO-GB000215.
XX
PR 05-FEB-1993; 93GB-00002289.
PR 20-OCT-1993; 93GB-00021592.
XX
PA (SMIK) SMITHKLINE BEECHAM PLC.
XX
PI Burnham MKR, Chopra I, Critchley IA, Knowles DJC;
XX
DR WPI; 1994-279748/34.
XX
PT Fibronectin binding protein and monoclonal antibodies specific for Fbp -
PT useful to prevent adherence of Gram-positive bacteria to indwelling
PT devices or wounds.
XX
PS Disclosure; Page 30; 40pp; English.
XX
CC Polypeptides corresponding to residues G709-T886 plus PPIVPT, G709-
CC P838(P838T) and G709-P838 (AAR58805-07, respectively) of *S. aureus* J2385
CC (NCIMB 40532) Fbp type A fibronectin binding domain D1-D4 region
CC (AAR58808) were expressed in *E. coli* BL21(DE4) and used to raise Mabs
CC specific for Fbp. (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ Sequence 130 AA;
XX
Query Match 100.0%; Score 52; DB 2; Length 130;
Best Local Similarity 100.0%; Pred. No. 0.12;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 1 KHTETIEEDT 10
Db 80 KHTETIEEDT 89
XX
RESULT 11
AAR91202
ID AAR91202 standard; peptide; 130 AA.

```

XX AC AAR91202;
XX XX 13-NOV-1996 (first entry)
XX DT
XX DE D1-D4 fibronectin binding domains.
XX XX
XX KW Fibronectin; oral hygiene; gingivitis; gum disease; adhesion;
XX KW periodontitis; oral pathogens; caries; calculus; candidiasis; oral surgery;
XX KW tissue regeneration; irrigation; toothpaste; dentifrice; mouthwash;
XX KM lozenge.
XX XX
XX OS Staphylococcus aureus.
XX XX
XX PN WO9604003-A1.
XX PD
XX PF 15-FEB-1996.
XX PF 18-JUL-1995; 95WO-EP002825.
XX PR 05-AUG-1994; 94GB-00015902.
XX PA (SMIK ) SMITHKLINE BEECHAM PLC.
XX PI Barnett P, Critchley IA, Dodd I;
XX DR WPI; 1996-129122/13.
XX XX
XX PT Prevention of adherence of oral pathogens in the oral cavity, partic.
XX PT tooth surfaces - by application of a fibronectin binding protein or
XX PT polypeptide or a monoclonal antibody or fragment against it.
XX PS Claim 5; Page 32; 41pp; English.
XX XX
XX CC Adherence of oral pathogens, particularly to tooth surfaces, can be
XX CC prevented by application of a fibronectin binding protein or polypeptide.
XX CC The fibronectin binding protein or polypeptide is useful in the
XX CC manufacture of oral hygiene compositions, eg. toothpaste, liquid
XX CC dentifrice, mouthwash or lozenge. They are useful to prevent the plaque-
XX CC related development of carious lesions, gingivitis, calculus or
XX CC periodontal disease and to combat oral cavity infections, e.g.
XX CC candidiasis. They may also be useful in oral surgery e.g. in guided
XX CC tissue regeneration procedures to prevent subsequent bacterial infection,
XX CC and for irrigation of periodontal pockets. This sequence corresponds to
XX CC amino acids 709-838 of the D1-D4 fibronectin binding domain of
XX CC Staphylococcus aureus
XX SQ Sequence 130 AA;
XX
XX Query Match 100.0%; Score 52; DB 2; Length 130;
XX Best Local Similarity 100.0%; Pred. No. 0.12;
XX Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 KHTFIIIEEDT 10
XX |||||
XX DB 80 KHTFIIIEEDT 89
XX
XX RESULT 12
XX ID AAR91201
XX ID AAR91201 standard; peptide; 130 AA.
XX AC AAR91201;
XX XX
XX DT 13-NOV-1996 (first entry)
XX DE D1-D4 fibronectin binding domains.
XX XX
XX KW Fibronectin; oral hygiene; gingivitis; gum disease; adhesion;
XX KW periodontitis; oral pathogens; caries; calculus; candidiasis; oral surgery;
XX KW tissue regeneration; irrigation; toothpaste; dentifrice; mouthwash;
XX KM lozenge.
XX XX

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OS Staphylococcus aureus.
XX XX
XX PN WO9604003-A1.
XX XX
XX PD 15-FEB-1996.
XX PF 18-JUL-1995; 95WO-EP002825.
XX PR 05-AUG-1994; 94GB-00015902.
XX PA (SMIK ) SMITHKLINE BEECHAM PLC.
XX PI Barnett P, Critchley IA, Dodd I;
XX DR WPI; 1996-129122/13.
XX XX
XX PT Prevention of adherence of oral pathogens in the oral cavity, partic.
XX PT tooth surfaces - by application of a fibronectin binding protein or
XX PT polypeptide or a monoclonal antibody or fragment against it.
XX PS Claim 5; Page 31-32; 41pp; English.
XX XX
XX CC Adherence of oral pathogens, particularly to tooth surfaces, can be
XX CC prevented by application of a fibronectin binding protein or polypeptide.
XX CC The fibronectin binding protein or polypeptide is useful in the
XX CC manufacture of oral hygiene compositions, eg. toothpaste, liquid
XX CC dentifrice, mouthwash or lozenge. They are useful to prevent the plaque-
XX CC related development of carious lesions, gingivitis, calculus or
XX CC periodontal disease and to combat oral cavity infections, e.g.
XX CC candidiasis. They may also be useful in oral surgery e.g. in guided
XX CC tissue regeneration procedures to prevent subsequent bacterial infection,
XX CC and for irrigation of periodontal pockets. This sequence corresponds to
XX CC amino acids 709-838 of the D1-D4 fibronectin binding domain of
XX CC Staphylococcus aureus with a P838T substitution
XX SQ Sequence 130 AA;
XX
XX Query Match 100.0%; Score 52; DB 2; Length 130;
XX Best Local Similarity 100.0%; Pred. No. 0.12;
XX Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 KHTFIIIEEDT 10
XX |||||
XX DB 80 KHTFIIIEEDT 89
XX
XX RESULT 13
XX ID AAY29089
XX ID AAY29089 standard; protein; 134 AA.
XX AC AAY29089;
XX XX
XX DT 28-SEP-1999 (first entry)
XX DE Cloned fibronectin binding protein binding domain (FnAB) sequence.
XX XX
XX KW Bovine herpes virus-2; BHV-2; cytokine; immune response; immunogen; IL;
XX KW interleukin; colony stimulating factor; CSF; interferon; IFN; TNF;
XX KW tumour necrosis factor; recombinant virus; vaccine; mucosal disease;
XX KW mastitis; breast cancer; stress-induced disease; binding domain; FnAB;
XX KW fibronectin binding protein.
XX XX
XX OS Staphylococcus aureus.
XX XX
XX PN WO9916892-A1.
XX PD
XX PF 08-APR-1999.
XX PF 29-SEP-1998; 98WO-GB002927.
XX PR 29-SEP-1997; 97GB-00020633.
XX PA (UTBR-) UNIV BRISTOL.
XX

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XX Bradley AJ, Duffas WPB;
XX WPI: 1999-255101/21.
DR N-PSDB; AAX91506.
XX New bovine herpes virus-2 vectors.
XX Example 2; Fig 8A-B; 130pp; English.
XX The invention provides bovine herpes virus-2 (BHV-2) based vectors that
CC comprise at least one cytokine-encoding DNA sequence. The expression of
CC cytokines in mammals can up-regulate immune responses to the immunogens.
CC The cytokine is selected from interleukins (IL), colony stimulating
CC factors (CSF), interferons (IFN) and tumour necrosis factors (TNF). The
CC BHV-2 based vector or recombinant virus can be used as vaccines. They can
CC be used for preventing or treating a mucosal disease in a subject, e.g.
CC ruminants, cattle, sheep, goats, dogs, cats, horses, or man, particularly
CC mastitis in cows or breast cancers in humans. They can also be used for
CC preventing or treating a stress-induced disease. The present sequence
CC represents a S. aureus fibronectin binding protein binding domain
CC sequence FNMBB, the gene cloned for use in this invention. The gene has
CC 97.8 percent identity when compared to the previously published sequences
CC FNBA and FNBB
CC
CC Sequence 134 AA:
SQ
Query Match 100.0%; Score 52; DB 2; Length 134;
Best Local Similarity 100.0%; Pred. No. 0.12;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 KHTETIEEDT 10
DB 80 KHTETIEEDT 89

```

RESULT 14
AAY29088
ID AAY29088 standard; protein; 134 AA.
XX AAY29088;
XX 28-SEP-1999 (first entry)
XX S. aureus fibronectin binding protein B (FnBB) binding domain.
XX Bovine herpes virus-2; BHV-2; cytokine; immune response; immunogen; IL;
XX interleukin; colony stimulating factor; CSF; interferon; IFN; TNF;
XX tumour necrosis factor; recombinant virus; vaccine; mucosal disease;
XX mastitis; breast cancer; stress-induced disease; binding domain; FNBB;
XX fibronectin binding protein.
XX Staphylococcus aureus.
XX OS
XX MO9916892-A1.
XX 08-APR-1999.
XX 29-SEP-1998; 98WO-GB002927.
XX PF
XX 29-SEP-1997; 97GB-00020633.
XX PR
XX (UYBR-) UNIV BRISTOL.
XX PA
XX Bradley AJ, Duffas WPB;
XX WPI: 1999-255101/21.
XX DR N-PSDB; AAX91505.
XX N-PSDB; AAX91505.
XX New bovine herpes virus-2 vectors.
XX PT
XX Example 2; Fig 8A-B; 130pp; English.

```

CC The invention provides bovine herpes virus-2 (BHV-2) based vectors that
CC comprise at least one cytokine-encoding DNA sequence. The expression of
CC cytokines in mammals can up-regulate immune responses to the immunogens.
CC The cytokine is selected from interleukins (IL), colony stimulating
CC factors (CSF), interferons (IFN) and tumour necrosis factors (TNF). The
CC BHV-2 based vector or recombinant virus can be used as vaccines. They can
CC be used for preventing or treating a mucosal disease in a subject, e.g.
CC ruminants, cattle, sheep, goats, dogs, cats, horses, or man, particularly
CC mastitis in cows or breast cancers in humans. They can also be used for
CC preventing or treating a stress-induced disease. The present sequence
CC represents the binding domain of a previously published S. aureus
CC fibronectin binding protein B (FNBB) sequence. The FNBB binding domain
CC gene sequence FNMBB, cloned for use in this invention has 97.8 percent
CC identity when compared to the previously published FNBA and FNBB gene
CC sequences
CC
CC Sequence 134 AA:
SQ
Query Match 100.0%; Score 52; DB 2; Length 134;
Best Local Similarity 100.0%; Pred. No. 0.12;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 KHTETIEEDT 10
DB 80 KHTETIEEDT 89

```

RESULT 15
AAY29087
ID AAY29087 standard; protein; 134 AA.
XX AAY29087;
XX 28-SEP-1999 (first entry)
XX S. aureus fibronectin binding protein A (FNBA) binding domain.
XX Bovine herpes virus-2; BHV-2; cytokine; immune response; immunogen; IL;
XX interleukin; colony stimulating factor; CSF; interferon; IFN; TNF;
XX tumour necrosis factor; recombinant virus; vaccine; mucosal disease;
XX mastitis; breast cancer; stress-induced disease; binding domain; FNBA;
XX fibronectin binding protein.
XX Staphylococcus aureus.
XX OS
XX MO9916892-A1.
XX 08-APR-1999.
XX 29-SEP-1998; 98WO-GB002927.
XX PF
XX 29-SEP-1997; 97GB-00020633.
XX PR
XX (UYBR-) UNIV BRISTOL.
XX PA
XX Bradley AJ, Duffas WPB;
XX WPI: 1999-255101/21.
XX DR N-PSDB; AAX91504.
XX N-PSDB; AAX91504.
XX New bovine herpes virus-2 vectors.
XX PT
XX Example 2; Fig 8A-B; 130pp; English.

The invention provides bovine herpes virus-2 (BHV-2) based vectors that comprise at least one cytokine-encoding DNA sequence. The expression of cytokines in mammals can up-regulate immune responses to the immunogens. The cytokine is selected from interleukins (IL), colony stimulating factors (CSF), interferons (IFN) and tumour necrosis factors (TNF). The BHV-2 based vector or recombinant virus can be used as vaccines. They can be used for preventing or treating a mucosal disease in a subject, e.g. ruminants, cattle, sheep, goats, dogs, cats, horses, or man, particularly mastitis in cows or breast cancers in humans. They can also be used for

CC preventing or treating a stress-induced disease. The present sequence
CC represents the binding domain of a previously published S. aureus
CC fibronectin binding protein A (FnBA) sequence. The FnB binding domain
CC gene sequence FNBA8, cloned for use in this invention has 97.8 percent
CC identity when compared to the previously published FnBA and FnB8 gene
CC sequences

XX
SQ Sequence 134 AA;

Query Match 100.0%; Score 52; DB 2; Length 134;

Best Local Similarity 100.0%; Pred. No. 0.12; Mismatches 0; Gaps 0;

Matches 10; Conservative 0; Indels 0; Gaps 0;

Qy 1 KHTFIREDT 10

Db 80 KHTFIREDT 89

Search completed: October 25, 2005, 21:29:10
Job time : 70.7126 secs

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OM protein - protein search, using sw model

Run on: October 22, 2005, 07:41:53 ; Search time 17.2989 Seconds
(without alignments)
43.153 Million cell updates/sec

Title: US-10-731-238-89
Perfect score: 52
Sequence: 1 KHTETIEDDT 10

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: /cgn2_6/ptodata/1/1aa/5A.COMB.pep:*
2: /cgn2_6/ptodata/1/1aa/5B.COMB.pep:*
3: /cgn2_6/ptodata/1/1aa/6A.COMB.pep:*
4: /cgn2_6/ptodata/1/1aa/6B.COMB.pep:*
5: /cgn2_6/ptodata/1/1aa/PTUS.COMB.pep:*
6: /cgn2_6/ptodata/1/1aa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	52	100.0	10	US-09-010-317-89	Sequence 89, Appl
2	52	100.0	37	US-08-234-622A-4	Sequence 4, Appl
3	52	100.0	38	US-08-729-767-5	Sequence 5, Appl
4	52	100.0	114	US-08-259-000-3	Sequence 3, Appl
5	52	100.0	130	US-08-459-135A-7	Sequence 7, Appl
6	52	100.0	130	US-08-459-135A-8	Sequence 8, Appl
7	52	100.0	130	US-08-495-559-7	Sequence 7, Appl
8	52	100.0	130	US-08-495-559-8	Sequence 8, Appl
9	52	100.0	139	US-08-856-253-8	Sequence 8, Appl
10	52	100.0	174	US-08-459-135A-10	Sequence 10, Appl
11	52	100.0	174	US-08-459-135A-13	Sequence 13, Appl
12	52	100.0	174	US-08-495-559-10	Sequence 10, Appl
13	52	100.0	174	US-08-495-559-13	Sequence 13, Appl
14	52	100.0	176	US-08-495-559-6	Sequence 6, Appl
15	52	100.0	178	US-08-459-135A-12	Sequence 12, Appl
16	52	100.0	178	US-08-495-559-12	Sequence 12, Appl
17	52	100.0	181	US-08-459-135A-6	Sequence 6, Appl
18	52	100.0	559	US-08-956-171E-5251	Sequence 5251, Ap
19	52	100.0	559	US-08-781-966A-5251	Sequence 5251, Ap
20	52	100.0	1027	US-08-956-171E-5254	Sequence 5254, Ap
21	52	100.0	1027	US-08-781-966A-5254	Sequence 5254, Ap
22	41	78.8	10	US-09-010-317-88	Sequence 88, Appl
23	39	75.0	10	US-09-010-317-90	Sequence 90, Appl
24	38	72.1	708	US-09-636-728-35	Sequence 35, Appl
25	37	71.2	1972	US-08-875-435B-4	Sequence 5719, A
26	36	69.2	89	US-09-270-767-57719	Sequence 5719, A
27	36	69.2	253	US-09-270-767-42427	Sequence 42427, A

28	36	69.2	267	3	US-08-935-263-10	Sequence 10, Appl
29	36	69.2	267	3	US-09-594-185-10	Sequence 10, Appl
30	36	69.2	267	4	US-10-033-078-10	Sequence 10, Appl
31	35	67.3	379	4	US-09-543-681A-7957	Sequence 7957, Ap
32	35	67.3	381	4	US-09-270-767-46589	Sequence 46589, A
33	35	67.3	569	4	US-09-602-787A-20	Sequence 20, Appl
34	35	67.3	1972	4	US-08-875-435B-3	Sequence 3, Appl
35	34	65.4	107	4	US-09-621-976-7619	Sequence 7619, Ap
36	34	65.4	119	4	US-09-513-999C-7908	Sequence 7908, Ap
37	34	65.4	157	4	US-09-270-767-32794	Sequence 32794, A
38	34	65.4	157	4	US-09-270-767-48011	Sequence 48011, A
39	34	65.4	273	4	US-09-107-433-4284	Sequence 4284, Ap
40	34	65.4	275	4	US-09-583-110-3006	Sequence 3006, Ap
41	34	65.4	395	4	US-09-270-767-45417	Sequence 45417, A
42	34	65.4	519	4	US-09-248-796A-18734	Sequence 18734, A
43	34	65.4	830	4	US-09-562-737-37	Sequence 37, Appl
44	33	63.5	114	4	US-09-107-532A-5154	Sequence 5154, Ap
45	33	63.5	127	4	US-09-107-532A-4663	Sequence 4663, Ap

ALIGNMENTS

RESULT 1
US-09-010-317-89
Sequence 89, Application US/09010317
Patent No. 6685943
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
APPLICANT: Patti, Joseph M.
APPLICANT: House-Pompeo, Karen L.
APPLICANT: Speciale, Pietro
APPLICANT: Joh, Danny
APPLICANT: McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
TITLE OF INVENTION: AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hidler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAMK.189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-5000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 89:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-09-010-317-89
Query Match 100.0%; Score 52; DB 4; Length 10;
Best local similarity 100.0%; Pred. No. 0.003;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KHTIIIEEDT 10
Db 1 KHTIIIEEDT 10

RESULT 2

US-08-234-622A-4
; Sequence 4, Application US/08234622A
; Patent No. 5440014
; GENERAL INFORMATION:
; APPLICANT: HOOK, Magnus
; APPLICANT: MCGAVIN, Martin
; APPLICANT: RAUCCI, Giuseppe
; TITLE OF INVENTION: A FIBRONECTIN BINDING PEPTIDE
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Doane, Swecker & Mathis
; STREET: P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/234,622A
; FILING DATE: 28-APR-1994
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: SE 9002617-0
; FILING DATE: 10-AUG-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/SE91/00534
; FILING DATE: 09-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Meuth, Donna M
; REGISTRATION NUMBER: 36,607
; REFERENCE/DOCKET NUMBER: 012885-044
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 37 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-234-622A-4

Query Match 100.0%; Score 52; DB 1; Length 37;
Best Local Similarity 100.0%; Pred. No. 0.012;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KHTIIIEEDT 10
Db 3 KHTIIIEEDT 12

RESULT 3

US-08-729-767-5
; Sequence 5, Application US/08729767
; Patent No. 5770702
; GENERAL INFORMATION:
; APPLICANT: HOOK, Magnus
; APPLICANT: LINDBERG, Martin Kjell
; APPLICANT: SIGNAS, Lars Christer
; APPLICANT: WADSTROM, Torkel Mikael

APPLICANT: FROMAN, Gunnar
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN AS WELL AS
; TITLE OF INVENTION: ITS PREPARATION
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Doane, Swecker & Mathis, L.L.P.
; STREET: P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/729,767
; FILING DATE: 07-OCT-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/259,000
; FILING DATE: 13-JUN-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/007,817
; FILING DATE: 22-JAN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/201,028
; FILING DATE: 01-JUN-1988
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: SE 8702272-9
; FILING DATE: 01-JUN-1987
; ATTORNEY/AGENT INFORMATION:
; NAME: McGowan, Malcolm K.
; REGISTRATION NUMBER: 39,300
; REFERENCE/DOCKET NUMBER: 012889-036
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 38 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-729-767-5

Query Match 100.0%; Score 52; DB 1; Length 38;
Best Local Similarity 100.0%; Pred. No. 0.013;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KHTIIIEEDT 10
Db 4 KHTIIIEEDT 13

RESULT 4

US-08-259-000-3
; Sequence 3, Application US/08259000
; Patent No. 5571514
; GENERAL INFORMATION:
; APPLICANT: HOOK, Magnus
; APPLICANT: LINDBERG, Martin Kjell
; APPLICANT: SIGNAS, Lars Christer
; APPLICANT: WADSTROM, Torkel Mikael
; APPLICANT: FROMAN, Gunnar
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN AS WELL AS
; TITLE OF INVENTION: ITS PREPARATION
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Doane, Swecker & Mathis
; STREET: P.O. Box 1404

CITY: Alexandria
STATE: Virginia
COUNTRY: United States
ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/259,000
FILING DATE: 13-JUN-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: SE 8702272-9
FILING DATE: 01-JUN-1987
ATTORNEY/AGENT INFORMATION:
NAME: Meuth, Donna M
REGISTRATION NUMBER: 36,607
REFERENCE/DOCKET NUMBER: 012885-062
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 114 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-259-000-3

Query Match 100.0%; Score 52; DB 1; Length 114;
Best Local Similarity 100.0%; Pred. No. 0.038;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KHTTEIIBEDT 10
|||
Db 80 KHTTEIIBEDT 89

RESULT 5
US-08-459-135A-7
Sequence 7, Application US/08459135A
Patent No. 5955078
GENERAL INFORMATION:
APPLICANT: BURHAM, Martin Karl Russel
APPLICANT: CHOPRA, Ian
APPLICANT: CRITCHLEY, Ian Alfred
APPLICANT: KNOWLES, David Justin Charles
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN: MONOCLONAL ANTIBODY AND THEIR US
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
STATE: PA
COUNTRY: U.S.A.
ZIP: 19406-0939
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: Fastseq, Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/459,135A
FILING DATE: 02-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB/94/00215
FILING DATE: 04-Feb-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:

NAME: Gimm, Edward R
REGISTRATION NUMBER: 38,891
REFERENCE/DOCKET NUMBER: P30591C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-4478
TELEFAX: 610-270-5090
TELEX:
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 130 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-459-135A-7

Query Match 100.0%; Score 52; DB 2; Length 130;
Best Local Similarity 100.0%; Pred. No. 0.043;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KHTTEIIBEDT 10
|||
Db 80 KHTTEIIBEDT 89

RESULT 6
US-08-459-135A-8
Sequence 8, Application US/08459135A
Patent No. 5955078
GENERAL INFORMATION:
APPLICANT: BURHAM, Martin Karl Russel
APPLICANT: CHOPRA, Ian
APPLICANT: CRITCHLEY, Ian Alfred
APPLICANT: KNOWLES, David Justin Charles
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN: MONOCLONAL ANTIBODY AND THEIR US
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
STATE: PA
COUNTRY: U.S.A.
ZIP: 19406-0939
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: Fastseq, Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/459,135A
FILING DATE: 02-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB/94/00215
FILING DATE: 04-Feb-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Gimm, Edward R
REGISTRATION NUMBER: 38,891
REFERENCE/DOCKET NUMBER: P30591C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-4478
TELEFAX: 610-270-5090
TELEX:
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 130 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-459-135A-8

Query Match 100.0%; Score 52; DB 2; Length 130;
Best Local Similarity 100.0%; Pred. No. 0.043;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KHTIIEEDT 10
Db 80 KHTIIEEDT 89

RESULT 7

US-08-495-559-7
; Sequence 7, Application US/08495559A
; Patent No. 6054572
; GENERAL INFORMATION:
; APPLICANT: BURHAM, Martin Karl Russel
; APPLICANT: CHOPRA, Ian
; APPLICANT: CRITCHLEY, Ian Alfred
; APPLICANT: KNOWLES, David Justin Charles
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN: MONOCLONAL
; FILE REFERENCE: P30591
; CURRENT APPLICATION NUMBER: US/08/495,559A
; EARLIER FILING DATE: 1995-08-03
; EARLIER APPLICATION NUMBER: GB 9302289.5
; EARLIER FILING DATE: 1993-02-05
; EARLIER APPLICATION NUMBER: GB 9321592.9
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 7
; LENGTH: 130
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-08-495-559-7

Query Match 100.0%; Score 52; DB 3; Length 130;
Best Local Similarity 100.0%; Pred. No. 0.043;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KHTIIEEDT 10
Db 80 KHTIIEEDT 89

RESULT 8

US-08-495-559-8
; Sequence 8, Application US/08495559A
; Patent No. 6054572
; GENERAL INFORMATION:
; APPLICANT: BURHAM, Martin Karl Russel
; APPLICANT: CHOPRA, Ian
; APPLICANT: CRITCHLEY, Ian Alfred
; APPLICANT: KNOWLES, David Justin Charles
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN: MONOCLONAL
; TITLE OF INVENTION: ANTIBODY AND THEIR USE IN PREVENTING BACTERIAL ADHESION
; FILE REFERENCE: P30591
; CURRENT APPLICATION NUMBER: US/08/495,559A
; EARLIER FILING DATE: 1995-08-03
; EARLIER APPLICATION NUMBER: GB 9302289.5
; EARLIER FILING DATE: 1993-02-05
; EARLIER APPLICATION NUMBER: GB 9321592.9
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 8
; LENGTH: 130
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-08-495-559-8

Query Match 100.0%; Score 52; DB 3; Length 130;
Best Local Similarity 100.0%; Pred. No. 0.043;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KHTIIEEDT 10

Db 80 KHTIIEEDT 89

RESULT 9

US-08-856-253-8
; Sequence 8, Application US/08856253
; Patent No. 6288214
; GENERAL INFORMATION:
; APPLICANT: Hook, Magnus
; APPLICANT: Partl, Joseph M.
; APPLICANT: House-Pompeo, Karen
; APPLICANT: Symanam, Narayana
; APPLICANT: Symesky, Jindrich
; TITLE OF INVENTION: COLLAGEN BINDING PROTEIN COMPOSITIONS
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: U.S.
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/856,253
; FILING DATE: Concurrently Herewith
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/017,678
; FILING DATE: 16-MAY-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Kitchell, Barbara S.
; REGISTRATION NUMBER: 33,928
; REFERENCE/DOCKET NUMBER: TANK:193
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (512) 418-3000
; TELEFAX: (512) 474-7577
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 139 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
US-08-856-253-8

Query Match 100.0%; Score 52; DB 3; Length 139;
Best Local Similarity 100.0%; Pred. No. 0.046;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KHTIIEEDT 10
Db 94 KHTIIEEDT 103

RESULT 10

US-08-459-135A-10
; Sequence 10, Application US/08459135A
; Patent No. 5955078
; GENERAL INFORMATION:
; APPLICANT: BURHAM, Martin Karl Russel
; APPLICANT: CHOPRA, Ian
; APPLICANT: CRITCHLEY, Ian Alfred
; APPLICANT: KNOWLES, David Justin Charles
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN: MONOCLONAL ANTIBODY AND THEIR USE
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corporation

STREET: 709 Swedeland Road
CITY: King of Prussia
STATE: PA
COUNTRY: U.S.A.
ZIP: 19406-0939
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: Fastseq, Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/459,135A
FILING DATE: 02-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB/94/00215
FILING DATE: 04-Feb-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Gimm, Edward R
REGISTRATION NUMBER: 38,891
REFERENCE/DOCKET NUMBER: P30591C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-4478
TELEFAX: 610-270-5090
TELEX:
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 174 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: Protein
US-08-459-135A-10

Query Match 100.0%; Score 52; DB 2; Length 174;
Best Local Similarity 100.0%; Pred. No. 0.057;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 KHTETIEEDT 10
|||||
DB 80 KHTETIEEDT 89

RESULT 11
US-08-459-135A-13
Sequence 13, Application US/08459135A
Patent No. 5955078
GENERAL INFORMATION:
APPLICANT: BURHAM, Martin Karl Russel
APPLICANT: CHOPRA, Ian
APPLICANT: CRITCHLEY, Ian Alfred
APPLICANT: KNOWLES, David Justin Charles
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN: MONOCLONAL ANTIBODY AND THEIR USE
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESSES:
ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
STATE: PA
COUNTRY: U.S.A.
ZIP: 19406-0939
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: Fastseq, Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/459,135A
FILING DATE: 02-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB/94/00215
FILING DATE: 04-Feb-1994

CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Gimm, Edward R
REGISTRATION NUMBER: 38,891
REFERENCE/DOCKET NUMBER: P30591C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-4478
TELEFAX: 610-270-5090
TELEX:
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 174 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-459-135A-13

Query Match 100.0%; Score 52; DB 2; Length 174;
Best Local Similarity 100.0%; Pred. No. 0.057;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 KHTETIEEDT 10
|||||
DB 80 KHTETIEEDT 89

RESULT 12
US-08-495-559-10
Sequence 10, Application US/08495559A
Patent No. 6054572
GENERAL INFORMATION:
APPLICANT: BURHAM, Martin Karl Russel
APPLICANT: CHOPRA, Ian
APPLICANT: CRITCHLEY, Ian Alfred
APPLICANT: KNOWLES, David Justin Charles
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN: MONOCLONAL
TITLE OF INVENTION: ANTIBODY AND THEIR USE IN PREVENTING BACTERIAL ADHESION
FILE REFERENCE: P30591
CURRENT APPLICATION NUMBER: US/08/495,559A
CURRENT FILING DATE: 1995-08-03
EARLIER APPLICATION NUMBER: GB 9302289.5
EARLIER FILING DATE: 1993-02-05
EARLIER APPLICATION NUMBER: GB 9321592.9
EARLIER FILING DATE: 1993-10-20
NUMBER OF SEQ ID NOS: 13
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 10
LENGTH: 174
TYPE: PRT
ORGANISM: Staphylococcus aureus
US-08-495-559-10

Query Match 100.0%; Score 52; DB 3; Length 174;
Best Local Similarity 100.0%; Pred. No. 0.057;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 KHTETIEEDT 10
|||||
DB 80 KHTETIEEDT 89

RESULT 13
US-08-495-559-13
Sequence 13, Application US/08495559A
Patent No. 6054572
GENERAL INFORMATION:
APPLICANT: BURHAM, Martin Karl Russel
APPLICANT: CHOPRA, Ian
APPLICANT: CRITCHLEY, Ian Alfred
APPLICANT: KNOWLES, David Justin Charles
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN: MONOCLONAL
TITLE OF INVENTION: ANTIBODY AND THEIR USE IN PREVENTING BACTERIAL ADHESION

```
FILE REFERENCE: P30591
CURRENT APPLICATION NUMBER: US/08/495,559A
CURRENT FILING DATE: 1995-08-03
EARLIER APPLICATION NUMBER: GB 9302289.5
EARLIER FILING DATE: 1993-02-05
EARLIER APPLICATION NUMBER: GB 9321592.9
EARLIER FILING DATE: 1993-10-20
NUMBER OF SEQ ID NOS: 13
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 13
LENGTH: 174
TYPE: PRT
ORGANISM: Staphylococcus aureus
US-08-495-559-13

Query Match      100.0%; Score 52; DB 3; Length 174;
Best Local Similarity 100.0%; Pred. No. 0.057;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KHTETIEEDT 10
DB      80 KHTETIEEDT 89

RESULT 14
US-08-495-559-6
Sequence 6, Application US/08495559A
GENERAL INFORMATION:
APPLICANT: BURHAM, Martin Karl Russel
APPLICANT: CHOPRA, Ian
APPLICANT: CRITCHLEY, Ian Alfred
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN: MONOCLONAL
TITLE OF INVENTION: ANTIBODY AND THEIR USE IN PREVENTING BACTERIAL ADHESION
FILE REFERENCE: P30591
CURRENT APPLICATION NUMBER: US/08/495,559A
CURRENT FILING DATE: 1995-08-03
EARLIER APPLICATION NUMBER: GB 9302289.5
EARLIER FILING DATE: 1993-02-05
EARLIER APPLICATION NUMBER: GB 9321592.9
EARLIER FILING DATE: 1993-10-20
NUMBER OF SEQ ID NOS: 13
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 6
LENGTH: 176
TYPE: PRT
ORGANISM: Staphylococcus aureus
US-08-495-559-6

Query Match      100.0%; Score 52; DB 3; Length 176;
Best Local Similarity 100.0%; Pred. No. 0.058;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KHTETIEEDT 10
DB      80 KHTETIEEDT 89

RESULT 15
US-08-459-135A-12
Sequence 12, Application US/08459135A
Patent No. 5955078
GENERAL INFORMATION:
APPLICANT: BURHAM, Martin Karl Russel
APPLICANT: CHOPRA, Ian
APPLICANT: CRITCHLEY, Ian Alfred
TITLE OF INVENTION: KNOWLES, David Justin Charles
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN: MONOCLONAL ANTIBODY AND THEIR USE
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESSES:
ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
```

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CITY: King of Prussia
STATE: PA
COUNTRY: U.S.A.
ZIP: 19406-0939
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: Fastseq, Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/459,135A
FILING DATE: 02-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB/94/00215
FILING DATE: 04-Feb-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Gimmil, Edward R
REGISTRATION NUMBER: 38,891
REFERENCE/DOCKET NUMBER: P30591C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-4478
TELEFAX: 610-270-5090
TELEX:
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 178 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: Protein
US-08-459-135A-12

Query Match      100.0%; Score 52; DB 2; Length 178;
Best Local Similarity 100.0%; Pred. No. 0.059;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KHTETIEEDT 10
DB      80 KHTETIEEDT 89

Search completed: October 22, 2005, 09:35:43
Job time: 18.2989 secs
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 22, 2005, 12:39:57 ; Search time 56.1494 Seconds
(without alignments)
74.354 Million cell updates/sec

Title: US-10-731-238-89
Perfect score: 52
Sequence: 1 KHTRIEDT 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1862951 seqs, 417491010 residues

Total number of hits satisfying chosen parameters: 1862951

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

Published Applications AA:*

- 1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
- 2: /cgn2_6/ptodata/2/pubpaa/PTCT_NEW_PUB.pep:*
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- 12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
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- 14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
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- 16: /cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pep:*
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- 18: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
- 19: /cgn2_6/ptodata/2/pubpaa/US11A_PUBCOMB.pep:*
- 20: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep:*
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- 22: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	52	100.0	10	US-10-731-238-89	Sequence 89, App1
2	52	100.0	37	US-11-066-697-1134	Sequence 1134, App1
3	52	100.0	139	US-09-813-820-8	Sequence 8, App1
4	52	100.0	388	US-08-901-062-1	Sequence 1, App1
5	52	100.0	559	US-08-781-986A-5251	Sequence 5251, App
6	52	100.0	559	US-10-329-624-5251	Sequence 5251, App
7	52	100.0	940	US-10-470-048B-424	Sequence 424, App
8	52	100.0	948	US-10-470-048B-69	Sequence 69, App1
9	52	100.0	1018	US-09-815-242-5797	Sequence 5797, App
10	52	100.0	1018	US-09-815-242-12838	Sequence 12838, App
11	52	100.0	1018	US-10-470-048B-68	Sequence 68, App1

12	52	100.0	1027	8	US-08-781-986A-5254	Sequence 5254, App
13	52	100.0	1027	15 <td>US-10-329-624-5254</td> <td>Sequence 5254, App</td>	US-10-329-624-5254	Sequence 5254, App
14	47	90.4	961	15 <td>US-10-282-122A-43778</td> <td>Sequence 43778, A</td>	US-10-282-122A-43778	Sequence 43778, A
15	47	90.4	978	9 <td>US-09-815-242-5456</td> <td>Sequence 5456, App</td>	US-09-815-242-5456	Sequence 5456, App
16	47	90.4	1001	9 <td>US-09-815-242-12686</td> <td>Sequence 12686, A</td>	US-09-815-242-12686	Sequence 12686, A
17	47	90.4	1038	15 <td>US-10-282-122A-43827</td> <td>Sequence 43827, A</td>	US-10-282-122A-43827	Sequence 43827, A
18	41	78.8	10	18 <td>US-10-731-238-89</td> <td>Sequence 88, App1</td>	US-10-731-238-89	Sequence 88, App1
19	39	75.0	10	18 <td>US-10-731-238-90</td> <td>Sequence 90, App1</td>	US-10-731-238-90	Sequence 90, App1
20	37	71.2	314	17 <td>US-10-774-355A-2428</td> <td>Sequence 2428, App</td>	US-10-774-355A-2428	Sequence 2428, App
21	37	71.2	842	16 <td>US-10-425-115-304416</td> <td>Sequence 304416, A</td>	US-10-425-115-304416	Sequence 304416, A
22	36	69.2	59	16 <td>US-10-425-115-201510</td> <td>Sequence 201510, A</td>	US-10-425-115-201510	Sequence 201510, A
23	36	69.2	267	13 <td>US-10-033-078-10</td> <td>Sequence 10, App1</td>	US-10-033-078-10	Sequence 10, App1
24	36	69.2	267	16 <td>US-10-763-933-110</td> <td>Sequence 10, App1</td>	US-10-763-933-110	Sequence 10, App1
25	36	69.2	392	16 <td>US-10-437-963-163286</td> <td>Sequence 163286, A</td>	US-10-437-963-163286	Sequence 163286, A
26	36	69.2	514	16 <td>US-10-437-963-163284</td> <td>Sequence 163284, A</td>	US-10-437-963-163284	Sequence 163284, A
27	36	69.2	1012	20 <td>US-11-097-143-27570</td> <td>Sequence 27570, A</td>	US-11-097-143-27570	Sequence 27570, A
28	35	67.3	336	15 <td>US-10-282-122A-77325</td> <td>Sequence 77325, A</td>	US-10-282-122A-77325	Sequence 77325, A
29	35	67.3	528	20 <td>US-11-097-143-41799</td> <td>Sequence 41799, A</td>	US-11-097-143-41799	Sequence 41799, A
30	35	67.3	569	9 <td>US-09-738-626-6179</td> <td>Sequence 6179, App</td>	US-09-738-626-6179	Sequence 6179, App
31	35	67.3	569	15 <td>US-10-627-476-20</td> <td>Sequence 20, App1</td>	US-10-627-476-20	Sequence 20, App1
32	35	67.3	855	15 <td>US-10-369-493-2692</td> <td>Sequence 2692, App</td>	US-10-369-493-2692	Sequence 2692, App
33	35	67.3	962	9 <td>US-09-738-626-4322</td> <td>Sequence 4322, App</td>	US-09-738-626-4322	Sequence 4322, App
34	35	67.3	962	17 <td>US-10-494-541-96</td> <td>Sequence 96, App1</td>	US-10-494-541-96	Sequence 96, App1
35	34	65.4	42	9 <td>US-09-864-761-45543</td> <td>Sequence 45543, A</td>	US-09-864-761-45543	Sequence 45543, A
36	34	65.4	118	16 <td>US-10-425-115-185256</td> <td>Sequence 185256, A</td>	US-10-425-115-185256	Sequence 185256, A
37	34	65.4	135	9 <td>US-08-764-888-247</td> <td>Sequence 247, App</td>	US-08-764-888-247	Sequence 247, App
38	34	65.4	135	9 <td>US-09-764-891-3248</td> <td>Sequence 3248, App</td>	US-09-764-891-3248	Sequence 3248, App
39	34	65.4	135	15 <td>US-10-264-049-2441</td> <td>Sequence 2441, App</td>	US-10-264-049-2441	Sequence 2441, App
40	34	65.4	160	10 <td>US-09-847-208-153</td> <td>Sequence 153, App</td>	US-09-847-208-153	Sequence 153, App
41	34	65.4	165	16 <td>US-10-842-740-15</td> <td>Sequence 15, App1</td>	US-10-842-740-15	Sequence 15, App1
42	34	65.4	176	16 <td>US-10-437-963-201469</td> <td>Sequence 201469, A</td>	US-10-437-963-201469	Sequence 201469, A
43	34	65.4	182	17 <td>US-10-899-557-50</td> <td>Sequence 50, App1</td>	US-10-899-557-50	Sequence 50, App1
44	34	65.4	191	15 <td>US-10-424-599-285285</td> <td>Sequence 285285, A</td>	US-10-424-599-285285	Sequence 285285, A
45	34	65.4	197	15 <td>US-10-424-599-285284</td> <td>Sequence 285284, A</td>	US-10-424-599-285284	Sequence 285284, A

ALIGNMENTS

RESULT 1
US-10-731-238-89
Sequence 89, Application US/10731238
Publication No. US20050123552A1
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
Patli, Joseph M.
House-Pompeo, Karen L.
Speziale, Pietro
John, Danny
McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/731,238
FILING DATE: 10-Dec-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/010,117
FILING DATE: 21-Jan-1998
APPLICATION NUMBER: US 60/036,139

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; FILING DATE: 21-JAN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Hibler, David W.
; REGISTRATION NUMBER: 41,071
; REFERENCE/DOCKET NUMBER: TANK:189
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 512-418-3000
; TELEFAX: 512-474-7577
; INFORMATION FOR SEQ ID NO: 89:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 89:
US-10-731-238-89

Query Match      100.0%; Score 52; DB 18; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0082;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KHTETLEEDT 10
DB 1 KHTETLEEDT 10

RESULT 2
US-11-066-697-1134
; Sequence 1134, Application US/11066697
; Publication No. US20050187159A1
; GENERAL INFORMATION:
; APPLICANT: Bridon, Dominique P.
; APPLICANT: Ezrin, Alan M.
; APPLICANT: Milner, Peter G.
; APPLICANT: Holmes, Darren L.
; APPLICANT: Thibaudau, Karen
; TITLE OF INVENTION: PROTECTION OF ENDOGENOUS THERAPEUTIC PEPTIDES FROM
; TITLE OF INVENTION: PEPTIDASE ACTIVITY THROUGH CONJUGATION TO BLOOD
; FILE REFERENCE: 500863002301
; CURRENT APPLICATION NUMBER: US/11/066,697
; CURRENT FILING DATE: 2005-02-25
; PRIOR APPLICATION NUMBER: 09/657,276
; PRIOR FILING DATE: 2000-09-07
; PRIOR APPLICATION NUMBER: 60/153,406
; PRIOR FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: 60/159,783
; PRIOR FILING DATE: 1999-10-15
; NUMBER OF SEQ ID NOS: 1617
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1134
; LENGTH: 37
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptide
US-11-066-697-1134

Query Match      100.0%; Score 52; DB 20; Length 37;
Best Local Similarity 100.0%; Pred. No. 0.034;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KHTETLEEDT 10
DB 3 KHTETLEEDT 12

RESULT 3
US-09-813-820-8
; Sequence 8, Application US/09813820
; Patent No. US20020102262A1
; GENERAL INFORMATION:
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; APPLICANT: Hook, Magnus
; Patti, Joseph M.
; House-Pompeo, Karen
; Sthanam, Narayana
; Symersky, Jindrich
; TITLE OF INVENTION: COLLAGEN BINDING PROTEIN COMPOSITIONS
; AND METHODS OF USE
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: U.S.
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/813,820
; FILING DATE: 22-Mar-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/856,253
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Kitchell, Barbara S.
; REGISTRATION NUMBER: 33,928
; REFERENCE/DOCKET NUMBER: TANK:193
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (512) 418-3000
; TELEFAX: (512) 474-7577
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 139 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-09-813-820-8

Query Match      100.0%; Score 52; DB 9; Length 139;
Best Local Similarity 100.0%; Pred. No. 0.15;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KHTETLEEDT 10
DB 94 KHTETLEEDT 103

RESULT 4
US-08-901-062-1
; Sequence 1, Application US/08901062
; Publication No. US20020025324A1
; GENERAL INFORMATION:
; APPLICANT: SEALS, JONATHAN R.
; TITLE OF INVENTION: RECOMBINANT BIVALENT BACTERIAL VACCINE
; TITLE OF INVENTION: FOR THE PREVENTION OF MASTITIS
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HALB AND DORR LLP
; STREET: 60 State Street
; CITY: Boston
; STATE: MA
; COUNTRY: United States Of America
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/901.062
FILING DATE: 25-JUL-1997
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Baker, Hollie L.
REGISTRATION NUMBER: 31,321
REFERENCE/DOCKET NUMBER: 106941.153
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 526-6000
TELEFAX: (617) 526-5000
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 388 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-901-062-1

Query Match 100.0%; Score 52; DB 8; Length 388;
Best Local Similarity 100.0%; Pred. No. 0.45;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KHTTEIIBDT 10
DB 343 KHTTEIIBDT 352

RESULT 5
US-08-781-986A-5251
Sequence 5251, Application US/08781986A
Publication No. US20030054436A1
GENERAL INFORMATION:
APPLICANT: Charles Kunesh
TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
NUMBER OF SEQUENCES: 5255
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COUNTRY: USA
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/781,986A
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Benson, Bob
REGISTRATION NUMBER: 30,446
REFERENCE/DOCKET NUMBER: PB248PP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 5251:
SEQUENCE CHARACTERISTICS:
LENGTH: 559 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-781-986A-5251

Query Match 100.0%; Score 52; DB 8; Length 559;
Best Local Similarity 100.0%; Pred. No. 0.68;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KHTTEIIBDT 10
DB 379 KHTTEIIBDT 388

RESULT 6
US-10-329-624-5251
Sequence 5251, Application US/10329624
Publication No. US20040043037A1
GENERAL INFORMATION:
APPLICANT: Charles Kunesh
Gill H. Choi
Patrick S. Dillon
Craig A. Rosen
Steven C. Barash
Michael R. Fannon
TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
NUMBER OF SEQUENCES: 5256
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COUNTRY: USA
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/329,624
FILING DATE: 27-Dec-2002
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/956,171
FILING DATE: October 20, 1997
APPLICATION NUMBER: 60/009,861
FILING DATE: January 5, 1996
APPLICATION NUMBER: 08/781,986
FILING DATE: January 3, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Mark J. Hyman
REGISTRATION NUMBER: 46,789
REFERENCE/DOCKET NUMBER: PB248P1D1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (240) 314-1224
TELEFAX: (301) 309-8439
INFORMATION FOR SEQ ID NO: 5251:
SEQUENCE CHARACTERISTICS:
LENGTH: 559 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 5251:
US-10-329-624-5251

Query Match 100.0%; Score 52; DB 15; Length 559;
Best Local Similarity 100.0%; Pred. No. 0.68;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KHTTEIIBDT 10
DB 379 KHTTEIIBDT 388

RESULT 7
US-10-470-048B-424

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; Sequence 424, Application US/10470048B
; Publication No. US20050037444A1
; GENERAL INFORMATION:
; APPLICANT: MEINKE ET AL.
; TITLE OF INVENTION: A METHOD FOR IDENTIFICATION, ISOLATION AND PRODUCTION OF
; FILE REFERENCE: SONN:03505
; CURRENT APPLICATION NUMBER: US/10/470,048B
; CURRENT FILING DATE: 2003-07-25
; NUMBER OF SEQ ID NOS: 603
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 424
; LENGTH: 940
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-10-470-048B-424

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Query Match          100.0%; Score 52; DB 17; Length 940;
Best Local Similarity 100.0%; Pred. No. 1.2;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 KHTEIIEDT 10
Db      760 KHTEIIEDT 769

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RESULT 8
US-10-470-048B-69
; Sequence 69, Application US/10470048B
; Publication No. US20050037444A1
; GENERAL INFORMATION:
; APPLICANT: MEINKE ET AL.
; TITLE OF INVENTION: A METHOD FOR IDENTIFICATION, ISOLATION AND PRODUCTION OF
; FILE REFERENCE: SONN:03505
; CURRENT APPLICATION NUMBER: US/10/470,048B
; CURRENT FILING DATE: 2003-07-25
; NUMBER OF SEQ ID NOS: 603
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 69
; LENGTH: 948
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-10-470-048B-69

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Query Match          100.0%; Score 52; DB 17; Length 948;
Best Local Similarity 100.0%; Pred. No. 1.2;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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```

Qy      1 KHTEIIEDT 10
Db      768 KHTEIIEDT 777

```

```

RESULT 9
US-09-815-242-5797
; Sequence 5797, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haeselbeck, Robert
; APPLICANT: Ohlsen, Kari L.
; APPLICANT: Zyckind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; FILE REFERENCE: ELITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078

```

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; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 1410
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5797
; LENGTH: 1018
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-09-815-242-5797

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```

Query Match          100.0%; Score 52; DB 9; Length 1018;
Best Local Similarity 100.0%; Pred. No. 1.3;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      1 KHTEIIEDT 10
Db      824 KHTEIIEDT 833

```

```

RESULT 10
US-09-815-242-12838
; Sequence 12838, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haeselbeck, Robert
; APPLICANT: Ohlsen, Kari L.
; APPLICANT: Zyckind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; FILE REFERENCE: ELITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 1410
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12838
; LENGTH: 1018
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-09-815-242-12838

```

OY 1 KHTLEIEDT 10
|||
Db 824 KHTLEIEDT 833

RESULT 11
US-10-470-048B-68
; Sequence 68, Application US/10470048B
; Publication No. US20050037444A1
; GENERAL INFORMATION:
; APPLICANT: MEINKE ET AL.
; TITLE OF INVENTION: A METHOD FOR IDENTIFICATION, ISOLATION AND PRODUCTION OF
; FILE REFERENCE: SOMN-03505
; CURRENT FILING DATE: 2003-07-25
; NUMBER OF SEQ ID NOS: 603
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 68
; LENGTH: 1018
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-10-470-048B-68

Query Match 100.0%; Score 52; DB 17; Length 1018;
Best Local Similarity 100.0%; Pred. No. 1.3;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 KHTLEIEDT 10
|||
Db 824 KHTLEIEDT 833

RESULT 12
US-08-781-986A-5254
; Sequence 5254, Application US/08781986A
; Publication No. US20030054436A1
; GENERAL INFORMATION:
; APPLICANT: Charles Kunach
; TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
; NUMBER OF SEQUENCES: 5255
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4mb storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/781,986A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; ATTORNEY/AGENT INFORMATION:
; NAME: Benson, Bob
; REGISTRATION NUMBER: 30,446
; REFERENCE/DOCKET NUMBER: PB248PP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 5254:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1027 amino acids
; TYPE: amino acid
; STRANDEDNESS: single

TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-781-986A-5254

Query Match 100.0%; Score 52; DB 8; Length 1027;
Best Local Similarity 100.0%; Pred. No. 1.3;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 KHTLEIEDT 10
|||
Db 833 KHTLEIEDT 842

RESULT 13
US-10-329-624-5254
; Sequence 5254, Application US/10329624
; Publication No. US20040043037A1
; GENERAL INFORMATION:
; APPLICANT: Charles Kunach
; Gil H. Choi
; Patrick S. Dillon
; Craig A. Rosen
; Steven C. Barash
; Michael R. Fannon

TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
NUMBER OF SEQUENCES: 5256
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COUNTRY: USA
ZIP: 20850

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/329,624
FILING DATE: 27-Dec-2002
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/956,171
FILING DATE: October 20, 1997
APPLICATION NUMBER: 60/009,861
FILING DATE: January 5, 1996
APPLICATION NUMBER: 08/781,986
FILING DATE: January 3, 1997

ATTORNEY/AGENT INFORMATION:
NAME: Mark J. Hyman
REGISTRATION NUMBER: 46,789
REFERENCE/DOCKET NUMBER: PB248P1D1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (240) 314-1224
TELEFAX: (301) 309-8439
INFORMATION FOR SEQ ID NO: 5254:
SEQUENCE CHARACTERISTICS:
LENGTH: 1027 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 5254:
US-10-329-624-5254

Query Match 100.0%; Score 52; DB 15; Length 1027;
Best Local Similarity 100.0%; Pred. No. 1.3;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 KHTLEIEDT 10
|||
Db 833 KHTLEIEDT 842


```
RESULT 14
US-10-282-122A-43778
; Sequence 43778, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zykkind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PAM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 43778
; LENGTH: 961
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-10-282-122A-43778

Query Match          90.4%; Score 47; DB 15; Length 961;
Best Local Similarity 90.0%; Pred. No. 9.9;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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QY      1 KHTETIEEDT 10
Db      771 KHNTEIEEDT 780

RESULT 15
US-09-815-242-5456
; Sequence 5456, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari L.
; APPLICANT: Zykkind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
```

```
; TITLE OF INVENTION: Identification of Essential Genes in
; FILE REFERENCE: ELITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5456
; LENGTH: 978
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-09-815-242-5456

Query Match          90.4%; Score 47; DB 9; Length 978;
Best Local Similarity 90.0%; Pred. No. 10;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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```
QY      1 KHTETIEEDT 10
Db      802 KHNTEIEEDT 811

Search completed: October 22, 2005, 12:56:24
Job time : 57.1494 secs
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 22, 2005, 08:04:46 ; Search time 11.6092 Seconds
(without alignments)
82.880 Million cell updates/sec

Title: US-10-731-238-89
Perfect score: 52
Sequence: 1 KHTRIEDDT 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	52	100.0	940	2	S19702 fibronectin-binding
2	52	100.0	1018	2	A32192 fibronectin-binding
3	47	90.4	961	2	G90053 hypothetical prote
4	47	90.4	1038	2	H90053 hypothetical prote
5	39	75.0	1670	2	T06754 DNA-directed RNA p
6	37	71.2	210	2	G83929 hypothetical prote
7	37	71.2	788	2	H96545 hypothetical prote
8	37	71.2	1143	2	B84431 probable receptor
9	37	71.2	1572	1	A41604 myosin heavy chain
10	36	69.2	55	2	T03337 gene 630 protein -
11	36	69.2	700	2	S57020 clathrin-associate
12	35	67.3	217	2	F70817 conserved ABC trans
13	35	67.3	240	1	A70031 methionine aminope
14	35	67.3	299	2	C69039 transcription regu
15	35	67.3	336	2	A82165 protein W109.4 (l
16	35	67.3	403	2	E88021 smooth muscle myos
17	35	67.3	855	2	S77252 smooth muscle myos
18	35	67.3	1938	2	JC5421 smooth muscle myos
19	35	67.3	1972	2	JC5420 smooth muscle myos
20	35	65.4	215	2	S28062 homeotic protein g
21	34	65.4	216	2	B42756 hypothetical prote
22	34	65.4	243	2	T12485 hypothetical prote
23	34	65.4	251	2	E96637 exodeoxyribonuclea
24	34	65.4	275	2	E95215 exodeoxyribonuclea
25	34	65.4	275	2	A32301 exodeoxyribonuclea
26	34	65.4	275	2	B98079 exodeoxyribonuclea
27	34	65.4	364	2	T48628 hypothetical prote
28	34	65.4	411	2	UC1482 TYA protein - yeas
29	34	65.4	413	2	S52610 TYA protein - yeas

30	34	65.4	414	2	S31261
31	34	65.4	466	2	T22141
32	34	65.4	1086	1	B46335
33	33	63.5	144	2	H64659
34	33	63.5	147	2	H87649
35	33	63.5	169	2	A28146
36	33	63.5	174	2	B81145
37	33	63.5	192	2	A97014
38	33	63.5	224	2	AC3627
39	33	63.5	279	2	F87577
40	33	63.5	313	2	T29195
41	33	63.5	335	1	DELBC
42	33	63.5	347	2	T19685
43	33	63.5	349	2	F84980
44	33	63.5	373	2	G70355
45	33	63.5	733	2	G84668

ALIGNMENTS

RESULT 1

S19702 fibronectin-binding protein B - Staphylococcus aureus
C:Species: Staphylococcus aureus
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
C:Accession: S19702
R:Jonsen, K.; Signaes, C.; Mueller, H.P.; Lindberg, M.
Eur. J. Biochem. 202, 1041-1048, 1991
A:Title: Two different genes encode fibronectin binding proteins in Staphylococcus aure
A:Reference number: S19702; MUID:92111475; PMID:1837266
A:Accession: S19702
A:Status: Preliminary
A:Molecule type: DNA
A:Residues: 1-940 <JOB>
A:Cross-references: UNIPROT:Q53682; EMBL:X62922; NID:g49040; PIDN:CAA44726.1; PID:G5815
C:Keywords: fibronectin binding

Query Match 100.0%; Score 52; DB 2; Length 940;
Best Local Similarity 100.0%; Pred. No. 0.09;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KHTRIEDDT 10
DB 760 KHTRIEDDT 769

RESULT 2

A32192 fibronectin-binding protein - Staphylococcus aureus
C:Species: Staphylococcus aureus
C:Date: 31-Jul-1989 #sequence_revision 31-Jul-1989 #text_change 16-Feb-1997
A:Accession: A32192
R:Signaes, C.; Raucsi, G.; Jonsen, K.; Lindgren, P.E.; Anantharamiah, G.M.; Hoeoek,
Proc. Natl. Acad. Sci. U.S.A. 86, 699-703, 1989
A:Title: Nucleotide sequence of the gene for a fibronectin-binding protein from Staphyl
A:Reference number: A32192; MUID:89098998; PMID:2521391
A:Accession: A32192
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1018 <SIG>
A:Cross-references: GB:J04151
C:Keywords: fibronectin binding

Query Match 100.0%; Score 52; DB 2; Length 1018;
Best Local Similarity 100.0%; Pred. No. 0.098;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KHTRIEDDT 10
DB 824 KHTRIEDDT 833

Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 2 HTEIIEEDT 10
|||::||
452 HTEVIQADT 460

Db 452 HTEVIQADT 460

RESULT 8

B84431

probable receptor protein kinase [imported] - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)

C>Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004

C:Accession: B84431

R:Lin, X.; Kaul, S.; Rounsailey, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;

M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Vanaken, S.E.; Umayam, L.; Tallon, L.

ense, D.; Nieman, W.C.; White, O.; Elsen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.

Nature 402, 761-768, 1999

A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.

A:Reference number: A84420; MUID:20083487; PMID:10617157

A:Accession: B84431

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-1143 <STO>

A:Cross-references: UNIPROT:O9ZPS9; GB:AE002093; NID:g4406778; PIDN:AA020088.1; GSPDB:GN

C:Genetics:

A:Gene: At2g01950

A:Map position: 2

Query Match

Best Local Similarity 66.7%; Pred. No. 86;

Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KHTRIEED 9
|||::||
1065 KHTREVIDED 1073

RESULT 9

A41604

myosin heavy chain, smooth muscle, long splice form - rabbit

C:Species: Oryctolagus cuniculus (domestic rabbit)

C>Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 19-Apr-2002

C:Accession: A41604; A33501

R:Barb, P.; Kelly, C.; Periaesamy, M.

Proc. Natl. Acad. Sci. U.S.A. 88, 10676-10680, 1991

A:Title: Characterization of a mammalian smooth muscle myosin heavy-chain gene: complete

A:Reference number: A41604; MUID:92073350; PMID:1961735

A:Accession: A41604

A:Molecule type: mRNA

A:Residues: 1-1972 <BAB>

A:Cross-references: GB:M77812

R:Nagai, R.; Kuro-o, M.; Barb, P.; Periaesamy, M.

J. Biol. Chem. 264, 9734-9737, 1989

A:Title: Identification of two types of smooth muscle myosin heavy chain isoforms by CDN

A:Reference number: A33501; MUID:89255535; PMID:2722872

A:Accession: A33501

A:Molecule type: mRNA

A:Residues: 1451-1972 <NAG>

A:Cross-references: GB:J04833; NID:g165519; PIDN:AAA11407.1; PID:g165520

A:Experimental source: smooth muscle

A>Note: examination by Southern blotting for the regions of difference between this iso-

form and the

active splicing

C:Superfamily: myosin heavy chain; myosin motor domain homology

C:Keywords: actin binding; alternative splicing; ATP; coiled coil; hydrolase; methylated

F:88-771/Domain: myosin motor domain homology <MMOT>

F:178-185/Region: nucleotide-binding motif A (P-loop)

F:559-572/Region: actin binding #status predicted

F:633-647/Region: actin binding #status predicted

F:844-1938/Domain: coiled coil #status predicted <COI>

F:844-1284/Region: S2

F:1285-1972/Region: light meromyosin

F:1939-1972/Domain: carboxyl-terminal <CBT>

F:129/Modified site: N6,N6,N6-trimethyllysine (Lys) #status predicted

F:184/Binding site: ATP (Lys) #status predicted

F:701,711/Active site: Cys #status predicted

Query Match

Best Local Similarity 60.0%; Pred. No. 1.6e+02;

Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KHTRIEEDT 10
|||::||
1200 KHTQVEHET 1209

RESULT 10

T03337

gene e30 protein - Lactococcus phage b11170

C:Species: Lactococcus phage b11170

C>Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 09-Jul-2004

C:Accession: T03337

R:Crutz-Le Coq, A.M.; Ceasejin, B.; Commissaire, J.; Anba, J.; Kyriakidis, S.; Chopin,

submitted to the EMBL Data Library, June 1997

A:Description: Sequence and organization of the lactococcal isometric b11170 phage gene

A:Reference number: Z14903

A:Accession: T03337

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-55 <CRU>

A:Cross-references: UNIPROT:O80130; EMBL:AF009630; NID:g3282260; PIDN:AA027209.1; PID:g

C:Genetics:

A:Gene: e30

Query Match

Best Local Similarity 100.0%; Pred. No. 4.6;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KHTRIIE 7
|||::||
46 KHTRIIE 52

RESULT 11

S57020

glutathione-associated protein complex beta chain homolog YAP80 - yeast (Saccharomyces cer

N)Alternative names: beta-adaptin; protein J1422; protein YR005w

C:Species: Saccharomyces cerevisiae

C>Date: 08-Jul-1995 #sequence_revision 08-Sep-1995 #text_change 09-Jul-2004

C:Accession: S57020; S55193; S12934

R:de Haan, M.; Grivell, L.A.; Smits, P.H.M.

submitted to the Protein Sequence Database, September 1995

A:Reference number: S56771

A:Accession: S57020

A:Molecule type: DNA

A:Residues: 1-700 <ZAG>

A:Cross-references: UNIPROT:P27351; EMBL:Z49505; NID:g1015627; PIDN:CAA09527.1; PID:g10

R:de Haan, M.; Smits, P.H.M.; Grivell, L.A.

submitted to the EMBL Data Library, May 1995

A:Reference number: S55183

A:Accession: S55193

A:Molecule type: DNA

A:Residues: 'MAK',53-700 <DEH>

A:Cross-references: EMBL:X87611; NID:g854567; PIDN:CAA0927.1; PID:g854578

R:Kirchhausen, T.

Mol. Cell. Biol. 10, 6089-6090, 1990

A:Title: Identification of a putative yeast homolog of the mammalian beta chains of the

A:Accession: S12934; MUID:91042546; PMID:2122239

A:Status: nucleic acid sequence not shown

A:Molecule type: DNA

A:Residues: 1-54, 'L',56-483, 'N',485-503, 'N',505-520, 'T',522-628, 'I',630-700 <KIR>

A:Cross-references: EMBL:M64998; NID:g173201; PIDN:AAA35226.1; PID:g173202

C:Genetics:

A:Gene: SGD:APL1; YAP80

A:Cross-references: MIPS:YJR005w; SGD:S0003765

A:Map position: 10R

Query Match 69.3%; Score 36; DB 2; Length 700;
Best Local Similarity 62.5%; Pred. No. 78;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

OY 1 KHTEIEE 8
||||:|
Db 443 KHTEVVE 450

RESULT 12

F70817
probable ABC transporter - Mycobacterium tuberculosis (strain H37RV)

C:Species: Mycobacterium tuberculosis
C>Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 09-Jul-2004

C:Accession: F70817
R:Coile, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Fellwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Raibaud, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.

Nature 393, 537-544, 1998
A:Authors: Sgaree, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.

A>Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome
A:Reference number: A70500; MUID:98295987; PMID:9634230

A:Accession: F70817

A:Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-217 <COL>

A:Cross-references: UNIPROT:O53915; GB:AL022002; GB:AL123456; NID:93261544; PIDN:CAAL1755

A:Experimental source: strain H37RV

C:Genetics:

A:Gene: RV167C

Query Match 67.3%; Score 35; DB 2; Length 217;
Best Local Similarity 66.7%; Pred. No. 33;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 KHTEIEED 9
||||:|
Db 173 KHTELAHED 181

RESULT 13

A70031
conserved hypothetical protein yvbY - Bacillus subtilis

C:Species: Bacillus subtilis

C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004

C:Accession: A70031

R:Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azavedo, V.; Bertez, C.; Bron, S.; Brouillet, S.; Brusch, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Cho, A.; Ehrlich, S.D.; Emmeron, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrarri, E.

Nature 390, 249-256, 1997

A:Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Gallier, A.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holst, S.; Hosono, S.; Hult, M.F.; Koeter, P.; Konings, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois, Y.M.; Ogasawara, N.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portecelle, R.; Rigger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadleir, Y.; Sato, T.; Scanlon, A.; Schleich, S.; Schroeder, R.; Scrofano, F.; Sekiguchi, J.; Sekowska, A.; Serot, A.; Tamakoshi, A.; Tanaka, T.; Terpetra, P.; Tognoni, A.; Tosato, V.; Uchiyama, T.; Winkler, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K.

A:Authors: Yoshikawa, H.F.; Zumbstein, E.; Yoshikawa, H.; Danchin, A.

A>Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.

A:Reference number: A69580; MUID:98044033; PMID:9384377

A:Accession: A70031

A:Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-240 <KTN>

A:Cross-references: UNIPROT:O32259; GB:Z99121; GB:AL009126; NID:92635827; PIDN:CAB15408.

A:Experimental source: strain 168

C:Genetics:

A:Gene: yvbY

A:Superfamily: yxgG protein

Query Match 67.3%; Score 35; DB 1; Length 240;
Best Local Similarity 66.7%; Pred. No. 37;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 2 HTEIEEDT 10
||||:|
Db 63 HTEIETDS 71

RESULT 14

C69039
methionine aminopeptidase - Methanobacterium thermoautotrophicum (strain Delta H)

C:Species: Methanobacterium thermoautotrophicum

C>Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004

C:Accession: C69039

R:Smith, D.R.; Doucette-Stamm, L.A.; Delonghery, C.; Lee, H.; Dubois, J.; Aldredge, T.; Qu, D.; Spadafora, R.; Vicaire, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiwani, N.

J. Bacteriol. 179, 7135-7155, 1997

A>Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: func.

A:Reference number: A69000; MUID:98037514; PMID:9371463

A:Accession: C69039

A:Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-299 <MTH>

A:Cross-references: UNIPROT:Q27355; GB:AB000894; GB:AB000666; NID:92622392; PIDN:AA857

A:Experimental source: strain Delta H

C:Genetics:

A:Gene: MTH1296

A:Start codon: GTG

C:Superfamily: Escherichia coli methionyl aminopeptidase

Query Match 67.3%; Score 35; DB 2; Length 299;
Best Local Similarity 66.7%; Pred. No. 47;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 1 KHTEIEED 9
||||:|
Db 284 EHTVIVED 292

RESULT 15

A82165
transcription regulator lacI family VC1721 [imported] - Vibrio cholerae (strain N16961)

C:Species: Vibrio cholerae

C>Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004

C:Accession: A82165

R:Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwin, M.L.; Dodson, R.J.; Haidelberg, D.; Ermolaeva, M.D.; Vamathevan, J.; Baas, S.; Qin, H.; Dragoti, I.; Sellers, J.

1, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.

Nature 406, 477-483, 2000

A>Title: DNA sequence of both chromosomes of the cholera pathogen Vibrio cholerae.

A:Reference number: A82035; MUID:20406833; PMID:10952301

A:Accession: A82165

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-336 <HEI>

A:Cross-references: UNIPROT:O9KRC1; GB:AB004250; GB:AB003852; NID:9656237; PIDN:AAE948

A:Experimental source: serogroup O1, strain N16961, biotype El Tor

C:Genetics:

A:Gene: VC1721

A:Map position: 1

C:Superfamily: lac repressor

Query Match 67.3%; Score 35; DB 2; Length 336;
Best Local Similarity 66.7%; Pred. No. 54;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 2 HTEIEEDT 10
||||:|
Db 321 HPEIIVERT 329

Wed Oct 26 15:03:14 2005

us-10-731-238-89.rpr

Page 5

Search completed: October 22, 2005, 09:55:40
Job time : 13.6092 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 22, 2005, 08:01:06 ; Search time 56.2069 Seconds
(without alignments)
91.106 Million cell updates/sec

Title: US-10-731-238-89
Perfect score: 52
Sequence: 1 KHTELIEBDT 10

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_03: *
1: uniprot_sprot: *
2: uniprot_trembl: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB ID	Description
1	52	100.0	152	2	Q9AEP9
2	52	100.0	940	2	Q53682
3	52	100.0	943	2	Q8NUU8
4	52	100.0	957	2	Q6G6H4
5	52	100.0	1015	2	Q8NUU7
6	52	100.0	1015	2	Q6G6H3
7	52	100.0	1018	1	FNBA_STAAU
8	47	90.4	961	2	Q99RD3
9	47	90.4	961	2	Q7A3J8
10	47	90.4	965	2	Q6GDU5
11	47	90.4	1038	2	Q99RD2
12	47	90.4	1038	2	Q7A3J7
13	41	78.8	818	2	Q6PFM2
14	41	78.8	863	2	Q803V1
15	40	76.9	378	2	Q64OT9
16	39	75.0	455	2	Q7RAC1
17	39	75.0	499	2	Q6RIAT
18	39	75.0	798	2	Q8UT55
19	39	75.0	931	2	Q6LU36
20	39	75.0	1028	1	FTSK_VIHPA
21	39	75.0	1670	2	Q9SVT0
22	38	73.1	445	2	Q09487
23	38	73.1	708	2	Q9C1Q7
24	38	73.1	1077	2	Q7RDA2
25	38	73.1	1401	2	Q7QXR1
26	37	71.2	175	2	Q9Q8G9
27	37	71.2	210	2	Q9KAP8
28	37	71.2	246	2	Q87R06
29	37	71.2	314	2	Q8VEZ8
30	37	71.2	585	2	Q8TXG6
31	37	71.2	788	2	Q9C6J1

32	37	71.2	1143	2	Q9ZPS9	Q9ZPS9 arabidopsis
33	37	71.2	1972	1	MYHB_RABIT	P35748 cryocollagus
34	36	69.2	55	2	Q80130	Q80130 bacteriophage
35	36	69.2	203	2	Q9FW86	Q9FW86 oryza sativ
36	36	69.2	267	2	Q9AJM9	Q9AJM9 kurtzia sp.
37	36	69.2	269	2	Q87066	Q87066 vibrio para
38	36	69.2	324	2	Q82315	Q82315 chlamydomon
39	36	69.2	360	2	Q6R7D8	Q6R7D8 cestrid her
40	36	69.2	461	2	Q64ZS7	Q64ZS7 bacterioides
41	36	69.2	485	2	Q05160	Q05160 saccharomyc
42	36	69.2	514	2	Q9FW87	Q9FW87 oryza sativ
43	36	69.2	577	2	Q75B65	Q75B65 ashybysa goes
44	36	69.2	599	2	Q7MKY3	Q7MKY3 vibrio vuln
45	36	69.2	599	2	Q8DPF6	Q8DPF6 vibrio vuln

ALIGNMENTS

RESULT 1

ID	Q9AEP9	PRELIMINARY;	PRT;	152 AA.
AC	Q9AEP9;			
DT	01-JUN-2001 (TREMBLrel. 17, Created)			
DT	01-JUN-2001 (TREMBLrel. 17, Last sequence update)			
DT	01-DEC-2001 (TREMBLrel. 19, Last annotation update)			
DE	Fibronectin-binding protein (fragment).			
GN	Name=fnb;			
OS	Staphylococcus aureus.			
OC	Bacteria; Firmicutes; Bacillales; Staphylococcus.			
OX	NCBI_TaxID=1280;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=CMRSA-1;			
RX	MEDLINE=21246681; PubMed=11349044;			
RY	DOI=10.1128/IAI.69.6.3791-3799.2001;			
RA	Rice K., Huesca M., Vaz D., McGavin M.J.;			
RT	"Variance in fibronectin binding and fnb locus polymorphisms in			
RT	Staphylococcus aureus: identification of antigenic variation in a			
RT	fibronectin binding protein adhesin of the epidemic CMRSA-1 strain of			
RT	methicillin-resistant S. aureus."			
RL	Infect. Immun. 69:3791-3799 (2001).			
DR	EMBL; AY029184; AAK31588.1; --			
FT	NON_TER	1		
FT	NON_TER	152		
SQ	SEQUENCE	152 AA;	17193 MW;	CFA3913C2B11C025 CRC64;
Query Match				
Best local Similarity 100.0%; Score 52; DB 2; Length 152;				
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;				
Qy	1 KHTELIEBDT 10			
Db	117 KHTELIEBDT 126			
RESULT 2				
ID	Q53682	PRELIMINARY;	PRT;	940 AA.
AC	Q53682;			
DT	01-NOV-1996 (TREMBLrel. 01, Created)			
DT	01-NOV-1996 (TREMBLrel. 01, Last sequence update)			
DT	01-MAR-2004 (TREMBLrel. 26, Last annotation update)			
DE	Fibronectin binding protein B.			
GN	Name=fnbB;			
OS	Staphylococcus aureus.			
OC	Bacteria; Firmicutes; Bacillales; Staphylococcus.			
OX	NCBI_TaxID=1280;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=8325-4;			
RX	MEDLINE=92111475; PubMed=1837266;			
RA	Jonsson K., Signes C., Muller H.P., Lindberg M.;			


```
RT "Two different genes encode fibronectin binding proteins in
RT Staphylococcus aureus. The complete nucleotide sequence and
RT characterization of the second gene."
RT Eur. J. Biochem 202:1041-1048 (1991).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC an amide bond (By similarity).
DR EMBL: X62992; CAA44726.1; -.
DR PIR: S19702; S19702.
DR HSP: Q53653; I167.
DR GO: GO:0009986; C:cell surface; IEA.
DR GO: GO:0005618; C:cell wall; IEA.
DR GO: GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO: GO:0016020; C:membrane; IEA.
DR GO: GO:0007155; P:cell adhesion; IEA.
DR InterPro: IPR008966; Adhes_bact.
DR InterPro: IPR004237; Fn_bind.
DR InterPro: IPR005877; Gpos_YsIRK.
DR Pfam: PF02986; Fn_bind; 2.
DR Pfam: PF04650; YsIRK_signal; 1.
DR TIGRFAMs: TIGR01167; LPXTG_anchor; 1.
DR TIGRFAMs: TIGR01168; YsIRK_signal; 1.
DR PROSITE: PS50847; GRAM_POS_ANCHORING; 1.
DR Cell wall; Peptidoglycan-anchor.
SQ SEQUENCE 940 AA; 10355 MW; E35FBBCA907AE345 CRC64;

Query Match 100.0%; Score 52; DB 2; Length 940;
Best Local Similarity 100.0%; Pred. No. 0.96;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KHTETIEEDT 10
Db 760 KHTETIEEDT 769

RESULT 3
Q8NTU8 PRELIMINARY; PRT; 943 AA.
ID Q8NTU8
AC Q8NTU8
DT 01-OCT-2002 (TREMBlrel. 22, Created)
DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE FmbB protein.
GN Name=fmbB; OrderedLocustNames=MM2420;
OS Staphylococcus aureus (strain MM2).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=196620;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MM2;
RX MEDLINE=22040717; PubMed=12044378; DOI=10.1016/S0140-6736(02)08713-5;
RA Baba T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Oguchi A.,
RA Negai Y., Iwama N., Asano K., Nami T., Kuroda H., Cui L.,
RA Yamamoto K., Hiramatsu K.,
RT "Genome and virulence determinants of high virulence community-
RT acquired MRSA."
RL Lancet 359:1819-1827 (2002).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC an amide bond (By similarity).
DR EMBL: AF004830; BAB96285.1; -.
DR HSP: Q53653; I167.
DR GO: GO:0009986; C:cell surface; IEA.
DR GO: GO:0005618; C:cell wall; IEA.
DR GO: GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO: GO:0016020; C:membrane; IEA.
DR GO: GO:0007155; P:cell adhesion; IEA.
DR InterPro: IPR008966; Adhes_bact.
DR InterPro: IPR004237; Fn_bind.
DR InterPro: IPR005877; Gpos_YsIRK.
DR Pfam: PF02986; Fn_bind; 1.
DR Pfam: PF04650; YsIRK_signal; 1.
DR TIGRFAMs: TIGR01167; LPXTG_anchor; 1.
DR TIGRFAMs: TIGR01168; YsIRK_signal; 1.
DR PROSITE: PS50847; GRAM_POS_ANCHORING; 1.
DR Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ SEQUENCE 957 AA; 105980 MW; 28F8BA7FFDFD3EAF CRC64;

Query Match 100.0%; Score 52; DB 2; Length 957;
Best Local Similarity 100.0%; Pred. No. 0.98;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KHTETIEEDT 10
Db 767 KHTETIEEDT 776
```

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DR Pfam: PF04650; YsIRK_signal; 1.
DR TIGRFAMs: TIGR01167; LPXTG_anchor; 1.
DR TIGRFAMs: TIGR01168; YsIRK_signal; 1.
DR PROSITE: PS50847; GRAM_POS_ANCHORING; 1.
DR Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ SEQUENCE 943 AA; 104537 MW; DA8A5F31997E1B6A CRC64;

Query Match 100.0%; Score 52; DB 2; Length 943;
Best Local Similarity 100.0%; Pred. No. 0.96;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KHTETIEEDT 10
Db 767 KHTETIEEDT 776

RESULT 4
Q6G6H4 PRELIMINARY; PRT; 957 AA.
ID Q6G6H4
AC Q6G6H4
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE Fibronectin-binding protein.
GN Name=fmbB; OrderedLocustNames=SAS2387;
OS Staphylococcus aureus (strain MSSA476).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=282459;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=15213324; DOI=10.1073/pnas.0402521101;
RA Holden M.T.G., Fell E.J., Lindsey J.A., Peacock S.J., Day N.P.J.,
RA Enright M.C., Foster T.J., Moore C.E., Hurst L., Atkin R., Barron A.,
RA Bason N., Bentley S.D., Chillingworth C., Chillingworth T.,
RA Churcher C., Clark L., Cotton C., Cronin A., Doggett J., Dowd L.,
RA Felwell T., Hance Z., Harris B., Hauser H., Holtroyd S., Jags K.,
RA James K.D., Lennard N., Line M.A., Mayes R., Moule S., Mungall K.,
RA Ormond D., Quail M.A., Rabinowitsch E., Rutherford K.M., Sanders M.,
RA Sharp S., Simmonds M., Stevens K., Whitehead S., Barrett B.G.,
RA Spratt B.G., Parkhill J.,
RT "Complete genomes of two clinical Staphylococcus aureus strains:
RT evidence for the rapid evolution of virulence and drug resistance."
RT Proc. Natl. Acad. Sci. U.S.A. 101:9786-9791(2004).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC an amide bond (By similarity).
DR EMBL: BK571857; CAG44201.1; -.
DR GO: GO:0009986; C:cell surface; IEA.
DR GO: GO:0005618; C:cell wall; IEA.
DR GO: GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO: GO:0016020; C:membrane; IEA.
DR GO: GO:0007155; P:cell adhesion; IEA.
DR InterPro: IPR008966; Adhes_bact.
DR InterPro: IPR004237; Fn_bind.
DR InterPro: IPR005877; Gpos_YsIRK.
DR InterPro: IPR001899; Gram_pos_anchor.
DR Pfam: PF02986; Fn_bind; 1.
DR Pfam: PF04650; YsIRK_signal; 1.
DR TIGRFAMs: TIGR01167; LPXTG_anchor; 1.
DR TIGRFAMs: TIGR01168; YsIRK_signal; 1.
DR PROSITE: PS50847; GRAM_POS_ANCHORING; 1.
DR Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ SEQUENCE 957 AA; 105980 MW; 28F8BA7FFDFD3EAF CRC64;

Query Match 100.0%; Score 52; DB 2; Length 957;
Best Local Similarity 100.0%; Pred. No. 0.98;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KHTETIEEDT 10
Db 767 KHTETIEEDT 776
```

RESULT 5	
ID	Q88NU7
AC	Q88NU7; PRELIMINARY; PRT; 1015 AA.
DT	01-OCT-2002 (TREMBLREL. 22, Created)
DT	01-OCT-2002 (TREMBLREL. 22, Last sequence update)
DT	01-OCT-2003 (TREMBLREL. 25, Last annotation update)
DE	Fmb protein.
GN	Name=Fmb; OrderedLocustNames=MW2421;
OS	Staphylococcus aureus (strain MW2).
OC	Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX	NCBI_TaxID=196620;
RN	[1]
RP	SEQUENCE FROM N.A.
RC	STRAIN=MW2;
RX	MEDLINE=22040717; PubMed=12044378; DOI=10.1016/S0140-6736(02)08713-5;
RA	Baba T., Takuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Oguchi A.,
RA	Nagai Y., Iwama N., Asano K., Naito T., Kuroda H., Cui L.,
RA	Yanamoto K., Hiratacsu K.;
RT	"Genome and virulence determinants of high virulence community-
RT	acquired MRSA.";
RL	Lancet 359:1819-1827(2002).
CC	-1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC	an amide bond (by similarity).
DR	EMBL; AP004830; BAB96286.1; -.
DR	GO; GO:0009986; C:cell surface; IEA.
DR	GO; GO:0005618; C:cell wall; IEA.
DR	GO; GO:0009275; C:cell wall (sensus Gram-positive Bacteria); IEA.
DR	GO; GO:0016020; C:membrane; IEA.
DR	GO; GO:007155; P:cell adhesion; IEA.
DR	InterPro; IPR008966; Adhes_bact.
DR	InterPro; IPR004237; Fm_bind.
DR	InterPro; IPR005877; Gpos_YsIRK.
DR	InterPro; IPR001899; Gram_pos_anchor.
DR	Pfam; PF02986; Fm_bind; 1.
DR	Pfam; PF00746; Gram_pos_anchor; 1.
DR	Pfam; PF04650; YsIRK_signal; 1.
DR	TIGRFAMS; TIGR01167; LpxTG_anchor; 1.
DR	TIGRFAMS; TIGR01168; YsIRK_signal; 1.
DR	PROSITE; PS0847; GRAM_POS_ANCHORING; 1.
KM	Cell wall; Complete proteome; Peptidoglycan-anchor.
SO	SEQUENCE 1015 AA; 111145 MW; D0F9281BB64D4D2 CRC64;
Query Match 100.0%; Score 52; DB 2; Length 1015;	
Best Local Similarity 100.0%; Pred. No. 1;	
Matches	10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	1 KHTETIEEDT 10
DB	825 KHTETIEEDT 834
RESULT 6	
ID	Q6G6H3
AC	Q6G6H3; PRELIMINARY; PRT; 1015 AA.
DT	05-JUL-2004 (TREMBLREL. 27, Created)
DT	05-JUL-2004 (TREMBLREL. 27, Last sequence update)
DT	05-JUL-2004 (TREMBLREL. 27, Last annotation update)
DE	Fibronectin-binding protein.
GN	OrderedLocustNames=SA52388;
OS	Staphylococcus aureus (strain MSS4476).
OC	Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX	NCBI_TaxID=282459;
RN	[1]
RP	SEQUENCE FROM N.A.
RX	Pubmed=15213324; DOI=10.1073/pnas.0402521101;
RA	Holden M.T.G., Fell E.J., Lindsey J.A., Peacock S.J., Day N.P.J.,
RA	Enright M.C., Foster T.J., Moore C.E., Hurst L., Atkin R., Barron A.,
RA	Bason N., Bentley S.D., Chillingworth C., Chillingworth T.,
RA	Churcher C., Clark L., Corton C., Cronin A., Doggett J., Dowd L.,
RA	Felwell T., Hance Z., Harris B., Hauser H., Holroyd S., Jagsels K.,
RA	James K.D., Leonard N., Line A., Mayes R., Moutle S., Mungall K.,

Ormond D., Quail M.A., Rabbिनowitsch E., Rutherford K.M., Sanders M., Sharp S.G., Simmonds M., Stevens K., Whitehead S., Barrett B.G., Spratt B.G., Parkhill J., "Complete genomes of two clinical *Staphylococcus aureus* strains: RT evidence for the rapid evolution of virulence and drug resistance."; Proc. Natl. Acad. Sci. U.S.A. 101:9786-9791(2004).

CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by an amide bond (By similarity).

CC EMBL: BX571857; CAC44202.1; -

CC DR GO: GO:0009986; C:cell surface; IEA.

CC DR GO: GO:0005618; C:cell wall; IEA.

CC DR GO: GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.

CC DR GO: GO:0016020; C:membrane; IEA.

CC DR GO: GO:0007155; P:cell adhesion; IEA.

CC InterPro: IPR008966; Adhes_bact.

CC InterPro: IPR004237; Fn_bind.

CC InterPro: IPR005877; Gpos_YsIRK.

CC InterPro: IPR001899; Gram_pos_anchor.

CC Pfam: PF02986; Fn_bind; 1.

CC Pfam: PF00746; Gram_pos_anchor; 1.

CC Pfam: PF04650; YsIRK_signal; 1.

CC TIGRFAMs: TIGR01167; LPXTG_anchor; 1.

CC TIGRFAMs: TIGR01168; YsIRK_signal; 1.

CC PROSITE: PS50847; GRAM_POS_ANCHORING; 1.

CC Cell wall; Complete proteome; Peptidoglycan-anchor.

CC SEQUENCE 1015 AA; 111145 MW; D0F9281BB64D44D2 CRC64;

Query Match 100.0%; Score 52; DB 2; Length 1015;
Best Local Similarity 100.0%; Pred. No.1;
Matches 10; Conservative 0; Mismatches 0; Gaps 0;

Oy 1 KHTEIIEDT 10
|||||||
Db 825 KHTEIIEDT 834

RESULT 7
FNBA_STAAU STANDARD; PRT; 1018 AA.
ID FNBA_STAAU STANDARD; PRT; 1018 AA.
AC. P14738;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Fibronectin-binding protein precursor (FNBP).
GN Name:fnba;
OS *Staphylococcus aureus*.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
CC NCB1_TaxID=1280;
CC [1]
CC
CC RP SEQUENCE FROM N.A.;
CC STRAIN=NCTC 8325-4;
CC MEDLINE=89098998; PubMed=2521391;
CC Signaes C., Raucsi G., Joensson K., Lindgren P.-E.,
CC Anantharamiah G.M., Hoeoek M., Lindberg M.;
CC "Nucleotide sequence of the gene for a fibronectin-binding protein
CC from *Staphylococcus aureus*: use of this peptide sequence in the
CC synthesis of biologically active peptides.";
CC Proc. Natl. Acad. Sci. U.S.A. 86:699-703(1989).
CC
CC -1- FUNCTION: The ability of bacteria to bind fibronectin has been
CC proposed as a virulence factor enabling bacteria to colonize wound
CC tissues and blood clots. Binding of plasma fibronectin to the
CC bacterial surface might block adhesion receptors on *S.aureus*, thus
CC representing an important defense mechanism against tissue
CC invasion.
CC
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC an amide bond (potential).
CC
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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```
CC or send an email to license@lsb.sib.ch).
-----
CC EMBL: J04151; AAA2632.1; -.
DR InterPro: IPR004237; Fn_bind.
DR InterPro: IPR005877; Gpos_Ysirk.
DR InterPro: IPR001899; Gram_pos_anchor.
DR Pfam: PF02986; Fn_bind.1.
DR Pfam: PF00746; Gram_pos_anchor.1.
DR Pfam: PF04650; Ysirk_signal.1.
DR TIGRFAMs: TIGR01167; Lpxtg_anchor.1.
DR TIGRFAMs: TIGR01168; Ysirk_signal.1.
DR PROSITE: PS50847; GRAM_POS_ANCHORING.1.
DR Cell adhesion; Cell wall; Peptidoglycan-anchor; Repeat; Signal;
KM virulence.
FT SIGNAL 1 36 Fibronectin-binding protein.
FT CHAIN 37 985 Removed by sortase (Potential).
FT PROPEP 986 1018 B-1.
FT REPEAT 545 574 B-2.
FT REPEAT 545 604 4 X approximate tandem repeats,
FT DOMAIN 745 878 fibronectin-binding domain.
FT REPEAT 745 782 D-1.
FT REPEAT 783 820 D-2.
FT REPEAT 821 859 D-3.
FT REPEAT 860 878 D-4 (incomplete).
FT DOMAIN 879 948 5 X tandem repeats, Pro-rich (WR).
FT REPEAT 879 892 WR 1.
FT REPEAT 893 906 WR 2.
FT REPEAT 907 920 WR 3.
FT REPEAT 921 934 WR 4.
FT REPEAT 935 948 WR 5.
FT SITE 982 986 Lpxtg sorting signal (Potential).
FT MOD_RRS 985 985 Pentaglycyl murein peptidoglycan amidated
SQ SEQUENCE 1018 AA; 111780 MW; 58175E0D0B81F1F CRC64;
threonine (Potential).
Query Match 100.0%; Score 52; DB 1; Length 1018;
Best Local Similarity 100.0%; Pred. No. 1;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 KHTEIIEDT 10
Db 824 KHTEIIEDT 833
RESULT 8
Q99RD3 PRELIMINARY; PRT; 961 AA.
ID Q99RD3
AC Q99RD3;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Fibronectin-binding protein homolog.
GN Name=fnb3; OrderedLocNames=SAV2502;
OS Staphylococcus aureus (strain Mu50 / ATCC 700699).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxId=158878;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Mu50 / ATCC 700699;
RX MEDLINE=21311952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2;
RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Lian J.-O., Ito T.,
RA Kanamori M., Matsunaru H., Maruyama A., Murakami H., Hosoyama A.,
RA Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
RA Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
RA Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
RA Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
RT "Whole genome sequencing of methicillin-resistant Staphylococcus
aureus.";
RL Lancet 357:1225-1240(2001).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
an amide bond (by similarity).
```

```
DR EMBL: AP003365; BAB58664.1; -.
DR PIR: G90053; G90053.
DR HSSP: Q53653; 1N67.
DR GO: GO:0009986; C:cell surface; IEA.
DR GO: GO:0005618; C:cell wall; IEA.
DR GO: GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO: GO:0016020; C:membrane; IEA.
DR GO: GO:0007155; P:cell adhesion; IEA.
DR InterPro: IPR008966; Adhes_bact.
DR InterPro: IPR004237; Fn_bind.
DR InterPro: IPR005877; Gpos_Ysirk.
DR InterPro: IPR001899; Gram_pos_anchor.
DR Pfam: PF02986; Fn_bind.1.
DR Pfam: PF00746; Gram_pos_anchor.1.
DR Pfam: PF04650; Ysirk_signal.1.
DR TIGRFAMs: TIGR01167; Lpxtg_anchor.1.
DR TIGRFAMs: TIGR01168; Ysirk_signal.1.
DR PROSITE: PS50847; GRAM_POS_ANCHORING.1.
DR Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ SEQUENCE 961 AA; 106010 MW; 364940FB84EA4101 CRC64;
Query Match 90.4%; Score 47; DB 2; Length 961;
Best Local Similarity 90.0%; Pred. No. 8.3;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 KHTEIIEDT 10
Db 771 KHTEIIEDT 780
RESULT 9
Q7A3J8 PRELIMINARY; PRT; 961 AA.
ID Q7A3J8
AC Q7A3J8;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE FnbB protein.
GN Name=fnb3; OrderedLocNames=SA2290;
OS Staphylococcus aureus (strain N315).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxId=158879;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=21311952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2;
RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Lian J.-O., Ito T.,
RA Kanamori M., Matsunaru H., Maruyama A., Murakami H., Hosoyama A.,
RA Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
RA Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
RA Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
RA Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
RT "Whole genome sequencing of methicillin-resistant Staphylococcus
aureus.";
RL Lancet 357:1225-1240(2001).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
an amide bond (by similarity).
```

KW Cell wall; Complete proteome, Peptidoglycan-anchor.
 SQ SEQUENCE 961 AA; 106010 MW; 364940f884EA4101 CRC64;
 Query Match 90.4%; Score 47; DB 2; Length 961;
 Best Local Similarity 90.0%; Pred. No. 8.3;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KHTREIIBEDT 10
 |||||
 DB 771 KNEIIEEDT 780

RESULT 10
 O6GDUS PRELIMINARY; PRT; 965 AA.
 ID O6GDUS
 AC O6GDUS;
 DT 05-JUL-2004 (TREMBLrel. 27, Created)
 DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
 DE Fibronectin-binding protein.
 GN Name=fnbA; OrderedLocustNames=SA2580;
 OS Staphylococcus aureus (strain MRSA252).
 CC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 NCBI_TaxID=282458;
 RX SEQUENCE FROM N.A.
 RX Holden M.T.G., Fell E.J., Lindsay J.A., Peacock S.J., Day N.P.J.,
 RA Enright M.C., Foster T.J., Moore C.E., Hurst L., Atkin R., Barron A.,
 RA Baeson N., Bentley S.D., Chillingworth C., Chillingworth T.,
 RA Churcher C., Clark L., Cotton C., Cronin A., Doggett J., Dowd L.,
 RA Feltwell T., Hance Z., Harris B., Hauser H., Holtroyd S., Jagels K.,
 RA James K.D., Leonard N., Line A., Mayes R., Moule S., Mungall K.,
 RA Ommond D., Quail M.A., Rabinowitch E., Rutherford K.M., Sanders M.,
 RA Sharp S., Simmonds M., Stevens K., Whitehead S., Barrall B.G.,
 RA Spratt B.G., Parkhill J.;
 RT "Complete genomes of two clinical Staphylococcus aureus strains:
 RT evidence for the rapid evolution of virulence and drug resistance";
 RL Proc. Natl. Acad. Sci. U.S.A. 101:9786-9791(2004).
 CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
 an amide bond (By similarity).
 DR EMBL; BX571856; CAG41560.1; -;
 DR GO; GO:0009986; C:cell surface; IEA.
 DR GO; GO:0009275; C:cell wall (senu Gram-positive Bacteria); IEA.
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0007155; P:cell adhesion; IEA.
 DR InterPro; IPR008966; Adhes_bact.
 DR InterPro; IPR004237; Fn_bind.
 DR InterPro; IPR005877; Gpos_YsIRK.
 DR InterPro; IPR001899; Gram_pos_anchor.
 DR Pfam; PF02986; Fn_bind; 1.
 DR Pfam; PF00746; Gram_pos_anchor; 1.
 DR Pfam; PF04650; YsIRK_signal; 1.
 DR TIGRFAMs; TIGR01167; LpxTG_anchor; 1.
 DR TIGRFAMs; TIGR01168; YsIRK_signal; 1.
 DR PROSITE; PS50847; GRAM_POS_ANCHORING; 1.
 KW Cell wall; Complete proteome; Peptidoglycan-anchor.
 SQ SEQUENCE 965 AA; 105591 MW; 2982B13216400551 CRC64;

Query Match 90.4%; Score 47; DB 2; Length 965;
 Best Local Similarity 90.0%; Pred. No. 8.3;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KHTREIIBEDT 10
 |||||
 DB 789 KNEIIEEDT 798

RESULT 11
 O99RD2 PRELIMINARY; PRT; 1038 AA.
 ID O99RD2
 AC O99RD2;
 DT 01-JUN-2001 (TREMBLrel. 17, Created)

DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
 DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
 DE Fibronectin-binding protein homolog.
 GN Name=fnb; OrderedLocustNames=SAV2503;
 OS Staphylococcus aureus (strain Mu50 / ATCC 700699).
 CC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 NCBI_TaxID=158878;
 RX SEQUENCE FROM N.A.
 RC STRAIN=Mu50 / ATCC 700699;
 RX MEDLINE=21311952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2;
 RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
 RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Iian J.-O., Ito T.,
 RA Kanamori M., Matsunaru H., Maruyama A., Murakami H., Hoshoyama A.,
 RA Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
 RA Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
 RA Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
 RA Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
 RT "Whole genome sequencing of methicillin-resistant Staphylococcus
 RT aureus";
 RL Lancet 357:1225-1240(2001).
 CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
 an amide bond (By similarity).
 DR EMBL; AP003365; BAB58665.1; -;
 DR PIR; H90053; H90053.
 DR GO; GO:0009986; C:cell surface; IEA.
 DR GO; GO:0005618; C:cell wall; IEA.
 DR GO; GO:0009275; C:cell wall (senu Gram-positive Bacteria); IEA.
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0007155; P:cell adhesion; IEA.
 DR InterPro; IPR008966; Adhes_bact.
 DR InterPro; IPR004237; Fn_bind.
 DR InterPro; IPR005877; Gpos_YsIRK.
 DR InterPro; IPR001899; Gram_pos_anchor.
 DR Pfam; PF02986; Fn_bind; 1.
 DR Pfam; PF00746; Gram_pos_anchor; 1.
 DR Pfam; PF04650; YsIRK_signal; 1.
 DR TIGRFAMs; TIGR01167; LpxTG_anchor; 1.
 DR TIGRFAMs; TIGR01168; YsIRK_signal; 1.
 DR PROSITE; PS50847; GRAM_POS_ANCHORING; 1.
 KW Cell wall; Complete proteome; Peptidoglycan-anchor.
 SQ SEQUENCE 1038 AA; 113618 MW; 666BF6F2FBB12 CRC64;

Query Match 90.4%; Score 47; DB 2; Length 1038;
 Best Local Similarity 90.0%; Pred. No. 9;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KHTREIIBEDT 10
 |||||
 DB 820 KNEIIEEDT 829

RESULT 12
 Q7A3J7 PRELIMINARY; PRT; 1038 AA.
 ID Q7A3J7
 AC Q7A3J7;
 DT 05-JUL-2004 (TREMBLrel. 27, Created)
 DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
 DE Fnb protein.
 GN Name=fnb; OrderedLocustNames=SA2291;
 OS Staphylococcus aureus (strain N315).
 CC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 NCBI_TaxID=158879;
 RX SEQUENCE FROM N.A.
 RX MEDLINE=21311952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2;
 RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
 RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Iian J.-O., Ito T.,
 RA Kanamori M., Matsunaru H., Maruyama A., Murakami H., Hoshoyama A.,
 RA Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
 RA Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
 RA Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,

FT NON_TER 1 1
SQ SEQUENCE 863 AA; 93639 MW; B916C9694D5389CC CRC64;

Query Match 78.8%; Score 41; DB 2; Length 863;
Best Local Similarity 70.0%; Pred. No. 94;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 KHTEIIEDT 10
|:|||||
Db 397 KETELVEEDT 406

RESULT 15

064QT9 PRELIMINARY; PRT; 378 AA.
ID 064QT9
AC 064QT9:
DT 25-OCT-2004 (TREMBLrel. 28, Created)
DT 25-OCT-2004 (TREMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TREMBLrel. 28, Last annotation update)
DE Hypothetical protein.
GN ORFNames=BF3398;
OS Bacteroides fragilis.
OC Bacteroidetes; Bacteroides (class); Bacteroidales;
OC Bacteria; Bacteroidetes; Bacteroides.
OX NCBI_TaxID=817;
RX [1]
RN RP SEQUENCE FROM N.A.
RC STRAIN=YCH46;
RA Kuwahara T., Yamashita A., Hirakawa H., Nakayama H., Toh H., Okada N.,
RA Kuwaha S., Hattori M., Hayashi T., Onishi Y.,
RT "Genomic analysis of Bacteroides fragilis reveals extensive DNA
RT inversions regulating cell surface adaptation.";
RL Proc. Natl. Acad. Sci. U.S.A. 0:0-0(2004).
DR EMBL; AP006841; BAD50142.1;-.
KW Hypothetical protein.
SQ SEQUENCE 378 AA; 43337 MW; 097B703726FA9F8C CRC64;

Query Match 76.9%; Score 40; DB 2; Length 378;
Best Local Similarity 77.8%; Pred. No. 60;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 HTEIIEDT 10
|:|||||
Db 24 HOEVIEDT 32

Search completed: October 22, 2005, 09:52:13
Job time : 58.2069 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 25, 2005, 20:58:51 ; Search time 69.7126 Seconds
(without alignments)
55.479 Million cell updates/sec

Title: US-10-731-238-90
Perfect score: 50
Sequence: 1 TEIEEDPTNK 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:*

- 1: Geneseqp1980s:*
- 2: Geneseqp1990s:*
- 3: Geneseqp2000s:*
- 4: Geneseqp2001s:*
- 5: Geneseqp2002s:*
- 6: Geneseqp2003as:*
- 7: Geneseqp2003bs:*
- 8: Geneseqp2004as:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	50	100.0	10	2	AAW65746
2	50	100.0	37	1	AAW65746 Fibronect
3	50	100.0	37	4	AAW65746 Fibronect
4	50	100.0	38	1	AAW65746 Fibronect
5	50	100.0	77	2	AAW65746 Fibronect
6	50	100.0	101	2	AAW65746 Fibronect
7	50	100.0	113	2	AAW65746 Fibronect
8	50	100.0	124	2	AAW65746 Fibronect
9	50	100.0	128	2	AAW65746 Fibronect
10	50	100.0	130	2	AAW65746 Fibronect
11	50	100.0	130	2	AAW65746 Fibronect
12	50	100.0	130	2	AAW65746 Fibronect
13	50	100.0	130	2	AAW65746 Fibronect
14	50	100.0	134	2	AAW65746 Fibronect
15	50	100.0	134	2	AAW65746 Fibronect
16	50	100.0	134	2	AAW65746 Fibronect
17	50	100.0	139	2	AAW65746 Fibronect
18	50	100.0	162	2	AAW65746 Fibronect
19	50	100.0	164	2	AAW65746 Fibronect
20	50	100.0	174	2	AAW65746 Fibronect
21	50	100.0	174	2	AAW65746 Fibronect
22	50	100.0	181	2	AAW65746 Fibronect
23	50	100.0	181	2	AAW65746 Fibronect
24	50	100.0	559	2	AAW65746 Fibronect
25	50	100.0	940	2	AAW65746 Fibronect

26	50	100.0	940	6	ABJ19111
27	50	100.0	948	6	ADA89470
28	50	100.0	948	6	ABJ18923
29	50	100.0	948	6	ABW72536
30	50	100.0	1018	1	AAW65746
31	50	100.0	1018	4	AAW65746
32	50	100.0	1018	4	AAW65746
33	50	100.0	1018	4	ABJ18922
34	50	100.0	1018	6	ABW72537
35	50	100.0	1027	2	AAW65746
36	50	100.0	1027	6	ABW15854
37	45	90.0	978	4	AAU37093
38	45	90.0	1001	4	ABU15903
39	45	90.0	1038	6	ABU15903
40	40	80.0	10	2	AAW65746
41	40	80.0	387	7	ADJ70426
42	40	80.0	403	5	ABG31768
43	40	80.0	413	8	ADL66350
44	40	80.0	430	6	ABP75913
45	39	78.0	10	2	AAW65746

ALIGNMENTS

RESULT 1
AAW65746 standard; peptide; 10 AA.

AAW65746;

16-OCY-1998 (first entry)

Fibronectin binding protein-derived peptide #90.

microbial surface components recognising adhesive matrix molecule;

MSCRAMM; fibronectin; fibronectin-binding protein; antibody; epitope;

antibiotic; bacterial infection; antibiotic-resistant strain.

Synthetic.

Staphylococcus aureus.

21-JAN-1998; 98WO-US001222.

21-JAN-1997; 97US-0036139P.

(TEXAS) UNIV TEXAS A & M SYSTEM.

Hoeek M, Patti JM, House-Pompeo KL, Speziale P, Joh D;

Megavir M;

WPI, 1998-413816/35.

Antibody that binds to fibronectin-binding protein, preventing its

binding to fibronectin - used to treat or prevent bacterial infection,

especially by Staphylococci and Streptococci.

Example 9; Page 11; 201pp; English.

The invention relates to antibodies that bind to a fibronectin-binding domain of a fibronectin-binding protein, and inhibit binding of the protein to a fibronectin. Also claimed are: (1) isolated peptides of a fibronectin-binding protein that do not bind to fibronectin; (2) fusion protein containing at least one peptide of a fibronectin-binding protein linked to a second amino acid sequence; (3) nucleic acid encoding the isolated peptide of (1). Antibodies, the isolated peptides of (1) and the nucleic acids are all useful for immunisation (active or passive) and (b) inhibiting binding of bacteria to fibronectin (for preventing or treating infection in humans or other animals, particularly by staphylococci or

CC streptococci, e.g. meningitis, otitis media, pneumonia, endocarditis,
 CC mastitis in cattle, abortion in horses and many others. Since the
 CC antibodies block binding of bacteria, they should be effective against
 CC antibiotic-resistant strains, and may replace antibiotic therapy or
 CC increase its effectiveness. Sequences AAW5744-58 represent peptides
 CC which were synthesised to span the D3 motif of S. aureus fibronectin
 CC binding protein A
 CC
 XX

Sequence 10 AA;

Query Match 100.0%; Score 50; DB 2; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.025;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TEIIEDTNN 10
 |||||
 1 TEIIEDTNN 10

RESULT 2

ID AAB82118 standard; protein; 37 AA.

XX AAB82118;

XX 25-MAR-2003 (revised)

DT 05-JAN-1990 (first entry)

XX Fibronectin binding protein.

XX Fibronectin binding protein; S.aureus; immunisation; mastitis; ruminants;
 wound infection; diagnosis.

XX Staphylococcus aureus.

XX EP294349-A.

XX 07-DEC-1988.

XX 30-MAY-1988; 88EP-00850188.

XX 01-JUN-1987; 87SE-00002272.

XX (ALFA) ALFA LAVAL AGRIC INT AB.

XX Lindberg MK, Signas LC, Wadstrom TM, Froman G;

XX WPI; 1988-347978/49.

XX N-PSDB; AAN82056.

PT Hybrid DNA encoding Staphylococcus aureus fibronectin binding protein -
 PT useful for immunisation and topical application to prevent staphylococcal
 PT infections.

XX Claim 11; Page 12; 23pp; English.

XX The S. aureus fibronectin binding protein may be included in a hybrid
 CC protein. The protein may be used to immunise ruminants against
 CC staphylococcal mastitis, pref. when given at 0.5-5 microg/kg, using 3
 CC doses at 1-3 week intervals; and for topical applicn. to prevent wound
 CC infection, pref. using isotonic saline soln. of concn. 25-250 microg/mg.
 CC The DNA encoding the binding protein and the hybrid protein may be
 CC immobilised on a carrier and used to diagnose staphylococcal infections.
 CC (Updated on 25-MAR-2003 to correct PA field.)
 CC
 XX

Sequence 37 AA;

Query Match 100.0%; Score 50; DB 1; Length 37;
 Best Local Similarity 100.0%; Pred. No. 0.097;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TEIIEDTNN 10
 |||||

DB 6 TEIIEDTNN 15

RESULT 3

ID AAB91958 standard; peptide; 37 AA.

XX AAB91958;

XX 22-JUN-2001 (first entry)

DE Fibronectin fragment and fibrin related peptide SEQ ID NO.1134.

XX Protection; endogenous therapeutic peptide; peptidase; conjugation;
 KM blood component; modification; succinimide; maleimido group; amino;
 KM hydroxyl; thiol; hormone; growth factor; neurotransmitter.

XX Homo sapiens.

XX Synthetic.

XX WO200069900-A2.

XX 23-NOV-2000.

XX 17-MAY-2000; 2000WO-US013576.

XX 17-MAY-1999; 99US-0134406P.

XX 10-SEP-1999; 99US-0153406P.

XX 15-OCT-1999; 99US-0159783P.

XX (CONU-) CONUCHEM INC.

XX Bridon DP, Ezrin AM, Milner PG, Holmes DL, Thibaudau K;

XX WPI; 2001-112059/12.

XX Modifying and attaching therapeutic peptides to albumin prevents
 PT peptidase degradation, useful for increasing length of in vivo activity.

XX Disclosure; Page 566; 733pp; English.

XX The present invention describes a modified therapeutic peptide (I)
 CC comprising a therapeutically active amino acid region (III) and a
 CC reactive group (II) (e.g. succinimide and maleimido groups) attached to
 CC a less therapeutically active amino acid region (IV), which covalently
 CC bonds with amino/hydroxyl/thiol groups on blood components to form a
 CC peptidase stabilized therapeutic peptide composed of 3-50 amino acids.
 CC (I) are useful for modifying therapeutic peptides e.g. hormones, growth
 CC factors and neurotransmitters, to protect them from peptidase activity in
 CC vivo for the treatment of various disorders. Endogenous therapeutic
 CC peptides are not suitable as drug candidates as they require frequent
 CC administration due to rapid degradation by peptidases in the body.
 CC Modifying and attaching therapeutic peptides to albumin prevents or
 CC reduces the action of peptidases to increase length of activity (half
 CC life) and specificity as bonding to large molecules decreases.
 CC Intracellular uptake and interference with physiological processes.
 CC AAB90829 to AAB92441 represent peptides which can be used in the
 CC exemplification of the present invention
 CC
 XX

Sequence 37 AA;

Query Match 100.0%; Score 50; DB 4; Length 37;
 Best Local Similarity 100.0%; Pred. No. 0.097;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TEIIEDTNN 10
 |||||

DB 5 TEIIEDTNN 14

RESULT 4

ID AAB80662 standard; protein; 38 AA.

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XX AAP80662;
AC
XX 25-MAR-2003 (revised)
DT 07-OCT-1990 (first entry)
DE Protein with fibronectin binding ability.
XX Hybrid DNA molecule; fibronectin binding; mastitis; ruminants;
KW wound infection.
XX Staphylococcus aureus.
OS EP294349-A.
XX 07-DEC-1988.
XX 30-MAY-1988; 88EP-00850188.
XX 01-JUN-1987; 87SB-00002272.
XX (ALFA ) ALFA LAVAL AGRIC INT AB.
XX Lindberg MK, Signas LC, Wadstrom TM, Froman G;
XX WPI; 1988-347978/49.
XX N-PSDB; AAN81099.
XX Hybrid DNA encoding Staphylococcus aureus fibronectin binding protein -
PT useful for immunisation and topical application to prevent staphylococcal
PT infections.
XX Claim 11; Page 12; 23pp; English.
XX The peptide has fibronectin binding ability. It is useful for immunising
XX ruminants against staphylococcal mastitis, pref. when used at 0.5-5
XX micrograms/kg, using 3 doses given at 1-3 week intervals; for topical
XX application to prevent wound infection, using an isotonic saline soln. of
XX concn. 25-250 micrograms/ml; and, when immobilised on a carrier, for
XX diagnosing staphylococcal infections. (Updated on 25-MAR-2003 to correct
XX PF field.) (Updated on 25-MAR-2003 to correct PA field.)
CC
CC Sequence 38 AA;
SQ
Query Match 100.0%; Score 50; DB 1; Length 38;
Best Local Similarity 100.0%; Pred. No. 0.1; Mismatches 0; Indels 0; Gaps 0;
Matches 10; Conservative 0;
QY 1 TEIIEEDTNK 10
DB 6 TEIIEEDTNK 15
RESULT 5
AAR88749
ID AAR88749 standard; protein; 77 AA.
XX
XX AAR88749;
AC
XX 24-SEP-1996 (first entry)
DT
XX S. aureus fibronectin binding protein D2D3 polypeptide.
DE
XX Fibronectin binding protein; D2D3; prevention; adhesion; bacteria;
XX gram positive; extracellular matrix protein; in-dwelling device;
XX catheter; wound; D2D3; oral pathogen; oral cavity; J2385; NCIMB 40532.
XX Staphylococcus aureus.
OS
XX WO9604380-A1.
XX 15-FEB-1996.
XX

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PF 28-JUL-1995; 95WO-EP003039.
XX
XX 05-AUG-1994; 94GB-00015901.
XX (SMIK ) SMITHKLINE BEECHAM PLC.
XX
XX Critchley IA, Dodd I, Barnett P, Mossakowska DEI;
XX WPI; 1996-129396/13.
XX N-PSDB; AAT12582.
XX
XX Staphylococcus aureus fibronectin binding protein D2D3 polypeptide -
PT useful for combating infection at wound sites, surgical implants, etc.
PT and as antiadherent agent in oral hygiene.
XX Claim 5; Page 26; 38pp; English.
XX
XX The present sequence is the S. aureus fibronectin binding protein
XX polypeptide D2D3, which can be used to prevent adhesion of (e.g. gram
XX positive) bacteria, to extra-cellular matrix proteins on in-dwelling
XX devices, e.g. catheters or in wounds. D2D3 can also be used to prevent
XX oral pathogens from binding to extra-cellular matrix proteins, in the
XX oral cavity. D2D3 was found to be effective at inhibiting S. aureus 8325-
XX 4, and 120 adhesion to fibronectin coated PMMA coverlips, at a min.
XX adhesion inhibitor concn. of 10 microg/ml. D2D3 was derived from the D2
XX and D3 regions of the S. aureus J2385 (NCIMB 40532) fibronectin binding
XX protein
CC
CC Sequence 77 AA;
SQ
Query Match 100.0%; Score 50; DB 2; Length 77;
Best Local Similarity 100.0%; Pred. No. 0.21; Mismatches 0; Indels 0; Gaps 0;
Matches 10; Conservative 0;
QY 1 TEIIEEDTNK 10
DB 44 TEIIEEDTNK 53
RESULT 6
AAR90939
ID AAR90939 standard; peptide; 101 AA.
XX
XX AAR90939;
AC
XX 23-SEP-1996 (first entry)
DT
XX D3D4 polypeptide #3.
DE
XX Fibronectin binding protein; Fbp; S.aureus J2385; monoclonal antibody;
XX infection; surgical implant; antiadherent agent; hygiene; adhesion;
XX extracellular matrix protein; oral pathogen; oral cavity.
XX Staphylococcus aureus.
OS
XX
XX Key Location/Qualifiers
XX Region 1..35
XX FT /note= "D3 region fragment"
XX FT 36..50
XX FT /note= "D4 region"
XX FT 51..101
XX FT /note= "WPI region fragment"
XX
XX WO9604381-A1.
XX 15-FEB-1996.
XX
XX 28-JUL-1995; 95WO-EP003040.
XX 05-AUG-1994; 94GB-00015900.
XX (SMIK ) SMITHKLINE BEECHAM PLC.
XX

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PI Critchley IA, Dodd I, Barnett P, McDay DL;
XX
XX WPI; 1996-129397/13.
PT Polypeptide(s) derived from Staphylococcus aureus fibronectin binding
PT protein - inhibit binding of bacteria to extracellular matrix proteins,
PT for combating infection at the site of wounds and surgical implants, and
PT in oral hygiene.
XX
PS Claim 6; Page 24; 35pp; English.
XX
CC AAR90937-R90942 represent D3D4 polypeptides. These sequences correspond
CC to fragments of the Staphylococcus aureus fibronectin binding protein
CC (Fbp). This sequence corresponds to residues 81-181 of S.aureus J2385
CC Fbp, and also contains a portion of the wall region 1 (WR1). These
CC sequences, and monoclonal antibodies against them can be used to combat
CC infection at the site of wounds, surgical implants and other in-dwelling
CC devices (such as catheters), and as antiadherent agents in oral hygiene.
CC They can also be used in the manufacture of a medicament for the
CC prevention of adhesion of bacteria to extracellular matrix proteins
CC present on in-dwelling devices or in wounds, or of oral pathogens to
CC similar proteins on surfaces in the oral cavity
XX
SQ Sequence 101 AA;
Query Match 100.0%; Score 50; DB 2; Length 101;
Best Local Similarity 100.0%; Pred. No. 0.28;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TEIIEDDTNK 10
|||
Db 2 TEIIEDDTNK 11
RESULT 7
AAR90937
ID AAR90937 standard; peptide; 113 AA.
XX
AC AAR90937;
XX
DT 23-SEP-1996 (first entry)
XX
DE D3D4 polypeptide #1.
XX
KM Fibronectin binding protein; Fbp; S.aureus J2385; monoclonal antibody;
KM infection; surgical implant; antiadherent agent; hygiene; adhesion;
KM extracellular matrix protein; oral pathogen; oral cavity.
XX
OS Staphylococcus aureus.
XX
FH Key Location/Qualifiers
FT Region 1..21
FT /note= "D1 region fragment"
FT Region 22..59
FT /note= "D2 region"
FT Region 60..98
FT /note= "D3 region"
FT Region 99..113
FT /note= "D4 region"
FT Misc-difference 113
FT /note= "P113T"
XX
PN WO9604381-A1.
XX
PD 15-FEB-1996.
XX
PF 28-JUL-1995; 95WO-EP003040.
XX
PR 05-AUG-1994; 94GB-00015900.
XX
PA (SMIK) SMITHKLINE BEECHAM PLC.
XX
PI Critchley IA, Dodd I, Barnett P, McDay DL;

XX
DR WPI; 1996-129397/13.
XX
XX Polypeptide(s) derived from Staphylococcus aureus fibronectin binding
PT protein - inhibit binding of bacteria to extracellular matrix proteins,
PT for combating infection at the site of wounds and surgical implants, and
PT in oral hygiene.
XX
PS Claim 6; Page 24; 35pp; English.
XX
CC AAR90937-R90942 represent D3D4 polypeptides. These sequences correspond
CC to fragments of the Staphylococcus aureus fibronectin binding protein
CC (Fbp). This sequence corresponds to residues 18-130 of S.aureus J2385
CC Fbp, and also contains the D2 region, and a portion of the D1 region.
CC These sequences, and monoclonal antibodies against them can be used to
CC combat infection at the site of wounds, surgical implants and other in-
CC dwelling devices (such as catheters), and as antiadherent agents in oral
CC hygiene. They can also be used in the manufacture of a medicament for the
CC prevention of adhesion of bacteria to extracellular matrix proteins
CC present on in-dwelling devices or in wounds, or of oral pathogens to
CC similar proteins on surfaces in the oral cavity
XX
SQ Sequence 113 AA;
Query Match 100.0%; Score 50; DB 2; Length 113;
Best Local Similarity 100.0%; Pred. No. 0.31;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TEIIEDDTNK 10
|||
Db 65 TEIIEDDTNK 74
RESULT 8
AAR90940
ID AAR90940 standard; peptide; 124 AA.
XX
AC AAR90940;
XX
DT 23-SEP-1996 (first entry)
XX
DE D3D4 polypeptide #4.
XX
KM Fibronectin binding protein; Fbp; S.aureus J2385; monoclonal antibody;
KM infection; surgical implant; antiadherent agent; hygiene; adhesion;
KM extracellular matrix protein; oral pathogen; oral cavity.
XX
OS Staphylococcus aureus.
XX
FH Key Location/Qualifiers
FT Region 1..19
FT /note= "D2 region fragment"
FT Region 20..58
FT /note= "D3 region"
FT Region 59..62
FT /note= "D4 region"
FT Region 63..124
FT /note= "WR1 region"
XX
PN WO9604381-A1.
XX
PD 15-FEB-1996.
XX
PF 28-JUL-1995; 95WO-EP003040.
XX
PR 05-AUG-1994; 94GB-00015900.
XX
PA (SMIK) SMITHKLINE BEECHAM PLC.
XX
PI Critchley IA, Dodd I, Barnett P, McDay DL;
XX
DR WPI; 1996-129397/13.

PT Polypeptide(s) derived from Staphylococcus aureus fibronectin binding
 PT protein - inhibit binding of bacteria to extracellular matrix proteins,
 PT for combating infection at the site of wounds and surgical implants, and
 PT in oral hygiene.

PS Claim 6; Page 24; 35pp; English.

XX AAR90937-R90942 represent D3D4 polypeptides. These sequences correspond
 CC to fragments of the Staphylococcus aureus fibronectin binding protein
 CC (Fbp). This sequence corresponds to residues 58-181 of S. aureus J2385
 CC Fbp, and also contains a portion of the D2 region, and a portion of the
 CC wall region 1 (Wrl). These sequences, and monoclonal antibodies against
 CC Fbp, can be used to combat infection at the site of wounds, surgical
 CC implants and other in-dwelling devices (such as catheters), and as
 CC antiadherent agents in oral hygiene. They can also be used in the
 CC manufacture of a medicament for the prevention of adhesion of bacteria to
 CC extracellular matrix proteins present on in-dwelling devices or in
 CC wounds, or of oral pathogens to similar proteins on surfaces in the oral
 CC cavity.

XX Sequence 124 AA;

Query Match 100.0%; Score 50; DB 2; Length 124;
 Best Local Similarity 100.0%; Pred. No. 0.34;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TEIIEEDTNK 10
 |||||
 DB 25 TEIIEEDTNK 34

RESULT 9
 AAR90941

ID AAR90941 standard; peptide; 128 AA.

XX AAR90941;

DT 23-SEP-1996 (first entry)

XX D3D4 polypeptide #5.

XX Fibronectin binding protein; Fbp; S. aureus J2385; monoclonal antibody;
 KW infection; surgical implant; antiadherent agent; hygiene; adhesion;
 KW extracellular matrix protein; oral pathogen; oral cavity.

XX Staphylococcus aureus.

XX Key Location/Qualifiers

FT Region 1..23
 /note= "D2 region"

FT Region 24..62
 /note= "D3 region"

FT Region 63..77
 /note= "D4 region"

FT Region 78..128
 /note= "Wrl region"

XX WO9604381-A1.

XX 15-FEB-1996.

XX 28-JUL-1995; 95WO-EP003040.

XX 05-AUG-1994; 94GB-00015900.

XX (SMIK) SMITHKLINE BEECHAM PLC.
 XX Critchley IA, Dodd I, Barnett P, Mcbay DL;
 XX WPI, 1996-129397/13.

XX Polypeptide(s) derived from Staphylococcus aureus fibronectin binding
 PT protein - inhibit binding of bacteria to extracellular matrix proteins,

PT for combating infection at the site of wounds and surgical implants, and
 PT in oral hygiene.

PS Claim 6; Page 24; 35pp; English.

XX AAR90937-R90942 represent D3D4 polypeptides. These sequences correspond
 CC to fragments of the Staphylococcus aureus fibronectin binding protein
 CC (Fbp). This sequence corresponds to residues 54-181 of S. aureus J2385
 CC Fbp, and also contains the D2 region, and a portion of the wall region 1
 CC (Wrl). These sequences, and monoclonal antibodies against them can be
 CC used to combat infection at the site of wounds, surgical implants and
 CC other in-dwelling devices (such as catheters), and as antiadherent agents
 CC in oral hygiene. They can also be used in the manufacture of a medicament
 CC for the prevention of adhesion of bacteria to extracellular matrix
 CC proteins present on in-dwelling devices or in wounds, or of oral
 CC pathogens to similar proteins on surfaces in the oral cavity

XX Sequence 128 AA;

Query Match 100.0%; Score 50; DB 2; Length 128;
 Best Local Similarity 100.0%; Pred. No. 0.35;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TEIIEEDTNK 10
 |||||
 DB 29 TEIIEEDTNK 38

RESULT 10
 AAR58806

ID AAR58806 standard; protein; 130 AA.

XX AAR58806;

DT 25-MAR-2003 (revised)
 DT 30-MAR-1995 (first entry)

XX Fibronectin binding domain D1-D4(709-838 (P838T)).

XX Fibronectin binding protein; Fbp; fibronectin binding domain;
 KW monoclonal antibody; MAb; adhesion; Gram-positive bacterium; bacteremia;
 KW Escherichia coli.

XX Staphylococcus aureus.

XX WO9418327-A1.

XX 18-AUG-1994.

XX 04-FEB-1994; 94WO-GB000215.

XX 05-FEB-1993; 93GB-00002289.

XX 20-OCT-1993; 93GB-00021592.

XX (SMIK) SMITHKLINE BEECHAM PLC.

XX Burnham MKR, Chopra I, Critchley IA, Knowles DJC;
 XX WPI, 1994-279748/34.

XX Fibronectin binding protein and monoclonal antibodies specific for Fbp -
 PT devices or wounds.

XX Disclosure: Page 30; 40pp; English.

XX Polypeptides corresponding to residues G709-T886 plus PRVPT, G709-
 CC P838(P838T) and G709-P838 (AAR58805-07, respectively) of S. aureus J2385
 CC (NCIMB 40532) Fbp type A fibronectin binding domain D1-D4 region
 CC (AAR58808) were expressed in E. coli BL21 (DE4) and used to raise MAbs
 CC specific for Fbp. (Updated on 25-MAR-2003 to correct PN field.)

XX Sequence 130 AA;

Query Match 100.0%; Score 50; DB 2; Length 130;
 Best Local Similarity 100.0%; Pred. No. 0.36;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TEIIEEDTNK 10
 |||||
 DB 82 TEIIEEDTNK 91

RESULT 11

AAR5807
 ID AAR58807 standard; protein; 130 AA.

XX AAR58807;

AC AAR58807;
 XX 25-MAR-2003 (revised)
 DT 30-MAR-1995 (first entry)

XX Fibronectin binding domain D1-D4(709-838).

XX Fibronectin binding protein; Fbp; fibronectin binding domain;

KW monoclonal antibody; MAb; adhesion; Gram-positive bacterium; bacteremia;

KM Escherichia coli.

OS Staphylococcus aureus.

XX WO9418327-A1.

XX 18-AUG-1994.

XX 04-FEB-1994; 94WO-GB000215.

XX 05-FEB-1993; 93GB-00002289.

XX 20-OCT-1993; 93GB-00021592.

XX (SMIK) SMITHKLINE BEECHAM PLC.

XX Burnham MKR, Chopra I, Critchley IA, Knowles DVC;

XX WPI; 1994-279748/34.

XX Fibronectin binding protein and monoclonal antibodies specific for Fbp -
 PT useful to prevent adherence of Gram-positive bacteria to indwelling
 PT devices or wounds.

XX Disclosure; Page 30; 40pp; English.

XX Polypeptides corresponding to residues G709-T886 plus PRIVPT, G709-
 CC P838(P838T) and G709-P838 (AAR58805-07, respectively) of S. aureus J2385

CC (NCIMB 40532) Fbp type A fibronectin binding domain D1-D4 region
 CC (AAR58808) were expressed in E. coli BL21(DE4) and used to raise MAbs

CC specific for Fbp. (Updated on 25-MAR-2003 to correct PN field.)

XX Sequence 130 AA;

Query Match 100.0%; Score 50; DB 2; Length 130;
 Best Local Similarity 100.0%; Pred. No. 0.36;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TEIIEEDTNK 10
 |||||
 DB 82 TEIIEEDTNK 91

RESULT 12

AAR91202
 ID AAR91202 standard; peptide; 130 AA.

XX AAR91202;

XX 13-NOV-1996 (first entry)

DE D1-D4 fibronectin binding domains.

XX Fibronectin; oral hygiene; gingivitis; gum disease; adhesion;

KW periodontitis; oral pathogens; caries; calculus; candidiasis; oral surgery;

KW tissue regeneration; irrigation; toothpaste; dentifrice; mouthwash;

KM lozenge.

XX Staphylococcus aureus.

XX WO9604003-A1.

XX 15-FEB-1996.

XX 18-JUL-1995; 95WO-EP002825.

XX 05-AUG-1994; 94GB-00015902.

XX (SMIK) SMITHKLINE BEECHAM PLC.

XX Barnett P, Critchley IA, Dodd I;

XX WPI; 1996-129122/13.

XX Prevention of adherence of oral pathogens in the oral cavity, partic-
 PT tooth surfaces - by application of a fibronectin binding protein or
 PT polypeptide or a monoclonal antibody or fragment against it.

XX Claim 5; Page 32; 41pp; English.

XX Adherence of oral pathogens, particularly to tooth surfaces, can be
 CC prevented by application of a fibronectin binding protein or polypeptide.

CC The fibronectin binding protein or polypeptide is useful in the
 CC manufacture of oral hygiene compositions, eg. toothpaste, liquid

CC dentifrice, mouthwash or lozenge. They are useful to prevent the plaque-
 CC related development of carious lesions, gingivitis, calculus or

CC periodontal disease and to combat oral cavity infections, e.g.
 CC candidiasis. They may also be useful in oral surgery e.g. in guided

CC tissue regeneration procedures to prevent subsequent bacterial infection,
 CC and for irrigation of periodontal pockets. This sequence corresponds to

CC amino acids 709-838 of the D1-D4 fibronectin binding domain of
 CC Staphylococcus aureus

XX Sequence 130 AA;

Query Match 100.0%; Score 50; DB 2; Length 130;
 Best Local Similarity 100.0%; Pred. No. 0.36;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TEIIEEDTNK 10
 |||||
 DB 82 TEIIEEDTNK 91

RESULT 13

AAR91201
 ID AAR91201 standard; peptide; 130 AA.

XX AAR91201;

XX 13-NOV-1996 (first entry)

XX D1-D4 fibronectin binding domains.

XX Fibronectin; oral hygiene; gingivitis; gum disease; adhesion;

KW periodontitis; oral pathogens; caries; calculus; candidiasis; oral surgery;

KW tissue regeneration; irrigation; toothpaste; dentifrice; mouthwash;

XX lozenge.

XX Staphylococcus aureus.

XX WO9604003-A1.

XX 15-FEB-1996.

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XX PF 18-JUL-1995; 95WO-EP002825.
XX PR 05-AUG-1994; 94GB-00015902.
XX PA (SMIK ) SMITHKLINE BEECHAM PLC.
XX PI Barnett P, Critchley IA, Dodd I;
XX DR WPI; 1996-129122/13.
XX PT Prevention of adherence of oral pathogens in the oral cavity, partic.
XX PF tooth surfaces - by application of a fibronectin binding protein or
XX PT polypeptide or a monoclonal antibody or fragment against it.
XX PS Claim 5; Page 31-32; 41pp; English.
XX CC Adherence of oral pathogens, particularly to tooth surfaces, can be
XX CC prevented by application of a fibronectin binding protein or polypeptide.
XX CC The fibronectin binding protein or polypeptide is useful in the
XX CC manufacture of oral hygiene compositions, eg. toothpaste, liquid
XX CC dentifrice, mouthwash or lozenge. They are useful to prevent the plaque-
XX CC related development of carious lesions, gingivitis, calculus or
XX CC periodontal disease and to combat oral cavity infections, e.g. in guided
XX CC candidiasis. They may also be useful in oral surgery e.g. in guided
XX CC tissue regeneration procedures to prevent subsequent bacterial infection,
XX CC and for irrigation of periodontal pockets. This sequence corresponds to
XX CC amino acids 709-838 of the D1-D4 fibronectin binding domain of
XX CC Staphylococcus aureus with a P838T substitution
XX SQ Sequence 130 AA;

Query Match 100.0%; Score 50; DB 2; Length 130;
Best Local Similarity 100.0%; Pred. No. 0.36; Mismatches 0; Indels 0; Gaps 0;
Matches 10; Conservative 0;

QY 1 TEIIEEDTNK 10
DB 82 TEIIEEDTNK 91

RESULT 14
AAV29089
ID AAV29089 standard; protein; 134 AA.
XX AC AAV29089;
XX DT 28-SEP-1999 (first entry)
XX DE Cloned fibronectin binding protein binding domain (FnBAB) sequence.
XX KM Bovine herpes virus-2; BHV-2; cytokine; immune response; immunogen; IL;
XX KM interleukin; colony stimulating factor; CSF; interferon; IFN; TNF;
XX KM tumour necrosis factor; recombinant virus; vaccine; mucosal disease;
XX KM mastitis; breast cancer; stress-induced disease; binding domain; FnBAB;
XX KM fibronectin binding protein.
XX OS Staphylococcus aureus.
XX PN WO9916892-A1.
XX PD 08-APR-1999.
XX PF 29-SEP-1998; 98WO-GB002927.
XX PR 29-SEP-1997; 97GB-00020633.
XX PA (UYBR-) UNIV BRISTOL.
XX PI Bradley AJ, Duffas WP;
XX DR WPI; 1999-255101/21.
XX DR N-PSDB; AAX91506.

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XX PF New bovine herpes virus-2 vectors.
XX PS Example 2; Fig 8A-B; 130pp; English.
XX CC The invention provides bovine herpes virus-2 (BHV-2) based vectors that
XX CC comprise at least one cytokine-encoding DNA sequence. The expression of
XX CC cytokines in mammals can up-regulate immune responses to the immunogens.
XX CC The cytokine is selected from interleukins (IL), colony stimulating
XX CC factors (CSF), interferons (IFN) and tumour necrosis factors (TNF). The
XX CC BHV-2 based vector or recombinant virus can be used as vaccine. They can
XX CC be used for preventing or treating a mucosal disease in a subject, e.g.
XX CC ruminants, cattle, sheep, goats, dogs, cats, horses, or man, particularly
XX CC mastitis in cows or breast cancers in humans. They can also be used for
XX CC preventing or treating a stress-induced disease. The present sequence
XX CC represents a S. aureus fibronectin binding protein binding domain
XX CC sequence FnBAB, the gene cloned for use in this invention. The gene has
XX CC 97.8 percent identity when compared to the previously published sequences
XX CC FnBA and FnBB
XX SQ Sequence 134 AA;

Query Match 100.0%; Score 50; DB 2; Length 134;
Best Local Similarity 100.0%; Pred. No. 0.37; Mismatches 0; Indels 0; Gaps 0;
Matches 10; Conservative 0;

QY 1 TEIIEEDTNK 10
DB 82 TEIIEEDTNK 91

RESULT 15
AAV29088
ID AAV29088 standard; protein; 134 AA.
XX AC AAV29088;
XX DT 28-SEP-1999 (first entry)
XX DE S. aureus fibronectin binding protein B (FnBB) binding domain.
XX KM Bovine herpes virus-2; BHV-2; cytokine; immune response; immunogen; IL;
XX KM interleukin; colony stimulating factor; CSF; interferon; IFN; TNF;
XX KM tumour necrosis factor; recombinant virus; vaccine; mucosal disease;
XX KM mastitis; breast cancer; stress-induced disease; binding domain; FnBB;
XX KM fibronectin binding protein.
XX OS Staphylococcus aureus.
XX PN WO9916892-A1.
XX PD 08-APR-1999.
XX PF 29-SEP-1998; 98WO-GB002927.
XX PR 29-SEP-1997; 97GB-00020633.
XX PA (UYBR-) UNIV BRISTOL.
XX PI Bradley AJ, Duffas WP;
XX DR WPI; 1999-255101/21.
XX DR N-PSDB; AAX91505.
XX PT New bovine herpes virus-2 vectors.
XX PS Example 2; Fig 8A-B; 130pp; English.
XX CC The invention provides bovine herpes virus-2 (BHV-2) based vectors that
XX CC comprise at least one cytokine-encoding DNA sequence. The expression of
XX CC cytokines in mammals can up-regulate immune responses to the immunogens.
XX CC The cytokine is selected from interleukins (IL), colony stimulating
XX CC factors (CSF), interferons (IFN) and tumour necrosis factors (TNF). The

```

CC BHV-2 based vector or recombinant virus can be used as vaccines. They can
CC be used for preventing or treating a mucosal disease in a subject, e.g.
CC ruminants, cattle, sheep, goats, dogs, cats, horses, or man, particularly
CC mastitis in cows or breast cancers in humans. They can also be used for
CC preventing or treating a stress-induced disease. The present sequence
CC represents the binding domain of a previously published S. aureus
CC fibronectin binding protein B (FnBB) sequence. The FnB binding domain
CC gene sequence FNBAB, cloned for use in this invention has 97.8 percent
CC identity when compared to the previously published FNB A and FnBB gene
CC sequences
XX
SQ Sequence 134 AA;

Query Match 100.0%; Score 50; DB 2; Length 134;
Best local Similarity 100.0%; Pred. No. 0.37;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TEIIEEDTNK 10
Db 82 TEIIEEDTNK 91

Search completed: October 25, 2005, 21:29:10
Job time : 69.7126 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 22, 2005, 07:41:53 ; Search time 17.2989 Seconds
(without alignments)
43.153 Million cell updates/sec

Title: US-10-731-238-90
Perfect score: 50
Sequence: 1 TEILEDPYTK 10

Scoring table: BIOSUM62
Gapop 10.0, Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :
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4: /cgn2_6/ptodata/1/1aa/6B COMB.pep:*
5: /cgn2_6/ptodata/1/1aa/PTUS COMB.pep:*
6: /cgn2_6/ptodata/1/1aa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	50	100.0	10	US-09-010-317-90	Sequence 90, Appl
2	50	100.0	37	US-08-234-622A-4	Sequence 4, Appl
3	50	100.0	38	US-08-729-767-5	Sequence 5, Appl
4	50	100.0	114	US-08-259-000-3	Sequence 3, Appl
5	50	100.0	130	US-08-459-135A-7	Sequence 7, Appl
6	50	100.0	130	US-08-459-135A-8	Sequence 8, Appl
7	50	100.0	130	US-08-495-559-7	Sequence 7, Appl
8	50	100.0	130	US-08-495-559-8	Sequence 8, Appl
9	50	100.0	139	US-08-856-253-8	Sequence 8, Appl
10	50	100.0	174	US-08-459-135A-10	Sequence 10, Appl
11	50	100.0	174	US-08-459-135A-13	Sequence 13, Appl
12	50	100.0	174	US-08-495-559-10	Sequence 10, Appl
13	50	100.0	174	US-08-495-559-13	Sequence 13, Appl
14	50	100.0	176	US-08-495-559-6	Sequence 6, Appl
15	50	100.0	178	US-08-459-135A-12	Sequence 12, Appl
16	50	100.0	178	US-08-495-559-12	Sequence 12, Appl
17	50	100.0	181	US-08-459-135A-6	Sequence 6, Appl
18	50	100.0	559	US-08-956-171E-5251	Sequence 5251, Ap
19	50	100.0	559	US-08-781-986A-5251	Sequence 5251, Ap
20	50	100.0	1027	US-08-956-171E-5254	Sequence 5254, Ap
21	50	100.0	1027	US-08-781-986A-5254	Sequence 5254, Ap
22	40	80.0	10	US-09-010-317-91	Sequence 91, Appl
23	40	80.0	38	US-08-294-189-8	Sequence 8, Appl
24	39	78.0	10	US-09-010-317-89	Sequence 89, Appl
25	36	72.0	335	US-09-248-796A-20532	Sequence 20532, A
26	35	70.0	351	US-09-248-796A-15236	Sequence 15236, A
27	34	68.0	285	US-09-107-532A-3967	Sequence 3967, Ap

28	34	68.0	285	6	5171685-4	Patent No. 5171685
29	34	68.0	285	6	5518916-4	Patent No. 5518916
30	34	68.0	285	6	5171685-4	Patent No. 5171685
31	34	68.0	285	6	5518916-4	Patent No. 5518916
32	34	68.0	360	1	US-09-043-627-2	Sequence 2, Appl
33	34	68.0	473	3	US-08-073-383-6	Sequence 6, Appl
34	34	68.0	473	3	US-09-460-421-17	Sequence 17, Appl
35	34	68.0	473	5	PCT-US94-06365-6	Sequence 6, Appl
36	34	68.0	637	4	US-09-248-796A-19134	Sequence 19134, A
37	34	68.0	650	4	US-09-248-796A-15925	Sequence 15925, A
38	34	68.0	1014	4	US-09-949-016-8229	Sequence 8229, Ap
39	33	66.0	1395	4	US-09-270-767-45417	Sequence 45417, A
40	33	66.0	401	4	US-09-248-796A-15172	Sequence 15172, A
41	33	66.0	557	4	US-09-138-277C-3	Sequence 3, Appl
42	33	66.0	806	4	US-08-684-005-2	Sequence 2, Appl
43	33	66.0	1045	4	US-09-489-039A-8589	Sequence 8589, Ap
44	33	66.0	1179	4	US-09-792-024-89	Sequence 89, Appl
45	32	64.0	10	4	US-09-010-317-92	Sequence 92, Appl

ALIGNMENTS

RESULT 1
US-09-010-317-90
Sequence 90, Application US/09010317
Patent No. 6685943
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
APPLICANT: Patti, Joseph M.
APPLICANT: House-Pompeo, Karen L.
APPLICANT: Speziale, Pietro
APPLICANT: Job, Danny
APPLICANT: McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
TITLE OF INVENTION: AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAMK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 90:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-09-010-317-90
Query Match 100.0%; Score 50; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0074;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 TEIIIEDTNK 10
Db 1 TEIIIEDTNK 10

RESULT 2
US-08-234-622A-4
; Sequence 4, Application US/08234622A
; Patent No. 5440014
; GENERAL INFORMATION:
; APPLICANT: HOOK, Magnus
; APPLICANT: MCGAVIN, Martin
; APPLICANT: RAUCCI, Giuseppe
; TITLE OF INVENTION: A FIBRONECTIN BINDING PEPTIDE
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Doane, Swecker & Mathis
; STREET: P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/234,622A
; FILING DATE: 28-APR-1994
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: SE 9002617-0
; FILING DATE: 10-AUG-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/SE91/00534
; FILING DATE: 09-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Meuth, Donna M
; REGISTRATION NUMBER: 36,607
; REFERENCE/DOCKET NUMBER: 012885-044
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 37 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-234-622A-4
Query Match 100.0%; Score 50; DB 1; Length 37;
Best Local Similarity 100.0%; Pred. No. 0.028;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 TEIIIEDTNK 10
Db 5 TEIIIEDTNK 14

RESULT 3
US-08-729-767-5
; Sequence 5, Application US/08729767
; Patent No. 5770702
; GENERAL INFORMATION:
; APPLICANT: HOOK, Magnus
; APPLICANT: LINDBERG, Martin Kjell
; APPLICANT: SIGNAS, Lars Christer
; APPLICANT: WADSTROM, Torkel Mikael

; APPLICANT: FROMAN, Gunnar
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN AS WELL AS
; TITLE OF INVENTION: ITS PREPARATION
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Doane, Swecker & Mathis, L.L.P.
; STREET: P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/729,767
; FILING DATE: 07-OCT-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/259,000
; FILING DATE: 13-JUN-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/007,817
; FILING DATE: 22-JAN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/201,028
; FILING DATE: 01-JUN-1988
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: SE 8702272-9
; FILING DATE: 01-JUN-1987
; ATTORNEY/AGENT INFORMATION:
; NAME: McGowan, Malcolm K.
; REGISTRATION NUMBER: 39,300
; REFERENCE/DOCKET NUMBER: 012889-036
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 38 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-729-767-5

Query Match 100.0%; Score 50; DB 1; Length 38;
Best Local Similarity 100.0%; Pred. No. 0.029;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 TEIIIEDTNK 10
Db 6 TEIIIEDTNK 15

RESULT 4
US-08-259-000-3
; Sequence 3, Application US/08259000
; Patent No. 5571514
; GENERAL INFORMATION:
; APPLICANT: HOOK, Magnus
; APPLICANT: LINDBERG, Martin Kjell
; APPLICANT: SIGNAS, Lars Christer
; APPLICANT: WADSTROM, Torkel Mikael
; APPLICANT: FROMAN, Gunnar
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN AS WELL AS
; TITLE OF INVENTION: ITS PREPARATION
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Doane, Swecker & Mathis
; STREET: P.O. Box 1404

Wed Oct 26 15:03:15 2005

us-10-731-238-90.rat

Page 3

CITY: Alexandria
STATE: Virginia
COUNTRY: United States
ZIP: 22113-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA: US/08/259,000
APPLICATION NUMBER: 13-JUN-1994
FILING DATE: 13-JUN-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA: SE 8702272-9
APPLICATION NUMBER: SE 8702272-9
FILING DATE: 01-JUN-1987
ATTORNEY/AGENT INFORMATION:
NAME: Meuth, Donna M
REGISTRATION/DOCKET NUMBER: 012885-062
REFERENCE/DOCKET NUMBER: 836-6620
TELEPHONE: (703) 836-2021
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 114 amino acids
TYPE: amino acid
STRANDEDNESS: linear
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-259-000-3
Query Match 100.0%; Score 50; DB 1; Length 114; Gaps 0;
Best Local Similarity 100.0%; Pred. No. 0.089; 0; Indels 0; Mismatches 0;
Matches 10; Conservative 0;
QY 1 TEIIEEDTNK 10
82 TEIIEEDTNK 91
DB
RESULT 5
US-08-459-135A-7
Sequence 7, Application US/08459135A
GENERAL INFORMATION:
PATENT NO. 5955078
APPLICANT: BURHAM, Martin Karl Russel
APPLICANT: CHOPRA, Ian
APPLICANT: CRITCHLEY, Ian Alfred Charles
APPLICANT: KNOWLES, David Justin Charles
APPLICANT: MONOCLONAL ANTIBODY AND THEIR US
TITLE OF INVENTION: 15
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
ADDRESS: 709 Swedeland Road
STREET: King of Prussia
CITY: PA
STATE: PA
COUNTRY: U.S.A.
ZIP: 19406-0939
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: Fastseq, Version 2.0
CURRENT APPLICATION DATA: US/08/459,135A
APPLICATION NUMBER: 02-JUN-1995
FILING DATE: 02-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA: PCT/GB/94/00215
APPLICATION NUMBER: PCT/GB/94/00215
FILING DATE: 04-Feb-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:

NAME: Gimm, Edward R 38, 891
REGISTRATION/DOCKET NUMBER: P30591C2
REFERENCE/DOCKET INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-4478
TELEFAX: 610-270-5090
TELEX: 610-270-5090
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 130 amino acids
TYPE: amino acid
STRANDEDNESS: linear
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-459-135A-8
Query Match 100.0%; Score 50; DB 2; Length 130; Gaps 0;
Best Local Similarity 100.0%; Pred. No. 0.1; 0; Indels 0; Mismatches 0;
Matches 10; Conservative 0;
QY 1 TEIIEEDTNK 10
82 TEIIEEDTNK 91
DB
RESULT 6
US-08-459-135A-8
Sequence 8, Application US/08459135A
GENERAL INFORMATION:
PATENT NO. 5955078
APPLICANT: BURHAM, Martin Karl Russel
APPLICANT: CHOPRA, Ian
APPLICANT: CRITCHLEY, Ian Alfred Charles
APPLICANT: KNOWLES, David Justin Charles
APPLICANT: MONOCLONAL ANTIBODY AND THEIR US
TITLE OF INVENTION: 15
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
ADDRESS: 709 Swedeland Road
STREET: King of Prussia
CITY: PA
STATE: PA
COUNTRY: U.S.A.
ZIP: 19406-0939
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: Fastseq, Version 2.0
CURRENT APPLICATION DATA: US/08/459,135A
APPLICATION NUMBER: 02-JUN-1995
FILING DATE: 02-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA: PCT/GB/94/00215
APPLICATION NUMBER: PCT/GB/94/00215
FILING DATE: 04-Feb-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Gimm, Edward R 38, 891
REGISTRATION/DOCKET NUMBER: P30591C2
REFERENCE/DOCKET INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-4478
TELEFAX: 610-270-5090
TELEX: 610-270-5090
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 130 amino acids
TYPE: amino acid
STRANDEDNESS: linear
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-459-135A-8
Query Match 100.0%; Score 50; DB 2; Length 130; Gaps 0;
Best Local Similarity 100.0%; Pred. No. 0.1; 0; Indels 0; Mismatches 0;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 TEIEEDTNK 10
Db 82 TEIEEDTNK 91

Page

RESULT 7
US-08-495-559-7
Sequence 7, Application US/08495559A
Patent No. 6054572
GENERAL INFORMATION:
APPLICANT: BURHAM, Martin Karl Russel
APPLICANT: CHOPRA, Ian
APPLICANT: CRITCHLEY, Ian Alfred
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN, MONOCLONAL
FILE REFERENCE: P30591
CURRENT APPLICATION NUMBER: US/08/495,559A
EARLIER FILING DATE: 1995-08-03
EARLIER APPLICATION NUMBER: GB 9302289.5
EARLIER FILING DATE: 1993-02-05
NUMBER OF SEQ ID NOS: 13
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO: 7
LENGTH: 130
TYPE: PRT
ORGANISM: Staphylococcus aureus

Query Match
Best Local Similarity 100.0%; Score 50; DB 3; Length 130;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 TEIEEDTNK 10
Db 82 TEIEEDTNK 91

RESULT 8
US-08-495-559-8
Sequence 8, Application US/08495559A
Patent No. 6054572
GENERAL INFORMATION:
APPLICANT: BURHAM, Martin Karl Russel
APPLICANT: CHOPRA, Ian
APPLICANT: CRITCHLEY, Ian Alfred
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN, MONOCLONAL
FILE REFERENCE: P30591
CURRENT APPLICATION NUMBER: US/08/495,559A
EARLIER FILING DATE: 1995-08-03
EARLIER APPLICATION NUMBER: GB 9302289.5
EARLIER FILING DATE: 1993-02-05
NUMBER OF SEQ ID NOS: 13
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO: 8
LENGTH: 130
TYPE: PRT
ORGANISM: Staphylococcus aureus

Query Match
Best Local Similarity 100.0%; Score 50; DB 3; Length 130;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 TEIEEDTNK 10

Db 82 TEIEEDTNK 91

RESULT 9
US-08-856-253-8
Sequence 8, Application US/08856253
Patent No. 6288214
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
APPLICANT: Patti, Joseph M.
APPLICANT: House-Pompeo, Karen
APPLICANT: Schanam, Narayana
TITLE OF INVENTION: COLLAGEN BINDING PROTEIN COMPOSITIONS
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: Texas
COUNTRY: U.S.
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: 514
CLASSIFICATION: US/08/856,253
FILING DATE: Concurrently Herewith
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 60/017,678
ATTORNEY/AGENT INFORMATION:
NAME: Kitchell, Barbara S.
REGISTRATION NUMBER: 33,928
TELECOMMUNICATIONS INFORMATION:
TELEPHONE: (512) 418-3000
TELEFAX: (512) 474-7577
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 139 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear

Query Match
Best Local Similarity 100.0%; Score 50; DB 3; Length 139;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 TEIEEDTNK 10
Db 96 TEIEEDTNK 105

RESULT 10
US-08-459-135A-10
Sequence 10, Application US/08459135A
Patent No. 5935078
GENERAL INFORMATION:
APPLICANT: BURHAM, Martin Karl Russel
APPLICANT: CHOPRA, Ian
APPLICANT: CRITCHLEY, Ian Alfred
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN, MONOCLONAL ANTIBODY AND THEIR USE
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation

```

; STREET: 709 Swedeland Road
; CITY: King of Prussia
; STATE: PA
; COUNTRY: U.S.A.
; ZIP: 19406-0939
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: DOS
; SOFTWARE: Fastseq, Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/459,135A
; FILING DATE: 02-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB/94/00215
; FILING DATE: 04-Feb-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Gimm, Edward R
; REGISTRATION NUMBER: 38,891
; REFERENCE/DOCKET NUMBER: P30591C2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-270-4478
; TELEFAX: 610-270-5090
; TELEX:
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 174 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: Protein
; US-08-459-135A-10

Query Match      100.0%; Score 50; DB 2; Length 174;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 TEIIEEDPTNK 10
Db      82 TEIIEEDPTNK 91

RESULT 11
US-08-459-135A-13
; Sequence 13, Application US/08459135A
; Patent No. 5955078
; GENERAL INFORMATION:
; APPLICANT: BURHAM, Martin Karl Russel
; APPLICANT: CHOPRA, Ian
; APPLICANT: CRITCHLEY, Ian Alfred
; APPLICANT: KNOWLES, David Justin Charles
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN: MONOCLONAL ANTIBODY AND THEIR US
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corporation
; STREET: 709 Swedeland Road
; CITY: King of Prussia
; STATE: PA
; COUNTRY: U.S.A.
; ZIP: 19406-0939
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: DOS
; SOFTWARE: Fastseq, Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/459,135A
; FILING DATE: 02-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB/94/00215
; FILING DATE: 04-Feb-1994
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; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Gimm, Edward R
; REGISTRATION NUMBER: 38,891
; REFERENCE/DOCKET NUMBER: P30591C2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-270-4478
; TELEFAX: 610-270-5090
; TELEX:
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 174 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-459-135A-13

Query Match      100.0%; Score 50; DB 2; Length 174;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 TEIIEEDPTNK 10
Db      82 TEIIEEDPTNK 91

RESULT 12
US-08-495-559-10
; Sequence 10, Application US/08495559A
; Patent No. 6054572
; GENERAL INFORMATION:
; APPLICANT: BURHAM, Martin Karl Russel
; APPLICANT: CHOPRA, Ian
; APPLICANT: CRITCHLEY, Ian Alfred
; APPLICANT: KNOWLES, David Justin Charles
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN: MONOCLONAL
; TITLE OF INVENTION: ANTIBODY AND THEIR USE IN PREVENTING BACTERIAL ADHESION
; FILE REFERENCE: P30591
; CURRENT APPLICATION NUMBER: US/08/495,559A
; CURRENT FILING DATE: 1995-08-03
; EARLIER FILING DATE: 1993-02-05
; EARLIER APPLICATION NUMBER: GB 9302289.5
; EARLIER FILING DATE: 1993-02-05
; EARLIER APPLICATION NUMBER: GB 9321592.9
; EARLIER FILING DATE: 1993-10-20
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 10
; LENGTH: 174
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
; US-08-495-559-10

Query Match      100.0%; Score 50; DB 3; Length 174;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 TEIIEEDPTNK 10
Db      82 TEIIEEDPTNK 91

RESULT 13
US-08-495-559-13
; Sequence 13, Application US/08495559A
; Patent No. 6054572
; GENERAL INFORMATION:
; APPLICANT: BURHAM, Martin Karl Russel
; APPLICANT: CHOPRA, Ian
; APPLICANT: CRITCHLEY, Ian Alfred
; APPLICANT: KNOWLES, David Justin Charles
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN: MONOCLONAL
; TITLE OF INVENTION: ANTIBODY AND THEIR USE IN PREVENTING BACTERIAL ADHESION
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; FILE REFERENCE: P30591
; CURRENT APPLICATION NUMBER: US/08/495.559A
; CURRENT FILING DATE: 1995-08-03
; EARLIER APPLICATION NUMBER: GB 9302289.5
; EARLIER FILING DATE: 1993-02-05
; EARLIER APPLICATION NUMBER: GB 9321592.9
; EARLIER FILING DATE: 1993-10-20
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 13
; LENGTH: 174
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-08-495-559-13

Query Match      100.0%; Score 50; DB 3; Length 174;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 TEIIEEDTNK 10
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        82 TEIIEEDTNK 91

RESULT 14
US-08-495-559-6
; Sequence 6, Application US/08495559A
; Patent No. 6054572
; GENERAL INFORMATION:
; APPLICANT: BURHAM, Martin Karl Russel
; APPLICANT: CHOPRA, Ian
; APPLICANT: CRITCHLEY, Ian Alfred
; APPLICANT: KNOWLES, David Justin Charles
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN: MONOCLONAL
; TITLE OF INVENTION: ANTIBODY AND THEIR USE IN PREVENTING BACTERIAL ADHESION
; FILE REFERENCE: P30591
; CURRENT APPLICATION NUMBER: US/08/495.559A
; CURRENT FILING DATE: 1995-08-03
; EARLIER APPLICATION NUMBER: GB 9302289.5
; EARLIER FILING DATE: 1993-02-05
; EARLIER APPLICATION NUMBER: GB 9321592.9
; EARLIER FILING DATE: 1993-10-20
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 176
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-08-495-559-6

Query Match      100.0%; Score 50; DB 3; Length 176;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 TEIIEEDTNK 10
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        82 TEIIEEDTNK 91

RESULT 15
US-08-459-135A-12
; Sequence 12, Application US/08459135A
; Patent No. 5955078
; GENERAL INFORMATION:
; APPLICANT: BURHAM, Martin Karl Russel
; APPLICANT: CHOPRA, Ian
; APPLICANT: CRITCHLEY, Ian Alfred
; APPLICANT: KNOWLES, David Justin Charles
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN: MONOCLONAL ANTIBODY AND THEIR US
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: SmithKline Beecham Corporation
; STREET: 709 Swedeland Road
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; CITY: King of Prussia
; STATE: PA
; COUNTRY: U.S.A.
; ZIP: 19406-0939
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: Fastseq, Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/459,135A
; FILING DATE: 02-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB/94/00215
; FILING DATE: 04-Feb-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Glimml, Edward R
; REGISTRATION NUMBER: 38,891
; REFERENCE/DOCKET NUMBER: P30591C2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-270-4478
; TELEFAX: 610-270-5090
; TELEX:
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 178 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Protein
US-08-459-135A-12

Query Match      100.0%; Score 50; DB 2; Length 178;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 TEIIEEDTNK 10
        |||||
        82 TEIIEEDTNK 91
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Search completed: October 22, 2005, 09:35:44
Job time : 18.2989 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 22, 2005, 12:39:57 ; Search time 56.1494 Seconds
(without alignments)
74.354 Million cell updates/sec

Title: US-10-731-238-90
Perfect score: 50
Sequence: 1 TEIIEPTNK 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1862951 seqs, 417491010 residues

Total number of hits satisfying chosen parameters: 1862951

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database :

Published Applications_AA:*

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12: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*

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14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*

15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep:*

16: /cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pep:*

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21: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*

22: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	50	100.0	10	US-10-731-238-90	Sequence 90, Appl
2	50	100.0	37	US-11-066-697-1134	Sequence 1134, Ap
3	50	100.0	139	US-09-813-820-8	Sequence 8, Appl
4	50	100.0	388	US-08-901-062-1	Sequence 1, Appl
5	50	100.0	559	US-08-781-986A-5251	Sequence 5251, Ap
6	50	100.0	559	US-10-329-624-5251	Sequence 5251, Ap
7	50	100.0	940	US-10-470-048B-424	Sequence 424, Ap
8	50	100.0	948	US-10-470-048B-69	Sequence 69, Appl
9	50	100.0	1018	US-09-815-242-5797	Sequence 5797, Ap
10	50	100.0	1018	US-09-815-242-12838	Sequence 12838, A
11	50	100.0	1018	US-10-470-048B-68	Sequence 68, Appl

12	50	100.0	1027	8	US-08-781-986A-5254	Sequence 5254, Ap
13	50	100.0	1027	15	US-10-329-624-5254	Sequence 5254, Ap
14	45	90.0	961	15	US-10-282-122A-43778	Sequence 43778, A
15	45	90.0	978	9	US-09-815-242-5456	Sequence 5456, Ap
16	45	90.0	1001	9	US-09-815-242-12686	Sequence 12686, A
17	45	90.0	1038	15	US-10-282-122A-43827	Sequence 43827, A
18	40	80.0	10	10	US-10-731-238-91	Sequence 91, Appl
19	40	80.0	387	16	US-10-408-765A-2232	Sequence 2232, Ap
20	40	80.0	403	16	US-10-469-864-2	Sequence 2, Appl
21	39	78.0	10	18	US-10-731-238-89	Sequence 89, Appl
22	38	76.0	142	9	US-10-424-599-149795	Sequence 149795, A
23	38	76.0	61	9	US-09-864-761-45543	Sequence 45543, A
24	37	74.0	61	14	US-10-091-483-166	Sequence 166, Ap
25	37	74.0	283	15	US-10-424-599-203454	Sequence 203454, Ap
26	37	74.0	168	16	US-10-165-289A-2	Sequence 2, Appl
27	36	72.0	889	18	US-10-450-763-34639	Sequence 34639, A
28	36	72.0	108	20	US-11-097-143-21987	Sequence 21987, A
29	35	70.0	283	18	US-10-510-408-129	Sequence 129, Ap
30	35	70.0	362	16	US-10-425-115-363098	Sequence 363098, A
31	35	70.0	456	15	US-10-282-122A-60636	Sequence 60636, A
32	35	70.0	1255	20	US-11-097-143-22923	Sequence 22923, A
33	35	70.0	76	16	US-10-767-701-36626	Sequence 36626, A
34	34	68.0	98	20	US-11-097-143-22923	Sequence 22923, A
35	34	68.0	265	15	US-10-437-963-163286	Sequence 163286, A
36	34	68.0	352	16	US-10-444-795B-815	Sequence 815, Ap
37	34	68.0	400	15	US-10-444-795B-815	Sequence 369, App
38	34	68.0	433	15	US-10-220-120-369	Sequence 369, App
39	34	68.0	473	9	US-09-797-500-3	Sequence 3, Appl
40	34	68.0	473	14	US-10-081-119-26	Sequence 26, Appl
41	34	68.0	473	15	US-10-353-274-17	Sequence 17, Appl
42	34	68.0	473	15	US-10-444-795B-813	Sequence 813, Appl
43	34	68.0	473	17	US-10-951-389-26	Sequence 26, Appl
44	34	68.0	473	17	US-10-951-389-26	Sequence 26, Appl
45	34	68.0	473	17	US-10-951-406-26	Sequence 26, Appl

ALIGNMENTS

RESULT 1

US-10-731-238-90
Sequence 90, Application US/10731238
Publication No. US20050123552A1

GENERAL INFORMATION:

APPLICANT: Hook, Magnus
Patt, Joseph M.
House-Pompeo, Karen L.
Speziale, Pietro
John, Danny
McGavin, Martin J.

TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS

AND METHODS OF USE

NUMBER OF SEQUENCES: 105

CORRESPONDENCE ADDRESSES:

ADDRESSER: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston

STATE: TX
COUNTRY: USA

ZIP: 77210-4433

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10731, 238
FILING DATE: 10-Dec-2003
CLASSIFICATION: <unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/010, 317
FILING DATE: 21-Jan-1998
APPLICATION NUMBER: US 60/036, 139

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;
; FILING DATE: 21-JAN-1997
; ATTORNEY/AGENT INFORMATION:
;   NAME: Hibler, David W.
;   REGISTRATION NUMBER: 41,071
;   REFERENCE/DOCKET NUMBER: TAMK:189
; TELECOMMUNICATION INFORMATION:
;   TELEPHONE: 512-418-3000
;   TELEFAX: 512-474-7577
; INFORMATION FOR SEQ ID NO: 90:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 10 amino acids
;   TYPE: amino acid
;   STRANDEDNESS: <Unknown>
;   TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 90:
US-10-731-238-90

Query Match      100.0%; Score 50; DB 18; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.037;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 TEIEEDTNK 10
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Db      1 TEIEEDTNK 10

RESULT 2
US-11-066-697-1134
; Sequence 1134, Application US/11066697
; Publication No. US20050187159A1
; GENERAL INFORMATION:
;   APPLICANT: Bridon, Dominique P.
;   APPLICANT: Ezrin, Alan M.
;   APPLICANT: Milner, Peter G.
;   APPLICANT: Holmes, Darren L.
;   APPLICANT: Thibadeau, Karen
; TITLE OF INVENTION: PROTECTION OF ENDOGENOUS THERAPEUTIC PEPTIDES FROM
; TITLE OF INVENTION: PEPTIDASE ACTIVITY THROUGH COMUGATION TO BLOOD
; FILE REFERENCE: 50086202301
; CURRENT APPLICATION NUMBER: US/11/066,697
; PRIOR FILING DATE: 2005-02-25
; PRIOR APPLICATION NUMBER: 09/657,276
; PRIOR FILING DATE: 2000-09-07
; PRIOR APPLICATION NUMBER: 60/153,406
; PRIOR FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: 60/159,783
; PRIOR FILING DATE: 1999-10-15
; NUMBER OF SEQ ID NOS: 1617
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1134
; LENGTH: 37
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptide
US-11-066-697-1134

Query Match      100.0%; Score 50; DB 20; Length 37;
Best Local Similarity 100.0%; Pred. No. 0.15;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 TEIEEDTNK 10
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Db      5 TEIEEDTNK 14

RESULT 3
US-09-813-820-8
; Sequence 8, Application US/09813820
; Patent No. US20020102262A1
; GENERAL INFORMATION:
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; APPLICANT: Hook, Magnus
;   Patti, Joseph M.
;   House-Pompeo, Karen
;   Sthanam, Narayana
;   Syneraky, Jindrich
; TITLE OF INVENTION: COLLAGEN BINDING PROTEIN COMPOSITIONS
;   AND METHODS OF USE
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
;   ADDRESS: Arnold, White & Durkee
;   STREET: P.O. Box 4433
;   CITY: Houston
;   STATE: Texas
;   COUNTRY: U.S.
; ZIP: 77210
; COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/09/813,820
;   FILING DATE: 22-Mar-2001
;   CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: 08/856,253
;   FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
;   NAME: Kitchell, Barbara S.
;   REGISTRATION NUMBER: 33,928
; TELECOMMUNICATION INFORMATION:
;   TELEPHONE: (512) 418-3000
;   TELEFAX: (512) 474-7577
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 139 amino acids
;   TYPE: amino acid
;   STRANDEDNESS: <Unknown>
;   TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-09-813-820-8

Query Match      100.0%; Score 50; DB 9; Length 139;
Best Local Similarity 100.0%; Pred. No. 0.61;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 TEIEEDTNK 10
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Db      96 TEIEEDTNK 105

RESULT 4
US-08-901-062-1
; Sequence 1, Application US/08901062
; Publication No. US20020025324A1
; GENERAL INFORMATION:
;   APPLICANT: SEALS, JONATHAN R.
; TITLE OF INVENTION: RECOMBINANT BIVALENT BACTERIAL VACCINE
; TITLE OF INVENTION: FOR THE PREVENTION OF MASTITIS
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
;   ADDRESS: HALE AND DORR LLP
;   STREET: 60 State Street
;   CITY: Boston
;   STATE: MA
;   COUNTRY: United States of America
; ZIP: 02109
; COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: PatentIn Release #1.0, Version #1.30
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/901.062
FILING DATE: 25-JUL-1997
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Baker, Hollie L.
REGISTRATION NUMBER: 31,321
REFERENCE/DOCKET NUMBER: 106941.153
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 526-6000
TELEFAX: (617) 526-5000
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 388 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-901-062-1

Query Match 100.0%; Score 50; DB 8; Length 388;
Best Local Similarity 100.0%; Pred. No. 1.8;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TEIIEEDTNK 10
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DB 345 TEIIEEDTNK 354

RESULT 5
US-08-781-986A-5251
Sequence 5251, Application US/08781986A
Publication No. US20030054436A1
GENERAL INFORMATION:
APPLICANT: Charles Kunach
TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
NUMBER OF SEQUENCES: 5255
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COUNTRY: USA
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/781.986A
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Benson, Bob
REGISTRATION NUMBER: 30,446
REFERENCE/DOCKET NUMBER: PB248PP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 5251:
SEQUENCE CHARACTERISTICS:
LENGTH: 559 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-781-986A-5251

Query Match 100.0%; Score 50; DB 8; Length 559;
Best Local Similarity 100.0%; Pred. No. 2.7;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TEIIEEDTNK 10
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DB 381 TEIIEEDTNK 390

RESULT 6
US-10-329-624-5251
Sequence 5251, Application US/10329624
Publication No. US20040043037A1
GENERAL INFORMATION:
APPLICANT: Charles Kunach
Gil H. Choi
Patrick S. Dillon
Craig A. Rosen
Steven C. Barash
Michael R. Fannon
TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
NUMBER OF SEQUENCES: 5256
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COUNTRY: USA
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/329.624
FILING DATE: 27-Dec-2002
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/956,171
FILING DATE: October 20, 1997
APPLICATION NUMBER: 60/009,861
FILING DATE: January 5, 1996
APPLICATION NUMBER: 08/781,986
FILING DATE: January 3, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Mark J. Hyman
REGISTRATION NUMBER: 46,789
REFERENCE/DOCKET NUMBER: PB248P1D1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (240) 314-1224
TELEFAX: (301) 309-8439
INFORMATION FOR SEQ ID NO: 5251:
SEQUENCE CHARACTERISTICS:
LENGTH: 559 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 5251:
US-10-329-624-5251

Query Match 100.0%; Score 50; DB 15; Length 559;
Best Local Similarity 100.0%; Pred. No. 2.7;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TEIIEEDTNK 10
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DB 381 TEIIEEDTNK 390

RESULT 7
US-10-470-048B-424


```
; Sequence 424, Application US/10470048B
; Publication No. US20050037444A1
; GENERAL INFORMATION:
; APPLICANT: MEINKE ET AL.
; TITLE OF INVENTION: A METHOD FOR IDENTIFICATION, ISOLATION AND PRODUCTION OF
; FILE REFERENCE: SONN:03505
; CURRENT APPLICATION NUMBER: US/10/470,048B
; CURRENT FILING DATE: 2003-07-25
; NUMBER OF SEQ ID NOS: 603
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 424
; LENGTH: 940
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-10-470-048B-424

Query Match          100.0%; Score 50; DB 17; Length 940;
Best Local Similarity 100.0%; Pred. No. 4.7;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 TEIEEDPTNK 10
        |||||||
Db      762 TEIEEDPTNK 771

RESULT 8
US-10-470-048B-69
; Sequence 69, Application US/10470048B
; Publication No. US20050037444A1
; GENERAL INFORMATION:
; APPLICANT: MEINKE ET AL.
; TITLE OF INVENTION: A METHOD FOR IDENTIFICATION, ISOLATION AND PRODUCTION OF
; FILE REFERENCE: SONN:03505
; CURRENT APPLICATION NUMBER: US/10/470,048B
; CURRENT FILING DATE: 2003-07-25
; NUMBER OF SEQ ID NOS: 603
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 69
; LENGTH: 948
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-10-470-048B-69

Query Match          100.0%; Score 50; DB 17; Length 948;
Best Local Similarity 100.0%; Pred. No. 4.7;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 TEIEEDPTNK 10
        |||||||
Db      770 TEIEEDPTNK 779

RESULT 9
US-09-815-242-5797
; Sequence 5797, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haeselbeck, Robert
; APPLICANT: Ohlsen, Karl L.
; APPLICANT: Zyekind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; FILE REFERENCE: ELITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
```

```
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 1410
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5797
; LENGTH: 1018
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-09-815-242-5797

Query Match          100.0%; Score 50; DB 9; Length 1018;
Best Local Similarity 100.0%; Pred. No. 5.1;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 TEIEEDPTNK 10
        |||||||
Db      826 TEIEEDPTNK 835

RESULT 10
US-09-815-242-12838
; Sequence 12838, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haeselbeck, Robert
; APPLICANT: Ohlsen, Karl L.
; APPLICANT: Zyekind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; FILE REFERENCE: ELITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 1410
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12838
; LENGTH: 1018
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-09-815-242-12838

Query Match          100.0%; Score 50; DB 9; Length 1018;
Best Local Similarity 100.0%; Pred. No. 5.1;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 1 TEIIEEDTNK 10
|||
Db 826 TEIIEEDTNK 835

RESULT 11
US-10-470-048B-68
; Sequence 68, Application US/10470048B
; Publication No. US20050037444A1
; GENERAL INFORMATION:
; APPLICANT: WEINKE ET AL.
; TITLE OF INVENTION: A METHOD FOR IDENTIFICATION, ISOLATION AND PRODUCTION OF
; FILE REFERENCE: SOINN:035US
; CURRENT APPLICATION NUMBER: US/10/470,048B
; NUMBER OF SEQ ID NOS: 603
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 68
; LENGTH: 1018
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-10-470-048B-68

Query Match 100.0%; Score 50; DB 17; Length 1018;
Best Local Similarity 100.0%; Pred. No. 5.1;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TEIIEEDTNK 10
|||
Db 826 TEIIEEDTNK 835

RESULT 12
US-08-781-986A-5254
; Sequence 5254, Application US/08781986A
; Publication No. US20030054436A1
; GENERAL INFORMATION:
; APPLICANT: Charles Kunsch
; TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
; NUMBER OF SEQUENCES: 5255
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4mb storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/781,986A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Benson, Bob
; REGISTRATION NUMBER: 30,446
; REFERENCE/DOCKET NUMBER: PB248PP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 5254:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1027 amino acids
; TYPE: amino acid
; STRANDEDNESS: single

; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-781-986A-5254

Query Match 100.0%; Score 50; DB 8; Length 1027;
Best Local Similarity 100.0%; Pred. No. 5.1;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TEIIEEDTNK 10
|||
Db 835 TEIIEEDTNK 844

RESULT 13
US-10-329-624-5254
; Sequence 5254, Application US/10329624
; Publication No. US20040043037A1
; GENERAL INFORMATION:
; APPLICANT: Charles Kunsch
; GIL H. Choi
; Patrick S. Dillon
; Craig A. Rosen
; Steven C. Barash
; Michael R. Fannon
; TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
; NUMBER OF SEQUENCES: 5256
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4mb storage

COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/329,624

FILING DATE: 27-Dec-2002

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/956,171

FILING DATE: October 20, 1997

APPLICATION NUMBER: 60/009,861

FILING DATE: January 5, 1996

APPLICATION NUMBER: 08/781,986

FILING DATE: January 3, 1997

ATTORNEY/AGENT INFORMATION:
NAME: Mark J. Hyman

REGISTRATION NUMBER: 46,789

REFERENCE/DOCKET NUMBER: PB248P1D1

TELECOMMUNICATION INFORMATION:
TELEPHONE: (240) 314-1224

TELEFAX: (301) 309-8439

INFORMATION FOR SEQ ID NO: 5254:
SEQUENCE CHARACTERISTICS:

LENGTH: 1027 amino acids
TYPE: amino acid

STRANDEDNESS: single
TOPOLOGY: linear

MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 5254:

US-10-329-624-5254

Query Match 100.0%; Score 50; DB 15; Length 1027;
Best Local Similarity 100.0%; Pred. No. 5.1;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TEIIEEDTNK 10
|||
Db 835 TEIIEEDTNK 844

RESULT 14

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US-10-282-122A-43778
; Sequence 43778, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Karl
; APPLICANT: Zyklich, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See file wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 43778
; LENGTH: 961
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-10-282-122A-43778

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Query Match          90.0%; Score 45; DB 15; Length 961;
Best Local Similarity 100.0%; Pred. No. 35;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      2 EIIEDTNNK 10
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Db      774 EIIEDTNNK 782

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RESULT 15

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US-09-815-242-5456
; Sequence 5456, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Karl L.
; APPLICANT: Zyklich, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard

```

```

; TITLE OF INVENTION: Identification of Essential Genes in
; PROKARYOTES
; FILE REFERENCE: ELITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5456
; LENGTH: 978
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-09-815-242-5456

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Query Match          90.0%; Score 45; DB 9; Length 978;
Best Local Similarity 100.0%; Pred. No. 36;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      2 EIIEDTNNK 10
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Db      805 EIIEDTNNK 813

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Job time : 58.1494 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using SW model

Run on: October 22, 2005, 08:04:46 ; Search time 11.6092 Seconds
(without alignments)
82.880 Million cell updates/sec

Title: US-10-731-238-90
Perfect score: 50
Sequence: 1 TEIIEBDTNK 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	50	100.0	940	2	S19702 fibronectin-binding
2	50	100.0	1018	2	A32192 fibronectin-binding
3	45	90.0	961	2	G90053 hypothetical prote
4	45	90.0	1038	2	H90053 hypothetical prote
5	39	78.0	183	2	G81351 probable Holliday
6	37	74.0	121	2	H70471 conserved hypothet
7	37	74.0	806	2	T41930 ribonucleotide red
8	36	72.0	200	2	E81314 probable periplasm
9	36	72.0	207	2	G84983 5-amino-6-(5-phosp
10	36	72.0	237	2	A12062 hypothetical prote
11	36	72.0	384	2	T37271 probable H+-export
12	35	72.0	678	2	A71287 probable cytoplasm
13	35	70.0	124	2	T45973 hypothetical prote
14	35	70.0	283	2	I40442 DNA-binding protei
15	35	70.0	456	2	AC1336 argininosuccinate
16	35	70.0	608	2	H72292 hypothetical prote
17	34	68.0	100	2	G97040 hypothetical prote
18	34	68.0	226	2	B90581 hypothetical prote
19	34	68.0	274	2	T21284 hypothetical prote
20	34	68.0	284	2	F97216 probable aminoglyc
21	34	68.0	285	2	A48444 mezozoite surface
22	34	68.0	411	2	JC1482 TYA protein - yeas
23	34	68.0	413	2	S52610 TYA protein - yeas
24	34	68.0	414	2	S31261 protein-tyrosine-p
25	34	68.0	473	1	A38874 fusion, PTS system
26	34	68.0	627	2	H96951 hypothetical prote
27	34	68.0	795	2	T07709 demoglein 3 precu
28	34	68.0	999	1	I0HUG3 protein kinase - s
29	34	68.0	1094	2	S49313

30	34	68.0	1146	2	B70376 reverse gyrase - A
31	34	68.0	1244	2	T19068 hypothetical prote
32	34	68.0	2823	2	F87908 protein T22A3 a [i
33	34	68.0	2823	2	T23064 hypothetical prote
34	34	68.0	3102	2	T43291 laminin alpha chain
35	34	68.0	123	2	G86745 hypothetical prote
36	33	66.0	182	2	B86396 T2P11.11 protein -
37	33	66.0	182	2	S46667 meloitis-specific p
38	33	66.0	330	2	E82936 conserved hypothet
39	33	66.0	341	2	AC1528 alpha-1,6-mannanas
40	33	66.0	406	2	T42561 DNA polymerase pro
41	33	66.0	453	2	T20965 hypothetical prote
42	33	66.0	484	2	S25002 1-aminocyclopropan
43	33	66.0	557	2	JC6539 tumor necrosis fac
44	33	66.0	806	2	A12428 sucrose synthase [
45	33	66.0	810	2	A97852 vitB4 protein prec

ALIGNMENTS

RESULT 1

S19702 fibronectin-binding protein B - Staphylococcus aureus
C:Species: Staphylococcus aureus
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
C:Accession: S19702
R:Joensson, K.; Signaes, C.; Mueller, H.P.; Lindberg, M.
Eur. J. Biochem. 202, 1041-1048, 1991
A:Title: Two different genes encode fibronectin binding proteins in Staphylococcus aure
A:Reference number: S19702, MUID:92111475, PMID:1837266
A:Accession: S19702
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-940 <JOB>
A:Cross-references: UNIPROT:Q53682; EMBL:X62992; NID:G49040; PIDN:CAA44726.1; PID:G5815
C:Keywords: fibronectin binding

Query Match 100.0%; Score 50; DB 2; Length 940;
Best Local Similarity 100.0%; Pred. No. 0.27;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TEIIEBDTNK 10
DB 762 TEIIEBDTNK 771

RESULT 2

A32192 fibronectin-binding protein - Staphylococcus aureus
C:Species: Staphylococcus aureus
C:Date: 31-Jul-1989 #sequence_revision 31-Jul-1989 #text_change 16-Feb-1997
R:Signaes, C.; Raucel, G.; Joensson, K.; Lindgren, P.E.; Anantharamaiah, G.M.; Hoeoek
Proc. Natl. Acad. Sci. U.S.A. 86, 699-703, 1989
A:Title: Nucleotide sequence of the gene for a fibronectin-binding protein from Staph
A:Reference number: A32192; MUID:89098998; PMID:2521391
A:Accession: A32192
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1018 <SIG>
A:Cross-references: GB:J04151
C:Keywords: fibronectin binding

Query Match 100.0%; Score 50; DB 2; Length 1018;
Best Local Similarity 100.0%; Pred. No. 0.3;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TEIIEBDTNK 10
DB 826 TEIIEBDTNK 835

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RESULT 3
G90053
hypothetical protein fnbB [imported] - Staphylococcus aureus (strain N315)
C/Species: Staphylococcus aureus
C/Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C/Accession: G90053
R/Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Ogud
ma, A.; Mitutani, U.; Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.;
C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
A/Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.
A/Reference number: A89758; PMID:21311952; PMID:11418146
A/Accession: G90053
A/Status: Preliminary
A/Molecule type: DNA
A/Residues: 1-961 <KUR>
A/Cross-references: UNIPROT:Q99RD3; GB:BA000018; PID:gl3702452; PIDN:BAB43593.1; GSPDB:G
A/Experimental source: strain N315
C/Genetics:
A/Gene: fnbB

Query Match          90.0%; Score 45; DB 2; Length 961;
Best Local Similarity 100.0%; Pred. No. 2.4;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EIEEDTNK 10
DB 774 EIEEDTNK 782

RESULT 4
H90053
hypothetical protein fnb [imported] - Staphylococcus aureus (strain N315)
C/Species: Staphylococcus aureus
C/Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C/Accession: H90053
R/Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Ogud
ma, A.; Mitutani, U.; Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.;
C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
A/Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.
A/Reference number: A89758; PMID:21311952; PMID:11418146
A/Accession: H90053
A/Status: Preliminary
A/Molecule type: DNA
A/Residues: 1-1038 <KUR>
A/Cross-references: UNIPROT:Q99RD3; GB:BA000018; PID:gl3702453; PIDN:BAB43594.1; GSPDB:G
A/Experimental source: strain N315
C/Genetics:
A/Gene: fnbB

Query Match          90.0%; Score 45; DB 2; Length 1038;
Best Local Similarity 100.0%; Pred. No. 2.7;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EIEEDTNK 10
DB 823 EIEEDTNK 831

RESULT 5
G81351
probable Holliday junction DNA helicase Cj0799c [imported] - Campylobacter jejuni (strain
C/Species: Campylobacter jejuni
C/Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004
C/Accession: G81351
R/Parkhill, J.; Wren, B.W.; Mungall, K.; Kettle, J.M.; Churcher, C.; Basham, D.; Chilling
C.W.; Quail, M.; Rajandream, M.A.; Rutherford, K.M.; VanVleet, A.; Whitehead, S.; Barrell
Nature 403, 665-668, 2000
A/Title: The genome sequence of the food-borne pathogen Campylobacter jejuni reveals hyl
A/Reference number: A81250; PMID:20150912; PMID:10688204
A/Accession: G81351
C/Genetics:
A/Gene: preliminary
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A/Molecule type: DNA
A/Residues: 1-183 <PAR>
A/Cross-references: UNIPROT:Q9PCL1; GB:AL139076; GB:AL111168; NID:G6368128; PIDN:CA
A/Experimental source: serotype O2, strain NCTC 11168
C/Genetics:
A/Gene: ruvA; Cj0799c
C/Superfamily: holliday junction DNA helicase ruvA

Query Match          78.0%; Score 39; DB 2; Length 183;
Best Local Similarity 70.0%; Pred. No. 5.6;
Matches 7; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 TEIEEDTNK 10
DB 50 TOLIEEDTNK 59

RESULT 6
H70471
conserved hypothetical protein aq_2000 - Aquifex aeolicus
C/Species: Aquifex aeolicus
C/Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 09-Jul-2004
C/Accession: H70471
R/Dekert, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.; O
V.
Nature 392, 353-358, 1998
A/Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.
A/Reference number: A70300; PMID:9819666; PMID:9537320
A/Accession: H70471
A/Status: preliminary; nucleic acid sequence not shown; translation not shown
A/Molecule type: DNA
A/Residues: 1-121 <AQF>
A/Cross-references: UNIPROT:Q67804; GB:AE000767; NID:G2384235; PIDN:AAC07774.1; PID G238
A/Experimental source: strain VFS
C/Genetics:
A/Gene: aq_2000

Query Match          74.0%; Score 37; DB 2; Length 121;
Best Local Similarity 77.8%; Pred. No. 8.5;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 EIEEDTNK 10
DB 84 KIEEDTNK 92

RESULT 7
T41930
ribonucleotide reductase, large subunit - human herpesvirus 7 (strain J1)
C/Species: human herpesvirus 7
A/Variety: strain J1
C/Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C/Accession: T41930
R/Nicholas, J.
submitted to the EMBL Data Library, December 1995
A/Description: Determination and analysis of the complete nucleotide sequence of human
A/Reference number: Z22022
A/Accession: T41930
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1806 <NIC>
A/Cross-references: UNIPROT:P50641; EMBL:U43400; PIDN:AAC54690.1
A/Experimental source: strain J1
C/Genetics:
A/Note: U28

Query Match          74.0%; Score 37; DB 2; Length 806;
Best Local Similarity 66.7%; Pred. No. 66;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 2 EIEEDTNK 10
DB 287 QIVEKDTNK 295
```

RESULT 8
E81314
probable periplasmic thioredoxin Cj1106 [imported] - Campylobacter jejuni (strain NCTC 1)
C:Species: Campylobacter jejuni
C:Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004
C:Accession: E81314
R:Parkhill, J.; Wren, B.W.; Mungall, K.; Kelsey, J.M.; Churcher, C.; Baeham, D.; Chilling
C.W.; Quail, M.; Rajandream, M.A.; Rutherford, K.M.; VanVleet, A.; Whitehead, S.; Barrer
Nature 403, 665-668, 2000
A:Title: The genome sequence of the food-borne pathogen Campylobacter jejuni reveals h
A:Reference number: A81250; MUID:20150912; PMID:10688204
A:Accession: E81314
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-200 <PAR>
A:Cross-references: UNIPROT:O9PN18; GB:AL139077; GB:AL111168; NID:g65968444; PIDN:CA87336
A:Experimental source: serotype O2, strain NCTC 1168
C:Genetics:
A:Gene: Cj1106

Query Match 72.0%; Score 36; DB 2; Length 200;
Best Local Similarity 60.0%; Pred. No. 23;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Oy 1 TEIEEDTNK 10
:::|||||
Db 186 TELMEDLNK 195

RESULT 9
G84983
5-amin-6-(5-phosphoribosylamino)uracil reductase (EC 1.1.1.193) [imported] - Buchnera
N:Alternate names: riboflavin reductase
C:Species: Buchnera sp.
C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 02-Mar-2001
C:Accession: G84983
R:Shigenobu, S.; Matanabe, H.; Hattori, M.; Sakaki, Y.; Ishikawa, H.
Nature 407, 81-86, 2000
A:Title: Genome sequence of the endocellular bacterial symbiont of aphids Buchnera sp. A
A:Reference number: A84930; MUID:20445173; PMID:10993077
A:Accession: G84983
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-207 <STO>
A:Cross-references: GB:AP000398; GSPDB:GN00144
A:Experimental source: strain APS
C:Genetics:
A:Gene: ribD2; BU462
C:Keywords: oxidoreductase

Query Match 72.0%; Score 36; DB 2; Length 207;
Best Local Similarity 70.0%; Pred. No. 23;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Oy 1 TEIEEDTNK 10
:::|||||
Db 106 TQIEEDHNK 115

RESULT 10
A12062
hypothetical protein a1r2055 [imported] - Nostoc sp. (strain PCC 7120)
C:Species: Nostoc sp. PCC 7120
A:Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C:Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004
C:Accession: A12062
R:Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kurita, T.; Sasamoto, S.; Matanabe, A.; Iriguchi
Nakazaki, N.; Shimo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S
DNA Res. 8, 205-213, 2001
A:Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana
A:Reference number: AB1807; MUID:21595285; PMID:11759840

A:Accession: A12062
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-237 <KIR>
A:Cross-references: UNIPROT:O8YVC3; GB:BA000019; PIDN:BA873754.1; PID:g17131146; GSPDB:
A:Experimental source: strain PCC 7120
C:Genetics:
A:Gene: a1r2055

Query Match 72.0%; Score 36; DB 2; Length 237;
Best Local Similarity 66.7%; Pred. No. 27;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Oy 2 EIEEDTNK 10
:::|||||
Db 135 QIIDODTNK 143

RESULT 11
T37271
probable H+-exporting ATPase (EC 3.6.3.6) chain Vha11, vacuolar - Caenorhabditis elegans
N:Alternate names: Vha11 protein
C:Species: Caenorhabditis elegans
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C:Accession: T37271
R:Okazaki, T.; Yamamoto, R.; Futai, M.
J. Biol. Chem. 273, 22570-22576, 1998
A:Title: Multiple genes for vacuolar-type ATPase proteolipids in Caenorhabditis elegans
A:Reference number: 221659; MUID:98380481; PMID:9712884
A:Accession: T37271
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-384 <OKA>
A:Cross-references: UNIPROT:Q9XXU9; EMBL:AB009567; NID:g4579711; PIDN:BAA75067.1; PID:
C:Superfamily: vacuolar H+-transporting ATPase 16k chain
C:Keywords: ATP; hydrogen ion transport; hydrolase; transmembrane protein

Query Match 72.0%; Score 36; DB 2; Length 384;
Best Local Similarity 60.0%; Pred. No. 46;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Oy 1 TEIEEDTNK 10
:::|||||
Db 79 TEVEEDKSK 88

RESULT 12
A71287
probable cytoplasmic filament protein A (cfpA) - syphilis spirochete
C:Species: Treponema pallidum subsp. pallidum (syphilis spirochete)
C:Date: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 09-Jul-2004
C:Accession: A71287
R:Fraser, C.M.; Norris, S.J.; Weinstock, G.M.; White, O.; Sutton, G.G.; Dodson, R.; Gw
Leon, J.; Khailak, H.; Richardson, D.; Howell, J.K.; Chidambaram, M.; Uterback, T.; Mc
they, L.; Weidman, J.; Smith, H.O.; Venter, J.C.
Science 281, 375-388, 1998
A:Title: Complete genome sequence of Treponema pallidum, the syphilis spirochete.
A:Reference number: A71250; MUID:98332770; PMID:9665876
A:Accession: A71287
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-678 <CO>
A:Cross-references: UNIPROT:Q56336; GB:AE001246; GB:AE000520; NID:g3323046; PIDN:AA65
A:Experimental source: strain Nichols
C:Genetics:
A:Gene: TP0748

Query Match 72.0%; Score 36; DB 2; Length 678;
Best Local Similarity 66.7%; Pred. No. 84;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Oy 2 EIEEDTNK 10
:::|||||

Db 40 QLIBEETNK 48

RESULT 13

T45973

hypothetical protein F9D24.40 - *Arabidopsis thaliana*C/Species: *Arabidopsis thaliana* (mouse-ear cress)

C/Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 09-Jul-2004

C/Accession: T45973

R/D/Author: M.; Vazzi, A.; Modesto, D.; Pigazzi, M.; Valle, G.; Mewes, H.W.; Lemcke, K.;

submitted to the Protein Sequence Database, January 2000

A/Accession: T45973

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-124 <DAN>

A/Cross-references: UNIPROT:Q9W2K3; EMBL:AL137081

A/Experimental source: cultivar Columbia; BAC clone F9D24

C/Genetics:

A/Map position: 3

A/Introns: 30/1; 51/3; 66/3; 93/3

A/Note: F9D24.40

Query Match	70.0%;	Score 35;	DB 2;	Length 124;
Best Local Similarity	70.0%;	Pred. No. 21;		
Matches	7;	Conservative 1;	Mismatches 2;	Indels 0;
			Gaps 0;	

OY	1	TEIIEEDTNK 10
	:	
Db	79	TEIIEEVTYK 88

RESULT 14

I40442

DNA-binding protein Spo0J-like homolog yyaA - *Bacillus subtilis*

N/Alternate names: probable DNA binding protein (replication origin region)

C/Species: *Bacillus subtilis*

C/Date: 12-Aug-1996 #sequence_revision 12-Aug-1996 #text_change 09-Jul-2004

C/Accession: I40442; S66023; H70083; S18078

R/Ogasawara, N.; Yoshikawa, H.

Mol. Microbiol. 6, 629-634, 1992

A/Title: Genes and their organization in the replication origin region of the bacterial

A/Reference number: I40435; MUID:92204018; PMID:1552862

A/Accession: I40442

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: DNA

A/Residues: 1-283 <RBS>

A/Cross-references: UNIPROT:P37524; EMBL:X62539; NID:940020; PIDN:CAA44406.1; PID:940028

R/Ogasawara, N.; Nakai, S.; Yoshikawa, H.

DNA Res. 1, 1-14, 1994

A/Title: Systematic sequencing of the 180 kilobase region of the *Bacillus subtilis* chrom

A/Reference number: S65967; MUID:96051385; PMID:7584024

A/Accession: S66023

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-283 <OGA>

A/Cross-references: EMBL:D26185; NID:9467326; PIDN:BA05229.1; PID:9467383

R/Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berter

C.; Bron, S.; Brouillet, S.; Brunsch, C.V.; Caldwell, B.; Capiano, V.; Carter, N.M.; Chc

A.; Ehrlich, S.D.; Emerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.;

Nature 390, 249-256, 1997

A/Authors: Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galleron, N.; Ghim

wood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.; Itaya, M.;

Kontingstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois, S.; Lauber,

A.; Authors: Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Maeda, S.; Maueel, C.; Medigt

, K.; Ogihara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle, D.; Potwol

Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadate, Y.; Sato, T.; Scanlon, E.; Schied

A.; Authors: Schroeter, R.; Scofield, F.; Sekiguchi, J.; Sekowska, A.; Seror, S.J.; Serro

amakoshi, A.; Tanaka, T.; Terpestra, P.; Tognoni, A.; Tosato, V.; Uchiyama, S.; Vandendol

; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K.; Yoshikawa,

A.; Authors: Zumbstein, E.; Yoshikawa, H.; Danchin, A.

A/Title: The complete genome sequence of the Gram-positive bacterium *Bacillus subtilis*.

A/Reference number: A69580; MUID:98044033; PMID:9384377

A/Accession: H70083

A/Status: preliminary; nucleic acid sequence not shown; translation not shown

A/Molecule type: DNA

A/Residues: 1-283 <KUN>

A/Cross-references: GB:299124; GB:AL009126; NID:92636442; PIDN:CAB16136.1; PID:9263646

A/Experimental source: strain 168

C/Genetics:

A/Gene: yyaA

C/Superfamily: *Bacillus subtilis* transport protein spo0J

Query Match	70.0%;	Score 35;	DB 2;	Length 263;
Best Local Similarity	77.8%;	Pred. No. 51;		
Matches	7;	Conservative 0;	Mismatches 2;	Indels 0;
			Gaps 0;	

OY	2	EIIEEDTNK 10
	:	
Db	19	EIAEHDTNK 27

RESULT 15

AC1336

argininosuccinate lyase homolog argH [imported] - *Listeria monocytogenes* (strain EGD-e)C/Species: *Listeria monocytogenes*

C/Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004

C/Accession: AC1336

R/Glaser, P.; Frangoul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Blocke

D.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Duseurget, O.; Entian, K.D.; Fahl, H

D.; Jones, L.M.; Karst, U.

Science 294, 849-852, 2001

A/Authors: Kreft, U.; Kuhn, M.; Kunst, F.; Kurapkai, G.; Madueno, E.; Maltournam, A.; M

ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland,

A/Title: Comparative genomics of *Listeria* species.

A/Reference number: AB1077; MUID:21537279; PMID:11679669

A/Accession: AC1336

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-456 <GLA>

A/Cross-references: UNIPROT:Q8Y5H1; GB:NC_003210; PIDN:CAD00169.1; PID:g16411561; GSPDB

A/Experimental source: strain EGD-e

C/Genetics:

A/Gene: argH

C/Superfamily: argininosuccinate lyase

Query Match	70.0%;	Score 35;	DB 2;	Length 456;
Best Local Similarity	70.0%;	Pred. No. 85;		
Matches	7;	Conservative 1;	Mismatches 2;	Indels 0;
			Gaps 0;	

OY	1	TEIIEEDTNK 10
	:	
Db	353	TEIIEESTYK 362

Search completed: October 22, 2005, 09:55:41
 Job time : 12.6092 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 22, 2005, 08:01:06 ; Search time 56.2069 Seconds
(without alignments)
91.106 Million cell updates/sec

Title: US-10-731-238-90
Perfect score: 50
Sequence: 1 TEIIEEDTNK 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_03:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Length	DB	ID	Description
1	50	100.0	152	2	Q9AEP9	Q9AEP9 staphylococ
2	50	100.0	940	2	Q53682	Q53682 staphylococ
3	50	100.0	943	2	Q8NUU8	Q8NUU8 staphylococ
4	50	100.0	957	2	Q6G6H4	Q6G6H4 staphylococ
5	50	100.0	1015	2	Q8NUU7	Q8NUU7 staphylococ
6	50	100.0	1015	2	Q6G6H3	Q6G6H3 staphylococ
7	50	100.0	1018	1	FNBA_STRAU	P14738 staphylococ
8	45	90.0	961	2	Q99RD3	Q99RD3 staphylococ
9	45	90.0	961	2	Q7A3J8	Q7A3J8 staphylococ
10	45	90.0	965	2	Q6GDU5	Q6GDU5 staphylococ
11	45	90.0	1038	2	Q99RD2	Q99RD2 staphylococ
12	45	90.0	1038	2	Q7A3J7	Q7A3J7 staphylococ
13	40	80.0	403	2	Q75138	Q75138 homo sapien
14	40	80.0	413	2	Q96AJ1	Q96AJ1 homo sapien
15	40	80.0	413	2	Q65ZAJ	Q65ZAJ homo sapien
16	39	78.0	183	1	RUVA_CAMUE	O9PPC1 campylobact
17	39	78.0	331	2	Q7RLK5	Q7RLK5 plasmodium
18	39	78.0	1288	2	Q8IKY1	Q8IKY1 plasmodium
19	38	76.0	93	1	RPOL_SULTO	O67804 aquiflex aeo
20	37	74.0	121	2	Q88SHO	Q88SHO lacobacilli
21	37	74.0	190	2	Q88SHO	Q88SHO lacobacilli
22	37	74.0	618	2	Q7UZP4	Q7UZP4 prochloroco
23	37	74.0	806	1	RIRL_HNV7J	P50641 human herpe
24	37	74.0	806	2	Q77Y78	Q77Y78 human herpe
25	37	74.0	829	2	Q6C1W0	Q6C1W0 yarrowia li
26	36	72.0	168	2	Q8LPD3	Q8LPD3 linum usita
27	36	72.0	200	2	Q93PM0	Q93PM0 campylobact
28	36	72.0	200	2	Q9PN18	Q9PN18 campylobact
29	36	72.0	207	1	R1D2_BUCAI	P57534 buchnera ap
30	36	72.0	237	2	Q8YVC3	Q8YVC3 anabaena sp
31	36	72.0	328	2	Q8JW16	Q8JW16 japanese ya

32	36	72.0	384	1	VATC_CAREL	Q9XU9 caenorhabdi
33	36	72.0	664	2	Q9ROT8	Q9ROT8 treponema d
34	36	72.0	667	2	Q9RBN3	Q9RBN3 treponema p
35	36	72.0	674	2	Q9LAX1	Q9LAX1 treponema v
36	36	72.0	677	1	CFPA_TREPA	Q56336 treponema p
37	36	72.0	679	2	Q9R47	Q9R47 treponema p
38	36	72.0	682	2	Q73PF7	Q73PF7 treponema d
39	36	72.0	818	2	Q6PFM2	Q6PFM2 brachydantio
40	36	72.0	863	2	Q803V1	Q803V1 brachydantio
41	36	72.0	1186	2	Q895W7	Q895W7 clostridium
42	35	70.0	104	2	Q8E7B5	Q8E7B5 streptococc
43	35	70.0	108	2	Q9V960	Q9V960 drosophila
44	35	70.0	121	2	Q6YRJ3	Q6YRJ3 onion yello
45	35	70.0	124	2	Q9M2K3	Q9M2K3 arabidopsis

ALIGNMENTS

RESULT 1

ID	Q9AEP9	PRELIMINARY;	PRT;	152 AA.
AC	Q9AEP9;			
DT	01-JUN-2001 (TREMBLrel. 17, Created)			
DT	01-JUN-2001 (TREMBLrel. 17, Last sequence update)			
DT	01-DEC-2001 (TREMBLrel. 19, Last annotation update)			
DE	Fibronectin-binding protein (fragment).			
GN	Name=fnb;			
OS	Staphylococcus aureus.			
OC	Bacteria; Firmicutes; Bacillales; Staphylococcus.			
OX	NCBI_TaxID=1280;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=CMRSA-1;			
RX	MEDLINE=21246681; PubMed=11349044;			
RX	DOI=10.1128/IAI.69.6.3791-3799.2001;			
RA	Rice K., Huesca M., Vaz D., McGavin M.J.;			
RT	"Variance in fibronectin binding and fnb locus polymorphisms in a			
RT	Staphylococcus aureus: Identification of antigenic variation in a			
RT	fibronectin binding protein adhesin of the epidemic CMRSA-1 strain of			
RT	methicillin-resistant S. aureus."			
RI	Infect. Immun. 69:3791-3799 (2001).			
RI	EMBL; AY029184; AAK31588.1; --			
DR	EMBL; AY029184; AAK31588.1; --			
FT	NON_TER			
FT	NON_TER			
FT	NON_TER			
SQ	SEQUENCE 152 AA; 17193 MW; CFA3913C2B11C025 CRC64;			
Query Match				
Best Local Similarity 100.0%; Score 50; DB 2; Length 152;				
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;				
QY	1 TEIIEEDTNK 10			
DB	119 TEIIEEDTNK 128			
RESULT 2				
ID	Q53682	PRELIMINARY;	PRT;	940 AA.
AC	Q53682;			
DT	01-NOV-1996 (TREMBLrel. 01, Created)			
DT	01-NOV-1996 (TREMBLrel. 01, Last sequence update)			
DT	01-MAR-2004 (TREMBLrel. 26, Last annotation update)			
DE	Fibronectin binding protein B.			
GN	Name=fnbB;			
OS	Staphylococcus aureus.			
OC	Bacteria; Firmicutes; Bacillales; Staphylococcus.			
OX	NCBI_TaxID=1280;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=8325-4;			
RX	MEDLINE=92111475; PubMed=1837266;			
RA	Jonsson K., Sigfus C., Muller H.P., Lindberg M.;			


```
RT "Two different genes encode fibronectin binding proteins in
Staphylococcus aureus. The complete nucleotide sequence and
RT characterization of the second gene.";
RL Bur. J. Biochem. 202:1041-1048 (1991).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
an amide bond (By similarity).
DR EMBL; X62992; CAA44726.1; -.
DR PIR; S19702; S19702.
DR HSP; O53653; IN67.
DR GO; GO:0009986; C:cell surface; IEA.
DR GO; GO:0005618; C:cell wall; IEA.
DR GO; GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0007155; P:cell adhesion; IEA.
DR InterPro; IPR008966; Adhes_bact.
DR InterPro; IPR004237; Fn_bind.
DR InterPro; IPR05877; Gpos_YsIRK.
DR Pfam; PF02986; Fn_bind_2.
DR Pfam; PF00746; Gram_pos_anchor_1.
DR TIGRFAMs; TIGR01167; LPTXG_anchor; 1.
DR TIGRFAMs; TIGR01168; YsIRK_signal; 1.
DR PROSITE; PS50847; GRAM_POS_ANCHORING; 1.
KM Cell wall; Peptidoglycan-anchor.
SQ SEQUENCE 940 AA; 10355 MW; E35FBBCA907AE345 CRC64;

Query Match 100.0%; Score 50; DB 2; Length 940;
Best Local Similarity 100.0%; Pred. No. 2.1;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TEIIEEDTNK 10
Db 762 TEIIEEDTNK 771

RESULT 3
Q88NU8 PRELIMINARY; PRT; 943 AA.
ID Q88NU8;
AC Q88NU8;
DT 01-OCT-2002 (TReMBLrel. 22, Created)
DT 01-OCT-2002 (TReMBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE FnBb protein.
GN Name=fnbB; OrderedLocuNames=MM2420;
OS Staphylococcus aureus (strain MM2).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=196620;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MM2;
RX MEDLINE=22040717; PubMed=12044378; DOI=10.1016/S0140-6736(02)08713-5;
RA Baba T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Oguchi A.,
RA Nagai Y., Iwama N., Asano K., Naito T., Kuroda H., Cui L.,
RA Yamamoto K., Hiramatsu K.;
RT "Genome and virulence determinants of high virulence community-
RT acquired MRSA.";
RL Lancet 359:1819-1827 (2002).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
an amide bond (By similarity).
DR EMBL; AP004830; BAB96285.1; -.
DR HSP; O53653; IN67.
DR GO; GO:0009986; C:cell surface; IEA.
DR GO; GO:0005618; C:cell wall; IEA.
DR GO; GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0007155; P:cell adhesion; IEA.
DR InterPro; IPR008966; Adhes_bact.
DR InterPro; IPR004237; Fn_bind.
DR InterPro; IPR05877; Gpos_YsIRK.
DR Pfam; PF02986; Fn_bind_1.
DR Pfam; PF00746; Gram_pos_anchor_1.
SQ SEQUENCE 957 AA; 105980 MW; 28F8BA7FFD3EAF CRC64;

Query Match 100.0%; Score 50; DB 2; Length 940;
Best Local Similarity 100.0%; Pred. No. 2.1;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DR Pfam; PF04650; YsIRK_signal; 1.
DR TIGRFAMs; TIGR01167; LPTXG_anchor; 1.
DR TIGRFAMs; TIGR01168; YsIRK_signal; 1.
DR PROSITE; PS50847; GRAM_POS_ANCHORING; 1.
KM Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ SEQUENCE 943 AA; 104537 MW; DA8A5F3197E1B6A CRC64;

Query Match 100.0%; Score 50; DB 2; Length 943;
Best Local Similarity 100.0%; Pred. No. 2.1;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TEIIEEDTNK 10
Db 769 TEIIEEDTNK 778

RESULT 4
Q6G6H4 PRELIMINARY; PRT; 957 AA.
ID Q6G6H4;
AC Q6G6H4;
DT 05-JUL-2004 (TReMBLrel. 27, Created)
DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TReMBLrel. 27, Last annotation update)
DE Fibronectin-binding protein.
GN Name=fnbB; OrderedLocuNames=SAS2387;
OS Staphylococcus aureus (strain MSSA476).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=282459;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=1521324; DOI=10.1073/pnas.0402521101;
RA Holden M.T.G., Fell E.J., Lindsey J.A., Peacock S.J., Day N.P.J.,
RA Enright M.C., Foster T.J., Moore C.E., Hurst L., Atkin R., Barron A.,
RA Bason N., Bentley S.D., Chillingworth C., Chillingworth T.,
RA Churcher C., Clark L., Cotton C., Cronin A., Doggett J., Dowd L.,
RA Felwell T., Hance Z., Harris B., Hauser H., Holtroyd S., Jags K.,
RA James K.D., Lennard N., Line A., Mayes R., Moule S., Mungall K.,
RA Ormond D., Quail M.A., Rabinowitsch E., Rutherford K.M., Sanders M.,
RA Sharp S., Simmonds M., Stevens K., Whitehead S., Barrett B.G.,
RA Spratt B.G., Parkhill J.;
RT "Complete genomes of two clinical Staphylococcus aureus strains:
RT evidence for the rapid evolution of virulence and drug resistance.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:9786-9791 (2004).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
an amide bond (By similarity).
DR EMBL; BX571857; CAG44201.1; -.
DR GO; GO:0009986; C:cell surface; IEA.
DR GO; GO:0005618; C:cell wall; IEA.
DR GO; GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0007155; P:cell adhesion; IEA.
DR InterPro; IPR008966; Adhes_bact.
DR InterPro; IPR004237; Fn_bind.
DR InterPro; IPR05877; Gpos_YsIRK.
DR InterPro; IPR001899; Gram_pos_anchor.
DR Pfam; PF02986; Fn_bind_1.
DR Pfam; PF00746; Gram_pos_anchor_1.
DR Pfam; PF04650; YsIRK_signal; 1.
DR TIGRFAMs; TIGR01167; LPTXG_anchor; 1.
DR TIGRFAMs; TIGR01168; YsIRK_signal; 1.
DR PROSITE; PS50847; GRAM_POS_ANCHORING; 1.
KM Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ SEQUENCE 957 AA; 105980 MW; 28F8BA7FFD3EAF CRC64;

Query Match 100.0%; Score 50; DB 2; Length 957;
Best Local Similarity 100.0%; Pred. No. 2.2;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TEIIEEDTNK 10
Db 769 TEIIEEDTNK 778
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CC or send an email to jlicense@lsb-sib.ch).
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CC EMBL: J04151; AAA26632.1; -.
DR InterPro: IPR004237; Fn_bind.
DR InterPro: IPR005877; Gpoa_YsIRK.
DR InterPro: IPR01899; Gram_pos_anchor.
DR Pfam: PF02986; Fn_bind. 1.
DR Pfam: PF00746; Gram_pos_anchor; 1.
DR Pfam: PF04650; YsIRK_signal; 1.
DR TIGRFAMs: TIGR01167; LPXTG_anchor; 1.
DR TIGRFAMs: TIGR01168; YsIRK_signal; 1.
DR PROSITE: PS50847; GRAM_POS_ANCHORING; 1.
KM Cell adhesion; Cell wall; Peptidoglycan-anchor; Repeat; Signal;
KW Virulence.
FT SIGNAL 1 36
FT CHAIN 37 985 Fibronectin-binding protein..
FT PROPEP 986 1018 Removed by sortase (potential).
FT REPEAT 545 574 B-1.
FT REPEAT 575 604 B-2.
FT DOMAIN 745 878 4 X approximate tandem repeats,
fibronectin-binding domain.
FT REPEAT 745 782 D-1.
FT REPEAT 783 820 D-2.
FT REPEAT 821 859 D-3.
FT REPEAT 860 878 D-4 (incomplete).
FT DOMAIN 879 948 5 X tandem repeats, Pro-rich (WR).
FT REPEAT 879 892 WR 1.
FT REPEAT 893 906 WR 2.
FT REPEAT 907 920 WR 3.
FT REPEAT 921 934 WR 4.
FT REPEAT 935 948 WR 5.
FT SITE 982 986 LPXTG sorting signal (potential).
FT MOD_RSS 985 985 Pentaglycyl murein peptidoglycan amidated
chreonine (potential).
SQ SEQUENCE 1018 AA; 111780 MW; 58175E0020E81F1F CRC64;

Query Match 100.0%; Score 50; DB 1; Length 1018;
Best Local Similarity 100.0%; Pred. No. 2.3;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY 1 TEIIEEDTNK 10
Db 826 TEIIEEDTNK 835

RESULT 8
Q99RD3 PRELIMINARY; PRT; 961 AA.
ID Q99RD3
AC Q99RD3;
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE Fibronectin-binding protein homolog.
GN Name=fnb3; OrderedLocustNames=SAV2502;
OS Staphylococcus aureus (strain Mu50 / ATCC 700699).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
CX NCBI_TaxID=158878;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MU50 / ATCC 700699;
RX MEDLINE=21311952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2;
RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
Cui L., Oguchi A., Aoki K.-I., Nagai Y., Lian J.-Q., Ito T.,
Kanamori M., Matsunaru H., Maruyama A., Murakami H., Hosoyama A.,
Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
RT "Whole genome sequencing of methicillin-resistant Staphylococcus
aureus.";
RL Lancel 357:1225-1240(2001).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
an amide bond (by similarity).
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DR EMBL: AP003365; BAB58664.1; -.
DR PIR: G90053; G90053.
DR HSSP: Q53653; 1N67.
DR GO: GO:0009986; C:cell surface; IEA.
DR GO: GO:0005618; C:cell wall; IEA.
DR GO: GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO: GO:0016020; C:membrane; IEA.
DR GO: GO:0007155; P:cell adhesion; IEA.
DR InterPro: IPR008966; Adhes_bact.
DR InterPro: IPR004237; Fn_bind.
DR InterPro: IPR005877; Gpoa_YsIRK.
DR InterPro: IPR001899; Gram_pos_anchor.
DR Pfam: PF02986; Fn_bind; 1.
DR Pfam: PF00746; Gram_pos_anchor; 1.
DR TIGRFAMs: TIGR01167; LPXTG_anchor; 1.
DR TIGRFAMs: TIGR01168; YsIRK_signal; 1.
DR PROSITE: PS50847; GRAM_POS_ANCHORING; 1.
KM Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ SEQUENCE 961 AA; 106010 MW; 364940F84EA4101 CRC64;

Query Match 90.0%; Score 45; DB 2; Length 961;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY 2 EIIIEEDTNK 10
Db 774 EIIIEEDTNK 782

RESULT 9
Q7A3J8 PRELIMINARY; PRT; 961 AA.
ID Q7A3J8
AC Q7A3J8;
DT 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE FnbB protein.
GN Name=fnbB; OrderedLocustNames=SA2290;
OS Staphylococcus aureus (strain N315).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
CX NCBI_TaxID=158879;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=21311952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2;
RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
Cui L., Oguchi A., Aoki K.-I., Nagai Y., Lian J.-Q., Ito T.,
Kanamori M., Matsunaru H., Maruyama A., Murakami H., Hosoyama A.,
Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
RT "Whole genome sequencing of methicillin-resistant Staphylococcus
aureus.";
RL Lancel 357:1225-1240(2001).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
an amide bond (by similarity).
CX EMBL: AP003337; BAB43593.1; -.
DR GO: GO:0009986; C:cell surface; IEA.
DR GO: GO:0005618; C:cell wall; IEA.
DR GO: GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO: GO:0016020; C:membrane; IEA.
DR GO: GO:0007155; P:cell adhesion; IEA.
DR InterPro: IPR008966; Adhes_bact.
DR InterPro: IPR004237; Fn_bind.
DR InterPro: IPR005877; Gpoa_YsIRK.
DR InterPro: IPR001899; Gram_pos_anchor.
DR Pfam: PF02986; Fn_bind; 1.
DR Pfam: PF00746; Gram_pos_anchor; 1.
DR TIGRFAMs: TIGR01167; LPXTG_anchor; 1.
DR TIGRFAMs: TIGR01168; YsIRK_signal; 1.
DR PROSITE: PS50847; GRAM_POS_ANCHORING; 1.
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KW Cell wall; Complete proteome; Peptidoglycan-anchor.
 SQ SEQUENCE 961 AA; 106010 MW; 364940f884EA4101 CRC64;
 Query Match 90.0%; Score 45; DB 2; Length 961;
 Best Local Similarity 100.0%; Pred. No. 18;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EIIEDPTNK 10
 |||||
 Db 774 EIIEDPTNK 782

RESULT 10
 O6GDUS PRELIMINARY; PRT; 965 AA.
 ID O6GDUS
 AC O6GDUS;
 DT 05-JUL-2004 (TREMBlrel. 27, Created)
 DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
 DE Fibronectin-binding protein.
 GN Name=fnbA; OrderedLocustNames=SA2580;
 OS Staphylococcus aureus (strain MRSA252).
 CC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 NCBI_TaxID=282458;
 [1]
 RN SEQUENCE FROM N.A.
 RP PubMed:15213324; DOI=10.1073/pnas.0402521101;
 RX Holden M.T.G., Fell E.J., Lindsay J.A., Peacock S.J., Day N.P.J.,
 RA Enright M.C., Foster T.J., Moore C.E., Hurrell L., Atkin R., Barron A.,
 RA Baeson N., Bentley S.D., Chillingworth C., Chillingworth I.,
 RA Churcher C., Clark L., Corton C., Cronin A., Doggett J., Dowd L.,
 RA Felwell T., Hance Z., Harris B., Hauser H., Holroyd S., Jagsels K.,
 RA James K.D., Lennard N., Line A., Mayes R., Moulis S., Mungall K.,
 RA Ormond D., Quail M.A., Rabinowitch E., Rutherford K.M., Sanders M.,
 RA Sharp S., Simmonds M., Stevens K., Whitehead S., Barrall B.G.,
 RA Spratt B.G., Parkhill J.;
 RT "Complete genomes of two clinical Staphylococcus aureus strains:
 RT evidence for the rapid evolution of virulence and drug resistance";
 RL Proc. Natl. Acad. Sci. U.S.A. 101:9786-9791(2004).
 CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
 CC an amide bond (By similarity).
 DR EMBL; BX571856; CAG41560.1; -;
 DR GO; GO:0009986; C:cell surface; IEA.
 DR GO; GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0007155; P:cell adhesion; IEA.
 DR InterPro; IPR008966; Adhes_bact.
 DR InterPro; IPR004237; Fn_bind.
 DR InterPro; IPR005877; Gpos_YsIRK.
 DR InterPro; IPR001899; Gram_pos_anchor.
 DR Pfam; PF02986; Fn_bind; 1.
 DR Pfam; PF00746; Gram_pos_anchor; 1.
 DR Pfam; PF04650; YsIRK_signal; 1.
 DR TIGRFAMs; TIGR01167; LpxTG_anchor; 1.
 DR TIGRFAMs; TIGR01168; YsIRK_signal; 1.
 DR PROSITE; PS50847; GRAM_POS_ANCHORING; 1.
 KW Cell wall; Complete proteome; Peptidoglycan-anchor.
 SQ SEQUENCE 965 AA; 105691 MW; 2982E132164D0551 CRC64;

Query Match 90.0%; Score 45; DB 2; Length 965;
 Best Local Similarity 100.0%; Pred. No. 18;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EIIEDPTNK 10
 |||||
 Db 792 EIIEDPTNK 800

RESULT 11
 O99RD2 PRELIMINARY; PRT; 1038 AA.
 ID O99RD2;
 AC O99RD2;
 DT 01-JUN-2001 (TREMBlrel. 17, Created)

DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
 DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
 DE Fibronectin-binding protein homolog.
 GN Name=fnb; OrderedLocustNames=SAV2503;
 OS Staphylococcus aureus (strain Mu50 / ATCC 700699).
 CC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 NCBI_TaxID=158878;
 [1]
 RN SEQUENCE FROM N.A.
 RP STRAIN=Mu50 / ATCC 700699;
 RX MEDLINE=21311952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2;
 RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
 RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Iino J.-Q., Ito T.,
 RA Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,
 RA Mizutani U. Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
 RA Sekimizu K., Hirakawa H., Kihara S., Goto S., Yabuzaki J.,
 RA Kanehisa M., Yamauchi A., Oshima K., Furuya K., Yoshino C., Shiba T.,
 RA Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
 RT "Whole genome sequencing of methicillin-resistant Staphylococcus
 RT aureus";
 RL Lancet 357:1225-1240(2001).
 CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
 CC an amide bond (By similarity).
 DR EMBL; AP003365; BAB58665.1; -;
 DR PIR; H90053; H90053.
 DR GO; GO:0009986; C:cell surface; IEA.
 DR GO; GO:0005618; C:cell wall; IEA.
 DR GO; GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0007155; P:cell adhesion; IEA.
 DR InterPro; IPR008966; Adhes_bact.
 DR InterPro; IPR004237; Fn_bind.
 DR InterPro; IPR005877; Gpos_YsIRK.
 DR InterPro; IPR001899; Gram_pos_anchor.
 DR Pfam; PF02986; Fn_bind; 1.
 DR Pfam; PF00746; Gram_pos_anchor; 1.
 DR Pfam; PF04650; YsIRK_signal; 1.
 DR TIGRFAMs; TIGR01167; LpxTG_anchor; 1.
 DR TIGRFAMs; TIGR01168; YsIRK_signal; 1.
 DR PROSITE; PS50847; GRAM_POS_ANCHORING; 1.
 KW Cell wall; Complete proteome; Peptidoglycan-anchor.
 SQ SEQUENCE 1038 AA; 113618 MW; 666BF6F2FBE12 CRC64;

Query Match 90.0%; Score 45; DB 2; Length 1038;
 Best Local Similarity 100.0%; Pred. No. 20;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EIIEDPTNK 10
 |||||
 Db 823 EIIEDPTNK 831

RESULT 12
 O7A3J7 PRELIMINARY; PRT; 1038 AA.
 ID O7A3J7;
 AC O7A3J7;
 DT 05-JUL-2004 (TREMBlrel. 27, Created)
 DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
 DE Fmb protein.
 GN Name=fmb; OrderedLocustNames=SA2291;
 OS Staphylococcus aureus (strain N315).
 CC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 NCBI_TaxID=158879;
 [1]
 RN SEQUENCE FROM N.A.
 RP MEDLINE=21311952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2;
 RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
 RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Iino J.-Q., Ito T.,
 RA Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,
 RA Mizutani U. Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
 RA Sekimizu K., Hirakawa H., Kihara S., Goto S., Yabuzaki J.,
 RA Kanehisa M., Yamauchi A., Oshima K., Furuya K., Yoshino C., Shiba T.,

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RA Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
RT "Whole genome sequencing of methicillin-resistant Staphylococcus
RT aureus.";
RL Lancel 357:1225-1240(2001).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC an amide bond (by similarity).
DR EMBL: AP003137; BAB3594.1; -.
DR GO: GO:0009986; C:cell surface; IEA.
DR GO: GO:0005618; C:cell wall; IEA.
DR GO: GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO: GO:0007155; P:cell adhesion; IEA.
DR InterPro: IPR008966; A:hes_dact.
DR InterPro: IPR004237; F:bind.
DR InterPro: IPR005877; G:pos_YSIK.
DR InterPro: IPR001899; G:pos_pos_anchor.
DR Pfam: PF02986; F:bind_1.
DR Pfam: PF00746; G:pos_anchor_1.
DR Pfam: PF04650; YSIK_signal; 1.
DR TIGRFAMs: TIGR01167; LPXTG_anchor; 1.
DR TIGRFAMs: TIGR01168; YSIK_signal; 1.
DR PROSITE: PS50847; GRAM_POS_ANCHORING; 1.
KM Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ SEQUENCE 1038 AA; 113618 MW; 665BFBF2FBEB12 CRC64;

Query March 90.0%; Score 45; DB 2; Length 1038;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EIIEDPTNK 10
Db 823 EIIEDPTNK 831

RESULT 13
O75138
ID O75138 PRELIMINARY; PRT; 403 AA.
AC O75138;
DT 01-NOV-1998 (TREMBlrel. 08, Created)
DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE KIAA0643 protein (Fragment).
GN Name=KIAA0643;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=98403880; PubMed=9734811;
RA Ishikawa K., Nagase T., Suyama M., Miyajima N., Tanaka A., Kotani H.,
RA Nomura N., Ohara O.;
RT "Prediction of the coding sequences of unidentified human genes. X.
RT The complete sequences of 100 new cDNA clones from brain which can
RT code for large proteins in vitro.";
RL DNA Res. 5:169-176(1998).
DR EMBL: AB014543; BAA31618.1; -.
DR InterPro: IPR001715; Calponin-like.
FT NON_TER
SQ SEQUENCE 403 AA; 46389 MW; 2BB4B81FF2381453 CRC64;

Query March 80.0%; Score 40; DB 2; Length 403;
Best Local Similarity 70.0%; Pred. No. 63;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 TEIIEPTNK 10
Db 132 SEIIEPTNK 141

RESULT 14
Q96AJ1

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ID Q96AJ1 PRELIMINARY; PRT; 413 AA.
AC Q96AJ1;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-MAR-2004 (TREMBlrel. 26, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE Clusterin associated protein 1.
GN Name=CLUAP1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Skin;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko U., Matulis A.K., Farmer A.A., Rubin G.M., Hong L.,
RA Saplinton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Uedin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raba S.S., Loughellano N.A., Peters G.J., Abramson R.D., Mullan S.J.,
RA Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.R., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimmett J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smalins D.E., Schmech A., Schein J.E.,
RA Jones S.V., Maira M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Skin;
RA Director MGC Project;
RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: BC017070; AAH17070.3; -.
SQ SEQUENCE 413 AA; 48155 MW; 7A23D4FA2AE5A9F CRC64;

Query March 80.0%; Score 40; DB 2; Length 413;
Best Local Similarity 70.0%; Pred. No. 64;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 TEIIEPTNK 10
Db 116 SEIIEPTNK 125

RESULT 15
O652A3
ID O652A3 PRELIMINARY; PRT; 413 AA.
AC O652A3;
DT 25-OCT-2004 (TREMBlrel. 28, Created)
DT 25-OCT-2004 (TREMBlrel. 28, Last sequence update)
DT 25-OCT-2004 (TREMBlrel. 28, Last annotation update)
DE Clusterin associated protein 1.
GN Name=CLUAP1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Takahashi M., Miwa N., Furukawa Y., Nakamura Y.;
RT "Isolation and characterization of a novel gene CLUAP1 whose
RT expression is frequently upregulated in colon cancer.";
RL Oncogene 0:0-0(2004).
DR EMBL: AB089691; BAD44779.1; -.
SQ SEQUENCE 413 AA; 48125 MW; 7A23D4FA2AE5A9F CRC64;

```

Query Match 80.0%; Score 40; DB 2; Length 413;
Best Local Similarity 70.0%; Pred. No. 64;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TEIEEDTNK 10
:|||||
Db 116 SEIVEDVNK 125

Search completed: October 22, 2005, 09:52:14
Job time : 57.2069 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using bw model

Run on: October 25, 2005, 20:58:51 ; Search time 69.7126 Seconds
(without alignments)
55.479 Million cell updates/sec

Title: US-10-731-238-91

Perfect score: 51
Sequence: 1 IIEBDYTKDK 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:*

- 1: Geneseqp1980s:*
- 2: Geneseqp1990s:*
- 3: Geneseqp2000s:*
- 4: Geneseqp2001s:*
- 5: Geneseqp2002s:*
- 6: Geneseqp2003as:*
- 7: Geneseqp2003bs:*
- 8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	51	100.0	10	2	AAM65747
2	51	100.0	37	1	AAP82118
3	51	100.0	37	4	AAB91958
4	51	100.0	38	1	AAP80662
5	51	100.0	77	2	AAR88749
6	51	100.0	101	2	AAR90939
7	51	100.0	113	2	AAR90937
8	51	100.0	124	2	AAR90940
9	51	100.0	128	2	AAR90941
10	51	100.0	130	2	AAR58806
11	51	100.0	130	2	AAR58807
12	51	100.0	130	2	AAR91202
13	51	100.0	130	2	AAR91201
14	51	100.0	134	2	AAY29089
15	51	100.0	134	2	AAY29088
16	51	100.0	134	2	AAY29087
17	51	100.0	139	2	AAM31556
18	51	100.0	162	2	AAR90942
19	51	100.0	164	2	AAR90938
20	51	100.0	174	2	AAR58808
21	51	100.0	174	2	AAR91203
22	51	100.0	181	2	AAR58805
23	51	100.0	181	2	AAR91200
24	51	100.0	559	2	AAM69803
25	51	100.0	940	2	AAR07070

26	51	100.0	940	6	ABJ19111
27	51	100.0	948	6	ADA89470
28	51	100.0	948	6	ABJ18923
29	51	100.0	948	6	ABM72536
30	51	100.0	961	6	ABU15854
31	51	100.0	978	4	AAU33960
32	51	100.0	1001	4	AAU37093
33	51	100.0	1018	1	AAU37245
34	51	100.0	1018	4	AAU34301
35	51	100.0	1018	6	ABJ18922
36	51	100.0	1018	6	ABM72537
37	51	100.0	1018	6	ABM72537
38	51	100.0	1027	2	AAW69806
39	51	100.0	1038	6	ABU15903
40	43	84.3	10	2	AAM65748
41	41	80.4	928	8	ADN19097
42	40	78.4	10	2	AAM65746
43	38	74.5	249	3	AAW60593
44	38	74.5	249	3	AAW64316
45	38	74.5	268	3	AAW60592

ALIGNMENTS

RESULT 1
AAM65747 standard; peptide; 10 AA.

XX AC AAM65747;

DT 16-OCT-1998 (first entry)

DE Fibronection binding protein-derived peptide #91.

XX microbial surface components recognising adhesive matrix molecule;

KW MSCRAMM; fibronection; fibronection-binding protein; antibody; epitope;

KW antiserum; bacterial infection; antibiotic-resistant strain.

XX Synthetic.

OS Staphylococcus aureus.

XX WO9831389-A2.

XX 23-JUL-1998.

XX 21-JAN-1998; 98WO-US001222.

XX 21-JAN-1997; 97US-0036139P.

XX (TEXA) UNIV TEXAS A & M SYSTEM.

XX Hooeek M, Patti JM, House-Pompeo KL, Speziale P, Joh D;

XX Mcgavin M;

XX WPI; 1998-413816/35.

XX Example 9; Page 111; 201pp; English.

XX The invention relates to antibodies that bind to a fibronection-binding

XX domain of a fibronection-binding protein, and inhibit binding of the

XX protein to fibronection. Also claimed are: (1) isolated peptides of a

XX fibronection-binding protein that do not bind to fibronection; (2) fusion

XX protein containing at least one peptide of a fibronection-binding protein

XX linked to a second amino acid sequence; (3) nucleic acid encoding the

XX isolated peptide of (1). Antibodies, the isolated peptides of (1) and the

XX nucleic acids are all useful for immunisation (active or passive) and (by

XX inhibiting binding of bacteria to fibronection) for preventing or treating

XX infection in humans or other animals, particularly by staphylococci or


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XX AAP80662;
AC 25-MAR-2003 (revised)
XX 07-OCT-1990 (first entry)
DT
XX Protein with fibronectin binding ability.
XX Hybrid DNA molecule; fibronectin binding; mastitis; ruminants;
XX wound infection.
XX Staphylococcus aureus.
XX EP294349-A.
XX 07-DEC-1988.
XX 30-MAY-1988; 88EP-00850188.
XX 01-JUN-1987; 87SE-00002272.
XX (ALFA ) ALFA LAVAL AGRIC INT AB.
XX Lindberg MK, Signas LC, Wadstrom TM, Froman G;
XX WPI; 1988-347978/49.
XX N-PSDB; AAN81099.
XX Hybrid DNA encoding Staphylococcus aureus fibronectin binding protein -
XX useful for immunisation and topical application to prevent staphylococcal
XX infections.
XX Claim 11; Page 12; 23pp; English.
XX The peptide has fibronectin binding ability. It is useful for immunising
XX ruminants against staphylococcal mastitis, pref. when used at 0.5-5
XX micrograms/kg, using 3 doses given at 1-3 week intervals; for topical
XX application to prevent wound infection, using an isotonic saline soln. of
XX concn. 25-250 micrograms/ml; and, when immobilised on a carrier, for
XX diagnosing staphylococcal infections. (Updated on 25-MAR-2003 to correct
XX PF field.)
XX Sequence 38 AA:
SQ
Query Match 100.0%; Score 51; DB 1; Length 38;
Best Local Similarity 100.0%; Pred. No. 0.073; Indels 0; Gaps 0;
Matches 10; Conservative 0; Mismatches 0;
QY 1 IIEEDTNKDK 10
DB 8 IIEEDTNKDK 17
RESULT 5
AAR88749
ID AAR88749 standard; protein; 77 AA.
XX AAR88749;
XX 24-SEP-1996 (first entry)
XX S. aureus fibronectin binding protein D2D3 polypeptide.
XX Fibronectin binding protein; D2D3; prevention; adhesion; bacteria;
XX gram positive; extra-cellular matrix protein; in-dwelling device;
XX catheter; wound; D2D3; oral pathogen; oral cavity; J2385; NCIMB 40532.
XX Staphylococcus aureus.
OS
XX WO9604380-A1.
XX 15-FEB-1996.

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PF 28-JUL-1995; 95WO-EP003039.
XX 05-AUG-1994; 94GB-00015901.
XX (SMIK ) SMITHKLINE BEECHAM PLC.
XX Critchley IA, Dodd I, Barnett P, Mossakowska DEI;
XX WPI; 1996-129396/13.
XX N-PSDB; AAT12582.
XX Staphylococcus aureus fibronectin binding protein D2D3 polypeptide -
XX useful for combating infection at wound sites, surgical implants, etc.
XX and as antiadherent agent in oral hygiene.
XX Claim 5; Page 26; 38pp; English.
XX The present sequence is the S. aureus fibronectin binding protein
XX polypeptide D2D3, which can be used to prevent adhesion of (e.g. gram
XX positive) bacteria, to extra-cellular matrix proteins on in-dwelling
XX devices, e.g. catheters or in wounds. D2D3 can also be used to prevent
XX oral pathogens from binding to extra-cellular matrix proteins, in the
XX oral cavity. D2D3 was found to be effective at inhibiting S. aureus 8325-
XX 4, and 120 adhesion to fibronectin coated PMA coverslips, at a min.
XX adhesion inhibitor concn. of 10 microg/ml. D2D3 was derived from the D2
XX and D3 regions of the S. aureus J2385 (NCIMB 40532) fibronectin binding
XX protein
XX Sequence 77 AA:
SQ
Query Match 100.0%; Score 51; DB 2; Length 77;
Best Local Similarity 100.0%; Pred. No. 0.16; Indels 0; Gaps 0;
Matches 10; Conservative 0; Mismatches 0;
QY 1 IIEEDTNKDK 10
DB 46 IIEEDTNKDK 55
RESULT 6
AAR90939
ID AAR90939 standard; peptide; 101 AA.
XX AAR90939;
XX 23-SEP-1996 (first entry)
XX D3D4 polypeptide #3.
XX Fibronectin binding protein; Fbp; S. aureus J2385; monoclonal antibody;
XX infection; surgical implant; antiadherent agent; hygiene; adhesion;
XX extracellular matrix protein; oral pathogen; oral cavity.
XX Staphylococcus aureus.
OS
XX WO9604381-A1.
XX 15-FEB-1996.
XX 28-JUL-1995; 95WO-EP003040.
XX 05-AUG-1994; 94GB-00015900.
XX (SMIK ) SMITHKLINE BEECHAM PLC.

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PI Critchley IA, Dodd I, Barnett P, Mcday DL;
 XX
 DR WPI; 1996-129397/13.
 XX
 PT Polypeptide(s) derived from Staphylococcus aureus fibrinectin binding
 PT protein - inhibit binding of bacteria to extracellular matrix proteins,
 PT for combating infection at the site of wounds and surgical implants, and
 PT in oral hygiene.
 XX
 PS Claim 6; Page 24; 35pp; English.
 XX
 CC AAR90937-R90942 represent D3D4 polypeptides. These sequences correspond
 CC to fragments of the Staphylococcus aureus fibrinectin binding protein
 CC (Fbp). This sequence corresponds to residues 81-181 of S.aureus J2385
 CC (Fbp), and also contains a portion of the wall region 1 (WR1). These
 CC sequences, and monoclonal antibodies against them can be used to combat
 CC infection at the site of wounds, surgical implants and other in-dwelling
 CC devices (such as catheters), and as antiadherent agents in oral hygiene.
 CC They can also be used in the manufacture of a medicament for the
 CC prevention of adhesion of bacteria to extracellular matrix proteins
 CC present on in-dwelling devices or in wounds, or of oral pathogens to
 CC similar proteins on surfaces in the oral cavity
 CC
 SQ Sequence 101 AA;
 Query Match 100.0%; Score 51; DB 2; Length 101;
 Best Local Similarity 100.0%; Pred. No. 0.21;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 IIEEDTNKDK 10
 |||||
 Db 4 IIEEDTNKDK 13
 |||||
 RESULT 7
 AAR90937
 ID AAR90937 standard; peptide; 113 AA.
 XX
 AC AAR90937;
 XX
 DT 23-SEP-1996 (first entry)
 XX
 DE D3D4 polypeptide #1.
 XX
 KM Fibrinectin binding protein; Fbp; S.aureus J2385; monoclonal antibody;
 KM infection; surgical implant; antiadherent agent; hygiene; adhesion;
 KM extracellular matrix protein; oral pathogen; oral cavity.
 XX
 OS Staphylococcus aureus.
 XX
 FH Key Location/Qualifiers
 FT Region 1..21
 FT /note= "D1 region fragment"
 FT Region 22..59
 FT /note= "D2 region"
 FT Region 60..98
 FT /note= "D3 region"
 FT Region 99..113
 FT /note= "D4 region"
 FT Misc-difference 113
 FT /note= "P113T"
 XX
 PN WO9604381-A1.
 XX
 PD 15-FEB-1996.
 XX
 PF 28-JUL-1995; 95WO-EP003040.
 XX
 PR 05-AUG-1994; 94GB-00015900.
 XX
 PA (SMIK) SMITHKLINE BEECHAM PLC.
 XX
 PI Critchley IA, Dodd I, Barnett P, Mcday DL;

XX
 DR WPI; 1996-129397/13.
 XX
 PT Polypeptide(s) derived from Staphylococcus aureus fibrinectin binding
 PT protein - inhibit binding of bacteria to extracellular matrix proteins,
 PT for combating infection at the site of wounds and surgical implants, and
 PT in oral hygiene.
 XX
 PS Claim 6; Page 24; 35pp; English.
 XX
 CC AAR90937-R90942 represent D3D4 polypeptides. These sequences correspond
 CC to fragments of the Staphylococcus aureus fibrinectin binding protein
 CC (Fbp). This sequence corresponds to residues 18-130 of S.aureus J2385
 CC (Fbp), and also contains the D2 region, and a portion of the D1 region.
 CC These sequences, and monoclonal antibodies against them can be used to
 CC combat infection at the site of wounds, surgical implants and other in-
 CC dwelling devices (such as catheters), and as antiadherent agents in oral
 CC hygiene. They can also be used in the manufacture of a medicament for the
 CC prevention of adhesion of bacteria to extracellular matrix proteins
 CC present on in-dwelling devices or in wounds, or of oral pathogens to
 CC similar proteins on surfaces in the oral cavity
 CC
 SQ Sequence 113 AA;
 Query Match 100.0%; Score 51; DB 2; Length 113;
 Best Local Similarity 100.0%; Pred. No. 0.23;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 IIEEDTNKDK 10
 |||||
 Db 67 IIEEDTNKDK 76
 |||||
 RESULT 8
 AAR90940
 ID AAR90940 standard; peptide; 124 AA.
 XX
 AC AAR90940;
 XX
 DT 23-SEP-1996 (first entry)
 XX
 DE D3D4 polypeptide #4.
 XX
 KM Fibrinectin binding protein; Fbp; S.aureus J2385; monoclonal antibody;
 KM infection; surgical implant; antiadherent agent; hygiene; adhesion;
 KM extracellular matrix protein; oral pathogen; oral cavity.
 XX
 OS Staphylococcus aureus.
 XX
 FH Key Location/Qualifiers
 FT Region 1..19
 FT /note= "D2 region fragment"
 FT Region 20..58
 FT /note= "D3 region"
 FT Region 59..62
 FT /note= "D4 region"
 FT Region 63..124
 FT /note= "WR1 region"
 XX
 PN WO9604381-A1.
 XX
 PD 15-FEB-1996.
 XX
 PF 28-JUL-1995; 95WO-EP003040.
 XX
 PR 05-AUG-1994; 94GB-00015900.
 XX
 PA (SMIK) SMITHKLINE BEECHAM PLC.
 XX
 PI Critchley IA, Dodd I, Barnett P, Mcday DL;
 XX
 DR WPI; 1996-129397/13.

PT polypeptide(s) derived from Staphylococcus aureus fibronectin binding
PT protein - inhibit binding of bacteria to extracellular matrix proteins,
PT for combating infection at the site of wounds and surgical implants, and
PT in oral hygiene.

XX Claim 6; Page 24; 35pp; English.

XX AAR90937-R90942 represent D3D4 polypeptides. These sequences correspond
CC to fragments of the Staphylococcus aureus fibronectin binding protein
CC (Fbp). This sequence corresponds to residues 58-181 of S. aureus J2385
CC (Fbp), and also contains a portion of the D2 region, and a portion of the
CC wall region 1 (WRI). These sequences, and monoclonal antibodies against
CC them can be used to combat infection at the site of wounds, surgical
CC implants and other in-dwelling devices (such as catheters), and as
CC antiadherent agents in oral hygiene. They can also be used in the
CC manufacture of a medicament for the prevention of adhesion of bacteria to
CC extracellular matrix proteins present on in-dwelling devices or in
CC wounds, or of oral pathogens to similar proteins on surfaces in the oral
CC cavity.

XX Sequence 124 AA;

Query Match 100.0%; Score 51; DB 2; Length 124;
Best Local Similarity 100.0%; Pred. No. 0.26; Mismatches 0; Gaps 0;
Matches 10; Conservative 0; Indels 0;

OY 1 IIEEDTNKDK 10
|||
DB 27 IIEEDTNKDK 36

RESULT 9

AAR90941 ID AAR90941 standard; peptide; 128 AA.

AC AAR90941;

DT 23-SEP-1996 (first entry)

XX D3D4 polypeptide #5.

XX Fibronectin binding protein; Fbp; S. aureus J2385; monoclonal antibody;
KW infection; surgical implant; antiadherent agent; hygiene; adhesion;
KW extracellular matrix protein; oral pathogen; oral cavity.

XX Staphylococcus aureus.

XX Key Location/Qualifiers

FT Region 1..23 /note= "D2 region"

FT Region 24..62 /note= "D3 region"

FT Region 63..77 /note= "D4 region"

FT Region 78..128 /note= "WRI region"

XX WO9604381-A1.

XX 15-FEB-1996.

XX 28-JUL-1995; 95WO-EP003040.

XX 05-AUG-1994; 94GB-00015900.

XX (SMITK) SMITHKLINE BEECHAM PLC.

XX Critchley IA, Dodd I, Barnett P, Mcbay DL;

XX WPI, 1996-129397/13.

PT Polypeptide(s) derived from Staphylococcus aureus fibronectin binding
PT protein - inhibit binding of bacteria to extracellular matrix proteins,

PT for combating infection at the site of wounds and surgical implants, and
PT in oral hygiene.

XX Claim 6; Page 24; 35pp; English.

XX AAR90937-R90942 represent D3D4 polypeptides. These sequences correspond
CC to fragments of the Staphylococcus aureus fibronectin binding protein
CC (Fbp). This sequence corresponds to residues 54-181 of S. aureus J2385
CC (Fbp), and also contains the D2 region, and a portion of the wall region 1
CC (WRI). These sequences, and monoclonal antibodies against them can be
CC used to combat infection at the site of wounds, surgical implants and
CC other in-dwelling devices (such as catheters), and as antiadherent agents
CC in oral hygiene. They can also be used in the manufacture of a medicament
CC for the prevention of adhesion of bacteria to extracellular matrix
CC proteins present on in-dwelling devices or in wounds, or of oral
CC pathogens to similar proteins on surfaces in the oral cavity

XX Sequence 128 AA;

Query Match 100.0%; Score 51; DB 2; Length 128;
Best Local Similarity 100.0%; Pred. No. 0.27; Mismatches 0; Gaps 0;
Matches 10; Conservative 0; Indels 0;

OY 1 IIEEDTNKDK 10
|||
DB 31 IIEEDTNKDK 40

RESULT 10

AAR58806 ID AAR58806 standard; protein; 130 AA.

XX AAR58806;

DT 25-MAR-2003 (revised)

DT 30-MAR-1995 (first entry)

XX Fibronectin binding domain D1-D4(709-838(P838T)).

XX Fibronectin binding protein; Fbp; fibronectin binding domain;
KW monoclonal antibody; MAb; adhesion; Gram-positive bacterium; bacteremia;
KW Escherichia coli.

XX Staphylococcus aureus.

XX WO9418327-A1.

XX 18-AUG-1994.

XX 04-FEB-1994; 94WO-GB000215.

XX 05-FEB-1993; 93GB-00002289.

XX 20-OCT-1993; 93GB-00021592.

XX (SMITK) SMITHKLINE BEECHAM PLC.

XX Burnham MKR, Chopra I, Critchley IA, Knowles DVC;

XX WPI, 1994-279748/34.

PT Polypeptide(s) derived from Staphylococcus aureus fibronectin binding
PT protein - inhibit binding of bacteria to extracellular matrix proteins,
PT for combating infection at the site of wounds and surgical implants, and
PT in oral hygiene.

XX Disclousure; Page 30; 40pp; English.

XX Polypeptides corresponding to residues 709-T886 plus PRIVPT, 709-
CC P838(P838T) and 709-P838 (AAR58805-07, respectively) of S. aureus J2385
CC (NCTMB 40532) Fbp type A fibronectin binding domain D1-D4 region
CC (AAR58808) were expressed in E. coli BL21(DE4) and used to raise Mabs
CC specific for Fbp. (Updated on 25-MAR-2003 to correct PN field.)

XX Sequence 130 AA;

Query Match 100.0%; Score 51; DB 2; Length 130;
 Best Local Similarity 100.0%; Pred. No. 0.27;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IIEEDTNKDK 10
 |||||
 84 IIEEDTNKDK 93

RESULT 11

AAR58807
 ID AAR58807 standard; protein; 130 AA.

XX AAR58807;

AC 25-MAR-2003 (revised)

DT 30-MAR-1995 (first entry)

XX Fibronectin binding domain D1-D4(709-838).

XX Fibronectin binding protein; Fbp; fibronectin binding domain;

KM monoclonal antibody; Mab; adhesion; Gram-positive bacterium; bacteremia;

XX Escherichia coli.

OS Staphylococcus aureus.

XX WO9418327-A1.

XX 18-AUG-1994.

XX 04-FEB-1994; 94WO-GB000215.

XX 05-FEB-1993; 93GB-00002289.

XX 20-OCT-1993; 93GB-00021592.

XX (SMIK) SMITHKLINE BEECHAM PLC.

XX Burnham MKR, Chopra I, Critchley IA, Knowles DJC;

XX WPI; 1994-279746/34.

XX Fibronectin binding protein and monoclonal antibodies specific for Fbp -

XX useful to prevent adherence of Gram-positive bacteria to indwelling

XX devices or wounds.

XX Disclosure; Page 30; 40pp; English.

XX Polypeptides corresponding to residues G709-T886 plus PIVPT, G709-

XX P838(P838T) and G709-P838 (AAR58805-07, respectively) of S. aureus J2385

XX (NCIMB 40532) Fbp type A fibronectin binding domain D1-D4 region

XX (AAR58808) were expressed in E. coli BL21(DE4) and used to raise Mabs

XX specific for Fbp. (Updated on 25-MAR-2003 to correct PN field.)

XX Sequence 130 AA;

XX Query Match 100.0%; Score 51; DB 2; Length 130;

XX Best Local Similarity 100.0%; Pred. No. 0.27;

XX Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IIEEDTNKDK 10
 |||||
 84 IIEEDTNKDK 93

RESULT 12

AAR91202
 ID AAR91202 standard; peptide; 130 AA.

XX AAR91202;

XX 13-NOV-1996 (first entry)

DE D1-D4 fibronectin binding domains.

XX Fibronectin; oral hygiene; gingivitis; gum disease; adhesion;

KM periodontitis; oral pathogens; caries; calculus; candidiasis; oral surgery;

KM tissue regeneration; irrigation; toothpaste; dentifrice; mouthwash;

XX lozenge.

XX Staphylococcus aureus.

XX WO9604003-A1.

XX 15-FEB-1996.

XX 18-JUL-1995; 95WO-EP002825.

XX 05-AUG-1994; 94GB-00015902.

XX (SMIK) SMITHKLINE BEECHAM PLC.

XX Barnett P, Critchley IA, Dodd I;

XX WPI; 1996-129122/13.

XX Prevention of adherence of oral pathogens in the oral cavity, partic-

XX tooth surfaces - by application of a fibronectin binding protein or

XX polypeptide or a monoclonal antibody or fragment against it.

XX Claim 5; Page 32; 41pp; English.

XX Adherence of oral pathogens, particularly to tooth surfaces, can be

XX prevented by application of a fibronectin binding protein or polypeptide.

XX The fibronectin binding protein or polypeptide is useful in the

XX manufacture of oral hygiene compositions, eg. toothpaste, liquid

XX dentifrice, mouthwash or lozenge. They are useful to prevent the plaque-

XX related development of carious lesions, gingivitis, calculus or

XX periodontal disease and to combat oral cavity infections, e.g.

XX candidiasis. They may also be useful in oral surgery e.g. in guided

XX tissue regeneration procedures to prevent subsequent bacterial infection,

XX and for irrigation of periodontal pockets. This sequence corresponds to

XX amino acids 709-838 of the D1-D4 fibronectin binding domain of

XX Staphylococcus aureus

XX Sequence 130 AA;

XX Query Match 100.0%; Score 51; DB 2; Length 130;

XX Best Local Similarity 100.0%; Pred. No. 0.27;

XX Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IIEEDTNKDK 10
 |||||
 84 IIEEDTNKDK 93

XX AAR91201 standard; peptide; 130 AA.

XX AAR91201;

XX 13-NOV-1996 (first entry)

XX D1-D4 fibronectin binding domains.

XX Fibronectin; oral hygiene; gingivitis; gum disease; adhesion;

KM periodontitis; oral pathogens; caries; calculus; candidiasis; oral surgery;

KM tissue regeneration; irrigation; toothpaste; dentifrice; mouthwash;

XX lozenge.

XX Staphylococcus aureus.

XX WO9604003-A1.

XX 15-FEB-1996.

XX 18-JUL-1995; 95WO-EP002825.
 PF 05-AUG-1994; 94GB-00015902.
 XX (SMIK) SMITHLINE BEECHAM PLC.
 PA Barnett P, Critchley IA, Dodd I;
 XX WPI, 1996-129122/13.
 DR
 XX Prevention of adherence of oral pathogens in the oral cavity, partic.
 PT tooth surfaces - by application of a fibronectin binding protein or
 PF polypeptide or a monoclonal antibody or fragment against it.
 XX
 PS Claim 5; Page 31-32; 41pp; English.
 XX
 CC Adherence of oral pathogens, particularly to tooth surfaces, can be
 CC prevented by application of a fibronectin binding protein or polypeptide.
 CC The fibronectin binding protein or polypeptide is useful in the
 CC manufacture of oral hygiene compositions, eg. toothpaste, liquid
 CC dentifrice, mouthwash or lozenge. They are useful to prevent the plaque-
 CC related development of carious lesions, gingivitis, calculus or
 CC periodontal disease and to combat oral cavity infections, e.g.
 CC candidiasis. They may also be useful in oral surgery e.g. in guided
 CC tissue regeneration procedures to prevent subsequent bacterial infection,
 CC and for irrigation of periodontal pockets. This sequence corresponds to
 CC amino acids 709-838 of the D1-D4 fibronectin binding domain of
 CC Staphylococcus aureus with a P838T substitution
 XX
 SQ Sequence 130 AA;

Query Match 100.0%; Score 51; DB 2; Length 130;
 Best Local Similarity 100.0%; Pred. No. 0.27;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 IIEEDTNKDK 10
 |||||
 DB 84 IIEEDTNKDK 93

RESULT 14
 AAY29089
 ID AAY29089 standard; protein; 134 AA.
 XX
 AC AAY29089;

XX 28-SEP-1999 (first entry)
 DT

DE Cloned fibronectin binding protein binding domain (FnBAB) sequence.

XX Bovine herpes virus-2; BHV-2; cytokine; immune response; immunogen; IL;
 KM interleukin; colony stimulating factor; CSF; interferon; IFN; TNF;
 KM tumour necrosis factor; recombinant virus; vaccine; mucosal disease;
 KM mastitis; breast cancer; stress-induced disease; binding domain; FnBAB;
 KM fibronectin binding protein.
 XX

OS Staphylococcus aureus.
 XX

PN WO9916892-A1.
 XX

PD 08-APR-1999.
 XX

PF 29-SEP-1998; 98WO-GB002927.
 XX

PR 29-SEP-1997; 97GB-00020633.
 XX

PA (UYBR-) UNIV BRISTOL.
 XX

PI Bradley AJ, Duffas WPH;
 XX

DR WPI, 1999-255101/21.
 DR

DR N-PSDB; AAX91506.
 DR

XX New bovine herpes virus-2 vectors.
 PF
 XX
 PS Example 2; Fig 8A-B; 130pp; English.
 XX

CC The invention provides bovine herpes virus-2 (BHV-2) based vectors that
 CC comprise at least one cytokine-encoding DNA sequence. The expression of
 CC cytokines in mammals can up-regulate immune responses to the immunogens.
 CC The cytokine is selected from interleukins (IL), colony stimulating
 CC factors (CSF), interferons (IFN) and tumour necrosis factors (TNF). The
 CC BHV-2 based vector or recombinant virus can be used as vaccines. They can
 CC be used for preventing or treating a mucosal disease in a subject, e.g.
 CC ruminants, cattle, sheep, dogs, cats, horses, or man, particularly
 CC mastitis in cows or breast cancers in humans. They can also be used for
 CC preventing or treating a stress-induced disease. The present sequence
 CC represents a S. aureus fibronectin binding protein binding domain
 CC sequence FnBAB, the gene cloned for use in this invention. The gene has
 CC 97.8 percent identity when compared to the previously published sequences
 CC FnBA and FnBB
 XX

SQ Sequence 134 AA;

Query Match 100.0%; Score 51; DB 2; Length 134;
 Best Local Similarity 100.0%; Pred. No. 0.28;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 IIEEDTNKDK 10
 |||||
 DB 84 IIEEDTNKDK 93

RESULT 15
 AAY29088
 ID AAY29088 standard; protein; 134 AA.
 XX
 AC AAY29088;

XX 28-SEP-1999 (first entry)
 DT

DE S. aureus fibronectin binding protein B (FnBB) binding domain.

XX Bovine herpes virus-2; BHV-2; cytokine; immune response; immunogen; IL;
 KM interleukin; colony stimulating factor; CSF; interferon; IFN; TNF;
 KM tumour necrosis factor; recombinant virus; vaccine; mucosal disease;
 KM mastitis; breast cancer; stress-induced disease; binding domain; FnBB;
 KM fibronectin binding protein.
 XX

OS Staphylococcus aureus.
 XX

PN WO9916892-A1.
 XX

PD 08-APR-1999.
 XX

PF 29-SEP-1998; 98WO-GB002927.
 XX

PR 29-SEP-1997; 97GB-00020633.
 XX

PA (UYBR-) UNIV BRISTOL.
 XX

PI Bradley AJ, Duffas WPH;
 XX

DR WPI, 1999-255101/21.
 DR

DR N-PSDB; AAX91505.
 XX

PT New bovine herpes virus-2 vectors.
 XX

PS Example 2; Fig 8A-B; 130pp; English.
 XX

CC The invention provides bovine herpes virus-2 (BHV-2) based vectors that
 CC comprise at least one cytokine-encoding DNA sequence. The expression of
 CC cytokines in mammals can up-regulate immune responses to the immunogens.
 CC The cytokine is selected from interleukins (IL), colony stimulating
 CC factors (CSF), interferons (IFN) and tumour necrosis factors (TNF). The

CC BHV-2 based vector or recombinant virus can be used as vaccines. They can
CC be used for preventing or treating a mucosal disease in a subject, e.g.
CC ruminants, cattle, sheep, goats, dogs, cats, horses, or man, particularly
CC mastitis in cows or breast cancers in humans. They can also be used for
CC preventing or treating a stress-induced disease. The present sequence
CC represents the binding domain of a previously published S. aureus
CC fibronectin binding protein B (FnBB) sequence. The FnB binding domain
CC gene sequence FNBBAB, cloned for use in this invention has 97.8 percent
CC identity when compared to the previously published FNBA and FNBB gene
CC sequences

XX
SQ Sequence 134 AA;

Query Match 100.0%; Score 51; DB 2; Length 134;
Best Local Similarity 100.0%; Pred. No. 0.28;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IIEEDTNKDK 10
Db 84 IIEEDTNKDK 93

Search completed: October 25, 2005, 21:29:11
Job time : 70.7126 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 22, 2005, 07:41:53 ; Search time 17.2989 Seconds
(without alignments)
43.153 Million cell updates/sec

Title: US-10-731-238-91
Perfect score: 51
Sequence: 1 IIBEDTNKDK 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: /cgn2_6/ptodata/1/1aa/5A.COMB.pep:*
2: /cgn2_6/ptodata/1/1aa/5B.COMB.pep:*
3: /cgn2_6/ptodata/1/1aa/6A.COMB.pep:*
4: /cgn2_6/ptodata/1/1aa/6B.COMB.pep:*
5: /cgn2_6/ptodata/1/1aa/PCITUS.COMB.pep:*
6: /cgn2_6/ptodata/1/1aa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	51	100.0	10	4	US-09-010-317-91
2	51	100.0	37	1	US-08-234-622A-4
3	51	100.0	38	1	US-08-294-189-8
4	51	100.0	38	1	US-08-729-767-5
5	51	100.0	114	1	US-08-259-000-3
6	51	100.0	130	2	US-08-459-135A-7
7	51	100.0	130	2	US-08-459-135A-8
8	51	100.0	130	3	US-08-495-559-7
9	51	100.0	130	3	US-08-495-559-8
10	51	100.0	139	3	US-08-856-253-8
11	51	100.0	174	2	US-08-459-135A-10
12	51	100.0	174	2	US-08-459-135A-13
13	51	100.0	174	3	US-08-495-559-10
14	51	100.0	174	3	US-08-495-559-13
15	51	100.0	176	3	US-08-495-559-6
16	51	100.0	178	2	US-08-459-135A-12
17	51	100.0	178	3	US-08-495-559-12
18	51	100.0	181	2	US-08-459-135A-6
19	51	100.0	559	4	US-08-956-171E-5251
20	51	100.0	559	4	US-08-781-986A-5251
21	51	100.0	1027	4	US-08-956-171E-5254
22	51	100.0	1027	4	US-08-781-986A-5254
23	43	84.3	10	4	US-09-010-317-92
24	40	78.4	10	4	US-09-010-317-90
25	37	72.5	10	4	US-09-010-317-7
26	37	72.5	10	4	US-09-010-317-85
27	37	72.5	12	4	US-09-010-317-62

28	37	72.5	36	4	US-09-010-317-58	Sequence 58, Appl
29	37	72.5	36	4	US-09-010-317-59	Sequence 59, Appl
30	37	72.5	38	1	US-08-234-622A-3	Sequence 3, Appl
31	37	72.5	38	1	US-08-729-767-4	Sequence 7, Appl
32	37	72.5	38	4	US-09-010-317-7	Sequence 8, Appl
33	37	72.5	38	4	US-09-010-317-8	Sequence 45, Appl
34	37	72.5	38	4	US-09-010-317-45	Sequence 49, Appl
35	37	72.5	38	4	US-09-010-317-49	Sequence 2, Appl
36	36	70.6	360	3	US-09-043-627-2	Sequence 14, Appl
37	36	70.6	890	2	US-08-483-101-14	Sequence 2, Appl
38	35	68.6	652	3	US-08-559-896B-2	Sequence 2, Appl
39	35	68.6	652	4	US-09-351-794A-2	Sequence 49, Appl
40	34	66.7	23	4	US-09-383-062-49	Sequence 5939, Ap
41	34	66.7	176	4	US-09-328-352-5939	Sequence 4839, Ap
42	34	66.7	225	4	US-09-328-352-4839	Sequence 35302, A
43	34	66.7	228	4	US-09-270-767-35302	Sequence 50519, A
44	34	66.7	228	4	US-09-270-767-50519	Sequence 2, Appl
45	34	66.7	376	2	US-08-704-548-2	

ALIGNMENTS

RESULT 1
US-09-010-317-91
; Sequence 91, Application US/09010317
; Patent No. 6685943
; GENERAL INFORMATION:
; APPLICANT: Hook, Magnus
; APPLICANT: Patti, Joseph M.
; APPLICANT: House-Pompeo, Karen L.
; APPLICANT: Speziale, Pietro
; APPLICANT: Joh, Danny
; APPLICANT: McGavin, Martin J.
; TITLE OF INVENTION: FIBROECTIN BINDING PROTEIN COMPOSITIONS
; TITLE OF INVENTION: AND METHODS OF USE
; NUMBER OF SEQUENCES: 105
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: TX
; COUNTRY: USA
; ZIP: 77210-4433
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/010.317
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/036,139
; FILING DATE: 21-JAN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Hibler, David W.
; REGISTRATION NUMBER: 41,071
; REFERENCE/DOCKET NUMBER: TAMK.189
; TELECOMMUNICATIONS INFORMATION:
; TELEPHONE: 542-418-3000
; TELEFAX: 542-474-7577
; INFORMATION FOR SEQ ID NO: 91:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; US-09-010-317-91
Query Match 100.0%; Score 51; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0061;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 IIEEDTNKDK 10
| | | | | | | |
Db 1 IIEEDTNKDK 10

RESULT 2

US-08-234-622A-4
; Sequence 4, Application US/08234622A
; Patent No. 5440014
; GENERAL INFORMATION:
; APPLICANT: HOOK, Magnus
; APPLICANT: MCGAVIN, Martin
; APPLICANT: RAUCCI, Giuseppe
; TITLE OF INVENTION: A FIBRONECTIN BINDING PEPTIDE
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Doane, Swecker & Mathis
; STREET: P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/234,622A
; FILING DATE: 28-APR-1994
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: SE 9002617-0
; FILING DATE: 10-AUG-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/SE91/00534
; FILING DATE: 09-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Meuth, Donna M
; REGISTRATION NUMBER: 36,607
; REFERENCE/DOCKET NUMBER: 012885-044
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 37 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-234-622A-4

Query Match 100.0%; Score 51; DB 1; Length 37;
Best Local Similarity 100.0%; Pred. No. 0.023;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 IIEEDTNKDK 10
| | | | | | | |
Db 7 IIEEDTNKDK 16

RESULT 3

US-08-294-189-8
; Sequence 8, Application US/08294189
; Patent No. 5707822
; GENERAL INFORMATION:
; APPLICANT: Fischecci, Vincent A.
; APPLICANT: Rakonjac, Jasna
; APPLICANT: Robbins, John
; TITLE OF INVENTION: GENE SERUM OPACITY FACTOR

NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack Avenue
City: Hackensack
STATE: New Jersey
COUNTRY: USA
ZIP: 07601

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/294,189
FILING DATE: 22-AUG-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Bsq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-118
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 487-5800
TELEFAX: 201 343-1684
TELEX: 133521
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
ORGANISM: Streptococcus pyogenes
STRAIN: D734
IMMEDIATE SOURCE:
CLONE: SAU3a
US-08-294-189-8

Query Match 100.0%; Score 51; DB 1; Length 38;
Best Local Similarity 100.0%; Pred. No. 0.024;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 IIEEDTNKDK 10
| | | | | | | |
Db 1 IIEEDTNKDK 10

RESULT 4

US-08-729-767-5
; Sequence 5, Application US/08729767
; Patent No. 5770702
; GENERAL INFORMATION:
; APPLICANT: HOOK, Magnus
; APPLICANT: LINDBERG, Martin Kjel
; APPLICANT: SIGNAS, Lars Christel
; APPLICANT: MADSTROM, Torkel Mikael
; APPLICANT: FROMAN, Gunnar
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN AS WELL AS
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Doane, Swecker & Mathis, L.L.P.
; STREET: P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/729,767
FILING DATE: 07-OCT-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/259,000
FILING DATE: 13-JUN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/007,817
FILING DATE: 22-JAN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/201,028
FILING DATE: 01-JUN-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: SE 8702272-9
FILING DATE: 01-JUN-1987
ATTORNEY/AGENT INFORMATION:
NAME: McGowan, Malcolm K.
REGISTRATION NUMBER: 39,300
REFERENCE/DOCKET NUMBER: 012889-036
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-729-767-5

Query Match 100.0%; Score 51; DB 1; Length 38;
Best Local Similarity 100.0%; Pred. No. 0.024;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IIEEDTNKDK 10
|||
Db 8 IIEEDTNKDK 17

RESULT 5
US-08-259-000-3
Sequence 3, Application US/08259000
Patent No. 5571514
GENERAL INFORMATION:
APPLICANT: HOOK, Magnus
APPLICANT: LINDBERG, Martin Kjell
APPLICANT: SIGNAS, Lars Christer
APPLICANT: WADSTROM, Torkel Mikael
APPLICANT: FROMAN, Gunnar
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN AS WELL AS
TITLE OF INVENTION: ITS PREPARATION
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Burns, Doane, Swecker & Mathis
STREET: P.O. Box 1404
CITY: Alexandria
STATE: Virginia
COUNTRY: United States
ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/259,000
FILING DATE: 13-JUN-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: SE 8702272-9

FILING DATE: 01-JUN-1987
ATTORNEY/AGENT INFORMATION:
NAME: Meuth, Donna M
REGISTRATION NUMBER: 36,607
REFERENCE/DOCKET NUMBER: 012885-062
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 114 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-259-000-3

Query Match 100.0%; Score 51; DB 1; Length 114;
Best Local Similarity 100.0%; Pred. No. 0.075;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IIEEDTNKDK 10
|||
Db 84 IIEEDTNKDK 93

RESULT 6
US-08-459-135A-7
Sequence 7, Application US/08459135A
Patent No. 5955078
GENERAL INFORMATION:
APPLICANT: BURHAM, Martin Karl Russel
APPLICANT: CHOPRA, Ian
APPLICANT: CRITCHLEY, Ian Alfred
APPLICANT: KNOWLES, David Justin Charles
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN: MONOCLONAL ANTIBODY AND THEIR US
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
STATE: PA
COUNTRY: U.S.A.
ZIP: 19406-0939
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: Fastseq, Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/459,135A
FILING DATE: 02-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB/94/00215
FILING DATE: 04-Feb-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Gimmil, Edward R
REGISTRATION NUMBER: 38,891
REFERENCE/DOCKET NUMBER: P30591C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-4478
TELEFAX: 610-270-5090
TELEX:
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 130 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-459-135A-7

Query Match 100.0%; Score 51; DB 2; Length 130;
 Best Local Similarity 100.0%; Pred. No. 0.086;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IIEEDTNKDK 10
 |||||
 DB 84 IIEEDTNKDK 93

RESULT 7

US-08-459-135A-8
 ; Sequence 8, Application US/08459135A
 ; Patent No. 5955078

GENERAL INFORMATION:

APPLICANT: BURHAM, Martin Karl Russel

APPLICANT: CHOPRA, Ian

APPLICANT: CRITCHLEY, Ian Alfred

APPLICANT: KNOWLES, David Justin Charles

TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN: MONOCLONAL ANTIBODY AND THEIR US

NUMBER OF SEQUENCES: 15

CORRESPONDENCE ADDRESS:

ADDRESSEE: SmithKline Beecham Corporation

STREET: 709 Swedeland Road

CITY: King of Prussia

STATE: PA

COUNTRY: U.S.A.

ZIP: 19406-0939

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

OPERATING SYSTEM: DOS

SOFTWARE: Fastseq, Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/459,135A

FILING DATE: 02-JUN-1995

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/GB/94/00215

FILING DATE: 04-Feb-1994

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Gilmul, Edward R

REGISTRATION NUMBER: 38,891

REFERENCE/DOCKET NUMBER: P30591C2

TELECOMMUNICATION INFORMATION:

TELEPHONE: 610-270-4478

TELEFAX: 610-270-5090

TELEX:

INFORMATION FOR SEQ ID NO: 8:

SEQUENCE CHARACTERISTICS:

LENGTH: 130 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-459-135A-8

Query Match 100.0%; Score 51; DB 2; Length 130;

Best Local Similarity 100.0%; Pred. No. 0.086;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IIEEDTNKDK 10
 |||||
 DB 84 IIEEDTNKDK 93

RESULT 8

US-08-495-559-7

; Sequence 7, Application US/08495559A

; Patent No. 6054572

GENERAL INFORMATION:

APPLICANT: BURHAM, Martin Karl Russel

APPLICANT: CHOPRA, Ian

APPLICANT: CRITCHLEY, Ian Alfred

APPLICANT: KNOWLES, David Justin Charles

TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN: MONOCLONAL

TITLE OF INVENTION: ANTIBODY AND THEIR USE IN PREVENTING BACTERIAL ADHESION

FILE REFERENCE: P30591

CURRENT APPLICATION NUMBER: US/08/495,559A

CURRENT FILING DATE: 1995-08-03

EARLIER APPLICATION NUMBER: GB 9302289.5

EARLIER FILING DATE: 1993-02-05

EARLIER APPLICATION NUMBER: GB 9321592.9

EARLIER FILING DATE: 1993-10-20

NUMBER OF SEQ ID NOS: 13

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 7

LENGTH: 130

TYPE: PRT

ORGANISM: Staphylococcus aureus

US-08-495-559-7

Query Match 100.0%; Score 51; DB 3; Length 130;
 Best Local Similarity 100.0%; Pred. No. 0.086;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IIEEDTNKDK 10
 |||||
 DB 84 IIEEDTNKDK 93

RESULT 9

US-08-495-559-8

; Sequence 8, Application US/08495559A

; Patent No. 6054572

GENERAL INFORMATION:

APPLICANT: BURHAM, Martin Karl Russel

APPLICANT: CHOPRA, Ian

APPLICANT: CRITCHLEY, Ian Alfred

APPLICANT: KNOWLES, David Justin Charles

TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN: MONOCLONAL

TITLE OF INVENTION: ANTIBODY AND THEIR USE IN PREVENTING BACTERIAL ADHESION

FILE REFERENCE: P30591

CURRENT APPLICATION NUMBER: US/08/495,559A

CURRENT FILING DATE: 1995-08-03

EARLIER APPLICATION NUMBER: GB 9302289.5

EARLIER FILING DATE: 1993-02-05

EARLIER APPLICATION NUMBER: GB 9321592.9

EARLIER FILING DATE: 1993-10-20

NUMBER OF SEQ ID NOS: 13

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 8

LENGTH: 130

TYPE: PRT

ORGANISM: Staphylococcus aureus

US-08-495-559-8

Query Match 100.0%; Score 51; DB 3; Length 130;

Best Local Similarity 100.0%; Pred. No. 0.086;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IIEEDTNKDK 10
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 DB 84 IIEEDTNKDK 93

RESULT 10

US-08-856-253-8

; Sequence 8, Application US/08856253

; Patent No. 6288214

GENERAL INFORMATION:

APPLICANT: Hook, Magnus

APPLICANT: Patti, Joseph M.

APPLICANT: House-Pompeo, Karen

APPLICANT: Stahanam, Narayana

APPLICANT: Symeraky, Jindrich

TITLE OF INVENTION: COLLAGEN BINDING PROTEIN COMPOSITIONS

TITLE OF INVENTION: AND METHODS OF USE
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P. O. Box 4433
CITY: Houston
STATE: Texas
COUNTRY: U.S.
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/856,253
FILING DATE: Concurrently Herewith
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/017,678
FILING DATE: 16-MAY-1996
ATTORNEY/AGENT INFORMATION:
NAME: Kitchell, Barbara S.
REGISTRATION NUMBER: 33,928
REFERENCE/DOCKET NUMBER: TANK:193
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
TELEFAX: (512) 474-7577
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 139 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-08-856-253-8

Query Match 100.0%; Score 51; DB 3; Length 139;
Best Local Similarity 100.0%; Pred. No. 0.093;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IIEEDTNKDK 10
DB 98 IIEEDTNKDK 107

RESULT 11
US-08-459-135A-10
Sequence 10, Application US/08459135A
Patent No. 5955078
GENERAL INFORMATION:
APPLICANT: BURNHAM, Martin Karl Russel
APPLICANT: CHOPRA, Ian
APPLICANT: CRITCHLEY, Ian Alfred
APPLICANT: KNOWLES, David Justin Charles
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN: MONOCLONAL ANTIBODY AND THEIR US
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
STATE: PA
COUNTRY: U.S.A.
ZIP: 19406-0939
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: Fastseq, Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/459,135A
FILING DATE: 02-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/GB/94/00215
FILING DATE: 04-Feb-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Gimm1, Edward R
REGISTRATION NUMBER: 38,891
REFERENCE/DOCKET NUMBER: P30591C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-4478
TELEFAX: 610-270-5090
TELEX:
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 174 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: Protein
US-08-459-135A-10

Query Match 100.0%; Score 51; DB 2; Length 174;
Best Local Similarity 100.0%; Pred. No. 0.12;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IIEEDTNKDK 10
DB 84 IIEEDTNKDK 93

RESULT 12
US-08-459-135A-13
Sequence 13, Application US/08459135A
Patent No. 5955078
GENERAL INFORMATION:
APPLICANT: BURNHAM, Martin Karl Russel
APPLICANT: CHOPRA, Ian
APPLICANT: CRITCHLEY, Ian Alfred
APPLICANT: KNOWLES, David Justin Charles
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN: MONOCLONAL ANTIBODY AND THEIR US
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
STATE: PA
COUNTRY: U.S.A.
ZIP: 19406-0939
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: Fastseq, Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/459,135A
FILING DATE: 02-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB/94/00215
FILING DATE: 04-Feb-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Gimm1, Edward R
REGISTRATION NUMBER: 38,891
REFERENCE/DOCKET NUMBER: P30591C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-4478
TELEFAX: 610-270-5090
TELEX:
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 174 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear

MOLECULE TYPE: protein
US-08-495-135A-13

Query Match 100.0%; Score 51; DB 2; Length 174;
Best Local Similarity 100.0%; Pred. No. 0.12;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IIEEDTNKDK 10
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84 IIEEDTNKDK 93

RESULT 13

US-08-495-559-10
; Sequence 10, Application US/08495559A
; Patent No. 6054572
; GENERAL INFORMATION:
; APPLICANT: BURHAM, Martin Karl Russel
; APPLICANT: CHOPRA, Ian
; APPLICANT: CRITCHLEY, Ian Alfred
; APPLICANT: KNOWLES, David Justin Charles
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN: MONOCLONAL
; FILE REFERENCE: P30591
; CURRENT APPLICATION NUMBER: US/08/495,559A
; EARLIER FILING DATE: 1995-08-03
; EARLIER APPLICATION NUMBER: GB 9302289.5
; EARLIER FILING DATE: 1993-02-05
; EARLIER APPLICATION NUMBER: GB 9321592.9
; EARLIER FILING DATE: 1993-10-20
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 10
; LENGTH: 174
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-08-495-559-10

Query Match 100.0%; Score 51; DB 3; Length 174;
Best Local Similarity 100.0%; Pred. No. 0.12;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IIEEDTNKDK 10
|||
84 IIEEDTNKDK 93

RESULT 14

US-08-495-559-13
; Sequence 13, Application US/08495559A
; Patent No. 6054572
; GENERAL INFORMATION:
; APPLICANT: BURHAM, Martin Karl Russel
; APPLICANT: CHOPRA, Ian
; APPLICANT: CRITCHLEY, Ian Alfred
; APPLICANT: KNOWLES, David Justin Charles
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN: MONOCLONAL
; FILE REFERENCE: P30591
; CURRENT APPLICATION NUMBER: US/08/495,559A
; EARLIER FILING DATE: 1995-08-03
; EARLIER APPLICATION NUMBER: GB 9302289.5
; EARLIER FILING DATE: 1993-02-05
; EARLIER APPLICATION NUMBER: GB 9321592.9
; EARLIER FILING DATE: 1993-10-20
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 13
; LENGTH: 174
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-08-495-559-13

Query Match 100.0%; Score 51; DB 3; Length 174;
Best Local Similarity 100.0%; Pred. No. 0.12;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IIEEDTNKDK 10
|||
84 IIEEDTNKDK 93

RESULT 15

US-08-495-559-6
; Sequence 6, Application US/08495559A
; Patent No. 6054572
; GENERAL INFORMATION:
; APPLICANT: BURHAM, Martin Karl Russel
; APPLICANT: CHOPRA, Ian
; APPLICANT: CRITCHLEY, Ian Alfred
; APPLICANT: KNOWLES, David Justin Charles
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN: MONOCLONAL
; FILE REFERENCE: P30591
; CURRENT APPLICATION NUMBER: US/08/495,559A
; EARLIER FILING DATE: 1995-08-03
; EARLIER APPLICATION NUMBER: GB 9302289.5
; EARLIER FILING DATE: 1993-02-05
; EARLIER APPLICATION NUMBER: GB 9321592.9
; EARLIER FILING DATE: 1993-10-20
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 176
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-08-495-559-6

Query Match 100.0%; Score 51; DB 3; Length 176;
Best Local Similarity 100.0%; Pred. No. 0.12;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IIEEDTNKDK 10
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84 IIEEDTNKDK 93

Search completed: October 22, 2005, 09:35:44
Job time : 17.2989 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 22, 2005, 12:39:57 ; Search time 56.1494 Seconds
(without alignments)

74.354 Million cell updates/sec

Title: US-10-731-238-91

Perfect score: 51

Sequence: 1 IIEEDTNKDK 10

Scoring table: BLOSUM62

Searched: 1862951 seqs, 417491010 residues

Total number of hits satisfying chosen parameters: 1862951

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: Published Applications AA:*

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2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
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16: /cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pep:*
17: /cgn2_6/ptodata/2/pubpaa/US10E_PUBCOMB.pep:*
18: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
19: /cgn2_6/ptodata/2/pubpaa/US11A_PUBCOMB.pep:*
20: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep:*
21: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*
22: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	51	100.0	10	18	US-10-731-238-91
2	51	100.0	37	20	US-11-066-697-1134
3	51	100.0	139	9	US-09-813-820-8
4	51	100.0	388	8	US-08-901-062-1
5	51	100.0	559	8	US-08-781-986A-5251
6	51	100.0	559	15	US-10-329-624-5251
7	51	100.0	940	17	US-10-470-048B-424
8	51	100.0	948	17	US-10-470-048B-69
9	51	100.0	961	15	US-10-282-122A-43778
10	51	100.0	978	9	US-09-815-242-5456
11	51	100.0	1001	9	US-09-815-242-12686

Result No.	Score	Query Match	Length	DB ID	Description
12	51	100.0	1018	9	US-09-815-242-5797
13	51	100.0	1018	9	US-09-815-242-12838
14	51	100.0	1018	17	US-10-470-048B-68
15	51	100.0	1027	8	US-08-781-986A-5254
16	51	100.0	1027	15	US-10-329-624-5254
17	51	100.0	1038	15	US-10-282-122A-43827
18	43	84.3	928	10	US-10-731-238-92
19	41	80.4	928	9	US-09-801-368-282
20	41	80.4	928	15	US-10-369-493-1750
21	40	78.4	10	18	US-10-731-238-90
22	37	72.5	10	18	US-10-731-238-2
23	37	72.5	10	18	US-10-731-238-85
24	37	72.5	12	18	US-10-731-238-62
25	37	72.5	30	14	US-10-287-821-1
26	37	72.5	31	14	US-10-287-821-2
27	37	72.5	36	18	US-10-731-238-58
28	37	72.5	36	18	US-10-731-238-59
29	37	72.5	38	18	US-10-731-238-7
30	37	72.5	38	18	US-10-731-238-8
31	37	72.5	38	18	US-10-731-238-45
32	37	72.5	38	18	US-10-731-238-49
33	37	72.5	767	9	US-09-815-242-5899
34	37	72.5	767	9	US-09-815-242-13140
35	37	72.5	889	18	US-10-450-763-34639
36	36	70.6	214	15	US-10-108-2608-3351
37	36	70.6	281	9	US-09-775-879-18
38	36	70.6	281	9	US-09-775-879-21
39	36	70.6	281	16	US-10-736-318-18
40	36	70.6	281	16	US-10-736-318-21
41	36	70.6	379	18	US-10-450-763-45254
42	36	70.6	387	16	US-10-408-765A-2232
43	36	70.6	603	16	US-10-469-864-2
44	36	70.6	633	15	US-10-335-977-5854
45	36	70.6	685	16	US-10-437-963-187620

ALIGNMENTS

RESULT 1
US-10-731-238-91
Sequence 91, Application US/10731238
Publication No. US20050123552A1
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
Pattl, Joseph M.
House-Pompeo, Karen L.
Speziale, Pietro
John, Danny
McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSER: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/731, 238
FILING DATE: 10-Dec-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/010, 217
FILING DATE: 21-Jan-1998
APPLICATION NUMBER: US 60/036, 139

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; FILING DATE: 21-JAN-1997
; ATTORNEY/AGENT INFORMATION:
;   NAME: Hibler, David W.
;   REGISTRATION NUMBER: 41,071
;   REFERENCE/DOCKET NUMBER: TAMK:189
; TELECOMMUNICATION INFORMATION:
;   TELEPHONE: 512-418-3000
;   TELEFAX: 512-474-7577
; INFORMATION FOR SEQ ID NO: 91:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH: 10 amino acids
;     TYPE: amino acid
;     STRANDEDNESS: <Unknown>
;     TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 91:
US-10-731-238-91

Query Match      100.0%; Score 51; DB 18; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.058;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 IIEEDTNKDK 10
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Db      1 IIEEDTNKDK 10

RESULT 2
US-11-066-697-1134
; Sequence 1134, Application US/11066697
; Publication No. US20050187159A1
; GENERAL INFORMATION:
;   APPLICANT: Bridon, Dominique P.
;   APPLICANT: Ezrin, Alan M.
;   APPLICANT: Milner, Peter G.
;   APPLICANT: Holmes, Darren L.
;   APPLICANT: Thibaudau, Karen
; TITLE OF INVENTION: PROTECTION OF ENDOGENOUS THERAPEUTIC PEPTIDES FROM
; TITLE OF INVENTION: PEPTIDASE ACTIVITY THROUGH CONJUGATION TO BLOOD
; TITLE OF INVENTION: COMPONENTS
; FILE REFERENCE: 500862002301
; CURRENT APPLICATION NUMBER: US/11/066,697
; CURRENT FILING DATE: 2005-02-25
; PRIOR APPLICATION NUMBER: 09/657,276
; PRIOR FILING DATE: 2000-09-07
; PRIOR APPLICATION NUMBER: 60/153,406
; PRIOR FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: 60/159,783
; PRIOR FILING DATE: 1999-10-15
; NUMBER OF SEQ ID NOS: 1617
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1134
; LENGTH: 37
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptide
US-11-066-697-1134

Query Match      100.0%; Score 51; DB 20; Length 37;
Best Local Similarity 100.0%; Pred. No. 0.23;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 IIEEDTNKDK 10
        |||||
Db      7 IIEEDTNKDK 16

RESULT 3
US-09-813-820-8
; Sequence 8, Application US/09813820
; Patent No. US20020102262A1
; GENERAL INFORMATION:
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```

; APPLICANT: Hook, Magnus
;   Patti, Joseph M.
;   House-Pompeo, Karen
;   Stahanam, Narayana
;   Symekey, Jindrich
; TITLE OF INVENTION: COLLAGEN BINDING PROTEIN COMPOSITIONS
; AND METHODS OF USE
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: U.S.
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/813,820
; FILING DATE: 22-Mar-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/856,253
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
;   NAME: Kitchell, Barbara S.
;   REGISTRATION NUMBER: 33,928
;   REFERENCE/DOCKET NUMBER: TAMK:193
; TELECOMMUNICATION INFORMATION:
;   TELEPHONE: (512) 418-3000
;   TELEFAX: (512) 474-7577
; INFORMATION FOR SEQ ID NO: 8:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH: 139 amino acids
;     TYPE: amino acid
;     STRANDEDNESS: <Unknown>
;     TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-09-813-820-8

Query Match      100.0%; Score 51; DB 9; Length 139;
Best Local Similarity 100.0%; Pred. No. 0.9;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 IIEEDTNKDK 10
        |||||
Db      98 IIEEDTNKDK 107

RESULT 4
US-08-901-062-1
; Sequence 1, Application US/08901062
; Publication No. US20020025324A1
; GENERAL INFORMATION:
;   APPLICANT: SEALS, JONATHAN R.
; TITLE OF INVENTION: RECOMBINANT BIVALENT BACTERIAL VACCINE
; TITLE OF INVENTION: FOR THE PREVENTION OF MASTITIS
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HALE AND DORR LLP
; STREET: 60 State Street
; CITY: Boston
; STATE: MA
; COUNTRY: United States Of America
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/901.062
FILING DATE: 25-JUL-1997
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Baker, Hollie L.
REGISTRATION NUMBER: 31,321
REFERENCE/DOCKET NUMBER: 106941.153
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 526-6000
TELEFAX: (617) 526-5000
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 388 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-901-062-1

Query Match 100.0%; Score 51; DB 8; Length 388;
Best Local Similarity 100.0%; Pred. No. 2.6;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 IIEEDTNKDK 10
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Db 347 IIEEDTNKDK 356

RESULT 5
US-08-781-986A-5251
Sequence 5251, Application US/08781986A
Publication No. US20030054436A1
GENERAL INFORMATION:
APPLICANT: Charles Kunsch
TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
NUMBER OF SEQUENCES: 5255
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COUNTRY: USA
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/781,986A
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Benson, Bob
REGISTRATION NUMBER: 30,446
REFERENCE/DOCKET NUMBER: PB248PP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 5251:
SEQUENCE CHARACTERISTICS:
LENGTH: 559 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-781-986A-5251

Query Match 100.0%; Score 51; DB 8; Length 559;
Best Local Similarity 100.0%; Pred. No. 3.8;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 IIEEDTNKDK 10
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Db 383 IIEEDTNKDK 392

RESULT 6
US-10-329-624-5251
Sequence 5251, Application US/10329624
Publication No. US20040043037A1
GENERAL INFORMATION:
APPLICANT: Charles Kunsch
Gil H. Choi
Patrick S. Dillon
Craig A. Rosen
Steven C. Barash
Michael R. Rannon
TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
NUMBER OF SEQUENCES: 5256
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COUNTRY: USA
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/329,624
FILING DATE: 27-Dec-2002
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/956,171
FILING DATE: October 20, 1997
APPLICATION NUMBER: 60/009,861
FILING DATE: January 5, 1996
APPLICATION NUMBER: 08/781,986
FILING DATE: January 3, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Mark J. Hyman
REGISTRATION NUMBER: 46,789
REFERENCE/DOCKET NUMBER: PB248P1D1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (240) 314-1224
TELEFAX: (301) 309-8439
INFORMATION FOR SEQ ID NO: 5251:
SEQUENCE CHARACTERISTICS:
LENGTH: 559 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 5251:
US-10-329-624-5251

Query Match 100.0%; Score 51; DB 15; Length 559;
Best Local Similarity 100.0%; Pred. No. 3.8;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 IIEEDTNKDK 10
|||
Db 383 IIEEDTNKDK 392

RESULT 7
US-10-470-048B-424


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; Sequence 424, Application US/10470048B
; Publication No. US20050037444A1
; GENERAL INFORMATION:
; APPLICANT: MEINKE ET AL.
; TITLE OF INVENTION: A METHOD FOR IDENTIFICATION, ISOLATION AND PRODUCTION OF
; FILE REFERENCE: SONN:03505
; CURRENT APPLICATION NUMBER: US/10/470,048B
; CURRENT FILING DATE: 2003-07-25
; NUMBER OF SEQ ID NOS: 603
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 424
; LENGTH: 940
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-10-470-048B-424

Query Match      100.0%; Score 51; DB 17; Length 940;
Best Local Similarity 100.0%; Pred. No. 6.5;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 IIEEDTNKDK 10
Db      764 IIEEDTNKDK 773

RESULT 8
US-10-470-048B-69
; Sequence 69, Application US/10470048B
; Publication No. US20050037444A1
; GENERAL INFORMATION:
; APPLICANT: MEINKE ET AL.
; TITLE OF INVENTION: A METHOD FOR IDENTIFICATION, ISOLATION AND PRODUCTION OF
; FILE REFERENCE: SONN:03505
; CURRENT APPLICATION NUMBER: US/10/470,048B
; CURRENT FILING DATE: 2003-07-25
; NUMBER OF SEQ ID NOS: 603
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 69
; LENGTH: 948
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-10-470-048B-69

Query Match      100.0%; Score 51; DB 17; Length 948;
Best Local Similarity 100.0%; Pred. No. 6.6;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 IIEEDTNKDK 10
Db      772 IIEEDTNKDK 781

RESULT 9
US-10-282-122A-43778
; Sequence 43778, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Karl
; APPLICANT: Zyekind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
```

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; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2001-02-16
; PRIOR APPLICATION NUMBER: 60/269,308
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 43778
; LENGTH: 961
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-10-282-122A-43778

Query Match      100.0%; Score 51; DB 15; Length 961;
Best Local Similarity 100.0%; Pred. No. 6.7;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 IIEEDTNKDK 10
Db      775 IIEEDTNKDK 784

RESULT 10
US-09-815-242-5456
; Sequence 5456, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Karl L.
; APPLICANT: Zyekind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; FILE REFERENCE: ELITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
```

```
SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5456
; LENGTH: 978
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-09-815-242-5456
```

```
Query Match      100.0%; Score 51; DB 9; Length 978;
Best Local Similarity 100.0%; Pred. No. 6.8;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 11EEDTNKDX 10
        |||||
        806 11EEDTNKDX 815
```

```
RESULT 11
US-09-815-242-12686
; Sequence 12686, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; FILE REFERENCE: ELITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12686
; LENGTH: 1001
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-09-815-242-12686
```

```
Query Match      100.0%; Score 51; DB 9; Length 1001;
Best Local Similarity 100.0%; Pred. No. 7;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 11EEDTNKDX 10
        |||||
        829 11EEDTNKDX 838
```

```
RESULT 12
US-09-815-242-5797
; Sequence 5797, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari L.
; APPLICANT: Zyskind, Judith W.
```

```
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John D.
APPLICANT: Carr, Grant J.
APPLICANT: Yamamoto, Robert T.
APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; FILE REFERENCE: ELITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5797
; LENGTH: 1018
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-09-815-242-5797
```

```
Query Match      100.0%; Score 51; DB 9; Length 1018;
Best Local Similarity 100.0%; Pred. No. 7.1;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 11EEDTNKDX 10
        |||||
        828 11EEDTNKDX 837
```

```
RESULT 13
US-09-815-242-12838
; Sequence 12838, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; FILE REFERENCE: ELITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
```

```

; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12838
; LENGTH: 1018
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-09-815-242-12838

```

```

Query Match          100.0%; Score 51; DB 9; Length 1018;
Best Local Similarity 100.0%; Pred. No. 7.1;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      1 IIEEDTNKDK 10
        |||||
Db       828 IIEEDTNKDK 837

```

```

RESULT 14
US-10-470-048B-68
; Sequence 68, Application US/10470048B
; Publication No. US20050037444A1
; GENERAL INFORMATION:
; APPLICANT: MEINKE ET AL.
; TITLE OF INVENTION: A METHOD FOR IDENTIFICATION, ISOLATION AND PRODUCTION OF
; FILE REFERENCE: SONN:035US
; CURRENT APPLICATION NUMBER: US/10/470,048B
; CURRENT FILING DATE: 2003-07-25
; NUMBER OF SEQ ID NOS: 603
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 68
; LENGTH: 1018
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-10-470-048B-68

```

```

Query Match          100.0%; Score 51; DB 17; Length 1018;
Best Local Similarity 100.0%; Pred. No. 7.1;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      1 IIEEDTNKDK 10
        |||||
Db       828 IIEEDTNKDK 837

```

```

RESULT 15
US-08-781-986A-5254
; Sequence 5254, Application US/08781986A
; Publication No. US20030054436A1
; GENERAL INFORMATION:
; APPLICANT: Charles Kunsch
; TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
; NUMBER OF SEQUENCES: 5255
; CORRESPONDENCE ADDRESSES:
; ADDRESSSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4mb storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/781,986A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:

```

```

; NAME: Benson, Bob
; REGISTRATION NUMBER: 30,446
; REFERENCE/DOCKET NUMBER: PB248PP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 5254:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1027 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-781-986A-5254

```

```

Query Match          100.0%; Score 51; DB 8; Length 1027;
Best Local Similarity 100.0%; Pred. No. 7.1;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      1 IIEEDTNKDK 10
        |||||
Db       837 IIEEDTNKDK 846

```

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Search completed: October 22, 2005, 12:56:26
Job time : 56.1494 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 22, 2005, 08:04:46 ; Search time 11.6092 Seconds
(without alignments)
82.880 Million cell updates/sec

Title: US-10-731-238-91
Perfect score: 51
Sequence: 1 IIEEDTNKDK 10

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	51	100.0	940	2	S19702
2	51	100.0	961	2	G90053
3	51	100.0	1018	2	A32192
4	51	100.0	1038	2	H90053
5	41	80.4	928	2	S50578
6	40	78.4	237	2	A12062
7	38	74.5	375	1	A49107
8	38	74.5	963	2	T09911
9	36	70.6	121	2	H70471
10	36	70.6	274	2	T12184
11	36	70.6	281	2	S71251
12	36	70.6	748	2	D64585
13	36	70.6	748	2	F71927
14	36	70.6	872	2	S49538
15	36	70.6	1820	1	CHBE
16	35	68.6	806	2	T41930
17	35	68.6	932	2	S62555
18	34	66.7	131	2	F89838
19	34	66.7	224	2	F96668
20	34	66.7	227	2	D97091
21	34	66.7	290	2	F70362
22	34	66.7	376	2	A56480
23	34	66.7	466	2	AH2453
24	34	66.7	470	2	T41409
25	34	66.7	476	1	KCHUS2
26	34	66.7	529	2	T08684
27	34	66.7	530	2	A84847
28	34	66.7	549	2	A56461
29	34	66.7	555	2	A56560

30	34	66.7	678	2	A71287	probable cytoplasm
31	34	66.7	682	2	G84539	hypothetical prote
32	34	66.7	894	2	G82260	leucyl-tRNA synthe
33	34	66.7	902	2	T01127	curly leaf protein
34	34	66.7	1094	2	S49313	protein kinase - B
35	34	66.7	1097	2	A29943	Toll protein precu
36	34	66.7	1244	2	T19068	hypothetical prote
37	33	64.7	105	2	C69848	hypothetical prote
38	33	64.7	117	2	T18123	hypothetical prote
39	33	64.7	150	1	M6WL11	66 protein - human
40	33	64.7	173	2	B86396	T2P1.11 protein -
41	33	64.7	182	2	S46667	meiosis-specific p
42	33	64.7	193	2	H97224	protease subunit
43	33	64.7	196	2	PD0004	self-incompatibili
44	33	64.7	201	2	A89804	hypothetical prote
45	33	64.7	214	2	H87093	ATP-dependent Clp

ALIGNMENTS

RESULT 1

S19702
fibronectin-binding protein B - Staphylococcus aureus
C/Species: Staphylococcus aureus
C/Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
C/Accession: S19702
R/Jensenon, K.; Signaes, C.; Mueller, H.P.; Lindberg, M.
Eur. J. Biochem. 202, 1041-1048, 1991
A/Title: Two different genes encode fibronectin binding proteins in Staphylococcus aure
A/Reference number: S19702; MUID:92111475; PMID:1837266
A/Accession: S19702
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-940 <JOB>
A/Cross-references: UNIPROT:Q53682; EMBL:X62992; NID:949040; PIDN:CA44726.1; PID g5815
C/Keywords: fibronectin binding

Query Match 100.0%; Score 51; DB 2; Length 940;
Best Local Similarity 100.0%; Pred. No. 0.34;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 IIEEDTNKDK 10
Db 764 IIEEDTNKDK 773

RESULT 2

G90053
hypothetical protein fnbB [imported] - Staphylococcus aureus (strain N315)
C/Species: Staphylococcus aureus
C/Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
R/Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Ima, A.; Mizutani-Oi, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayaishi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
A/Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.
A/Reference number: AB9758; MUID:21311952; PMID:11418146
A/Accession: G90053
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-961 <KUR>
A/Cross-references: UNIPROT:Q99RD3; GB:BA000018; PID:g13702452; PIDN:BA43593.1; C
A/Experimental source: strain N315
C/Genetics:
A/Genes: fnbB

Query Match 100.0%; Score 51; DB 2; Length 961;
Best Local Similarity 100.0%; Pred. No. 0.34;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 IIEEDTNKDK 10

Db 775 IIEEDTNKDK 784

RESULT 3

A32192
fibronectin-binding protein - Staphylococcus aureus
C:Species: Staphylococcus aureus
C>Date: 31-Jul-1989 #sequence_revision 31-Jul-1989 #text_change 16-Feb-1997
C/Accession: A32192
R:Signes, C.; Rancici, G.; Joensen, K.; Lindgren, P.E.; Anantharamaiah, G.M.; Hoeoek, M.
Proc. Natl. Acad. Sci. U.S.A. 86, 699-703, 1989
A>Title: Nucleotide sequence of the gene for a fibronectin-binding protein from Staphylococcus aureus
A/Reference number: A32192; MUID:89098998; PMID:2521391
A/Accession: A32192
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-1018 <SIG>
A/Cross-references: GB:J04151
C:Keywords: fibronectin binding

Query Match 100.0%; Score 51; DB 2; Length 1018;
Best Local Similarity 100.0%; Pred. No. 0.36; Mismatches 0; Indels 0; Gaps 0;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 IIEEDTNKDK 10
Db 828 IIEEDTNKDK 837

RESULT 4

H90053
hypothetical protein fnb [imported] - Staphylococcus aureus (strain N315)
C:Species: Staphylococcus aureus
C>Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C/Accession: H90053
R:Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Ogura, A.; Mizutani, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.; C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
A>Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.
A/Reference number: A89758; MUID:21311952; PMID:11418146
A/Accession: H90053
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-1038 <KUR>
A/Cross-references: UNIPROT:Q99RD2; GB:BA000018; PID:g13702453; PIDN:BA843594.1; GSPDB:A; Experimental source: strain N315
C:Genetics:
A:Gene: fnb

Query Match 100.0%; Score 51; DB 2; Length 1038;
Best Local Similarity 100.0%; Pred. No. 0.37; Mismatches 0; Indels 0; Gaps 0;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 IIEEDTNKDK 10
Db 824 IIEEDTNKDK 833

RESULT 5

S50578
hypothetical protein YER075C - Yeast (Saccharomyces cerevisiae)
C:Species: Saccharomyces cerevisiae
C>Date: 28-May-1993 #sequence_revision 24-Feb-1995 #text_change 09-Jul-2004
C/Accession: S50578
R:Dirich, F.S.
Submitted to the EMBL Data Library, December 1994
A/Description: The sequence of S. cerevisiae lambda clone 3612 and cosmid 9747.
A/Reference number: S50438
A/Accession: S50578
A/Molecule type: DNA
A/Residues: 1-928 <DIE>

A/Cross-references: UNIPROT:P40048; EMBL:U18814; NID:g603309; PIDN:AAB64614.1; PIR: A; Genetics:
A:Gene: SGD:PRP3
A/Cross-references: SGD:S0000877; MIPS:YER075C

A/Map position: 5R
C:Keywords: phosphoprotein
F:527-867/Domain: protein-tyrosine-phosphatase homology <PRP>
F:804/Active site: Cys (phosphocysteine intermediate) #status predicted
F:810/Binding site: substrate phosphate (Arg) #status predicted

Query Match 80.4%; Score 41; DB 2; Length 928;
Best Local Similarity 77.8%; Pred. No. 21; Mismatches 0; Indels 0; Gaps 0;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 2 IIEEDTNKDK 10
Db 381 IIEEDTNKDK 389

RESULT 6

A12062
hypothetical protein alr2055 [imported] - Nostoc sp. (strain PCC 7120)
C:Species: Nostoc sp. PCC 7120
A/Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C/Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004
C/Accession: A12062
R:Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kunitz, T.; Sasamoto, S.; Watanabe, A.; Iriyuchi, Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, DNA Res. 8, 205-213, 2001
A>Title: Complete genomic sequence of the filamentous nitrogen-fixing Cyanobacterium Anabaena PCC 7120
A/Reference number: AB1807; MUID:21595285; PMID:11759840
A/Accession: A12062
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-237 <KUR>
A/Cross-references: UNIPROT:Q8YVC3; GB:BA000019; PIDN:BA873754.1; PID:g17131146; GSPDB:A; Experimental source: strain PCC 7120
C:Genetics:
A:Gene: alr2055

Query Match 78.4%; Score 40; DB 2; Length 237;
Best Local Similarity 77.8%; Pred. No. 7.7; Mismatches 0; Indels 0; Gaps 0;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 1 IIEEDTNKDK 9
Db 136 IIEEDTNKDK 144

RESULT 7

B49107
alcohol dehydrogenase (EC 1.1.1.1) 2 - deer mouse
N/Alternate names: alcohol dehydrogenase 2; aldehyde reductase
C:Species: Peromyscus maniculatus (deer mouse)
C/Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004
C/Accession: B49107
R:Zheng, Y.W.; Bey, M.; Liu, H.; Felder, M.R.
J. Biol. Chem. 268, 24933-24939, 1993
A>Title: Molecular basis of the alcohol dehydrogenase-negative deer mouse. Evidence for
A/Reference number: A49107; MUID:94043358; PMID:8227055
A/Accession: B49107
A/Molecule type: mRNA
A/Residues: 1-375 <ZHE>
A/Cross-references: UNIPROT:P41681; GB:L15704; NID:g416389; PIDN:AAA40592.1; PID:g416391
C/Comment: Although most similar to the class VI human enzyme, this protein may represent
C/Function:
A/Description: catalyzes the oxidation of primary and secondary alcohols to aldehydes and
C/Superfamily: alcohol dehydrogenase; long-chain alcohol dehydrogenase homology
C:Keywords: alcohol metabolism; metalloprotein; NAD; oxidoreductase; zinc
F:2-366/Product: alcohol dehydrogenase VI #status predicted <MNT>
F:32-366/Domain: long-chain alcohol dehydrogenase homology <LADH>
F:195-324/Region: beta-alpha-beta NAD nucleotide-binding fold
F:47,69,175/Binding site: zinc, catalytic (Cys, His, Cys) #status predicted

F:99,102,105,113/Binding site: zinc, noncatalytic (Cys) #status predicted

Query Match 74.5%; Score 38; DB 1; Length 375;
Best Local Similarity 80.0%; Pred. No. 29;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 IIEEDTNKDK 10
|||
Db 220 IIAVDTRNKK 229

RESULT 8

T09911

probable serine/threonine-specific protein kinase (EC 2.7.1.-) T22A6.310 - Arabidopsis thaliana (mouse-ear cress)

C:Species: Arabidopsis thaliana (mouse-ear cress)

C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004

C:Accession: T09911

R:Bevan, M.; Zimmermann, W.; Gruenisen, A.; Wambutt, R.; Bancroft, I.; Mewes, H.W.; May submitted to the Protein Sequence Database, June 1999

A:Reference number: Z16896

A:Accession: T09911

A:Molecule type: DNA

A:Residues: 1-963 <BBV>

A:Cross-references: UNIPROT:Q9STU7; EMBL:AL078637; GSPDB:GN00062; ATSP:T22A6.310

A:Experimental source: cultivar Columbia; BAC clone T22A6

C:Genetics:

A:Gene: ATSP:T22A6.310

A:Map position: 4

A:Introns: 286/3; 386/2; 434/3; 473/2; 543/1; 678/1; 691/3; 719/3; 753/2; 788/3; 821/3;

C:Keywords: phosphotransferase; protein kinase

Query Match 74.5%; Score 38; DB 2; Length 963;
Best Local Similarity 70.0%; Pred. No. 77;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 IIEEDTNKDK 10
|||
Db 629 IVEADTRKDK 638

RESULT 9

H70471

conserved hypothetical protein aq_2000 - Aquifex aeolicus

C:Species: Aquifex aeolicus

C:Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 09-Jul-2004

C:Accession: H70471

R:Decker, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.; O'V.

Nature 392, 353-358, 1998

A:Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.

A:Reference number: A70300; MUID:98196666; PMID:9537320

A:Accession: H70471

A:Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-121 <AQP>

A:Cross-references: UNIPROT:O67804; GB:AE000767; NID:92984235; PIDN:AAC0774.1; PID:9298

A:Experimental source: strain VFS

C:Genetics:

A:Gene: aq_2000

Query Match 70.6%; Score 36; DB 2; Length 121;
Best Local Similarity 87.5%; Pred. No. 20;

Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 IIEEDTNK 8
|||
Db 85 IIEKDTNK 92

RESULT 10

T21284

hypothetical protein F23A7.3 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004

C:Accession: T21284

R:McMurray, A. submitted to the EMBL Data Library, October 1996

A:Reference number: Z19401

A:Accession: T21284

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-274 <WIL>

A:Cross-references: UNIPROT:Q93556; EMBL:Z81067; PIDN:CAB02977.1; GSPDB:GN00028; CESP:F

A:Experimental source: clone F23A7

C:Genetics:

A:Gene: CESP:F23A7.3

A:Map position: X

A:Introns: 51/3; 97/3; 114/3

Query Match 70.6%; Score 36; DB 2; Length 274;
Best Local Similarity 75.0%; Pred. No. 48;

Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 2 IIEEDTNKDK 9
|||
Db 138 IIEEDTNKDK 145

RESULT 11

S71251

C-5 sterol desaturase (EC 1.-.-.-) - Arabidopsis thaliana

N:Alternate names: delta7-sterol-C5-desaturase; sterol-C5-desaturase

C:Species: Arabidopsis thaliana (mouse-ear cress)

C:Date: 28-Oct-1996 #sequence_revision 27-Feb-1997 #text_change 09-Jul-2004

C:Accession: S71251

R:Gachotte, D.; Husselsstein, T.; Bard, M.; Benveniste, P.

submitted to the EMBL Data Library, July 1995

A:Description: Cloning a plant sterol-C5-desaturase by functional complementation of a

A:Reference number: S71251

A:Accession: S71251

A:Molecule type: mRNA

A:Residues: 1-281 <GAC>

A:Cross-references: UNIPROT:Q39208; EMBL:X90454; NID:g1061037; PID:g1061038

C:Superfamily: Saccharomyces cerevisiae ERG25 protein

C:Keywords: oxidoreductase

Query Match 70.6%; Score 36; DB 2; Length 281;
Best Local Similarity 66.7%; Pred. No. 49;

Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 IIEEDTNKDK 9
|||
Db 267 IIEEDTNKDK 275

RESULT 12

cg pathogenicity island protein cags - Helicobacter pylori (strain 26995)

C:Species: Helicobacter pylori

C:Date: 09-Aug-1997 #sequence_revision 09-Aug-1997 #text_change 09-Jul-2004

C:Accession: D64585

R:Tomb, J.F.; White, O.; Kierlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.I.

Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khatalik, H.G.; Glodek, A.; McKen-

son, J.D.; Kelley, J.M.; Cotton, M.D.; Meldman, J.M.; Fujii, C.; Bowman, C.; Watthey, I.

son, J.D.; Kelley, J.M.; Cotton, M.D.; Meldman, J.M.; Fujii, C.; Bowman, C.; Watthey, I.

A:Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Frazer,

A:Title: The complete genome sequence of the gastric pathogen Helicobacter pylori.

A:Reference number: A64520; MUID:97394467; PMID:9252185

A:Accession: D64585

A:Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-748 <TON>

A:Cross-references: UNIPROT:O25260; GB:AE000566; GB:AE000511; NID:g2313628; PIDN:AAD07E

Query Match 70.6%; Score 36; DB 2; Length 748;
Best Local Similarity 60.0%; Pred. No. 14e+02;

Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 IIEEDTNKDK 10
:|||||:
Db 412 LIEDDTNMEK 421

RESULT 13
F71927
cag island protein, DNA transfer protein - Helicobacter pylori (strain J99)

C/Species: Helicobacter pylori
A/Variety: strain J99
C/Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 09-Jul-2004
C/Accession: F71927
R/Alt: R.A.; Ling, L.S.L.; Moir, D.T.; King, B.L.; Brown, E.D.; Doly, P.C.; Smith, D.R.;
Fred, C.; Gibson, R.; Werberg, D.; Mills, S.D.; Jiang, Q.; Taylor, D.E.; Vovis, G.F.;
Nature 397, 176-180, 1999
A/Title: Genomic sequence comparison of two unrelated isolates of the human gastric path
A/Reference number: A71800; MUID:99120557; PMID:9923682
A/Accession: F71927
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-748 <ANN>
A/Cross-references: UNIPROT:Q9ZLV3; GB:AE001481; GB:AE001439; NID:94155005; PIDN:AD0605
A/Experimental source: strain J99
C/Genetic:
A/Gene: vlrD4

Query Match 70.6%; Score 36; DB 2; Length 748;
Best Local Similarity 60.0%; Pred. No. 1.4e+02;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 IIEEDTNKDK 10
:|||||:
Db 412 LIEDDTNMEK 421

RESULT 14
S49538
Cooc protein precursor - Escherichia coli
C/Species: Escherichia coli
C/Date: 15-Feb-1996 #sequence_revision 01-Mar-1996 #text_change 09-Jul-2004
C/Accession: S49538
R/Froehlich, B.J.; Karakashian, A.; Melsen, L.R.; Wakefield, J.C.; Scott, J.R.
Mol. Microbiol. 12, 387-401, 1994
A/Title: Cooc and Cooc are required for assembly of CSI pili.
A/Reference number: S49538; MUID:94344028; PMID:7915003
A/Accession: S49538
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-872 <PRO>
A/Cross-references: UNIPROT:Q47114; EMBL:X76908; NID:9488735; PIDN:CAA54229.1; PID:94887

Query Match 70.6%; Score 36; DB 2; Length 872;
Best Local Similarity 77.8%; Pred. No. 1.6e+02;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 IIEEDTNKDK 10
:|||||:
Db 731 IIEEDTNKSK 739

RESULT 15
CHEE
sodium channel protein - electric eel
C/Species: Electrophorus electricus (electric eel)
C/Date: 28-May-1986 #sequence_revision 28-May-1986 #text_change 09-Jul-2004
C/Accession: A03178; I50536
R/Noda, M.; Shimizu, S.; Tanabe, T.; Takai, T.; Kayano, T.; Ikeda, T.; Takahashi, H.; Na
da, H.; Miyata, T.; Numa, S.
Nature 312, 121-127, 1984
A/Title: Primary structure of Electrophorus electricus sodium channel deduced from cDNA
A/Reference number: A03178; MUID:85061498; PMID:6209577

A/Accession: A03178
A/Molecule type: mRNA
A/Residues: 1-1820 <NOD>
A/Cross-references: UNIPROT:P02719; GB:X01119; NID:962776; PIDN:CAA55587.1; PID:962777
R/Noda, M.; Numa, S.
J. Recept. Res. 7, 467-497, 1987
A/Title: Structure and function of sodium channel.
A/Reference number: I50536; MUID:87311395; PMID:2442385
A/Accession: I50536
A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: mRNA
A/Residues: 1-1820 <NO2>
A/Cross-references: GB:M22252; NID:91041048; PIDN:AAA79960.1; PID:91041049
A/Comment: This membrane glycoprotein mediates the voltage-dependent sodium-ion permeab
as the membrane, the protein forms a sodium-selective channel through which sodium ions
C/Comment: This sequence contains four highly homologous internal repeats (excluding re
Each repeat has a similar overall structure containing six subregions located in ident
has a net positive charge (S4), and one is neutral (S2).
C/Comment: The four repeating units are thought to be oriented pseudosymmetrically acro
e. The presence of four homologous structures within this molecule is consistent with t
C/Comment: Available data suggest that activation and inactivation gates are located ne
955 might, in conjunction with the positively charged residues of S4, act as a voltage
C/Superfamily: sodium channel protein

C/Keywords: duplication; glycoprotein; ion transport; membrane protein; sodium channel;
F/111-419,555-807,989-1281,1311-1587/Region: duplication internal repeats I, II, III an
F/111-141,555-585,989-1019,1311-1341/Region: S1 of repeats I through IV
F/150-171,597-620,1033-1057,1353-1376/Region: S2 of repeats I through IV
F/177-197,626-643,1062-1079,1381-1398/Region: S3 of repeats I through IV
F/204-224,651-671,1092-1112,1417-1437/Region: S4 of repeats I through IV
F/244-264,691-711,1132-1152,1454-1474/Region: S5 of repeats I through IV
F/379-402,767-790,1236-1264,1544-1567/Region: S6 of repeats I through IV
F/205,278,288,317,591,690,797,1160,1174,1806/Binding site: carbohydrate (Asn) (covalent

Query Match 70.6%; Score 36; DB 1; Length 1820;
Best Local Similarity 87.5%; Pred. No. 3.4e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 EEDTNKDK 10
:|||||:
Db 908 EEDTNKDK 915

Search completed: October 22, 2005, 09:55:42
Job time : 12.6092 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 22, 2005, 08:01:06 ; Search time 56.2069 Seconds
(without alignments)
91.106 Million cell updates/sec

Title: US-10-731-238-91
Perfect score: 51
Sequence: 1 IIEEDTNKDK 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_03:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	51	100.0	152 2 Q9AEP9	Q9AEP9 staphylococ
2	51	100.0	940 2 Q53682	Q53682 staphylococ
3	51	100.0	943 2 Q8NUU8	Q8NUU8 staphylococ
4	51	100.0	957 2 Q6G6H4	Q6G6H4 staphylococ
5	51	100.0	961 2 Q99RD3	Q99RD3 staphylococ
6	51	100.0	961 2 Q7A3J8	Q7A3J8 staphylococ
7	51	100.0	965 2 Q6GDU5	Q6GDU5 staphylococ
8	51	100.0	1015 2 Q8NUU7	Q8NUU7 staphylococ
9	51	100.0	1015 2 Q6G6H3	Q6G6H3 staphylococ
10	51	100.0	1018 1 FNBA STRAU	FNBA STRAU
11	51	100.0	1038 2 Q99RD2	Q99RD2 staphylococ
12	51	100.0	1038 2 Q7A3J7	Q7A3J7 staphylococ
13	41	80.4	928 1 PTP3 YEAST	PTP3 YEAST
14	40	78.4	89 2 Q7RSR0	Q7RSR0 giardia lam
15	40	78.4	237 2 Q8YVC3	Q8YVC3 anabaena sp
16	39	76.5	245 2 Q73R01	Q73R01 treponema d
17	38	74.5	190 2 Q88SH0	Q88SH0 lactobacill
18	38	74.5	268 2 Q8LFT2	Q8LFT2 aradidopsis
19	38	74.5	375 1 ADH2 PERMA	ADH2 PERMA
20	38	74.5	435 2 Q8XLU3	Q8XLU3 peromyces
21	38	74.5	606 2 Q9FIW8	Q9FIW8 aradidopsis
22	38	74.5	963 2 Q9STU7	Q9STU7 aradidopsis
23	38	74.5	1026 2 Q6V495	Q6V495 drosophila
24	37	72.5	136 2 Q8EP70	Q8EP70 xanthomonas
25	37	72.5	263 2 Q6BHD9	Q6BHD9 debaryomyces
26	37	72.5	613 2 Q6UDM5	Q6UDM5 brachydanio
27	37	72.5	897 2 Q8ID14	Q8ID14 plasmodium
28	37	72.5	1225 2 Q8ILF3	Q8ILF3 plasmodium
29	37	72.5	2367 2 Q7R607	Q7R607 giardia lam
30	36	70.6	98 2 Q91PH6	Q91PH6 chilo iride
31	36	70.6	121 2 Q67804	Q67804 aquilex aeo

32	36	70.6	140 2 Q8TOM9	Q8TOM9 methanosarc
33	36	70.6	144 2 Q8ERK2	Q8ERK2 oceanobacil
34	36	70.6	170 1 Y79B_METUA	P81233 mechanococ
35	36	70.6	195 2 Q7UK66	Q7UK66 rhodospirill
36	36	70.6	214 2 Q8N929	Q8N929 homo sapien
37	36	70.6	253 2 Q6FP89	Q6FP89 candida gla
38	36	70.6	274 2 Q93556	Q93556 caenorhabdi
39	36	70.6	281 1 SC51_ARATH	Q39208 aradidopsis
40	36	70.6	282 1 Q6YU76	Q6YU76 oryza sativ
41	36	70.6	403 2 Q75138	Q75138 homo sapien
42	36	70.6	413 2 Q96AJ1	Q96AJ1 homo sapien
43	36	70.6	413 2 Q65Z43	Q65Z43 homo sapien
44	36	70.6	464 2 Q8EO50	Q8EO50 oceanobacil
45	36	70.6	543 1 PCK_KLULA	Q43112 kluyveromyces

ALIGNMENTS

```

RESULT 1
Q9AEP9 PRELIMINARY; PRT; 152 AA.
ID Q9AEP9
AC Q9AEP9;
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Fibronectin-binding protein (Fragment).
GN Name=fnb;
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxId=1280;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=CMRSA-1;
RX MEDLINE=21246681; PubMed=11349044;
RX DOI=10.1128/IAI.69.6.3791-3799.2001;
RA Rice K., Huesca M., Vaz D., McGavin M.J.;
RT "Variance in fibronectin binding and fnb locus polymorphisms in
RT Staphylococcus aureus: identification of antigenic variation in a
RT fibronectin binding protein adhesin of the epidemic CMRSA-1 strain of
RT methicillin-resistant S. aureus.";
RL Infect Immun. 69:3791-3799 (2001).
DR EMBL, AY029184; AAK31588.1; -.
FT NON_TER
FT NON_TER 152
SQ SEQUENCE 152 AA; 17193 MW; CFA3913C2B11C025 CRC64;

Query Match 100.0%; Score 51; DB 2; Length 152;
Best Local Similarity 100.0%; Pred. No. 0.47; Mismatches 0; Indels 0; Gaps 0;
Matches 10; Conservative

Qy 1 IIEEDTNKDK 10
Db 121 IIEEDTNKDK 130

RESULT 2
Q53682 PRELIMINARY; PRT; 940 AA.
ID Q53682;
AC Q53682;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Fibronectin binding protein B.
GN Name=fnb;
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxId=1280;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=8325-4;
RX MEDLINE=92111475; PubMed=1837266;
RX Jonsson K., Signas C., Muller H.P., Lindberg M.;

```


RT "Two different genes encode fibronectin binding proteins in
 RT Staphylococcus aureus. The complete nucleotide sequence and
 RT characterization of the second gene.";
 RL Bur. J. Biochem. 202:1041-1048 (1991).
 CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
 CC an amide bond (By similarity).
 DR EMBL: X62992; CAA44726.1; -.
 DR PIR: S19702; S19702.
 DR HSSP: O53653; IN67.
 DR GO: GO:0009986; C:cell surface; IEA.
 DR GO: GO:0005618; C:cell wall; IEA.
 DR GO: GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
 DR GO: GO:0016020; C:membrane; IEA.
 DR GO: GO:0007155; P:cell adhesion; IEA.
 DR InterPro: IPR008966; Adhes_bact.
 DR InterPro: IPR004237; Fn_bind.
 DR InterPro: IPR005877; Gpos_Ysirk.
 DR InterPro: IPR01899; Gram_pos_anchor.
 DR Pfam: PF02986; Fn_bind; 2.
 DR Pfam: PF04650; Ysirk_signal; 1.
 DR TIGRFAMs: TIGR01167; LpXtg_anchor; 1.
 DR TIGRFAMs: TIGR01168; Ysirk_signal; 1.
 DR PROSITE: PS50847; GRAM_POS_ANCHORING; 1.
 DR Cell wall; Peptidoglycan-anchor.
 SQ SEQUENCE 940 AA; 10355 MW; E35FBBCA907AE345 CRC64;

Query Match 100.0%; Score 51; DB 2; Length 940;
 Best Local Similarity 100.0%; Pred. No. 3;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 IIEEDTNKDK 10
 |||||
 Db 764 IIEEDTNKDK 773

RESULT 3
 Q8N8UB PRELIMINARY; PRT; 943 AA.
 ID Q8N8UB
 AC Q8N8UB
 DT 01-OCT-2002 (TREMBlrel. 22, Created)
 DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
 DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
 DE FnbB protein.
 GN Name=fnbB; OrderedLocuNames=MM2420;
 OS Staphylococcus aureus (strain MM2).
 CC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 CX NCBI_TaxID=196620;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=MM2;
 RX MEDLINE=22040717; PubMed=12044378; DOI=10.1016/S0140-6736(02)08713-5;
 RA Baba T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Oguchi A.,
 RA Nagai Y., Iwama N., Asano K., Naito T., Kuroda H., Cui L.,
 RA Yamamoto K., Hiramatsu K.;
 RT "Genome and virulence determinants of high virulence community-
 RT acquired MRSA.";
 RL Lancet 359:1819-1827 (2002).
 CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
 CC an amide bond (By similarity).
 DR EMBL: AP004830; BAB96285.1; -.
 DR HSSP: O53653; IN67.
 DR GO: GO:0009986; C:cell surface; IEA.
 DR GO: GO:0005618; C:cell wall; IEA.
 DR GO: GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
 DR GO: GO:0016020; C:membrane; IEA.
 DR GO: GO:0007155; P:cell adhesion; IEA.
 DR InterPro: IPR008966; Adhes_bact.
 DR InterPro: IPR004237; Fn_bind.
 DR InterPro: IPR005877; Gpos_Ysirk.
 DR InterPro: IPR001899; Gram_pos_anchor.
 DR Pfam: PF02986; Fn_bind; 1.
 DR Pfam: PF00746; Gram_pos_anchor; 1.

DR Pfam: PF04650; Ysirk_signal; 1.
 DR TIGRFAMs: TIGR01167; LpXtg_anchor; 1.
 DR TIGRFAMs: TIGR01168; Ysirk_signal; 1.
 DR PROSITE: PS50847; GRAM_POS_ANCHORING; 1.
 DR Cell wall; Complete proteome; Peptidoglycan-anchor.
 SQ SEQUENCE 943 AA; 104537 MW; DA8A5F3197EB6A CRC64;

Query Match 100.0%; Score 51; DB 2; Length 943;
 Best Local Similarity 100.0%; Pred. No. 3;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 IIEEDTNKDK 10
 |||||
 Db 771 IIEEDTNKDK 780

RESULT 4
 Q6G6H4 PRELIMINARY; PRT; 957 AA.
 ID Q6G6H4
 AC Q6G6H4
 DT 05-JUL-2004 (TREMBlrel. 27, Created)
 DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
 DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
 DE Fibronectin-binding protein.
 GN Name=fnbB; OrderedLocuNames=SAS2387;
 OS Staphylococcus aureus (strain MSSA476).
 CC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 CX NCBI_TaxID=282459;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX PubMed=1521324; DOI=10.1073/pnas.0402521101;
 RA Holden M.T.G., Fell E.J., Lindsay J.A., Peacock S.J., Day N.P.J.,
 RA Enright M.C., Foster T.J., Moore C.E., Hurst L., Atkin R., Barron A.,
 RA Bason N., Bentley S.D., Chillingworth C., Chillingworth T.,
 RA Churcher C., Clark L., Cotton C., Cronin A., Doggett J., Dowd L.,
 RA Felwell T., Hance Z., Harris B., Hauser H., Holtroyd S., Jagels K.,
 RA James K.D., Leonard N., Line A., Mayes R., Moule S., Mungall K.,
 RA Ormond D., Quail M.A., Rabinowitch E., Rutherford K.M., Sanders M.,
 RA Sharp S., Simmonds M., Stevens K., Whitehead S., Barrett B.G.,
 RA Spratt B.G., Parkhill J.;
 RT "Complete genomes of two clinical Staphylococcus aureus strains:
 RT evidence for the rapid evolution of virulence and drug resistance.";
 RL Proc. Natl. Acad. Sci. U.S.A. 101:9786-9791 (2004).
 CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
 CC an amide bond (By similarity).
 DR EMBL: BX571857; CAG44201.1; -.
 DR GO: GO:0009986; C:cell surface; IEA.
 DR GO: GO:0005618; C:cell wall; IEA.
 DR GO: GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
 DR GO: GO:0016020; C:membrane; IEA.
 DR GO: GO:0007155; P:cell adhesion; IEA.
 DR InterPro: IPR008966; Adhes_bact.
 DR InterPro: IPR004237; Fn_bind.
 DR InterPro: IPR005877; Gpos_Ysirk.
 DR InterPro: IPR001899; Gram_pos_anchor.
 DR InterPro: IPR001899; Gram_pos_anchor.
 DR Pfam: PF02986; Fn_bind; 1.
 DR Pfam: PF00746; Gram_pos_anchor; 1.
 DR Pfam: PF04650; Ysirk_signal; 1.
 DR TIGRFAMs: TIGR01167; LpXtg_anchor; 1.
 DR TIGRFAMs: TIGR01168; Ysirk_signal; 1.
 DR PROSITE: PS50847; GRAM_POS_ANCHORING; 1.
 DR Cell wall; Complete proteome; Peptidoglycan-anchor.
 SQ SEQUENCE 957 AA; 105980 MW; 28FBBA7FFD3EAF CRC64;

Query Match 100.0%; Score 51; DB 2; Length 957;
 Best Local Similarity 100.0%; Pred. No. 3;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 IIEEDTNKDK 10
 |||||
 Db 771 IIEEDTNKDK 780

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RESULT 5
099RD3 PRELIMINARY; PRT; 961 AA.
ID 099RD3
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE Fibronectin-binding protein homolog.
GN Name=fnb3; OrderedLocustNames=SAV2502;
OS Staphylococcus aureus (strain Muso / ATCC 700699).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OK NCBI_TaxID=158878;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Muso / ATCC 700699;
RX MEDLINE=21311952; Pubmed=11418146; DOI=10.1016/S0140-6736(00)04403-2;
RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Iian J.-Q., Ito T.,
RA Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,
RA Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
RA Sekimizu K., Hiraoka H., Kuhara S., Goto S., Yabuzaki J.,
RA Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
RA Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
RA "Whole genome sequencing of methicillin-resistant Staphylococcus
RT aureus."
RL Lancet 357:1225-1240(2001).
CC -1 SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
an amide bond (By similarity).
EMBL, AP003365; BAB58664.1; -.
DR PIR; G90053; G90053.
DR HSSP; Q53653; IN67.
DR GO; GO:0009986; C:cell surface; IEA.
DR GO; GO:0005618; C:cell wall; IEA.
DR GO; GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0007155; P:cell adhesion; IEA.
DR InterPro; IPR008966; Adhes_bact.
DR InterPro; IPR004237; Fn_bind.
DR InterPro; IPR005877; Gpos_YsIRK.
DR InterPro; IPR001899; Gram_pos_anchor.
DR Pfam; PF02986; Fn_bind; 1.
DR Pfam; PF00746; Gram_pos_anchor; 1.
DR Pfam; PF04650; YsIRK_signal; 1.
DR TIGRFAMs; TIGR01167; LPTXG_anchor; 1.
DR TIGRFAMs; TIGR01168; YsIRK_signal; 1.
DR PROSITE; PS50847; GRAM_POS_ANCHORING; 1.
KW Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ SEQUENCE 961 AA; 106010 MW; 364940F884EA4101 CRC64;

Query Match 100.0%; Score 51; DB 2; Length 961;
Best Local Similarity 100.0%; Pred. No. 3.1;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 IIEEDTNKDK 10
DB 775 IIEEDTNKDK 784
ID 07A3J8 PRELIMINARY; PRT; 961 AA.
ID 07A3J8
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE FnB3 protein.
GN Name=fnb3; OrderedLocustNames=SA2290;
OS Staphylococcus aureus (strain N315).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OK NCBI_TaxID=158879;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21311952; Pubmed=11418146; DOI=10.1016/S0140-6736(00)04403-2;

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RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Iian J.-Q., Ito T.,
RA Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,
RA Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
RA Sekimizu K., Hiraoka H., Kuhara S., Goto S., Yabuzaki J.,
RA Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
RA Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
RA "Whole genome sequencing of methicillin-resistant Staphylococcus
RT aureus."
RL Lancet 357:1225-1240(2001).
CC -1 SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
an amide bond (By similarity).
EMBL, AP003365; BAB58664.1; -.
DR GO; GO:0009986; C:cell surface; IEA.
DR GO; GO:0005618; C:cell wall; IEA.
DR GO; GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0007155; P:cell adhesion; IEA.
DR InterPro; IPR008966; Adhes_bact.
DR InterPro; IPR004237; Fn_bind.
DR InterPro; IPR005877; Gpos_YsIRK.
DR InterPro; IPR001899; Gram_pos_anchor.
DR Pfam; PF02986; Fn_bind; 1.
DR Pfam; PF00746; Gram_pos_anchor; 1.
DR Pfam; PF04650; YsIRK_signal; 1.
DR TIGRFAMs; TIGR01167; LPTXG_anchor; 1.
DR TIGRFAMs; TIGR01168; YsIRK_signal; 1.
DR PROSITE; PS50847; GRAM_POS_ANCHORING; 1.
KW Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ SEQUENCE 961 AA; 106010 MW; 364940F884EA4101 CRC64;

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Query Match 100.0%; Score 51; DB 2; Length 961;
Best Local Similarity 100.0%; Pred. No. 3.1;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 IIEEDTNKDK 10
DB 775 IIEEDTNKDK 784
ID 06GDUS PRELIMINARY; PRT; 965 AA.
ID 06GDUS
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE Fibronectin-binding protein.
GN Name=fnbA; OrderedLocustNames=SA2580;
OS Staphylococcus aureus (strain WRS4252).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OK NCBI_TaxID=282458;
RN [1]
RP SEQUENCE FROM N.A.
RX Pubmed=15213324; DOI=10.1073/pnas.0402521101;
RA Holden M.T.G., Fell E.J., Lindsay J.A., Peacock S.J., Day N.P.J.,
RA Enright M.C., Foster T.J., Moore C.E., Hurst L., Atkin R., Barron A.,
RA Bason N., Bentley S.D., Chillingworth T.,
RA Churcher C., Clark L., Cotton C., Cronin A., Doggett J., Dowd L.,
RA Fellwell T., Hance Z., Harris B., Hauser H., Holroyd S., Jagels K.,
RA James K.D., Lennard N., Line A., Mayes R., Moulie S., Mungall K.,
RA Ormond D., Quail M.A., Rabinowitsch E., Rutherford K.M., Sanders M.,
RA Sharp S., Simmonds M., Stevens K., Whitehead S., Barrett B.G.,
RA Spratt B.G., Parkhill J.;
RA "Complete genomes of two clinical Staphylococcus aureus strains:
RT evidence for the rapid evolution of virulence and drug resistance";
RL Proc. Natl. Acad. Sci. U.S.A. 101:9786-9791(2004).
CC -1 SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
an amide bond (By similarity).
EMBL, BX571856; CAG41560.1; -.
DR GO; GO:0009986; C:cell surface; IEA.
DR GO; GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO; GO:0016020; C:membrane; IEA.

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DR GO:0007155; P:cell adhesion; IEA.
DR InterPro: IPR008966; Adhes_bact.
DR InterPro: IPR004237; Fn_bind.
DR InterPro: IPR005877; Gpos_YsIRK.
DR InterPro: IPR01899; Gram_pos_anchor.
DR Pfam: PF02986; Fn_bind. 1.
DR Pfam: PF00746; Gram_pos_anchor; 1.
DR Pfam: PF04650; YsIRK_signal; 1.
DR TIGRFAMs: TIGR01167; LPXTG_anchor; 1.
DR TIGRFAMs: TIGR01168; YsIRK_signal; 1.
DR PROSITE: PS50847; GRAM_POS_ANCHORING; 1.
DR Cell wall; Complete proteome; Peptidoglycan-anchor.
KW SEQUENCE 965 AA; 105691 MW; 2982813164D0551 CRC64;

Query Match 100.0%; Score 51; DB 2; Length 965;
Best Local Similarity 100.0%; Pred. No. 3.1;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 IIEEDTNKDK 10
Db 793 IIEEDTNKDK 802

RESULT 8
Q8NUU7 PRELIMINARY; PRT; 1015 AA.
ID Q8NUU7
AC Q8NUU7;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Fnb protein.
GN Name=fnb; OrderedLocustNames=WM2421;
OS Staphylococcus aureus (strain WM2).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
NC NCB1_TaxID=196620;
NX [1]
RP SEQUENCE FROM N.A.
RC STRAIN=WM2;
RX MEDLINE=22040717; PubMed=12044378; DOI=10.1016/S0140-6736(02)08713-5;
RA Baba T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Aoki A.,
RA Nagai Y., Iwama N., Asano K., Naito T., Kuroda H., Cui L.,
RA Yamamoto K., Hiramatsu K.;
RT "Genome and virulence determinants of high virulence community-
RT acquired MRSA.";
RL Lancet 359:1819-1827(2002).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC an amide bond (by similarity).
DR EMBL: AP004830; BAB96286.1; -.
DR GO: GO:0009986; C:cell surface; IEA.
DR GO: GO:0005618; C:cell wall; IEA.
DR GO: GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO: GO:0016020; C:membrane; IEA.
DR GO: GO:0007155; P:cell adhesion; IEA.
DR InterPro: IPR008966; Adhes_bact.
DR InterPro: IPR004237; Fn_bind.
DR InterPro: IPR005877; Gpos_YsIRK.
DR InterPro: IPR01899; Gram_pos_anchor.
DR Pfam: PF02986; Fn_bind. 1.
DR Pfam: PF00746; Gram_pos_anchor; 1.
DR Pfam: PF04650; YsIRK_signal; 1.
DR TIGRFAMs: TIGR01167; LPXTG_anchor; 1.
DR TIGRFAMs: TIGR01168; YsIRK_signal; 1.
DR PROSITE: PS50847; GRAM_POS_ANCHORING; 1.
KW Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ SEQUENCE 1015 AA; 111145 MW; D0F9281BB64D4D2 CRC64;

Query Match 100.0%; Score 51; DB 2; Length 1015;
Best Local Similarity 100.0%; Pred. No. 3.3;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 IIEEDTNKDK 10
Db 829 IIEEDTNKDK 838
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RESULT 9
Q6G6H3 PRELIMINARY; PRT; 1015 AA.
ID Q6G6H3
AC Q6G6H3;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Fibronectin-binding protein.
DE OrderedLocustNames=SA52388;
GN Staphylococcus aureus (strain MSSA476).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
NX NCB1_TaxID=282459;
RP SEQUENCE FROM N.A.
RX PubMed=1521324; DOI=10.1073/pnas.0402521101;
RA Holden M.T.G., Fell E.J., Lindsey J.A., Peacock S.J., Day N.P.J.,
RA Enright M.C., Foster T.J., Moore C.E., Hurst L., Atkin R., Barron A.,
RA Bason N., Bentley S.D., Chillingworth C., Chillingworth T.,
RA Churcher C., Clark L., Corton C., Cronin A., Doggett J., Dowd L.,
RA Fellwell T., Hance Z., Harris B., Hauser H., Holtroyd S., Jags K.,
RA James K.D., Leonard N., Line A., Mayes R., Moule S., Mungall K.,
RA Ormond D., Quail M.A., Rabinovitch E., Rutherford K.M., Sanders M.,
RA Sharp S., Simmonds M., Stevens K., Whitehead S., Barrett B.G.,
RA Spratt B.G., Parkhill J.;
RT "Complete genomes of two clinical Staphylococcus aureus strains:
RT evidence for the rapid evolution of virulence and drug resistance.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:9786-9791(2004).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC an amide bond (by similarity).
DR EMBL: BX571857; CA644202.1; -.
DR GO: GO:0009986; C:cell surface; IEA.
DR GO: GO:0005618; C:cell wall; IEA.
DR GO: GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO: GO:0016020; C:membrane; IEA.
DR GO: GO:0007155; P:cell adhesion; IEA.
DR InterPro: IPR008966; Adhes_bact.
DR InterPro: IPR004237; Fn_bind.
DR InterPro: IPR005877; Gpos_YsIRK.
DR InterPro: IPR01899; Gram_pos_anchor.
DR Pfam: PF02986; Fn_bind. 1.
DR Pfam: PF00746; Gram_pos_anchor; 1.
DR Pfam: PF04650; YsIRK_signal; 1.
DR TIGRFAMs: TIGR01167; LPXTG_anchor; 1.
DR TIGRFAMs: TIGR01168; YsIRK_signal; 1.
DR PROSITE: PS50847; GRAM_POS_ANCHORING; 1.
KW Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ SEQUENCE 1015 AA; 111145 MW; D0F9281BB64D4D2 CRC64;

Query Match 100.0%; Score 51; DB 2; Length 1015;
Best Local Similarity 100.0%; Pred. No. 3.3;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 IIEEDTNKDK 10
Db 829 IIEEDTNKDK 838

RESULT 10
FNBA_STNAU STANDARD; PRT; 1018 AA.
ID FNBA_STNAU
AC P14738;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Fibronectin-binding protein precursor (FNBP).
GN Name=fnbA;
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
NX NCB1_TaxID=1280;
RP SEQUENCE FROM N.A.
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RC STRAIN=NCTC 8325-4;
 RX MEDLINE=89098998; PubMed=2521391;
 RA Sinaas C., Raucel G., Joensen K., Lindgren P.-E.,
 RA Anantharamaiah G.M., Hoeck M., Lindberg M.;
 RT "Nucleotide sequence of the gene for a fibronectin-binding protein
 from *Staphylococcus aureus*: use of this peptide sequence in the
 RT synthesis of biologically active peptides.";
 RL Proc. Natl. Acad. Sci. U.S.A. 86:699-703(1989).
 CC -1- FUNCTION: The ability of bacteria to bind fibronectin has been
 CC proposed as a virulence factor enabling bacteria to colonize wound
 CC tissues and blood clots. Binding of plasma fibronectin to the
 CC bacterial surface might block adhesion receptors on *S.aureus*, thus
 CC representing an important defense mechanism against tissue
 CC invasion.
 CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
 CC an amide bond (potential).
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (see <http://www.isb-sib.ch/announce/>
 CC or send an email to license@sib-sib.ch).
 CC -----
 DR EMBL; J04151; AAA26632.1; -;
 DR InterPro; IPR004237; Fn_bind.
 DR InterPro; IPR005877; Gpos_YsIRK.
 DR InterPro; IPR001899; Gram_pos_anchor.
 DR Pfam; PF02986; Fn_bind; 1.
 DR Pfam; PF00746; Gram_pos_anchor; 1.
 DR Pfam; PF04650; YsIRK_signal; 1.
 DR TIGRFAMs; TIGR01167; LPXTG_anchor; 1.
 DR TIGRFAMs; TIGR01168; YsIRK_signal; 1.
 DR PROSITE; PS50847; GRAM_POS_ANCHORING; 1.
 DR Cell adhesion; Cell wall; Peptidoglycan-anchor; Repeat; Signal;
 KW Virulence.
 FT SIGNAL 1 36
 FT CHAIN 37 985
 FT PROPEP 96 1018
 FT REPEAT 545 574
 FT REPEAT 575 604
 FT DOMAIN 745 878
 FT REPEAT 745 782
 FT REPEAT 783 820
 FT REPEAT 821 859
 FT REPEAT 860 878
 FT DOMAIN 879 948
 FT REPEAT 879 892
 FT REPEAT 893 906
 FT REPEAT 907 920
 FT REPEAT 921 934
 FT REPEAT 935 948
 FT SITE 962 966
 FT MOD_RES 985 985
 SQ SEQUENCE 1018 AA; 111780 MW; 58175E0020881F1F CRC64;
 Query Match 100.0%; Score 51; DB 1; Length 1018;
 Best Local Similarity 100.0%; Pred. No. 3.3;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
 DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
 DE Fibronectin-binding protein homolog.
 GN Name=fnb; OrderedLocustNames=SAV2503;
 OS *Staphylococcus aureus* (strain Mu50 / ATCC 700699).
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 OX NCBI_TaxID=158878;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Mu50 / ATCC 700699;
 RX MEDLINE=21311952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2;
 RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
 RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Iian J.-O., Ito T.,
 RA Kanamori M., Matsunaru H., Maruyama A., Murakami H., Hoshoyama A.,
 RA Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
 RA Sekimizu K., Hiraoka H., Kihara S., Goto S., Yabuzaki J.,
 RA Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
 RA Hatori M., Ogasawara N., Hayashi H., Hiratake K.;
 RT "Whole genome sequencing of methicillin-resistant *Staphylococcus*
 RT *aureus*.";
 RL Lancet 357:1225-1240(2001).
 CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
 CC an amide bond (By similarity).
 CC -----
 DR EMBL; AP003365; BAB58665.1; -;
 DR PIR; H90053; H90053.
 DR GO; GO:0009986; C:cell surface; IEA.
 DR GO; GO:0005618; C:cell wall; IEA.
 DR GO; GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0007155; P:cell adhesion; IEA.
 DR InterPro; IPR009966; Adhes_bact.
 DR InterPro; IPR004237; Fn_bind.
 DR InterPro; IPR005877; Gpos_YsIRK.
 DR InterPro; IPR001899; Gram_pos_anchor.
 DR Pfam; PF02986; Fn_bind; 1.
 DR Pfam; PF00746; Gram_pos_anchor; 1.
 DR Pfam; PF04650; YsIRK_signal; 1.
 DR TIGRFAMs; TIGR01167; LPXTG_anchor; 1.
 DR TIGRFAMs; TIGR01168; YsIRK_signal; 1.
 DR PROSITE; PS50847; GRAM_POS_ANCHORING; 1.
 DR Cell wall; Complete proteome; Peptidoglycan-anchor.
 SQ SEQUENCE 1038 AA; 113618 MW; 666BF6BF2FBB12 CRC64;
 Query Match 100.0%; Score 51; DB 2; Length 1038;
 Best Local Similarity 100.0%; Pred. No. 3.3;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DT 07A337 PRELIMINARY; PRT; 1038 AA.
 AC 07A337;
 DT 05-JUL-2004 (TREMBlrel. 27, Created)
 DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
 DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
 DE Fnb protein.
 GN Name=fnb; OrderedLocustNames=SA2291;
 OS *Staphylococcus aureus* (strain N315).
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 OX NCBI_TaxID=158879;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC MEDLINE=21311952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2;
 RX Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
 RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Iian J.-O., Ito T.,
 RA Kanamori M., Matsunaru H., Maruyama A., Murakami H., Hoshoyama A.,
 RA Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
 RA Sekimizu K., Hiraoka H., Kihara S., Goto S., Yabuzaki J.,
 RA Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,

RA Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
 RT "Whole genome sequencing of methicillin-resistant *Staphylococcus*
 RT aureus".
 CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
 CC an amide bond (By similarity).
 CC EMBL: AP003137; BAB3594.1; -.
 CC GO: GO:0009986; C:cell surface; IEA.
 CC GO: GO:0005568; C:cell wall; IEA.
 CC GO: GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
 CC GO: GO:0016020; C:membrane; IEA.
 CC GO: GO:0007155; P:cell adhesion; IEA.
 CC InterPro: IPR008966; Aches_bact.
 CC InterPro: IPR004237; Fb_bind.
 CC InterPro: IPR005877; Gpos_YsIRK.
 CC InterPro: IPR001899; Gram_pos_anchor.
 CC Pfam: PF02986; Fb_bind; 1.
 CC Pfam: PF00746; Gram_pos_anchor; 1.
 CC Pfam: PF04650; YsIRK_signal; 1.
 CC TIGRFAMs: TIGR01167; LPTXG_anchor; 1.
 CC TIGRFAMs: TIGR01168; YsIRK_signal; 1.
 CC PROSITE: PS50847; GRAM_POS_ANCHORING; 1.
 CC KEGG: KEGG01168; Complete proteome; Peptidoglycan-anchor.
 CC SEQUENCE 1038 AA; 113618 MW; 666BFB52FBBE12 CRC64;
 SQ
 Query Match 100.0%; Score 51; DB 2; Length 1038;
 Best Local Similarity 100.0%; Pred. No. 3.3;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 IIEEDTNKDK 10
 DB 824 IIEEDTNKDK 833
 ID PTP3_YEAST STANDARD; PRT; 928 AA.
 AC P40048;
 DT 01-FEB-1995 (Rel. 31, Created)
 DT 01-FEB-1995 (Rel. 31, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Protein-tyrosine phosphatase 3 (EC 3.1.3.48) (PTPase 3).
 GN Name=PTP3; OrderedLocNames=YERO75C;
 OS *Saccharomyces cerevisiae* (Baker's yeast).
 CC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 CC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
 CC NCBI_TaxID=4932;
 CX [1]
 RN SEQUENCE FROM N.A., AND CHARACTERIZATION.
 RP MEDLINE=97367951; PubMed=9224718;
 RX Zhan X.-L., Deschenes R.J., Guan K.-L.;
 RT "Differential regulation of FUS3 MAP kinase by tyrosine-specific
 RT phosphatases PTP2/PTP3 and dual-specificity phosphatase MSG5 in
 RT *Saccharomyces cerevisiae*.";
 RL Genes Dev. 11:1690-1702(1997).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=5288C / AB972;
 RX MEDLINE=97313264; PubMed=9169868;
 RA Dietrich F.S., Mulligan J.T., Hennesey K.M., Yelton M.A., Allen E.,
 RA Areujo J.M., Aviles E., Berno A., Brennan T., Carpenter J., Chen E.,
 RA Cherry J.M., Chung E., Duncan M., Guzman E., Hartzell G.,
 RA Hunnicke-Smith S., Hyman R.W., Kayser A., Komp C., Laehkari D., Lew H.,
 RA Lin D., Mosedale D., Nakahara K., Namath A., Norgren R., Oefner P.,
 RA Oh C., Petrel P.X., Roberts D., Sehl P., Schramm S., Shogren T.,
 RA Smith V., Taylor P., Wei Y., Botstein D., Davis R.W.;
 RT "The nucleotide sequence of *Saccharomyces cerevisiae* chromosome V.";
 RL Nature 387:78-81(1997).
 CC -1- FUNCTION: Major phosphatase responsible for tyrosine
 CC dephosphorylation of MAP kinase FUS3 to inactivate its activity;
 CC it also has important roles, along with MSG5, in the inactivation
 CC of FUS3 following pheromone stimulation.
 CC -1- CATALYTIC ACTIVITY: Protein tyrosine phosphate + H(2)O = protein

CC tyrosine + phosphate.
 CC -1- SIMILARITY: Belongs to the protein-tyrosine phosphatase family.
 CC Non-receptor class subfamily.
 CC -1- SIMILARITY: Contains 1 rhodanese domain.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL: AF006304; AAB7081.1; -.
 CC EMBL: U18814; AAB64614.1; -.
 CC PIR: S50578; S50578.
 CC HSSP: P18052; LYFO.
 CC GerMOnline: 139155; -.
 CC SCD: S00000877; PTP3.
 CC GO: GO:0005737; C:cytoplasm; IDA.
 CC GO: GO:0004725; F:protein-tyrosine-phosphatase activity; IDA.
 CC GO: GO:0000173; P:inactivation of MAPK during osmolarity sensing; IMP.
 CC GO: GO:0006470; P:protein amino acid dephosphorylation; IDA.
 CC GO: GO:000750; P:signal transduction during conjugation with. . .; IMP.
 CC InterPro: IPR001763; Rhodanese-like.
 CC InterPro: IPR000387; TYR_phosphatase.
 CC InterPro: IPR000242; Tyr_PP.
 CC Pfam: PF00581; Rhodanese; 1.
 CC Pfam: PF00102; Y_phosphatase; 1.
 CC PRINTS: PR00700; PRTYPHPTASE.
 CC SMART: SM00194; PTPC; 1.
 CC SMART: SM00450; RHOD; 1.
 CC PROSITE: PSS0206; RHODANSE_3; 1.
 CC PROSITE: PSS0383; TYR_PHOSPHATASE_1; 1.
 CC PROSITE: PSS0056; TYR_PHOSPHATASE_2; 1.
 CC PROSITE: PSS0055; TYR_PHOSPHATASE_PTP; 1.
 CC KEGG: KEGG01168; Protein phosphatase.
 CC HYDROLASE; Protein phosphatase.
 CC FT DOMAIN 111 232
 FT ACT_SITE 804 804
 FT Rhodanese.
 FT Phosphocysteine intermediate (By
 FT similarity).
 FT DOMAIN 308 311
 FT POLY-SER.
 FT FT DOMAIN 592 597
 FT POLY-THR.
 FT FT DOMAIN 702 715
 FT POLY-ASN.
 FT FT DOMAIN 724 732
 FT POLY-ASP.
 SQ SEQUENCE 928 AA; 105250 MW; 6DEC5BA26B7ACBCB CRC64;
 Query Match 80.4%; Score 41; DB 1; Length 928;
 Best Local Similarity 77.8%; Pred. No. 1.7e+02;
 Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 QY 2 IIEEDTNKDK 10
 DB 381 LEKDTNKDK 389
 ID Q7R5R0 PRELIMINARY; PRT; 89 AA.
 AC Q7R5R0;
 DT 01-MAR-2004 (TEMBLrel. 26, Created)
 DT 01-MAR-2004 (TEMBLrel. 26, Last sequence update)
 DT 01-MAR-2004 (TEMBLrel. 26, Last annotation update)
 DE GIP_487_20953_21222.
 OS *Giardia lamblia* ATCC 50803.
 CC Eukaryota; Diplomonadida; Hexamitidae; Giardinae; Giardia.
 CC NCBI_TaxID=184922;
 CX [1]
 RN SEQUENCE FROM N.A.
 RP STRAIN=WB C6;
 RC Morrison H.G., McArthur A.G., Adam R.D., Aley S.B., Gillin F.D.,
 RA Olsen G.J., Sogin M.L.;
 RT "Draft sequence of the *Giardia lamblia* genome.";
 RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.

-1- CAUTION: The sequence shown here is derived from an
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.
 DR EMBL: AAC01000004; EAA42582.1; -
 SQ SEQUENCE 89 AA; 10841 MW; F17C1E1523D44176 CRC64;

Query Match 78.4%; Score 40; DB 2; Length 89;
 Best Local Similarity 77.8%; Pred. No. 23;
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 IIEPTNKDK 10
 :|||
 Db 78 VEEDRNKDK 86

RESULT 15

08YVC3 PRELIMINARY; PRT; 237 AA.
 ID 08YVC3;
 AC 08YVC3;
 DT 01-MAR-2002 (TRENBLrel. 20, Created)
 DT 01-MAR-2002 (TRENBLrel. 20, Last sequence update)
 DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)
 DE A12055 protein.
 GN OrderedLocusNames=A12055;
 OS Anabaena sp. (strain PCC 7120).
 OC Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Nostoc.
 OX NCBI_TaxID=103690;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21595285; PubMed=11759840;
 RA Kaneko T., Nakamura Y., Molk C.P., Kuritz T., Sasamoto S.,
 RA Watanabe A., Iriuchi M., Ishikawa A., Kawashina K., Kimura T.,
 RA Kishida Y., Kohara M., Matsumoto M., Takazawa M., Yamada M.,
 RA Nakazaki N., Shimo S., Sugimoto M.,
 RA Yasuda M., Tabata S.,
 RT "Complete genomic sequence of the filamentous nitrogen-fixing
 RT cyanobacterium Anabaena sp. strain PCC 7120."
 RL DNA Rep. 8:205-213(2001).
 DR EMBL: AP003588; BAB73754.1; -
 DR PIR: A12062; A12062.
 KW Complete proteome.
 SQ SEQUENCE 237 AA; 26766 MW; 29EA6C0DA2E88D5F CRC64;

Query Match 78.4%; Score 40; DB 2; Length 237;
 Best Local Similarity 77.8%; Pred. No. 62;
 Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 IIEPTNKDK 9
 :|||
 Db 136 IIDQPTNKD 144

Search completed: October 22, 2005, 09:52:16
 Job time : 58.2069 secs

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CC streptococci, e.g. meningitis, otitis media, pneumonia, endocarditis,
CC mastitis in cattle, abortion in horses and many others. Since the
CC antibodies block binding of bacteria, they should be effective against
CC antibiotic-resistant strains, and may replace antibiotic therapy or
CC increase its effectiveness. Sequences AAW65744-58 represent peptides
CC which were synthesised to span the D3 motif of S. aureus fibronectin
CC binding protein A
XX
SQ Sequence 10 AA;
Query Match 100.0%; Score 54; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0078;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 EBDTNKDKPS 10
1 EBDTNKDKPS 10
Db 1 EBDTNKDKPS 10
RESULT 2
AAP82118
ID AAP82118 standard; protein; 37 AA.
XX
AC AAP82118;
XX
DT 25-MAR-2003 (revised)
DT 05-JUN-1990 (first entry)
XX
DE Fibronectin binding protein.
XX
KM Fibronectin binding protein; S.aureus; immunisation; mastitis; ruminants;
KM wound infection; diagnosis.
XX
OS Staphylococcus aureus.
XX
PN EP294349-A.
XX
PD 07-DEC-1988.
XX
PF 30-MAY-1988; 88EP-00850188.
XX
PR 01-JUN-1987; 87SE-00002272.
XX
XX (ALFA) ALFA LAVAL AGRIC INT AB.
XX
PI Lindberg MK, Signae LC, Wadstrom TM, Froman G;
XX
DR WPI; 1988-347978/49.
DR N-PSDB; AAN82056.
XX
PT Hybrid DNA encoding Staphylococcus aureus fibronectin binding protein -
PT useful for immunisation and topical application to prevent staphylococcal
PT infections.
XX
PS Claim 11; Page 12; 23pp; English.
XX
CC The S. aureus fibronectin binding protein may be included in a hybrid
CC protein. The protein may be used to immunise ruminants against
CC staphylococcal mastitis, pref. when given at 0.5-5 microg/kg, using 3
CC doses at 1-3 week intervals; and for topical applicn. to prevent wound
CC infection, pref. using isotonic saline soln. of concn. 25-250 microg/mg.
CC The DNA encoding the binding protein and the hybrid protein may be
CC immobilised on a carrier and used to diagnose staphylococcal infections.
CC (updated on 25-MAR-2003 to correct PA field.)
XX
SQ Sequence 37 AA;
Query Match 100.0%; Score 54; DB 1; Length 37;
Best Local Similarity 100.0%; Pred. No. 0.029;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 EBDTNKDKPS 10
1 EBDTNKDKPS 10

Db 10 EBDTNKDKPS 19
RESULT 3
AAB91958
ID AAB91958 standard; peptide; 37 AA.
XX
AC AAB91958;
XX
DT 22-JUN-2001 (first entry)
XX
DE Fibronectin fragment and fibrin related peptide SEQ ID NO.1134.
XX
KM Protection; endogenous therapeutic peptide; peptidase; conjugation;
KM blood component; modification; succinimidyl; maleimido group; amino;
KM hydroxyl; thiol; hormone; growth factor; neurotransmitter.
XX
OS Homo sapiens.
OS Synthetic.
PN WO200069900-A2.
XX
PD 23-NOV-2000.
XX
PF 17-MAY-2000; 2000WO-US013576.
XX
PR 17-MAY-1999; 99US-0134406P.
PR 10-SEP-1999; 99US-0153406P.
PR 15-OCT-1999; 99US-0159783P.
XX
PA (CONU-) CONUTCHEM INC.
XX
PI Bridon DP, Ezrin AM, Milner PG, Holmes DL, Thibaudau K;
XX
DR WPI; 2001-112059/12.
XX
PT Modifying and attaching therapeutic peptides to albumin prevents
PT peptidase degradation, useful for increasing length of in vivo activity.
XX
PS Disclosure; Page 566; 733pp; English.
XX
CC The present invention describes a modified therapeutic peptide (I)
CC comprising a therapeutically active amino acid region (III) and a
CC reactive group (II) (e.g. succinimidyl and maleimido groups) attached to
CC a less therapeutically active amino acid region (IV), which covalently
CC bonds with amino/hydroxyl/thiol groups on blood components to form a
CC peptidase stabilised therapeutic peptide composed of 3-50 amino acids.
CC (I) are useful for modifying therapeutic peptides e.g. hormones, growth
CC factors and neurotransmitters, to protect them from peptidase activity in
CC vivo for the treatment of various disorders. Endogenous therapeutic
CC peptides are not suitable as drug candidates as they require frequent
CC administration due to rapid degradation by peptidases in the body.
CC Modifying and attaching therapeutic peptides to albumin prevents or
CC reduces the action of peptidases to increase length of activity (half
CC life) and specificity as bonding to large molecules decreases
CC intracellular uptake and interference with physiological processes.
CC AAB90829 to AAB92441 represent peptides which can be used in the
CC exemplification of the present invention
XX
SQ Sequence 37 AA;
Query Match 100.0%; Score 54; DB 4; Length 37;
Best Local Similarity 100.0%; Pred. No. 0.029;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 EBDTNKDKPS 10
1 EBDTNKDKPS 10
Db 9 EBDTNKDKPS 18
RESULT 4
AAP80662
ID AAP80662 standard; protein; 38 AA.

```

XX AAP80662;
AC 25-MAR-2003 (revised)
XX 07-OCT-1990 (first entry)
DT
XX Protein with fibronectin binding ability.
DE
XX Hybrid DNA molecule; fibronectin binding; mastitis; ruminants;
KM wound infection.
XX
XX Staphylococcus aureus.
OS
XX EP294349-A.
PN
XX 07-DEC-1988.
PD
XX 30-MAY-1988; 88EP-00850188.
PF
XX 01-JUN-1987; 87SE-00002272.
PR
XX (ALFA ) ALFA LAVAL AGRIC INT AB.
PA
XX Lindberg MK, Signas LC, Wadstrom TM, Froman G;
PI WPI; 1988-347978/49.
XX N-PSDB; AAN81099.
DR
XX Hybrid DNA encoding Staphylococcus aureus fibronectin binding protein -
PT useful for immunisation and topical application to prevent staphylococcal
XX infections.
XX
XX Claim 11; Page 12; 23pp; English.
PS
XX The peptide has fibronectin binding ability. It is useful for immunising
CC ruminants against staphylococcal mastitis, pref. when used at 0.5-5
CC micrograms/kg; using 3 doses given at 1-3 week intervals; for topical
CC application to prevent wound infection, using an isotonic saline soln. of
CC concn. 25-250 micrograms/ml; and, when immobilised on a carrier, for
CC diagnosing staphylococcal infections. (Updated on 25-MAR-2003 to correct
CC PF field.) (Updated on 25-MAR-2003 to correct PA field.)
CC
XX
XX Sequence 38 AA;
SQ
Query Match 100.0%; Score 54; DB 1; Length 38;
Best Local Similarity 100.0%; Pred. No. 0.03; 0; Indels 0; Gaps 0;
Matches 10; Conservative 0; Mismatches 0;
QY 1 EEDTNKDKPS 10
DB 10 EEDTNKDKPS 19

```

RESULT 5
AAV29087
ID AAV29087 standard; protein; 134 AA.
XX
AC AAV29087;
XX
XX 28-SEP-1999 (first entry)
DT
XX
XX S. aureus fibronectin binding protein A (FnBA) binding domain.
DE
XX
XX Bovine herpes virus-2; BHV-2; cytokine; immune response; immunogen; IL;
KM interleukin; colony stimulating factor; CSF; interferon; IFN; TNF;
KM tumour necrosis factor; recombinant virus; vaccine; mucosal disease;
KM mastitis; breast cancer; stress-induced disease; binding domain; FnBA;
KM fibronectin binding protein.
XX
OS Staphylococcus aureus.
XX
XX WO9916892-A1.
PN
XX

```

PD 08-APR-1999.
XX
XX 29-SEP-1998; 98WO-GB002927.
PF
XX 29-SEP-1997; 97GB-00020633.
PR
XX (UYBR-) UNIV BRISTOL.
PA
XX Bradley AJ, Duffae WPI;
PI WPI; 1999-255101/21.
XX N-PSDB; AAX91504.
DR
XX New bovine herpes virus-2 vectors.
FT
XX
XX Example 2; Fig 8A-B; 130pp; English.
PS
XX The invention provides bovine herpes virus-2 (BHV-2) based vectors that
CC comprise at least one cytokine-encoding DNA sequence. The expression of
CC cytokines in mammals can up-regulate immune responses to the immunogens.
CC The cytokine is selected from interleukins (IL), colony stimulating
CC factors (CSF), interferons (IFN) and tumour necrosis factors (TNF). The
CC BHV-2 based vector or recombinant virus can be used as vaccines. They can
CC be used for preventing or treating a mucosal disease in a subject, e.g.
CC ruminants, cattle, sheep, goats, dogs, cats, horses, or man, particularly
CC mastitis in cows or breast cancers in humans. They can also be used for
CC preventing or treating a stress-induced disease. The present sequence
CC represents the binding domain of a previously published S. aureus
CC fibronectin binding protein A (FnBA) sequence. The Fnb binding domain
CC gene sequence FNBA9, cloned for use in this invention has 97.8 percent
CC identity when compared to the previously published FnBA and FnBB gene
CC sequences
CC
XX
XX Sequence 134 AA;
SQ
Query Match 100.0%; Score 54; DB 2; Length 134;
Best Local Similarity 100.0%; Pred. No. 0.11; 0; Indels 0; Gaps 0;
Matches 10; Conservative 0; Mismatches 0;
QY 1 EEDTNKDKPS 10
DB 86 EEDTNKDKPS 95

```

RESULT 6
AAW31556
ID AAW31556 standard; protein; 139 AA.
XX
AC AAW31556;
XX
XX 27-AUG-2003 (revised)
DT 25-MAR-2003 (revised)
DT 21-MAY-1998 (first entry)
XX
XX Fibronection-binding MSCRAMM derivative PQD.
DE
XX
XX Fibronection; PQD; collagen binding protein; sepsis; infection;
KM microbial surface component recognising adhesive matrix molecule; MSCRAMM;
KM adhesin; vaccine; immunisation; diagnosis; therapy; mastitis.
XX
XX Staphylococcus aureus.
OS
XX
XX Key Location/Qualifiers
FT Peptide 1..12
FT /note= "vector PQE30-derived peptide"
XX
XX WO9743314-A2.
XX
XX 20-NOV-1997.
PD
XX
XX 14-MAY-1997; 97WO-US008210.
PF
XX
XX 16-MAY-1996; 96US-0017678P.
PN
XX

```
XX (TEXTA ) UNIV TEXAS A & M SYSTEM.
PA (UABR-) UAB RES FOUND.
XX
PI Hoeoek M, Patti JM, House-Pompeo K, Sthanam N, Symersky J;
XX WPI; 1998-008801/01.
DR
XX Antibody that interacts with collagen binding domain of Staphylococcal
PT cna gene product - useful to prevent bacterial sepsis in animal infected
XX with Staphylococcus aureus.
XX
PS Disclosure; Page 91; 143pp; English.
XX
XX This protein comprises Staphylococcus aureus fibronectin-binding
CC microbial surface component recognizing adhesive matrix molecule (MSCRAMM)
CC derivative pOD, plus a vector-derived N-terminal peptide. The invention
CC relates to claimed nucleic acid sequences (see AAU93436-38) encoding S.
CC aureus collagen binding protein (CBP) epitopes M17, M31 and M55 (see
CC AAU31552-54) that confer protection against S. aureus infection. CBP
CC protein and antigenic epitopes are contemplated for use in the treatment
CC of pathological infections, especially to prevent bacterial adhesion to
CC collagen. The epitopes are also contemplated for use in the preparation to
CC of vaccines and as carrier proteins in vaccine formulations, as well as
CC in the formulation of compositions for the prevention of S. aureus
CC infection. pCF33 and pOD (see AAU31556) were used to raise anti-MSCRAMM
CC polyclonal antibodies used in passive immunisation against bovine
CC mastitis. (Updated on 25-MAR-2003 to correct PI field.) (Updated on 27-
CC AUG-2003 to correct OS field.)
XX
SQ Sequence 139 AA;
XX
XX Query Match 100.0%; Score 54; DB 2; Length 139;
XX Best Local Similarity 100.0%; Pred. No. 0.11;
XX Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1 EEDTNKD KPS 10
XX |||||
Db 100 EEDTNKD KPS 109
XX
RESULT 7
AAP82115
ID AAP82115 standard; protein; 1018 AA.
XX
AC AAP82115;
XX
XX 25-MAR-2003 (revised)
DT 05-JAN-1990 (first entry)
XX
XX Fibronectin binding protein.
DE
XX Fibronectin binding protein; S.aureus; immunisation; mastitis; ruminants;
KM wound infection; diagnosis.
XX
XX Staphylococcus aureus.
OS
XX EP294349-A.
XX
XX 07-DEC-1988.
PD
XX
XX 30-MAY-1988; 88EP-00850188.
PF
XX 01-JUN-1987; 87SE-00002272.
PR
XX (ALFA ) ALFA LAVAL AGRIC INT AB.
PA
XX
XX Lindberg MK, Signas LC, Wadstrom TW, Froman G;
PI WPI; 1988-347978/49.
DR P-PSDB; AAP82115.
XX
XX Hybrid DNA encoding Staphylococcus aureus fibronectin binding protein -
```

```
PT useful for immunisation and topical application to prevent staphylococcal
PT infections.
XX
XX Disclosure; Fig. 8A:1-8A:2; 23pp; English.
XX
XX The S.aureus fibronectin binding protein may be included in a hybrid
CC protein. The protein may be used to immunise ruminants against
CC staphylococcal mastitis, pref. when given at 0.5-5 microg/kg, using 3
CC doses at 1-3 week intervals; and for topical applicn. to prevent wound
CC infection, pref. using isotonic saline soln. of concn. 25-250 microg/mg.
CC The DNA encoding the binding protein and the hybrid protein may be
CC immobilised on a carrier and used to diagnose staphylococcal infections.
CC (Updated on 25-MAR-2003 to correct PA field.)
XX
SQ Sequence 1018 AA;
XX
XX Query Match 100.0%; Score 54; DB 1; Length 1018;
XX Best Local Similarity 100.0%; Pred. No. 0.85;
XX Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1 EEDTNKD KPS 10
XX |||||
Db 630 EEDTNKD KPS 839
XX
RESULT 8
AAU37245
ID AAU37245 standard; protein; 1018 AA.
XX
AC AAU37245;
XX
XX 14-FEB-2002 (first entry)
DT
XX
XX Staphylococcus aureus cellular proliferation protein #415.
DE
XX Antisense; prokaryotic cellular proliferation protein; antibiotic;
KM antibacterial; drug design.
XX
XX Staphylococcus aureus.
OS
XX WO200170955-A2.
XX
XX 27-SEP-2001.
PD
XX
XX 21-MAR-2001; 2001WO-US009180.
PF
XX
XX 21-MAR-2000; 2000US-0191078P.
PR 23-MAY-2000; 2000US-0206848P.
PR 26-MAY-2000; 2000US-0207727P.
PR 23-OCT-2000; 2000US-0242578P.
PR 27-NOV-2000; 2000US-0253625P.
PR 22-DEC-2000; 2000US-0257931P.
PR 16-FEB-2001; 2001US-0269308P.
XX
XX (ELIT-) ELITRA PHARM INC.
PA
XX
XX Haselbeck R, Ohlsen KL, Zykkind JW, Wall D, Trawick JD, Carr GJ;
PI Yamamoto RT, Xu HH;
XX
XX WPI; 2001-611495/70.
DR N-PSDB; AAS55104.
XX
XX New polynucleotides for the identification and development of
PT antibiotics, comprise sequences of antisense nucleic acids.
XX
XX Example 3; SEQ ID NO 12838; 51pp; English.
PS
XX
XX The invention relates to antisense inhibitors of genes essential to
CC prokaryotic cellular proliferation, their use in identifying the genes,
CC their use in the discovery of novel antibiotics, the essential genes
CC themselves and the encoded proteins. The prokaryotes used are Escherichia
CC coli, Staphylococcus aureus, Salmonella typhi, Klebsiella pneumoniae,
CC Pseudomonas aeruginosa and Enterococcus faecalis. The invention is also
```


CC infections or colonisation against *S. aureus* or *S. epidermidis*. The
CC preparation of antibodies is useful for the manufacture of a medicament
CC for treating or preventing staphylococcal infections or colonisation
CC against *S. aureus* or *S. epidermidis*. The antibody preparations may also
CC be used for diagnostic and imaging purposes. Other conditions that can be
CC treated include cancer, autoimmune diseases or infections caused by viral
CC (e.g. HIV, hepatitis A, B or C), fungal or protozoan pathogens. This
CC sequence represents a staphylococcal protein relating to the method for
CC identifying and producing pathogen specific antigens of the invention
XX
SQ Sequence 1018 AA;

Query Match 100.0%; Score 54; DB 6; Length 1018;
Best Local Similarity 100.0%; Pred. No. 0.85;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EEDTNKDKPS 10
Db 830 EEDTNKDKPS 839

RESULT 11
ABM72537
ID ABM72537 standard; protein; 1018 AA.

XX
AC ABM72537;

XX
DT 20-NOV-2003 (first entry)

XX
DE Staphylococcus aureus protein #1777.

XX
KM Antibacterial; vaccine; gene therapy; infection; sepsis; diagnosis;
KM enzymatic assay; antibiotic target.

XX
OS Staphylococcus aureus.

XX
PN W0200294868-A2.

XX
PD 28-NOV-2002.

XX
PF 27-MAR-2002; 2002WO-IB002637.

XX
PR 27-MAR-2001; 2001GB-00007661.

XX
PA (CHIR-) CHIRON SPA.

XX
PI Masignani V, Mora M, Scarcelli M;

XX
DR WPI; 2003-120786/11.

XX
DR N-PSDB; ACF74097.

XX
PT New Staphylococcus aureus protein, useful as a vaccine for treating or
PT preventing Staphylococcal infection, specifically an infection caused by
PT *S. aureus*, e.g. sepsis.

XX
PS Claim 1; SEQ ID NO 3554; 49pp; English.

XX
CC The invention relates to novel genes and encoded proteins from
CC Staphylococcus aureus. A composition comprising the *S. aureus* protein, a
CC nucleic acid encoding the protein, or an antibody to the protein, is
CC useful as a pharmaceutical, particularly as a vaccine for treating or
CC preventing infection due to Staphylococcus bacteria, specifically an
CC infection caused by *S. aureus*. The composition is particularly useful for
CC treating or preventing sepsis in a patient. The composition can also be
CC used for diagnostics. The protein is also used in an assay for enzymatic
CC studies and as a target for antibodies. This sequence represents one of
CC the novel *S. aureus* proteins of the invention
XX

SQ Sequence 1018 AA;

Query Match 100.0%; Score 54; DB 6; Length 1018;
Best Local Similarity 100.0%; Pred. No. 0.85;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EEDTNKDKPS 10
Db 830 EEDTNKDKPS 839

RESULT 12
AAW89806
ID AAW89806 standard; protein; 1027 AA.

XX
AC AAW89806;

XX
DT 16-MAR-1999 (first entry)

XX
DE Staphylococcus aureus protein SEQ ID #5254.

XX
KM Computer readable medium; vaccine; *S. aureus* infection; immunodetection;
KM cellulitis; eyelid infection; food poisoning; osteomyelitis; therapy;
KM skin infection; surgical wound infection; scalded skin syndrome;
KM toxic shock syndrome.

XX
OS Staphylococcus aureus.

XX
PN EP786519-A2.

XX
PD 30-JUL-1997.

XX
PF 07-JAN-1997; 97EP-00100117.

XX
PR 05-JAN-1996; 96US-0009861P.

XX
PA (HUMA-) HUMAN GENOME SCI INC.

XX
PI Kunsch CA, Choi GH, Barash SC, Dillon PJ, Fannon MR, Rosen CA;

XX
DR WPI; 1997-374922/35.

XX
PT Polynucleotide(s) and proteins derived from Staphylococcus aureus -
PT stored on computer readable medium and used in the production of anti-
PT *S. aureus* vaccines.

XX
PS Claim 23; Page 3263-3267; 3271pp; English.

XX
CC This sequence represents a Staphylococcus aureus protein sequence of the
CC invention. The DNA sequences encoding the *S. aureus* proteins are recorded
CC on a computer readable medium, preferably selected from a floppy or hard
CC disk, random access memory (RAM), read-only memory (ROM) or CD-ROM.
CC Homology searches using the *S. aureus* DNA sequences allows putative
CC functions to be assigned so that protein-encoding or regulatory regions
CC of commercial, therapeutic or industrial importance can be obtained.
CC Specifically, sequences which are likely to encode antigens have been
CC identified and these polypeptides can be used in a vaccine composition
CC against *S. aureus* infection. The polypeptides can also be used in a kit
CC for the immunodetection of *S. aureus* in a sample. *S. aureus* is implicated
CC in numerous human diseases, including cellulitis, eyelid infections, food
CC poisoning, osteomyelitis, skin and surgical wound infections, scalded
CC skin syndrome, toxic shock syndrome, etc. Organisms transformed with the
CC DNA sequences can be used for recombinant production of the polypeptides.
CC The new DNA sequences (and their fragments) are useful as primers or
CC probes for isolating homologues of any of the 5191 *S. aureus* DNA sequences
CC contained on the computer readable medium
XX

SQ Sequence 1027 AA;

Query Match 100.0%; Score 54; DB 2; Length 1027;
Best Local Similarity 100.0%; Pred. No. 0.86;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EEDTNKDKPS 10
Db 839 EEDTNKDKPS 848

RESULT 13
 AAR88749
 ID AAR88749 standard; protein; 77 AA.
 XX
 AC AAR88749;
 XX
 DT 24-SEP-1996 (first entry)
 XX
 DE S. aureus fibrinectin binding protein D2D3 polypeptide.
 XX
 KW Fibrinectin binding protein; D2D3; prevention; adhesion; bacteria;
 KW gram positive; extra-cellular matrix protein; in-dwelling device;
 KW catheter; wound; D2D3; oral pathogen; oral cavity; J2385; NCIMB 40532.
 XX
 OS Staphylococcus aureus.
 XX
 PN MO9604380-A1.
 PD 15-FEB-1996.
 XX
 PE 28-JUL-1995; 95WO-EP003039.
 XX
 PR 05-AUG-1994; 94GB-00015901.
 XX
 PA (SMIK) SMITHKLINE BEECHAM PLC.
 XX
 PI Critchley IA, Dodd I, Barnett P, Mosakowska DEI;
 XX
 DR WPI; 1996-129396/13.
 DR N-PSDB; AAT12582.
 XX
 PT Staphylococcus aureus fibrinectin binding protein D2D3 polypeptide -
 PT useful for combating infection at wound sites, surgical implants, etc.
 PT and as antiadherent agent in oral hygiene.
 XX
 PS Claim 5, Page 26; 38pp; English.
 XX
 CC The present sequence is the S. aureus fibrinectin binding protein
 CC polypeptide D2D3, which can be used to prevent adhesion of (e.g. gram
 CC positive) bacteria, to extra-cellular matrix proteins on in-dwelling
 CC devices, e.g. catheters or in wounds. D2D3 can also be used to prevent
 CC oral pathogens from binding to extra-cellular matrix proteins, in the
 CC oral cavity. D2D3 was found to be effective at inhibiting S. aureus 8325-
 CC 4, and 120 adhesion to fibrinectin coated PMMA coverslips, at a min.
 CC adhesion inhibitor concn. of 10 microg/ml. D2D3 was derived from the D2
 CC and D3 regions of the S. aureus J2385 (NCIMB 40532) fibrinectin binding
 CC protein
 CC
 SQ Sequence 77 AA;
 Query Match 94.4%; Score 51; DB 2; Length 77;
 Best Local Similarity 90.0%; Pred. No. 0.21; Mismatches 0; Gaps 0;
 Matches 9; Conservative 1; Indels 0; Gaps 0;
 QY 1 EEDTNKDKPS 10
 DB 48 EEDTNKDKPN 57
 RESULT 14
 AAR90939
 ID AAR90939 standard; peptide; 101 AA.
 XX
 AC AAR90939;
 XX
 DT 23-SEP-1996 (first entry)
 XX
 DE D3D4 polypeptide #3.
 XX
 KW Fibrinectin binding protein; Fbp; S. aureus J2385; monoclonal antibody;
 KW infection; surgical implant; antiadherent agent; hygiene; adhesion;
 KW extracellular matrix protein; oral pathogen; oral cavity.
 XX

OS Staphylococcus aureus.
 XX
 FH Key Location/Qualifiers
 FT Region 1..35
 FT Region /note= "D3 region fragment"
 FT Region 36..50
 FT Region /note= "D4 region"
 FT Region 51..101
 FT Region /note= "WRI region fragment"
 XX
 PN MO9604381-A1.
 PD 15-FEB-1996.
 XX
 PE 28-JUL-1995; 95WO-EP003040.
 XX
 PR 05-AUG-1994; 94GB-00015900.
 XX
 PA (SMIK) SMITHKLINE BEECHAM PLC.
 XX
 PI Critchley IA, Dodd I, Barnett P, Mcday DL;
 XX
 DR WPI; 1996-129397/13.
 XX
 PT Polypeptide(s) derived from Staphylococcus aureus fibrinectin binding
 PT protein - inhibit binding of bacteria to extracellular matrix proteins,
 PT for combating infection at the site of wounds and surgical implants, and
 PT in oral hygiene.
 XX
 PS Claim 6, Page 24; 35pp; English.
 XX
 CC AAR90937-R90942 represent D3D4 polypeptides. These sequences correspond
 CC to fragments of the Staphylococcus aureus fibrinectin binding protein
 CC (Fbp). This sequence corresponds to residues 81-181 of S. aureus J2385
 CC (Fbp). This sequence contains a portion of the wall region 1 (WRI). These
 CC sequences, and monoclonal antibodies against them can be used to combat
 CC infection at the site of wounds, surgical implants and other in-dwelling
 CC devices (such as catheters), and as antiadherent agents in oral hygiene.
 CC They can also be used in the manufacture of a medicament for the
 CC prevention of adhesion of bacteria to extracellular matrix proteins
 CC present on in-dwelling devices or in wounds, or of oral pathogens to
 CC similar proteins on surfaces in the oral cavity
 CC
 SQ Sequence 101 AA;
 Query Match 94.4%; Score 51; DB 2; Length 101;
 Best Local Similarity 90.0%; Pred. No. 0.28; Mismatches 0; Gaps 0;
 Matches 9; Conservative 1; Indels 0; Gaps 0;
 QY 1 EEDTNKDKPS 10
 DB 6 EEDTNKDKPN 15
 RESULT 15
 AAR90937
 ID AAR90937 standard; peptide; 113 AA.
 XX
 AC AAR90937;
 XX
 DT 23-SEP-1996 (first entry)
 XX
 DE D3D4 polypeptide #1.
 XX
 KW Fibrinectin binding protein; Fbp; S. aureus J2385; monoclonal antibody;
 KW infection; surgical implant; antiadherent agent; hygiene; adhesion;
 KW extracellular matrix protein; oral pathogen; oral cavity.
 XX
 OS Staphylococcus aureus.
 XX
 FH Key Location/Qualifiers
 FT Region 1..21
 FT Region /note= "D1 region fragment"

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OM protein - protein search, using bw model

Run on: October 22, 2005, 07:41:53 ; Search time 17.2989 Seconds
(without alignments)
43.153 Million cell updates/sec

Title: US-10-731-238-92
Perfect score: 54
Sequence: 1 EEDTKDKPS 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
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2: /cgn2_6/ptodata/1/1aa/5B.COMB.pep:*
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5: /cgn2_6/ptodata/1/1aa/6CTUS.COMB.pep:*
6: /cgn2_6/ptodata/1/1aa/Backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match length	ID	Description
1	54	100.0	10 4 US-09-010-317-92	Sequence 92, Appl
2	54	100.0	37 1 US-08-234-622A-4	Sequence 4, Appl
3	54	100.0	38 1 US-08-294-189-8	Sequence 8, Appl
4	54	100.0	38 1 US-08-729-767-5	Sequence 5, Appl
5	54	100.0	114 1 US-08-259-000-3	Sequence 3, Appl
6	54	100.0	139 3 US-08-856-253-8	Sequence 8, Appl
7	54	100.0	178 2 US-08-459-135A-12	Sequence 12, Appl
8	54	100.0	178 3 US-08-495-559-12	Sequence 12, Appl
9	54	100.0	1027 4 US-08-956-171E-5254	Sequence 5254, Ap
10	54	100.0	1027 4 US-08-781-986A-5254	Sequence 5254, Ap
11	51	94.4	130 2 US-08-459-135A-7	Sequence 7, Appl
12	51	94.4	130 2 US-08-459-135A-8	Sequence 8, Appl
13	51	94.4	130 3 US-08-495-559-7	Sequence 7, Appl
14	51	94.4	130 3 US-08-495-559-8	Sequence 8, Appl
15	51	94.4	174 2 US-08-459-135A-10	Sequence 10, Appl
16	51	94.4	174 2 US-08-459-135A-11	Sequence 10, Appl
17	51	94.4	174 3 US-08-495-559-13	Sequence 13, Appl
18	51	94.4	174 3 US-08-495-559-10	Sequence 13, Appl
19	51	94.4	176 3 US-08-495-559-6	Sequence 6, Appl
20	51	94.4	181 2 US-08-459-135A-6	Sequence 6, Appl
21	51	94.4	559 4 US-08-956-171E-5251	Sequence 5251, Ap
22	51	94.4	559 4 US-08-781-986A-5251	Sequence 5251, Ap
23	44	81.5	10 4 US-09-010-317-2	Sequence 2, Appl
24	44	81.5	10 4 US-09-010-317-93	Sequence 93, Appl
25	44	81.5	12 4 US-09-010-317-62	Sequence 62, Appl
26	44	81.5	38 1 US-08-234-622A-3	Sequence 3, Appl
27	44	81.5	38 1 US-08-729-767-4	Sequence 4, Appl

28	44	81.5	38 4 US-09-010-317-7	Sequence 7, Appl
29	44	81.5	38 4 US-09-010-317-8	Sequence 8, Appl
30	44	81.5	38 4 US-09-010-317-45	Sequence 45, Appl
31	44	81.5	38 4 US-09-010-317-49	Sequence 49, Appl
32	43	79.6	10 4 US-09-010-317-91	Sequence 91, Appl
33	43	79.6	10 4 US-09-010-317-67	Sequence 67, Appl
34	40	74.1	14 4 US-09-010-317-105	Sequence 105, Ap
35	40	74.1	38 1 US-08-234-622A-2	Sequence 2, Appl
36	40	74.1	38 1 US-08-729-767-3	Sequence 3, Appl
37	40	74.1	38 4 US-09-010-317-5	Sequence 5, Appl
38	40	74.1	38 4 US-09-010-317-6	Sequence 6, Appl
39	40	74.1	38 4 US-09-010-317-35	Sequence 35, Appl
40	40	74.1	38 4 US-09-010-317-43	Sequence 43, Appl
41	40	74.1	39 4 US-09-010-317-57	Sequence 57, Appl
42	40	74.1	39 4 US-09-010-317-56	Sequence 56, Appl
43	39	72.2	38 4 US-09-010-317-46	Sequence 46, Appl
44	38	70.4	38 4 US-09-010-317-40	Sequence 40, Appl
45	38	70.4	38 4 US-09-010-317-41	Sequence 41, Appl

ALIGNMENTS

RESULT 1
US-09-010-317-92
; Sequence 92, Application US/09010317
; Patent No. 6685943
; GENERAL INFORMATION:
; APPLICANT: Hook, Magnus
; APPLICANT: Patil, Joseph M.
; APPLICANT: House-Pompeo, Karen L.
; APPLICANT: Speziale, Pietro
; APPLICANT: Joh, Danny
; APPLICANT: McGavin, Martin J.
; TITLE OF INVENTION: FIBROBLAST BINDING PROTEIN COMPOSITIONS
; TITLE OF INVENTION: AND METHODS OF USE
; NUMBER OF SEQUENCES: 105
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: TX
; COUNTRY: USA
; ZIP: 77210-4433
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/010.317
; FILING DATE:
; CLASSIFICATION:
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: US 60/036,139
; FILING DATE: 21-JAN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Hbliler, David W.
; REGISTRATION NUMBER: 41,071
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 512-418-3000
; TELEFAX: 512-474-7577
; INFORMATION FOR SEQ ID NO: 92:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; US-09-010-317-92
Query Match 100.0%; Score 54; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0013;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EEDTNKDKPS 10
Db 1 EEDTNKDKPS 10

RESULT 2

US-08-234-622A-4
; Sequence 4, Application US/08234622A
; Patent No. 5440014
; GENERAL INFORMATION:
; APPLICANT: HOOK, Magnus
; APPLICANT: MCGAVIN, Martin
; APPLICANT: RAUCCI, Giuseppe
; TITLE OF INVENTION: A FIBRONECTIN BINDING PEPTIDE
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Doane, Swecker & Mathis
; STREET: P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/234,622A
; FILING DATE: 28-APR-1994
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: SE 9002617-0
; FILING DATE: 10-AUG-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/SE91/00534
; FILING DATE: 09-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Meuth, Donna M
; REGISTRATION NUMBER: 36,607
; REFERENCE/DOCKET NUMBER: 012885-044
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 37 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-234-622A-4

Query Match 100.0%; Score 54; DB 1; Length 37;
Best Local Similarity 100.0%; Pred. No. 0.0052;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EEDTNKDKPS 10
Db 9 EEDTNKDKPS 18

RESULT 3

US-08-294-189-8
; Sequence 8, Application US/08294189
; Patent No. 5707822
; GENERAL INFORMATION:
; APPLICANT: Fischetti, Vincent A.
; APPLICANT: Rakonjac, Jasna
; APPLICANT: Robbins, John
; TITLE OF INVENTION: GENE SERUM OPACITY FACTOR

NUMBER OF SEQUENCES: 23

CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack Avenue
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
ZIP: 07601

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/294,189
FILING DATE: 22-AUG-1994
CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-118
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 487-5800
TELEFAX: 201 343-1684
TELEX: 133521

INFORMATION FOR SEQ ID NO: 8:

SEQUENCE CHARACTERISTICS:

LENGTH: 38 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: unknown

MOLECULE TYPE: peptide

ORGANISM: Streptococcus pyogenes

STRAIN: D734

INDIVIDUAL ISOLATE: 22

IMMEDIATE SOURCE:

CLONE: 8A03a

US-08-294-189-8
Qy 1 EEDTNKDKPS 10
Db 3 EEDTNKDKPS 12

Query Match 100.0%; Score 54; DB 1; Length 38;
Best Local Similarity 100.0%; Pred. No. 0.0053;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 4

US-08-729-767-5
; Sequence 5, Application US/08729767
; Patent No. 5770702
; GENERAL INFORMATION:
; APPLICANT: HOOK, Magnus
; APPLICANT: LINDBERG, Martin Kjell
; APPLICANT: SIGNAS, Lars Christer
; APPLICANT: WADSTROM, Torkel Mikael
; APPLICANT: FROMAN, Gunnar
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN AS WELL AS
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Doane, Swecker & Mathis, L.L.P.
; STREET: P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/729,767
FILING DATE: 07-OCT-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/259,000
FILING DATE: 13-JUN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/007,817
FILING DATE: 22-JAN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/201,028
FILING DATE: 01-JUN-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: SE 8702272-9
FILING DATE: 01-JUN-1987
ATTORNEY/AGENT INFORMATION:
NAME: McGowan, Malcolm K.
REGISTRATION NUMBER: 39,300
REFERENCE/DOCKET NUMBER: 012889-036
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-729-767-5

Query Match 100.0%; Score 54; DB 1; Length 38;
Best Local Similarity 100.0%; Pred. No. 0.0053;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EEDTNKD KPS 10
|||||||
Db 10 EEDTNKD KPS 19

RESULT 5
US-08-259-000-3
Sequence 3, Application US/08259000
Patent No. 5571514
GENERAL INFORMATION:
APPLICANT: HOOK, Magnus
APPLICANT: LINDERBERG, Martin Kjell
APPLICANT: SIGNAS, Lars Christer
APPLICANT: WADSTROM, Torkel Mikael
APPLICANT: FROMAN, Gunnar
TITLE OF INVENTION: FIBROBLAST BINDING PROTEIN AS WELL AS
NUMBER OF SEQUENCES: 4
TITLE OF INVENTION: ITS PREPARATION
CORRESPONDENCE ADDRESS:
ADDRESSEE: Burns, Doane, Swecker & Mathis
STREET: P.O. Box 1404
CITY: Alexandria
STATE: Virginia
COUNTRY: United States
ZIP: 22113-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/259,000
FILING DATE: 13-JUN-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: SE 8702272-9

FILING DATE: 01-JUN-1987
ATTORNEY/AGENT INFORMATION:
NAME: Meuth, Donna M
REGISTRATION NUMBER: 36,607
REFERENCE/DOCKET NUMBER: 012885-062
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 114 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-259-000-3

Query Match 100.0%; Score 54; DB 1; Length 114;
Best Local Similarity 100.0%; Pred. No. 0.017;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EEDTNKD KPS 10
|||||||
Db 86 EEDTNKD KPS 95

RESULT 6
US-08-856-253-8
Sequence 8, Application US/08856253
Patent No. 6288214
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
APPLICANT: Patti, Joseph M.
APPLICANT: House-Pompeo, Karen
APPLICANT: Schanam, Narayana
APPLICANT: Symersky, Jindrich
TITLE OF INVENTION: AND METHODS OF USE
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: Texas
COUNTRY: U.S.
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/856,253
FILING DATE: Concurrently Herewith
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/017,678
FILING DATE: 16-MAY-1996
ATTORNEY/AGENT INFORMATION:
NAME: Kitchell, Barbara S.
REGISTRATION NUMBER: 33,928
REFERENCE/DOCKET NUMBER: TANK-193
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
TELEFAX: (512) 474-7577
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 139 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-08-856-253-8

Query Match 100.0%; Score 54; DB 3; Length 139;
 Best Local Similarity 100.0%; Pred. No. 0.021;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EEDTNKDKPS 10
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 Db 100 EEDTNKDKPS 109

RESULT 7

US-08-459-135A-12
 ; Sequence 12, Application US/08459135A
 ; Patent No. 5955078
 ; GENERAL INFORMATION:
 ; APPLICANT: BURHAM, Martin Karl Russel
 ; APPLICANT: CRITCHLEY, Ian Alfred
 ; APPLICANT: KNOWLES, David Justin Charles
 ; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN: MONOCLONAL ANTIBODY AND THEIR US
 ; NUMBER OF SEQUENCES: 15
 ; CORRESPONDENCE ADDRESSES:
 ; ADDRESSEE: SmithKline Beecham Corporation
 ; STREET: 709 Swedeland Road
 ; CITY: King of Prussia
 ; STATE: PA
 ; COUNTRY: U.S.A.
 ; ZIP: 19406-0939
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: DOS
 ; SOFTWARE: Fastseq, Version 2.0
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/459,135A
 ; FILING DATE: 02-JUN-1995
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: PCT/GB/94/00215
 ; FILING DATE: 04-Feb-1994
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Gimmil, Edward R
 ; REGISTRATION NUMBER: 38,891
 ; REFERENCE/DOCKET NUMBER: P30591C2
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 610-270-4478
 ; TELEFAX: 610-270-5090
 ; TELEX:
 ; INFORMATION FOR SEQ ID NO: 12:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 178 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-08-459-135A-12

Query Match 100.0%; Score 54; DB 2; Length 178;
 Best Local Similarity 100.0%; Pred. No. 0.028;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EEDTNKDKPS 10
 |||||
 Db 86 EEDTNKDKPS 95

RESULT 8

US-08-495-559-12
 ; Sequence 12, Application US/08495559A
 ; Patent No. 6054572
 ; GENERAL INFORMATION:
 ; APPLICANT: BURHAM, Martin Karl Russel
 ; APPLICANT: CHOPRA, Ian

; APPLICANT: CRITCHLEY, Ian Alfred
 ; APPLICANT: KNOWLES, David Justin Charles
 ; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN: MONOCLONAL
 ; TITLE OF INVENTION: ANTIBODY AND THEIR USE IN PREVENTING BACTERIAL ADHESION
 ; FILE REFERENCE: P30591
 ; CURRENT APPLICATION NUMBER: US/08/495,559A
 ; CURRENT FILING DATE: 1995-08-03
 ; EARLIER APPLICATION NUMBER: GB 9302289.5
 ; EARLIER FILING DATE: 1993-02-05
 ; EARLIER APPLICATION NUMBER: GB 9321592.9
 ; EARLIER FILING DATE: 1993-10-20
 ; NUMBER OF SEQ ID NOS: 13
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 12
 ; LENGTH: 178
 ; TYPE: PRT
 ; ORGANISM: Staphylococcus aureus
 ; US-08-495-559-12

Query Match 100.0%; Score 54; DB 3; Length 178;
 Best Local Similarity 100.0%; Pred. No. 0.028;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EEDTNKDKPS 10
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 Db 86 EEDTNKDKPS 95

RESULT 9

US-08-956-171E-5254
 ; Sequence 5254, Application US/08956171E
 ; Patent No. 6593114
 ; GENERAL INFORMATION:
 ; APPLICANT: Charles Kunsch
 ; Gil H. Choi
 ; Patrick S. Dillon
 ; Craig A. Rosen
 ; Steven C. Barash
 ; Michael R. Fannon
 ; TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
 ; NUMBER OF SEQUENCES: 5256
 ; CORRESPONDENCE ADDRESSES:
 ; ADDRESSEE: Human Genome Sciences, Inc.
 ; STREET: 9410 Key West Avenue
 ; CITY: Rockville
 ; STATE: Maryland
 ; COUNTRY: USA
 ; ZIP: 20850
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette, 3.50 inch, 1.4mb storage
 ; COMPUTER: HP Vectra 486/33
 ; OPERATING SYSTEM: MSDOS version 6.2
 ; SOFTWARE: ASCII Text
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/956,171E
 ; FILING DATE: 20-Oct-1997
 ; CLASSIFICATION: <Unknown>
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 60/009,861
 ; FILING DATE: January 5, 1996
 ; APPLICATION NUMBER: 08/781,986
 ; FILING DATE: January 3, 1997
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Mark J. Hyman
 ; REGISTRATION NUMBER: 46,789
 ; REFERENCE/DOCKET NUMBER: PB248P1
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (240) 314-1224
 ; TELEFAX: (301) 309-8439
 ; INFORMATION FOR SEQ ID NO: 5254:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 1027 amino acids
 ; TYPE: amino acid

STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 5254:
US-08-956-171E-5254

Query Match 100.0%; Score 54; DB 4; Length 1027;
Best Local Similarity 100.0%; Pred. No. 0.18;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EEDTKDKPS 10
Db 839 EEDTKDKPS 848

RESULT 10
US-08-781-986A-5254
Sequence 5254, Application US/08781986A
Patent No. 6737248
GENERAL INFORMATION:
APPLICANT: Charles Kunsch
TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
NUMBER OF SEQUENCES: 5255
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COUNTRY: USA
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/781,986A
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Benson, Bob
REGISTRATION NUMBER: 30,446
REFERENCE/DOCKET NUMBER: PB248PP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 5254:
SEQUENCE CHARACTERISTICS:
LENGTH: 1027 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-781-986A-5254

Query Match 100.0%; Score 54; DB 4; Length 1027;
Best Local Similarity 100.0%; Pred. No. 0.18;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EEDTKDKPS 10
Db 839 EEDTKDKPS 848

RESULT 11
US-08-459-135A-7
Sequence 7, Application US/08459135A
Patent No. 5955078
GENERAL INFORMATION:
APPLICANT: BURNHAM, Martin Karl Russel

APPLICANT: CHOPRA, Ian
APPLICANT: CRITCHLEY, Ian Alfred
APPLICANT: KNOWLES, David Justin Charles
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN: MONOCLONAL ANTIBODY AND THEIR US
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
STATE: PA
COUNTRY: U.S.A.
ZIP: 19406-0939
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: Fastseq, Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/459,135A
FILING DATE: 02-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB/94/00215
FILING DATE: 04-Feb-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Gimmil, Edward R
REGISTRATION NUMBER: 38,891
REFERENCE/DOCKET NUMBER: P30591C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-4478
TELEFAX: 610-270-5090
TELEX:
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 130 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-459-135A-7

Query Match 94.4%; Score 51; DB 2; Length 130;
Best Local Similarity 90.0%; Pred. No. 0.069;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EEDTKDKPS 10
Db 86 EEDTKDKPN 95

RESULT 12
US-08-459-135A-8
Sequence 8, Application US/08459135A
Patent No. 5955078
GENERAL INFORMATION:
APPLICANT: BURNHAM, Martin Karl Russel
APPLICANT: CHOPRA, Ian
APPLICANT: CRITCHLEY, Ian Alfred
APPLICANT: KNOWLES, David Justin Charles
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN: MONOCLONAL ANTIBODY AND THEIR US
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
STATE: PA
COUNTRY: U.S.A.
ZIP: 19406-0939
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: Fastseq, Version 2.0

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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/459,135A
; FILING DATE: 02-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB/94/00215
; FILING DATE: 04-Feb-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Gimmi, Edward R
; REGISTRATION NUMBER: 38,891
; REFERENCE/DOCKET NUMBER: P30591C2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-270-4478
; TELEFAX: 610-270-5090
;
; TELEX:
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 130 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
;
US-08-459-135A-8

Query Match          94.4%; Score 51; DB 3; Length 130;
Best Local Similarity 90.0%; Pred. No. 0.069;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 EEDTNKDKPS 10
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      :
Db      86 EEDTNKDKPN 95

RESULT 13
US-08-495-559-7
; Sequence 7, Application US/08495559A
; Patent No. 6054572
; GENERAL INFORMATION:
; APPLICANT: BURHAM, Martin Karl Russel
; APPLICANT: CHOPRA, Ian
; APPLICANT: CRITCHLEY, Ian Alfred
; APPLICANT: KNOWLES, David Justin Charles
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN: MONOCLONAL
; FILE REFERENCE: P30591
; CURRENT APPLICATION NUMBER: US/08/495,559A
; CURRENT FILING DATE: 1995-08-03
; EARLIER APPLICATION NUMBER: GB 9302289.5
; EARLIER FILING DATE: 1993-02-05
; EARLIER APPLICATION NUMBER: GB 9321592.9
; EARLIER FILING DATE: 1993-10-20
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 7
; LENGTH: 130
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
;
US-08-495-559-7

Query Match          94.4%; Score 51; DB 3; Length 130;
Best Local Similarity 90.0%; Pred. No. 0.069;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 EEDTNKDKPS 10
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Db      86 EEDTNKDKPN 95

RESULT 14
US-08-495-559-8
; Sequence 8, Application US/08495559A
; Patent No. 6054572
; GENERAL INFORMATION:
; APPLICANT: BURHAM, Martin Karl Russel
; APPLICANT: CHOPRA, Ian
; APPLICANT: CRITCHLEY, Ian Alfred
; APPLICANT: KNOWLES, David Justin Charles
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN: MONOCLONAL
; FILE REFERENCE: P30591
; CURRENT APPLICATION NUMBER: US/08/495,559A
; CURRENT FILING DATE: 1995-08-03
; EARLIER APPLICATION NUMBER: GB 9302289.5
; EARLIER FILING DATE: 1993-02-05
; EARLIER APPLICATION NUMBER: GB 9321592.9
; EARLIER FILING DATE: 1993-10-20
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 8
; LENGTH: 130
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
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US-08-495-559-8

Query Match          94.4%; Score 51; DB 3; Length 130;
Best Local Similarity 90.0%; Pred. No. 0.069;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 EEDTNKDKPS 10
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      :
Db      86 EEDTNKDKPN 95

RESULT 15
US-08-459-135A-10
; Sequence 10, Application US/08459135A
; Patent No. 5955078
; GENERAL INFORMATION:
; APPLICANT: BURHAM, Martin Karl Russel
; APPLICANT: CHOPRA, Ian
; APPLICANT: CRITCHLEY, Ian Alfred
; APPLICANT: KNOWLES, David Justin Charles
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN: MONOCLONAL ANTIBODY AND THEIR US
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corporation
; STREET: 709 Swedeland Road
; CITY: King of Prussia
; STATE: PA
; COUNTRY: U.S.A.
; ZIP: 19406-0939
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq, Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/459,135A
; FILING DATE: 02-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB/94/00215
; FILING DATE: 04-Feb-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Gimmi, Edward R
; REGISTRATION NUMBER: 38,891
; REFERENCE/DOCKET NUMBER: P30591C2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-270-4478
; TELEFAX: 610-270-5090
;
; TELEX:
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 174 amino acids
; TYPE: amino acid
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 22, 2005, 12:39:57 ; Search time 56.1494 Seconds
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74.354 Million cell updates/sec

Title: US-10-731-238-92
Perfect score: 54
Sequence: 1 EEDTNKDKPS 10

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Gapop 10.0 , Gapext 0.5

Searched: 1862951 seqs, 417491010 residues
Total number of hits satisfying chosen parameters: 1862951

Minimum DB seq length: 0
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Listing first 45 summaries

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19: /cgn2_6/ptodata/2/pubpaa/US11A_PUBCOMB.pep:*
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21: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*
22: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	54	100.0	10	18	US-10-731-238-92
2	54	100.0	37	20	US-11-066-697-1134
3	54	100.0	139	9	US-09-813-820-8
4	54	100.0	1018	9	US-09-815-242-5797
5	54	100.0	1018	9	US-09-815-242-12838
6	54	100.0	1018	17	US-10-470-048B-68
7	54	100.0	1027	8	US-08-781-986A-5254
8	54	100.0	1027	15	US-10-328-624-5254
9	51	94.4	388	8	US-08-901-062-1
10	51	94.4	559	8	US-08-781-986A-5251
11	51	94.4	559	15	US-10-329-624-5251

12	51	94.4	940	17	US-10-470-048B-424	Sequence 424, App
13	51	94.4	948	17	US-10-470-048B-69	Sequence 69, Appl
14	51	94.4	961	15	US-10-282-122A-43778	Sequence 43778, A
15	51	94.4	978	9	US-09-815-242-5456	Sequence 5456, Ap
16	51	94.4	1001	9	US-09-815-242-12686	Sequence 12686, A
17	51	94.4	1038	15	US-10-282-122A-43827	Sequence 43827, A
18	44	81.5	10	18	US-10-731-238-92	Sequence 2, Appl1
19	44	81.5	10	18	US-10-731-238-93	Sequence 93, Appl
20	44	81.5	12	18	US-10-731-238-62	Sequence 62, Appl
21	44	81.5	30	14	US-10-287-821-1	Sequence 1, Appl1
22	44	81.5	31	14	US-10-287-821-2	Sequence 2, Appl1
23	44	81.5	38	18	US-10-731-238-7	Sequence 8, Appl1
24	44	81.5	38	18	US-10-731-238-8	Sequence 8, Appl1
25	44	81.5	38	18	US-10-731-238-45	Sequence 45, Appl
26	44	81.5	38	18	US-10-731-238-49	Sequence 49, Appl
27	44	81.5	767	9	US-09-815-242-5899	Sequence 5899, Ap
28	44	81.5	767	9	US-09-815-242-13140	Sequence 13140, A
29	43	79.6	10	18	US-10-731-238-67	Sequence 1, Appl
30	40	74.1	10	18	US-10-731-238-67	Sequence 67, Appl
31	40	74.1	14	18	US-10-731-238-105	Sequence 105, App
32	40	74.1	18	18	US-10-731-238-15	Sequence 5, Appl1
33	40	74.1	38	18	US-10-731-238-6	Sequence 6, Appl1
34	40	74.1	38	18	US-10-731-238-35	Sequence 35, Appl
35	40	74.1	38	18	US-10-731-238-43	Sequence 43, Appl
36	40	74.1	39	18	US-10-731-238-56	Sequence 56, Appl
37	40	74.1	39	18	US-10-731-238-57	Sequence 57, Appl
38	39	72.2	38	18	US-10-731-238-46	Sequence 46, Appl
39	39	72.2	928	15	US-09-801-368-282	Sequence 282, App
40	39	72.2	928	15	US-10-369-493-1750	Sequence 1750, Ap
41	38	70.4	38	18	US-10-731-238-40	Sequence 40, Appl
42	38	70.4	38	18	US-10-731-238-41	Sequence 41, Appl
43	38	70.4	38	18	US-10-731-238-47	Sequence 47, Appl
44	37	68.5	10	18	US-10-731-238-85	Sequence 85, Appl
45	37	68.5	36	18	US-10-731-238-58	Sequence 58, Appl

ALIGNMENTS

RESULT 1
US-10-731-238-92
; Sequence 92, Application US/10731238
; Publication No. US20050123552A1
; GENERAL INFORMATION:
; APPLICANT: Hook, Magnus
; Patti, Joseph M.
; House-Pompeo, Karen L.
; Speziale, Pietro
; John, Danny
; McGavin, Martin J.
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
; AND METHODS OF USE
; NUMBER OF SEQUENCE: 105
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: TX
; COUNTRY: USA
; ZIP: 77210-4433
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Releasee #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/731,238
; FILING DATE: 10-Dec-2003
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/010,317
; FILING DATE: 21-Jan-1998
; APPLICATION NUMBER: US 60/036,139


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; FILING DATE: 21-JAN-1997
; ATTORNEY/AGENT INFORMATION:
;   NAME: Hibler, David W.
;   REGISTRATION NUMBER: 41,071
;   REFERENCE/DOCKET NUMBER: TAMK:189
; TELECOMMUNICATION INFORMATION:
;   TELEPHONE: 512-418-3000
;   TELEFAX: 512-474-7577
; INFORMATION FOR SEQ ID NO: 92:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH: 10 amino acids
;     TYPE: amino acid
;     STRANDEDNESS: <Unknown>
;     TOPOLOGY: linear
;
; SEQUENCE DESCRIPTION: SEQ ID NO: 92:
US-10-731-238-92

Query Match      100.0%; Score 54; DB 18; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0085;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 EEDTNKD KPS 10
Db      1 EEDTNKD KPS 10

RESULT 2
US-11-066-697-1134
; Sequence 1134, Application US/11066697
; Publication No. US20050187159A1
; GENERAL INFORMATION:
;   APPLICANT: Ezrin, Alan M.
;   APPLICANT: Bidon, Dominique P.
;   APPLICANT: Milner, Peter G.
;   APPLICANT: Holmes, Darren L.
;   APPLICANT: Thibaudau, Karen
; TITLE OF INVENTION: PROTECTION OF ENDOGENOUS THERAPEUTIC PEPTIDES FROM
; TITLE OF INVENTION: PEPTIDASE ACTIVITY THROUGH CONJUGATION TO BLOOD
; FILE REFERENCE: 500862002301
; CURRENT APPLICATION NUMBER: US/11/066,697
; CURRENT FILING DATE: 2005-02-25
; PRIOR APPLICATION NUMBER: 09/657,276
; PRIOR FILING DATE: 2000-09-07
; PRIOR APPLICATION NUMBER: 60/153,406
; PRIOR FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: 60/159,783
; PRIOR FILING DATE: 1999-10-15
; NUMBER OF SEQ ID NOS: 1617
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1134
; LENGTH: 37
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
;
; US-11-066-697-1134

Query Match      100.0%; Score 54; DB 20; Length 37;
Best Local Similarity 100.0%; Pred. No. 0.034;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 EEDTNKD KPS 10
Db      9 EEDTNKD KPS 18

RESULT 3
US-09-813-820-8
; Sequence 8, Application US/09813820
; Patent No. US20020102262A1
; GENERAL INFORMATION:
```

```

; APPLICANT: Hook, Magnus
;   Patli, Joseph M.
;   House-Pompeo, Karen
;   Shanam, Narayana
;   Symerky, Jindrich
; TITLE OF INVENTION: COLLAGEN BINDING PROTEIN COMPOSITIONS
; AND METHODS OF USE
;
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: U.S.
; ZIP: 77210
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/09/813,820
;   FILING DATE: 22-Mar-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: 08/856,253
;   FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
;   NAME: Kitchell, Barbara S.
;   REGISTRATION NUMBER: 33,928
;   REFERENCE/DOCKET NUMBER: TAMK:193
; TELECOMMUNICATION INFORMATION:
;   TELEPHONE: (512) 418-3000
;   TELEFAX: (512) 474-7577
; INFORMATION FOR SEQ ID NO: 8:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH: 139 amino acids
;     TYPE: amino acid
;     STRANDEDNESS: <Unknown>
;     TOPOLOGY: linear
;
; SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-09-813-820-8

Query Match      100.0%; Score 54; DB 9; Length 139;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 EEDTNKD KPS 10
Db      100 EEDTNKD KPS 109

RESULT 4
US-09-815-242-5797
; Sequence 5797, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
;   APPLICANT: Haselbeck, Robert
;   APPLICANT: Ohlsen, Karl L.
;   APPLICANT: Zyskind, Judith W.
;   APPLICANT: Wall, Daniel
;   APPLICANT: Trawick, John D.
;   APPLICANT: Carr, Grant J.
;   APPLICANT: Yamamoto, Robert T.
;   APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; TITLE OF INVENTION: Prokaryotes
; FILE REFERENCE: ELITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
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PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 5797
LENGTH: 1018
TYPE: PRT
ORGANISM: Staphylococcus aureus
US-09-815-242-5797

Query Match 100.0%; Score 54; DB 9; Length 1018;
Best Local Similarity 100.0%; Pred. No. 1.1;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EEDTNKD KPS 10
Db 830 EEDTNKD KPS 839

RESULT 5
US-09-815-242-12838
Sequence 12838, Application US/09815242
Patent No. US20020061569A1
GENERAL INFORMATION:
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Karl L.
APPLICANT: Zyskind, Judith W.
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John D.
APPLICANT: Carr, Grant J.
APPLICANT: Yamamoto, Robert T.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in
FILE REFERENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 12838
LENGTH: 1018
TYPE: PRT
ORGANISM: Staphylococcus aureus
US-09-815-242-12838

Query Match 100.0%; Score 54; DB 9; Length 1018;
Best Local Similarity 100.0%; Pred. No. 1.1;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 EEDTNKD KPS 10

Db 830 EEDTNKD KPS 839

RESULT 6
US-10-470-048B-68
Sequence 68, Application US/10470048B
Publication No. US2005003744A1
GENERAL INFORMATION:
APPLICANT: MEINKE ET AL.
TITLE OF INVENTION: A METHOD FOR IDENTIFICATION, ISOLATION AND PRODUCTION OF
FILE REFERENCE: SOGN.035US
CURRENT APPLICATION NUMBER: US/10/470,048B
CURRENT FILING DATE: 2003-07-25
NUMBER OF SEQ ID NOS: 603
SOFTWARE: PatentIn version 3.1
SEQ ID NO 68
LENGTH: 1018
TYPE: PRT
ORGANISM: Staphylococcus aureus
US-10-470-048B-68

Query Match 100.0%; Score 54; DB 17; Length 1018;
Best Local Similarity 100.0%; Pred. No. 1.1;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EEDTNKD KPS 10
Db 830 EEDTNKD KPS 839

RESULT 7
US-08-781-986A-5254
Sequence 5254, Application US/08781986A
Publication No. US20030054436A1
GENERAL INFORMATION:
APPLICANT: Charles Kunsch
TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
NUMBER OF SEQUENCES: 5255
CORRESPONDENCE ADDRESS:
ADDRESS: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COUNTRY: USA
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/781,986A
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Benson, Bob
REGISTRATION NUMBER: 30,446
REFERENCE/DOCKET NUMBER: PB248BP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 5254:
SEQUENCE CHARACTERISTICS:
LENGTH: 1027 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein

US-08-781-986A-5254

Query Match 100.0%; Score 54; DB 8; Length 1027;
Best Local Similarity 100.0%; Pred. No. 1.1;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EEDTNKD KPS 10
|||||
DB 839 EEDTNKD KPS 848

RESULT 8
US-10-329-624-5254

; Sequence 5254, Application US/10329624
; Publication No. US20040043037A1

; GENERAL INFORMATION:

; APPLICANT: Charles Kunach

; Gil H. Choi

; Patrick S. Dillon

; Craig A. Rosen

; Steven C. Barash

; Michael R. Fannon

; TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences

; NUMBER OF SEQUENCES: 5256

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Human Genome Sciences, Inc.

; STREET: 9410 Key West Avenue

; CITY: Rockville

; STATE: Maryland

; COUNTRY: USA

; ZIP: 20850

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette, 3.50 inch, 1.4MB storage

; COMPUTER: HP Vectra 486/33

; OPERATING SYSTEM: MSDOS version 6.2

; SOFTWARE: ASCII Text

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/10/329,624

; FILING DATE: 27-Dec-2002

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/956,171

; FILING DATE: October 20, 1997

; APPLICATION NUMBER: 60/009,861

; FILING DATE: January 5, 1996

; APPLICATION NUMBER: 08/781,986

; FILING DATE: January 3, 1997

; ATTORNEY/AGENT INFORMATION:

; NAME: Mark J. Hyman

; REGISTRATION NUMBER: 46,789

; REFERENCE/DOCKET NUMBER: PB248P1D1

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (240) 314-1224

; TELEFAX: (301) 309-8439

; INFORMATION FOR SEQ ID NO: 5254:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 1027 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; SEQUENCE DESCRIPTION: SEQ ID NO: 5254:

; US-10-329-624-5254

Query Match 100.0%; Score 54; DB 15; Length 1027;
Best Local Similarity 100.0%; Pred. No. 1.1;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EEDTNKD KPS 10
|||||
DB 839 EEDTNKD KPS 848

RESULT 9

US-08-901-062-1

; Sequence 1, Application US/08901062
; Publication No. US20020025324A1

; GENERAL INFORMATION:

; APPLICANT: SEALS, JONATHAN R.

; TITLE OF INVENTION: RECOMBINANT BIVALENT BACTERIAL VACCINE

; TITLE OF INVENTION: FOR THE PREVENTION OF MASTITIS

; NUMBER OF SEQUENCES: 2

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: HALE AND DOR LLP

; STREET: 60 State Street

; CITY: Boston

; STATE: MA

; COUNTRY: United States Of America

; ZIP: 02109

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/901,062

; FILING DATE: 25-JUL-1997

; CLASSIFICATION: 424

; ATTORNEY/AGENT INFORMATION:

; NAME: Baker, Hollie L.

; REGISTRATION NUMBER: 31,321

; REFERENCE/DOCKET NUMBER: 106941.153

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (617) 526-6000

; TELEFAX: (617) 526-5000

; INFORMATION FOR SEQ ID NO: 1:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 388 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; HYPOTHETICAL: NO

; ANTI-SENSE: NO

; US-08-901-062-1

Query Match 94.4%; Score 51; DB 8; Length 388;
Best Local Similarity 90.0%; Pred. No. 1.3;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EEDTNKD KPS 10
|||||
DB 349 EEDTNKD KPS 358

RESULT 10
US-08-781-986A-5251

; Sequence 5251, Application US/08781986A
; Publication No. US20030054436A1

; GENERAL INFORMATION:

; APPLICANT: Charles Kunach

; TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences

; NUMBER OF SEQUENCES: 5255

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Human Genome Sciences, Inc.

; STREET: 9410 Key West Avenue

; CITY: Rockville

; STATE: Maryland

; COUNTRY: USA

; ZIP: 20850

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette, 3.50 inch, 1.4MB storage

; COMPUTER: HP Vectra 486/33

; OPERATING SYSTEM: MSDOS version 6.2

; SOFTWARE: ASCII Text

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/781,986A

;; FILING DATE:
;; CLASSIFICATION: 435
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER:
;; FILING DATE:
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Benson, Bob
;; REGISTRATION NUMBER: 30,446
;; REFERENCE/DOCKET NUMBER: PB248BP
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (301) 309-8504
;; TELEFAX: (301) 309-8512
;; INFORMATION FOR SEQ ID NO: 5251:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 559 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; US-08-781-986A-5251

Query Match 94.4%; Score 51; DB 8; Length 559;
Best Local Similarity 90.0%; Pred. No. 2;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EEDTKDKRPS 10
|||
Db 385 EEDTKDKRPN 394

RESULT 11
US-10-329-624-5251
; Sequence 5251, Application US/10329624
; Publication No. US20040043037A1
; GENERAL INFORMATION:
; APPLICANT: Charles Kunesh
; Gal H. Choi
; Patrick S. Dillon
; Craig A. Rosen
; Steven C. Barash
; Michael R. Fannon
; TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
; NUMBER OF SEQUENCES: 5256
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4MB storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/329,624
; FILING DATE: 27-Dec-2002
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/956,111
; FILING DATE: October 20, 1997
; APPLICATION NUMBER: 60/009,861
; FILING DATE: January 5, 1996
; APPLICATION NUMBER: 08/781,986
; FILING DATE: January 3, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Mark J. Hyman
; REGISTRATION/DOCKET NUMBER: 46,789
; REFERENCE/DOCKET NUMBER: PB248P1D1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (240) 314-1224
; TELEFAX: (301) 309-8439
; INFORMATION FOR SEQ ID NO: 5251:

;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 559 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; SEQUENCE DESCRIPTION: SEQ ID NO: 5251:
US-10-329-624-5251

Query Match 94.4%; Score 51; DB 15; Length 559;
Best Local Similarity 90.0%; Pred. No. 2;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EEDTKDKRPS 10
|||
Db 385 EEDTKDKRPN 394

RESULT 12
US-10-470-048B-424
; Sequence 424, Application US/10470048B
; Publication No. US2005003744A1
; GENERAL INFORMATION:
; APPLICANT: MEINKE ET AL.
; TITLE OF INVENTION: A METHOD FOR IDENTIFICATION, ISOLATION AND PRODUCTION OF
; FILE REFERENCE: SONN:035US
; CURRENT APPLICATION NUMBER: US/10/470,048B
; CURRENT FILING DATE: 2003-07-25
; NUMBER OF SEQ ID NOS: 603
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 424
; LENGTH: 940
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-10-470-048B-424

Query Match 94.4%; Score 51; DB 17; Length 940;
Best Local Similarity 90.0%; Pred. No. 3.4;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EEDTKDKRPS 10
|||
Db 766 EEDTKDKRPN 775

RESULT 13
US-10-470-048B-69
; Sequence 69, Application US/10470048B
; Publication No. US2005003744A1
; GENERAL INFORMATION:
; APPLICANT: MEINKE ET AL.
; TITLE OF INVENTION: A METHOD FOR IDENTIFICATION, ISOLATION AND PRODUCTION OF
; FILE REFERENCE: SONN:035US
; CURRENT APPLICATION NUMBER: US/10/470,048B
; CURRENT FILING DATE: 2003-07-25
; NUMBER OF SEQ ID NOS: 603
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 69
; LENGTH: 948
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-10-470-048B-69

Query Match 94.4%; Score 51; DB 17; Length 948;
Best Local Similarity 90.0%; Pred. No. 3.5;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EEDTKDKRPS 10
|||
Db 774 EEDTKDKRPN 783

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RESULT 14
US-10-282-122A-43778
; Sequence 43778, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zykkind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See file wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 43778
; LENGTH: 961
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-10-282-122A-43778

Query Match          94.4%; Score 51; DB 15; Length 961;
Best Local Similarity 90.0%; Pred. No. 3.5;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 EEDTNKDKPS 10
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Db       777 EEDTNKDKPN 786
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RESULT 15
US-09-815-242-5456
; Sequence 5456, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari L.
; APPLICANT: Zykkind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
```

```
; TITLE OF INVENTION: Identification of Essential Genes in
; FILE REFERENCE: Prokaryotes
; FILE REFERENCE: ELITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5456
; LENGTH: 978
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-09-815-242-5456

Query Match          94.4%; Score 51; DB 9; Length 978;
Best Local Similarity 90.0%; Pred. No. 3.6;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 EEDTNKDKPS 10
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Db       808 EEDTNKDKPN 817

Search completed: October 22, 2005, 12:56:26
Job time : 56.1494 secs
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GenCore version 5.1.6
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OM protein - protein search, using bw model

Run on: October 22, 2005, 08:04:46 ; Search time 11.6092 Seconds
(without alignments)
82.880 Million cell updates/sec

Title: US-10-731-238-92
Perfect score: 54
Sequence: 1 EEDTNKDKPS 10

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match length	ID	Description
1	54	100.0	1018 2 A32192	fibronectin-binding
2	51	94.4	940 2 S19702	fibronectin-binding
3	51	94.4	961 2 G90053	hypothetical prote
4	51	94.4	1038 2 H90053	hypothetical prote
5	39	72.2	467 2 S16915	gamma-aminobutyric
6	39	72.2	603 2 S15074	calpastatin - rat
7	39	72.2	654 2 T10772	calpastatin - rat
8	39	72.2	928 2 S50578	hypothetical prote
9	37	68.5	323 2 T47574	embryonic abundant
10	37	68.5	384 2 H96829	probable RNA-bind
11	37	68.5	590 1 S55095	myd-related protei
12	37	68.5	772 2 T06154	hypothetical prote
13	36	66.7	261 2 S20610	calpastatin - mous
14	36	66.7	631 2 T26232	hypothetical prote
15	36	66.7	817 2 F83073	probable ATP-depen
16	36	66.7	1820 1 CHEE	sodium channel pro
17	36	66.7	4869 2 S65572	ryanodine receptor
18	35	64.8	82 2 G83011	translocation prot
19	35	64.8	172 1 NKVGBG	core protein p19 -
20	35	64.8	238 1 CQBE74	US4 protein - huma
21	35	64.8	591 2 C84220	propionyl-CoA carb
22	34	63.0	131 2 F89838	conserved hypotet
23	34	63.0	165 2 B84486	probable Athlia re
24	34	63.0	167 2 E81028	conserved hypotet
25	34	63.0	167 2 A81973	hypothetical prote
26	34	63.0	180 2 T33142	hypothetical prote
27	34	63.0	204 2 T47457	hypothetical prote
28	34	63.0	238 1 VOCH	riboflavin-binding
29	34	63.0	269 1 WZVZ13	I3 protein - vacci

30	34	63.0	269 2 T37340	30K DNA binding ph
31	34	63.0	269 2 G72157	L3L protein - vari
32	34	63.0	269 2 A36843	K3L protein - vari
33	34	63.0	269 2 T28495	hypothetical prote
34	34	63.0	274 2 T21284	hypothetical prote
35	34	63.0	328 1 MBMSB	golli-myeilin basic
36	34	63.0	376 2 A56480	N-acetylglucosamin
37	34	63.0	430 2 T04678	hypothetical prote
38	34	63.0	434 2 D96716	probable alpha/bet
39	34	63.0	438 2 T37786	probable RNA-bind
40	34	63.0	440 1 A35875	transcription fact
41	34	63.0	440 2 I48291	transcription fact
42	34	63.0	441 1 A53988	transcription fact
43	34	63.0	441 1 TVCHTE	transcription fact
44	34	63.0	441 1 TVHBT	transcription fact
45	34	63.0	467 2 S19317	gamma-aminobutyric

ALIGNMENTS

RESULT 1
A32192
fibronectin-binding protein - Staphylococcus aureus
C:Species: Staphylococcus aureus
C:Date: 31-Jul-1989 #sequence_revision 31-Jul-1989 #text_change 16-Feb-1997
C:Accession: A32192
R:Signaes, C.; Raucci, G.; Joensen, K.; Lindgren, P.E.; Anantharamiah, G.M.; Hoeck,
Proc. Natl. Acad. Sci. U.S.A. 86, 699-703, 1989
A:Title: Nucleotide sequence of the gene for a fibronectin-binding protein from Staphyl.
A:Reference number: A32192; MUID:8908998; PMID:2521391
A:Accession: A32192
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1018 <SIG>
A:Cross-references: GB:J04151
C:Keywords: fibronectin binding

Query Match 100.0%; Score 54; DB 2; Length 1018;
Best Local Similarity 100.0%; Pred. No. 0.08;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EEDTNKDKPS 10
DB 830 EEDTNKDKPS 839

RESULT 2

S19702
fibronectin-binding protein B - Staphylococcus aureus
C:Species: Staphylococcus aureus
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
C:Accession: S19702
R:Joensen, K.; Signaes, C.; Mueller, H.P.; Lindberg, M.
Eur. J. Biochem. 202, 1041-1048, 1991
A:Title: Two different genes encode fibronectin binding proteins in Staphylococcus aure
A:Reference number: S19702; MUID:9211475; PMID:1837266
A:Accession: S19702
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-940 <JOB>
A:Cross-references: UNIPROT:Q53682; EMBL:X62992; NID:949040; PIDD:CAA44726.1; PID:95815
C:Keywords: fibronectin binding

Query Match 94.4%; Score 51; DB 2; Length 940;
Best Local Similarity 90.0%; Pred. No. 0.26;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EEDTNKDKPS 10
DB 766 EEDTNKDKPS 775

```

RESULT 3
G90053
hypothetical protein fnb [imported] - Staphylococcus aureus (strain N315)
C:Species: Staphylococcus aureus
C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C:Accession: G90053
R:Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguc
ma, A.; Mitutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.;
C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
A:Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.
A:Reference number: A89758; MUID:21311952; PMID:11418146
A:Accession: G90053
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-961 <KUR>
A:Cross-references: UNIPROT:Q99RD3; GB:BA000018; PID:g13702452; PIDN:BA03593.1; GSPDB:C
A:Experimental source: strain N315
C:Genetics:
A:Gene: fnb

Query Match          94.4%; Score 51; DB 2; Length 961;
Best Local Similarity 90.0%; Pred. No. 0.27;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EEDTNKDKPS 10
    |||||
    |||||
Db 777 EEDTNKDKPN 786

RESULT 4
H90053
hypothetical protein fnb [imported] - Staphylococcus aureus (strain N315)
C:Species: Staphylococcus aureus
C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C:Accession: H90053
R:Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguc
ma, A.; Mitutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.;
C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
A:Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.
A:Reference number: A89758; MUID:21311952; PMID:11418146
A:Accession: H90053
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1038 <KUR>
A:Cross-references: UNIPROT:Q99RD2; GB:BA000018; PID:g13702453; PIDN:BA03594.1; GSPDB:C
A:Experimental source: strain N315
C:Genetics:
A:Gene: fnb

Query Match          94.4%; Score 51; DB 2; Length 1038;
Best Local Similarity 90.0%; Pred. No. 0.29;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EEDTNKDKPS 10
    |||||
    |||||
Db 826 EEDTNKDKPN 835

RESULT 5
S16915
gamma-aminobutyric acid/benzodiazepine receptor gamma-3 chain precursor - mouse
N:Alternate names: GABA(A) receptor gamma-3 chain
C:Species: Mus musculus (house mouse)
C:Date: 12-Mar-1993 #sequence_revision 12-Mar-1993 #text_change 09-Jul-2004
C:Accession: S16915; S15469
R:Wilson-Shaw, D.; Robinson, M.; Gambarana, C.; Siegel, R.E.; Sikela, J.M.
FEBS Lett. 284, 211-215, 1991
A:Title: A novel gamma subunit of the GABA(A) receptor identified using the polymerase c
A:Reference number: S16915; MUID:91285135; PMID:1647983
A:Accession: S16915
A:Molecule type: mRNA

```

```

A:Residues: 1-467 <NIL>
A:Cross-references: UNIPROT:P27681; EMBL:X59300; NID:G51121; PIDN:CAA1988.1; PID:G51122
C:Superfamily: acetylcholine receptor
C:Keywords: disulfide bond; glycoprotein; ion channel; neurotransmitter receptor; transm
F:1-17/Domain: signal sequence #status predicted <Sig>
F:18-467/Product: gamma-aminobutyric acid/benzodiazepine receptor gamma-3 chain #status
F:255-277/Domain: transmembrane #status predicted <TM1>
F:281-303/Domain: transmembrane #status predicted <TM2>
F:315-337/Domain: transmembrane #status predicted <TM3>
F:444-467/Domain: transmembrane #status predicted <TM4>
F:110,228/Binding site: carbohydrate (Asn) (covalent) #status predicted
F:111-185/Disulfide bonds: #status predicted

Query Match          72.2%; Score 39; DB 2; Length 467;
Best Local Similarity 70.0%; Pred. No. 21;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 EEDTNKDKPS 10
    |||||
    |||||
Db 23 EEDNEDSPS 32

RESULT 6
S15074
calpastatin - rat
C:Species: Rattus sp. (rat)
C:Date: 18-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004
C:Accession: S15074
R:Ichida, S.; Emori, Y.; Suzuki, K.
Biochim. Biophys. Acta 1088, 436-438, 1991
A:Title: Rat calpastatin has diverged primary sequence from other mammalian calpastatin.
A:Reference number: S15074; MUID:91198152; PMID:2015306
A:Accession: S15074
A:Molecule type: mRNA
A:Residues: 1-603 <ISH>
A:Cross-references: UNIPROT:P27321; EMBL:X56729; NID:G57783; PIDN:CAA0053.1; PID:G5778
C:Superfamily: calpain inhibitor

Query Match          72.2%; Score 39; DB 2; Length 603;
Best Local Similarity 87.5%; Pred. No. 27;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 EEDTNKDKP 9
    |||||
    |||||
Db 96 EEDTNKDDP 103

RESULT 7
T10772
calpastatin - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004
C:Accession: T10772
R:de Tullio, R.; Sparatore, B.; Salimino, F.; Melloni, E.; Pontremoli, S.
FEBS Lett. 422, 113-117, 1998
A:Title: Rat brain contains multiple mRNAs for calpastatin.
A:Reference number: 217133; MUID:98133328; PMID:9475181
A:Accession: T10772
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-654 <DBT>
A:Cross-references: UNIPROT:Q55152; EMBL:Y13586; NID:G2765339; PIDN:CAA73916.1; PID:G27
A:Experimental source: strain Sprague Dawley, brain
C:Genetics:
A:Gene: CAST

Query Match          72.2%; Score 39; DB 2; Length 654;
Best Local Similarity 87.5%; Pred. No. 29;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 EEDTNKDKP 9
    |||||
    |||||

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Db 147 EDTNKDMP 154

RESULT 8

550578
hypothetical protein YER075c - yeast (Saccharomyces cerevisiae)
C:Species: Saccharomyces cerevisiae
C:Date: 28-May-1993 #sequence_revision 24-Feb-1995 #text_change 09-Jul-2004
C:Accession: S50578
R:Dieterich, F.S.
submitted to the EMBL Data Library, December 1994
A:Description: The sequence of S. cerevisiae lambda clone 3612 and cosmid 9747.
A:Reference number: S50438
A:Accession: S50578
A:Molecule type: DNA
A:Residues: 1-928 <DIR>
A:Cross-references: UNIPROT:P40048; EMBL:U18814; NID:g603309; PIDN:AAB64614.1; PID:g6033

A:Gene: SGD:PTP3
A:Cross-references: SGD:S0000877; MIPS:YER075c
A:Map position: 5R
C:Keywords: phosphoprotein
F:527-867/Domain: protein-tyrosine-phosphatase homology <PTP>
F:804/Active site: Cys (phosphocysteine intermediate) #status predicted
F:810/Binding site: substrate phosphate (Arg) #status predicted

Query Match 72.2%; Score 39; DB 2; Length 928;
Best Local Similarity 87.5%; Pred. No. 42;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EDTNKDK 8
|:|||||
Db 382 EDTNKDK 389

RESULT 9

T47574
embryonic abundant protein-like - Arabidopsis thaliana
N:Alternate names: protein F24B22.110
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 09-Jul-2004
C:Accession: T47574
R:Bloecker, H.; Mewes, H.W.; Lemcke, K.; Mayer, K.F.X.; Quehier, F.; Salanoubat, M.
submitted to the Protein Sequence Database, January 2000
A:Reference number: Z23016
A:Accession: T47574
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-333 <BL>
A:Cross-references: UNIPROT:Q9M389; EMBL:AL132957
A:Experimental source: cultivar Columbia; BAC clone F24B22

C:Genetics:
A:Map position: 3
A:introns: 50/3; 259/3
A>Note: F24B22.110
C:Superfamily: Arabidopsis thaliana hypothetical protein T20K12.110

Query Match 68.5%; Score 37; DB 2; Length 323;
Best Local Similarity 70.0%; Pred. No. 33;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 EDTNKDKPS 10
|:|||||
Db 305 EDDACKDKPS 314

RESULT 10

H96829
probable RNA-binding protein, 55844-57764 (imported) - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C:Accession: H96829
R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,

Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.
ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000

A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marzalli
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shim, P.; Southwick, A.M.; Sun, H.; Tallon,
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.

A:Reference number: A86141; MUID:21016719; PMID:11130712
A:Accession: H96829
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-384 <STO>
A:Cross-references: UNIPROT:Q9CA91; GB:AE005173; NID:g6453879; PIDN:AA09063.1; GSPDB:G
C:Genetics:
A:Gene: F19K16.16
A:Map position: 1

Query Match 68.5%; Score 37; DB 2; Length 384;
Best Local Similarity 70.0%; Pred. No. 39;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 EDTNKDKPS 10
|:|||||
Db 230 EKVTKDKPS 239

RESULT 11

S55095
myb-related protein YMR213w - yeast (Saccharomyces cerevisiae)
N:Alternate names: hypothetical protein YMR261.07
C:Species: Saccharomyces cerevisiae
C:Date: 08-Jul-1995 #sequence_revision 01-Sep-1995 #text_change 09-Jul-2004
C:Accession: S55095
R:Pedman, K.; Brown, D.; Bowman, S.

submitted to the EMBL Data Library, June 1995
A:Reference number: S55089
A:Accession: S55095
A:Molecule type: DNA
A:Residues: 1-590 <DED>
A:Cross-references: UNIPROT:Q03654; EMBL:Z49809; NID:g854459; PIDN:CNA89928.1; PID:g854
A:Experimental source: strain AB972
A:Genetics:
A:Gene: SGD:CEP1; MIPS:YMR213w
A:Cross-references: SGD:S0004826
A:Map position: 13R

C:Superfamily: myb DNA-binding repeat homology <MYB1>
F:5-56/Domain: myb DNA-binding repeat homology <MYB2>
F:57-106/Domain: myb DNA-binding repeat homology <MYB2>

Query Match 68.5%; Score 37; DB 1; Length 590;
Best Local Similarity 87.5%; Pred. No. 61;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 DTNKDKPS 10
|:|||||
Db 254 DGNKDKPS 261

RESULT 12

T06154
hypothetical protein F24J7.162 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)

C:Date: 30-Apr-1999 #sequence_revision 30-Apr-1999 #text_change 09-Jul-2004
C:Accession: T06154
R:Bevan, M.; Vitale, D.; Liguori, R.; Argiriou, A.; De Simone, V.; Bancroft, I.; Mewes,
submitted to the Protein Sequence Database, April 1999
A:Reference number: Z15493
A:Accession: T06154
A:Molecule type: DNA
A:Residues: 1-772 <BEV>

A:Cross-references: UNIPROT:Q9SN69; EMBL:AL021768; GSPDB:GN00062; ATSP:F24J7.162


```
A:Experimental source: cultivar Columbia; BAC clone F24J7
C:Genetics:
A:Gene: ATSP:F24J7.162
A:Map position: 4
A:Insertions: 4/2; 42/3; 273/2; 303/2; 342/3; 346/1; 463/3; 485/2; 536/3; 548/3; 576/3; 610
Query Match 68.5%; Score 37; DB 2; Length 772;
Best Local Similarity 75.0%; Pred. No. 81;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 EDTNKDKP 9
Db 649 KDSNKDKP 656

RESULT 13
S20610
calpastatin - mouse (fragment)
C:Species: Mus musculus (house mouse)
C>Date: 20-May-1994 #sequence_revision 12-Apr-1996 #text_change 13-Aug-1999
C:Accession: S20610; S17344
R:Lee, W.U.; Hatanaka, M.; Maki, M.
Biochim. Biophys. Acta 1129, 251-253, 1992
A:Title: Multiple forms of rat calpastatin cDNA in the coding region of functionally unk
A:Reference number: S20610; MUID:92110395; PMID:1730065
A:Accession: S20610
A:Molecule type: mRNA
A:Residues: 1-261 <LEB>
A:Cross-references: EMBL:X62519; NID:950296; PIDN:CAA4385.1; PID:950297
C:Superfamily: calpain inhibitor

Query Match 66.7%; Score 36; DB 2; Length 261;
Best Local Similarity 75.0%; Pred. No. 40;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 EDTNKDKP 9
Db 147 EDTNRDDP 154

RESULT 14
T26232
hypothetical protein W06D12.5 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T26232
R:Baaham, V.
submitted to the EMBL Data Library, November 1996
A:Reference number: Z20177
A:Accession: T26232
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-631 <WIL>
A:Cross-references: UNIPROT:O45894; EMBL:Z82073; PIDN:CAB04926.1; GSPDB:GNO0023; CESP:W0
A:Experimental source: clone W06D12
C:Genetics:
A:Gene: CESP:W06D12.5
A:Map position: 5
A:Insertions: 4/3; 50/1; 89/2; 153/1; 244/3; 285/3; 333/1; 384/2; 509/1; 553/3

Query Match 66.7%; Score 36; DB 2; Length 631;
Best Local Similarity 60.0%; Pred. No. 1e+02;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 EDTNKDKPS 10
Db 36 EDTNLKPS 45

RESULT 15
F83073
probable ATP-dependent proteinase PA4576 [imported] - Pseudomonas aeruginosa (strain PAC
C:Species: Pseudomonas aeruginosa
```

```
C>Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004
C:Accession: F83073
R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.D.; Br
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lfm,
.; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathc
A:Reference number: A82950; MUID:20437337; PMID:10984043
A:Accession: F83073
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-817 <STO>
A:Cross-references: UNIPROT:Q9HYK8; GB:AE004871; GB:AE004091; NID:9950819; PIDN:AAG079e
A:Experimental source: strain PA01
C:Genetics:
A:Gene: PA4576

Query Match 66.7%; Score 36; DB 2; Length 817;
Best Local Similarity 60.0%; Pred. No. 1.3e+02;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 EDTNKDKPS 10
Db 792 EDDKXDKPA 801

Search completed: October 22, 2005, 09:55:43
Job time : 12.6092 secs
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 22, 2005, 08:01:06 ; Search time 56.2069 Seconds
(without alignments)
91.106 Million cell updates/sec

Title: US-10-731-238-92
Perfect score: 54
Sequence: 1 EEDTNKDKPS 10

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_03: *
1: uniprot_sprot: *
2: uniprot_trembl: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	54	100.0	152	2	Q9AEP9
2	54	100.0	1018	1	FNBA STAAU
3	51	94.4	940	2	Q53682
4	51	94.4	943	2	Q8NTU8
5	51	94.4	957	2	Q6G6H4
6	51	94.4	961	2	Q99RD3
7	51	94.4	961	2	Q7A3V8
8	51	94.4	965	2	Q6GDUS
9	51	94.4	1015	2	Q8NUU7
10	51	94.4	1015	2	Q6G6H3
11	51	94.4	1038	2	Q99RD2
12	51	94.4	1038	2	Q7A3V7
13	40	74.1	461	2	Q7QAC5
14	40	74.1	613	2	Q6UDM5
15	39	72.2	145	2	Q8BOW9
16	39	72.2	176	2	Q55155
17	39	72.2	190	1	GRPE_ACHLA
18	39	72.2	467	1	GAC3_MOUSE
19	39	72.2	529	2	Q81100
20	39	72.2	593	2	Q99MG2
21	39	72.2	616	2	Q55151
22	39	72.2	654	1	ICAL_RAT
23	39	72.2	654	2	Q55152
24	39	72.2	654	2	Q99MG1
25	39	72.2	742	2	Q8BS96
26	39	72.2	928	1	PTP3_YEAST
27	39	72.2	1123	2	Q68Z55
28	39	72.2	1293	2	Q698P5
29	38	70.4	574	2	Q7YZ15
30	37	68.5	89	2	Q7RSR0
31	37	68.5	254	2	Q7OKS2

32	37	68.5	323	2	Q8L913	Q8L913 arabidopsis
33	37	68.5	323	2	Q9M389	Q9M389 arabidopsis
34	37	68.5	382	2	Q6CYC7	Q6CYC7 kluyveromy
35	37	68.5	384	2	Q9CA91	Q9CA91 arabidopsis
36	37	68.5	397	2	Q7Y1E4	Q7Y1E4 oryza sativ
37	37	68.5	434	2	Q6MU64	Q6MU64 mycoplasma
38	37	68.5	513	2	Q851P1	Q851P1 oryza sativ
39	37	68.5	590	1	CEP1_YEAST	CEP1_YEAST saccharomyc
40	37	68.5	590	2	Q6B1D8	Q6B1D8 saccharomyc
41	37	68.5	772	2	Q9SN69	Q9SN69 arabidopsis
42	37	68.5	1225	2	Q81LF3	Q81LF3 plasmodium
43	37	68.5	1395	2	Q7SC01	Q7SC01 neurospora
44	36	66.7	121	2	Q8BGM3	Q8BGM3 mus muscu
45	36	66.7	164	2	Q7RT09	Q7RT09 plasmodium

ALIGNMENTS

RESULT 1

ID	Q9AEP9	PRELIMINARY;	PRT;	152 AA.
AC	Q9AEP9:			
DT	01-JUN-2001 (TREMBLrel. 17, Created)			
DT	01-JUN-2001 (TREMBLrel. 17, Last sequence update)			
DT	01-DEC-2001 (TREMBLrel. 19, Last annotation update)			
DE	Fibronectin-binding protein (Fragment).			
GN	Name=fnb;			
OS	Staphylococcus aureus.			
OC	Bacteria; Firmicutes; Bacillales; Staphylococcus.			
OX	NCBI_TaxID=1280;			
RP	SEQUENCE FROM N.A.			
RP	STRAIN=CMRSA-1;			
RX	MEDLINE=21246681; PubMed=11349044;			
RX	DOI=10.1128/IAI.69.6.3791-3799.2001;			
RA	Rice K., Huasca M., Vaz D., McGavin M.J.			
RT	"Variance in fibronectin binding and fnb locus polymorphisms in a			
RT	Staphylococcus aureus: Identification of antigenic variation in a			
RT	fibronectin binding protein adhesin of the epidemic CMRSA-1 strain of			
RT	methicillin-resistant S. aureus."			
RL	Infect. Immun. 69:3791-3799 (2001).			
DR	EMBL; AY029184; AAK31588.1; ..			
FT	NON_TER	1		
FT	NON_TER	152		
SQ	SEQUENCE	152 AA;	17193 MW;	CFA3913C2B11C025 CRC64;

Query Match 100.0%; Score 54; DB 2; Length 152;
Best local Similarity 100.0%; Pred. No. 0.12; Mismatches 0; Gaps 0;
Matches 10; Conservative 0; Indels 0;

QY 1 EEDTNKDKPS 10
|||
Db 123 EEDTNKDKPS 132

RESULT 2

ID	FNBA STAAU	STANDARD;	PRT;	1018 AA.
AC	P14738;			
DT	01-APR-1990 (Rel. 14, Created)			
DT	01-APR-1990 (Rel. 14, Last sequence update)			
DT	25-OCT-2004 (Rel. 45, Last annotation update)			
DE	Fibronectin-binding protein precursor (FNBP).			
GN	Name=fnbA;			
OS	Staphylococcus aureus.			
OC	Bacteria; Firmicutes; Bacillales; Staphylococcus.			
OX	NCBI_TaxID=1280;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RP	STRAIN=NCIC 8325-4;			
RX	MEDLINE=89098998; PubMed=2521391;			
RA	Signaas C., Raucsi G., Joensson K., Lindgren P.-E.,			

RA Anantharamiah G.M., Hoecek M., Lindberg M.;
 RT "Nucleotide sequence of the gene for a fibronectin-binding protein
 from *Staphylococcus aureus*: use of this peptide sequence in the
 synthesis of biologically active peptides.";
 RL Proc. Natl. Acad. Sci. U.S.A. 86:699-703(1989).
 CC -1- FUNCTION: The ability of bacteria to bind fibronectin has been
 proposed as a virulence factor enabling bacteria to colonize wound
 tissues and blood clots. Binding of plasma fibronectin to the
 bacterial surface might block adhesion receptors on *S. aureus*, thus
 representing an important defense mechanism against tissue
 invasion.
 CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
 an amide bond (potential).
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 between the Swiss Institute of Bioinformatics and the EMBL outstation -
 the European Bioinformatics Institute. There are no restrictions on its
 use by non-profit institutions as long as its content is in no way
 modified and this statement is not removed. Usage by and for commercial
 entities requires a license agreement (See [http://www.ebi.ac.uk/announcements/](http://www.ebi.ac.uk/announcements)
 or send an email to license@ebi.ac.uk).
 CC -----
 DR EMBL, J04151, AAA26632.1, -.
 DR InterPro: IPR004237; Fn_bind.
 DR InterPro: IPR005877; Gpos_YsIRK.
 DR InterPro: IPR001899; Gram_pos_anchor.
 DR Pfam: PF02986; Fn_bind; 1.
 DR Pfam: PF00746; Gram_pos_anchor; 1.
 DR Pfam: PF04650; YsIRK_signal; 1.
 DR TIGRFAMs: TIGR01167; LPXTG_anchor; 1.
 DR TIGRFAMs: TIGR01168; YsIRK_signal; 1.
 DR PROSITE: PSS0847; GRAM_POS_ANCHORING; 1.
 KM Cell adhesion; Cell wall; Peptidoglycan-anchor; Repeat; Signal;
 KW virulence.
 FT SIGNAL 1 36
 FT CHAIN 37 985 Fibronectin-binding protein.
 FT PROPEP 986 1018 Removed by sortase (potential).
 FT REPEAT 545 574 B-1.
 FT REPEAT 575 604 B-2.
 FT DOMAIN 745 878 4 X approximate tandem repeats,
 fibronectin-binding domain.
 FT REPEAT 745 782 D-1.
 FT REPEAT 783 820 D-2.
 FT REPEAT 821 859 D-3.
 FT REPEAT 860 878 D-4 (incomplete).
 FT DOMAIN 879 948 5 X tandem repeats, Pro-rich (WR).
 FT REPEAT 879 892 WR 1.
 FT REPEAT 893 906 WR 2.
 FT REPEAT 907 920 WR 3.
 FT REPEAT 921 934 WR 4.
 FT REPEAT 935 948 WR 5.
 FT SITE 982 986 LPXTG sorting signal (potential).
 FT MOD_RES 985 985 Pentaglycyl aurein peptidoglycan amidated
 threonine (potential).
 SQ SEQUENCE 1018 AA; 111780 MW; 58175E0020E81F1F CRC64;
 Query Match 100.0%; Score 54; DB 1; Length 1018;
 Best Local Similarity 100.0%; Pred. No. 0.87; Mismatches 0; Indels 0; Gaps 0;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 EEDTNKDKPS 10
 DB 830 EEDTNKDKPS 839
 RESULT 3
 Q53682 PRELIMINARY; PRT; 940 AA.
 AC Q53682;
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
 DE Fibronectin binding protein B.

GN Name=fnbB;
 OS *Staphylococcus aureus*.
 OC Bacteria; Firmicutes; Bacillales; *Staphylococcus*.
 OX NCBI_TaxID=1280;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=8325-4;
 RX MEDLINE=22040717; PubMed=1837266;
 RA Jonsson K., Signas C., Muller H.P., Lindberg M.;
 RT "Two different genes encode fibronectin binding proteins in
Staphylococcus aureus. The complete nucleotide sequence and
 characterization of the second gene.";
 RL Eur. J. Biochem. 202:1041-1048(1991).
 CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
 an amide bond (By similarity).
 CC EMBL: X62992; CAA44726.1; -.
 DR PIR, S19702, S19702.
 DR HSP, Q53653, 1N67.
 DR GO: GO:0009986; C:cell surface; IEA.
 DR GO: GO:0005618; C:cell wall; IEA.
 DR GO: GO:0009375; C:cell wall (sensu Gram-positive Bacteria); IEA.
 DR GO: GO:0016020; C:membrane; IEA.
 DR GO: GO:0007155; P:cell adhesion; IEA.
 DR InterPro: IPR008966; Adhes_Bact.
 DR InterPro: IPR004237; Fn_bind.
 DR InterPro: IPR005877; Gpos_YsIRK.
 DR InterPro: IPR001899; Gram_pos_anchor.
 DR Pfam: PF02986; Fn_bind; 2.
 DR Pfam: PF00746; Gram_pos_anchor; 1.
 DR Pfam: PF04650; YsIRK_signal; 1.
 DR TIGRFAMs: TIGR01167; LPXTG_anchor; 1.
 DR TIGRFAMs: TIGR01168; YsIRK_signal; 1.
 DR PROSITE: PSS0847; GRAM_POS_ANCHORING; 1.
 KM Cell wall; Peptidoglycan-anchor.
 KW SEQUENCE 940 AA; 103555 MW; E35FBBCA907AE345 CRC64;
 Query Match 94.4%; Score 51; DB 2; Length 940;
 Best Local Similarity 90.0%; Pred. No. 2.7;
 Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 EEDTNKDKPS 10
 DB 766 EEDTNKDKPS 775
 RESULT 4
 Q8NNU8 PRELIMINARY; PRT; 943 AA.
 AC Q8NNU8;
 DT 01-OCT-2002 (TREMBLrel. 22, Created)
 DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update)
 DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
 DE Pdb protein.
 GN Name=fnbB; Ordered locus Names=MW2420;
 OS *Staphylococcus aureus* (strain MW2).
 OC Bacteria; Firmicutes; Bacillales; *Staphylococcus*.
 OX NCBI_TaxID=196620;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=MW2;
 RX MEDLINE=22040717; PubMed=12044378; DOI=10.1016/S0140-6736(02)08713-5;
 RA Baba T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Oguchi A.,
 RA Nagai Y., Iwama N., Aono K., Naimi T., Kuroda H., Cui L.,
 RA Yamamoto K., Hiramatsu K.;
 RT "Genome and virulence determinants of high virulence community-
 acquired MRSA.";
 RL Lancet 359:1819-1827(2002).
 CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
 an amide bond (By similarity).
 DR EMBL: AP004830; BAB96285.1; -.
 DR HSP, Q53653, 1N67.
 DR GO: GO:0009986; C:cell surface; IEA.
 DR GO: GO:0005618; C:cell wall; IEA.

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DR GO: GO:0009275; C:cell wall (senu Gram-positive Bacteria); IEA.
DR GO: GO:0016020; C:membrane; IEA.
DR GO: GO:0007155; P:cell adhesion; IEA.
DR InterPro: IPR008966; Adhes_bact.
DR InterPro: IPR004237; Fn_bind.
DR InterPro: IPR005877; Gpos_YsIRK.
DR InterPro: IPR001899; Gram_pos_anchor.
DR Pfam: PF02986; Fn_bind; 1.
DR Pfam: PF00746; Gram_pos_anchor; 1.
DR Pfam: PF04650; YsIRK_signal; 1.
DR TIGRfams: TIGR01167; LpxTG_anchor; 1.
DR TIGRfams: TIGR01168; YsIRK_signal; 1.
DR PROSITE: PS50847; GRAM_POS_ANCHORING; 1.
KW Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ SEQUENCE 943 AA; 104537 MW; DABA5F31947E1B6A CRC64;

Query Match 94.4%; Score 51; DB 2; Length 943;
Best Local Similarity 90.0%; Pred. No. 2.7;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 EEDTKDKRPS 10
DB 773 EEDTKDKRPN 782

RESULT 5
O6G6H4 PRELIMINARY; PRT; 957 AA.
ID O6G6H4
AC O6G6H4;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Fibronectin-binding protein.
CN Name=fnbB; OrderedlocusNames=SA52387;
OS Staphylococcus aureus (strain MSSA476).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=282459;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed:15233324; DOI=10.1073/pnas.040251101;
RA Holden M.T.G., Fell E.J., Linday J.A., Peacock S.J., Day N.P.J.,
RA Enright M.C., Foster T.J., Moore C.E., Hurst L., Atkin R., Barton A.,
RA Benson N., Bentley S.D., Chillingworth C., Chillingworth T.,
RA Churcher C., Clark L., Corbin C., Cronin A., Doggett J., Dowd L.,
RA Feltham T., Hance Z., Harris B., Hauser H., Holtroyd S., Jagels K.,
RA James K.D., Lennard N., Line A., Mayes R., Moule S., Mungall K.,
RA Ormond D., Quail M.A., Rabinowitch E., Rutherford K.M., Sanders M.,
RA Sharp S., Simmonds M., Stevens K., Whitehead S., Barrett B.G.,
RA Spratt B.G., Parkhill J.;
RT "Complete genomes of two clinical Staphylococcus aureus strains:
RT evidence for the rapid evolution of virulence and drug resistance.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:9786-9791(2004).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC an amide bond (By similarity).
EMBL: BX571857; CAG44201.1; -.
DR GO: GO:0009986; C:cell surface; IEA.
DR GO: GO:0005618; C:cell wall; IEA.
DR GO: GO:0009275; C:cell wall (senu Gram-positive Bacteria); IEA.
DR GO: GO:0016020; C:membrane; IEA.
DR GO: GO:0007155; P:cell adhesion; IEA.
DR InterPro: IPR008966; Adhes_bact.
DR InterPro: IPR004237; Fn_bind.
DR InterPro: IPR005877; Gpos_YsIRK.
DR InterPro: IPR001899; Gram_pos_anchor.
DR Pfam: PF02986; Fn_bind; 1.
DR Pfam: PF00746; Gram_pos_anchor; 1.
DR TIGRfams: TIGR01167; LpxTG_anchor; 1.
DR TIGRfams: TIGR01168; YsIRK_signal; 1.
DR PROSITE: PS50847; GRAM_POS_ANCHORING; 1.
KW Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ SEQUENCE 957 AA; 105980 MW; 28F8BA7FFD5EAF CRC64;

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Query Match 94.4%; Score 51; DB 2; Length 957;
Best Local Similarity 90.0%; Pred. No. 2.8;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 EEDTKDKRPS 10
DB 773 EEDTKDKRPN 782

RESULT 6
O99RD3 PRELIMINARY; PRT; 961 AA.
ID O99RD3
AC O99RD3;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DE 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Fibronectin-binding protein homolog.
CN Name=fnbB; OrderedlocusNames=SAV2502;
OS Staphylococcus aureus (strain Mu50 / ATCC 700699).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=158878;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=Mu50 / ATCC 700699;
RX MEDLINE=21311952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2;
RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Iian J.-O., Ito T.,
RA Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,
RA Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
RA Sekimizu K., Hiraoka H., Kubara S., Goto S., Yabuzaki J.,
RA Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
RA Hattori M., Ogasawara N., Hayashi H., Hiramoto K.,
RT "Whole genome sequencing of methicillin-resistant Staphylococcus
RT aureus.";
RL Lancet 357:1225-1240(2001).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC an amide bond (By similarity).
EMBL: AP003365; BAB58664.1; -.
DR PIR: G90053; G90053.
DR HSP: Q53653; IN67.
DR GO: GO:0009986; C:cell surface; IEA.
DR GO: GO:0005618; C:cell wall; IEA.
DR GO: GO:0009275; C:cell wall (senu Gram-positive Bacteria); IEA.
DR GO: GO:0016020; C:membrane; IEA.
DR GO: GO:0007155; P:cell adhesion; IEA.
DR InterPro: IPR008966; Adhes_bact.
DR InterPro: IPR004237; Fn_bind.
DR InterPro: IPR005877; Gpos_YsIRK.
DR InterPro: IPR001899; Gram_pos_anchor.
DR Pfam: PF02986; Fn_bind; 1.
DR Pfam: PF00746; Gram_pos_anchor; 1.
DR Pfam: PF04650; YsIRK_signal; 1.
DR TIGRfams: TIGR01167; LpxTG_anchor; 1.
DR TIGRfams: TIGR01168; YsIRK_signal; 1.
DR PROSITE: PS50847; GRAM_POS_ANCHORING; 1.
KW Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ SEQUENCE 961 AA; 106010 MW; 364940F884EA4101 CRC64;

Query Match 94.4%; Score 51; DB 2; Length 961;
Best Local Similarity 90.0%; Pred. No. 2.8;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 EEDTKDKRPS 10
DB 777 EEDTKDKRPN 786

RESULT 7
O7A3J8 PRELIMINARY; PRT; 961 AA.
ID O7A3J8
AC O7A3J8;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)

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DT 05-JUL-2004 (TrEMBLrel. 27, last annotation update)
DE FnbB protein.
GN Name=fnbB; OrderedlocusNames=SA2290;
OS Staphylococcus aureus (strain NJ15);
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
NCI_TaxID=15879;
RX MEDLINE=2311952; PubMed=1418146; DOI=10.1016/S0140-6736(00)04403-2;
RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
RA Cui L., Oguchi A., Aoki K.-I., Negai Y., Iian J.-O., Ito T.,
RA Kanamori M., Mabumaru H., Maruyama A., Murakami H., Hoshiyama A.,
RA Mitutani Y., Takahashi N.K., Sawano T., Inoue R.-I., Kato C.,
RA Sekimizu K., Hatakeyama H., Kuhara S., Goto S., Yabuzaki J.,
RA Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
RA Hattori M., Ogasawara N., Hayashi H., Hiramoto K.;
RT "Whole genome sequencing of methicillin-resistant Staphylococcus
RT aureus."
RL Lancet 357:1225-1240(2001).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC an amide bond (By similarity).
DR EMBL: AP003137; BAB43593.1; -
DR GO: GO:0009986; C:cell surface; IEA.
DR GO: GO:0005618; C:cell wall; IEA.
DR GO: GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO: GO:0016020; C:membrane; IEA.
DR GO: GO:0007155; P:cell adhesion; IEA.
DR InterPro: IPR008966; Adhes_bact.
DR InterPro: IPR004237; Fn_bind.
DR InterPro: IPR005877; Gpos_YsIRK.
DR InterPro: IPR001899; Gram_pos_anchor.
DR Pfam: PF02986; Fn_bind. 1.
DR Pfam: PF00746; Gram_pos_anchor. 1.
DR TIGRFAMs: TIGR01167; LpxTG_anchor. 1.
DR TIGRFAMs: TIGR01168; YsIRK_signal. 1.
DR PROSITE: PS50847; GRAM_POS_ANCHORING. 1.
KW Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ SEQUENCE 961 AA; 106010 MW; 364940F84E4101 CRC64;

Query Match 94.4%; Score 51; DB 2; Length 961;
Best Local Similarity 90.0%; Pred. No. 2.8;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 EEDTNKDKPS 10
Db 777 EEDTNKDKPN 786

RESULT 8
ID OEGDUS PRELIMINARY; PRT; 965 AA.
AC OEGDUS;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, last sequence update)
DE Fibronectin-binding protein.
GN Name=fnbA; OrderedlocusNames=SA2580;
OS Staphylococcus aureus (strain MRSA252).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
NCI_TaxID=282458;
RX MEDLINE=1513324; DOI=10.1073/pnas.040251101;
RA Holden M.T.G., Fell E.J., Lindsay J.A., Peacock S.J., Day N.P.J.,
RA Enright M.C., Foster T.J., Moore C.E., Hurst L., Atkin R., Barron A.,
RA Baeson N., Bentley S.D., Chillingworth C., Chillingworth T.,
RA Churcher C., Clark L., Cotton C., Cronin A., Doggett J., Dowd L.,
RA Feltham T., Hance Z., Harris B., Hauser H., Holtroyd S., Jegerle K.,
RA James K.D., Lennard N., Line A., Mayes R., Moule S., Mungall K.,
RA Ormond D., Quail M.A., Rabinowitsch E., Rutherford K.M., Sanders M.,
RA Sharp S., Simmonds M., Stevens K., Whitehead S., Barrett B.G.,
RA Spratt B.G., Parkhill J.;

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RT "Complete genomes of two clinical Staphylococcus aureus strains:
RT evidence for the rapid evolution of virulence and drug resistance.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:9786-9791(2004).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC an amide bond (By similarity).
DR EMBL: BX571856; CAG41560.1; -
DR GO: GO:0009986; C:cell surface; IEA.
DR GO: GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO: GO:0016020; C:membrane; IEA.
DR GO: GO:0007155; P:cell adhesion; IEA.
DR InterPro: IPR008966; Adhes_bact.
DR InterPro: IPR004237; Fn_bind.
DR InterPro: IPR005877; Gpos_YsIRK.
DR InterPro: IPR001899; Gram_pos_anchor.
DR Pfam: PF02986; Fn_bind. 1.
DR Pfam: PF00746; Gram_pos_anchor. 1.
DR TIGRFAMs: TIGR01167; LpxTG_anchor. 1.
DR TIGRFAMs: TIGR01168; YsIRK_signal. 1.
DR PROSITE: PS50847; GRAM_POS_ANCHORING. 1.
KW Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ SEQUENCE 965 AA; 105691 MW; 2982E132164D0551 CRC64;

Query Match 94.4%; Score 51; DB 2; Length 965;
Best Local Similarity 90.0%; Pred. No. 2.8;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 EEDTNKDKPS 10
Db 795 EEDTNKDKPN 804

RESULT 9
ID O8NUJ7 PRELIMINARY; PRT; 1015 AA.
AC O8NUJ7;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, last annotation update)
DE FnbB protein.
GN Name=fnb; OrderedlocusNames=MM2421;
OS Staphylococcus aureus (strain MW2).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
NCI_TaxID=196620;
RX MEDLINE=22040717; PubMed=12044378; DOI=10.1016/S0140-6736(02)08713-5;
RA Baba T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Oguchi A.,
RA Nagai Y., Iwama N., Asano K., Naimi T., Kuroda H., Cui L.,
RA Yamamoto K., Hiramoto K.;
RT "Genome and virulence determinants of high virulence community-
RT acquired MRSA.";
RL Lancet 359:1819-1827(2002).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC an amide bond (By similarity).
DR EMBL: AP004830; BAB96286.1; -
DR GO: GO:0009986; C:cell surface; IEA.
DR GO: GO:0005618; C:cell wall; IEA.
DR GO: GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO: GO:0016020; C:membrane; IEA.
DR GO: GO:0007155; P:cell adhesion; IEA.
DR InterPro: IPR008966; Adhes_bact.
DR InterPro: IPR004237; Fn_bind.
DR InterPro: IPR005877; Gpos_YsIRK.
DR InterPro: IPR001899; Gram_pos_anchor.
DR Pfam: PF02986; Fn_bind. 1.
DR Pfam: PF00746; Gram_pos_anchor. 1.
DR TIGRFAMs: TIGR01167; LpxTG_anchor. 1.
DR TIGRFAMs: TIGR01168; YsIRK_signal. 1.
DR PROSITE: PS50847; GRAM_POS_ANCHORING. 1.
KW Cell wall; Complete proteome; Peptidoglycan-anchor.

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SQ SEQUENCE 1015 AA; 111145 MW; D0F9281BB64D44D2 CRC64;
 Query Match 94.4%; Score 51; DB 2; Length 1015;
 Best Local Similarity 90.0%; Pred. No. 2.9;
 Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EEDTNKDKPS 10
 |||||
 DB 831 EEDTNKDKPN 840

RESULT 10
 O6G6H3 PRELIMINARY; PRT; 1015 AA.
 ID O6G6H3
 AC O6G6H3;
 DT 05-JUN-2004 (TREMBlrel. 27, Created)
 DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
 DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
 DE Fibrinectin-binding protein.
 GN OrderedLocustNames=SA52388;
 OS Staphylococcus aureus (strain MSSA476).
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 NCBI_TaxID=282459;
 RX PubMed=15213324; DOI=10.1073/pnas.0402521101;
 RA Holden M.T.G., Fell E.J., Lindsey J.A., Peacock S.J., Day N.P.J.,
 RA Enright M.C., Foster T.J., Moore C.E., Hurst L., Atkin R., Barron A.,
 RA Baon N., Bentley S.D., Chillingworth C., Chillingworth T.,
 RA Churcher C., Clark L., Cotton C., Cronin A., Doggett J., Dowd L.,
 RA Fellwell T., Hance Z., Harris B., Hauser H., Holtroyd S., Jagsle K.,
 RA James K.D., Lennard N., Line A., Mayes R., Moule S., Mungall K.,
 RA Ormond D., Quail M.A., Rabinowitch E., Rutherford K.M., Sanders M.,
 RA Sharp S., Simmonds M., Stevens K., Whitehead S., Barrall B.G.,
 RA Spratt B.G., Parkhill J.;
 RT "Complete genomes of two clinical Staphylococcus aureus strains:
 RT evidence for the rapid evolution of virulence and drug resistance";
 RL Proc. Natl. Acad. Sci. U.S.A. 101:9786-9791(2004).
 CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
 CC an amide bond (By similarity).
 CC EMBL; BX571857; CAG4202.1; -;
 DR GO; GO:0009986; C:cell surface; IEA.
 DR GO; GO:0005618; C:cell wall; IEA.
 DR GO; GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0007155; P:cell adhesion; IEA.
 DR InterPro; IPR008966; Adhes_bact.
 DR InterPro; IPR004237; Fn_bind.
 DR InterPro; IPR005877; Gpos_YsIRK.
 DR InterPro; IPR001899; Gram_pos_anchor.
 DR Pfam; PF02986; Fn_bind; 1.
 DR Pfam; PF00746; Gram_pos_anchor; 1.
 DR Pfam; PF04650; YsIRK_signal; 1.
 DR TIGRFAMs; TIGR01167; LPTG_anchor; 1.
 DR TIGRFAMs; TIGR01168; YsIRK_signal; 1.
 DR PROSITE; PS50847; GRAM_POS_ANCHORING; 1.
 KW Cell wall; Complete proteome; Peptidoglycan-anchor.
 SQ SEQUENCE 1015 AA; 111145 MW; D0F9281BB64D44D2 CRC64;

Query Match 94.4%; Score 51; DB 2; Length 1015;
 Best Local Similarity 90.0%; Pred. No. 2.9;
 Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EEDTNKDKPS 10
 |||||
 DB 831 EEDTNKDKPN 840

RESULT 11
 O99RD2 PRELIMINARY; PRT; 1038 AA.
 ID O99RD2;
 AC O99RD2;
 DT 01-JUN-2001 (TREMBlrel. 17, Created)

DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
 DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
 DE Fibrinectin-binding protein homolog.
 GN Name=fnb; OrderedLocustNames=SAV2503;
 OS Staphylococcus aureus (strain Mu50 / ATCC 700699).
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 NCBI_TaxID=158878;
 RX PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2;
 RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
 RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Iian J.-Q., Ito T.,
 RA Kanamori M., Matsunaru H., Maruyama A., Murakami H., Hosoyama A.,
 RA Mizutani Y., Takahashi N.K., Sawano T., Inoue R.-i., Kaito C.,
 RA Sekimizu K., Hiraoka H., Kunara S., Goto S., Yabuzaki J.,
 RA Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
 RA Hattori M., Ogasawara N., Hayashi H., Hiramoto K.;
 RT "Whole genome sequencing of methicillin-resistant Staphylococcus
 RT aureus";
 RL Lancet 357:1225-1240(2001).
 CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
 CC an amide bond (By similarity).
 CC EMBL; AP003365; BAB58665.1; -;
 DR PIR; H90053; H90053.
 DR GO; GO:0009986; C:cell surface; IEA.
 DR GO; GO:0005618; C:cell wall; IEA.
 DR GO; GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0007155; P:cell adhesion; IEA.
 DR InterPro; IPR008966; Adhes_bact.
 DR InterPro; IPR004237; Fn_bind.
 DR InterPro; IPR005877; Gpos_YsIRK.
 DR InterPro; IPR001899; Gram_pos_anchor.
 DR Pfam; PF02986; Fn_bind; 1.
 DR Pfam; PF00746; Gram_pos_anchor; 1.
 DR Pfam; PF04650; YsIRK_signal; 1.
 DR TIGRFAMs; TIGR01167; LPTG_anchor; 1.
 DR TIGRFAMs; TIGR01168; YsIRK_signal; 1.
 DR PROSITE; PS50847; GRAM_POS_ANCHORING; 1.
 KW Cell wall; Complete proteome; Peptidoglycan-anchor.
 SQ SEQUENCE 1038 AA; 113618 MW; 666BF6BF2BFBBE12 CRC64;

Query Match 94.4%; Score 51; DB 2; Length 1038;
 Best Local Similarity 90.0%; Pred. No. 3;
 Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EEDTNKDKPS 10
 |||||
 DB 826 EEDTNKDKPN 835

RESULT 12
 Q7A3J7 PRELIMINARY; PRT; 1038 AA.
 ID Q7A3J7;
 AC Q7A3J7;
 DT 05-JUN-2004 (TREMBlrel. 27, Created)
 DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
 DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
 DE Fnb protein.
 GN Name=fnb; OrderedLocustNames=SA2291;
 OS Staphylococcus aureus (strain N315).
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 NCBI_TaxID=158879;
 RX PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2;
 RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
 RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Iian J.-Q., Ito T.,
 RA Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,
 RA Mizutani Y., Takahashi N.K., Sawano T., Inoue R.-i., Kaito C.,
 RA Sekimizu K., Hiraoka H., Kunara S., Goto S., Yabuzaki J.,
 RA Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,

RA Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
 RT "Whole genome sequencing of methicillin-resistant *Staphylococcus aureus*."
 RL Lancet 357:1225-1240(2001).
 CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by an amide bond (By similarity).
 DR EMBL: AP003137; BAB3594.1; -.
 DR GO: GO:0009986; C:cell surface; IEA.
 DR GO: GO:0005618; C:cell wall; IEA.
 DR GO: GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
 DR GO: GO:0016020; C:membrane; IEA.
 DR GO: GO:0007155; P:cell adhesion; IEA.
 DR InterPro: IPR008966; Adhes_bact.
 DR InterPro: IPR004237; Fn_bind.
 DR InterPro: IPR005877; Gcos_Ysirk.
 DR InterPro: IPR001899; Gram_pos_anchor.
 DR Pfam: PF02986; Fn_bind; 1.
 DR Pfam: PF00746; Gram_pos_anchor; 1.
 DR Pfam: PF04650; Ysirk_signal; 1.
 DR TIGRFAMs: TIGR01167; Lpxtg_anchor; 1.
 DR TIGRFAMs: TIGR01168; Ysirk_signal; 1.
 DR PROSITE: PS50847; GRAM_POS_ANCHORING; 1.
 KW Cell wall; Complete proteome; Peptidoglycan-anchor.
 SQ SEQUENCE 1038 AA; 113618 MW; 666BFB2FBEB12 CRC64;

Query Match 94.4%; Score 51; DB 2; Length 1038;
 Best Local Similarity 90.0%; Pred. No. 3;
 Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EEDTNKDKPS 10
 Db 826 EEDTNKDKPN 835

RESULT 13
 Q7QAC5 PRELIMINARY; PRT; 461 AA.
 AC Q7QAC5;
 DT 01-MAR-2004 (TREMBLrel. 26, Created)
 DT 01-MAR-2004 (TREMBLrel. 26, Last sequence update)
 DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
 DE EbiP3522 (Fragment).
 GN Name=ebiG3522; ORFNames=ENSANG0000002822;
 OS Anopheles gambiae str. PEST.
 CC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Nematocera; Anophelinae.
 OX NCBI_TaxID=180454;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=PEST;
 RA Anopheles Genome Sequencing Consortium;
 RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
 CC -1- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is preliminary data.
 DR EMBL: AAA01008898; EAA09218.1; -.
 DR GO: GO:0016021; C:integral to membrane; IEA.
 DR GO: GO:0005215; F:transporter activity; IEA.
 DR GO: GO:0006810; P:transport; IEA.
 DR InterPro: IPR007114; MFS.
 DR PROSITE: PS50850; MFS; 1.
 FT NON_TER 1
 FT NON_TER 1
 SQ SEQUENCE 461 AA; 51332 MW; 2991B63947F01465 CRC64;

Query Match 74.1%; Score 40; DB 2; Length 461;
 Best Local Similarity 70.0%; Pred. No. 1.1e+02;
 Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 EEDTNKDKPS 10
 Db 257 QEDTNERKPS 266

RESULT 14
 O6UDM5 PRELIMINARY; PRT; 613 AA.
 ID O6UDM5;
 AC O6UDM5;
 DT 05-JUL-2004 (TREMBLrel. 27, Created)
 DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
 DE Staraker.
 GN Name=stm;
 OS Brachydanio rerio (Zebrafish) (Danio rerio).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes; OC Cyprinidae; Danio.
 OX NCBI_TaxID=7955;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Seelinger C., Burghammer M., Busch-Neutwich E., Berger J., Schwarz H., Riekel C., Nicolson T.;
 RL Submitted (JUG-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AY372242; AAQ93680.1; -.
 DR ZFIN: ZDB-GENE-031112-4; stm.
 SQ SEQUENCE 613 AA; 66119 MW; E93D6C2F1C4217F9 CRC64;

Query Match 74.1%; Score 40; DB 2; Length 613;
 Best Local Similarity 70.0%; Pred. No. 1.5e+02;
 Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 EEDTNKDKPS 10
 Db 155 DSDENKDKPS 164

RESULT 15
 O8BQW9 PRELIMINARY; PRT; 145 AA.
 ID O8BQW9;
 AC O8BQW9;
 DT 01-MAR-2003 (TREMBLrel. 23, Created)
 DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)
 DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
 DE Mus musculus adult male corpora quadrigemina cDNA, RIKEN full-length enriched library, clone:8230362M20 product:gamma-aminobutyric acid DE (GABA-A) receptor, subunit gamma 3, full insert sequence.
 GN Name=B230362M20Rik;
 OS Mus musculus (Mouse).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Corpora quadrigemina;
 RX MEDLINE=9279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
 RA Carninci P., Hayashizaki Y.;
 RT "High-efficiency full-length cDNA cloning."
 RL Meth. Enzymol. 303:19-44(1999).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Corpora quadrigemina;
 RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
 RA RIKEN FANTOM Consortium;
 RT "Functional annotation of a full-length mouse cDNA collection."
 RL Nature 409:685-690(2001).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Corpora quadrigemina;
 RA The RIKEN Consortium;
 RT "The RIKEN Genome Exploration Research Group Phase I & II Team; Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs."
 RL Nature 420:563-573(2002).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Corpora quadrigemina;

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RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Kono H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtration of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630(2000).
RN
RN
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Corpora quadrigemina;
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA Kono H., Akiyama J., Nishi K., Kitsuai T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishino T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwara S., Inoue K., Ozawa K., Izawa M., Ohara E., Wachihi M.,
RA Yoneda Y., Ishikawa T., Tanaka T., Matsura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kita A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771(2000).
RN
RN
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Corpora quadrigemina;
RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
RA Hayashida K., Hayatsu N., Hiramoto K., Hirooka T., Hirozane T.,
RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
RA Kato H., Kawai J., Kojima Y., Kondo S., Kono H., Kouda M., Koya S.,
RA Kurahara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohse N., Okazaki Y.,
RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
RA Sasaki D., Shibata K., Shingawa A., Shiraki T., Sogabe Y., Tagami M.,
RA Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR GBD; MGI:2444828; B230362M20Rik.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005230; P:extracellular ligand-gated ion channel acti. . .; IEA.
DR GO; GO:0004890; P:GABA-A receptor activity; IEA.
DR GO; GO:0004872; P:receptor activity; IEA.
DR GO; GO:0006821; P:chloride transport; IEA.
DR GO; GO:0007214; P:gamma-aminobutyric acid signalling pathway; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro: IPR005437; GABRG1 receptor.
DR InterPro: IPR006202; Neur_chan_LBD.
DR Pfam: PF02931; Neur_chan_LBD; I.
DR PRINTS; PR01620; GABARG1MMA.
KW Receptor.
SQ SEQUENCE 145 AA; 16307 MW; C2375D074C1C19F CRC64;
Query Match 72.2%; Score 39; DB 2; Length 145;
Best Local Similarity 70.0%; Pred. No. 51;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 1 EEDTKDKXPS 10
DB 23 EEDENEDSPS 32

```

Search completed: October 22, 2005, 09:52:17
 Job time : 57.2069 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 25, 2005, 20:58:51 ; Search time 69.7126 Seconds
(without alignments)
55.479 Million cell updates/sec

Title: US-10-731-238-93

Perfect score: 56

Sequence: 1 DTNKPSPSYQ 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

1: A_Geneseq_16Dec04: *
2: Geneseqp1980s: *
3: Geneseqp1990s: *
4: Geneseqp2000s: *
5: Geneseqp2001s: *
6: Geneseqp2002s: *
7: Geneseqp2003as: *
8: Geneseqp2003bs: *
9: Geneseqp2004s: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	56	100.0	10	2	AAW65749
2	56	100.0	37	4	AAW65749
3	56	100.0	38	1	AAW65749
4	56	100.0	134	2	AAW65749
5	56	100.0	139	2	AAW65749
6	56	100.0	1018	1	AAW65749
7	56	100.0	1018	4	AAW65749
8	56	100.0	1018	6	AAW65749
9	56	100.0	1018	6	AAW65749
10	56	100.0	1018	6	AAW65749
11	56	100.0	1027	2	AAW65749
12	56	94.6	77	2	AAW65749
13	53	94.6	101	2	AAW65749
14	53	94.6	113	2	AAW65749
15	53	94.6	124	2	AAW65749
16	53	94.6	128	2	AAW65749
17	53	94.6	130	2	AAW65749
18	53	94.6	130	2	AAW65749
19	53	94.6	130	2	AAW65749
20	53	94.6	130	2	AAW65749
21	53	94.6	134	2	AAW65749
22	53	94.6	134	2	AAW65749
23	53	94.6	162	2	AAW65749
24	53	94.6	164	2	AAW65749
25	53	94.6	174	2	AAW65749

26	53	94.6	174	2	AAW65749
27	53	94.6	181	2	AAW65749
28	53	94.6	181	2	AAW65749
29	53	94.6	559	2	AAW65749
30	53	94.6	940	2	AAW65749
31	53	94.6	940	6	AAW65749
32	53	94.6	948	6	AAW65749
33	53	94.6	948	6	AAW65749
34	53	94.6	948	6	AAW65749
35	53	94.6	961	6	AAW65749
36	53	94.6	978	4	AAW65749
37	53	94.6	1001	4	AAW65749
38	53	94.6	1038	6	AAW65749
39	51	91.1	37	1	AAW65749
40	45	80.4	10	2	AAW65749
41	44	78.6	10	2	AAW65749
42	43	76.8	30	4	AAW65749
43	43	76.8	30	7	AAW65749
44	43	76.8	31	7	AAW65749
45	43	76.8	38	1	AAW65749

ALIGNMENTS

RESULT 1
AAW65749
ID AAW65749 standard; peptide; 10 AA.

AC AAW65749;

DT 16-OCT-1998 (first entry)

DE Fibronectin binding protein-derived peptide #93.

KW Microbial surface components recognising adhesive matrix molecule;

KW MSCRAMM; fibronectin; fibronectin-binding protein; antibody; epitope;

KW antibiotic; bacterial infection; antibiotic-resistant strain.

XX Synthetic.

XX Staphylococcus aureus.

XX WO9831389-A2.

XX 21-JAN-1998; 98WO-US001222.

XX 21-JAN-1997; 97US-0036139P.

XX (TEXAS) UNIV TEXAS A & M SYSTEM.

XX Hooeek M, Patti JM, House-Pompeo KL, Speciale P, Joh D;

XX Mcgavin M;

XX WPI; 1998-413816/35.

XX Antibody that binds to fibronectin-binding protein, preventing its

XX binding to fibronectin - used to treat or prevent bacterial infection,

XX especially by Staphylococci and Streptococci.

XX Example 9; Page 111, 201pp; English.

XX The invention relates to antibodies that bind to a fibronectin-binding

XX domain of a fibronectin-binding protein, and inhibit binding of the

XX protein to fibronectin. Also claimed are: (1) isolated peptides of a

XX fibronectin-binding protein that do not bind to fibronectin; (2) fusion

XX protein containing at least one peptide of a fibronectin-binding protein

XX linked to a second amino acid sequence; (3) nucleic acid encoding the

XX isolated peptide of (1). Antibodies, the isolated peptides of (1) and the

XX nucleic acids are all useful for immunisation (active or passive) and (by

XX inhibiting binding of bacteria to fibronectin) for preventing or treating

XX infection in humans or other animals, particularly by staphylococci or

CC streptococci, e.g. meningitis, otitis media, pneumonia, endocarditis,
 CC mastitis in cattle, abortion in horses and many others. Since the
 CC antibodies block binding of bacteria, they should be effective against
 CC antibiotic-resistant strains, and may replace antibiotic therapy or
 CC increase its effectiveness. Sequences AAM65744-58 represent peptides
 CC which were synthesised to span the D3 motif of S. aureus fibronectin
 CC binding protein A
 CC
 XX
 SQ Sequence 10 AA;
 Query Match 100.0%; Score 56; DB 2; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.0022;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Db 1 DTNKKRPSYQ 10
 1 DTNKKRPSYQ 10
 RESULT 2
 ID AAB91958 standard; peptide; 37 AA.
 XX
 AC AAB91958;
 XX
 DT 22-JUN-2001 (first entry)
 XX
 DE Fibronectin fragment and fibrin related peptide SEQ ID NO:1134.
 XX
 KM Protection; endogenous therapeutic peptide; peptidase; conjugation;
 KM blood component; modification; succinimidyl; maleimido group; amino;
 KM hydroxyl; thiol; hormone; growth factor; neurotransmitter.
 XX
 OS Homo sapiens.
 OS Synthetic.
 OS
 PN WO200069900-A2.
 XX
 PD 23-NOV-2000.
 XX
 PF 17-MAY-2000; 2000WO-US013576.
 XX
 PR 17-MAY-1999; 99US-0134406P.
 PR 10-SEP-1999; 99US-0153406P.
 PR 15-OCT-1999; 99US-0159783P.
 XX
 PA (CONT-) CONUTCHEM INC.
 XX
 PI Bridon DP, Ezrin AM, Milner PG, Holmes DL, Thibaudau K;
 XX
 DR WPI; 2001-112059/12.
 XX
 PT Modifying and attaching therapeutic peptides to albumin prevents
 PT peptidase degradation, useful for increasing length of in vivo activity.
 XX
 PS Disclosure; Page 566; 733pp; English.
 XX
 The present invention describes a modified therapeutic peptide (I)
 CC comprising a therapeutically active amino acid region (III) and a
 CC reactive group (II) (e.g. succinimidyl and maleimido groups) attached to
 CC a less therapeutically active amino acid region (IV), which covalently
 CC bonds with amino/hydroxyl/thiol groups on blood components to form a
 CC peptidase stabilised therapeutic peptide composed of 3-50 amino acids.
 CC (I) are useful for modifying therapeutic peptides e.g. hormones, growth
 CC factors and neurotransmitters, to protect them from peptidase activity in
 CC vivo for the treatment of various disorders. Endogenous therapeutic
 CC peptides are not suitable as drug candidates as they require frequent
 CC administration due to rapid degradation by peptidases in the body.
 CC Modifying and attaching therapeutic peptides to albumin prevents or
 CC reduces the action of peptidases to increase length of activity (half
 CC life) and specifically as bonding to large molecules decreases
 CC intracellular uptake and interference with physiological processes.
 CC AAB90829 to AAB92441 represent peptides which can be used in the

CC exemplification of the present invention
 XX
 SQ Sequence 37 AA;
 Query Match 100.0%; Score 56; DB 4; Length 37;
 Best Local Similarity 100.0%; Pred. No. 0.0083;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Db 1 DTNKKRPSYQ 10
 11 DTNKKRPSYQ 20
 RESULT 3
 ID AAP80662 standard; protein; 38 AA.
 XX
 AC AAP80662;
 XX
 DT 25-MAR-2003 (revised)
 DT 07-OCT-1990 (first entry)
 XX
 DE Protein with fibronectin binding ability.
 XX
 KM Hybrid DNA molecule; fibronectin binding; mastitis; ruminants;
 KM wound infection.
 XX
 OS Staphylococcus aureus.
 OS
 PN EP294349-A.
 XX
 PD 07-DEC-1988.
 XX
 PF 30-MAY-1988; 88EP-00850186.
 XX
 PR 01-JUN-1987; 87SE-00002272.
 XX
 PA (ALFA) ALFA LAVAL AGRIC INT AB.
 XX
 PI Lindberg MK, Signas LC, Wadstrom TM, Froman G;
 XX
 DR WPI; 1988-347978/49.
 DR N-PSDB; AAN81099.
 XX
 PT Hybrid DNA encoding Staphylococcus aureus fibronectin binding protein -
 PT useful for immunisation and topical application to prevent staphylococcal
 PT infections.
 XX
 PS Claim 11; Page 12; 23pp; English.
 XX
 The peptide has fibronectin binding ability. It is useful for immunising
 CC ruminants against staphylococcal mastitis, pref. when used at 0.5-5
 CC micrograms/kg, using 3 doses given at 1-3 week intervals; for topical
 CC application to prevent wound infection, using an isotonic saline soln. of
 CC concn. 25-250 micrograms/ml; and, when immobilised on a carrier, for
 CC diagnosing staphylococcal infections. (Updated on 25-MAR-2003 to correct
 CC PF field.) (Updated on 25-MAR-2003 to correct PA field.)
 CC
 XX
 SQ Sequence 38 AA;
 Query Match 100.0%; Score 56; DB 1; Length 38;
 Best Local Similarity 100.0%; Pred. No. 0.0085;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Db 1 DTNKKRPSYQ 10
 12 DTNKKRPSYQ 21
 RESULT 4
 ID AAY29087 standard; protein; 134 AA.
 XX

AC AAY29087;
 XX
 DT 28-SEP-1999 (first entry)
 XX
 DE S. aureus fibronectin binding protein A (FnBA) binding domain.
 XX
 KM Bovine herpes virus-2; BHV-2; cytokine; immune response; immunogen; IL;
 KM interleukin; colony stimulating factor; CSF; interferon; IFN; TNF;
 KM tumour necrosis factor; recombinant virus; vaccine; mucosal disease;
 KM mastitis; breast cancer; stress-induced disease; binding domain; FnBA;
 KM Fibronectin binding protein.
 XX
 OS Staphylococcus aureus.
 XX
 PN MO9916892-A1.
 XX
 PD 08-APR-1999.
 XX
 PP 29-SEP-1998; 98WO-GB002927.
 XX
 PR 29-SEP-1997; 97GB-00020633.
 XX
 PA (UTBR-) UNIV BRISTOL.
 XX
 PI Bradley AJ, Duffas WP;
 XX
 DR WPI: 1999-255101/21.
 DR N-PSDB: AAX91504.
 XX
 PT New bovine herpes virus-2 vectors.
 XX
 PS Example 2; Fig 8A-B; 130bp; English.
 XX
 CC The invention provides bovine herpes virus-2 (BHV-2) based expressions that
 CC comprise at least one cytokine-encoding DNA sequence. The expression of
 CC cytokines in mammals can up-regulate immune responses to the immunogens.
 CC The cytokine is selected from interleukins (IL), colony stimulating
 CC factors (CSF), interferons (IFN) and tumour necrosis factors (TNF). The
 CC BHV-2 based vector or recombinant virus can be used as vaccines. They can
 CC be used for preventing or treating a mucosal disease in a subject, e.g.
 CC ruminants, cattle, sheep, goats, dogs, cats, horses, or man, particularly
 CC mastitis in cows or breast cancers in humans. They can also be used for
 CC preventing or treating a stress-induced disease. The present sequence
 CC represents the binding domain of a previously published S. aureus
 CC fibronectin binding protein A (FnBA) sequence. The FnB binding domain
 CC gene sequence FnBA, cloned for use in this invention has 97.8 percent
 CC identity when compared to the previously published FnBA and FnBB gene
 CC sequences
 XX
 SQ Sequence 134 AA;
 XX
 QY Query Match 100.0%; Score 56; DB 2; Length 134;
 Best Local Similarity 100.0%; Pred. No. 0.031;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 1 DTNKKPSYQ 10
 |||||
 88 DTNKKPSYQ 97
 DB

KM microbial surface component recognising adhesive matrix molecule; MSCRAMM;
 KM adhesin; vaccine; immunisation; diagnosis; therapy; mastitis.
 XX
 OS Staphylococcus aureus.
 XX
 FT Key Location/Qualifiers
 FT Peptide 1..12
 FT /note="vector PQB30-derived peptide"
 XX
 PN MO9743314-A2.
 XX
 PD 20-NOV-1997.
 XX
 PF 14-MAY-1997; 97MO-US008210.
 XX
 PR 16-MAY-1996; 96US-0017678P.
 XX
 PA (TEXA) UNIV TEXAS A & M SYSTEM.
 PA (UABR-) UAB RES FOUND.
 XX
 PI Hoeoek M, Patti JM, House-Pompeo K, Sthanam N, Symersky J;
 XX
 DR WPI: 1998-008801/01.
 XX
 PT Antibody that interacts with collagen binding domain of Staphylococcal
 PT cna gene product - useful to prevent bacterial sepsis in animal infected
 PT with Staphylococcus aureus.
 XX
 PS Disclosure; Page 91; 143bp; English.
 XX
 CC This protein comprises Staphylococcus aureus fibronectin-binding
 CC microbial surface component recognising adhesive matrix molecule (MSCRAMM)
 CC derivative pQD, plus a vector-derived N-terminal peptide. The invention
 CC relates to claimed nucleic acid sequences (see AAT93436-38) encoding S.
 CC aureus collagen binding protein (CBP) epitopes M17, M31 and M55 (see
 CC AAT93436-54) that confer protection against S. aureus infection. CBP
 CC protein and antigenic epitopes are contemplated for use in the treatment
 CC of pathological infections, especially to prevent bacterial adhesion to
 CC collagen. The epitopes are also contemplated for use in the preparation
 CC of vaccines and as carrier proteins in vaccine formulations, as well as
 CC in the formulation of compositions for the prevention of S. aureus
 CC infection. pQF33 and pQD (see AAT93436) were used to raise anti-MSCRAMM
 CC polyclonal antibodies used in passive immunisation against bovine
 CC mastitis. (Updated on 25-MAR-2003 to correct PI field.) (Updated on 27-
 CC AUG-2003 to correct OS field.)
 XX
 SQ Sequence 139 AA;
 XX
 QY Query Match 100.0%; Score 56; DB 2; Length 139;
 Best Local Similarity 100.0%; Pred. No. 0.032;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 1 DTNKKPSYQ 10
 |||||
 102 DTNKKPSYQ 111
 DB

RESULT 5
 AAM31556
 ID AAM31556 standard; protein; 139 AA.
 XX
 AC AAM31556;
 XX
 DT 27-AUG-2003 (revised)
 DT 25-MAR-2003 (revised)
 DT 21-MAY-1998 (first entry)
 XX
 DE Fibronectin-binding MSCRAMM derivative pQD.
 XX
 KM Fibronectin; pQD; collagen binding protein; sepsis; infection;
 XX

RESULT 6
 AAP82115
 ID AAP82115 standard; protein; 1018 AA.
 XX
 AC AAP82115;
 XX
 DT 25-MAR-2003 (revised)
 DT 05-JAN-1990 (first entry)
 XX
 DE Fibronectin binding protein.
 XX
 KM Fibronectin binding protein; S.aureus; immunisation; mastitis; ruminants;
 KM wound infection; diagnosis.
 XX
 OS Staphylococcus aureus.
 XX

```
PN EP294349-A.
XX
XX 07-DEC-1988.
PD
XX 30-MAY-1988; 88EP-00850188.
XX
XX 01-JUN-1987; 87SE-00002272.
XX
XX (ALFA ) ALFA LAVAL AGRIC INT AB.
PA
XX
XX Lindberg MK, Signas LC, Wadstrom TM, Froman G;
XX WPI; 1988-347978/49.
DR P-PSDB; AAP82115.
XX
XX Hybrid DNA encoding Staphylococcus aureus fibronectin binding protein -
PT useful for immunisation and topical application to prevent staphylococcal
PT infections.
XX
XX Disclosure; Fig. 8A:1-8A:2; 23pp; English.
XX
XX The S. aureus fibronectin binding protein may be included in a hybrid
CC protein. The protein may be used to immunise ruminants against
CC staphylococcal mastitis, pref. when given at 0.5-5 microg/Kg, using 3
CC doses at 1-3 week intervals; and for topical applicn. to prevent wound
CC infection, pref. using isotonic saline soln. of concn. 25-250 microg/mg.
CC The DNA encoding the binding protein and the hybrid protein may be
CC immobilised on a carrier and used to diagnose staphylococcal infections.
CC (Updated on 25-MAR-2003 to correct PA field.)
CC
XX
SQ Sequence 1018 AA;
Query Match 100.0%; Score 56; DB 1; Length 1018;
Best Local Similarity 100.0%; Pred. No. 0.24;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 DTNKKRPSYQ 10
Db 832 DTNKKRPSYQ 841
RESULT 7
AAU37245
ID AAU37245 standard; protein; 1018 AA.
XX
XX AAU37245;
AC
XX
XX 14-FEB-2002 (first entry)
DT
XX
XX Staphylococcus aureus cellular proliferation protein #1415.
DE
XX
XX Antisense; prokaryotic cellular proliferation protein; antibiotic;
KW antibacterial; drug design.
XX
XX Staphylococcus aureus.
OS
XX WO200170955-A2.
PN
XX
XX 27-SEP-2001.
PD
XX
XX 21-MAR-2001; 2001WO-US009180.
PF
XX
XX 21-MAR-2000; 2000US-0191078P.
PR 23-MAY-2000; 2000US-0206848P.
PR 26-MAY-2000; 2000US-0297272P.
PR 23-OCT-2000; 2000US-0242578P.
PR 27-NOV-2000; 2000US-0253625P.
PR 22-DEC-2000; 2000US-0257931P.
PR 16-FEB-2001; 2001US-0269308P.
XX
XX (ELIT-) ELITRA PHARM INC.
PA
XX
XX Haseelbeck R, Ohlsen KL, Zyskind JW, Wall D, Trawick JD, Carr GJ;
PI
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PI Yamamoto RT, Xu HH;
XX
XX WPI; 2001-611495/70.
DR N-PSDB; AAS55104.
XX
XX New polynucleotides for the identification and development of
PT antibiotics, comprise sequences of antisense nucleic acids.
PT
XX
XX Example 3; SEQ ID NO 12838; 511pp; English.
XX
XX The invention relates to antisense inhibitors of genes essential to
CC prokaryotic cellular proliferation, their use in identifying the genes,
CC their use in the discovery of novel antibiotics, the essential genes
CC themselves and the encoded proteins. The prokaryotes used are Escherichia
CC coli, Staphylococcus aureus, Salmonella typhi, Klebsiella pneumoniae,
CC Pseudomonas aeruginosa and Enterococcus faecalis. The invention is also
CC useful for the identification of potential new targets for antibiotic
CC development. The antisense nucleic acids can also be used to identify
CC proteins used in proliferation, to express these proteins, and to obtain
CC antibodies capable of binding to the expressed proteins. The proteins can
CC be used to screen compounds in rational drug discovery programmes. The
CC antisense nucleic acid sequence is also useful to screen for homologous
CC nucleic acids which are required for cell proliferation in a wide variety
CC of organisms. The present sequence represents an essential prokaryotic
CC cellular proliferation protein. Note: The sequence data for this patent
CC did not form part of the printed specification, but was obtained in
CC electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX
SQ Sequence 1018 AA;
Query Match 100.0%; Score 56; DB 4; Length 1018;
Best Local Similarity 100.0%; Pred. No. 0.24;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 DTNKKRPSYQ 10
Db 832 DTNKKRPSYQ 841
RESULT 8
AAU34301
ID AAU34301 standard; protein; 1018 AA.
XX
XX AAU34301;
AC
XX
XX 14-FEB-2002 (first entry)
DT
XX
XX Staphylococcus aureus cellular proliferation protein #577.
DE
XX
XX Antisense; prokaryotic cellular proliferation protein; antibiotic;
KW antibacterial; drug design.
XX
XX Staphylococcus aureus.
OS
XX WO200170955-A2.
PN
XX
XX 27-SEP-2001.
PD
XX
XX 21-MAR-2001; 2001WO-US009180.
PF
XX
XX 21-MAR-2000; 2000US-0191078P.
PR 23-MAY-2000; 2000US-0206848P.
PR 26-MAY-2000; 2000US-0207727P.
PR 23-OCT-2000; 2000US-0242578P.
PR 27-NOV-2000; 2000US-0253625P.
PR 22-DEC-2000; 2000US-0257931P.
PR 16-FEB-2001; 2001US-0269308P.
XX
XX (ELIT-) ELITRA PHARM INC.
PA
XX
XX Haseelbeck R, Ohlsen KL, Zyskind JW, Wall D, Trawick JD, Carr GJ;
PI Yamamoto RT, Xu HH;
```

XX DR WPI; 2001-611495/70.
XX DR N-PSDB; AAS52160.
XX PT New polynucleotides for the identification and development of
XX PT antibiotics, comprise sequences of antisense nucleic acids.
XX PS Example 3; SEQ ID NO 5797; 511pp; English.
XX CC The invention relates to antisense inhibitors of genes essential to
XX CC prokaryotic cellular proliferation, their use in identifying the genes,
XX CC their use in the discovery of novel antibiotics, the essential genes
XX CC themselves and the encoded proteins. The prokaryotes used are Escherichia
XX CC coli, Staphylococcus aureus, Salmonella typhi, Klebsiella pneumoniae,
XX CC Pseudomonas aeruginosa and Enterococcus faecalis. The invention is also
XX CC useful for the identification of potential new targets for antibiotic
XX CC development. The antisense nucleic acids can also be used to identify
XX CC proteins used in proliferation, to express these proteins, and to obtain
XX CC antibodies capable of binding to the expressed proteins. The proteins can
XX CC be used to screen compounds in rational drug discovery programmes. The
XX CC antisense nucleic acid sequence is also useful to screen for homologous
XX CC nucleic acids which are required for cell proliferation in a wide variety
XX CC of organisms. The present sequence represents an essential prokaryotic
XX CC cellular proliferation protein. Note: The sequence data for this patent
XX CC did not form part of the printed specification, but was obtained in
XX CC electronic format directly from WIPO at
XX CC ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 1018 AA;
XX
XX Query Match 100.0%; Score 56; DB 4; Length 1018;
XX Best Local Similarity 100.0%; Pred. No. 0.24;
XX Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 DTNKKPSYQ 10
DB 832 DTNKKPSYQ 841
XX
XX RESULT 9
XX ABJ18922
XX ID ABJ18922 standard; protein; 1018 AA.
XX AC ABJ18922;
XX DT 06-MAR-2003 (first entry)
XX DE Pathogen specific antigen related staphylococcal protein SEQ ID No 68.
XX XX
XX XX Antibacterial; virucide; fungicide; protozoacide; cytostatic; anti-HIV;
XX XX hyperimmune; serum-reactive; antigen; pathogen; tumour; allergen;
XX XX auto-immunity; vaccine; staphylococcal infection; antibody; cancer;
XX XX autoimmune disease; HIV; hepatitis.
XX XX
XX XX Staphylococcus sp.
XX XX
XX XX WO200259148-A2.
XX XX
XX XX 01-AUG-2002.
XX XX
XX XX 21-JAN-2002; 2002WO-EP000546.
XX XX
XX XX 26-JAN-2001; 2001AT-00000130.
XX XX
XX XX (CIST-) CISTEM BIOTECHNOLOGIES GMBH.
XX XX
XX XX Meinke A, Nagy B, Von Ahnen U, Klade C, Henics T, Zauner W;
XX XX Minh DB, Vytvyteka O, Eitz H, Dryla A, Weichardt T, Hafner M;
XX XX Tempelmeier B;
XX XX WPI; 2003-075410/07.
XX DR
XX PT Identifying, isolating and producing hyperimmune serum-reactive antigens

XX PT from a pathogen, for preparing vaccine or medicament for treating or
XX PT preventing e.g. staphylococcal infections, comprises providing antibody
XX PT preparation.
XX XX
XX PS Example 7; Page 157; 252pp; English.
XX CC The invention relates to a novel method for identifying, isolating and
XX CC producing hyperimmune serum-reactive antigens from a pathogen, tumour,
XX CC allergen, a tissue or host prone to auto-immunity, where the antigens are
XX CC used in a vaccine, comprises providing antibody preparation from a plasma
XX CC pool of a type of animal, or individual sera with antibodies against the
XX CC specific pathogen, tumour, allergen, tissue or host prone to auto-
XX CC immunity. The hyperimmune serum-reactive antigens comprising any of the
XX CC 62 sequences of 53-2261 amino acids fully defined in the specification,
XX CC or their hyperimmune fragments are useful for the manufacture of a
XX CC pharmaceutical preparation, particularly a vaccine against staphylococcal
XX CC infections or colonisation against S. aureus or S. epidermidis. The
XX CC preparation of antibodies is useful for the manufacture of a medicament
XX CC for treating or preventing staphylococcal infections or colonisation
XX CC against S. aureus or S. epidermidis. The antibody preparations may also
XX CC be used for diagnostic and imaging purposes. Other conditions that can be
XX CC treated include cancer, autoimmune diseases or infections caused by viral
XX CC (e.g. HIV, hepatitis A, B or C), fungal or protozoan pathogens. This
XX CC sequence represents a staphylococcal protein relating to the method for
XX CC identifying and producing pathogen specific antigens of the invention
XX XX
XX SQ Sequence 1018 AA;
XX
XX Query Match 100.0%; Score 56; DB 6; Length 1018;
XX Best Local Similarity 100.0%; Pred. No. 0.24;
XX Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 DTNKKPSYQ 10
DB 832 DTNKKPSYQ 841
XX
XX RESULT 10
XX ABM72537
XX ID ABM72537 standard; protein; 1018 AA.
XX XX
XX AC ABM72537;
XX DT 20-NOV-2003 (first entry)
XX DE Staphylococcus aureus protein #1777.
XX DE
XX XX
XX XX Antibacterial; vaccine; gene therapy; infection; sepsis; diagnosis;
XX XX enzymatic assay; antibiotic target.
XX XX
XX XX Staphylococcus aureus.
XX OS
XX XX WO200294868-A2.
XX XX
XX XX 28-NOV-2002.
XX XX
XX XX 27-MAR-2002; 2002WO-IB002637.
XX XX
XX XX 27-MAR-2001; 2001GB-00007661.
XX XX
XX XX (CHIR-) CHIRON SPA.
XX XX
XX XX Maignani V, Mora M, Scarselli M;
XX XX
XX XX WPI; 2003-120786/11.
XX XX
XX XX N-PSDB; ACF74097.
XX XX
XX XX New Staphylococcus aureus protein, useful as a vaccine for treating or
XX XX preventing Staphylococcal infection, specifically an infection caused by
XX XX S. aureus, e.g. sepsis.
XX XX
XX PS Claim 1; SEQ ID NO 3554; 49pp; English.
XX XX

CC The invention relates to novel genes and encoded proteins from
CC Staphylococcus aureus. A composition comprising the S. aureus protein, a
CC nucleic acid encoding the protein, or an antibody to the protein, is
CC useful as a pharmaceutical, particularly as a vaccine for treating or
CC preventing infection due to Staphylococcus bacteria, specifically an
CC infection caused by S. aureus. The composition is particularly useful for
CC treating or preventing sepsis in a patient. The composition can also be
CC used for diagnostics. The protein is also used in an assay for enzymatic
CC studies and as a target for antibiotics. This sequence represents one of
CC the novel S. aureus proteins of the invention
XX
SQ Sequence 1018 AA;
QY
Query Match 100.0%; Score 56; DB 6; Length 1018;
Best Local Similarity 100.0%; Pred. No. 0.24;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 832 DTNKKRPSYQ 841
1 DTNKKRPSYQ 10
|||||
AAW89806 standard; protein; 1027 AA.
XX
AC AAW89806;
XX
DT 16-MAR-1999 (first entry)
XX
DE Staphylococcus aureus protein SEQ ID #5254.
XX
KM Computer readable medium; vaccine; S.aureus infection; immunodetection;
KM cellulitis; eyelid infection; food poisoning; osteomyelitis; therapy;
KM skin infection; surgical wound infection; scalded skin syndrome;
KM toxic shock syndrome.
XX
OS Staphylococcus aureus.
XX
PN EP786519-A2.
XX
PD 30-JUL-1997.
XX
PF 07-JAN-1997; 97EP-00100117.
XX
PR 05-JAN-1996; 96US-0009861P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Kunesh CA, Choi GH, Barash SC, Dillon PJ, Fannon MR, Rosen CA;
XX
XX WPI; 1997-374922/35.
XX
XX Polynucleotide(s) and proteins derived from Staphylococcus aureus -
PT scored on computer readable medium and used in the production of anti-
PT S. aureus vaccines.
XX
PS Claim 23; Page 3263-3267; 3271pp; English.
XX
XX This sequence represents a Staphylococcus aureus protein sequence of the
CC invention. The DNA sequences encoding the S.aureus proteins are recorded
CC on a computer readable medium, preferably selected from a floppy or hard
CC disk, random access memory (RAM), read-only memory (ROM) or CD-ROM.
CC Homology searches using the S. aureus DNA sequences allows putative
CC functions to be assigned so that protein-encoding or regulatory regions
CC of commercial, therapeutic or industrial importance can be obtained.
CC Specifically, sequences which are likely to encode antigens have been
CC identified and these polypeptides can be used in a vaccine composition
CC against S.aureus infection. The polypeptides can also be used in a kit
CC for the immunodetection of S.aureus in a sample. S.aureus is implicated
CC in numerous human diseases, including cellulitis, eyelid infections, food
CC poisoning, osteomyelitis, skin and surgical wound infections, scalded
CC skin syndrome, toxic shock syndrome, etc. Organisms transformed with the

CC DNA sequences can be used for recombinant production of the polypeptides.
CC The new DNA sequences (and their fragments) are useful as primers or
CC probes for isolating homologues of any of the 5191 S.aureus DNA sequences
CC contained on the computer readable medium
XX
SQ Sequence 1027 AA;
QY
Query Match 100.0%; Score 56; DB 2; Length 1027;
Best Local Similarity 100.0%; Pred. No. 0.25;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 841 DTNKKRPSYQ 850
1 DTNKKRPSYQ 10
|||||
AAR8749 standard; protein; 77 AA.
XX
AC AAR8749;
XX
DT 24-SEP-1996 (first entry)
XX
DE S. aureus fibronectin binding protein D2D3 polypeptide.
XX
KM Fibronectin binding protein; D2D3; prevention; adhesion; bacteria;
KM gram positive; extra-cellular matrix protein; in-dwelling device;
KM catheter; wound; D2D3; oral pathogen; oral cavity; J2385; NCIMB 40532.
XX
OS Staphylococcus aureus.
XX
PN WO9604380-A1.
XX
PD 15-FEB-1996.
XX
PF 28-JUL-1995; 95WO-EP003039.
XX
PR 05-AUG-1994; 94GB-00015901.
XX
PA (SMIX) SMITHKLINE BEECHAM PLC.
XX
PI Critchley IA, Dodd I, Barnett P, Mossakowska DEI;
XX
XX WPI; 1996-129396/13.
XX
DR N-PSDB; AAT12582.
XX
PT Staphylococcus aureus fibronectin binding protein D2D3 polypeptide -
PT useful for combating infection at wound sites, surgical implants, etc.
XX
XX Claim 5; Page 26; 38pp; English.
XX
XX The present sequence is the S. aureus fibronectin binding protein
CC polypeptide D2D3, which can be used to prevent adhesion of (e.g. gram
CC positive) bacteria, to extra-cellular matrix proteins on in-dwelling
CC devices, e.g. catheters or in wounds. D2D3 can also be used to prevent
CC oral pathogens from binding to extra-cellular matrix proteins, in the
CC oral cavity. D2D3 was found to be effective at inhibiting S. aureus 8325-
CC 4, and 120 adhesion to fibronectin coated PMMA coverslips, at a min.
CC adhesion inhibitor concn. of 10 microg/ml. D2D3 was derived from the D2
CC and D3 regions of the S. aureus J2385 (NCIMB 40532) fibronectin binding
CC protein
XX
SQ Sequence 77 AA;
QY
Query Match 94.6%; Score 53; DB 2; Length 77;
Best Local Similarity 90.0%; Pred. No. 0.062;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Db 50 DTNKKRPSYQ 59
1 DTNKKRPSYQ 10
|||||
50 DTNKKRPSYQ 59

RESULT 13

AAR90939 standard; peptide; 101 AA.

AAR90939;

23-SEP-1996 (first entry)

D3D4 polypeptide #3.

XX Fibronectin binding protein; Fbp; S.aureus J2385; monoclonal antibody;
 XX infection; surgical implant; antiadherent agent; hygiene; adhesion;
 XX extracellular matrix protein; oral pathogen; oral cavity.

Staphylococcus aureus.

Key Location/Qualifiers

Region 1..35 /note= "D3 region fragment"

Region 36..50 /note= "D4 region"

Region 51..101 /note= "WRI region fragment"

W09604381-A1.

15-FEB-1996.

28-JUL-1995; 95WO-EP003040.

05-AUG-1994; 94GB-00015900.

(SMIK) SMITHKLINE BEECHAM PLC.

Critchley IA, Dodd I, Barnett P, Mcbay DL;

WPI; 1996-129397/13.

XX Polypeptide(s) derived from Staphylococcus aureus fibronectin binding
 XX protein - inhibit binding of bacteria to extracellular matrix proteins,
 XX for combating infection at the site of wounds and surgical implants, and
 XX in oral hygiene.

Claim 6; Page 24; 35pp; English.

XX AAR90937-R90942 represent D3D4 polypeptides. These sequences correspond
 CC to fragments of the Staphylococcus aureus fibronectin binding protein
 CC (Fbp). This sequence corresponds to residues 81-181 of S.aureus J2385
 CC Fbp, and also contains a portion of the wall region 1 (WRI). These
 CC sequences, and monoclonal antibodies against them can be used to combat
 CC infection at the site of wounds, surgical implants and other in-dwelling
 CC devices (such as catheters), and as antiadherent agents in oral hygiene.
 CC They can also be used in the manufacture of a medicament for the
 CC prevention of adhesion of bacteria to extracellular matrix proteins
 CC present on in-dwelling devices or in wounds, or of oral pathogens to
 CC similar proteins on surfaces in the oral cavity

SQ Sequence 101 AA;

Query Match 94.6%; Score 53; DB 2; Length 101;

Best Local Similarity 90.0%; Pred. No. 0.082; Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DTNKKPSYQ 10

DB 8 DTNKKPMYQ 17

RESULT 14

AAR90937 standard; peptide; 113 AA.

AAR90937;

23-SEP-1996 (first entry)

D3D4 polypeptide #1.

XX Fibronectin binding protein; Fbp; S.aureus J2385; monoclonal antibody;
 XX infection; surgical implant; antiadherent agent; hygiene; adhesion;
 XX extracellular matrix protein; oral pathogen; oral cavity.

Staphylococcus aureus.

Key Location/Qualifiers

Region 1..21 /note= "D1 region fragment"

Region 22..59 /note= "D2 region"

Region 60..98 /note= "D3 region"

Region 99..113 /note= "D4 region"

Misc-difference 113 /note= "P113T"

W09604381-A1.

15-FEB-1996.

28-JUL-1995; 95WO-EP003040.

05-AUG-1994; 94GB-00015900.

(SMIK) SMITHKLINE BEECHAM PLC.

Critchley IA, Dodd I, Barnett P, Mcbay DL;

WPI; 1996-129397/13.

XX Polypeptide(s) derived from Staphylococcus aureus fibronectin binding
 XX protein - inhibit binding of bacteria to extracellular matrix proteins,
 XX for combating infection at the site of wounds and surgical implants, and
 XX in oral hygiene.

Claim 6; Page 24; 35pp; English.

XX AAR90937-R90942 represent D3D4 polypeptides. These sequences correspond
 CC to fragments of the Staphylococcus aureus fibronectin binding protein
 CC (Fbp). This sequence corresponds to residues 18-130 of S.aureus J2385
 CC Fbp, and also contains the D2 region, and a portion of the D1 region.
 CC These sequences, and monoclonal antibodies against them can be used to
 CC combat infection at the site of wounds, surgical implants and other in-
 CC dwelling devices (such as catheters), and as antiadherent agents in oral
 CC hygiene. They can also be used in the manufacture of a medicament for the
 CC prevention of adhesion of bacteria to extracellular matrix proteins
 CC present on in-dwelling devices or in wounds, or of oral pathogens to
 CC similar proteins on surfaces in the oral cavity

SQ Sequence 113 AA;

Query Match 94.6%; Score 53; DB 2; Length 113;

Best Local Similarity 90.0%; Pred. No. 0.091; Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DTNKKPSYQ 10

DB 71 DTNKKPMYQ 80

RESULT 15

AAR90940 standard; peptide; 124 AA.


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AC  AAR90940;
XX
DT  23-SEP-1996 (first entry)
XX
DE  D3D4 polypeptide #4.
XX
KM  Fibronectin binding protein; Fbp; S.aureus J2385; monoclonal antibody;
XX  infection; surgical implant; antiadherent agent; hygiene; adhesion;
KM  extracellular matrix protein; oral pathogen; oral cavity.
XX
OS  Staphylococcus aureus.
XX
XX  Key
XX  FH      Location/Qualifiers
XX  FT      Region
XX  FT      1..19
XX  FT      /note= "D2 region fragment"
XX  FT      20..58
XX  FT      /note= "D3 region"
XX  FT      59..62
XX  FT      /note= "D4 region"
XX  FT      63..124
XX  FT      /note= "WRI region"
XX
XX  WO9604381-A1.
XX
XX  15-FEB-1996.
XX
XX  28-JUL-1995; 95WO-EP003040.
XX
XX  05-AUG-1994; 94GB-00015900.
XX
XX  (SMIK ) SMITHKLINE BEECHAM PLC.
XX
XX  Critchley IA, Dodd I, Barnett P, Mcbay DL;
XX
XX  WPI; 1996-129397/13.
XX
XX  Polypeptide(s) derived from Staphylococcus aureus fibronectin binding
XX  PT  protein - inhibit binding of bacteria to extracellular matrix proteins,
XX  PT  for combatting infection at the site of wounds and surgical implants, and
XX  PT  in oral hygiene.
XX
XX  Claim 6; Page 24; 35pp; English.
XX
XX  AAR90937-R90942 represent D3D4 polypeptides. These sequences correspond
XX  CC  to fragments of the Staphylococcus aureus fibronectin binding protein
XX  CC  (Fbp). This sequence corresponds to residues 58-181 of S.aureus J2385
XX  CC  Fbp, and also contains a portion of the D2 region, and a portion of the
XX  CC  wall region 1 (WRI). These sequences, and monoclonal antibodies against
XX  CC  them can be used to combat infection at the site of wounds, surgical
XX  CC  implants and other in-dwelling devices (such as catheters), and as
XX  CC  antiadherent agents in oral hygiene. They can also be used in the
XX  CC  manufacture of a medicament for the prevention of adhesion of bacteria to
XX  CC  extracellular matrix proteins present on in-dwelling devices or in
XX  CC  wounds, or of oral pathogens to similar proteins on surfaces in the oral
XX  CC  cavity.
XX
XX  Sequence 124 AA:
XX
XX  Query Match 94.6%; Score 53; DB 2; Length 124;
XX  Best Local Similarity 90.0%; Pred. No. 0.1;
XX  Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
XX
QY  1 DTNKKPSYQ 10
XX  |||||:|
Db  31 DTNKKPSYQ 40

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Search completed: October 25, 2005, 21:29:11
 Job time : 69.7126 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 22, 2005, 07:41:53 ; Search time 17.2989 Seconds
(without alignments)
43.153 Million cell updates/sec

Title: US-10-731-238-93
Perfect score: 56
Sequence: 1 DTNKPSPYQ 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA*
1: /cgn2_6/ptodata/1/1aa/5A.COMB.pep:*
2: /cgn2_6/ptodata/1/1aa/5B.COMB.pep:*
3: /cgn2_6/ptodata/1/1aa/6A.COMB.pep:*
4: /cgn2_6/ptodata/1/1aa/6B.COMB.pep:*
5: /cgn2_6/ptodata/1/1aa/PCITUS.COMB.pep:*
6: /cgn2_6/ptodata/1/1aa/backfill1est1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	56	100.0	10	4	US-09-010-317-93 Sequence 93, Appl
2	56	100.0	37	1	US-08-234-622A-4 Sequence 4, Appl
3	56	100.0	38	1	US-08-294-189-8 Sequence 8, Appl
4	56	100.0	38	1	US-08-729-767-5 Sequence 5, Appl
5	56	100.0	114	1	US-08-259-000-3 Sequence 3, Appl
6	56	100.0	139	3	US-08-856-253-8 Sequence 8, Appl
7	56	100.0	178	2	US-08-459-135A-12 Sequence 12, Appl
8	56	100.0	178	3	US-08-495-559-12 Sequence 12, Appl
9	56	100.0	1027	4	US-08-956-171E-5254 Sequence 5254, Ap
10	56	100.0	1027	4	US-08-781-986A-5254 Sequence 5254, Ap
11	53	94.6	130	2	US-08-459-135A-7 Sequence 7, Appl
12	53	94.6	130	2	US-08-459-135A-8 Sequence 8, Appl
13	53	94.6	130	3	US-08-495-559-7 Sequence 7, Appl
14	53	94.6	130	3	US-08-495-559-8 Sequence 8, Appl
15	53	94.6	174	2	US-08-459-135A-10 Sequence 10, Appl
16	53	94.6	174	2	US-08-459-135A-13 Sequence 13, Appl
17	53	94.6	174	3	US-08-495-559-10 Sequence 10, Appl
18	53	94.6	174	3	US-08-495-559-13 Sequence 13, Appl
19	53	94.6	176	3	US-08-495-559-6 Sequence 6, Appl
20	53	94.6	181	2	US-08-459-135A-6 Sequence 6, Appl
21	53	94.6	559	4	US-08-956-171E-5251 Sequence 5251, Ap
22	53	94.6	559	4	US-08-781-986A-5251 Sequence 5251, Ap
23	45	80.4	10	4	US-09-010-317-94 Sequence 94, Appl
24	44	76.8	10	4	US-09-010-317-92 Sequence 92, Appl
25	43	76.8	38	1	US-08-234-622A-3 Sequence 3, Appl
26	43	76.8	38	1	US-08-729-767-4 Sequence 4, Appl
27	43	76.8	38	4	US-09-010-317-7 Sequence 7, Appl

28	43	76.8	38	4	US-09-010-317-8 Sequence 8, Appl
29	43	76.8	38	4	US-09-010-317-45 Sequence 45, Appl
30	43	76.8	38	4	US-09-010-317-46 Sequence 46, Appl
31	43	76.8	38	4	US-09-010-317-47 Sequence 47, Appl
32	43	76.8	38	4	US-09-010-317-49 Sequence 49, Appl
33	43	76.8	38	4	US-09-010-317-50 Sequence 50, Appl
34	39	69.6	10	4	US-09-010-317-68 Sequence 68, Appl
35	39	69.6	14	4	US-09-010-317-105 Sequence 105, App
36	39	69.6	38	1	US-08-234-622A-2 Sequence 2, Appl
37	39	69.6	38	1	US-08-729-767-3 Sequence 3, Appl
38	39	69.6	38	4	US-09-010-317-5 Sequence 5, Appl
39	39	69.6	38	4	US-09-010-317-6 Sequence 6, Appl
40	39	69.6	38	4	US-09-010-317-35 Sequence 35, Appl
41	39	69.6	38	4	US-09-010-317-36 Sequence 36, Appl
42	39	69.6	38	4	US-09-010-317-43 Sequence 43, Appl
43	39	69.6	38	4	US-09-010-317-44 Sequence 44, Appl
44	39	69.6	38	4	US-09-010-317-44 Sequence 44, Appl
45	39	69.6	39	4	US-09-010-317-56 Sequence 56, Appl

ALIGNMENTS

RESULT 1
US-09-010-317-93
Sequence 93, Application US/09010317
Patent No. 6685943
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
APPLICANT: Patti, Joseph M.
APPLICANT: House-Pompeo, Karen L.
APPLICANT: Speziale, Pietro
APPLICANT: McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
TITLE OF INVENTION: AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hübner, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAMK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-474-7577
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 93:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-09-010-317-93
Query Match 100.0%; Score 56; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0002;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DTNKDKPSYQ 10
Db 1 DTNKDKPSYQ 10

RESULT 2

US-08-234-622A-4
; Sequence 4, Application US/08234622A
; Patent No. 5440014
; GENERAL INFORMATION:
; APPLICANT: HOOK, Magnus
; APPLICANT: MCGAVIN, Martin
; APPLICANT: RAUCCI, Giuseppe
; TITLE OF INVENTION: A FIBRONECTIN BINDING PEPTIDE
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Doane, Swecker & Mathis
; STREET: P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/234,622A
; FILING DATE: 28-APR-1994
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: SE 9002617-0
; FILING DATE: 10-AUG-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/SE91/00534
; FILING DATE: 09-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Meuth, Donna M
; REGISTRATION NUMBER: 36,607
; REFERENCE/DOCKET NUMBER: 012885-044
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 37 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-234-622A-4

Query Match 100.0%; Score 56; DB 1; Length 37;
Best Local Similarity 100.0%; Pred. No. 0.00088;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DTNKDKPSYQ 10
Db 11 DTNKDKPSYQ 20

RESULT 3

US-08-234-189-8
; Sequence 8, Application US/08234189
; Patent No. 5707822
; GENERAL INFORMATION:
; APPLICANT: Fischetti, Vincent A.
; APPLICANT: Rakonjac, Jasna
; APPLICANT: Robbins, John
; TITLE OF INVENTION: GENE SERUM OPACITY FACTOR

NUMBER OF SEQUENCES: 23

CORRESPONDENCE ADDRESS:

ADDRESSEE: Klauber & Jackson

STREET: 411 Hackensack Avenue

CITY: Hackensack

STATE: New Jersey

COUNTRY: USA

ZIP: 07601

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/294,189

FILING DATE: 22-AUG-1994

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Jackson Esq., David A.

REGISTRATION NUMBER: 26,742

REFERENCE/DOCKET NUMBER: 600-1-118

TELECOMMUNICATION INFORMATION:

TELEPHONE: 201 487-5800

TELEFAX: 201 343-1684

TELEX: 133521

INFORMATION FOR SEQ ID NO: 8:

SEQUENCE CHARACTERISTICS:

LENGTH: 38 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: unknown

MOLECULE TYPE: peptide

ORIGINAL SOURCE:

ORGANISM: Streptococcus pyogenes

STRAIN: D734

INDIVIDUAL ISOLATE: 22

IMMEDIATE SOURCE:

CLONE: SAU3a

US-08-294-189-8

Query Match 100.0%; Score 56; DB 1; Length 38;
Best Local Similarity 100.0%; Pred. No. 0.00091;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DTNKDKPSYQ 10
Db 5 DTNKDKPSYQ 14

RESULT 4

US-08-729-767-5
; Sequence 5, Application US/08729767
; Patent No. 5770702
; GENERAL INFORMATION:
; APPLICANT: HOOK, Magnus
; APPLICANT: LINDBERG, Martin Kjell
; APPLICANT: SIGNAS, Lars Christer
; APPLICANT: MADSTROM, Torkel Mikael
; APPLICANT: FROWAN, Gunnar
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN AS WELL AS
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Doane, Swecker & Mathis, L.L.P.
; STREET: P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/729,767
FILING DATE: 07-OCT-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/259,000
FILING DATE: 13-JUN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/007,817
FILING DATE: 22-JAN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/201,028
FILING DATE: 01-JUN-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: SE 8702272-9
FILING DATE: 01-JUN-1987
ATTORNEY/AGENT INFORMATION:
NAME: McGowan, Malcolm K.
REGISTRATION NUMBER: 39,300
REFERENCE/DOCKET NUMBER: 012889-036
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-729-767-5

Query Match 100.0%; Score 56; DB 1; Length 38;
Best Local Similarity 100.0%; Pred. No. 0.00091;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DTNKDKPSYQ 10
Db 12 DTNKDKPSYQ 21

RESULT 5
US-08-259-000-3
Sequence 3, Application US/08259000
Patent No. 5571514
GENERAL INFORMATION:
APPLICANT: HOOK, Magnus
APPLICANT: LINDBERG, Martin Kjell
APPLICANT: SIGNAS, Lars Christer
APPLICANT: MADSTROM, Torkel Mikael
APPLICANT: FROMAN, Gunnar
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN AS WELL AS
NUMBER OF INVENTIONS: 4
TITLE OF INVENTION: ITS PREPARATION
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Burns, Doane, Swecker & Mathis
STREET: P.O. Box 1404
CITY: Alexandria
STATE: Virginia
COUNTRY: United States
ZIP: 22113-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/259,000
FILING DATE: 13-JUN-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: SE 8702272-9

FILING DATE: 01-JUN-1987
ATTORNEY/AGENT INFORMATION:
NAME: Meuth, Donna M
REGISTRATION NUMBER: 36,607
REFERENCE/DOCKET NUMBER: 012885-062
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 114 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-259-000-3

Query Match 100.0%; Score 56; DB 1; Length 114;
Best Local Similarity 100.0%; Pred. No. 0.0031;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DTNKDKPSYQ 10
Db 88 DTNKDKPSYQ 97

RESULT 6
US-08-856-253-8
Sequence 8, Application US/08856253
Patent No. 6288214
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
APPLICANT: Patti, Joseph M.
APPLICANT: House-Pompeo, Karen
APPLICANT: Stahanam, Narayana
APPLICANT: Symersky, Jindrich
TITLE OF INVENTION: COLLAGEN BINDING PROTEIN COMPOSITIONS
NUMBER OF INVENTIONS: 8
TITLE OF INVENTION: AND METHODS OF USE
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: Texas
COUNTRY: U.S.
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/856,253
FILING DATE: Concurrently Herewith
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/017,678
FILING DATE: 16-MAY-1996
ATTORNEY/AGENT INFORMATION:
NAME: Kitchell, Barbara S.
REGISTRATION NUMBER: 33,928
REFERENCE/DOCKET NUMBER: TANK:193
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
TELEFAX: (512) 474-7577
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 139 amino acids
TYPE: amino acid
STRANDEDNESS: linear
TOPOLOGY: linear
US-08-856-253-8

Query Match 100.0%; Score 56; DB 3; Length 139;
Best Local Similarity 100.0%; Pred. No. 0.0039;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DTNKKPSYQ 10
|||||
Db 102 DTNKKPSYQ 111

RESULT 7

US-08-459-135A-12
; Sequence 12, Application US/08459135A
; Patent No. 5955078
; GENERAL INFORMATION:
; APPLICANT: BURHAM, Martin Karl Russel
; APPLICANT: CHOPRA, Ian
; APPLICANT: CRITCHLEY, Ian Alfred
; APPLICANT: KNOWLES, David Justin Charles
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN: MONOCLONAL ANTIBODY AND THEIR US
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corporation
; STREET: 709 Swedeland Road
; CITY: King of Prussia
; STATE: PA
; COUNTRY: U.S.A.
; ZIP: 19406-0939
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq, Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/459,135A
; FILING DATE: 02-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB/94/00215
; FILING DATE: 04-Feb-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Gimm1, Edward R
; REGISTRATION NUMBER: 38,891
; REFERENCE/DOCKET NUMBER: P30591C2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-270-4478
; TELEFAX: 610-270-5090
; TELEX:
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 178 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Protein
US-08-459-135A-12

Query Match 100.0%; Score 56; DB 2; Length 178;
Best Local Similarity 100.0%; Pred. No. 0.0052;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DTNKKPSYQ 10
|||||
Db 88 DTNKKPSYQ 97

RESULT 8

US-08-495-559-12
; Sequence 12, Application US/08495559A
; Patent No. 6054572
; GENERAL INFORMATION:
; APPLICANT: BURHAM, Martin Karl Russel
; APPLICANT: CHOPRA, Ian

; APPLICANT: CRITCHLEY, Ian Alfred
; APPLICANT: KNOWLES, David Justin Charles
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN: MONOCLONAL
; TITLE OF INVENTION: ANTIBODY AND THEIR USE IN PREVENTING BACTERIAL ADHESION
; FILE REFERENCE: P30591
; CURRENT APPLICATION NUMBER: US/08/495,559A
; CURRENT FILING DATE: 1995-08-03
; EARLIER APPLICATION NUMBER: GB 9302289.5
; EARLIER FILING DATE: 1993-02-05
; EARLIER APPLICATION NUMBER: GB 9321592.9
; EARLIER FILING DATE: 1993-10-20
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 12
; LENGTH: 178
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-08-495-559-12

Query Match 100.0%; Score 56; DB 3; Length 178;
Best Local Similarity 100.0%; Pred. No. 0.0052;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DTNKKPSYQ 10
|||||
Db 88 DTNKKPSYQ 97

RESULT 9

US-08-956-171E-5254
; Sequence 5254, Application US/08956171E
; Patent No. 6593114
; GENERAL INFORMATION:
; APPLICANT: Charles Kunsch
; Gil H. Choi
; Patrick S. Dillon
; Craig A. Rosen
; Steven C. Barash
; Michael R. Pannon
; TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
; NUMBER OF SEQUENCES: 5256
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4mb storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/956,171E
; FILING DATE: 20-Oct-1997
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/009,861
; FILING DATE: January 5, 1996
; APPLICATION NUMBER: 08/781,986
; FILING DATE: January 3, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Mark J. Hyman
; REGISTRATION NUMBER: 46,789
; REFERENCE/DOCKET NUMBER: PB248P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (240) 314-1224
; TELEFAX: (301) 309-8439
; INFORMATION FOR SEQ ID NO: 5254:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1027 amino acids
; TYPE: amino acid

STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 5254:
US-08-956-1718-5254

Query Match 100.0%; Score 56; DB 4; Length 1027;
Best Local Similarity 100.0%; Pred. No. 0.037;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DTNKKPSYQ 10
|||||
Db 841 DTNKKPSYQ 850

RESULT 10
US-08-781-986A-5254
Sequence 5254, Application US/08781986A
Patent No. 6737248
GENERAL INFORMATION:
APPLICANT: Charles Kunsch
TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
NUMBER OF SEQUENCES: 5255
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COUNTRY: USA
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/781,986A
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION NUMBER:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Benson, Bob
REGISTRATION NUMBER: 30,446
REFERENCE/DOCKET NUMBER: PB248PP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 5254:
SEQUENCE CHARACTERISTICS:
LENGTH: 1027 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-781-986A-5254

Query Match 100.0%; Score 56; DB 4; Length 1027;
Best Local Similarity 100.0%; Pred. No. 0.037;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DTNKKPSYQ 10
|||||
Db 841 DTNKKPSYQ 850

RESULT 11
US-08-459-135A-7
Sequence 7, Application US/08459135A
Patent No. 5955078
GENERAL INFORMATION:
APPLICANT: BURHAM, Martin Karl Russel

APPLICANT: CHOPRA, Ian
APPLICANT: CRITCHLEY, Ian Alfred
APPLICANT: KNOWLES, David Justin Charles
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN: MONOCLONAL ANTIBODY AND THEIR US
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
STATE: PA
COUNTRY: U.S.A.
ZIP: 19406-0939
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: Fastseq, Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/459,135A
FILING DATE: 02-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: PCT/GB/94/00215
APPLICATION NUMBER: 04-Feb-1994
FILING DATE: 04-Feb-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Gimm1, Edward R
REGISTRATION NUMBER: 38,891
REFERENCE/DOCKET NUMBER: P30591C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-4478
TELEFAX: 610-270-5090
TELEX:
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 130 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-459-135A-7

Query Match 94.6%; Score 53; DB 2; Length 130;
Best Local Similarity 90.0%; Pred. No. 0.013;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DTNKKPSYQ 10
|||||
Db 88 DTNKKPSYQ 97

RESULT 12
US-08-459-135A-8
Sequence 8, Application US/08459135A
Patent No. 5955078
GENERAL INFORMATION:
APPLICANT: BURHAM, Martin Karl Russel
APPLICANT: CHOPRA, Ian
APPLICANT: CRITCHLEY, Ian Alfred
APPLICANT: KNOWLES, David Justin Charles
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN: MONOCLONAL ANTIBODY AND THEIR U
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
STATE: PA
COUNTRY: U.S.A.
ZIP: 19406-0939
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: Fastseq, Version 2.0

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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/459,135A
; FILING DATE: 02-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB/94/00215
; FILING DATE: 04-Feb-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Gimmi, Edward R
; REGISTRATION NUMBER: 38,891
; REFERENCE/DOCKET NUMBER: P30591C2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-270-4478
; TELEFAX: 610-270-5090
; TELEX:
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 130 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
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US-08-459-135A-8

Query Match          94.6%; Score 53; DB 2; Length 130;
Best Local Similarity 90.0%; Pred. No. 0.013;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 DTNKKPSYQ 10
      |||||:|
Db      88 DTNKKPNYQ 97

RESULT 13
; Sequence 7, Application US/08495559A
; Patent No. 6054572
; GENERAL INFORMATION:
; APPLICANT: BURHAM, Martin Karl Russel
; APPLICANT: CHOPRA, Ian
; APPLICANT: CRITCHLEY, Ian Alfred
; APPLICANT: KNOWLES, David Justin Charles
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN: MONOCLONAL
; FILE REFERENCE: P30591
; CURRENT APPLICATION NUMBER: US/08/495,559A
; CURRENT FILING DATE: 1995-08-03
; EARLIER APPLICATION NUMBER: GB 9302289.5
; EARLIER FILING DATE: 1993-02-05
; EARLIER APPLICATION NUMBER: GB 9321592.9
; EARLIER FILING DATE: 1993-10-20
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 7
; LENGTH: 130
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
;
US-08-495-559-7

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Best Local Similarity 90.0%; Pred. No. 0.013;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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Db      88 DTNKKPNYQ 97

RESULT 14
; Sequence 8, Application US/08495559A
; Patent No. 6054572
; GENERAL INFORMATION:
; APPLICANT: BURHAM, Martin Karl Russel
; APPLICANT: CHOPRA, Ian
; APPLICANT: CRITCHLEY, Ian Alfred
; APPLICANT: KNOWLES, David Justin Charles
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN: MONOCLONAL
; FILE REFERENCE: P30591
; CURRENT APPLICATION NUMBER: US/08/495,559A
; CURRENT FILING DATE: 1995-08-03
; EARLIER APPLICATION NUMBER: GB 9302289.5
; EARLIER FILING DATE: 1993-02-05
; EARLIER APPLICATION NUMBER: GB 9321592.9
; EARLIER FILING DATE: 1993-10-20
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 8
; LENGTH: 130
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
;
US-08-495-559-8

Query Match          94.6%; Score 53; DB 3; Length 130;
Best Local Similarity 90.0%; Pred. No. 0.013;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 DTNKKPSYQ 10
      |||||:|
Db      88 DTNKKPNYQ 97

RESULT 15
; Sequence 10, Application US/08459135A
; Patent No. 5955078
; GENERAL INFORMATION:
; APPLICANT: BURHAM, Martin Karl Russel
; APPLICANT: CHOPRA, Ian
; APPLICANT: CRITCHLEY, Ian Alfred
; APPLICANT: KNOWLES, David Justin Charles
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN: MONOCLONAL ANTIBODY AND THEIR US
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corporation
; STREET: 709 Swedeland Road
; CITY: King of Prussia
; STATE: PA
; COUNTRY: U.S.A.
; ZIP: 19406-0939
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq, Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/459,135A
; FILING DATE: 02-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB/94/00215
; FILING DATE: 04-Feb-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Gimmi, Edward R
; REGISTRATION NUMBER: 38,891
; REFERENCE/DOCKET NUMBER: P30591C2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-270-4478
; TELEFAX: 610-270-5090
; TELEX:
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 174 amino acids
; TYPE: amino acid
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;
; APPLICANT: BURHAM, Martin Karl Russel
; APPLICANT: CHOPRA, Ian
; APPLICANT: CRITCHLEY, Ian Alfred
; APPLICANT: KNOWLES, David Justin Charles
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN: MONOCLONAL
; FILE REFERENCE: P30591
; CURRENT APPLICATION NUMBER: US/08/495,559A
; CURRENT FILING DATE: 1995-08-03
; EARLIER APPLICATION NUMBER: GB 9302289.5
; EARLIER FILING DATE: 1993-02-05
; EARLIER APPLICATION NUMBER: GB 9321592.9
; EARLIER FILING DATE: 1993-10-20
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 8
; LENGTH: 130
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
;
US-08-495-559-8

Query Match          94.6%; Score 53; DB 3; Length 130;
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Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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Db      88 DTNKKPNYQ 97

RESULT 15
; Sequence 10, Application US/08459135A
; Patent No. 5955078
; GENERAL INFORMATION:
; APPLICANT: BURHAM, Martin Karl Russel
; APPLICANT: CHOPRA, Ian
; APPLICANT: CRITCHLEY, Ian Alfred
; APPLICANT: KNOWLES, David Justin Charles
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN: MONOCLONAL ANTIBODY AND THEIR US
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corporation
; STREET: 709 Swedeland Road
; CITY: King of Prussia
; STATE: PA
; COUNTRY: U.S.A.
; ZIP: 19406-0939
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq, Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/459,135A
; FILING DATE: 02-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB/94/00215
; FILING DATE: 04-Feb-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Gimmi, Edward R
; REGISTRATION NUMBER: 38,891
; REFERENCE/DOCKET NUMBER: P30591C2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-270-4478
; TELEFAX: 610-270-5090
; TELEX:
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 174 amino acids
; TYPE: amino acid
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! TOPOLOGY: linear
! MOLECULE TYPE: Protein
US-08-459-135A-10

Query March 94.6%; Score 53; DB 2; Length 174;
Best Local Similarity 90.0%; Pred. NO. 0.018;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DTNKKPPSYQ 10
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Db 88 DTNKKPPSYQ 97

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Job time : 17.2989 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using SW model

Run on: October 22, 2005, 12:39:57 ; Search time 56.1494 Seconds
(without alignments)
74.354 Million cell updates/sec

Title: US-10-731-238-93
Perfect score: 56
Sequence: 1 DTNKPSPYQ 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1862951 seqs, 417491010 residues

Total number of hits satisfying chosen parameters: 1862951

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

Published Applications AA:*

1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
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22: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	56	100.0	10	US-10-731-238-93	Sequence 93, Appl
2	56	100.0	37	US-11-066-697-1134	Sequence 1134, Ap
3	56	100.0	139	US-09-813-820-8	Sequence 8, Appl
4	56	100.0	1018	US-09-815-242-5797	Sequence 5797, Ap
5	56	100.0	1018	US-09-815-242-12838	Sequence 12838, A
6	56	100.0	1018	US-10-470-0488-68	Sequence 68, Appl
7	56	100.0	1027	US-08-781-986A-5254	Sequence 5254, Ap
8	56	100.0	1027	US-10-329-624-5254	Sequence 5254, Ap
9	53	94.6	388	US-08-901-062-1	Sequence 1, Appl
10	53	94.6	559	US-08-781-986A-5251	Sequence 5251, Ap
11	53	94.6	559	US-10-329-624-5251	Sequence 5251, Ap

12	53	94.6	940	US-10-470-0488-424	Sequence 424, App
13	53	94.6	948	US-10-470-0488-69	Sequence 69, Appl
14	53	94.6	961	US-10-282-122A-4378	Sequence 4378, A
15	53	94.6	978	US-09-815-242-5456	Sequence 5456, Ap
16	53	94.6	1001	US-09-815-242-12686	Sequence 12686, A
17	53	94.6	1038	US-10-282-122A-43827	Sequence 43827, A
18	45	80.4	10	US-10-731-238-94	Sequence 94, Appl
19	44	78.6	10	US-10-731-238-92	Sequence 92, Appl
20	43	76.8	30	US-10-287-821-1	Sequence 1, Appl
21	43	76.8	31	US-10-287-821-2	Sequence 2, Appl
22	43	76.8	31	US-10-731-238-7	Sequence 7, Appl
23	43	76.8	38	US-10-731-238-8	Sequence 8, Appl
24	43	76.8	38	US-10-731-238-45	Sequence 45, Appl
25	43	76.8	38	US-10-731-238-46	Sequence 46, Appl
26	43	76.8	38	US-10-731-238-47	Sequence 47, Appl
27	43	76.8	38	US-10-731-238-49	Sequence 49, Appl
28	43	76.8	38	US-10-731-238-50	Sequence 50, Appl
29	43	76.8	767	US-09-815-242-5899	Sequence 5899, Ap
30	43	76.8	767	US-09-815-242-13140	Sequence 13140, A
31	39	69.6	10	US-10-731-238-68	Sequence 68, Appl
32	39	69.6	14	US-10-731-238-105	Sequence 105, App
33	39	69.6	38	US-10-731-238-5	Sequence 5, Appl
34	39	69.6	38	US-10-731-238-6	Sequence 6, Appl
35	39	69.6	38	US-10-731-238-35	Sequence 35, Appl
36	39	69.6	38	US-10-731-238-36	Sequence 36, Appl
37	39	69.6	38	US-10-731-238-37	Sequence 37, Appl
38	39	69.6	38	US-10-731-238-43	Sequence 43, Appl
39	39	69.6	38	US-10-731-238-44	Sequence 44, Appl
40	39	69.6	39	US-10-731-238-56	Sequence 56, Appl
41	39	69.6	39	US-10-731-238-57	Sequence 57, Appl
42	39	69.6	112	US-09-864-408A-942	Sequence 942, App
43	38	67.9	31	US-09-764-877-1401	Sequence 1401, Ap
44	38	67.9	15	US-10-242-515-1401	Sequence 1401, Ap
45	38	67.9	928	US-09-801-368-282	Sequence 282, App

ALIGNMENTS

RESULT 1
US-10-731-238-93
Sequence 93, Application US/10731238
Publication No. US20050123552A1
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
Patti, Joseph M.
House-Pompeo, Karen L.
Speziale, Pietro
Joh, Danny
McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P. O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/731, 238
FILING DATE: 10-Dec-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE: 21-Jan-1998
APPLICATION NUMBER: US 60/036,139

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;
; FILING DATE: 21-JAN-1997
; ATTORNEY/AGENT INFORMATION:
;   NAME: Hibler, David W.
;   REGISTRATION NUMBER: 41,071
;   REFERENCE/DOCKET NUMBER: TAMK:189
; TELECOMMUNICATION INFORMATION:
;   TELEPHONE: 512-418-3000
;   TELEFAX: 512-474-7577
; INFORMATION FOR SEQ ID NO: 93:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH: 10 amino acids
;     TYPE: amino acid
;     STRANDEDNESS: <Unknown>
;     TOPOLOGY: linear
;
; SEQUENCE DESCRIPTION: SEQ ID NO: 93:
US-10-731-238-93

Query Match          100.0%; Score 56; DB 18; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0024;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DTNKDKPSYQ 10
Db 1 DTNKDKPSYQ 10

RESULT 2
US-11-066-697-1134
; Sequence 1134, Application US/11066697
; Publication No. US20050187159A1
; GENERAL INFORMATION:
;   APPLICANT: Bridon, Dominique P.
;   APPLICANT: Ezrin, Alan M.
;   APPLICANT: Milner, Peter G.
;   APPLICANT: Holmes, Darren U.
;   APPLICANT: Thibaudau, Karen
; TITLE OF INVENTION: PROTECTION OF ENDOGENOUS THERAPEUTIC PEPTIDES FROM
; TITLE OF INVENTION: PEPTIDASE ACTIVITY THROUGH CONJUGATION TO BLOOD
; FILE REFERENCE: 500862002301
; CURRENT APPLICATION NUMBER: US/11/066,697
; CURRENT FILING DATE: 2005-02-25
; PRIOR APPLICATION NUMBER: 09/657,276
; PRIOR FILING DATE: 2000-09-07
; PRIOR APPLICATION NUMBER: 60/153,406
; PRIOR FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: 60/159,783
; PRIOR FILING DATE: 1999-10-15
; NUMBER OF SEQ ID NOS: 1617
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1134
; LENGTH: 37
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptide
US-11-066-697-1134

Query Match          100.0%; Score 56; DB 20; Length 37;
Best Local Similarity 100.0%; Pred. No. 0.0093;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DTNKDKPSYQ 10
Db 11 DTNKDKPSYQ 20

RESULT 3
US-09-813-820-8
; Sequence 8, Application US/09813820
; Patent No. US20020102262A1
; GENERAL INFORMATION:
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; APPLICANT: Hook, Magnus
;   Patti, Joseph M.
;   House-Pompeo, Karen
;   Stenham, Narayana
;   Synerky, Jindrich
; TITLE OF INVENTION: COLLAGEN BINDING PROTEIN COMPOSITIONS
;   AND METHODS OF USE
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Arnold, White & Durkee
;   STREET: P.O. Box 4433
;   CITY: Houston
;   STATE: Texas
;   COUNTRY: U.S.
;   ZIP: 77210
;
; COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: PatentIn Release #1.0, Version #1.30
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;   APPLICATION NUMBER: US/09/813,820
;   FILING DATE: 22-Mar-2001
;   CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: 08/856,253
;   FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
;   NAME: Kitchell, Barbara S.
;   REGISTRATION NUMBER: 33,928
;   REFERENCE/DOCKET NUMBER: TAMK:193
; TELECOMMUNICATION INFORMATION:
;   TELEPHONE: (512) 418-3000
;   TELEFAX: (512) 474-7577
; INFORMATION FOR SEQ ID NO: 8:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH: 139 amino acids
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;     STRANDEDNESS: <Unknown>
;     TOPOLOGY: linear
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; SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-09-813-820-8

Query Match          100.0%; Score 56; DB 9; Length 139;
Best Local Similarity 100.0%; Pred. No. 0.036;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DTNKDKPSYQ 10
Db 102 DTNKDKPSYQ 111

RESULT 4
US-09-815-242-5797
; Sequence 5797, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
;   APPLICANT: Haeelbeck, Robert
;   APPLICANT: Ohlsen, Karl L.
;   APPLICANT: Zyskind, Judith W.
;   APPLICANT: Wall, Daniel
;   APPLICANT: Trawick, John D.
;   APPLICANT: Carr, Grant J.
;   APPLICANT: Yamamoto, Robert T.
;   APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
;   TITLE OF INVENTION: Prokaryotes
; FILE REFERENCE: ELITRA.01A
; CURRENT APPLICATION NUMBER: US/09/815,242
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
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;; PRIOR FILING DATE: 2000-05-23
;; PRIOR APPLICATION NUMBER: 60/207,727
;; PRIOR FILING DATE: 2000-05-26
;; PRIOR APPLICATION NUMBER: 60/242,578
;; PRIOR FILING DATE: 2000-10-23
;; PRIOR APPLICATION NUMBER: 60/253,625
;; PRIOR FILING DATE: 2000-11-27
;; PRIOR APPLICATION NUMBER: 60/257,931
;; PRIOR FILING DATE: 2000-12-22
;; PRIOR APPLICATION NUMBER: 60/269,308
;; PRIOR FILING DATE: 2001-02-16
;; NUMBER OF SEQ ID NOS: 14110
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO: 5797
;; LENGTH: 1018
;; TYPE: PRT
;; ORGANISM: Staphylococcus aureus
US-09-815-242-5797

Query Match 100.0%; Score 56; DB 9; Length 1018;
Best Local Similarity 100.0%; Pred. No. 0.29;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DTNKKPSYQ 10
Db 832 DTNKKPSYQ 841

RESULT 5
US-09-815-242-12838
; Sequence 12838, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:

;; APPLICANT: Haselbeck, Robert
;; APPLICANT: Ohlsen, Karl U.
;; APPLICANT: Zyskind, Judith W.
;; APPLICANT: Wall, Daniel
;; APPLICANT: Trawick, John D.
;; APPLICANT: Carr, Grant J.
;; APPLICANT: Yamamoto, Robert T.
;; APPLICANT: Xu, H. Howard
;; TITLE OF INVENTION: Identification of Essential Genes in
;; FILE REFERENCE: ELITRA.011A
;; CURRENT APPLICATION NUMBER: US/09/815,242
;; CURRENT FILING DATE: 2001-03-21
;; PRIOR APPLICATION NUMBER: 60/191,078
;; PRIOR FILING DATE: 2000-03-21
;; PRIOR APPLICATION NUMBER: 60/206,848
;; PRIOR FILING DATE: 2000-05-23
;; PRIOR APPLICATION NUMBER: 60/207,727
;; PRIOR FILING DATE: 2000-05-26
;; PRIOR APPLICATION NUMBER: 60/242,578
;; PRIOR FILING DATE: 2000-10-23
;; PRIOR APPLICATION NUMBER: 60/253,625
;; PRIOR FILING DATE: 2000-11-27
;; PRIOR APPLICATION NUMBER: 60/257,931
;; PRIOR FILING DATE: 2000-12-22
;; PRIOR APPLICATION NUMBER: 60/269,308
;; PRIOR FILING DATE: 2001-02-16
;; NUMBER OF SEQ ID NOS: 14110
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO: 12838
;; LENGTH: 1018
;; TYPE: PRT
;; ORGANISM: Staphylococcus aureus
US-09-815-242-12838

Query Match 100.0%; Score 56; DB 9; Length 1018;
Best Local Similarity 100.0%; Pred. No. 0.29;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 DTNKKPSYQ 10

Db 832 DTNKKPSYQ 841

RESULT 6
US-10-470-048B-68
; Sequence 68, Application US/10470048B
; Publication No. US20050037444A1
; GENERAL INFORMATION:
;; APPLICANT: MEINKE ET AL.
;; TITLE OF INVENTION: A METHOD FOR IDENTIFICATION, ISOLATION AND PRODUCTION OF
;; FILE REFERENCE: SONN.035US
;; CURRENT APPLICATION NUMBER: US/10/470,048B
;; CURRENT FILING DATE: 2003-07-25
;; NUMBER OF SEQ ID NOS: 603
;; SOFTWARE: PatentIn version 3.1
;; SEQ ID NO: 68
;; LENGTH: 1018
;; TYPE: PRT
;; ORGANISM: Staphylococcus aureus
US-10-470-048B-68

Query Match 100.0%; Score 56; DB 17; Length 1018;
Best Local Similarity 100.0%; Pred. No. 0.29;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DTNKKPSYQ 10
Db 832 DTNKKPSYQ 841

RESULT 7
US-08-781-986A-5254
; Sequence 5254, Application US/08781986A
; Publication No. US20030054436A1
; GENERAL INFORMATION:

;; APPLICANT: Charles Kunsch
;; TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
;; NUMBER OF SEQUENCES: 5255
;; CORRESPONDENCE ADDRESS:
;; STREET: 9410 Key West Avenue
;; CITY: Rockville
;; STATE: Maryland
;; COUNTRY: USA
;; ZIP: 20850
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Diskette, 3.50 inch, 1.4mb storage
;; COMPUTER: HP Vectra 486/33
;; OPERATING SYSTEM: MSDOS version 6.2
;; SOFTWARE: ASCII Text
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/781,986A
;; FILING DATE:
;; CLASSIFICATION: 435
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER:
;; FILING DATE:
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Benson, Bob
;; REGISTRATION NUMBER: 30,446
;; REFERENCE/DOCKET NUMBER: PB248BP
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (301) 309-8504
;; TELEFAX: (301) 309-8512
;; INFORMATION FOR SEQ ID NO: 5254:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 1027 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein

US-08-781-986A-5254

Query Match 100.0%; Score 56; DB 8; Length 1027;
Best Local Similarity 100.0%; Pred. No. 0.29; Mismatches 0; Indels 0; Gaps 0;
Matches 10; Conservative 0;

QY 1 DTNKKPSYQ 10
|||||
Db 841 DTNKKPSYQ 850

RESULT 8

US-10-329-624-5254

; Sequence 5254, Application US/10329624

; Publication No. US20040043037A1

; GENERAL INFORMATION:

; APPLICANT: Charles Kunach

; Gil H. Choi

; Patrick S. Dillon

; Craig A. Rosen

; Steven C. Barash

; Michael R. Fannon

; TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences

; NUMBER OF SEQUENCES: 5256

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Human Genome Sciences, Inc.

; STREET: 9410 Key West Avenue

; CITY: Rockville

; STATE: Maryland

; COUNTRY: USA

; ZIP: 20850

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage

; COMPUTER: HP Vectra 486/33

; OPERATING SYSTEM: MSDOS version 6.2

; SOFTWARE: ASCII Text

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/10/329,624

; FILING DATE: 27-Dec-2002

; PRIORITY APPLICATION DATA:

; APPLICATION NUMBER: 08/956,171

; FILING DATE: October 20, 1997

; APPLICATION NUMBER: 60/009,861

; FILING DATE: January 5, 1996

; APPLICATION NUMBER: 08/781,986

; FILING DATE: January 3, 1997

; ATTORNEY/AGENT INFORMATION:

; NAME: Mark J. Hyman

; REGISTRATION NUMBER: 46,789

; REFERENCE/DOCKET NUMBER: PB248P1D1

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (240) 314-1224

; TELEFAX: (301) 309-8439

; INFORMATION FOR SEQ ID NO: 5254:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 1027 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; SEQUENCE DESCRIPTION: SEQ ID NO: 5254:

US-10-329-624-5254

Query Match 100.0%; Score 56; DB 15; Length 1027;

Best Local Similarity 100.0%; Pred. No. 0.29; Mismatches 0; Indels 0; Gaps 0;

Matches 10; Conservative 0;

QY 1 DTNKKPSYQ 10

Db 841 DTNKKPSYQ 850

RESULT 9

US-08-901-062-1

; Sequence 1, Application US/08901062

; Publication No. US20020025324A1

; GENERAL INFORMATION:

; APPLICANT: SEALS, JONATHAN R.

; TITLE OF INVENTION: RECOMBINANT BIVALENT BACTERIAL VACCINE

; NUMBER OF SEQUENCES: 2

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: HALE AND DOR LLP

; STREET: 60 State Street

; CITY: Boston

; STATE: MA

; COUNTRY: United States Of America

; ZIP: 02109

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/901,062

; FILING DATE: 25-JUL-1997

; CLASSIFICATION: 424

; ATTORNEY/AGENT INFORMATION:

; NAME: Baker, Hollie L.

; REGISTRATION NUMBER: 31,321

; REFERENCE/DOCKET NUMBER: 106941.153

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (617) 526-6000

; TELEFAX: (617) 526-5000

; INFORMATION FOR SEQ ID NO: 1:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 388 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; HYPOTHETICAL: NO

; ANTI-SENSE: NO

US-08-901-062-1

Query Match 94.6%; Score 53; DB 8; Length 388;

Best Local Similarity 90.0%; Pred. No. 0.36; Mismatches 9; Conservative 1; Indels 0; Gaps 0;

Matches 9; Conservative 1; Indels 0; Gaps 0;

QY 1 DTNKKPSYQ 10

Db 351 DTNKKPSYQ 360

RESULT 10

US-08-781-986A-5251

; Sequence 5251, Application US/08781986A

; Publication No. US20030054436A1

; GENERAL INFORMATION:

; APPLICANT: Charles Kunach

; TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences

; NUMBER OF SEQUENCES: 5255

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Human Genome Sciences, Inc.

; STREET: 9410 Key West Avenue

; CITY: Rockville

; STATE: Maryland

; COUNTRY: USA

; ZIP: 20850

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage

; COMPUTER: HP Vectra 486/33

; OPERATING SYSTEM: MSDOS version 6.2

; SOFTWARE: ASCII Text

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/781,986A

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/ FILING DATE:
/ CLASSIFICATION: 435
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER:
/ FILING DATE:
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Benson, Bob
/ REGISTRATION NUMBER: 30,446
/ REFERENCE/DOCKET NUMBER: PB248PP
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (301) 309-8504
/ TELEFAX: (301) 309-8512
/ INFORMATION FOR SEQ ID NO: 5251:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 559 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ US-08-781-986A-5251

Query Match          94.6%; Score 53; DB 8; Length 559;
Best Local Similarity 90.0%; Pred. No 0.53;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 DTNKRPSYQ 10
        |||||:|
Db      387 DTNKKRKNYQ 396

RESULT 11
US-10-329-624-5251
/ Sequence 5251, Application US/10329624
/ Publication No. US20040043037A1
GENERAL INFORMATION:
APPLICANT: Charles Kunsch
          Gil H. Choi
          Patrick S. Dillon
          Craig A. Rosen
          Steven C. Barash
          Michael R. Fannon
TITLE OF INVENTION: Staphylococcus aureus polynucleotides and Sequences
NUMBER OF SEQUENCES: 5256
CORRESPONDENCE ADDRESS:
ADDRESSSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COUNTRY: USA
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4MB storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/329,624
FILING DATE: 27-Dec-2002
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/956,171
FILING DATE: October 20, 1997
APPLICATION NUMBER: 60/009,861
FILING DATE: January 5, 1996
APPLICATION NUMBER: 08/781,986
FILING DATE: January 3, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Mark J. Hyman
REGISTRATION NUMBER: 46,789
REFERENCE/DOCKET NUMBER: PB248P1D1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (240) 314-1224
TELEFAX: (301) 309-8439
INFORMATION FOR SEQ ID NO: 5251:

```

```

SEQUENCE CHARACTERISTICS:
LENGTH: 559 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 5251:
US-10-329-624-5251

Query Match      94.6%; Score 53; DB 15; Length 559;
Best Local Similarity 90.0%; Pred. No. 0.53;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 DTNKDKPSYQ 10
| | | | | | | |
DB 387 DTNKDKPNIQ 396

RESULT 12
US-10-470-048B-424
; Sequence 424, Application US/10470048B
; Publication No. US20050037444A1
; GENERAL INFORMATION:
; APPLICANT: MEINKE ET AL.
; TITLE OF INVENTION: A METHOD FOR IDENTIFICATION, ISOLATION AND PRODUCTION OF
; TITLE OF INVENTION: ANTIGENS TO A SPECIFIC PATHOGEN
; FILE REFERENCE: SONN.035US
; CURRENT APPLICATION NUMBER: US/10/470.048B
; CURRENT FILING DATE: 2003-07-25
; NUMBER OF SEQ ID NOS: 603
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 424
; LENGTH: 940
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-10-470-048B-424

Query Match      94.6%; Score 53; DB 17; Length 940;
Best Local Similarity 90.0%; Pred. No. 0.91;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 DTNKDKPSYQ 10
| | | | | | | |
DB 768 DTNKDKPNIQ 777

RESULT 13
US-10-470-048B-69
; Sequence 69, Application US/10470048B
; Publication No. US20050037444A1
; GENERAL INFORMATION:
; APPLICANT: MEINKE ET AL.
; TITLE OF INVENTION: A METHOD FOR IDENTIFICATION, ISOLATION AND PRODUCTION OF
; TITLE OF INVENTION: ANTIGENS TO A SPECIFIC PATHOGEN
; FILE REFERENCE: SONN.035US
; CURRENT APPLICATION NUMBER: US/10/470.048B
; CURRENT FILING DATE: 2003-07-25
; NUMBER OF SEQ ID NOS: 603
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 69
; LENGTH: 948
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-10-470-048B-69

Query Match      94.6%; Score 53; DB 17; Length 948;
Best Local Similarity 90.0%; Pred. No. 0.92;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 DTNKDKPSYQ 10
| | | | | | | |
DB 776 DTNKDKPNIQ 785

```

RESULT 14

```

US-10-282-122A-43778
; Sequence 43778, Application US/10282122A
; Publication No. US20040028129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyckind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 43778
; LENGTH: 961
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-10-282-122A-43778

```

```

Query Match          94.6%; Score 53; DB 15; Length 961;
Best Local Similarity 90.0%; Pred. No. 0.93;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY      1 DTNKDKPSYQ 10
      |||||:|
Db      779 DTNKDKPNYQ 788

```

```

RESULT 15
US-09-815-242-5456
; Sequence 5456, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari L.
; APPLICANT: Zyckind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard

```

```

; TITLE OF INVENTION: Identification of Essential Genes in
; FILE REFERENCE: Prokaryotes
; CURRENT APPLICATION NUMBER: US/09/815,242
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5456
; LENGTH: 978
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-09-815-242-5456

```

```

Query Match          94.6%; Score 53; DB 9; Length 978;
Best Local Similarity 90.0%; Pred. No. 0.95;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY      1 DTNKDKPSYQ 10
      |||||:|
Db      810 DTNKDKPNYQ 819

```

Search completed: October 22, 2005, 12:56:27
Job time : 57.1494 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 22, 2005, 08:04:46 ; Search time 11.6092 Seconds
(without alignments)
82.880 Million cell updates/sec

Title: US-10-731-238-93
Perfect score: 56
Sequence: 1 DTNKKDPSYQ 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	56	100.0	1018	2 A32192	fibronectin-binding
2	53	94.6	940	2 S19702	fibronectin-binding
3	53	94.6	961	2 G90053	hypothetical prote
4	53	94.6	1038	2 H90053	hypothetical prote
5	40	71.4	603	2 S15074	calpastatin - rat
6	40	71.4	654	2 T10772	calpastatin - rat
7	38	67.9	399	2 E86348	P1408.16 protein -
8	38	67.9	928	2 S50578	hypothetical prote
9	37	66.1	261	2 S20610	calpastatin - mous
10	37	66.1	442	2 S39348	26S ATP/ubiquitin-
11	37	66.1	558	2 D82878	phosphomannomutase
12	37	66.1	590	2 S55095	myb-related protei
13	37	66.1	725	1 E64211	virulence-associated
14	37	66.1	941	2 I40772	hypothetical prote
15	37	66.1	946	2 F81361	probable cell divi
16	36	64.3	575	2 T28230	ORF MSV069 probabl
17	36	64.3	739	2 F86337	P14010.2 protein -
18	36	64.3	772	2 T06154	hypothetical prote
19	36	64.3	881	2 E87387	Tom-dependent rec
20	36	64.3	1578	2 AD1512	peptidoglycan boun
21	35	62.5	183	2 B97784	formylmethionine d
22	35	62.5	216	2 H71111	hypothetical prote
23	35	62.5	255	2 E70166	exodeoxyribonuclea
24	35	62.5	310	2 B69755	ion channel homolo
25	35	62.5	327	2 B71146	probable glucose-1
26	35	62.5	432	2 S20108	nuclear protein -
27	35	62.5	519	2 S74242	6-phosphofructo-2-
28	35	62.5	558	2 S68447	origin recognition
29	35	62.5	726	1 S73915	virulence-associated

30	34	60.7	165	2 B84486	probable Achila re
31	34	60.7	343	2 A97057	uncharacterized pr
32	34	60.7	384	2 H96829	probable RNA-bindi
33	34	60.7	410	2 S50191	L-sorbose 1-phosph
34	34	60.7	440	1 A35875	transcription fact
35	34	60.7	440	2 I48291	transcription fact
36	34	60.7	441	1 A51988	transcription fact
37	34	60.7	441	1 TVCHTE	transcription fact
38	34	60.7	441	1 TVHUBT	transcription fact
39	34	60.7	480	2 JC7866	endo-1,6-beta-D-gl
40	34	60.7	485	1 TVCHET	transcription fact
41	34	60.7	488	1 TVPVES	transcription fact
42	34	60.7	519	2 B71726	multidrug resistanc
43	34	60.7	607	2 S58151	hypothetical prote
44	34	60.7	623	2 A64774	ybaU protein
45	34	60.7	623	2 C85541	probable proteinas

ALIGNMENTS

RESULT 1

A32192
fibronectin-binding protein B - Staphylococcus aureus
C:Species: Staphylococcus aureus
C:Date: 31-Jul-1989 #sequence_revision 31-Jul-1989 #text_change 16-Feb-1997
C:Accession: A32192
R:Signaes, C.; Raucci, G.; Joensson, K.; Lindgren, P.E.; Anantharamiah, G.M.; Hoeoek, Proc. Natl. Acad. Sci. U.S.A. 86, 699-703, 1989
A:Title: Nucleotide sequence of the gene for a fibronectin-binding protein from Staphyl
A:Reference number: A32192, MUID:89098998, PMID:2521391
A:Accession: A32192
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1018 <SIG>
A:Cross-references: GB:J04151
C:Keywords: fibronectin binding

Query Match 100.0%; Score 56; DB 2; Length 1018;
Best Local Similarity 100.0%; Pred. No. 0.019;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DTNKKDPSYQ 10
DB 832 DTNKKDPSYQ 841

RESULT 2

A32192
fibronectin-binding protein B - Staphylococcus aureus
C:Species: Staphylococcus aureus
C:Date: 31-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
R:Joensson, K.; Signaes, C.; Mueller, H.P.; Lindberg, M., Eur. J. Biochem. 202, 1041-1048, 1991
A:Title: Two different genes encode fibronectin binding proteins in Staphylococcus aure
A:Reference number: S19702; MUID:92111475; PMID:1837266
A:Accession: S19702
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-940 <JOB>
A:Cross-references: UNIPROT:Q53682; EMBL:X62992; NID:g49040; P1DN:CAA44726.1; PID:g5815
C:Keywords: fibronectin binding

Query Match 94.6%; Score 53; DB 2; Length 940;
Best Local Similarity 90.0%; Pred. No. 0.064;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DTNKKDPSYQ 10
DB 766 DTNKKDPSYQ 777

RESULT 3

G90053

A: hypothetical protein fnbB [imported] - Staphylococcus aureus (strain N315)

C: Species: Staphylococcus aureus

C: Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004

C: Accession: G90053

R: Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguma, A.; Mitsuhashi, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.; C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramoto, K.

Lancet 357, 1225-1240, 2001

A: Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.

A: Reference number: A89758; MUID: 21311952; PMID: 11418146

A: Accession: G90053

A: Status: Preliminary

A: Molecule type: DNA

A: Residues: 1-961 <KIR>

A: Cross-references: UNIPROT: Q99RD3; GB: BA000018; PID: g13702452; PIDN: BAB43593.1; GSPDB: C

A: Experimental source: strain N315

C: Genetics:

A: Gene: fnbB

Query Match 94.6%; Score 53; DB 2; Length 961;

Best Local Similarity 90.0%; Pred. No. 0.066;

Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DTNKKPSYQ 10

Db 779 DTNKKDPYQ 788

RESULT 4

H90053

A: hypothetical protein fnbB [imported] - Staphylococcus aureus (strain N315)

C: Species: Staphylococcus aureus

C: Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004

C: Accession: H90053

R: Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguma, A.; Mitsuhashi, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.; C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramoto, K.

Lancet 357, 1225-1240, 2001

A: Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.

A: Reference number: A89758; MUID: 21311952; PMID: 11418146

A: Accession: H90053

A: Status: Preliminary

A: Molecule type: DNA

A: Residues: 1-1038 <KIR>

A: Cross-references: UNIPROT: Q99RD2; GB: BA000018; PID: g13702453; PIDN: BAB43594.1; GSPDB: C

A: Experimental source: strain N315

C: Genetics:

A: Gene: fnbB

Query Match 94.6%; Score 53; DB 2; Length 1038;

Best Local Similarity 90.0%; Pred. No. 0.071;

Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DTNKKPSYQ 10

Db 828 DTNKKDPYQ 837

RESULT 5

S15074

A: calpastatin - rat

C: Species: Rattus sp. (rat)

C: Date: 18-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004

C: Accession: S15074

R: Iihida, S.; Emori, Y.; Suzuki, K.

Biochim. Biophys. Acta 1088, 436-438, 1991

A: Title: Rat calpastatin has diverged primary sequence from other mammalian calpastatins

A: Reference number: S15074; MUID: 91198152; PMID: 2015306

A: Accession: S15074

A: Molecule type: mRNA

A: Residues: 1-603 <ISH>

A: Cross-references: UNIPROT: P27321; EMBL: X56729; NID: g57783; PIDN: CAA40053.1; PID: g57784

C: Superfamily: calpain inhibitor

Query Match 71.4%; Score 40; DB 2; Length 603;

Best Local Similarity 77.8%; Pred. No. 12;

Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 DTNKKPSY 9

Db 97 DTNKKDPY 105

RESULT 6

T10772

A: calpastatin - rat

C: Species: Rattus norvegicus (Norway rat)

C: Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004

C: Accession: T10772

R: de Tullio, R.; Sparatore, B.; Salamino, F.; Melloni, E.; Pontremoli, S.

FEBS Lett. 422, 113-117, 1998

A: Title: Rat brain contains multiple mRNAs for calpastatin.

A: Reference number: 217133; MUID: 98133328; PMID: 9475181

A: Accession: T10772

A: Status: Preliminary; translated from GB/EMBL/DBJ

A: Molecule type: mRNA

A: Residues: 1-654 <DET>

A: Cross-references: UNIPROT: O55152; EMBL: Y13588; NID: g2765339; PIDN: CAA73916.1; PID: g276

A: Experimental source: strain Sprague Dawley, brain

C: Genetics:

A: Gene: CAST

C: Superfamily: calpain inhibitor

Query Match 71.4%; Score 40; DB 2; Length 654;

Best Local Similarity 77.8%; Pred. No. 13;

Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 DTNKKPSY 9

Db 148 DTNKKDPY 156

RESULT 7

E86348

A: F1408.16 protein - Arabidopsis thaliana

C: Species: Arabidopsis thaliana (mouse-ear cress)

C: Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004

C: Accession: E86348

R: Theologis, A.; Becker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Hughes, B.; Hultzar, L.

Nature 408, 816-820, 2000

A: Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.

C.A.; Li, J.H.; Li, Y.; Liu, X.; Liu, S.X.; Liu, Z.A.; Lurie, J.S.; Maitl, R.; Marziani,

Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A: Authors: Salzberg, S.L.; Schwartz, J.R.; Shim, P.; Southwick, A.M.; Sun, H.; Tallon,

ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A: Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.

A: Reference number: A86141; MUID: 21016719; PMID: 11130712

A: Accession: E86348

A: Status: Preliminary

A: Molecule type: DNA

A: Residues: 1-399 <STO>

A: Cross-references: UNIPROT: Q9LPR4; GB: AE005172; NID: g9454579; PIDN: AAF87902.1; GSPDB: C

C: Genetics:

A: Map position: 1

Query Match 67.9%; Score 38; DB 2; Length 399;

Best Local Similarity 87.5%; Pred. No. 13;

Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 TNKKPSY 9

Db 335 TNKKPSY 342

RESULT 8

S50578

hypothetical protein YER075C - yeast (Saccharomyces cerevisiae)

C/Species: Saccharomyces cerevisiae

C/Date: 28-May-1993 #sequence_revision 24-Feb-1995 #text_change 09-Jul-2004

C/Accession: S50578

R/Dietrich, F.S.

submitted to the EMBL Data Library, December 1994

A/Description: The sequence of S. cerevisiae lambda clone 3612 and cosmid 9747.

A/Reference number: S50438

A/Accession: S50578

A/Molecule type: DNA

A/Residues: 1-928 <DIR>

A/Cross-references: UNIPROT:P40048; EMBL:U18814; NID:g603309; PIDN:AAB64614.1; PID:g6033

C/Genetics:

A/Gene: SGD:PTP3

A/Cross-references: SGD:S0000877; MIPS:YER075C

A/Map position: 5R

C/Keywords: phosphoprotein

F/527-867/Domain: protein-tyrosine-phosphatase homology <PTP2>

F/804/Active site: Cys (phosphocysteine intermediate) #status predicted

F/810/Binding site: Substrate phosphate (Arg) #status predicted

Query Match 67.1%; Score 37; DB 2; Length 928;
Best Local Similarity 70.0%; Pred. No. 46;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;Qy 1 DTNKKPSYQ 10
|||||
Db 384 DTNKKLGFG 393

RESULT 9

S20610

calpastatin - mouse (fragment)

C/Species: Mus musculus (house mouse)

C/Date: 20-May-1994 #sequence_revision 12-Apr-1996 #text_change 13-Aug-1999

C/Accession: S20610; S17344

R/Lee, W.J.; Hatanaka, M.; Maki, M.

Biochim. Biophys. Acta 1129, 251-253, 1992

A/Title: Multiple forms of rat calpastatin cDNA in the coding region of functionally unk

A/Reference number: S20610; MUID:92110395; PMID:1730065

A/Accession: S20610

A/Molecule type: mRNA

A/Residues: 1-261 <LEB>

A/Cross-references: EMBL:X62519; NID:g50296; PIDN:CAA44385.1; PID:g50297

C/Superfamily: calpain inhibitor

Query Match 66.1%; Score 37; DB 2; Length 261;
Best Local Similarity 66.7%; Pred. No. 19;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;Qy 1 DTNKKPSY 9
|||:
Db 148 DTNRDDPY 156

RESULT 10

S39348

26S ATP/ubiquitin-dependent proteinase chain 84 - fission yeast (Schizosaccharomyces pom

C/Species: Schizosaccharomyces pombe

C/Date: 18-Feb-1994 #sequence_revision 23-Feb-1996 #text_change 09-Jul-2004

C/Accession: S39348; T40421

R/Gordon, C.; McGurk, G.; Dillon, P.; Rosen, C.; Haerle, N.D.

Nature 366, 355-357, 1993

A/Title: Defective mitosis due to a mutation in the gene for a fission yeast 26S proteas

A/Reference number: S39348; MUID:94067321; PMID:8247131

A/Accession: S39348

A/Status: nucleic acid sequence not shown

A/Molecule type: DNA

A/Residues: 1-448 <GOR>

A/Cross-references: UNIPROT:P36612; EMBL:Z29366; NID:g442507; PIDN:CAA82554.1; PID:g442

R/McDougall, R.C.; Rajandream, M.A.; Barrall, B.G.; Brown, S.; Harris, D.

submitted to the EMBL Data Library, October 1999

A/Reference number: Z21927

A/Accession: T40421

A/Status: preliminary; translated from GB/EMBL/DDBJ

A/Molecule type: DNA

A/Residues: 1-448 <MCD>

A/Cross-references: EMBL:AL121863; PIDN:CA858406.1; GSPDB:GN00067; SPDB:SPBC4.07C

A/Experimental source: strain 972h-; cosmid c4

C/Genetics:

A/Gene: SPBC4.07C

A/Map position: 2

A/Introns: 1/3

C/Keywords: ATP-dependent 26S proteinase; FtsH/SEC18/CDC48-type ATP-binding domain h

F/205-416/Domain: FtsH/SEC18/CDC48-type ATP-binding domain homology <VATP>

F/232-239/Region: nucleotide-binding motif A (P-loop)

Query Match 66.1%; Score 37; DB 2; Length 448;
Best Local Similarity 60.0%; Pred. No. 33;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;Qy 1 DTNKKPSYQ 10
|||||
Db 23 DQKKPKRYE 32

RESULT 11

D82878

phosphomannomutase UUS30 [imported] - Ureaplasma urealyticum

C/Species: Ureaplasma urealyticum

C/Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000

C/Accession: D82878

R/Glass, J.I.; Leftkowitz, E.J.; Glass, J.S.; Heiner, C.R.; Chen, E.Y.; Caswell, G.H.

submitted to GenBank, February 2000

A/Description: The complete sequence of Ureaplasma urealyticum: Alternate views of a mi

A/Reference number: A82870

A/Accession: D82878

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-552 <GLA>

A/Cross-references: GB:A8002152; GB:AF222894; NID:g6899532; PIDN:AAF30943.1; GSPDB:GN00

A/Experimental source: serovar 3; biovar 1

C/Genetics:

A/Gene: cpsG; UUS30

A/Genetic code: SGC3

Query Match 66.1%; Score 37; DB 2; Length 552;
Best Local Similarity 70.0%; Pred. No. 41;
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;Qy 1 DTNKKPSYQ 10
|||||
Db 400 DINNDKSYQ 409

RESULT 12

S55095

myb-related protein YMR213W - yeast (Saccharomyces cerevisiae)

N/Alternate names: hypothetical protein YMR261.07

C/Species: Saccharomyces cerevisiae

C/Date: 08-Jul-1995 #sequence_revision 01-Sep-1995 #text_change 09-Jul-2004

C/Accession: S55095

R/Dedman, K.; Brown, D.; Bowman, S.

submitted to the EMBL Data Library, June 1995

A/Reference number: S55089

A/Accession: S55095

A/Molecule type: DNA

A/Residues: 1-590 <DED>

A/Cross-references: UNIPROT:Q03654; EMBL:Z49809; NID:g854459; PIDN:CAA89928.1; PID:g8544

A/Experimental source: strain AB972

C/Genetics:

A:Gene: SGD:CEP1; MIPS:YMR213W
 A:Cross-references: SGD:S0004826
 A:Map position: 13R
 C:Superfamily: myb DNA-binding protein cdc5; myb DNA-binding repeat homology
 F/5-56/Domain: myb DNA-binding repeat homology <MYB1>
 F/57-106/Domain: myb DNA-binding repeat homology <MYB2>

Query Match 66.1%; Score 37; DB 1; Length 590;
 Best Local Similarity 87.5%; Pred. No. 44;
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DTNKKPS 8
 |||||
 Db 254 DGNKKPS 261

RESULT 13

E64211
 virulence-associated protein vacB homolog - Mycoplasma genitalium
 C:Species: Mycoplasma genitalium
 C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
 C:Accession: E64211
 R:Fraser, C.M.; Gocayne, J.D.; White, O.; Adams, M.D.; Clayton, R.A.; Fleischmann, R.D.;
 M.; Fultmann, J.; Nguyen, D.; Usterback, T.R.; Saudek, D.M.; Phillips, C.A.; Merrick, J.
 , C.A.; Venter, J.C.
 Science 270, 397-403, 1995
 A:Title: The minimal gene complement of Mycoplasma genitalium.
 A:Reference number: A64200; MUID:96026346; PMID:7569993
 A:Accession: E64211
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-725 <TIGR>
 A:Cross-references: UNIPROT:P47350; GB:U39690; GB:I43967; NID:g1045782; PID:g1045783; TT
 A:Experimental source: strain G-37
 C:Genetics:
 A:Genetic code: SGC3
 C:Superfamily: virulence-associated protein vacB homolog

Query Match 66.1%; Score 37; DB 1; Length 725;
 Best Local Similarity 75.0%; Pred. No. 55;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 NKDKPSYQ 10
 |||||
 Db 531 NKDNPSYE 538

RESULT 14

I40772
 hypothetical protein 1 - Campylobacter jejuni
 C:Species: Campylobacter jejuni
 C:Date: 16-Aug-1996 #sequence_revision 16-Aug-1996 #text_change 08-Oct-1999
 C:Accession: I40772
 R:Miller, S.; Pesci, B.C.; Pickett, C.L.
 Gene 146, 31-38, 1994
 A:Title: Genetic organization of the region upstream from the Campylobacter jejuni flaga
 A:Reference number: I40772; MUID:94341566; PMID:8063102
 A:Accession: I40772
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-941 <RES>
 A:Cross-references: EMBL:U06951; NID:g472793; PID:AAA61512.1; PID:g633732

Query Match 66.1%; Score 37; DB 2; Length 941;
 Best Local Similarity 66.7%; Pred. No. 73;
 Matches 8; Conservative 2; Mismatches 0; Indels 2; Gaps 1;

QY 1 DTNK-DKPSYQ 10
 |||||
 Db 278 DTNKNLDEPSYK 269

RESULT 15

F81361
 probable cell division protein Cj0886c [imported] - Campylobacter jejuni (strain NCTC 11
 C:Species: Campylobacter jejuni
 C:Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004
 C:Accession: F81361
 R:Parkhill, J.; Wren, B.W.; Mungall, K.; Kellay, J.M.; Churcher, C.; Basham, D.; Chiller
 C.W.; Quail, M.; Rajandream, M.A.; Rutherford, K.M.; VanVleet, A.; Whitehead, S.; Barrell
 Nature 403, 665-668, 2000
 A:Title: The genome sequence of the food-borne pathogen Campylobacter jejuni reveals hyl
 A:Reference number: A81250; MUID:20150912; PMID:10688204
 A:Accession: F81361
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-946 <PAR>
 A:Cross-references: UNIPROT:Q46089; GB:AL139076; GB:AL111168; NID:g6968128; PID:CA8731.
 A:Experimental source: serotype O2, strain NCTC 11168
 C:Genetics:
 A:Gene: ftsK; Cj0886c

Query Match 66.1%; Score 37; DB 2; Length 946;
 Best Local Similarity 66.7%; Pred. No. 73;
 Matches 8; Conservative 2; Mismatches 0; Indels 2; Gaps 1;

QY 1 DTNK-DKPSYQ 10
 |||||
 Db 283 DTNKNLDEPSYK 294

Search completed: October 22, 2005, 09:55:44
 Job time : 12.6092 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 22, 2005, 08:01:06 ; Search time 56.2069 Seconds
(without alignments)
91.106 Million cell updates/sec

Title: US-10-731-238-93
Perfect score: 56
Sequence: 1 DTNKPSPSYQ 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt_03:*

1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	56	100.0	152	2	Q9AEP9	Q9AEP9 staphylococ
2	56	100.0	1018	1	FNBA STAAU	P14738 staphylococ
3	53	94.6	940	2	Q53682	Q53682 staphylococ
4	53	94.6	943	2	Q8NUU8	Q8NUU8 staphylococ
5	53	94.6	957	2	Q6G6H4	Q6G6H4 staphylococ
6	53	94.6	961	2	Q99RD3	Q99RD3 staphylococ
7	53	94.6	961	2	Q7A3J8	Q7A3J8 staphylococ
8	53	94.6	965	2	Q6GDUS	Q6GDUS staphylococ
9	53	94.6	1015	2	Q8NUU7	Q8NUU7 staphylococ
10	53	94.6	1015	2	Q6G6H3	Q6G6H3 staphylococ
11	53	94.6	1038	2	Q99RD2	Q99RD2 staphylococ
12	53	94.6	1038	2	Q7A3J7	Q7A3J7 staphylococ
13	42	75.0	517	2	Q7PNT2	Q7PNT2 anopheles g
14	40	71.4	176	2	O55155	O55155 rattus norv
15	40	71.4	267	2	Q6UCN4	Q6UCN4 unculured
16	40	71.4	593	2	Q99MG2	Q99MG2 rattus norv
17	40	71.4	616	2	O55151	O55151 rattus norv
18	40	71.4	654	1	ICAL RAT	P27321 rattus norv
19	40	71.4	654	2	O55152	O55152 rattus norv
20	40	71.4	654	2	Q99MG1	Q99MG1 rattus norv
21	39	69.6	382	2	Q8BRV7	Q8BRV7 mus musculu
22	39	69.6	382	2	Q6CYC7	Q6CYC7 kluyveromyc
23	39	69.6	523	2	Q8UZZ0	Q8UZZ0 mus musculu
24	39	69.6	523	2	Q8VC11	Q8VC11 m hypocheit
25	39	69.6	1067	2	Q747N2	Q747N2 geobacter s
26	39	69.6	1123	2	O6S255	O6S255 streptococc
27	39	69.6	1167	2	Q8QV02	Q8QV02 filii diseas
28	38	67.9	320	2	Q6A6X7	Q6A6X7 propionibac
29	38	67.9	325	2	Q6B1X9	Q6B1X9 aradidopsis
30	38	67.9	399	2	Q9LPK4	Q9LPK4 aradidopsis
31	38	67.9	613	2	Q6UDMS	Q6UDMS brachydanio

32	38	67.9	742	2	Q8ES96	Q8ES96 oceanobacil
33	38	67.9	928	1	PFP3 YEAST	P40048 saccharomyc
34	38	67.9	1069	2	Q6FXV0	Q6FXV0 candida gla
35	38	67.9	1069	2	Q6KEZ7	Q6KEZ7 candida gla
36	38	67.9	1293	2	Q698P5	Q698P5 avian ortho
37	37	66.1	155	2	Q7N5Q4	Q7N5Q4 photorhabdu
38	37	66.1	370	2	Q6PBD3	Q6PBD3 xenopus tro
39	37	66.1	401	2	Q9U0Z5	Q9U0Z5 leishmania
40	37	66.1	448	1	PRS4 SCHPO	P3612 schizosacch
41	37	66.1	485	2	Q9M8Z6	Q9M8Z6 aradidopsis
42	37	66.1	552	2	Q9PPW0	Q9PPW0 ureaplasma
43	37	66.1	590	1	CEFL YEAST	Q03654 saccharomyc
44	37	66.1	590	2	Q6B1D8	Q6B1D8 saccharomyc
45	37	66.1	674	2	Q921U7	Q921U7 mus musculu

ALIGNMENTS

RESULT 1

Q9AEP9 PRELIMINARY; PRT; 152 AA.
AC Q9AEP9;
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Fibronectin-binding protein (fragment).
GN Name=fnb;
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxId=1280;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=2124681; PubMed=11349044;
RX DOI=10.1128/IAI.69.6.3791-3799.2001;
RA Rice K., Huesca M., Var D., McGavin M.J.;
RT "Variance in fibronectin binding and fnb locus polymorphisms in a Staphylococcus aureus: identification of antigenic variation in a fibronectin binding protein adhesin of the epidemic CMRSA-1 strain of methicillin-resistant S. aureus.";
RL Infect. Immun. 69:3791-3799(2001).
DR EMBL; AY029184; AAK31588.1; -.
FT NON_TER
FT NON_TER
SQ SEQUENCE 152 AA; 17193 MW; CFA3913C2B11C025 CRC64;

Query Match 100.0%; Score 56; DB 2; Length 152;

Best local Similarity 100.0%; Pred. NO. 0.035;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DTNKPSPSYQ 10
DB 125 DTNKPSPSYQ 134

RESULT 2

FNBA STAAU STANDARD; PRT; 1018 AA.
AC P14738;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Fibronectin-binding protein precursor (FNBP).
GN Name=fnba;
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxId=1280;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NCIC 8325-4;
RX MEDLINE=89098998; PubMed=2521391;
RA Signaes C., Raucet G., Joensson K., Lindgren P.-E.,

RA Anantharamaiah G.M., Hoecek M., Lindberg M.;
 RT "Nucleotide sequence of the gene for a fibronectin-binding protein
 from *Staphylococcus aureus*: use of this peptide sequence in the
 RT synthesis of biologically active peptides.";
 RL Proc. Natl. Acad. Sci. U.S.A. 86:699-703(1989).
 CC -1- FUNCTION: The ability of bacteria to bind fibronectin has been
 CC proposed as a virulence factor enabling bacteria to colonize wound
 CC tissues and blood clots. Binding of plasma fibronectin to the
 CC bacterial surface might block adhesion receptors on *S. aureus*, thus
 CC representing an important defense mechanism against tissue
 CC invasion.
 CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
 CC an amide bond (potential).
 CC -----
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 CC -----
 CC EMBL, J04151, AAA26632.1, -.
 DR InterPro: IPR004237; Fn_bind.
 DR InterPro: IPR005877; Gpos_YsIRK.
 DR InterPro: IPR001899; Gram_pos_anchor.
 DR Pfam: PF02986; Fn_bind_1.
 DR Pfam: PF00746; Gram_pos_anchor_1.
 DR Pfam: PF04650; YsIRK_signal_1.
 DR TIGRFAMs: TIGR01167; LpXTG_anchor_1.
 DR TIGRFAMs: TIGR01168; YsIRK_signal_1.
 DR PROSITE: PSS0847; GRAM_POS_ANCHORING; 1.
 KW Cell adhesion; Cell wall; Peptidoglycan-anchor; Repeat; Signal;
 KM virulence.
 FT SIGNAL 1 36
 FT CHAIN 37 985 Fibronectin-binding protein.
 FT PROPEP 986 1018 Removed by sortase (potential).
 FT REPEAT 545 574 B-1.
 FT REPEAT 575 604 B-2.
 FT DOMAIN 745 878 4 X approximate tandem repeats,
 FT REPEAT 745 782 fibronectin-binding domain.
 FT REPEAT 783 820 D-1.
 FT REPEAT 821 859 D-2.
 FT REPEAT 860 878 D-3.
 FT DOMAIN 879 948 D-4 (incomplete).
 FT REPEAT 879 948 5 X tandem repeats, Pro-rich (WR).
 FT REPEAT 893 906 WR 1.
 FT REPEAT 907 920 WR 2.
 FT REPEAT 921 934 WR 3.
 FT REPEAT 935 948 WR 4.
 FT SITE 982 986 LpXTG sorting signal (potential).
 FT MOD_RES 985 985 Penicillin signal (potential).
 FT MOD_RES 985 985 Penicillin signal (potential).
 SQ SEQUENCE 1018 AA; 111780 MW; 58175E0020E81F1F CRC64;
 Query Match 100.0%; Score 56; DB 1; Length 1018;
 Best Local Similarity 100.0%; Pred. No. 0.25; Indels 0; Gaps 0;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DTNKKPSYQ 10
 DB 832 DTNKKPSYQ 841
 RESULT 3
 Q53682 PRELIMINARY; PRT; 940 AA.
 AC Q53682;
 DT 01-NOV-1996 (Tremblrel. 01, Created)
 DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
 DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)
 DE Fibronectin binding protein B.

GN Name=fnbB;
 OS *Staphylococcus aureus*.
 OC Bacteria; Firmicutes; Bacillales; Staphylococcaceae.
 OX NCBI_TaxID=1280;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=8325-4;
 RX MEDLINE=92111475; PubMed=1837266;
 RA Jonsson K., Signas C., Muller H.P., Lindberg M.;
 RT "Two different genes encode fibronectin binding proteins in
 RT *Staphylococcus aureus*. The complete nucleotide sequence and
 RT characterization of the second gene."
 RL Eur. J. Biochem. 202:1041-1048(1991).
 CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
 CC an amide bond (By similarity).
 CC EMBL: X62992; CAA44726.1; -.
 DR PIR, S19702; S19702.
 DR HSP, Q53653; I1N67.
 DR GO: GO:0009986; C:cell surface; IEA.
 DR GO: GO:0005618; C:cell wall; IEA.
 DR GO: GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
 DR GO: GO:0016020; C:membrane; IEA.
 DR GO: GO:0007155; P:cell adhesion; IEA.
 DR InterPro: IPR008966; Adhes_bact.
 DR InterPro: IPR004237; Fn_bind.
 DR InterPro: IPR005877; Gpos_YsIRK.
 DR InterPro: IPR001899; Gram_pos_anchor.
 DR Pfam: PF02986; Fn_bind_2.
 DR Pfam: PF00746; Gram_pos_anchor_1.
 DR Pfam: PF04650; YsIRK_signal_1.
 DR TIGRFAMs: TIGR01167; LpXTG_anchor_1.
 DR TIGRFAMs: TIGR01168; YsIRK_signal_1.
 DR PROSITE: PSS0847; GRAM_POS_ANCHORING; 1.
 KW Cell wall; Peptidoglycan-anchor.
 SQ SEQUENCE 940 AA; 103555 MW; E35FBBCA907AE345 CRC64;
 Query Match 94.6%; Score 53; DB 2; Length 940;
 Best Local Similarity 90.0%; Pred. No. 0.81;
 Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DTNKKPSYQ 10
 DB 768 DTNKKPSYQ 777
 RESULT 4
 Q8NTU8 PRELIMINARY; PRT; 943 AA.
 AC Q8NTU8;
 DT 01-OCT-2002 (Tremblrel. 22, Created)
 DT 01-OCT-2002 (Tremblrel. 22, Last sequence update)
 DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
 DE FnBb protein.
 GN Name=fnbB; Ordered locus names=MW2420;
 OS *Staphylococcus aureus* (strain MW2).
 OC Bacteria; Firmicutes; Bacillales; Staphylococcaceae.
 OX NCBI_TaxID=196620;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=MW2;
 RX MEDLINE=22040717; PubMed=12044378; DOI=10.1016/S0140-6736(02)08713-5;
 RA Baba T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Oguchi A.,
 RA Nagai Y., Iwama N., Asano K., Naimi T., Kuroda H., Cui L.,
 RA Yamamoto K., Hiramatsu K.;
 RT "Genome and virulence determinants of high virulence community-
 RT acquired MRSA."
 RL Lancet 359:1819-1827(2002).
 CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
 CC an amide bond (By similarity).
 CC EMBL: AP004830; BAB96285.1; -.
 DR HSP, Q53653; I1N67.
 DR GO: GO:0009986; C:cell surface; IEA.
 DR GO: GO:0005618; C:cell wall; IEA.

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DR GO: GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO: GO:0016020; C:membrane; IEA.
DR GO: GO:0007155; P:cell adhesion; IEA.
DR InterPro: IPR008966; Adhes_bact.
DR InterPro: IPR004237; Fn_bind.
DR InterPro: IPR005877; Gpos_YsIRK.
DR InterPro: IPR001899; Gram_pos_anchor.
DR Pfam: PF02986; Fn_bind; 1.
DR Pfam: PF00746; Gram_pos_anchor; 1.
DR TIGRPFAMs: TIGR01167; LPXTG_anchor; 1.
DR TIGRPFAMs: TIGR01168; YsIRK_signal; 1.
DR PROSITE: PS50847; GRAM_POS_ANCHORING; 1.
DR Cell wall; Complete proteome; Peptidoglycan-anchor.
KW SEQUENCE 943 AA; 104537 MW; DA8A5F31947E1B6A CRC64;

Query March 94.6%; Score 53; DB 2; Length 943;
Best Local Similarity 90.0%; Pred. No. 0.81;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DTNKKPSYQ 10
Db 775 DTNKKPNYQ 784
|||||
|

RESULT 5
ID O6G6H4 PRELIMINARY; PRT; 957 AA.
AC O6G6H4.
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Fibronectin-binding protein.
GN Name=fnbB; OrderedlocusNames=SA52387;
OS Staphylococcus aureus (strain MSSA476).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=282459;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=1521324; DOI=10.1073/pnas.0402521101;
RA Holden M.T.G., Fell E.J., Lindsey J.A., Peacock S.J., Day N.P.J.,
RA Enright M.C., Foster T.J., Moore C.E., Hurst L., Atkin R., Barron A.,
RA Baon N., Bentley S.D., Chillingworth C., Chillingworth T.,
RA Churcher C., Clark L., Cronin A., Doggett J., Dowd L.,
RA Fellwell T., Hance Z., Harris B., Hauser H., Holroyd S., Jagels K.,
RA James K.D., Leonard N., Line A., Mayes R., Moule S., Mungall K.,
RA Omund S., Quail M.A., Rabinowitch E., Rutherford K.M., Sanders M.,
RA Sharp S., Simmonds M., Stevens K., Whitehead S., Barrett B.G.,
RA Spratt B.G., Parkhill J.;
RT "Complete genomes of two clinical Staphylococcus aureus strains:
RT evidence for the rapid evolution of virulence and drug resistance.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:9786-9791(2004).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC an amide bond (By similarity).
DR EMBL; BX571857; CAG44201.1; -.
DR GO: GO:0009986; C:cell surface; IEA.
DR GO: GO:0005618; C:cell wall; IEA.
DR GO: GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO: GO:0016020; C:membrane; IEA.
DR InterPro: IPR008966; Adhes_bact.
DR InterPro: IPR004237; Fn_bind.
DR InterPro: IPR005877; Gpos_YsIRK.
DR InterPro: IPR001899; Gram_pos_anchor.
DR Pfam: PF02986; Fn_bind; 1.
DR Pfam: PF00746; Gram_pos_anchor; 1.
DR TIGRPFAMs: TIGR01167; LPXTG_anchor; 1.
DR TIGRPFAMs: TIGR01168; YsIRK_signal; 1.
DR PROSITE: PS50847; GRAM_POS_ANCHORING; 1.
DR Cell wall; Complete proteome; Peptidoglycan-anchor.
KW SEQUENCE 957 AA; 105980 MW; 28F8BA7FFDFD3EAF CRC64;
SQ

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Query March 94.6%; Score 53; DB 2; Length 957;
Best Local Similarity 90.0%; Pred. No. 0.82;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DTNKKPSYQ 10
Db 775 DTNKKPNYQ 784
|||||
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RESULT 6
ID O99RD3 PRELIMINARY; PRT; 961 AA.
AC O99RD3.
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Fibronectin-binding protein homolog.
GN Name=fnbB; OrderedlocusNames=SAV2502;
OS Staphylococcus aureus (strain Mu50 / ATCC 700699).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=158878;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=Mu50 / ATCC 700699;
RX MEDLINE=21311952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2;
RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Ii H., Ito T.,
RA Kanamori M., Matsunari H., Maruyama A., Miyakami H., Hosoyama A.,
RA Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
RA Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuuchi J.,
RA Kanehisa M., Yanaoishi A., Oshima K., Furuya K., Yoshino C., Shiba T.,
RA Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
RT "Whole genome sequencing of methicillin-resistant Staphylococcus
RT aureus.";
RL Lancet 357:1225-1240(2001).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC an amide bond (By similarity).
DR EMBL; AP003365; BAB58664.1; -.
DR PIR; G90053; G90053.
DR HSSP; Q53653; IN67.
DR GO: GO:0009986; C:cell surface; IEA.
DR GO: GO:0005618; C:cell wall; IEA.
DR GO: GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO: GO:0016020; C:membrane; IEA.
DR InterPro: IPR008966; Adhes_bact.
DR InterPro: IPR004237; Fn_bind.
DR InterPro: IPR005877; Gpos_YsIRK.
DR InterPro: IPR001899; Gram_pos_anchor.
DR Pfam: PF02986; Fn_bind; 1.
DR Pfam: PF00746; Gram_pos_anchor; 1.
DR TIGRPFAMs: TIGR01167; LPXTG_anchor; 1.
DR TIGRPFAMs: TIGR01168; YsIRK_signal; 1.
DR PROSITE: PS50847; GRAM_POS_ANCHORING; 1.
DR Cell wall; Complete proteome; Peptidoglycan-anchor.
KW SEQUENCE 961 AA; 106010 MW; 364940F884EA4101 CRC64;
SQ

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Query March 94.6%; Score 53; DB 2; Length 961;
Best Local Similarity 90.0%; Pred. No. 0.83;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DTNKKPSYQ 10
Db 779 DTNKKPNYQ 788
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|

RESULT 7
ID O7A3J8 PRELIMINARY; PRT; 961 AA.
AC O7A3J8.
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)

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DT 05-JUL-2004 (TReMBLrel. 27, last annotation update)
DE FnbB protein.
GN Name=fnbB: OrderedlocusNames=SA2290;
OS Staphylococcus aureus (strain N315)
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=158879;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=1311952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2;
RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Iian J.-Q., Ito T.,
RA Kanamori M., Matsunaru H., Maruyama A., Murakami H.,
RA Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
RA Sekimizu K., Hiraoka H., Kuhara S., Goto S., Yabuzaki J.,
RA Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
RA Hanebisa M., Ogasawara N., Hayashi H., Hiramatsu K.;
RT "Whole genome sequencing of methicillin-resistant Staphylococcus
RT aureus."
RL Lancet 357:1225-1240(2001).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC an amide bond (By similarity).
DR EMBL: AP003137; BAB3593.1; -.
DR GO: GO:0009986; C:cell surface; IEA.
DR GO: GO:0005618; C:cell wall; IEA.
DR GO: GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO: GO:0016020; C:membrane; IEA.
DR GO: GO:0007155; P:cell adhesion; IEA.
DR InterPro: IPR008966; Adhes_bact.
DR InterPro: IPR004237; Fn_bind.
DR InterPro: IPR005877; Gpos_YsIRK.
DR InterPro: IPR01899; Gram_pos_anchor.
DR Pfam: PF02986; Fn_bind; 1.
DR Pfam: PF00746; Gram_pos_anchor; 1.
DR TIGRFAMs: TIGR01167; LPXTG_anchor; 1.
DR TIGRFAMs: TIGR01168; YsIRK_signal; 1.
DR PROSITE: PS50847; GRAM_POS_ANCHORING; 1.
KM Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ SEQUENCE 961 AA; 106010 MW; 364940F84EA4101 CRC64;

Query Match 94.6%; Score 53; DB 2; Length 961;
Best Local Similarity 90.0%; Pred. No. 0.83;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DTNKKPSYQ 10
Db 779 DTNKKKPNYQ 788

RESULT 8
ID OGDUS PRELIMINARY; PRT; 965 AA.
AC OGDUS;
DT 05-JUL-2004 (TReMBLrel. 27, Created)
DT 05-JUL-2004 (TReMBLrel. 27, last sequence update)
DT 05-JUL-2004 (TReMBLrel. 27, last annotation update)
DE Fibronectin-binding protein.
GN Name=fnbA: OrderedlocusNames=SA2580;
OS Staphylococcus aureus (strain MRSA252).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=282458;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=1513324; DOI=10.1073/pnas.040251101;
RA Holden M.T.G., Feil E.J., Lindsay J.A., Peacock S.J., Day N.P.J.,
RA Enright M.C., Foster T.J., Moore C.E., Hurst L., Atkin R., Barron A.,
RA Baon N., Bentley S.D., Chillingworth C., Chillingworth T.,
RA Churcher C., Clark L., Cronin C., Cronin H., Doggett J., Dowd L.,
RA Fellwell T., Hance Z., Harris B., Hauser H., Holtroyd S., Jagsels K.,
RA James K.D., Leonard N., Line A., Mayes R., Moule S., Mungall K.,
RA Ormond D., Quail M.A., Rabinowitsch E., Rutherford K.M., Sanders M.,
RA Sharp S., Simmonds M., Stevens K., Whitehead S., Barrell B.G.,
RA Spratt B.G., Parkhill J.;

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RT "Complete genomes of two clinical Staphylococcus aureus strains:
RT evidence for the rapid evolution of virulence and drug resistance."
RL Proc. Natl. Acad. Sci. U.S.A. 101:9786-9791(2004).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC an amide bond (By similarity).
DR EMBL: BX571856; CAG41560.1; -.
DR GO: GO:0009986; C:cell surface; IEA.
DR GO: GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO: GO:0016020; C:membrane; IEA.
DR GO: GO:0007155; P:cell adhesion; IEA.
DR InterPro: IPR008966; Adhes_bact.
DR InterPro: IPR004237; Fn_bind.
DR InterPro: IPR005877; Gpos_YsIRK.
DR InterPro: IPR01899; Gram_pos_anchor.
DR Pfam: PF02986; Fn_bind; 1.
DR Pfam: PF00746; Gram_pos_anchor; 1.
DR TIGRFAMs: TIGR01167; LPXTG_anchor; 1.
DR TIGRFAMs: TIGR01168; YsIRK_signal; 1.
DR PROSITE: PS50847; GRAM_POS_ANCHORING; 1.
KM Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ SEQUENCE 965 AA; 105691 MW; 2982E132164D0551 CRC64;

Query Match 94.6%; Score 53; DB 2; Length 965;
Best Local Similarity 90.0%; Pred. No. 0.83;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DTNKKPSYQ 10
Db 797 DTNKKKPNYQ 806

RESULT 9
ID OGDU7 PRELIMINARY; PRT; 1015 AA.
AC OGDU7;
DT 01-OCT-2002 (TReMBLrel. 22, Created)
DT 01-OCT-2002 (TReMBLrel. 22, last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, last annotation update)
DE Fnb protein.
GN Name=fnb: OrderedlocusNames=MW2421;
OS Staphylococcus aureus (strain MW2).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=196620;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=MW2;
RX MEDLINE=22040717; PubMed=12044378; DOI=10.1016/S0140-6736(02)08713-5;
RA Baba T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Oguchi A.,
RA Nagai Y., Iwama N., Amano K., Naimi T., Kuroda H., Cui L.,
RA Yamamoto K., Hiramatsu K.;
RT "Genome and virulence determinants of high virulence community-
RT acquired MRSA."
RL Lancet 359:1819-1827(2002).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC an amide bond (By similarity).
DR EMBL: AP004830; BAB96286.1; -.
DR GO: GO:0009986; C:cell surface; IEA.
DR GO: GO:0005618; C:cell wall; IEA.
DR GO: GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO: GO:0016020; C:membrane; IEA.
DR GO: GO:0007155; P:cell adhesion; IEA.
DR InterPro: IPR008966; Adhes_bact.
DR InterPro: IPR004237; Fn_bind.
DR InterPro: IPR005877; Gpos_YsIRK.
DR InterPro: IPR01899; Gram_pos_anchor.
DR Pfam: PF02986; Fn_bind; 1.
DR Pfam: PF00746; Gram_pos_anchor; 1.
DR TIGRFAMs: TIGR01167; LPXTG_anchor; 1.
DR TIGRFAMs: TIGR01168; YsIRK_signal; 1.
DR PROSITE: PS50847; GRAM_POS_ANCHORING; 1.
KM Cell wall; Complete proteome; Peptidoglycan-anchor.

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SQ SEQUENCE 1015 AA; 111145 MW; D0F9281BB64D44D2 CRC64;
 Query Match 94.6%; Score 53; DB 2; Length 1015;
 Best Local Similarity 90.0%; Pred. No. 0.88;
 Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DTNKKPSYQ 10
 |||||:
 DB 833 DTNKKDPNYQ 842

RESULT 10
 Q6G6H3 PRELIMINARY; PRT; 1015 AA.
 AC Q6G6H3;
 DT 05-JUL-2004 (TREMBlrel. 27, Created)
 DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
 DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
 DE Fibrinectin-binding protein.
 GN OrderedlocusNames=SA52388;
 OS Staphylococcus aureus (strain MSSA476).
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 CX NCBI_TaxID=282459;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX PubMed=15213324; DOI=10.1073/pnas.0402521101;
 RA Holden M.T.G., Fell E.J., Lindsey J.A., Peacock S.J., Day N.P.J.,
 RA Enright M.C., Foster T.J., Moore C.E., Hurst L., Atkin R., Barron A.,
 RA Baeron N., Bentley S.D., Chillingworth C., Chillingworth T.,
 RA Churcher C., Clark L., Cotton C., Cronin A., Doggett J., Dowd L.,
 RA Feltwell T., Hance Z., Harris B., Hauser H., Holtroyd S., Jagels K.,
 RA James K.D., Lennard N., Line A., Mayes R., Moule S., Mungall K.,
 RA Ormond D., Quail M.A., Rabinovitch E., Rutherford K.M., Sanders M.,
 RA Sharp S., Simmonds M., Stevens K., Whitehead S., Barrett B.G.,
 RA Spratt B.G., Parkhill J.;
 RT "Complete genomes of two clinical Staphylococcus aureus strains:
 RT evidence for the rapid evolution of virulence and drug resistance.";
 RL Proc. Natl. Acad. Sci. U.S.A. 101:9786-9791(2004).
 CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
 CC an amide bond (By similarity).
 DR EMBL: BX571857; CAG44202.1; -;
 DR GO: GO:0009986; C:cell surface; IEA.
 DR GO: GO:0005618; C:cell wall; IEA.
 DR GO: GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
 DR GO: GO:0016020; C:membrane; IEA.
 DR GO: GO:0007155; P:cell adhesion; IEA.
 DR InterPro: IPR008966; Adhes_bact.
 DR InterPro: IPR004237; Fn_bind.
 DR InterPro: IPR005877; Gpos_Y5IRK.
 DR InterPro: IPR001899; Gram_pos_anchor.
 DR Pfam: PF02986; Fn_bind; 1.
 DR Pfam: PF00746; Gram_pos_anchor; 1.
 DR Pfam: PF04650; Y5IRK_signal; 1.
 DR TIGRFAMs: TIGR01167; LEXTG_anchor; 1.
 DR TIGRFAMs: TIGR01168; Y5IRK_signal; 1.
 DR PROSITE: PS0847; GRAM_POS_ANCHORING; 1.
 KW Cell wall; Complete proteome; Peptidoglycan-anchor.
 SQ SEQUENCE 1015 AA; 111145 MW; D0F9281BB64D44D2 CRC64;

Query Match 94.6%; Score 53; DB 2; Length 1015;
 Best Local Similarity 90.0%; Pred. No. 0.88;
 Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DTNKKPSYQ 10
 |||||:
 DB 833 DTNKKDPNYQ 842

RESULT 11
 Q99RD2 PRELIMINARY; PRT; 1038 AA.
 AC Q99RD2;
 DT 01-JUN-2001 (TREMBlrel. 17, Created)

DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
 DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
 DE Fibrinectin-binding protein homolog.
 GN Name=fnb; OrderedlocusNames=SAV2503;
 OS Staphylococcus aureus (strain Mu50 / ATCC 700699).
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 CX NCBI_TaxID=158878;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Mu50 / ATCC 700699;
 RX MEDLINE=21311952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2;
 RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
 RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Ito T.,
 RA Kanamori M., Matsunaru H., Maruyama A., Murakami H., Hosoyama A.,
 RA Sekimizu K., Hiraoka H., Kuhara S., Sawano T., Inoue R.-I., Kato C.,
 RA Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
 RA Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
 RT "Whole genome sequencing of methicillin-resistant Staphylococcus
 RT aureus.";
 RL Lancet 357:1225-1240(2001).
 CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
 CC an amide bond (By similarity).
 DR EMBL: AP003365; BAB58665.1; -;
 DR PIR: H90053; H90053.
 DR GO: GO:0009986; C:cell surface; IEA.
 DR GO: GO:0005618; C:cell wall; IEA.
 DR GO: GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
 DR GO: GO:0016020; C:membrane; IEA.
 DR GO: GO:0007155; P:cell adhesion; IEA.
 DR InterPro: IPR008966; Adhes_bact.
 DR InterPro: IPR004237; Fn_bind.
 DR InterPro: IPR005877; Gpos_Y5IRK.
 DR InterPro: IPR001899; Gram_pos_anchor.
 DR Pfam: PF02986; Fn_bind; 1.
 DR Pfam: PF00746; Gram_pos_anchor; 1.
 DR Pfam: PF04650; Y5IRK_signal; 1.
 DR TIGRFAMs: TIGR01167; LEXTG_anchor; 1.
 DR TIGRFAMs: TIGR01168; Y5IRK_signal; 1.
 DR PROSITE: PS0847; GRAM_POS_ANCHORING; 1.
 KW Cell wall; Complete proteome; Peptidoglycan-anchor.
 SQ SEQUENCE 1038 AA; 113618 MW; 666BF6BF2BBEB12 CRC64;

Query Match 94.6%; Score 53; DB 2; Length 1038;
 Best Local Similarity 90.0%; Pred. No. 0.9;
 Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DTNKKPSYQ 10
 |||||:
 DB 828 DTNKKDPNYQ 837

RESULT 12
 Q7A3J7 PRELIMINARY; PRT; 1038 AA.
 AC Q7A3J7;
 DT 05-JUL-2004 (TREMBlrel. 27, Created)
 DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
 DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
 DE Pnb protein.
 GN Name=fnb; OrderedlocusNames=SA2291;
 OS Staphylococcus aureus (strain N315).
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 CX NCBI_TaxID=158879;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21311952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2;
 RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
 RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Ito T.,
 RA Kanamori M., Matsunaru H., Maruyama A., Murakami H., Hosoyama A.,
 RA Mizutani Y., Takahashi N.K., Sawano T., Inoue R.-I., Kato C.,
 RA Sekimizu K., Hiraoka H., Kuhara S., Goto S., Yabuzaki J.,
 RA Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,

RA Hattori M., Ogasawara N., Hayashi H., Hiratake K.;
 RT "whole genome sequencing of methicillin-resistant *Staphylococcus*
 RT aureus..."
 RL Lancet 357:1225-1240(2001).
 CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
 CC an amide bond (By similarity).
 DR EMBL: AP003137; BAB3594.1; -.
 DR GO: GO:0009986; C:cell surface; IEA.
 DR GO: GO:0005618; C:cell wall; IEA.
 DR GO: GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
 DR GO: GO:0016020; C:membrane; IEA.
 DR GO: GO:0007155; P:cell adhesion; IEA.
 DR InterPro: IPR008966; Adhes_bact.
 DR InterPro: IPR04237; Fn_bind.
 DR InterPro: IPR005877; Gpds_YSTRK.
 DR InterPro: IPR001899; Gram_pos_anchor.
 DR Pfam: PF02986; Fn_bind; 1.
 DR Pfam: PF00746; Gram_pos_anchor; 1.
 DR Pfam: PF04650; YSTRK_signal; 1.
 DR TIGRfams: TIGR01167; LPXTG_anchor; 1.
 DR TIGRfams: TIGR01168; YSTRK_signal; 1.
 DR PROSITE: PS50847; GRAM_POS_ANCHORING; 1.
 DR Cell wall; Complete proteome; Peptidoglycan-anchor.
 KW SEQUENCE 1038 AA; 113618 MW; 666BF6BF2FBEB12 CRC64;
 SQ

Query Match 94.6%; Score 53; DB 2; Length 1038;
 Best Local Similarity 90.0%; Pred. No. 0.9;
 Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DTNKKPSYQ 10
 |||||:
 Db 828 DTNKKPNYQ 837

RESULT 13
 Q7PNT2 PRELIMINARY; PRT; 517 AA.
 ID Q7PNT2;
 AC Q7PNT2;
 DT 01-MAR-2004 (TrEMBLrel. 26, Created)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE ENSANGP0000005870 (Fragment).
 GN Name=ENSANGP0000004463;
 OS Anopheles gambiae str. PEST.
 CC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 CC Neoptera; Endopterygota; Diptera; Nematocera; Anophelinae;
 CC NCBI_TaxID=180454;
 ON [1]
 RN SEQUENCE FROM N.A.
 RC STRAIN=PEST;
 RA Anopheles Genome Sequencing Consortium;
 RL Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.
 CC -1- CAUTION: The sequence shown here is derived from an
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.
 DR EMBL: AAB01008960; EAA11663.2; -.
 DR HSSP: Q13153; 1F3M.
 DR GO: GO:0005524; F:ATP binding; IEA.
 DR GO: GO:0005515; F:protein binding; IEA.
 DR GO: GO:0004672; F:protein kinase activity; IEA.
 DR GO: GO:0006468; P:protein amino acid phosphorylation; IEA.
 DR GO: GO:0007165; P:signal transduction; IEA.
 DR InterPro: IPR011009; Kinase_lke.
 DR InterPro: IPR000719; Prot_kinase.
 DR InterPro: IPR011524; SARAH.
 DR Pfam: PF00069; Kinase; 1.
 DR Pfam: PF00001; Prot_kinase; 1.
 DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE: PS0011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE: PS50951; SARAH; 1.
 KW ATP-binding.
 KW NON_TER 1
 FT NON_TER 517 517

SQ SEQUENCE 517 AA; 58300 MW; 551C299264DDF70A CRC64;
 Query Match 75.0%; Score 42; DB 2; Length 517;
 Best Local Similarity 70.0%; Pred. No. 43;
 Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 DTNKKPSYQ 10
 |||||:
 Db 404 DTNPKPKYR 413

RESULT 14
 ID 05155 PRELIMINARY; PRT; 176 AA.
 AC 05155;
 DT 01-JUN-1998 (TrEMBLrel. 06, Created)
 DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Calpastatin.
 GN Name=CAS7;
 OS Rattus norvegicus (Rat).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 CC NCBI_TaxID=10116;
 ON [1]
 RN SEQUENCE FROM N.A.
 RC STRAIN=Sprague Dawley; TISSUE=Brain;
 RX MEDLINE=9813328; PubMed=9475181; DOI=10.1016/S0014-5793(97)01588-3;
 RA De Tullio R., Sparatore B., Salameo F., Melloni E., Pontremoli S.;
 RT "Rat brain contains multiple mRNAs for calpastatin."
 RL FEBS Lett. 422:113-117(1998).
 DR EMBL: Y13591; CAA73919.1; -.
 DR GO: GO:0030161; F:calpain inhibitor activity; IEA.
 DR InterPro: IPR001259; Prot_inh_calpain.
 DR Pfam: PF00748; Calpain_inhib; 1.
 DR SEQUENCE 176 AA; 18716 MW; 5C76B33F2BC7E15 CRC64;
 SQ

Query Match 71.4%; Score 40; DB 2; Length 176;
 Best Local Similarity 77.8%; Pred. No. 33;
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 DTNKKPSY 9
 |||||:
 Db 110 DTNKKDPY 118

RESULT 15
 ID 06UCN4 PRELIMINARY; PRT; 267 AA.
 AC 06UCN4;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Hypothetical protein.
 GN ORFNames=HOT2C01.47;
 OS Uncultured marine alpha proteobacterium HOT2C01.
 CC Bacteria; Proteobacteria; Alphaproteobacteria; environmental samples.
 CC NCBI_TaxID=248049;
 ON [1]
 RN SEQUENCE FROM N.A.
 RP PubMed=14566056; DOI=10.1073/pnas.2133554100;
 RX De la Torre J.R., Christianson L.M., Beja O., Suzuki M.T., Karl D.M.,
 RA Heidelberg J.F., DeLong E.F.;
 RT "Proteorhodopsin genes are distributed among divergent marine
 RT bacterial taxa."
 RT Proc. Natl. Acad. Sci. U.S.A. 100:12830-12835(2003).
 RN [2]
 RN SEQUENCE FROM N.A.
 RP de la Torre J.R., Christianson L.M., Beja O., Suzuki M.T., Karl D.M.,
 RA Heidelberg J.F., DeLong E.F.;
 RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AY172455; AAR05356.1; -.
 KW Hypothetical protein.

SQ SEQUENCE 267 AA; 30501 MM; B2FF024CDB32EFA9 CRC64;

Query Match 71.4%; Score 40; DB 2; Length 267;
Best Local Similarity 70.0%; Pred. No. 50;
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 DTNKDKPSYQ 10
||| |
Db 236 DTNADAPRYQ 245

Search completed: October 22, 2005, 09:52:18
Job time : 57.2069 secs

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GenCore version 5.1.6
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OM protein - protein search, using bw model

Run on: October 25, 2005, 20:58:51 ; Search time 69.7126 Seconds
(without alignments)
55.479 Million cell updates/sec

Title: US-10-731-238-94
Perfect score: 57
Sequence: 1 NKDKRSYQFG 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_GeneSeq_16Dec04:*

- 1: geneSeq1980s:*
- 2: geneSeq1990s:*
- 3: geneSeq2000s:*
- 4: geneSeq2001s:*
- 5: geneSeq2002s:*
- 6: geneSeq2003as:*
- 7: geneSeq2003bs:*
- 8: geneSeq2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	57	100.0	10	AAW65750
2	57	100.0	37	AA891958
3	57	100.0	38	AA880662
4	57	100.0	134	AAV29087
5	57	100.0	139	AAW31556
6	57	100.0	1018	AA882115
7	57	100.0	1018	AAU37245
8	57	100.0	1018	AAU34301
9	57	100.0	1018	ABJ18922
10	57	100.0	1018	ABW72537
11	57	100.0	1027	AAW89806
12	54	94.7	77	AA888749
13	54	94.7	101	AA890939
14	54	94.7	113	AA890937
15	54	94.7	124	AA890940
16	54	94.7	128	AA890941
17	54	94.7	130	AA888806
18	54	94.7	130	AA888807
19	54	94.7	130	AA891202
20	54	94.7	130	AA891201
21	54	94.7	134	AAV29089
22	54	94.7	134	AAV29088
23	54	94.7	162	AA890942
24	54	94.7	164	AA890938
25	54	94.7	174	AA888808

26	54	94.7	174	2	AA891203
27	54	94.7	181	2	AA888805
28	54	94.7	181	2	AA891200
29	54	94.7	559	2	AAW89803
30	54	94.7	940	2	AA890707
31	54	94.7	940	6	ABJ19111
32	54	94.7	948	6	ADA89470
33	54	94.7	948	6	ABJ18923
34	54	94.7	948	6	ABW72536
35	54	94.7	961	6	ABU15854
36	54	94.7	978	4	AAU33960
37	54	94.7	1001	4	AAU37093
38	54	94.7	1038	6	ABU15903
39	46	80.7	10	2	AAW65751
40	46	80.7	22	2	AA821340
41	45	78.9	10	2	AAW65749
42	43	75.4	157	6	ABM70007
43	41.5	72.8	37	1	AA882118
44	41	71.9	325	4	ABG29183
45	41	71.9	782	4	ABG29187

ALIGNMENTS

RESULT 1
AAW65750
ID AAW65750 standard; peptide; 10 AA.

AC AAW65750;

DT 16-OCT-1998 (first entry)

DE Fibronectin binding protein-derived peptide #94.

KW microbial surface components recognising adhesive matrix molecule;
MSCKRAM; fibronectin; fibronectin-binding protein; antibody; epitope;
antibiotic; bacterial infection; antibiotic-resistant strain.

OS Synthetic.

OS Staphylococcus aureus.

PN WO9831389-A2.

PD 23-JUL-1998.

PF 21-JAN-1998; 98WO-US001222.

PR 21-JAN-1997; 97US-0036139P.

PA (TEXA) UNIV TEXAS A & M SYSTEM.

PI Hoeck M, Partl JM, House-Pompeo KL, Speziale P, Joh D;
McGavin MJ;

DR WPI; 1998-413816/35.

PT Antibody that binds to fibronectin-binding protein, preventing its
binding to fibronectin - used to treat or prevent bacterial infection,
especially by Staphylococci and Streptococci.

PS Example 9; Page 111; 201pp; English.

The invention relates to antibodies that bind to a fibronectin-binding domain of a fibronectin-binding protein, and inhibit binding of the protein to fibronectin. Also claimed are: (1) isolated peptides of a fibronectin-binding protein that do not bind to fibronectin; (2) fusion protein containing at least one peptide of a fibronectin-binding protein linked to a second amino acid sequence; (3) nucleic acid encoding the isolated peptide of (1). Antibodies, the isolated peptides of (1) and the nucleic acids are all useful for immunisation (active or passive) and (b) inhibiting binding of bacteria to fibronectin) for preventing or treating infection in humans or other animals, particularly by staphylococci or

CC streptococci, e.g. meningitis, otitis media, pneumonia, endocarditis,
 CC mastitis in cattle, abortion in horses and many others. Since the
 CC antibodies block binding of bacteria, they should be effective against
 CC antibiotic-resistant strains, and may replace antibiotic therapy or
 CC increase its effectiveness. Sequences AAB65744-58 represent peptides
 CC which were synthesized to span the D3 motif of S. aureus fibronectin
 CC binding protein A
 CC
 XX
 SQ Sequence 10 AA;
 Query Match 100.0%; Score 57; DB 2; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.0014;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 NKDKPSYQFG 10
 Db 1 NKDKPSYQFG 10
 RESULT 2
 AAB91958
 ID AAB91958 standard; peptide; 37 AA.
 AC AAB91958;
 XX
 DT 22-JUN-2001 (first entry)
 XX
 DE Fibronectin fragment and fibrin related peptide SEQ ID NO:1134.
 XX
 KM Protection; endogenous therapeutic peptide; peptidase; conjugation;
 KM blood component; modification; succinimidyl; maleimido group; amino;
 KM hydroxyl; thiol; hormone; growth factor; neurotransmitter.
 XX
 OS Homo sapiens.
 OS Synthetic.
 OS
 PN WO20069900-A2.
 PN
 PD 23-NOV-2000.
 PD
 XX
 PF 17-MAY-2000; 2000WO-US013576.
 PF
 XX
 PR 17-MAY-1999; 99US-0134406P.
 PR 10-SEP-1999; 99US-0153406P.
 PR 15-OCT-1999; 99US-0159783P.
 XX
 PA (CONJ-) CONJUCHEM INC.
 XX
 PI Bridon DP, Ezrin AM, Milner PG, Holmes DL, Thibaudau K;
 XX
 DR WPI; 2001-112059/12.
 XX
 PT Modifying and attaching therapeutic peptides to albumin prevents
 PT peptidase degradation, useful for increasing length of in vivo activity.
 PT
 XX
 PS Disclosure; Page 566; 733pp; English.
 XX
 SQ The present invention describes a modified therapeutic peptide (I)
 CC comprising a therapeutically active amino acid region (III) and a
 CC reactive group (II) (e.g. succinimidyl and maleimido groups) attached to
 CC a less therapeutically active amino acid region (IV), which covalently
 CC bonds with amino/hydroxyl/thiol groups on blood components to form a
 CC peptidase stabilised therapeutic peptide composed of 3-50 amino acids.
 CC (I) are useful for modifying therapeutic peptides e.g. hormones, growth
 CC factors and neurotransmitters, to protect them from peptidase activity in
 CC vivo for the treatment of various disorders. Endogenous therapeutic
 CC peptides are not suitable as drug candidates as they require frequent
 CC administration due to rapid degradation by peptidases in the body.
 CC Modifying and attaching therapeutic peptides to albumin prevents or
 CC reduces the action of peptidases to increase length of activity (half
 CC life) and specificity as bonding to large molecules decreases
 CC intracellular uptake and interference with physiological processes.
 CC AAB90829 to AAB92441 represent peptides which can be used in the

CC exemplification of the present invention
 XX
 SQ Sequence 37 AA;
 Query Match 100.0%; Score 57; DB 4; Length 37;
 Best Local Similarity 100.0%; Pred. No. 0.0049;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 NKDKPSYQFG 10
 Db 13 NKDKPSYQFG 22
 RESULT 3
 AAP80662
 ID AAP80662 standard; protein; 38 AA.
 AC AAP80662;
 XX
 DT 25-MAR-2003 (revised)
 DT 07-OCT-1990 (first entry)
 XX
 DE Protein with fibronectin binding ability.
 XX
 KM Hybrid DNA molecule; fibronectin binding; mastitis; ruminants;
 KM wound infection.
 KM
 XX
 OS Staphylococcus aureus.
 OS
 PN EP294349-A.
 PN
 XX
 PD 07-DEC-1988.
 PD
 XX
 PF 30-MAY-1988; 88EP-00850188.
 PF
 XX
 PR 01-JUN-1987; 87SE-00002272.
 PR
 PA (ALFA) ALFA LAVAL AGRIC INT AB.
 PA
 XX
 PI Lindberg MK, Signas LC, Wadstrom TM, Froman G;
 XX
 DR WPI: 1988-347978/49.
 DR
 DR N-PSDB; AAN81099.
 DR
 XX
 PT Hybrid DNA encoding Staphylococcus aureus fibronectin binding protein -
 PT useful for immunisation and topical application to prevent staphylococcal
 PT infections.
 PT
 XX
 PS Claim 11; Page 12; 23pp; English.
 XX
 XX
 CC The peptide has fibronectin binding ability. It is useful for immunising
 CC ruminants against staphylococcal mastitis, pref. when used at 0.5-5
 CC micrograms/kg, using 3 doses given at 1-3 week intervals; for topical
 CC application to prevent wound infection, using an isotonic saline soln. of
 CC concn. 25-250 micrograms/ml; and, when immobilised on a carrier, for
 CC diagnosing staphylococcal infections. (Updated on 25-MAR-2003 to correct
 CC PF field.)
 CC
 XX
 SQ Sequence 38 AA;
 Query Match 100.0%; Score 57; DB 1; Length 38;
 Best Local Similarity 100.0%; Pred. No. 0.0051;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 NKDKPSYQFG 10
 Db 14 NKDKPSYQFG 23
 RESULT 4
 AAY29087
 ID AAY29087 standard; protein; 134 AA.
 XX

AC AAY29087;
XX
DT 28-SEP-1999 (first entry)
DE
XX S. aureus fibronectin binding protein A (FnBA) binding domain.
XX
KW Bovine herpes virus-2; BHV-2; cytokine; immune response; immunogen; IL;
KW interleukin; colony stimulating factor; CSF; interferon; IFN; TNF;
KW tumour necrosis factor; recombinant virus; vaccine; mucosal disease;
KW mastitis; breast cancer; stress-induced disease; binding domain; FnBA;
XX fibronectin binding protein.
XX
OS Staphylococcus aureus.
XX
PN WO9916892-A1.
XX
PD 08-APR-1999.
XX
PF 29-SEP-1998; 98WO-GB002927.
XX
PR 29-SEP-1997; 97GB-00020633.
XX
PA (UYBR-) UNIV BRISTOL.
XX
PI Bradley AJ, Duffas WP;
XX
DR WPI, 1999-255101/21.
XX
DR N-PSDB; AAX91504.
XX
PT New bovine herpes virus-2 vectors.
XX
PS Example 2; Fig 8A-B; 130pp; English.
XX
XX The invention provides bovine herpes virus-2 (BHV-2) based vectors that
CC comprises at least one cytokine-encoding DNA sequence. The expression of
CC cytokines in mammals can up-regulate immune responses to the immunogens.
CC The cytokine is selected from interleukins (IL), colony stimulating
CC factors (CSF), interferons (IFN) and tumour necrosis factors (TNF). The
CC BHV-2 based vector or recombinant virus can be used as vaccines. They can
CC be used for preventing or treating a mucosal disease in a subject, e.g.
CC ruminants, cattle, sheep, goats, dogs, cats, horses, or man, particularly
CC mastitis in cows or breast cancers in humans. They can also be used for
CC preventing or treating a stress-induced disease. The present sequence
CC represents the binding domain of a previously published S. aureus
CC fibronectin binding protein A (FnBA) sequence. The FnB binding domain
CC gene sequence FNBA8, cloned for use in this invention has 97.8 percent
CC identity when compared to the previously published FnBA and FnB8 gene
CC sequences
XX
SQ Sequence 134 AA;

Query Match 100.0%; Score 57; DB 2; Length 134;
Best Local Similarity 100.0%; Pred. No. 0.017;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0.

QY 1 NKDKPSYQFG 10
|||
DB 90 NKDKPSYQFG 99

RESULT 5
AAM31556
ID AAM31556 standard; protein; 139 AA.
XX
AC AAM31556;
XX
DT 27-AUG-2003 (revised)
DT 25-MAR-2003 (revised)
DT 21-MAY-1998 (first entry)
XX
XX Fibronectin-binding MSCRAMM derivative pDQ.
DE
XX Fibronectin; pDQ; collagen binding protein; sepsis; infection;

Query Match	Best Local Similarity	Score	DB 2;	Length	139;
Matches 10;	Conservative	0;	Mismatches	0;	Indels 0; Gaps 0
QY	1 NKDKPSYQFG 10				
DB	104 NKDKPSYQFG 113				
RESULT 6					
AA82115					
ID	AA82115 standard; protein; 1018 AA.				
AC	AA82115;				
DT	25-MAR-2003 (revised)				
DT	05-JAN-1990 (first entry)				
DE	Fibronectin binding protein.				
XX					
XX	Fibronectin binding protein; S.aureus; immunisation; mastitis; ruminant;				
XX	wound infection; diagnosis.				
XX					
OS	Staphylococcus aureus.				
XX					
XX	Staphylococcus aureus.				
XX					
XX	microbial surface component recognising adhesive matrix molecule; MSCRAMM;				
XX	adhesin; vaccine; immunisation; diagnosis; therapy; mastitis.				
XX					
XX	Key				
XX	Location/Qualifiers				
XX	1..12				
XX	/note= "vector pQE30-derived peptide"				
XX					
XX	MO9743314-A2.				
XX					
XX	20-NOV-1997.				
XX					
XX	14-MAY-1997; 97WO-US008210.				
XX					
XX	16-MAY-1996; 96US-0017678P.				
XX					
XX	(TEXA) UNIV TEXAS A & M SYSTEM.				
XX	(UABR-) UAB RES FOUND.				
XX					
XX	Hoecek M, Patti JM, House-Pompeo K, Stahanam N, Symersky J;				
XX					
XX	WPI; 1998-008801/01.				
XX					
XX	Antibody that interacts with collagen binding domain of Staphylococcal				
XX	cna gene product - useful to prevent bacterial sepsis in animal infected				
XX	with Staphylococcus aureus.				
XX					
XX	Disclosure; Page 91; 143pp; English.				
XX					
XX	This protein comprises Staphylococcus aureus fibronectin-binding				
XX	microbial surface component recognising adhesive matrix molecule (MSCRAMM)				
XX	derivative pQD, plus a vector-derived N-terminal peptide. The invention				
XX	relates to claimed nucleic acid sequences (see AA193436-38) encoding S.				
XX	aureus collagen binding protein (CBP) epitopes M17, M1 and M55 (see				
XX	AAW1552-54) that confer protection against S. aureus infection. CBP				
XX	protein and antigenic epitopes are contemplated for use in the treatment				
XX	of pathological infections, especially to prevent bacterial adhesion to				
XX	collagen. The epitopes are also contemplated for use in the preparation of				
XX	of vaccines and as carrier proteins in vaccine formulations, as well as				
XX	in the formulation of compositions for the prevention of S. aureus				
XX	infection. pCF33 and pQD (see AAW1556) were used to raise anti-MSCRAMM				
XX	polyclonal antibodies used in passive immunisation against bovine				
XX	mastitis. (Updated on 25-MAR-2003 to correct PI field.) (Updated on 27-				
XX	AUG-2003 to correct OS field.)				
XX					
XX	SQ				
XX	Sequence 139 AA;				

```

PN      EP294349-A.
XX
XX      07-DEC-1988.
PD
XX
XX      30-MAY-1988;      88EP-00850188.
PF
XX
XX      01-JUN-1987;      87SE-00002272.
PR
XX
XX      (ALFA ) ALFA LAVAL AGRIC INT AB.
PA
XX
PI      Lindberg MK, Signas LC, Wadstrom TM, Froman G;
XX
XX      WPI; 1988-347978/49.
DR
XX
XX      P-PSDB; AAP82115.
DR
XX
XX      Hybrid DNA encoding Staphylococcus aureus fibronectin binding protein -
PT      useful for immunisation and topical application to prevent staphylococcal
PT      infections.
XX
XX      Disclosure; Fig. 8A:1-8A:2; 23pp; English.
XX
XX      The S. aureus fibronectin binding protein may be included in a hybrid
CC
CC      protein. The protein may be used to immunise ruminants against
CC      Staphylococcal mastitis, pref. when given at 0.5-5 microg/kg, using 3
CC      doses at 1-3 week intervals; and for topical applicn. to prevent wound
CC      infection, pref. using isotonic saline soln. of concn. 25-250 microg/mg.
CC      The DNA encoding the binding protein and the hybrid protein may be
CC      immobilised on a carrier and used to diagnose staphylococcal infections.
CC      (updated on 25-MAR-2003 to correct PA field.)
XX
XX      Sequence 1018 AA;
SQ
XX
XX      Query Match      100.0%; Score 57; DB 1; Length 1018;
XX      Best Local Similarity 100.0%; Pred. No. 0.13;
XX      Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      1 NKDKPSYQFG 10
XX      |||||
Db      834 NKDKPSYQFG 843

RESULT 7
AAU37245
ID      AAU37245 standard; protein; 1018 AA.
XX
XX      AAU37245;
AC
XX
XX      14-FEB-2002 (first entry)
DT
XX
XX      Staphylococcus aureus cellular proliferation protein #1415.
DE
XX
XX      Antisense; prokaryotic cellular proliferation protein; antibiotic;
KM      antibacterial; drug design.
XX
XX      Staphylococcus aureus.
OS
XX
XX      WO200170955-A2.
XX
XX      27-SEP-2001.
PD
XX
XX      21-MAR-2001; 2001WO-US009180.
PF
XX
XX      21-MAR-2000; 2000US-0191078P.
PR      21-MAR-2000; 2000US-0206848P.
PR      26-MAY-2000; 2000US-0207727P.
PR      23-OCT-2000; 2000US-0242578P.
PR      27-NOV-2000; 2000US-0253625P.
PR      22-DEC-2000; 2000US-0257931P.
PR      16-FEB-2001; 2001US-0269308P.
XX
XX      (ELIT-) ELITRA PHARM INC.
PA
XX
PI      Haselbeck R, Ohlsen KL, Zyskind JW, Wall D, Trawick JD, Carr GJ;
PI

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PI      Yamamoto RT, Xu HH;
XX
XX      WPI; 2001-611495/70.
DR
XX
XX      N-PSDB; AAS55104.
DR
XX
XX      New polynucleotides for the identification and development of
PT      antibiotics, comprise sequences of antisense nucleic acids.
PT
XX
XX      Example 3; SEQ ID NO 12838; 511pp; English.
XX
XX      The invention relates to antisense inhibitors of genes essential to
CC      prokaryotic cellular proliferation, their use in identifying the genes,
CC      their use in the discovery of novel antibiotics, the essential genes
CC      themselves and the encoded proteins. The prokaryotes used are Escherichia
CC      coli, Staphylococcus aureus, Salmonella typhi, Klebsiella pneumoniae,
CC      Pseudomonas aeruginosa and Enterococcus faecalis. The invention is also
CC      useful for the identification of potential new targets for antibiotic
CC      development. The antisense nucleic acids can also be used to identify
CC      proteins used in proliferation, to express these proteins, and to obtain
CC      antibodies capable of binding to the expressed proteins. The proteins can
CC      be used to screen compounds in rational drug discovery programmes. The
CC      antisense nucleic acid sequence is also useful to screen for homologous
CC      nucleic acids which are required for cell proliferation in a wide variety
CC      of organisms. The present sequence represents an essential prokaryotic
CC      cellular proliferation protein. Note: The sequence data for this patent
CC      did not form part of the printed specification, but was obtained in
CC      electronic format directly from WIPO at
CC      ftp.wipo.int/pub/published_pct_sequences
XX
XX      Sequence 1018 AA;
SQ
XX
XX      Query Match      100.0%; Score 57; DB 4; Length 1018;
XX      Best Local Similarity 100.0%; Pred. No. 0.13;
XX      Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      1 NKDKPSYQFG 10
XX      |||||
Db      834 NKDKPSYQFG 843

RESULT 8
AAU34301
ID      AAU34301 standard; protein; 1018 AA.
XX
XX      AAU34301;
AC
XX
XX      14-FEB-2002 (first entry)
DT
XX
XX      Staphylococcus aureus cellular proliferation protein #577.
DE
XX
XX      Antisense; prokaryotic cellular proliferation protein; antibiotic;
KM      antibacterial; drug design.
XX
XX      Staphylococcus aureus.
OS
XX
XX      WO200170955-A2.
XX
XX      27-SEP-2001.
PD
XX
XX      21-MAR-2001; 2001WO-US009180.
PF
XX
XX      21-MAR-2000; 2000US-0191078P.
PR      21-MAR-2000; 2000US-0206848P.
PR      26-MAY-2000; 2000US-0207727P.
PR      23-OCT-2000; 2000US-0242578P.
PR      27-NOV-2000; 2000US-0253625P.
PR      22-DEC-2000; 2000US-0257931P.
PR      16-FEB-2001; 2001US-0269308P.
XX
XX      (ELIT-) ELITRA PHARM INC.
PA
XX
PI      Haselbeck R, Ohlsen KL, Zyskind JW, Wall D, Trawick JD, Carr GJ;
PI      Yamamoto RT, Xu HH;
PI

```

XX WPI; 2001-611495/70.
DR N-PSDB; AASS2160.
XX
PT New polynucleotides for the identification and development of
PT antibiotics, comprise sequences of antisense nucleic acids.
XX
PS Example 3; SEQ ID NO 5797; 511pp; English.
XX
CC The invention relates to antisense inhibitors of genes essential to
CC prokaryotic cellular proliferation, their use in identifying the genes,
CC their use in the discovery of novel antibiotics, the essential genes
CC themselves and the encoded proteins. The prokaryotes used are *Escherichia*
CC *coli*, *Staphylococcus aureus*, *Salmonella typhi*, *Klebsiella pneumoniae*,
CC *Pseudomonas aeruginosa* and *Enterococcus faecalis*. The invention is also
CC useful for the identification of potential new targets for antibiotic
CC development. The antisense nucleic acids can also be used to identify
CC proteins used in proliferation, to express these proteins, and to obtain
CC antibodies capable of binding to the expressed proteins. The proteins can
CC be used to screen compounds in rational drug discovery programmes. The
CC antisense nucleic acid sequence is also useful to screen for homologous
CC nucleic acids which are required for cell proliferation in a wide variety
CC of organisms. The present sequence represents an essential prokaryotic
CC cellular proliferation protein. Note: The sequence data for this patent
CC did not form part of the printed specification, but was obtained in
CC electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 1018 AA;
XX
Query Match 100.0%; Score 57; DB 4; Length 1018;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 NKDKPSYQFG 10
DB 834 NKDKPSYQFG 843
XX
RESULT 9
ABJ18922 ID ABJ18922 standard; protein; 1018 AA.
XX
XX AC ABJ18922;
XX
DT 06-MAR-2003 (first entry)
XX
DE Pathogen specific antigen related staphylococcal protein SEQ ID No 68.
XX
XX Antibacterial; virucide; fungicide; protozoacide; cytostatic; anti-HIV;
XX hyperimmune; serum-reactive; antigen; pathogen; tumour; allergen;
XX auto-immunity; vaccine; staphylococcal infection; antibody; cancer;
XX autoimmune disease; HIV; hepatitis.
XX
OS Staphylococcus sp.
XX
XX WO200259148-A2.
XX
XX 01-AUG-2002.
XX
XX 21-JAN-2002; 2002WO-EP000546.
XX
XX 26-JAN-2001; 2001AT-00000130.
XX
XX (CIST-) CISTEM BIOTECHNOLOGIES GMBH.
XX
XX Meinke A, Nagy B, Von Ahsen U, Klade C, Henics T, Zauner W,
XX Mihh DB, Vytvytska O, Etz H, Dryla A, Weichart T, Hafner M,
XX Tempelmeier B;
XX
XX WPI; 2003-075410/07.
XX
XX Identifying, isolating and producing hyperimmune serum-reactive antigens

PT from a pathogen, for preparing vaccine or medicament for treating or
PT preventing e.g. staphylococcal infections, comprises providing antibody
PT preparation.
XX
XX
PS Example 7; Page 157; 252pp; English.
XX
CC The invention relates to a novel method for identifying, isolating and
CC producing hyperimmune serum-reactive antigens from a pathogen, tumour,
CC allergen, a tissue or host prone to auto-immunity, where the antigens are
CC used in a vaccine, comprises providing antibody preparation from a plasma
CC pool of a type of animal, or individual sera with antibodies against the
CC specific pathogen, tumour, allergen, tissue or host prone to auto-
CC immunity. The hyperimmune serum-reactive antigens comprising any of the
CC 62 sequences of 53-2261 amino acids fully defined in the specification,
CC or their hyperimmune fragments are useful for the manufacture of a
CC pharmaceutical preparation, particularly a vaccine against staphylococcal
CC infections or colonisation against *S. aureus* or *S. epidermidis*. The
CC preparation of antibodies is useful for the manufacture of a medicament
CC for treating or preventing staphylococcal infections or colonisation
CC against *S. aureus* or *S. epidermidis*. The antibody preparations may also
CC be used for diagnostic and imaging purposes. Other conditions that can be
CC treated include cancer, autoimmune diseases or infections caused by viral
CC (e.g. HIV, hepatitis A, B or C), fungal or protozoan pathogens. This
CC sequence represents a staphylococcal protein relating to the method for
CC identifying and producing pathogen specific antigens of the invention
XX
SQ Sequence 1018 AA;
XX
Query Match 100.0%; Score 57; DB 6; Length 1018;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 NKDKPSYQFG 10
DB 834 NKDKPSYQFG 843
XX
RESULT 10
ABM72537 ID ABM72537 standard; protein; 1018 AA.
XX
XX AC ABM72537;
XX
XX 20-NOV-2003 (first entry)
XX
DE Staphylococcus aureus protein #1777.
XX
XX Antibacterial; vaccine; gene therapy; infection; sepsis; diagnosis;
XX enzymatic assay; antibiotic target.
XX
XX Staphylococcus aureus.
XX
XX WO200294868-A2.
XX
XX 28-NOV-2002.
XX
XX 27-MAR-2002; 2002WO-IB002637.
XX
XX 27-MAR-2001; 2001GB-00007661.
XX
XX (CHIR-) CHIRON SPA.
XX
XX Massignani V, Mora M, Scarselli M,
XX
XX WPI; 2003-120786/11.
XX
XX N-PSDB; ACF74097.
XX
XX New Staphylococcus aureus protein, useful as a vaccine for treating or
XX preventing Staphylococcal infection, specifically an infection caused by
XX *S. aureus*, e.g. sepsis.
XX
XX
XX Claim 1; SEQ ID NO 3554; 49pp; English.
XX

CC The invention relates to novel genes and encoded proteins from
CC Staphylococcus aureus. A composition comprising the S. aureus protein, a
CC nucleic acid encoding the protein, or an antibody to the protein, is
CC useful as a pharmaceutical, particularly as a vaccine for treating or
CC preventing infection due to Staphylococcus bacteria, specifically an
CC infection caused by S. aureus. The composition is particularly useful for
CC treating or preventing sepsis in a patient. The composition can also be
CC used for diagnostics. The protein is also used in an assay for enzymatic
CC studies and as a target for antibiotics. This sequence represents one of
CC the novel S. aureus proteins of the invention
XX
SQ Sequence 1018 AA;
Query Match 100.0%; Score 57; DB 6; Length 1018;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 NKDKPSYQFG 10
DB 834 NKDKPSYQFG 843
RESULT 11
AAW89806 standard; protein; 1027 AA.
XX
AC AAW89806;
XX
DT 16-MAR-1999 (first entry)
XX
DE Staphylococcus aureus protein SEQ ID #5254.
XX
KM Computer readable medium; vaccine; S.aureus infection; immunodetection;
KM cellulitis; eyelid infection; food poisoning; osteomyelitis; therapy;
KM skin infection; surgical wound infection; scalded skin syndrome;
KM toxic shock syndrome.
XX
OS Staphylococcus aureus.
XX
PN EP786519-A2.
XX
PD 30-JUL-1997.
XX
PF 07-JAN-1997; 97EP-00100117.
XX
PR 05-JAN-1996; 96US-0009861P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Kunsch CA, Choi GH, Barash SC, Dillon PJ, Fannon MR, Rosen CA;
XX
XX WPI; 1997-374922/35.
XX
PT Polynucleotide(s) and proteins derived from Staphylococcus aureus -
PT stored on computer readable medium and used in the production of anti-
PT S.aureus vaccines.
XX
XX
XX Claim 23; Page 3263-3267; 3271pp; English.
XX
CC This sequence represents a Staphylococcus aureus protein sequence of the
CC invention. The DNA sequences encoding the S.aureus proteins are recorded
CC on a computer readable medium, preferably selected from a floppy or hard
CC disk, random access memory (RAM), read-only memory (ROM) or CD-ROM.
CC Homology searches using the S.aureus DNA sequences allows putative
CC functions to be assigned so that protein-encoding or regulatory regions
CC of commercial, therapeutic or industrial importance can be obtained.
CC Specifically, sequences which are likely to encode antigens have been
CC identified and these polypeptides can be used in a vaccine composition
CC against S.aureus infection. The polypeptides can also be used in a kit
CC for the immunodetection of S.aureus in a sample. S.aureus is implicated
CC in numerous human diseases, including cellulitis, eyelid infections, food
CC poisoning, osteomyelitis, skin and surgical wound infections, scalded
CC skin syndrome, toxic shock syndrome, etc. Organisms transformed with the

CC DNA sequences can be used for recombinant production of the polypeptides.
CC The new DNA sequences (and their fragments) are useful as primers or
CC probes for isolating homologues of any of the 5191 S.aureus DNA sequences
CC contained on the computer readable medium
XX
SQ Sequence 1027 AA;
Query Match 100.0%; Score 57; DB 2; Length 1027;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 NKDKPSYQFG 10
DB 843 NKDKPSYQFG 852
RESULT 12
AAR8749 standard; protein; 77 AA.
XX
AC AAR8749;
XX
DT 24-SEP-1996 (first entry)
XX
DE S. aureus fibronectin binding protein D2D3 polypeptide.
XX
KM Fibronectin binding protein; D2D3; prevention; adhesion; bacteria;
KM gram positive; extra-cellular matrix protein; in-dwelling device;
KM catheter; wound; D2D3; oral pathogen; oral cavity; J2385; NCIMB 40532.
XX
OS Staphylococcus aureus.
XX
PN WO9604380-A1.
XX
PD 15-FEB-1996.
XX
PF 28-JUL-1995; 95WO-EP003039.
XX
PR 05-AUG-1994; 94GB-00015901.
XX
PA (SMIK) SMITHKLINE BEECHAM PLC.
XX
PI Critchley IA, Dodd I, Barnett P, Mossakowska DE;
XX
XX WPI; 1996-129396/13.
XX
DR N-PSDB; AAT12582.
XX
PT Staphylococcus aureus fibronectin binding protein D2D3 polypeptide -
PT useful for combating infection at wound sites, surgical implants, etc.
PT and as antiadherent agent in oral hygiene.
XX
XX
XX Claim 5; Page 26; 38pp; English.
XX
CC The present sequence is the S. aureus fibronectin binding protein
CC polypeptide D2D3, which can be used to prevent adhesion of (e.g. gram
CC positive) bacteria, to extra-cellular matrix proteins on in-dwelling
CC devices, e.g. catheters or in wounds. D2D3 can also be used to prevent
CC oral pathogens from binding to extra-cellular matrix proteins, in the
CC oral cavity. D2D3 was found to be effective at inhibiting S. aureus 8325-
CC 4, and 120 adhesion to fibronectin coated PMMA coverslips, at a min.
CC adhesion inhibitor concn. of 10 microg/ml. D2D3 was derived from the D2
CC and D3 regions of the S. aureus J2385 (NCIMB 40532) fibronectin binding
CC protein
XX
SQ Sequence 77 AA;
Query Match 94.7%; Score 54; DB 2; Length 77;
Best Local Similarity 90.0%; Pred. No. 0.036;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 NKDKPSYQFG 10
DB 52 NKDKPSYQFG 61

RESULT 13
 AAR90939 ID AAR90939 standard; peptide: 101 AA.
 AC XX
 AC AAR90939;
 DT 23-SEP-1996 (first entry)
 XX XX
 DE D3D4 polypeptide #3.
 XX
 KM Fibronectin binding protein; Fbp; S.aureus J2385; monoclonal antibody;
 KM infection; surgical implant; antiadherent agent; hygiene; adhesion;
 KM extracellular matrix protein; oral pathogen; oral cavity.
 KW
 OS Staphylococcus aureus.
 XX
 FH Key Location/Qualifiers
 FT Region 1..35
 FT /note= "D3 region fragment"
 FT Region 36..50
 FT /note= "D4 region"
 FT Region 51..101
 FT /note= "WRI region fragment"
 XX
 PN WO9604381-A1.
 PD 15-FEB-1996.
 PD
 PF 28-JUL-1995; 95WO-EP003040.
 PF
 PR 05-AUG-1994; 94GB-00015900.
 PR
 PA (SMIK) SMITHKLINE BEECHAM PLC.
 PA
 PI Critchley IA, Dodd I, Barnett P, Mcbay DL;
 PI WPI; 1996-129397/13.
 DR
 XX Polypeptide(s) derived from Staphylococcus aureus fibronectin binding
 PT protein - inhibit binding of bacteria to extracellular matrix proteins,
 PT for combating infection at the site of wounds and surgical implants, and
 PT in oral hygiene.
 XX
 PS Claim 6; Page 24; 35pp; English.
 PS
 CC AAR90937-R90942 represent D3D4 polypeptides. These sequences correspond
 CC to fragments of the Staphylococcus aureus fibronectin binding protein
 CC (Fbp). This sequence corresponds to residues 81-181 of S.aureus J2385
 CC (Fbp), and also contains a portion of the wall region 1 (WRI). These
 CC sequences, and monoclonal antibodies against them can be used to combat
 CC infection at the site of wounds, surgical implants and other in-dwelling
 CC devices (such as catheters), and as antiadherent agents in oral hygiene.
 CC They can also be used in the manufacture of a medicament for the
 CC prevention of adhesion of bacteria to extracellular matrix proteins
 CC present on in-dwelling devices or in wounds, or of oral pathogens to
 CC similar proteins on surfaces in the oral cavity
 CC
 SQ Sequence 101 AA;
 Query Match 94.7%; Score 54; DB 2; Length 101;
 Best Local Similarity 90.0%; Pred. No. 0.047;
 Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 NKDKPSYQFG 10
 |||||:
 DB 10 NKDKPNYQFG 19
 |||||:
 RESULT 14
 AAR90937 ID AAR90937 standard; peptide: 113 AA.

AC XX
 AC AAR90937;
 DT 23-SEP-1996 (first entry)
 XX XX
 DE D3D4 polypeptide #1.
 XX
 KM Fibronectin binding protein; Fbp; S.aureus J2385; monoclonal antibody;
 KM infection; surgical implant; antiadherent agent; hygiene; adhesion;
 KM extracellular matrix protein; oral pathogen; oral cavity.
 KW
 OS Staphylococcus aureus.
 XX
 FH Key Location/Qualifiers
 FT Region 1..21
 FT /note= "D1 region fragment"
 FT Region 22..59
 FT /note= "D2 region"
 FT Region 60..98
 FT /note= "D3 region"
 FT Region 99..113
 FT /note= "D4 region"
 FT Misc-difference 113
 FT /note= "P13T"
 XX
 PN WO9604381-A1.
 PD 15-FEB-1996.
 PD
 PF 28-JUL-1995; 95WO-EP003040.
 PF
 PR 05-AUG-1994; 94GB-00015900.
 PR
 PA (SMIK) SMITHKLINE BEECHAM PLC.
 PA
 PI Critchley IA, Dodd I, Barnett P, Mcbay DL;
 PI WPI; 1996-129397/13.
 DR
 XX Polypeptide(s) derived from Staphylococcus aureus fibronectin binding
 PT protein - inhibit binding of bacteria to extracellular matrix proteins,
 PT for combating infection at the site of wounds and surgical implants, and
 PT in oral hygiene.
 XX
 PS Claim 6; Page 24; 35pp; English.
 PS
 CC AAR90937-R90942 represent D3D4 polypeptides. These sequences correspond
 CC to fragments of the Staphylococcus aureus fibronectin binding protein
 CC (Fbp). This sequence corresponds to residues 18-130 of S.aureus J2385
 CC (Fbp), and also contains the D2 region, and a portion of the D1 region.
 CC These sequences, and monoclonal antibodies against them can be used to
 CC combat infection at the site of wounds, surgical implants and other in-
 CC dwelling devices (such as catheters), and as antiadherent agents in oral
 CC hygiene. They can also be used in the manufacture of a medicament for the
 CC prevention of adhesion of bacteria to extracellular matrix proteins
 CC present on in-dwelling devices or in wounds, or of oral pathogens to
 CC similar proteins on surfaces in the oral cavity
 CC
 SQ Sequence 113 AA;
 Query Match 94.7%; Score 54; DB 2; Length 113;
 Best Local Similarity 90.0%; Pred. No. 0.053;
 Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 NKDKPSYQFG 10
 |||||:
 DB 73 NKDKPNYQFG 82
 |||||:
 RESULT 15
 AAR90940 ID AAR90940 standard; peptide: 124 AA.

```

AC  AAR90940;
XX
DT  23-SEP-1996  (first entry)
XX
DE  D3D4 polypeptide #4.
XX
KM  Fibronectin binding protein; Fbp; S.aureus J2385; monoclonal antibody;
KM  infection; surgical implant; antiadherent agent; hygiene; adhesion;
KM  extracellular matrix protein; oral pathogen; oral cavity.
XX
OS  Staphylococcus aureus.
XX
Key      Location/Qualifiers
FH  Region      1..19
FT  Region      /note= "D2 region fragment"
FT  Region      20..58
FT  Region      /note= "D3 region"
FT  Region      59..62
FT  Region      /note= "D4 region"
FT  Region      63..124
FT  Region      /note= "WRI region"

XX  WO9604381-A1.
XX  FN
XX  PD  15-FEB-1996.
XX
XX  28-JUL-1995; 95WO-EP003040.
XX  PF
XX  PR  05-AUG-1994; 94GB-00015900.
XX
XX  (SMIK ) SMITHKLINE BEECHAM PLC.
XX  PA
XX  PI  Critchley IA, Dodd I, Barnett P, Mcbay DL;
XX  WPI; 1996-129397/13.
XX  DR
XX  PT  Polypeptide(s) derived from Staphylococcus aureus fibronectin binding
XX  PT  protein - inhibit binding of bacteria to extracellular matrix proteins,
XX  PT  for combatting infection at the site of wounds and surgical implants, and
XX  PT  in oral hygiene.
XX
XX  Claim 6, Page 24; 35pp; English.
XX  PS
XX
XX  AAR90937-R90942 represent D3D4 polypeptides. These sequences correspond
XX  CC  to fragments of the Staphylococcus aureus fibronectin binding protein
XX  CC  (Fbp). This sequence corresponds to residues 58-181 of S.aureus J2385
XX  CC  Fbp, and also contains a portion of the D2 region, and a portion of the
XX  CC  wall region 1 (WRI). These sequences, and monoclonal antibodies against
XX  CC  them can be used to combat infection at the site of wounds, surgical
XX  CC  implants and other in-dwelling devices (such as catheters), and as
XX  CC  antiadherent agents in oral hygiene. They can also be used in the
XX  CC  manufacture of a medicament for the prevention of adhesion of bacteria to
XX  CC  extracellular matrix proteins present on in-dwelling devices or in
XX  CC  wounds, or of oral pathogens to similar proteins on surfaces in the oral
XX  CC  cavity.
XX
XX  SQ  Sequence 124 AA;

```

```

Query Match      94.7%; Score 54; DB 2; Length 124;
Best Local Similarity 90.0%; Pred. No. 0.058;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```

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QY  1 NKDKPSYQFG 10
    |||||:||||
DB  33 NKDKPNYQFG 42

```

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 Job time : 70.7126 secs

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OM protein - protein search, using SW model

Run on: October 22, 2005, 07:41:53 ; Search time 17.2989 Seconds
(without alignments)
43.153 Million cell updates/sec

Title: US-10-731-238-94
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Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	57	100.0	10	4	US-09-010-317-94
2	57	100.0	37	1	US-08-234-622A-4
3	57	100.0	38	1	US-08-294-189-8
4	57	100.0	38	1	US-08-729-767-5
5	57	100.0	114	1	US-08-259-000-3
6	57	100.0	139	3	US-08-856-253-8
7	57	100.0	178	2	US-08-459-135A-12
8	57	100.0	178	3	US-08-495-559-12
9	57	100.0	1027	4	US-08-956-171E-5254
10	57	100.0	1027	4	US-08-781-986A-5254
11	54	94.7	130	2	US-08-459-135A-7
12	54	94.7	130	2	US-08-459-135A-8
13	54	94.7	130	3	US-08-495-559-7
14	54	94.7	130	3	US-08-495-559-8
15	54	94.7	174	2	US-08-459-135A-10
16	54	94.7	174	2	US-08-459-135A-13
17	54	94.7	174	3	US-08-495-559-10
18	54	94.7	174	3	US-08-495-559-13
19	54	94.7	176	3	US-08-495-559-6
20	54	94.7	181	2	US-08-459-135A-6
21	54	94.7	559	4	US-08-956-171E-5251
22	54	94.7	559	4	US-08-781-986A-5251
23	46	80.7	10	4	US-09-010-317-95
24	45	78.9	10	4	US-09-010-317-93
25	40	70.2	21	4	US-09-010-317-9
26	40	70.2	21	4	US-09-010-317-20
27	40	70.2	21	4	US-09-010-317-21

ALIGNMENTS

28	40	70.2	21	4	US-09-010-317-22	Sequence 22, Appl
29	40	70.2	21	4	US-09-010-317-23	Sequence 23, Appl
30	40	70.2	21	4	US-09-010-317-24	Sequence 24, Appl
31	40	70.2	21	4	US-09-010-317-25	Sequence 25, Appl
32	40	70.2	21	4	US-09-010-317-26	Sequence 26, Appl
33	40	70.2	21	4	US-09-010-317-27	Sequence 27, Appl
34	40	70.2	21	4	US-09-010-317-28	Sequence 28, Appl
35	40	70.2	21	4	US-09-010-317-29	Sequence 29, Appl
36	40	70.2	21	4	US-09-010-317-30	Sequence 30, Appl
37	40	70.2	21	4	US-09-010-317-31	Sequence 31, Appl
38	40	70.2	21	4	US-09-010-317-32	Sequence 32, Appl
39	40	70.2	21	4	US-09-010-317-33	Sequence 33, Appl
40	39	68.4	658	4	US-09-543-681A-5984	Sequence 34, Appl
41	37	64.9	38	1	US-08-234-622A-3	Sequence 35, Appl
42	37	64.9	38	1	US-08-729-767-4	Sequence 36, Appl
43	37	64.9	38	1	US-08-729-767-7	Sequence 37, Appl
44	37	64.9	38	4	US-09-010-317-45	Sequence 38, Appl
45	37	64.9	38	4	US-09-010-317-46	Sequence 39, Appl

RESULT 1
US-09-010-317-94
Sequence 94, Application US/09010317
Patent No. 6685943
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
APPLICANT: Patti, Joseph M.
APPLICANT: House-Pompeo, Karen L.
APPLICANT: Speziale, Pietro
APPLICANT: Joh, Danny
APPLICANT: McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
TITLE OF INVENTION: AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent'n Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/010.317
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibley, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAMK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 94:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-09-010-317-94
Query Match 100.0%; Score 57; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.00011;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NKDKPSYQFG 10
Db 1 NKDKPSYQFG 10

RESULT 2

US-08-234-622A-4
; Sequence 4, Application US/08234622A
; Patent No. 5440014
; GENERAL INFORMATION:
; APPLICANT: HOOK, Magnus
; APPLICANT: MCGAVIN, Martin
; APPLICANT: RAUCCI, Giuseppe
; TITLE OF INVENTION: A FIBRONECTIN BINDING PEPTIDE
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Doane, Swecker & Mathis
; STREET: P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/234,622A
; FILING DATE: 28-APR-1994
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: SE 9002617-0
; FILING DATE: 10-AUG-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/SE91/00534
; FILING DATE: 09-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Meuth, Donna M
; REGISTRATION NUMBER: 36,607
; REFERENCE/DOCKET NUMBER: 012885-044
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 37 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-234-622A-4
Query Match 100.0%; Score 57; DB 1; Length 37;
Best Local Similarity 100.0%; Pred. No. 0.00044;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 NKDKPSYQFG 10
Db 13 NKDKPSYQFG 22
RESULT 3
US-08-294-189-8
; Sequence 8, Application US/08294189
; Patent No. 5707822
; GENERAL INFORMATION:
; APPLICANT: Fischecci, Vincent A.
; APPLICANT: Rakonjac, Jasna
; APPLICANT: Robbins, John
; TITLE OF INVENTION: GENE SERUM OPACITY FACTOR

NUMBER OF SEQUENCES: 23

CORRESPONDENCE ADDRESS:

ADDRESSEE: Klauber & Jackson

STREET: 411 Hackensack Avenue

CITY: Hackensack

STATE: New Jersey

COUNTRY: USA

ZIP: 07601

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/294,189

FILING DATE: 22-AUG-1994

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Jackson Esq., David A.

REGISTRATION NUMBER: 26,742

REFERENCE/DOCKET NUMBER: 600-1-118

TELECOMMUNICATION INFORMATION:

TELEPHONE: 201 487-5800

TELEFAX: 201 343-1684

TELEX: 133521

INFORMATION FOR SEQ ID NO: 8:

SEQUENCE CHARACTERISTICS:

LENGTH: 38 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: unknown

MOLECULE TYPE: peptide

ORGANISM: Streptococcus pyogenes

STRAIN: D734

INDIVIDUAL ISOLATE: 22

IMMEDIATE SOURCE:

CLONE: 8AUA3a

US-08-294-189-8

Query Match 100.0%; Score 57; DB 1; Length 38;
Best Local Similarity 100.0%; Pred. No. 0.00045;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NKDKPSYQFG 10
Db 7 NKDKPSYQFG 16

RESULT 4

US-08-729-767-5
; Sequence 5, Application US/08729767
; Patent No. 570702
; GENERAL INFORMATION:
; APPLICANT: HOOK, Magnus
; APPLICANT: LINDBERG, Martin Kjell
; APPLICANT: SIGNAS, Lars Christer
; APPLICANT: WADSTROM, Torkei Mikael
; APPLICANT: FROMAN, Gunnar
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN AS WELL AS
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Doane, Swecker & Mathis, L.L.P.
; STREET: P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/729,767
FILING DATE: 07-OCT-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/259,000
FILING DATE: 13-JUN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/007,817
FILING DATE: 22-JAN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/201,028
FILING DATE: 01-JUN-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: SE 8702272-9
FILING DATE: 01-JUN-1987
ATTORNEY/AGENT INFORMATION:
NAME: McGowan, Malcolm K.
REGISTRATION NUMBER: 39,300
REFERENCE/DOCKET NUMBER: 012889-036
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-729-767-5

Query Match 100.0%; Score 57; DB 1; Length 38;
Best Local Similarity 100.0%; Pred. No. 0.00045;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NKDKPSYQFG 10
|||
14 NKDKPSYQFG 23

Db 14 NKDKPSYQFG 23

RESULT 5
US-08-259-000-3
Sequence 3, Application US/08259000
Patent No. 5571514
GENERAL INFORMATION:
APPLICANT: HOOK, Magnus
APPLICANT: LINDBERG, Martin Kjell
APPLICANT: SIGNAS, Lars Christer
APPLICANT: WADSTROM, Torkei Mikael
APPLICANT: PROMAN, Gunnar
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN AS WELL AS
TITLE OF INVENTION: ITS PREPARATION
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Burns, Doane, Swecker & Mathie
STREET: P.O. Box 1404
CITY: Alexandria
STATE: Virginia
COUNTRY: United States
ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/259,000
FILING DATE: 13-JUN-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: SE 8702272-9

FILING DATE: 01-JUN-1987
ATTORNEY/AGENT INFORMATION:
NAME: Meuth, Donna M.
REGISTRATION NUMBER: 36,607
REFERENCE/DOCKET NUMBER: 012885-062
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 114 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-259-000-3

Query Match 100.0%; Score 57; DB 1; Length 114;
Best Local Similarity 100.0%; Pred. No. 0.0015;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NKDKPSYQFG 10
|||
90 NKDKPSYQFG 99

Db 90 NKDKPSYQFG 99

RESULT 6
US-08-856-253-8
Sequence 8, Application US/08856253
Patent No. 6288214
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
APPLICANT: Patti, Joseph M.
APPLICANT: House-Pompeo, Karen
APPLICANT: Schanam, Narayana
APPLICANT: Symersky, Jindrich
TITLE OF INVENTION: COLLAGEN BINDING PROTEIN COMPOSITIONS
TITLE OF INVENTION: AND METHODS OF USE
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: Texas
COUNTRY: U.S.
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/856,253
FILING DATE: Concurrently Herewith
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/017,678
FILING DATE: 16-MAY-1996
ATTORNEY/AGENT INFORMATION:
NAME: Kitchell, Barbara S.
REGISTRATION NUMBER: 33,928
REFERENCE/DOCKET NUMBER: TANK.193
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
TELEFAX: (512) 474-7577
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 139 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-856-253-8

Query Match 100.0%; Score 57; DB 3; Length 139;
Best Local Similarity 100.0%; Pred. No. 0.0018;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NKDKPSYQFG 10
|||||
Db 104 NKDKPSYQFG 113

RESULT 7
US-08-459-135A-12

; Sequence 12, Application US/08459135A
; Patent No. 5955078

; GENERAL INFORMATION:

; APPLICANT: BURHAM, Martin Karl Russel

; APPLICANT: CHOPRA, Ian Alfred

; APPLICANT: CRITCHLEY, Ian Alfred

; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN: MONOCLONAL ANTIBODY AND THEIR US

; NUMBER OF SEQUENCES: 15

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: SmithKline Beecham Corporation

; STREET: 709 Swedeland Road

; CITY: King of Prussia

; STATE: PA

; COUNTRY: U.S.A.

; ZIP: 19406-0939

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; OPERATING SYSTEM: DOS

; SOFTWARE: Fastseq, Version 2.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/459,135A

; FILING DATE: 02-JUN-1995

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: PCT/GB/94/00215

; FILING DATE: 04-Feb-1994

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: Gimm, Edward R

; REGISTRATION NUMBER: 38,891

; REFERENCE/DOCKET NUMBER: P30591C2

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 610-270-4478

; TELEFAX: 610-270-5090

; TELEX:

; INFORMATION FOR SEQ ID NO: 12:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 178 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: Protein

US-08-459-135A-12

Query Match 100.0%; Score 57; DB 2; Length 178;
Best Local Similarity 100.0%; Pred. No. 0.0024;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NKDKPSYQFG 10
|||||
Db 90 NKDKPSYQFG 99

RESULT 8
US-08-495-559-12

; Sequence 12, Application US/08495559A

; Patent No. 6054572

; GENERAL INFORMATION:

; APPLICANT: BURHAM, Martin Karl Russel

; APPLICANT: CHOPRA, Ian

; APPLICANT: CRITCHLEY, Ian Alfred

; APPLICANT: KNOWLES, David Justin Charles

; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN: MONOCLONAL

; TITLE OF INVENTION: ANTIBODY AND THEIR USE IN PREVENTING BACTERIAL ADHESION

; FILE REFERENCE: P30591

; CURRENT APPLICATION NUMBER: US/08/495,559A

; CURRENT FILING DATE: 1995-08-03

; EARLIER APPLICATION NUMBER: GB 9302289.5

; EARLIER FILING DATE: 1993-02-05

; EARLIER APPLICATION NUMBER: GB 9321592.9

; EARLIER FILING DATE: 1993-10-20

; NUMBER OF SEQ ID NOS: 13

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 12

; LENGTH: 178

; TYPE: PRT

; ORGANISM: Staphylococcus aureus

US-08-495-559-12

Query Match 100.0%; Score 57; DB 3; Length 178;
Best Local Similarity 100.0%; Pred. No. 0.0024;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NKDKPSYQFG 10
|||||
Db 90 NKDKPSYQFG 99

RESULT 9
US-08-956-171E-5254

; Sequence 5254, Application US/08956171E

; Patent No. 6593114

; GENERAL INFORMATION:

; APPLICANT: Charles Kunsch

; Gil H. Choi

; Patrick S. Dillon

; Craig A. Rosen

; Steven C. Barash

; Michael R. Fannon

; TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences

; NUMBER OF SEQUENCES: 5256

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Human Genome Sciences, Inc.

; STREET: 9410 Key West Avenue

; CITY: Rockville

; STATE: Maryland

; COUNTRY: USA

; ZIP: 20850

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette, 3.50 inch, 1.4mb storage

; COMPUTER: HP Vectra 486/33

; OPERATING SYSTEM: MSDOS version 6.2

; SOFTWARE: ASCII Text

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/956,171E

; FILING DATE: 20-Oct-1997

; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 60/009,861

; FILING DATE: January 5, 1996

; APPLICATION NUMBER: 08/781,986

; FILING DATE: January 3, 1997

; ATTORNEY/AGENT INFORMATION:

; NAME: Mark J. Hyman

; REGISTRATION NUMBER: 46,789

; REFERENCE/DOCKET NUMBER: PB248P1

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (240) 314-1224

; TELEFAX: (301) 309-8439

; INFORMATION FOR SEQ ID NO: 5254:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 1027 amino acids

; TYPE: amino acid

STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 5254:
US-08-956-171E-5254

Query Match 100.0%; Score 57; DB 4; Length 1027;
Best Local Similarity 100.0%; Pred. No. 0.015;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NKDKPSYQFG 10
|||||
DB 843 NKDKPSYQFG 852

RESULT 10
US-08-781-986A-5254
Sequence 5254, Application US/08781986A
Patent No. 6737248
GENERAL INFORMATION:
APPLICANT: Charles Kunsch
TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
NUMBER OF SEQUENCES: 5255
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COUNTRY: USA
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/781,986A
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Benson, Bob
REGISTRATION NUMBER: 30,446
REFERENCE/DOCKET NUMBER: PB248PP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8512
TELEFAX: (301) 309-8504
INFORMATION FOR SEQ ID NO: 5254:
SEQUENCE CHARACTERISTICS:
LENGTH: 1027 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-781-986A-5254
Query Match 100.0%; Score 57; DB 4; Length 1027;
Best Local Similarity 100.0%; Pred. No. 0.015;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 NKDKPSYQFG 10
|||||
DB 843 NKDKPSYQFG 852
RESULT 11
US-08-459-135A-7
Sequence 7, Application US/08459135A
Patent No. 5955078
GENERAL INFORMATION:
APPLICANT: BURNHAM, Martin Karl Russel

APPLICANT: CHOPRA, Ian
APPLICANT: CRITCHLEY, Ian Alfred
APPLICANT: KNOWLES, David Justin Charles
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN: MONOCLONAL ANTIBODY AND THEIR US
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
STATE: PA
COUNTRY: U.S.A.
ZIP: 19406-0939
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: Fastseq, Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/459,135A
FILING DATE: 02-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB/94/00215
FILING DATE: 04-Feb-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Gimm, Edward R
REGISTRATION NUMBER: 38,891
REFERENCE/DOCKET NUMBER: P30591C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-4478
TELEFAX: 610-270-5090
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 130 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-459-135A-7

Query Match 94.7%; Score 54; DB 2; Length 130;
Best Local Similarity 90.0%; Pred. No. 0.0063;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 NKDKPSYQFG 10
|||||
DB 90 NKDKPSYQFG 99

RESULT 12
US-08-459-135A-8
Sequence 8, Application US/08459135A
Patent No. 5955078
GENERAL INFORMATION:
APPLICANT: BURNHAM, Martin Karl Russel
APPLICANT: CHOPRA, Ian
APPLICANT: CRITCHLEY, Ian Alfred
APPLICANT: KNOWLES, David Justin Charles
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN: MONOCLONAL ANTIBODY AND THEIR US
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
STATE: PA
COUNTRY: U.S.A.
ZIP: 19406-0939
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: Fastseq, Version 2.0


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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/459,135A
; FILING DATE: 02-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB/94/00215
; FILING DATE: 04-Feb-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Gimmil, Edward R
; REGISTRATION NUMBER: 38,891
; REFERENCE/DOCKET NUMBER: P30591C2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-270-4478
; TELEFAX: 610-270-5090
;
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 130 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-459-135A-8

Query Match          94.7%; Score 54; DB 3; Length 130;
Best Local Similarity 90.0%; Pred. No. 0.0063;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 NKDKPSYQFG 10
      |||||:||||
Db      90 NKDKPNYQFG 99

RESULT 13
; Sequence 7, Application US/08495559A
; Patent No. 6054572
; GENERAL INFORMATION:
; APPLICANT: BURHAM, Martin Karl Russel
; APPLICANT: CHOPRA, Ian
; APPLICANT: CRITCHLEY, Ian Alfred
; APPLICANT: KNOWLES, David Justin Charles
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN: MONOCLONAL
; FILE REFERENCE: P30591
; CURRENT APPLICATION NUMBER: US/08/495,559A
; EARLIER FILING DATE: 1995-08-03
; EARLIER APPLICATION NUMBER: GB 9302289.5
; EARLIER FILING DATE: 1993-02-05
; EARLIER APPLICATION NUMBER: GB 9321592.9
; EARLIER FILING DATE: 1993-10-20
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 7
; LENGTH: 130
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-08-495-559-7

Query Match          94.7%; Score 54; DB 3; Length 130;
Best Local Similarity 90.0%; Pred. No. 0.0063;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 NKDKPSYQFG 10
      |||||:||||
Db      90 NKDKPNYQFG 99

RESULT 14
US-08-495-559-8
; Sequence 8, Application US/08495559A
; Patent No. 6054572
; GENERAL INFORMATION:
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; APPLICANT: BURHAM, Martin Karl Russel
; APPLICANT: CHOPRA, Ian
; APPLICANT: CRITCHLEY, Ian Alfred
; APPLICANT: KNOWLES, David Justin Charles
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN: MONOCLONAL
; FILE REFERENCE: P30591
; CURRENT APPLICATION NUMBER: US/08/495,559A
; CURRENT FILING DATE: 1995-08-03
; EARLIER APPLICATION NUMBER: GB 9302289.5
; EARLIER FILING DATE: 1993-02-05
; EARLIER APPLICATION NUMBER: GB 9321592.9
; EARLIER FILING DATE: 1993-10-20
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 8
; LENGTH: 130
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-08-495-559-8

Query Match          94.7%; Score 54; DB 3; Length 130;
Best Local Similarity 90.0%; Pred. No. 0.0063;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 NKDKPSYQFG 10
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Db      90 NKDKPNYQFG 99

RESULT 15
US-08-459-135A-10
; Sequence 10, Application US/08459135A
; Patent No. 5955078
; GENERAL INFORMATION:
; APPLICANT: BURHAM, Martin Karl Russel
; APPLICANT: CHOPRA, Ian
; APPLICANT: CRITCHLEY, Ian Alfred
; APPLICANT: KNOWLES, David Justin Charles
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN: MONOCLONAL ANTIBODY AND THEIR US
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Smitkligne Beecham Corporation
; STREET: 709 Swedeland Road
; CITY: King of Prussia
; STATE: PA
; COUNTRY: U.S.A.
; ZIP: 19406-0939
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: Fastseq, Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/459,135A
; FILING DATE: 02-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB/94/00215
; FILING DATE: 04-Feb-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Gimmil, Edward R
; REGISTRATION NUMBER: 38,891
; REFERENCE/DOCKET NUMBER: P30591C2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-270-4478
; TELEFAX: 610-270-5090
;
; TELEX:
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 174 amino acids
; TYPE: amino acid
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! TOPOLOGY: linear
! MOLECULE TYPE: Protein
US-08-459-135A-10

Query Match 94.7%; Score 54; DB 2; Length 174;
Best Local Similarity 90.0%; Pred. NO. 0.0086;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 NKDKPSYQFG 10
|||:||||
Db 90 NKDKPNTQFG 99

Search completed: October 22, 2005, 09:35:45
Job time : 17.2989 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 22, 2005, 12:39:57 ; Search time 56.1494 Seconds
(without alignments)
74.354 Million cell updates/sec

Title: US-10-731-238-94
Perfect score: 57
Sequence: 1 NKDKPSYQFG 10

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1862951 seqs, 417491010 residues

Total number of hits satisfying chosen parameters: 1862951

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

Published Applications_AA:*

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2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*

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19: /cgn2_6/ptodata/2/pubpaa/US11A_PUBCOMB.pep:*

20: /cgn2_6/ptodata/2/pubpaa/US11A_NEW_PUB.pep:*

21: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*

22: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	57	100.0	37	US-10-731-238-94	Sequence 94, Appl
2	57	100.0	139	US-11-066-697-1134	Sequence 1134, Ap
3	57	100.0	37	US-09-813-820-8	Sequence 8, Appl
4	57	100.0	1018	US-09-815-242-5797	Sequence 5797, Ap
5	57	100.0	1018	US-10-470-048B-68	Sequence 12838, A
6	57	100.0	1027	US-10-470-048B-68	Sequence 68, Appl
7	57	100.0	1027	US-08-781-986A-5254	Sequence 5254, Ap
8	57	100.0	1027	US-10-329-624-5254	Sequence 5254, Ap
9	54	94.7	388	US-08-901-662-1	Sequence 1, Appl
10	54	94.7	559	US-08-781-986A-5251	Sequence 5251, Ap
11	54	94.7	559	US-10-329-624-5251	Sequence 5251, Ap

12	54	94.7	940	US-10-470-048B-424	Sequence 424, App
13	54	94.7	948	US-10-470-048B-69	Sequence 69, Appl
14	54	94.7	961	US-10-282-122A-43778	Sequence 43778, A
15	54	94.7	978	US-09-815-242-5456	Sequence 5456, Ap
16	54	94.7	1001	US-09-815-242-12686	Sequence 12686, A
17	54	94.7	1038	US-10-282-122A-43827	Sequence 43827, A
18	46	80.7	10	US-10-731-238-95	Sequence 95, Appl
19	45	78.9	10	US-10-731-238-93	Sequence 93, Appl
20	41	71.9	335	US-10-450-763-59542	Sequence 59542, A
21	41	71.9	782	US-10-450-763-59546	Sequence 59546, A
22	41	71.9	2280	US-10-437-963-198400	Sequence 198400, A
23	41	71.9	2681	US-10-450-763-59543	Sequence 59543, A
24	40	70.2	21	US-10-731-238-9	Sequence 9, Appl
25	40	70.2	21	US-10-731-238-20	Sequence 20, Appl
26	40	70.2	21	US-10-731-238-21	Sequence 21, Appl
27	40	70.2	21	US-10-731-238-22	Sequence 22, Appl
28	40	70.2	21	US-10-731-238-23	Sequence 23, Appl
29	40	70.2	21	US-10-731-238-24	Sequence 24, Appl
30	40	70.2	21	US-10-731-238-25	Sequence 25, Appl
31	40	70.2	21	US-10-731-238-26	Sequence 26, Appl
32	40	70.2	21	US-10-731-238-27	Sequence 27, Appl
33	40	70.2	21	US-10-731-238-28	Sequence 28, Appl
34	40	70.2	21	US-10-731-238-29	Sequence 29, Appl
35	40	70.2	21	US-10-731-238-30	Sequence 30, Appl
36	40	70.2	21	US-10-731-238-31	Sequence 31, Appl
37	40	70.2	21	US-10-731-238-32	Sequence 32, Appl
38	40	70.2	21	US-10-731-238-33	Sequence 33, Appl
39	40	70.2	21	US-10-731-238-34	Sequence 34, Appl
40	38	66.7	118	US-10-425-115-361027	Sequence 361027, A
41	40	70.2	317	US-11-097-143-16848	Sequence 16848, A
42	37	64.9	38	US-10-080-334-165	Sequence 165, App
43	37	64.9	38	US-10-731-238-7	Sequence 7, Appl
44	37	64.9	38	US-10-731-238-45	Sequence 45, Appl
45	37	64.9	38	US-10-731-238-46	Sequence 46, Appl
			18	US-10-731-238-47	Sequence 47, Appl

ALIGNMENTS

RESULT 1

US-10-731-238-94

Sequence 94, Application US/10731238

Publication No. US2005012552A1

GENERAL INFORMATION:

APPLICANT: Hook, Magnus

Patel, Joseph M.

House-Pompeo, Karen L.

Speziale, Pietro

John, Denny

McGavin, Martin J.

TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS

AND METHODS OF USE

NUMBER OF SEQUENCES: 105

CORRESPONDENCE ADDRESSES:

ADDRESSER: Arnold, White & Durkee

STREET: P. O. Box 4433

CITY: Houston

STATE: TX

COUNTRY: USA

ZIP: 77210-4433

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/731,238

FILING DATE: 10-Dec-2003

CLASSIFICATION: <unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/010,317

FILING DATE: 21-Jan-1998

APPLICATION NUMBER: US 60/036,139

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;
; FILING DATE: 21-JAN-1997
; ATTORNEY/AGENT INFORMATION:
;   NAME: Hibler, David W.
;   REGISTRATION NUMBER: 41,071
;   REFERENCE/DOCKET NUMBER: TBMK:189
; TELECOMMUNICATION INFORMATION:
;   TELEPHONE: 512-418-3000
;   TELEFAX: 512-474-7577
; INFORMATION FOR SEQ ID NO: 94:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH: 10 amino acids
;     TYPE: amino acid
;     STRANDEDNESS: <Unknown>
;     TOPOLOGY: linear
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; SEQUENCE DESCRIPTION: SEQ ID NO: 94:
US-10-731-238-94

Query Match      100.0%; Score 57; DB 18; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0014;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NKDKPSYQFG 10
DB 1 NKDKPSYQFG 10

RESULT 2
US-11-066-697-1134
; Sequence 1134, Application US/11066697
; Publication No. US20050187159A1
; GENERAL INFORMATION:
;   APPLICANT: Bridon, Dominique P.
;   APPLICANT: Ezrin, Alan M.
;   APPLICANT: Milner, Peter G.
;   APPLICANT: Holmes, Darren L.
;   APPLICANT: Thibadeau, Karen
; TITLE OF INVENTION: PROTECTION OF ENDOGENOUS THERAPEUTIC PEPTIDES FROM
; TITLE OF INVENTION: PEPTIDASE ACTIVITY THROUGH COMUGATION TO BLOOD
; FILE REFERENCE: 500862002301
; CURRENT APPLICATION NUMBER: US/11/066,697
; CURRENT FILING DATE: 2005-02-25
; PRIOR APPLICATION NUMBER: 09/657,276
; PRIOR FILING DATE: 2000-09-07
; PRIOR APPLICATION NUMBER: 60/153,406
; PRIOR FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: 60/159,783
; PRIOR FILING DATE: 1999-10-15
; NUMBER OF SEQ ID NOS: 1617
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1134
; LENGTH: 37
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptide
US-11-066-697-1134

Query Match      100.0%; Score 57; DB 20; Length 37;
Best Local Similarity 100.0%; Pred. No. 0.0052;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NKDKPSYQFG 10
DB 13 NKDKPSYQFG 22

RESULT 3
US-09-813-820-8
; Sequence 8, Application US/09813820
; Patent No. US20020102282A1
; GENERAL INFORMATION:
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;
; APPLICANT: Hook, Magnus
;   Patti, Joseph M.
;   House-Pompeo, Karen
;   Sthanam, Narayana
;   Symereky, Jindrich
; TITLE OF INVENTION: COLLAGEN BINDING PROTEIN COMPOSITIONS
;   AND METHODS OF USE
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
;   ADDRESSER: Arnold, White & Durkee
;   STREET: P.O. Box 4433
;   CITY: Houston
;   STATE: Texas
;   COUNTRY: U.S.
;   ZIP: 77210
;
; COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/09/813,820
;   FILING DATE: 22-Mar-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: 08/856,253
;   FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
;   NAME: Kitchell, Barbara S.
;   REGISTRATION NUMBER: 33,928
;   REFERENCE/DOCKET NUMBER: TBMK:193
; TELECOMMUNICATION INFORMATION:
;   TELEPHONE: (512) 418-3000
;   TELEFAX: (512) 474-7577
; INFORMATION FOR SEQ ID NO: 8:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH: 139 amino acids
;     TYPE: amino acid
;     STRANDEDNESS: <Unknown>
;     TOPOLOGY: linear
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; SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-09-813-820-8

Query Match      100.0%; Score 57; DB 9; Length 139;
Best Local Similarity 100.0%; Pred. No. 0.02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NKDKPSYQFG 10
DB 104 NKDKPSYQFG 113

RESULT 4
US-09-815-242-5797
; Sequence 5797, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
;   APPLICANT: Haeselbeck, Robert
;   APPLICANT: Ohlsen, Karl L.
;   APPLICANT: Zyskind, Judith W.
;   APPLICANT: Wall, Daniel
;   APPLICANT: Trawick, John D.
;   APPLICANT: Carr, Grant J.
;   APPLICANT: Yamamoto, Robert T.
;   APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
;   TITLE OF INVENTION: Prokaryotes
; FILE REFERENCE: ELITRA.01A
; CURRENT APPLICATION NUMBER: US/09/815,242
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
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PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO: 5797
LENGTH: 1018
TYPE: PRT
ORGANISM: Staphylococcus aureus
US-09-815-242-5797

Query Match 100.0%; Score 57; DB 9; Length 1018;
Best Local Similarity 100.0%; Pred. No. 0.15;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NKDKPSYQFG 10
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DB 834 NKDKPSYQFG 843

RESULT 5
US-09-815-242-12838
Sequence 12838, Application US/09815242
GENERAL INFORMATION:
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Karl L.
APPLICANT: Zyskind, Judith W.
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John D.
APPLICANT: Carr, Grant J.
APPLICANT: Yamamoto, Robert T.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in
FILE REFERENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO: 12838
LENGTH: 1018
TYPE: PRT
ORGANISM: Staphylococcus aureus
US-09-815-242-12838

Query Match 100.0%; Score 57; DB 9; Length 1018;
Best Local Similarity 100.0%; Pred. No. 0.15;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 NKDKPSYQFG 10

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DB 834 NKDKPSYQFG 843

RESULT 6
US-10-470-048B-68
Sequence 68, Application US/10470048B
Publication No. US20050037444A1
GENERAL INFORMATION:
APPLICANT: MEINKE ET AL.
TITLE OF INVENTION: A METHOD FOR IDENTIFICATION, ISOLATION AND PRODUCTION OF
FILE REFERENCE: SONN.035US
CURRENT APPLICATION NUMBER: US/10/470,048B
CURRENT FILING DATE: 2003-07-25
NUMBER OF SEQ ID NOS: 603
SOFTWARE: PatentIn version 3.1
SEQ ID NO: 68
LENGTH: 1018
TYPE: PRT
ORGANISM: Staphylococcus aureus
US-10-470-048B-68

Query Match 100.0%; Score 57; DB 17; Length 1018;
Best Local Similarity 100.0%; Pred. No. 0.15;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NKDKPSYQFG 10
|||||
DB 834 NKDKPSYQFG 843

RESULT 7
US-08-781-986A-5254
Sequence 5254, Application US/08781986A
Publication No. US20030054436A1
GENERAL INFORMATION:
APPLICANT: Charles Kunach
TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
NUMBER OF SEQUENCES: 5255
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COUNTRY: USA
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/781,986A
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Benson, Bob
REGISTRATION NUMBER: 30,446
REFERENCE/DOCKET NUMBER: PB248PP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 5254:
SEQUENCE CHARACTERISTICS:
LENGTH: 1027 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein

US-08-781-986A-5254

Query Match 100.0%; Score 57; DB 8; Length 1027;
Best Local Similarity 100.0%; Pred. No. 0.16; Indels 0; Gaps 0;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NKDKPSYQFG 10
|||
Db 843 NKDKPSYQFG 852

RESULT 8
US-10-329-624-5254

; Sequence 5254, Application US/10329624
; Publication No. US20040043037A1

; GENERAL INFORMATION:
; APPLICANT: Charles Kunsch

; GIL H. Choi
; Patrick S. Dillon
; Craig A. Rosen
; Steven C. Barash

; TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
; NUMBER OF SEQUENCES: 5256

; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.

; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA

; ZIP: 20850

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage

; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2

; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/329,624

; FILING DATE: 27-Dec-2002

; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: 08/956,171

; FILING DATE: October 20, 1997

; APPLICATION NUMBER: 60/009,861

; FILING DATE: January 5, 1996

; APPLICATION NUMBER: 08/781,986

; FILING DATE: January 3, 1997

; ATTORNEY/AGENT INFORMATION:
; NAME: Mark J. Hyman

; REGISTRATION NUMBER: 46,789

; REFERENCE/DOCKET NUMBER: PB248P1D1

; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (240) 314-1124

; TELEFAX: (301) 309-8439

; INFORMATION FOR SEQ ID NO: 5254:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1027 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 5254:

US-10-329-624-5254

Query Match 100.0%; Score 57; DB 15; Length 1027;
Best Local Similarity 100.0%; Pred. No. 0.16; Indels 0; Gaps 0;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NKDKPSYQFG 10
|||
Db 843 NKDKPSYQFG 852

RESULT 9

US-08-901-062-1

; Sequence 1, Application US/08901062
; Publication No. US20020025324A1

; GENERAL INFORMATION:
; APPLICANT: SEALS, JONATHAN R.

; TITLE OF INVENTION: RECOMBINANT BIVALENT BACTERIAL VACCINE
; NUMBER OF SEQUENCES: 2

; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HALE AND DORR LLP

; STREET: 60 State Street
; CITY: Boston

; STATE: MA

; COUNTRY: United States of America

; ZIP: 02109

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/901,062

; FILING DATE: 25-JUL-1997

; CLASSIFICATION: 424

; ATTORNEY/AGENT INFORMATION:
; NAME: Baker, Hollie L.

; REGISTRATION NUMBER: 31,321

; REFERENCE/DOCKET NUMBER: 106941.153

; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 526-6000

; TELEFAX: (617) 526-5000

; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 388 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO

US-08-901-062-1

Query Match 94.7%; Score 54; DB 8; Length 388;
Best Local Similarity 90.0%; Pred. No. 0.2; Indels 0; Gaps 0;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 NKDKPSYQFG 10
|||
Db 353 NKDKPSYQFG 362

RESULT 10
US-08-781-986A-5251

; Sequence 5251, Application US/08781986A
; Publication No. US20030054436A1

; GENERAL INFORMATION:
; APPLICANT: Charles Kunsch

; TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
; NUMBER OF SEQUENCES: 5255

; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.

; STREET: 9410 Key West Avenue
; CITY: Rockville

; STATE: Maryland

; COUNTRY: USA

; ZIP: 20850

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage

; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2

; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/781,986A

FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Benson, Bob
REGISTRATION NUMBER: 30,446
REFERENCE/DOCKET NUMBER: PB248PP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 5251:
SEQUENCE CHARACTERISTICS:
LENGTH: 559 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-781-986A-5251

Query Match 94.7%; Score 54; DB 8; Length 559;
Best Local Similarity 90.0%; Pred. No. 0.29;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NKDKPSYQFG 10
|||||
Db 389 NKDKPNYQFG 398

RESULT 11

US-10-329-624-5251
Sequence 5251, Application US/10329624
Publication No. US20040043037A1
GENERAL INFORMATION:

APPLICANT: Charles Kunsch

Gil H. Choi

Patrick S. Dillon

Craig A. Rosen

Steven C. Barash

Michael R. Fannon

TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences

NUMBER OF SEQUENCES: 5256

CORRESPONDENCE ADDRESS:

ADDRESSEE: Human Genome Sciences, Inc.

STREET: 9410 Key West Avenue

CITY: Rockville

STATE: Maryland

COUNTRY: USA

ZIP: 20850

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage

COMPUTER: HP Vectra 486/33

OPERATING SYSTEM: MSDOS version 6.2

SOFTWARE: ASCII Text

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/329,624

FILING DATE: 27-Dec-2002

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/956,171

FILING DATE: October 20, 1997

APPLICATION NUMBER: 60/009,861

FILING DATE: January 5, 1996

APPLICATION NUMBER: 08/781,986

FILING DATE: January 3, 1997

ATTORNEY/AGENT INFORMATION:

NAME: Mark J. Hyman

REGISTRATION NUMBER: 46,789

REFERENCE/DOCKET NUMBER: PB248P1D1

TELECOMMUNICATION INFORMATION:

TELEPHONE: (240) 314-1224

TELEFAX: (301) 309-8439

INFORMATION FOR SEQ ID NO: 5251:

SEQUENCE CHARACTERISTICS:
LENGTH: 559 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 5251:
US-10-329-624-5251

Query Match 94.7%; Score 54; DB 15; Length 559;
Best Local Similarity 90.0%; Pred. No. 0.29;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NKDKPSYQFG 10
|||||
Db 389 NKDKPNYQFG 398

RESULT 12

US-10-470-048B-424
Sequence 424, Application US/10470048B
Publication No. US20050037444A1
GENERAL INFORMATION:

APPLICANT: MEINKE ET AL.

TITLE OF INVENTION: A METHOD FOR IDENTIFICATION, ISOLATION AND PRODUCTION OF

FILE REFERENCE: SONN:03505

CURRENT APPLICATION NUMBER: US/10/470,048B

CURRENT FILING DATE: 2003-07-25

NUMBER OF SEQ ID NOS: 603

SOFTWARE: PatentIn version 3.1

SEQ ID NO 424

LENGTH: 940

TYPE: PRT

ORGANISM: Staphylococcus aureus

US-10-470-048B-424

Query Match 94.7%; Score 54; DB 17; Length 940;
Best Local Similarity 90.0%; Pred. No. 0.5;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NKDKPSYQFG 10
|||||
Db 770 NKDKPNYQFG 779

RESULT 13

US-10-470-048B-69
Sequence 69, Application US/10470048B
Publication No. US20050037444A1
GENERAL INFORMATION:

APPLICANT: MEINKE ET AL.

TITLE OF INVENTION: A METHOD FOR IDENTIFICATION, ISOLATION AND PRODUCTION OF

FILE REFERENCE: SONN:03505

CURRENT APPLICATION NUMBER: US/10/470,048B

CURRENT FILING DATE: 2003-07-25

NUMBER OF SEQ ID NOS: 603

SOFTWARE: PatentIn version 3.1

SEQ ID NO 69

LENGTH: 948

TYPE: PRT

ORGANISM: Staphylococcus aureus

US-10-470-048B-69

Query Match 94.7%; Score 54; DB 17; Length 948;
Best Local Similarity 90.0%; Pred. No. 0.5;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NKDKPSYQFG 10
|||||
Db 778 NKDKPNYQFG 787


```
RESULT 14
US-10-282-122A-43778
; Sequence 43778, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haebelbeck, Robert
; APPLICANT: Ohlsen, Karl
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 43778
; LENGTH: 961
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-10-282-122A-43778

Query Match          94.7%; Score 54; DB 15; Length 961;
Best Local Similarity 90.0%; Pred. No. 0.51;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 NKDKPSYQFG 10
      |||||:||||
Db      781 NKDKPNYQFG 730

RESULT 15
US-09-815-242-5456
; Sequence 5456, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haebelbeck, Robert
; APPLICANT: Ohlsen, Karl L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
```

```
; TITLE OF INVENTION: Identification of Essential Genes in
; FILE REFERENCE: ELITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5456
; LENGTH: 978
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-09-815-242-5456

Query Match          94.7%; Score 54; DB 9; Length 978;
Best Local Similarity 90.0%; Pred. No. 0.52;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 NKDKPSYQFG 10
      |||||:||||
Db      812 NKDKPNYQFG 821

Search completed: October 22, 2005, 12:56:28
Job time : 57.1494 secs
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GenCore version 5.1.6
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OM protein - protein search, using bw model

Run on: October 22, 2005, 08:04:46 ; Search time 11.6092 Seconds
(without alignments)
82.880 Million cell updates/sec

Title: US-10-731-238-94
Perfect score: 57
Sequence: 1 NKDKPSYQFG 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	57	100.0	1018 2	A32192 fibronectin-binding
2	54	94.7	940 2	S19702 fibronectin-binding
3	54	94.7	961 2	G90053 hypothetical prote
4	54	94.7	1038 2	H90053 hypothetical prote
5	38	66.7	645 2	S03208 type III site-spec
6	37	64.9	537 2	T34380 hypothetical prote
7	37	64.9	575 2	T28230 ORF MSY069 probabl
8	37	64.9	725 1	E64211 virulence-associat
9	37	64.9	1328 2	S78457 exonuclease II - f
10	37	64.9	1790 1	S27772 vitellinogenin precu
11	36	63.2	209 2	S07725 protein P1 - Param
12	36	63.2	289 2	A69405 hydroxymethylbilan
13	36	63.2	292 2	S58857 botulinum neurotox
14	36	63.2	318 2	S73381 rfbJ protein - Syn
15	36	63.2	352 2	AC3306 periplasmic dipept
16	35	61.4	183 2	B97784 formylmethionine d
17	35	61.4	206 2	AH0259 melanoma antigen M
18	35	61.4	347 2	I38008 oligopeptide ABC t
19	35	61.4	541 2	A70141 origin recognition
20	35	61.4	558 2	S68447 2',3'-cyclic-nucle
21	35	61.4	652 1	S52695 2',3'-cyclic-nucle
22	35	61.4	656 2	AC0429 virulence-associat
23	35	61.4	726 1	S73915 probable NADH2 deh
24	35	61.4	820 2	C81252 hypothetical prote
25	35	61.4	826 2	G90283 hypothetical prote
26	34	59.6	125 2	D83770 sortase [imported]
27	34	59.6	206 2	A90057 conserved hypochet
28	34	59.6	330 2	F64584 B. subtilis YggU p
29	34	59.6	350 2	AH1604

30	34	59.6	363 2	AD1242 B. subtilis YggU p
31	34	59.6	395 1	A46345 gene III protein -
32	34	59.6	413 2	C91229 hypothetical prote
33	34	59.6	413 2	B86076 hypothetical prote
34	34	59.6	418 2	S40824 hypothetical 48k p
35	34	59.6	449 2	JC2381 virulence ACVB pro
36	34	59.6	456 2	D97662 agrobacterium chro
37	34	59.6	456 2	AG2886 hsp 90-binding pro
38	34	59.6	458 1	A42386 immunophilin p59 -
39	34	59.6	458 2	JN0673 immunophilin FKBP5
40	34	59.6	459 2	A46372 oxidoreductase, GM
41	34	59.6	509 2	D87452 multidrug resistanc
42	34	59.6	519 2	B71726 ybaU protein - Esc
43	34	59.6	623 2	A64774 probable proteinase
44	34	59.6	623 2	C85541
45	34	59.6	623 2	G90690 probable proteinase

ALIGNMENTS

RESULT 1
A32192
fibronectin-binding protein - Staphylococcus aureus
C:Species: Staphylococcus aureus
C:Date: 31-Jul-1989 #sequence_revision 31-Jul-1989 #text_change 16-Feb-1997
C:Accession: A32192
R:Signaes, C.; Raucet, G.; Joensson, K.; Lindgren, P.E.; Anantharamaiah, G.M.; Hoeeck, Proc. Natl. Acad. Sci. U.S.A. 86, 699-703, 1989
A:Title: Nucleotide sequence of the gene for a fibronectin-binding protein from Staphyl
A:Reference number: A32192; MUID:89089898; PMID:2521391
A:Accession: A32192
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1018 <SIG>
A:Cross-references: GB:J04151
C:Keywords: fibronectin binding

Query Match 100.0%; Score 57; DB 2; Length 1018;
Best Local Similarity 100.0%; Pred. No. 0.0098;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NKDKPSYQFG 10
Db 834 NKDKPSYQFG 843

RESULT 2

S19702
fibronectin-binding protein B - Staphylococcus aureus
C:Species: Staphylococcus aureus
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
C:Accession: S19702
R:Joensson, K.; Signaes, C.; Mueller, H.P.; Lindberg, M.
Eur. J. Biochem. 202, 1041-1048, 1991
A:Title: Two different genes encode fibronectin binding proteins in Staphylococcus aure
A:Reference number: S19702; MUID:9211475; PMID:1837266
A:Accession: S19702
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-940 <JOB>
A:Cross-references: UNIPROT:Q53682; EMBL:X62992; NID:949040; PIDD:CAA44726.1; PID:95815
C:Keywords: fibronectin binding

Query Match 94.7%; Score 54; DB 2; Length 940;
Best Local Similarity 90.0%; Pred. No. 0.034;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NKDKPSYQFG 10
Db 770 NKDKPSYQFG 779

```

RESULT 3
G90053
hypothetical protein fnbB [imported] - Staphylococcus aureus (strain N315)
C/Species: Staphylococcus aureus
C/Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C/Accession: G90053
R/Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguc
ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.;
C.; Shibata, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
A/Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.
A/Reference number: A89758; MUID:21311952; PMID:11418146
A/Accession: G90053
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-961 <KIR>
A/Cross-references: UNIPROT:Q99RD3; GB:BA000018; PID:g13702452; PIDN:BAB43593.1; GSPDB:G
A/Experimental source: strain N315
C/Genetics:
A/Gene: fnbB

Query Match          94.7%; Score 54; DB 2; Length 961;
Best Local Similarity 90.0%; Pred. No. 0.035; Mismatches 0; Gaps 0;
Matches 9; Conservative 1; Indels 0; Gaps 0;

QY 1 NKDKPSYQFG 10
    |||||:||||
Db 781 NKDKENYQFG 790

RESULT 4
H90053
hypothetical protein fnb [imported] - Staphylococcus aureus (strain N315)
C/Species: Staphylococcus aureus
C/Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C/Accession: H90053
R/Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguc
ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.;
C.; Shibata, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
A/Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.
A/Reference number: A89758; MUID:21311952; PMID:11418146
A/Accession: H90053
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-1038 <KIR>
A/Cross-references: UNIPROT:Q99RD2; GB:BA000018; PID:g13702453; PIDN:BAB43594.1; GSPDB:G
A/Experimental source: strain N315
C/Genetics:
A/Gene: fnbB

Query Match          94.7%; Score 54; DB 2; Length 1038;
Best Local Similarity 90.0%; Pred. No. 0.038; Mismatches 0; Gaps 0;
Matches 9; Conservative 1; Indels 0; Gaps 0;

QY 1 NKDKPSYQFG 10
    |||||:||||
Db 830 NKDKENYQFG 839

RESULT 5
S03208
type III site-specific deoxyribonuclease (EC 3.1.21.5) Ecop15 chain mod - Escherichia co
N/Alternate names: type III restriction enzyme Ecop15 chain mod
C/Species: Escherichia coli
C/Date: 07-Jun-1990 #sequence_revision 31-Dec-1991 #text_change 09-Jul-2004
C/Accession: S03208
R/Hemmelin, M.; Surti, B.; Rao, D.N.; Hornby, D.P.; Eberle, H.; Pipfl, T.; Kenel, S.; E
J. Mol. Biol. 200, 23-29, 1988
A/Title: Type III DNA restriction and modification systems Ecop1 and Ecop15. Nucleotide
A/Reference number: S01511; MUID:88245189; PMID:2837577
A/Accession: S03208
A/Molecule type: DNA

```

```

A/Residues: 1-645 <HUE>
A/Cross-references: UNIPROT:P12364; EMBL:X06288; NID:g42236; PIDN:CAA29616.1; PID:g42237
A/Note: the amino acid sequence from Fig. 6 is inconsistent with the nucleotide sequence
C/Genetics:
A/Gene: mod
C/Keywords: DNA binding; hydrolase

Query Match          66.7%; Score 38; DB 2; Length 645;
Best Local Similarity 77.8%; Pred. No. 28;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 NKDKPSYQFG 9
    |||||:||||
Db 457 NKDKTSYQFG 465

RESULT 6
T34380
hypothetical protein T25G12.2 - Caenorhabditis elegans
C/Species: Caenorhabditis elegans
C/Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
C/Accession: T34380
R/Du, Z.
Submitted to the EMBL Data Library, December 1995
A/Description: The sequence of C. elegans cosmid T25G12.
A/Reference number: T21515
A/Accession: T34380
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-537 <DUZ>
A/Cross-references: UNIPROT:Q22787; EMBL:U43283; PIDN:AAC69018.1; GSPDB:GN00028; CESP:T2
A/Experimental source: strain Bristol N2; clone T25G12
C/Genetics:
A/Gene: CESP:T25G12.2
A/Map position: X
A/Intons: 59/2; 89/1; 136/2; 279/3; 342/2; 426/3; 475/2; 526/2

Query Match          64.9%; Score 37; DB 2; Length 537;
Best Local Similarity 66.7%; Pred. No. 36;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 NKDKPSYQFG 9
    |||||:||||
Db 129 NKDKPTYFG 137

RESULT 7
T28230
ORF MSY069 probable rifampicin resistance (RIF) protein, Heliothis armigera entomopoxvi
C/Species: Melanoplus sanguinipes entomopoxvirus
C/Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 09-Jul-2004
C/Accession: T28230
R/Afonso, C.L.; Tulman, E.R.; Lu, Z.; Oma, E.; Kutish, G.F.; Rock, D.L.
J. Virol. 73, 533-552, 1999
A/Title: The genome of Melanoplus sanguinipes entomopoxvirus.
A/Reference number: Z20484; MUID:99102612; PMID:9847359
A/Accession: T28230
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-575 <APO>
A/Cross-references: UNIPROT:Q9YW23; EMBL:AF063866; NID:g4049647; PIDN:AAC97814.1; PID:g
C/Genetics:
A/Note: MSY069
C/Superfamily: variola virus N3L protein

Query Match          64.9%; Score 37; DB 2; Length 575;
Best Local Similarity 55.6%; Pred. No. 39;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 NKDKPSYQFG 9
    |||||:||||
Db 469 NSDRPYEF 477

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RESULT 8

E64211

vintulence-associated protein vacb homolog - Mycoplasma genitalium

C:Species: Mycoplasma genitalium

C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004

C:Accession: E64211

R:Freese, C.M.; Gocayne, J.D.; White, O.; Adams, M.D.; Clayton, R.A.; Fleischmann, R.D.; M.; Fuhmann, J.; Nguyen, D.; Uterback, T.R.; Saudek, D.M.; Phillips, C.A.; Merrick, J.

C: A.; Venter, J.C.

Science 270, 397-403, 1995

A:Title: The minimal gene complement of Mycoplasma genitalium.

C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004

A:Accession: E64211

A:Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-725 <TIGR>

A:Cross-references: UNIPROT:P47350; GB:U39690; GB:LA3967; NID:G1045782; PID:G1045783; TI

A:Experimental source: strain G-37

C:Genetics:

A:Genetic code: SGC3

C:Superfamily: vintulence-associated protein vacb homolog

Query Match 64.9%; Score 37; DB 1; Length 725;
 Best Local Similarity 75.0%; Pred. No. 50;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 NKDRSYQ 8
 DB 531 NKDNPSYE 538

RESULT 9

S78457

exonuclease II - fission yeast (Schizosaccharomyces pombe)

C:Species: Schizosaccharomyces pombe

C:Date: 19-Mar-1998 #sequence_revision 17-Apr-1998 #text_change 09-Jul-2004

C:Accession: S78457; T37829; S72531

R:Szankasi, P.; Smith, G.R.

submitted to the EMBL Data Library, September 1994

A:Reference number: S78457

A:Accession: S78457

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-1328 <SZA>

A:Cross-references: UNIPROT:P40183; EMBL:L35232; NID:G51021; PID:AA842181.1; PID:G5310

R:Devlin, K.; Churcher, C.M.; Barrell, B.G.; Rajandream, M.A.; Wood, V.

submitted to the EMBL Data Library, August 1997

A:Reference number: 221737

A:Accession: T37829

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-1328 <DEV>

A:Cross-references: EMBL:Z98849; PIDN:CAB11514.1; GSPDB:GN00066; SPDB:SPAC17A5.14

A:Experimental source: strain 972h; cosmid cl7A5

R:Szankasi, P.; Smith, G.R.

Curr. Genet. 30, 284-293, 1996

A:Title: Requirement of S. pombe exonuclease II, a homologue of S. cerevisiae Sep1, for

A:Reference number: S72531; MUID:96376490; PMID:8781170

A:Accession: S72531

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-27,29-1328 <SZA>

A:Cross-references: EMBL:L35232

C:Genetics:

A:Gene: SPAC17A5.14; exo2

A:Map position: 1

A:introns: 5/3; 28/2

C:Superfamily: Schizosaccharomyces pombe exonuclease II

Query Match 64.9%; Score 37; DB 2; Length 1328;
 Best Local Similarity 66.7%; Pred. No. 96;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 NKDRSYQF 9
 DB 362 NSDKSFDF 370

RESULT 10

S27772

vitellogenin precursor - boll weevil

C:Species: Anthonomus grandis (boll weevil)

C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004

C:Accession: S27772

R:Trewitt, P.M.; Heilmann, L.J.; Kumaran, A.K.

submitted to the EMBL Data Library, October 1991

A:Description: Nucleotide sequence and structure of the vitellogenin gene from the boll

A:Reference number: S27772

A:Accession: S27772

A:Molecule type: DNA

A:Residues: 1-1790 <TRE>

A:Cross-references: UNIPROT:Q05808; EMBL:M72980; NID:G155707; PIDN:AAA27740.1; PID:G155

A:Genetics:

A:introns: 11/1; 678/3; 744/2; 845/2; 902/1; 1466/1

C:Superfamily: boll weevil vitellogenin

P:1-18/Domain: signal sequence #status predicted <SIG>

P:19-1790/Product: vitellogenin #status predicted <MAT>

Query Match 64.9%; Score 37; DB 1; Length 1790;
 Best Local Similarity 55.6%; Pred. No. 1.3e+02;
 Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 2 KDRPSYQFG 10
 DB 224 RDRPSYHYG 232

RESULT 11

S07725

protein P1 - Paramecium tetraurelia mitochondrion

C:Species: mitochondrion Paramecium tetraurelia

C:Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 12-Jul-2004

C:Accession: S07725

R:Pritchard, A.E.; Sellhammer, J.J.; Mahalingam, R.; Sable, C.L.; Vennuti, S.E.; Cummings

Nucleic Acids Res. 18, 173-180, 1990

A:Title: Nucleotide sequence of the mitochondrial genome of Paramecium.

A:Reference number: S07725; MUID:90174913; PMID:2308823

A:Accession: S07725

A:Status: translation not shown

A:Molecule type: DNA

A:Residues: 1-209 <PRI>

A:Cross-references: UNIPROT:P15600; EMBL:X15917; NID:G13256; PID:G578750

C:Genetics:

A:Genome: mitochondrion

A:Start codon: ATA

C:Superfamily: NADH:quinone oxidoreductase (complex I), subunit 30K/NdhJ/Nuoc

C:Keywords: mitochondrion

Query Match 63.2%; Score 36; DB 2; Length 209;
 Best Local Similarity 66.7%; Pred. No. 20;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 KDRPSYQFG 10
 DB 19 KKKPKYRFG 27

RESULT 12

A69405

hydroxymethylbilane synthase (EC 4.3.1.8) - Archaeoglobus fulgidus

N:Alternate names: porphobilinogen deaminase

C:Species: Archaeoglobus fulgidus

C:Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004

C:Accession: A69405

R;Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson
; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.F.;
Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.
Nature 390, 364-370, 1997

A;Authors: Overbeek, T.; Cotton, M.D.; Spriggs, T.; Artlich, P.; Kaine, B.P.; Sykes, S.
Smith, H.O.; Woese, C.R.; Venter, J.C.

A;Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaea
A;Accession: A69405

A;Status: preliminary; nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA

A;Residues: 1-289 <KLE>

A;Cross-references: UNIPROT:O29026; GB:AE001018; GB:AE000782; NID:G2689341; PIDD:AA89000

C;Superfamily: hydroxymethylbilane synthase

C;Keywords: ammonia-lyase; carbon-nitrogen lyase; porphyrin biosynthesis

F;234/Modified site: dipyrrolylmethanemethyl (Cys) (covalent) #status predicted

Query Match 63.2%; Score 36; DB 2; Length 289;
Best Local Similarity 75.0%; Pred. No. 29;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 KDKPSYOF 9
Db 43 KDKPLIEP 50

RESULT 13

S58857

botulinum neurotoxin type B hemagglutinin component, 33K - Clostridium botulinum (strain
N;Alternate names: protein HA-33

C;Species: Clostridium botulinum

A;Variety: strain Eklund 17B

C;Date: 15-Feb-1996 #sequence_revision 01-Mar-1996 #text_change 09-Jul-2004

C;Accession: S58857

R;East, A.K.; Stacey, J.M.; Collins, M.D.

Syst. Appl. Microbiol. 17, 306-312, 1994

A;Title: Cloning and sequencing of a hemagglutinin component of the botulinum neurotoxin

A;Reference number: S58855

A;Accession: S58857

A;Molecule type: DNA

A;Residues: 1-292 <EAS>

A;Cross-references: UNIPROT:Q45868; EMBL:X79103; NID:9870932; PIDD:CAA55714.1; PID:98709

A;Experimental source: strain Eklund 17B

C;Keywords: hemagglutinin; neurotoxin

Query Match 63.2%; Score 36; DB 2; Length 292;
Best Local Similarity 66.7%; Pred. No. 29;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 NKDKPSYOF 9
Db 195 NKEKAYOF 203

RESULT 14

S77381

rfbJ protein - *Synechocystis* sp. (strain PCC 6803)

N;Alternate names: protein sll1457

C;Species: *Synechocystis* sp.

A;Variety: PCC 6803

C;Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004

C;Accession: S77381

R;Kaneh, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.;
O, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda
DNA Res. 3, 109-116, 1996

A;Title: Sequence analysis of the genome of the unicellular cyanobacterium *Synechocystis*
S.

A;Reference number: S74322; MUID:97061201; PMID:8905231

A;Accession: S77381

A;Status: nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA

A;Residues: 1-318 <KAN>

A;Cross-references: UNIPROT:P73444; EMBL:D90906; GB:AB001339; NID:G1652492; PIDD:BA11748

A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996

C;Genetics:

A;Gene: rfbJ

A;Start codon: GNG

C;Superfamily: Methanobacterium thermoautotrophicum dolichyl-phosphate mannose synthase

Query Match 63.2%; Score 36; DB 2; Length 318;
Best Local Similarity 66.7%; Pred. No. 32;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 KDKPSYOF 10
Db 124 KDKAYRFG 132

RESULT 15

AC3306

periplasmic dipeptide transport protein precursor BME10433 [imported] - *Brucella melitensis*

C;Species: *Brucella melitensis*

C;Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 09-Jul-2004

C;Accession: AC3306

R;DelVecchio, V.G.; Kaputral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Log, T.; Ivanova,
; Mazur, M.; Goldsman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Letes
Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002

A;Title: The genome sequence of the facultative intracellular pathogen *Brucella melitensis*

A;Reference number: AD3252; PMID:11756688

A;Status: preliminary

A;Accession: AC3306

A;Molecule type: DNA

A;Residues: 1-352 <KUR>

A;Cross-references: UNIPROT:Q8Y1L1; GB:AE008917; PIDD:AA151614.1; PID:G17982340; GSPDB:1

A;Experimental source: strain 16M

C;Genetics:

A;Gene: BME10433

A;Map position: I

Query Match 63.2%; Score 36; DB 2; Length 352;
Best Local Similarity 66.7%; Pred. No. 36;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 NKDKPSYOF 9
Db 136 NKDNPMYQY 144

Search completed: October 22, 2005, 09:55:45
Job time : 12.6092 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 22, 2005, 08:01:06 ; Search time 56.2069 Seconds
(without alignments)
91.106 Million cell updates/sec

Title: US-10-731-238-94
Perfect score: 57
Sequence: 1 NKDKPSYQFG 10

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_03: *
1: uniprot_sprot: *
2: uniprot_trembl: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	57	100.0	152	2	Q9AEP9
2	57	100.0	1018	1	FNBA STAAU
3	54	94.7	940	2	Q53682
4	54	94.7	943	2	Q8NUU8
5	54	94.7	957	2	Q6G6H4
6	54	94.7	961	2	Q99RD3
7	54	94.7	961	2	Q7A3J8
8	54	94.7	965	2	Q6GDU5
9	54	94.7	1015	2	Q8NUU7
10	54	94.7	1015	2	Q6G6H3
11	54	94.7	1038	2	Q99RD2
12	54	94.7	1038	2	Q7A3J7
13	43	75.4	155	2	Q7N5Q4
14	41	71.9	199	2	Q6XCOC
15	41	71.9	280	2	Q8STZ5
16	39	68.4	601	2	Q8AAV3
17	39	68.4	651	2	Q7N0G2
18	39	68.4	1167	2	Q8QV02
19	38	66.7	158	2	Q81QG3
20	38	66.7	467	2	Q75HB3
21	38	66.7	542	2	Q6CD90
22	38	66.7	640	2	Q6CD46
23	38	66.7	645	1	T3MO_ECOLI
24	37	64.9	315	2	Q89008
25	37	64.9	331	2	Q72Q50
26	37	64.9	331	2	Q8R617
27	37	64.9	354	2	Q6UM82
28	37	64.9	390	2	Q6ZUS9
29	37	64.9	500	1	LIFE_HUMAN
30	37	64.9	500	1	LIFE_MOUSE
31	37	64.9	500	2	Q6P9C8

32	37	64.9	537	2	Q22787	Q22787 caenorhabdi
33	37	64.9	575	2	Q9YW23	Q9YW23 melanoplus
34	37	64.9	653	2	Q8DE70	Q8DE70 vibrio vuln
35	37	64.9	657	2	Q7MPF5	Q7MPF5 vibrio vuln
36	37	64.9	725	1	RNR_MYCGE	P47350 mycoplasma
37	37	64.9	747	2	Q8XN30	Q8XN30 clostridium
38	37	64.9	943	2	Q6P260	Q6P260 mesoplasma
39	37	64.9	961	2	Q81C12	Q81C12 plasmodium
40	37	64.9	1016	2	Q6BNX0	Q6BNX0 debaryomyce
41	37	64.9	1328	1	EXO2_SCHPO	P40383 schizosacch
42	37	64.9	1790	1	VIT_AMTGR	Q05808 anthronomus
43	36	63.2	40	2	Q35371	Q35371 paramacium
44	36	63.2	50	2	Q35372	Q35372 paramacium
45	36	63.2	59	2	Q35373	Q35373 paramacium

ALIGNMENTS

RESULT 1

ID	Q9AEP9	PRELIMINARY;	PRT;	152 AA.
AC	Q9AEP9;			
DT	01-JUN-2001 (TREMBLrel. 17, Created)			
DT	01-JUN-2001 (TREMBLrel. 17, Last sequence update)			
DT	01-DEC-2001 (TREMBLrel. 19, Last annotation update)			
DE	Fibronectin-binding protein (fragment).			
GN	Name=fnb;			
OS	Staphylococcus aureus.			
OC	Bacteria; Firmicutes; Bacillales; Staphylococcus.			
OK	NCBI_TaxID=1280;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=CMRSA-1;			
RX	MEDLINE=21246681; PubMed=11349044;			
RX	DOI=10.1128/IAI.69.6.3791-3799.2001;			
RA	Rice K., Huesca M., Vaz D., McGavin M.J.,			
RT	"Variance in fibronectin binding and fnb locus polymorphisms in			
RT	Staphylococcus aureus: identification of antigenic variation in a			
RT	fibronectin binding protein adhesion of the epidemic CMRSA-1 strain of			
RT	methicillin-resistant S. aureus."			
RL	Infect. Immun. 69:3791-3799 (2001).			
DR	EMBL; AY029184; AAK31588.1; -.			
FT	NON_TER			
FT	NON_TER			
SQ	SEQUENCE 152 AA; 17193 MW; CFA3913C2B11C025 CRC64;			

Query Match 100.0%; Score 57; DB 2; Length 152;
Best local Similarity 100.0%; Pred. No. 0.0055;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NKDKPSYQFG 10
|||
Db 127 NKDKPSYQFG 136

RESULT 2

ID	FNBA STAAU	STANDARD;	PRT;	1018 AA.
AC	P14738;			
DT	01-APR-1990 (Rel. 14, Created)			
DT	01-APR-1990 (Rel. 14, Last sequence update)			
DT	25-OCT-2004 (Rel. 45, Last annotation update)			
DE	Fibronectin-binding protein precursor (FNBP).			
GN	Name=fnbA;			
OS	Staphylococcus aureus.			
OC	Bacteria; Firmicutes; Bacillales; Staphylococcus.			
OK	NCBI_TaxID=1280;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=NCITC 8325-4;			
RX	MEDLINE=89098988; PubMed=2521391;			
RA	Signaas C., Raucis G., Joensen K., Lindgren P.-E.,			

RA Anantharamaiah G.M., Hoeck M., Lindberg M.;
 "Nucleotide sequence of the gene for a fibronectin-binding protein
 from *Staphylococcus aureus*: use of this peptide sequence in the
 RT synthesis of biologically active peptides";
 RU Proc. Natl. Acad. Sci. U.S.A. 86:699-703(1989).
 CC -1- FUNCTION: The ability of bacteria to bind fibronectin has been
 CC proposed as a virulence factor enabling bacteria to colonize wound
 CC tissues and blood clots. Binding of plasma fibronectin to the
 CC bacterial surface might block adhesion receptors on *S.aureus*, thus
 CC representing an important defense mechanism against tissue
 CC invasion.
 CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
 CC an amide bond (potential).
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL, J04151, AAA26632.1; -.
 DR InterPro, IPR004237; Fn_bind.
 DR InterPro, IPR005877; Gpos_YsIRK.
 DR InterPro, IPR001899; Gram_pos_anchor.
 DR Pfam, PF02986; Fn_bind, 1.
 DR Pfam, PF00746; Gram_pos_anchor, 1.
 DR Pfam, PF04650; YsIRK_signal, 1.
 DR TIGRFAMs, TIGR01167; LPTXG_anchor, 1.
 DR TIGRFAMs, TIGR01168; YsIRK_signal, 1.
 DR PROSITE, PS50847; GRAM_POS_ANCHORING, 1.
 KM Cell adhesion; Cell wall; Peptidoglycan-anchor; Repeat; Signal;
 KM Virulence.
 FT SIGNAL 1 36
 FT CHAIN 37 985 Fibronectin-binding protein.
 FT PROPE 986 1018 Removed by sortase (potential).
 FT REPEAT 545 574 B-1.
 FT REPEAT 575 604 B-2.
 FT DOMAIN 745 878 4 X approximate tandem repeats,
 FT 745 878 fibronectin-binding domain.
 FT REPEAT 745 782 D-1.
 FT REPEAT 783 820 D-2.
 FT REPEAT 821 859 D-3.
 FT REPEAT 860 878 D-4 (incomplete).
 FT DOMAIN 879 948 5 X tandem repeats, Pro-rich (WR).
 FT REPEAT 879 892 WR 1.
 FT REPEAT 893 906 WR 2.
 FT REPEAT 907 920 WR 3.
 FT REPEAT 921 934 WR 4.
 FT REPEAT 935 948 WR 5.
 FT SITE 982 986 LPTXG sorting signal (potential).
 FT MOD_RRS 985 985 Pentaglycyl muurin peptidoglycan amidated
 FT threonine (potential).
 SQ SEQUENCE 1018 AA, 111780 MW, 58175E0020E81F1F CRC64;
 Query Match 100.0%; Score 57; DB 1; Length 1018;
 Best Local Similarity 100.0%; Pred. No. 0.044;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 NKDKPSYQFG 10
 DB 834 NKDKPSYQFG 843
 RESULT 3
 OS3682 PRELIMINARY; PRT; 940 AA.
 ID Q53682
 AC Q53682;
 DT 01-NOV-1996 (TREMBlrel. 01, Created)
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
 DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
 DE Fibronectin binding protein B.

GN Name=fnb3;
 OS *Staphylococcus aureus*.
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 OX NCBI_TaxID=1280;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=8325-4;
 RX MEDLINE=92111475; PubMed=1837266;
 RA Jonsen K., Signas C., Muller H.P., Lindberg M.;
 RT "Two different genes encode fibronectin binding proteins in
 RT *Staphylococcus aureus*. The complete nucleotide sequence and
 RT characterization of the second gene";
 RU Eur. J. Biochem. 202:1041-1048(1991).
 CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
 CC an amide bond (By similarity).
 CC EMBL, X62992; CAA44726.1; -.
 DR PIR, S19702; S19702.
 DR HSP, Q53653; 1N67.
 DR GO, GO:0009986; C:cell surface; IEA.
 DR GO, GO:0005618; C:cell wall; IEA.
 DR GO, GO:0009375; C:cell wall (sensu Gram-positive Bacteria); IEA.
 DR GO, GO:0016020; C:membrane; IEA.
 DR GO, GO:0007155; P:cell adhesion; IEA.
 DR InterPro, IPR008966; Adhes_bact.
 DR InterPro, IPR004237; Fn_bind.
 DR InterPro, IPR005877; Gpos_YsIRK.
 DR InterPro, IPR001899; Gram_pos_anchor.
 DR Pfam, PF02986; Fn_bind, 2.
 DR Pfam, PF00746; Gram_pos_anchor, 1.
 DR Pfam, PF04650; YsIRK_signal, 1.
 DR TIGRFAMs, TIGR01167; LPTXG_anchor, 1.
 DR TIGRFAMs, TIGR01168; YsIRK_signal, 1.
 DR PROSITE, PS50847; GRAM_POS_ANCHORING, 1.
 KM Cell wall; Peptidoglycan-anchor.
 SQ SEQUENCE 940 AA, 103555 MW, E35FBBCA907AE345 CRC64;
 Query Match 94.7%; Score 54; DB 2; Length 940;
 Best Local Similarity 90.0%; Pred. No. 0.16;
 Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 NKDKPSYQFG 10
 DB 770 NKDKPSYQFG 779
 RESULT 4
 OS Q8NU8
 ID Q8NU8 PRELIMINARY; PRT; 943 AA.
 AC Q8NU8;
 DT 01-OCT-2002 (TREMBlrel. 22, Created)
 DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
 DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
 DE Fnb3 protein.
 GN Name=fnb3; OrderedLocusNames=MM2420;
 OS *Staphylococcus aureus* (strain MW2).
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 OX NCBI_TaxID=196620;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=MM2;
 RX MEDLINE=22040717; PubMed=12044378; DOI=10.1016/S0140-6736(02)08713-5;
 RA Baba T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Oguchi A.,
 RA Nagai Y., Iwama N., Asano K., Naimi T., Kuroda H., Cui L.,
 RA Yamamoto K., Hiramatsu K.;
 RT "Genome and virulence determinants of high virulence community-
 RT acquired MRSA";
 RU Lancet 359:1819-1827(2002).
 CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
 CC an amide bond (By similarity).
 CC EMBL, AP004630; BAB96285.1; -.
 DR HSP, Q53653; 1N67.
 DR GO, GO:0009986; C:cell surface; IEA.
 DR GO, GO:0005618; C:cell wall; IEA.

```

DR GO: GO:0009275; C:cell wall (senu Gram-positive Bacteria); IEA.
DR GO: GO:0016020; C:membrane; IEA.
DR GO: GO:0007155; P:cell adhesion; IEA.
DR InterPro: IPR008966; Adhes_bact.
DR InterPro: IPR004237; Fn_bind.
DR InterPro: IPR005877; Gpos_YsIRK.
DR InterPro: IPR001899; Gram_pos_anchor.
DR Pfam: PF02986; Fn_bind. 1.
DR Pfam: PF00746; Gram_pos_anchor. 1.
DR TIGRFAMs: TIGR01167; LpxTG_anchor. 1.
DR TIGRFAMs: TIGR01168; YsIRK_signal. 1.
DR PROSITE: PS50847; GRAM_POS_ANCHORING. 1.
DR Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ SEQUENCE 943 AA; 104537 MW; DA8A5F31947E1B6A CRC64;

Query Match 94.7%; Score 54; DB 2; Length 943;
Best Local Similarity 90.0%; Pred. No. 0.16;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NKDKPSYQFG 10
Db 777 NKDKPNYQFG 786

RESULT 5
06G6H4 PRELIMINARY; PRT; 957 AA.
ID 06G6H4
AC 06G6H4;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE Fibronectin-binding protein.
DE Name=fnbB; OrderedLocNames=SA52387;
CN Staphylococcus aureus (strain MSSA4476).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=282459;
[1]
RP SEQUENCE FROM N.A.
FX PubMed:15213324; DOI=10.1073/pnas.0402521101;
RA Holden M.T.G., Feil E.J., Lindsay J.A., Peacock S.J., Day N.P.J.,
RA Enright M.C., Foster T.J., Moore C.E., Hurst L., Atkin R., Barron A.,
RA Baon N., Bentley S.D., Chillingworth C., Chillingworth T.,
RA Churcher C., Cronin A., Doggett J., Dowd L.,
RA Feltwell T., Hance Z., Harris B., Hauser H., Holtroyd S., Jagels K.,
RA James K.D., Lennard N., Line A., Mayes R., Moule S., Mungall K.,
RA Omund D., Quail M.A., Rabinovitch E., Rutherford K.M., Sanders M.,
RA Sharp S., Simmonds M., Stevens K., Whitehead S., Barrall B.G.,
RA Spratt B.G., Parhill J.;
RT "Complete genomes of two clinical Staphylococcus aureus strains:
RT evidence for the rapid evolution of virulence and drug resistance.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:9786-9791(2004)
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC an amide bond (By similarity).
EMBL: BX571857; CAG44201.1; -.
DR GO: GO:0009986; C:cell surface; IEA.
DR GO: GO:0005618; C:cell wall; IEA.
DR GO: GO:0009275; C:cell wall (senu Gram-positive Bacteria); IEA.
DR GO: GO:0016020; C:membrane; IEA.
DR GO: GO:0007155; P:cell adhesion; IEA.
DR InterPro: IPR008966; Adhes_bact.
DR InterPro: IPR004237; Fn_bind.
DR InterPro: IPR005877; Gpos_YsIRK.
DR InterPro: IPR001899; Gram_pos_anchor.
DR Pfam: PF02986; Fn_bind. 1.
DR Pfam: PF00746; Gram_pos_anchor. 1.
DR TIGRFAMs: TIGR01167; LpxTG_anchor. 1.
DR TIGRFAMs: TIGR01168; YsIRK_signal. 1.
DR PROSITE: PS50847; GRAM_POS_ANCHORING. 1.
DR Cell wall; Complete proteome; Peptidoglycan-anchor.
KW SEQUENCE 957 AA; 105980 MW; 28F8BA7FFDFD3EAF CRC64;
SQ

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Query Match 94.7%; Score 54; DB 2; Length 957;
Best Local Similarity 90.0%; Pred. No. 0.16;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NKDKPSYQFG 10
Db 777 NKDKPNYQFG 786

RESULT 6
099RD3 PRELIMINARY; PRT; 961 AA.
ID 099RD3
AC 099RD3;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 24, Last annotation update)
DE Fibronectin-binding protein homolog.
DE Name=fnbB; OrderedLocNames=SAV2502;
CN Staphylococcus aureus (strain Mu50 / ATCC 700699).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=158878;
[1]
RP SEQUENCE FROM N.A.
FX STRAIN=Mu50 / ATCC 700699;
RA MEDLINE=21311952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2;
RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Iian J.-O., Ito T.,
RA Kanemori M., Matsunaru H., Maruyama A., Murakami H., Hoshoyama A.,
RA Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
RA Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
RA Kanehisa M., Yanaashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
RA Hattori M., Ogasawara N., Hayaishi H., Hiramatsu K.;
RT "Whole genome sequencing of methicillin-resistant Staphylococcus
RT aureus.";
RL Lancet 357:1225-1240(2001).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC an amide bond (By similarity).
EMBL: AP003365; BAB58664.1; -.
DR PIR: G90053; G90053.
DR HSP: Q53653; I1N67.
DR GO: GO:0009986; C:cell surface; IEA.
DR GO: GO:0005618; C:cell wall; IEA.
DR GO: GO:0009275; C:cell wall (senu Gram-positive Bacteria); IEA.
DR GO: GO:0016020; C:membrane; IEA.
DR GO: GO:0007155; P:cell adhesion; IEA.
DR InterPro: IPR008966; Adhes_bact.
DR InterPro: IPR004237; Fn_bind.
DR InterPro: IPR005877; Gpos_YsIRK.
DR InterPro: IPR001899; Gram_pos_anchor.
DR Pfam: PF02986; Fn_bind. 1.
DR Pfam: PF00746; Gram_pos_anchor. 1.
DR TIGRFAMs: TIGR01167; LpxTG_anchor. 1.
DR TIGRFAMs: TIGR01168; YsIRK_signal. 1.
DR PROSITE: PS50847; GRAM_POS_ANCHORING. 1.
DR Cell wall; Complete proteome; Peptidoglycan-anchor.
KW SEQUENCE 961 AA; 106010 MW; 364940F884BA4101 CRC64;
SQ

Query Match 94.7%; Score 54; DB 2; Length 961;
Best Local Similarity 90.0%; Pred. No. 0.16;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NKDKPSYQFG 10
Db 781 NKDKPNYQFG 790

RESULT 7
07A3J8 PRELIMINARY; PRT; 961 AA.
ID 07A3J8
AC 07A3J8;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)

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DT 05-JUL-2004 (TrEMBLrel. 27, last annotation update)
DE Fnb protein.
GN Name=fnb: OrderedlocusNames=SA2290;
OS Staphylococcus aureus (strain N315);
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=158879;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=1311952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2;
RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Iian J.-O., Ito T.,
RA Kanamori M., Matsunaru H., Maruyama A., Murakami H., Hosoyama A.,
RA Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
RA Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
RA Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
RA Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
RA "Whole genome sequencing of methicillin-resistant Staphylococcus
RA aureus."
RT Lancet 357:1225-1240(2001).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC an amide bond (By similarity).
EMBL: AP003137; BAB43593.1; -.
DR GO: GO:0009986; C:cell surface; IEA.
DR GO: GO:0005618; C:cell wall; IEA.
DR GO: GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO: GO:0016020; C:membrane; IEA.
DR GO: GO:0007155; P:cell adhesion; IEA.
DR InterPro: IPR008966; Adhes_bact.
DR InterPro: IPR004237; Fn_bind.
DR InterPro: IPR005877; Gpos_YsIRK.
DR InterPro: IPR01899; Gram_pos_anchor.
DR Pfam: PF02986; Fn_bind; 1.
DR Pfam: PF04650; YsIRK_signal; 1.
DR TIGRFAMs: TIGR01167; LPXTG_anchor; 1.
DR TIGRFAMs: TIGR01168; YsIRK_signal; 1.
DR PROSITE: PS50847; GRAM_POS_ANCHORING; 1.
KM Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ SEQUENCE 961 AA; 106010 MW; 364940F884BA4101 CRC64;

Query Match 94.7%; Score 54; DB 2; Length 961;
Best Local Similarity 90.0%; Pred. No. 0.16;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 NKDKPSYQFG 10
Db 781 NKDKPNYQFG 790

RESULT 8
ID 06GDUS PRELIMINARY; PRT; 965 AA.
AC 06GDUS;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Fibronectin-binding protein.
GN Name=fnbA: OrderedlocusNames=SA2580;
OS Staphylococcus aureus (strain MRSA252).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=282458;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=15213324; DOI=10.1073/pnas.0402521101;
RA Holden M.T.G., Fell E.J., Lindsay J.A., Peacock S.J., Day N.P.J.,
RA Bright M.C., Foster T.J., Moore C.E., Hurst L., Atkin R., Barron A.,
RA Baeson N., Bentley S.D., Chillingworth C., Chillingworth T.,
RA Churcher C., Clark L., Corton C., Cronin A., Doggett J., Dowd L.,
RA Feltwell T., Hance Z., Harris B., Hauser H., Holtroyd S., Jørgen K.,
RA James K.D., Lennard N., Line A., Mayes R., Moule S., Mungall K.,
RA Omond D., Quail M.A., Rabinowitsch E., Rutherford K.M., Sanders M.,
RA Sharp S., Simmonds M., Stevens K., Whitehead S., Barrell B.G.,
RA Spratt B.G., Parkhill J.;
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RT "Complete genomes of two clinical Staphylococcus aureus strains:
RT evidence for the rapid evolution of virulence and drug resistance.";
RT Proc. Natl. Acad. Sci. U.S.A. 101:9786-9791(2004).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC an amide bond (By similarity).
EMBL: BX571856; CAG41560.1; -.
DR GO: GO:0009986; C:cell surface; IEA.
DR GO: GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO: GO:0016020; C:membrane; IEA.
DR GO: GO:0007155; P:cell adhesion; IEA.
DR InterPro: IPR008966; Adhes_bact.
DR InterPro: IPR004237; Fn_bind.
DR InterPro: IPR005877; Gpos_YsIRK.
DR InterPro: IPR01899; Gram_pos_anchor.
DR Pfam: PF02986; Fn_bind; 1.
DR Pfam: PF04650; YsIRK_signal; 1.
DR TIGRFAMs: TIGR01167; LPXTG_anchor; 1.
DR TIGRFAMs: TIGR01168; YsIRK_signal; 1.
DR PROSITE: PS50847; GRAM_POS_ANCHORING; 1.
KM Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ SEQUENCE 965 AA; 105691 MW; 2982E132164D0551 CRC64;

Query Match 94.7%; Score 54; DB 2; Length 965;
Best Local Similarity 90.0%; Pred. No. 0.16;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 NKDKPSYQFG 10
Db 799 NKDKPNYQFG 808

RESULT 9
ID 08NTU7 PRELIMINARY; PRT; 1015 AA.
AC 08NTU7;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Fnb protein.
GN Name=fnb: OrderedlocusNames=MM2421;
OS Staphylococcus aureus (strain MM2).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=196620;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=MM2;
RX MEDLINE=22040717; PubMed=12044378; DOI=10.1016/S0140-6736(02)08713-5;
RA Baba T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Oguchi A.,
RA Nagai Y., Iwama N., Asano K., Naimi T., Kuroda H., Cui L.,
RA Yamamoto K., Hiramatsu K.;
RT "Genome and virulence determinants of high virulence community-
RT acquired MRSA.";
RT Lancet 359:1819-1827(2002).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC an amide bond (By similarity).
EMBL: AP004830; BAB96286.1; -.
DR GO: GO:0009986; C:cell surface; IEA.
DR GO: GO:0005618; C:cell wall; IEA.
DR GO: GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO: GO:0016020; C:membrane; IEA.
DR GO: GO:0007155; P:cell adhesion; IEA.
DR InterPro: IPR008966; Adhes_bact.
DR InterPro: IPR004237; Fn_bind.
DR InterPro: IPR005877; Gpos_YsIRK.
DR InterPro: IPR01899; Gram_pos_anchor.
DR Pfam: PF02986; Fn_bind; 1.
DR Pfam: PF04650; YsIRK_signal; 1.
DR TIGRFAMs: TIGR01167; LPXTG_anchor; 1.
DR TIGRFAMs: TIGR01168; YsIRK_signal; 1.
DR PROSITE: PS50847; GRAM_POS_ANCHORING; 1.
KM Cell wall; Complete proteome; Peptidoglycan-anchor.
```

SQ SEQUENCE 1015 AA; 111145 MW; D0F9281B864D44D2 CRC64;
 Query Match 94.7%; Score 54; DB 2; Length 1015;
 Best Local Similarity 90.0%; Pred. No. 0.17;
 Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 NKDKPSYQFG 10
 |||||
 DB 835 NKDKPNYQFG 844

RESULT 10
 Q6G6H3 PRELIMINARY; PRT; 1015 AA.
 AC Q6G6H3;
 DT 05-JUL-2004 (TReMBLrel. 27, Created)
 DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TReMBLrel. 27, Last annotation update)
 DE Fibronection-binding protein.
 GN OrderedLocusNames=SA52388;
 OS Staphylococcus aureus (strain MSSA476).
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 CX NCBI_TaxID=282459;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX PubMed=15213324; DOI=10.1073/pnas.0402521101;
 RA Holden M.T.G., Fell E.J., Lindsay J.A., Peacock S.J., Day N.P.J.,
 RA Enright M.C., Foster T.J., Moore C.E., Hurst L., Atkin R., Barron A.,
 RA Baeson N., Bentley S.D., Chillingworth C., Chillingworth T.,
 RA Churcher C., Clark L., Corson C., Cronin A., Doggett J., Doud L.,
 RA Fellwell T., Hance Z., Harris B., Hauser H., Holtroyd S., Jørgels K.,
 RA James K.D., Lennard N., Line A., Mayes R., Moule S., Mungall K.,
 RA Ormond D., Quail M.A., Rabinowitch E., Rutherford K.M., Sanders M.,
 RA Sharp S., Simmonds M., Stevens K., Whitehead S., Barrall B.G.,
 RA Spratt B.G., Parkhill J.,
 RA "Complete genomes of two clinical Staphylococcus aureus strains:
 RT evidence for the rapid evolution of virulence and drug resistance.",
 RL Proc. Natl. Acad. Sci. U.S.A. 101:9786-9791(2004).
 CC -1 SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
 an amide bond (By similarity).
 DR EMBL: BX571857; CAG44202.1; -.
 DR GO: GO:0009986; C:cell surface; IEA.
 DR GO: GO:0005618; C:cell wall; IEA.
 DR GO: GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
 DR GO: GO:0016020; C:membrane; IEA.
 DR GO: GO:0007155; P:cell adhesion; IEA.
 DR InterPro: IPR008966; Adhes_Bact.
 DR InterPro: IPR004237; Fn_bind.
 DR InterPro: IPR005877; Gpos_YsIRK.
 DR InterPro: IPR001899; Gram_pos_anchor.
 DR Pfam: PF002986; Fn_bind. 1.
 DR Pfam: PF00746; Gram_pos_anchor. 1.
 DR Pfam: PF04650; YsIRK_signal. 1.
 DR TIGRFAMs: TIGR01167; LpxTG_anchor. 1.
 DR TIGRFAMs: TIGR01168; YsIRK_signal. 1.
 DR PROSITE: PS50847; GRAM_POS_ANCHORING. 1.
 KW Cell wall; Complete proteome; Peptidoglycan-anchor.
 SQ SEQUENCE 1015 AA; 111145 MW; D0F9281B864D44D2 CRC64;

Query Match 94.7%; Score 54; DB 2; Length 1015;
 Best Local Similarity 90.0%; Pred. No. 0.17;
 Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 NKDKPSYQFG 10
 |||||
 DB 835 NKDKPNYQFG 844

RESULT 11
 Q99RD2 PRELIMINARY; PRT; 1038 AA.
 AC Q99RD2;
 DT 01-JUN-2001 (TReMBLrel. 17, Created)

DT 01-JUN-2001 (TReMBLrel. 17, Last sequence update)
 DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)
 DE Fibronection-binding protein homolog.
 GN Name=fnb; OrderedLocusNames=SAV2503;
 OS Staphylococcus aureus (strain Mu50 / ATCC 700699).
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 CX NCBI_TaxID=158878;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Mu50 / ATCC 700699;
 RX MEDLINE=21311952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2;
 RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
 RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Iino J.-O., Ito T.,
 RA Kanamori M., Matsunaru H., Maruyama A., Murakami H., Hosoyama A.,
 RA Mizutani U.Y., Hiraekawa H., Kuhnra S., Goto S., Yabuzaki J.,
 RA Sekimizu K., Hiraekawa H., Oshima K., Furuya K., Yoshino C., Shiba T.,
 RA Hattori M., Ogasawara N., Hayashi H., Hiratake K.,
 RT "Whole genome sequencing of methicillin-resistant Staphylococcus
 RT aureus.",
 RL Lancet 357:1225-1240(2001).
 CC -1 SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
 an amide bond (By similarity).
 DR EMBL: AP003365; BAB58665.1; -.
 DR PIR: H90053; H90053.
 DR GO: GO:0009986; C:cell surface; IEA.
 DR GO: GO:0005618; C:cell wall; IEA.
 DR GO: GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
 DR GO: GO:0016020; C:membrane; IEA.
 DR GO: GO:0007155; P:cell adhesion; IEA.
 DR InterPro: IPR008966; Adhes_bact.
 DR InterPro: IPR004237; Fn_bind.
 DR InterPro: IPR005877; Gpos_YsIRK.
 DR InterPro: IPR001899; Gram_pos_anchor.
 DR Pfam: PF002986; Fn_bind. 1.
 DR Pfam: PF00746; Gram_pos_anchor. 1.
 DR Pfam: PF04650; YsIRK_signal. 1.
 DR TIGRFAMs: TIGR01167; LpxTG_anchor. 1.
 DR TIGRFAMs: TIGR01168; YsIRK_signal. 1.
 DR PROSITE: PS50847; GRAM_POS_ANCHORING. 1.
 KW Cell wall; Complete proteome; Peptidoglycan-anchor.
 SQ SEQUENCE 1038 AA; 113618 MW; 666BF6BF28FBE12 CRC64;

Query Match 94.7%; Score 54; DB 2; Length 1038;
 Best Local Similarity 90.0%; Pred. No. 0.17;
 Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 NKDKPSYQFG 10
 |||||
 DB 830 NKDKPNYQFG 839

RESULT 12
 Q7A3J7 PRELIMINARY; PRT; 1038 AA.
 AC Q7A3J7;
 DT 05-JUL-2004 (TReMBLrel. 27, Created)
 DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TReMBLrel. 27, Last annotation update)
 DE Fnb protein.
 GN Name=fnb; OrderedLocusNames=SA2291;
 OS Staphylococcus aureus (strain N315).
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 CX NCBI_TaxID=158879;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21311952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2;
 RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
 RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Iino J.-O., Ito T.,
 RA Kanamori M., Matsunaru H., Maruyama A., Murakami H., Hosoyama A.,
 RA Mizutani U.Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
 RA Sekimizu K., Hiraekawa H., Kuhnra S., Goto S., Yabuzaki J.,
 RA Kanehisa M., Yanehisa A., Oshima K., Furuya K., Yoshino C., Shiba T.,

RA Hactori M., Ogasawara N., Hayashi H., Hiramatsu K.
 RT "Whole genome sequencing of methicillin-resistant *Staphylococcus aureus*."
 RL Lancet 357:1225-1240(2001).
 CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by an amide bond (By similarity).
 CC EMBL, AP003137; BAB43594.1; -.
 DR GO: GO:0009986; C:cell surface; IEA.
 DR GO: GO:0005618; C:cell wall; IEA.
 DR GO: GO:0009275; C:cell wall (genus Gram-positive Bacteria); IEA.
 DR GO: GO:0016020; P:cell adhesion; IEA.
 DR GO: GO:0007155; P:cell adhesion; IEA.
 DR InterPro: IPR004237; Fm bind.
 DR InterPro: IPR008966; Adhes bact.
 DR InterPro: IPR005877; Gpos YSRK.
 DR InterPro: IPR001899; Gram_pos_anchor.
 DR Pfam: PF02986; Fm_bind; 1.
 DR Pfam: PF00746; Gram_pos_anchor; 1.
 DR Pfam: PF04650; YSRK_signal; 1.
 DR TIGRFAMs: TIGR01167; LpxTG_anchor; 1.
 DR TIGRFAMs: TIGR01168; YSRK_signal; 1.
 DR PROSITE: PSS0847; GRAM_POS_ANCHORING; 1.
 DR Cell wall; Complete proteome; Peptidoglycan-anchor.
 KW SEQUENCE 1038 AA; 113618 MW; 666BFBFBFB12 CRC64;
 SQ

Query Match 94.7%; Score 54; DB 2; Length 1038;
 Best Local Similarity 90.0%; Pred. No. 0.17;
 Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 NKDKPSYQFG 10
 Db 830 NKDKPSYQFG 839

RESULT 13

ID Q7N5Q4 PRELIMINARY; PRT; 155 AA.
 AC Q7N5Q4;
 DT 01-MAR-2004 (TrEMBLrel. 26, Created)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Similarities with immunity protein of pyocin S3.
 GN OederedLocustNames-Plu1890;
 OS Photobacterium luminescens (subsp. laumondii).
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Photobacterus.
 OX NCBI_TaxID=141679;
 OX [1]
 RN SEQUENCE FROM N.A.
 RP STRAIN=TT01;
 RX MEDLINE=22957627; PubMed=14528314;
 RA Duchoud E., Rusliok C., Frangoul L., Buchrieser C., Givaudan A., Taurit S., Bosc S., Boursaux-Eude C., Chandler M., Charles J.-F., Dassa E., Depose R., Derzelle S., Freydisse G., Gaudriault S., Medigue C., Lanois A., Powell K., Siguler P., Vincent R., Wingate V., Zouine M., Glaeser P., Boemare N., Danchin A., Kunst F.;
 RA "The genome sequence of the entomopathogenic bacterium *Photobacterium luminescens*."
 RT Nature 414:450-453(2001).
 RL Nat. Biotechnol. 21:1307-1313(2003).
 DR EMBL, BX571865; CAET4183.1; -.
 DR Photobact; plu1890; -.
 KW Complete proteome.
 SQ SEQUENCE 155 AA; 18191 MW; F739BAC6A0BC78D CRC64;
 SO

Query Match 75.4%; Score 43; DB 2; Length 155;
 Best Local Similarity 77.8%; Pred. No. 3.1;
 Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 NKDKPSYQFG 9
 Db 69 DRDKPSYQFG 77

RESULT 14

ID Q6XOC0 PRELIMINARY; PRT; 199 AA.
 AC Q6XOC0;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Putative tail assembly protein.
 GN ORFNames=34;
 OS Enterobacteria phage T1.
 OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae;
 OC T1-like viruses.
 OX NCBI_TaxID=12355;
 OX [1]
 RN SEQUENCE FROM N.A.
 RX PubMed=14972552; DOI=10.1016/j.virol.2003.09.020;
 RA Roberts M.D., Martin N.L., Kropinski A.M.;
 RT "The genome and proteome of coliphage T1."
 RL Virology 318:245-266(2004).
 DR EMBL, AY216660; AAP49965.1; -.
 DR InterPro: IPR010654; Lambda_tail_1.
 DR Pfam: PF06805; Lambda_tail_1; 1.
 SQ SEQUENCE 199 AA; 20897 MW; 6DB4FA2C1914553B CRC64;
 SO

Query Match 71.9%; Score 41; DB 2; Length 199;
 Best Local Similarity 70.0%; Pred. No. 10;
 Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 NKDKPSYQFG 10
 Db 154 SKNKPSYQFG 163

RESULT 15

ID Q8STZ5 PRELIMINARY; PRT; 280 AA.
 AC Q8STZ5;
 DT 01-JUN-2002 (TrEMBLrel. 21, Created)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Hypothetical protein ECu1_1970.
 GN Name=ECu1_1970;
 OS Encephalitozoon cuniculi GB-M1.
 OC Eukaryota; Fungi; Microsporidia; Unikaryonidae; Encephalitozoon.
 OX NCBI_TaxID=284813;
 OX [1]
 RN SEQUENCE FROM N.A.
 RP STRAIN=GB-M1;
 RX MEDLINE=21576510; PubMed=11719806; DOI=10.1038/35106579;
 RA Kalinka M.D., Duprat S., Cornillot E., Metenier G., Thomarot F., Rauscher G., Barbe V., Peyretailade E., Broctier P., Wincker P., Delbac F., El Alaoui H., Peyret P., Saurin W., Gouy M., Weissenbach J., Vivares C.P.;
 RA "Genome sequence and gene compaction of the eukaryotic parasite *Encephalitozoon cuniculi*."
 RT Nature 414:450-453(2001).
 RL Nature 414:450-453(2001).
 RN [2]
 RP SEQUENCE FROM N.A.
 RP STRAIN=GB-M1;
 RA Genoscope; (Apr-2001) to the EMBL/GenBank/DBJ databases.
 RL Submitted (Apr-2001) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: Contains 3 WD repeats.
 DR EMBL, AL590450; CAD26107.1; -.
 DR InterPro: IPR001680; WD40.
 DR Pfam: PF00400; WD40; 3.
 DR PRINTS, PR00320; GPROTEINBRPT.
 DR SMART; SM00320; WD40; 4.
 DR PROSITE; PS00678; WD_REPEATS_1; 1.
 DR PROSITE; PS00682; WD_REPEATS_2; 3.
 DR PROSITE; PS50294; WD_REPEATS_REGION; 1.
 KW Hypothetical protein; Repeat; WD repeat.
 SQ SEQUENCE 280 AA; 31339 MW; 50176D5970F538 CRC64;
 SO

Query Match 71.9%; Score 41; DB 2; Length 280;
Best Local Similarity 66.7%; Pred. No. 14;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
QY 2 KDKPSYQFG 10
: : : : :
Db 237 EDRPNYQFG 245

Search completed: October 22, 2005, 09:52:20
Job time : 58.2069 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 25, 2005, 20:58:51 ; Search time 69.7126 Seconds
(without alignments)
55.479 Million cell updates/sec

Title: US-10-731-238-95
Perfect score: 60
Sequence: 1 DKPSYQFGGH 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:*

- 1: geneseqp1980s:*
- 2: geneseqp1990s:*
- 3: geneseqp2000s:*
- 4: geneseqp2001s:*
- 5: geneseqp2002s:*
- 6: geneseqp2003as:*
- 7: geneseqp2003bs:*
- 8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	60	100.0	10	2	AAM65751
2	60	100.0	22	2	AAR21340
3	60	100.0	37	4	AAB91958
4	60	100.0	38	1	AAP80662
5	60	100.0	134	2	AAI29087
6	60	100.0	139	2	AAW31556
7	60	100.0	1018	1	AAP82115
8	60	100.0	1018	4	AAU37245
9	60	100.0	1018	4	AAU34301
10	60	100.0	1018	6	ABJ18922
11	60	100.0	1018	6	ABM72537
12	60	100.0	1027	2	AAW89806
13	57	95.0	77	2	AAW88749
14	57	95.0	101	2	AAW80939
15	57	95.0	113	2	AAW90937
16	57	95.0	124	2	AAW90940
17	57	95.0	128	2	AAW90941
18	57	95.0	130	2	AAW88806
19	57	95.0	130	2	AAW88807
20	57	95.0	130	2	AAW88807
21	57	95.0	130	2	AAW88807
22	57	95.0	134	2	AAW88807
23	57	95.0	134	2	AAW88807
24	57	95.0	134	2	AAW88807
25	57	95.0	164	2	AAW88807

26	57	95.0	174	2	AAW88808
27	57	95.0	174	2	AAW88808
28	57	95.0	181	2	AAW88808
29	57	95.0	181	2	AAW88808
30	57	95.0	559	2	AAW88803
31	57	95.0	940	2	AAW88803
32	57	95.0	940	6	ABJ19111
33	57	95.0	948	6	ADA89470
34	57	95.0	948	6	ABU18923
35	57	95.0	948	6	ABM72536
36	57	95.0	961	6	ABU15854
37	57	95.0	978	4	AAU37093
38	57	95.0	1001	4	AAU37093
39	57	95.0	1038	6	ABU15903
40	54	90.0	21	2	AAW65680
41	54	90.0	21	2	AAW65683
42	54	90.0	21	2	AAW65689
43	54	90.0	21	2	AAW65679
44	54	90.0	21	2	AAW65684
45	54	90.0	21	2	AAW65685

ALIGNMENTS

RESULT 1
ID AAM65751 standard; peptide; 10 AA.

XX AAM65751;

XX AC 16-OCR-1998 (first entry)

XX DT Fibronectin binding protein-derived peptide #95.

XX DE microbial surface components recognising adhesive matrix molecule;

XX DE MSCRAMM; fibronectin; fibronectin-binding protein; antibody; epitope;

XX DE antibiotic; bacterial infection; antibiotic-resistant strain.

XX OS Synthetic.

XX OS Staphylococcus aureus.

XX PN WO9831389-A2.

XX PF 21-JUN-1998; 98WO-US001222.

XX PF 21-JAN-1997; 97US-0036139P.

XX (TEXAS) UNIV TEXAS A & M SYSTEM.

XX Hooeek M, Patci JM, House-Pompeo KL, Speziale P, Joh D;

XX McGeavin MJ;

XX WPI, 1998-413816/35.

XX Antibody that binds to fibronectin-binding protein, preventing its

XX binding to fibronectin - used to treat or prevent bacterial infection,

XX especially by Staphylococci and Streptococci.

XX Example 9; Page 111, 201pp; English.

XX The invention relates to antibodies that bind to a fibronectin-binding

XX domain of a fibronectin-binding protein, and inhibit binding of the

XX protein to fibronectin. Also claimed are: (1) isolated peptides of a

XX fibronectin-binding protein that do not bind to fibronectin; (2) fusion

XX protein containing at least one peptide of a fibronectin-binding protein

XX linked to a second amino acid sequence; (3) nucleic acid encoding the

XX isolated peptide of (1). Antibodies, the isolated peptides of (1) and the

XX nucleic acids are all useful for immunisation (active or passive) and (by

XX inhibiting binding of bacteria to fibronectin) for preventing or treating

XX infection in humans or other animals, particularly by staphylococci or

CC streptococci, e.g. meningitis, otitis media, pneumonia, endocarditis,
CC mastitis in cattle, abortion in horses and many others. Since the
CC antibodies block binding of bacteria, they should be effective against
CC antibiotic-resistant strains, and may replace antibiotic therapy or
CC increase its effectiveness. Sequences AAM65744-58 represent peptides
CC which were synthesised to span the D3 motif of S. aureus fibronectin
CC binding protein A
CC
CC
SQ Sequence 10 AA;

Query Match 100.0%; Score 60; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.00075;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DKPSYQFGGH 10
| | | | | | | |
Db 1 DKPSYQFGGH 10

RESULT 2
AAR21340
ID AAR21340 standard; peptide: 22 AA.
XX
AC AAR21340;
XX
DT 25-MAR-2003 (revised)
DT 15-JUN-1992 (first entry)
XX
DE Fibronectin binding protein.
XX
KM FMBP; wound infection reduction; vaccination; mastitis;
KM Staphylococcal infections; D3.
XX
OS Synthetic.
XX
FN W09202555-A.
XX
PD 20-FEB-1992.
XX
PF 10-AUG-1990; 90SE-00002617.
XX
PR 10-AUG-1990; 90SE-00002617.
XX
XX (ALFA) ALFA LAVAL AGRIC INT AB.
XX
PI Hook M, McGavin M, Raucel G;
XX
DR WPI; 1992-080035/10.
XX
XX
PT New fibronectin binding peptide - combines with fusion peptide to form
PT large antigen, used in immunisation, diagnosis and for treating wounds.
XX
XX
PS Claim 1; Page 22; 33pp; English.
XX
CC The sequence comprises amino acids 17-33 of a tandem repeat, designated
CC D3 of the fibronectin binding site of Staphylococcus aureus 8325-4 FMBP.
CC The N-terminal DK may be replaced with H or K, and the C-terminal LKP may
CC be replaced by either L, IP, or OH. The peptides were synthesised using
CC standard methods and purified using reverse phase HPLC. The appropriate
CC fractions were dialysed and lyophilised. Peptide sequencing was performed
CC and the peptides digested and chemically modified by dinitroxypropylation
CC of the amino side chain of lysine. The carboxylic side chains were
CC converted to glycine methyl esters. The phenyl side chains of tyrosine
CC residues were oxidised. Chemically modified peptide D3 was compared to
CC unmodified D3. Lysine and tyrosine modifications only partially
CC diminished its activity whereas modification of aspartic/glutamic
CC residues resulted in complete loss of activity. The peptide can be used
CC for the prevention or reduction of the risk of wound infection. The
CC peptide can be used to create a large antigen for vaccinating ruminants
CC against mastitis caused by Staphylococcal infections. It can also be used
CC to diagnose Staphylococcal infections using ELISA or DNA probes. (Updated
CC on 25-MAR-2003 to correct PA field.)
XX

SQ Sequence 22 AA;

Query Match 100.0%; Score 60; DB 2; Length 22;
Best Local Similarity 100.0%; Pred. No. 0.0016;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DKPSYQFGGH 10
| | | | | | | |
Db 1 DKPSYQFGGH 10

RESULT 3
AAB91958
ID AAB91958 standard; peptide: 37 AA.
XX
AC AAB91958;
XX
DT 22-JUN-2001 (first entry)
XX
DE Fibronectin fragment and fibrin related peptide SEQ ID NO:1134.
XX
KM Protection; endogenous therapeutic peptide; peptidase; conjugation;
KM blood component; modification; succinimidyl; maleimido group; amino;
KM hydroxyl; thiol; hormone; growth factor; neurotransmitter.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN W0200069900-A2.
XX
PD 23-NOV-2000.
XX
PF 17-MAY-2000; 2000WO-US013576.
XX
PR 17-MAY-1999; 99US-0134406P.
PR 10-SEP-1999; 99US-0153406P.
PR 15-OCT-1999; 99US-0159783P.
XX
XX (CONJ-) CONJUCHEM INC.
XX
PI Bridon DP, Ezrin AM, Milner PG, Holmes DL, Thibaudau K;
XX
DR WPI; 2001-112059/12.
XX
XX
PT Modifying and attaching therapeutic peptides to albumin prevents
PT peptidase degradation, useful for increasing length of in vivo activity.
XX
XX
PS Disclosure; Page 566; 733pp; English.
XX
CC The present invention describes a modified therapeutic peptide (I)
CC comprising a therapeutically active amino acid region (III) and a
CC reactive group (II) (e.g. succinimidyl and maleimido groups) attached to
CC a less therapeutically active amino acid region (IV), which covalently
CC bonds with amino/hydroxyl/thiol groups on blood components to form a
CC peptidease stabilised therapeutic peptide composed of 3-50 amino acids.
CC (I) are useful for modifying therapeutic peptides e.g. hormones, growth
CC factors and neurotransmitters, to protect them from peptidase activity in
CC vivo for the treatment of various disorders. Endogenous therapeutic
CC peptides are not suitable as drug candidates as they require frequent
CC administration due to rapid degradation by peptidases in the body.
CC Modifying and attaching therapeutic peptides to albumin prevents or
CC reduces the action of peptidases to increase length of activity (half
CC life) and specifically as bonding to large molecules decreases
CC intercellular uptake and interference with physiological processes.
CC AAB90829 to AAB92441 represent peptides which can be used in the
CC exemplification of the present invention
XX
SQ Sequence 37 AA;

Query Match 100.0%; Score 60; DB 4; Length 37;
Best Local Similarity 100.0%; Pred. No. 0.0026;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DKPSYQFGGH 10
 |||||
 DB 15 DKPSYQFGGH 24

RESULT 4

AA080662
 ID AAP80662 standard; protein; 38 AA.

XX
 AC AAP80662;

XX 25-MAR-2003 (revised)
 DT 07-OCT-1990 (first entry)

XX Protein with fibronectin binding ability.

XX Hybrid DNA molecule; fibronectin binding; mastitis; ruminants;
 KW wound infection.

OS Staphylococcus aureus.

XX EP294349-A.

XX 07-DEC-1988.

XX 30-MAY-1988; 88EP-00850188.

XX 01-JUN-1987; 87SE-00002272.

XX (ALFA) ALFA LAVAL AGRIC INT AB.

PI Lindberg MK, Signas LC, Wadstrom TM, Froman G;

XX WPI; 1988-347978/49.

DR N-PSDB; AAN81099.

PT Hybrid DNA encoding Staphylococcus aureus fibronectin binding protein -
 PF useful for immunisation and topical application to prevent staphylococcal
 PT infections.

XX Claim 11; Page 12; 23pp; English.

XX The peptide has fibronectin binding ability. It is useful for immunising
 CC ruminants against staphylococcal mastitis, pref. when used at 0.5-5
 CC micrograms/kg, using 3 doses given at 1-3 week intervals; for topical
 CC application to prevent wound infection, using an isotonic saline soln. of
 CC concn. 25-250 micrograms/ml; and, when immobilised on a carrier, for
 CC diagnosing staphylococcal infections. (Updated on 25-MAR-2003 to correct
 CC PF field.) (Updated on 25-MAR-2003 to correct PA field.)

XX Sequence 38 AA;

Query Match 100.0%; Score 60; DB 1; Length 38;
 Best Local Similarity 100.0%; Pred. No. 0.0027;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DKPSYQFGGH 10
 |||||
 DB 16 DKPSYQFGGH 25

RESULT 5

AA29087
 ID AA29087 standard; protein; 134 AA.

XX
 AC AA29087;

DT 28-SEP-1999 (first entry)

DE S. aureus fibronectin binding protein A (FnBA) binding domain.

XX Bovine herpes virus-2; BHV-2; cytokine; immune response; immunogen; IL;
 KW interleukin; colony stimulating factor; CSF; interferon; IFN; TNF;

KW tumour necrosis factor; recombinant virus; vaccine; mucosal disease;
 KW mastitis; breast cancer; stress-induced disease; binding domain; FnBA;
 KW fibronectin binding protein.

OS Staphylococcus aureus.

XX W09916892-A1.

XX 08-APR-1999.

XX 29-SEP-1998; 98WO-GS002927.

XX 29-SEP-1997; 97GB-00020633.

XX (UYBR-) UNIV BRISTOL.

PI Bradley AJ, Duffas MPH;

XX WPI; 1999-255101/21.

DR N-PSDB; AAX91504.

PT New bovine herpes virus-2 vectors.

XX Example 2; Fig 8A-B; 130pp; English.

XX The invention provides bovine herpes virus-2 (BHV-2) based vectors that
 CC comprise at least one cytokine-encoding DNA sequence. The expression of
 CC cytokines in mammals can up-regulate immune responses to the immunogens.
 CC The cytokine is selected from interleukins (IL), colony stimulating
 CC factors (CSF), interferons (IFN) and tumour necrosis factors (TNF). The
 CC BHV-2 based vector or recombinant virus can be used as vaccines. They can
 CC be used for preventing or treating a mucosal disease in a subject, e.g.
 CC ruminants, cattle, sheep, goats, dogs, cats, horses, or man, particularly
 CC mastitis in cows or breast cancers in humans. They can also be used for
 CC preventing or treating a stress-induced disease. The present sequence
 CC represents the binding domain of a previously published S. aureus
 CC fibronectin binding protein A (FnBA) sequence. The FnB binding domain
 CC gene sequence FnBAB, cloned for use in this invention has 97.8 percent
 CC identity when compared to the previously published FnBA and FnBB gene
 CC sequences

XX Sequence 134 AA;

Query Match 100.0%; Score 60; DB 2; Length 134;
 Best Local Similarity 100.0%; Pred. No. 0.0091;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DKPSYQFGGH 10
 |||||
 DB 92 DKPSYQFGGH 101

RESULT 6

AAW31556
 ID AAW31556 standard; protein; 139 AA.

XX
 AC AAW31556;

DT 27-AUG-2003 (revised)

DT 25-MAR-2003 (revised)

DT 21-MAY-1998 (first entry)

DE Fibronectin-binding MSCRAMM derivative pQD.

XX Fibronectin; pQD; collagen binding protein; sepsis; infection;
 KW microbial surface component recognising adhesive matrix molecule; MSCRAMM;
 KW adhesin; vaccine; immunisation; diagnosis; therapy; mastitis.

OS Staphylococcus aureus.

XX Key Location/Qualifiers

FT Peptide 1..12
 /note= "vector pQE30-derived peptide"


```

XX PN W09743314-A2.
XX PI
XX PD 20-NOV-1997.
XX PF 14-MAY-1997; 97WO-US008210.
XX PR 16-MAY-1996; 96US-0017678P.
XX PA (TEXA ) UNIV TEXAS A & M SYSTEM.
XX PA (UABR-) UAB RES FOUND.
XX PI
XX PI Hosoek M, Patti JM, House-Pompeo K, Sthanam N, Symersky J,
XX DR WPI; 1998-008801/01.
XX PT
XX PT Antibody that interacts with collagen binding domain of Staphylococcal
XX PT cna gene product - useful to prevent bacterial sepsis in animal infected
XX PT with Staphylococcus aureus.
XX PS Disclosure; Page 91, 143pp; English.
XX CC This protein comprises Staphylococcus aureus fibronectin-binding
XX CC microbial surface component recognizing adhesive matrix molecule (MSCRAM)
XX CC derivative pGD, plus a vector-derived N-terminal peptide. The invention
XX CC relates to claimed nucleic acid sequences (see AA793436-38) encoding S.
XX CC aureus collagen binding protein (CBP) epitopes M17, M31 and M55 (see
XX CC AA731552-54) that confer protection against S. aureus infection. CBP
XX CC protein and antigenic epitopes are contemplated for use in the treatment
XX CC of pathological infections, especially to prevent bacterial adhesion to
XX CC collagen. The epitopes are also contemplated for use in the preparation
XX CC of vaccines and as carrier proteins in vaccine formulations, as well as
XX CC in the formulation of compositions for the prevention of S. aureus
XX CC infection. pCF33 and pGD (see AA731556) were used to raise anti-MSCRAMM
XX CC polyclonal antibodies used in passive immunisation against bovine
XX CC mastitis. (Updated on 25-MAR-2003 to correct PI field.) (Updated on 27-
XX CC AUG-2003 to correct OS field.)
XX SQ Sequence 139 AA;
XX
XX Query Match 100.0%; Score 60; DB 2; Length 139;
XX Best Local Similarity 100.0%; Pred. No. 0.0094;
XX Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 DKPSYQFGGH 10
XX Db 106 DKPSYQFGGH 115
XX
XX RESULT 7
XX AAP82115
XX ID AAP82115 standard; protein; 1018 AA.
XX XX
XX AC AAP82115;
XX XX
XX DT 25-MAR-2003 (revised)
XX DT 05-JAN-1990 (first entry)
XX DE Fibronectin binding protein.
XX KM Fibronectin binding protein; S.aureus; immunisation; mastitis; ruminants;
XX KM wound infection; diagnosis.
XX OS Staphylococcus aureus.
XX OS EP294349-A.
XX PN
XX PD 07-DEC-1988.
XX PF 30-MAY-1988; 88EP-00850188.
XX PT 01-JUN-1987; 87SE-00002272.
XX

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PA (ALFA ) ALFA LAVAL AGRIC INT AB.
XX XX
XX PI Lindberg MK, Signas LC, Wadstrom TM, Froman G;
XX XX
XX DR WPI; 1988-347978/49.
XX DR P-PSDB; AAP82115.
XX XX
XX PT Hybrid DNA encoding Staphylococcus aureus fibronectin binding protein -
XX PT useful for immunisation and topical application to prevent staphylococcal
XX PT infections.
XX PS Disclosure; Fig. 8A:1-8A:2; 23pp; English.
XX XX
XX CC The S.aureus fibronectin binding protein may be included in a hybrid
XX CC protein. The protein may be used to immunise ruminants against
XX CC staphylococcal mastitis, pref. when given at 0.5-5 microg/kg, using 3
XX CC doses at 1-3 week intervals; and for topical applicn. to prevent wound
XX CC infection, pref. using isotonic saline soln. of concn. 25-250 microg/mg.
XX CC The DNA encoding the binding protein and the hybrid protein may be
XX CC immobilised on a carrier and used to diagnose staphylococcal infections.
XX CC (Updated on 25-MAR-2003 to correct PA field.)
XX SQ Sequence 1018 AA;
XX
XX Query Match 100.0%; Score 60; DB 1; Length 1018;
XX Best Local Similarity 100.0%; Pred. No. 0.064;
XX Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 DKPSYQFGGH 10
XX Db 836 DKPSYQFGGH 845
XX
XX RESULT 8
XX AAU37245
XX ID AAU37245 standard; protein; 1018 AA.
XX XX
XX AC AAU37245;
XX XX
XX DT 14-FEB-2002 (first entry)
XX DE Staphylococcus aureus cellular proliferation protein #1415.
XX KM Antisense; prokaryotic cellular proliferation protein; antibiotic;
XX KM antibacterial; drug design.
XX OS Staphylococcus aureus.
XX PN
XX PN W0200170955-A2.
XX XX
XX PD 27-SEP-2001.
XX PF 21-MAR-2001; 2001WO-US009180.
XX XX
XX PR 21-MAR-2000; 2000US-0191078P.
XX PR 23-MAY-2000; 2000US-0206848P.
XX PR 26-MAY-2000; 2000US-0207727P.
XX PR 23-OCT-2000; 2000US-0242578P.
XX PR 27-NOV-2000; 2000US-0253625P.
XX PR 22-DEC-2000; 2000US-0257931P.
XX PR 16-FEB-2001; 2001US-0269308P.
XX PA
XX PA (ELIT-) ELITRA PHARM INC.
XX PI
XX PI Haselbeck R, Ohlsen KL, Zyskind JM, Wall D, Trawick JD, Carr GJ;
XX PI Yamamoto RT, Xu HH;
XX DR WPI; 2001-611495/70.
XX DR N-PSDB; AAS55104.
XX PT New polymucleotides for the identification and development of
XX PT antibiotics, comprise sequences of antisense nucleic acids.
XX

```

PS Example 3; SEQ ID NO 12838; 511pp; English.

XX The invention relates to antisense inhibitors of genes essential to

CC prokaryotic cellular proliferation, their use in identifying the genes,

CC their use in the discovery of novel antibiotics, the essential genes

CC themselves and the encoded proteins. The prokaryotes used are *Escherichia*

CC coli, *Staphylococcus aureus*, *Salmonella typhi*, *Klebsiella pneumoniae*,

CC *Pseudomonas aeruginosa* and *Enterococcus faecalis*. The invention is also

CC useful for the identification of potential new targets for antibiotic

CC development. The antisense nucleic acids can also be used to identify

CC proteins used in proliferation, to express these proteins, and to obtain

CC antibodies capable of binding to the expressed proteins. The proteins can

CC be used to screen compounds in rational drug discovery programmes. The

CC antisense nucleic acid sequence is also useful to screen for homologous

CC nucleic acids which are required for cell proliferation in a wide variety

CC of organisms. The present sequence represents an essential prokaryotic

CC cellular proliferation protein. Note: The sequence data for this patent

CC did not form part of the printed specification, but was obtained in

CC electronic format directly from WIPO at

CC ftp.wipo.int/pub/published_pct_sequences

XX

SO Sequence 1018 AA:

Query Match 100.0%; Score 60; DB 4; Length 1018;

Best Local Similarity 100.0%; Pred. No. 0.064;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DKPSYQFGGH 10

DB 836 DKPSYQFGGH 845

RESULT 9

AAU34301

ID AAU34301 standard; protein; 1018 AA.

XX AAU34301;

XX 14-FEB-2002 (first entry)

DE Staphylococcus aureus cellular proliferation protein #577.

DE Antisense; prokaryotic cellular proliferation protein; antibiotic;

KW antibacterial; drug design.

XX

OS Staphylococcus aureus.

XX

PN WO200170955-A2.

XX

PD 27-SEP-2001.

XX

PF 21-MAR-2001; 2001WO-US009180.

XX

PR 21-MAR-2000; 2000US-0191078P.

PR 23-MAY-2000; 2000US-0206848P.

PR 26-MAY-2000; 2000US-0207727P.

PR 23-OCT-2000; 2000US-0242578P.

PR 27-NOV-2000; 2000US-0253625P.

PR 22-DEC-2000; 2000US-0257931P.

PR 16-FEB-2001; 2001US-0269308P.

XX

PA (ELIT-) ELITRA PHARM. INC.

XX

PI Haselbeck R, Ohlsen KL, Zyskind JW, Wall D, Trawick JD, Carr GJ;

PI Yamamoto RT, Xu HH;

XX

DR WPI; 2001-611495/70.

DR N-PSDB; AAS52160.

XX

PT New polynucleotides for the identification and development of

PT antibiotics, comprise sequences of antisense nucleic acids.

XX

PS Example 3; SEQ ID NO 5797; 511pp; English.

XX The invention relates to antisense inhibitors of genes essential to

CC prokaryotic cellular proliferation, their use in identifying the genes,

CC their use in the discovery of novel antibiotics, the essential genes

CC themselves and the encoded proteins. The prokaryotes used are *Escherichia*

CC coli, *Staphylococcus aureus*, *Salmonella typhi*, *Klebsiella pneumoniae*,

CC *Pseudomonas aeruginosa* and *Enterococcus faecalis*. The invention is also

CC useful for the identification of potential new targets for antibiotic

CC development. The antisense nucleic acids can also be used to identify

CC proteins used in proliferation, to express these proteins, and to obtain

CC antibodies capable of binding to the expressed proteins. The proteins can

CC be used to screen compounds in rational drug discovery programmes. The

CC antisense nucleic acid sequence is also useful to screen for homologous

CC nucleic acids which are required for cell proliferation in a wide variety

CC of organisms. The present sequence represents an essential prokaryotic

CC cellular proliferation protein. Note: The sequence data for this patent

CC did not form part of the printed specification, but was obtained in

CC electronic format directly from WIPO at

CC ftp.wipo.int/pub/published_pct_sequences

XX

SO Sequence 1018 AA:

Query Match 100.0%; Score 60; DB 4; Length 1018;

Best Local Similarity 100.0%; Pred. No. 0.064;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DKPSYQFGGH 10

DB 836 DKPSYQFGGH 845

RESULT 10

ABJ18922

ID ABJ18922 standard; protein; 1018 AA.

XX ABJ18922;

XX 06-MAR-2003 (first entry)

DE Pathogen specific antigen related staphylococcal protein SEQ ID No 68.

DE Antibacterial; virucide; fungicide; protozoacide; cytostatic; anti-HIV;

KW hyperimmune; serum-reactive; antigen; pathogen; tumour; allergen;

KW auto-immunity; vaccine; staphylococcal infection; antibody; cancer;

KW autoimmune disease; HIV; hepatitis.

XX

OS Staphylococcus sp.

XX

PN WO200259148-A2.

XX

PD 01-AUG-2002.

XX

PF 21-JAN-2002; 2002WO-EP000546.

XX

PR 26-JAN-2001; 2001AT-00000130.

XX

PA (CIST-) CISTEM BIOTECHNOLOGIES GMBH.

XX

PI Meinke A, Nagy B, Von Ahnen U, Klade C, Henice T, Zauner W;

PI Minh DB, Vytvytska O, Ecz H, Dryla A, Weichart T, Hafner M;

PI Tempelmeier B;

XX

DR WPI; 2003-075410/07.

XX

PT Identifying, isolating and producing hyperimmune serum-reactive antigens

PT from a pathogen, for preparing vaccine or medicament for treating or

PT preventing e.g. staphylococcal infections, comprises providing antibody

PT preparation.

XX

PS Example 7; Page 157; 252pp; English.

XX

CC The invention relates to a novel method for identifying, isolating and

CC producing hyperimmune serum-reactive antigens from a pathogen, tumour,

KM infection; surgical implant; antiadherent agent; hygiene; adhesion;
 KM extracellular matrix protein; oral pathogen; oral cavity.
 XX
 OS Staphylococcus aureus.

Key	Location/Qualifiers
FT Region	1..21 /note= "D1 region fragment"
FT Region	22..59 /note= "D2 region"
FT Region	60..98 /note= "D3 region"
FT Region	99..113 /note= "D4 region"
FT Misc-difference	113 /note= "P113T"

XX WO9604381-A1.

XX 15-FEB-1996.

XX 28-JUL-1995; 95MO-EP003040.

XX 05-AUG-1994; 94GB-00015900.

XX (SMIK) SMITHKLINE BEECHAM PLC.

XX Critchley IA, Dodd I, Barnett P, Mcbay DL;

XX WPI; 1996-129397/13.

XX Polypeptide(s) derived from Staphylococcus aureus fibronectin binding
 PT protein - inhibit binding of bacteria to extracellular matrix proteins,
 PT for combatting infection at the site of wounds and surgical implants, and
 PT in oral hygiene.

XX Claim 6; Page 24; 35pp; English.

XX AAR90937-R90942 represent D3d4 polypeptides. These sequences correspond
 CC to fragments of the Staphylococcus aureus fibronectin binding protein
 CC (Fbp). This sequence corresponds to residues 18-130 of S.aureus 02385
 CC Fbp, and also contains the D2 region, and a portion of the D1 region.
 CC These sequences, and monoclonal antibodies against them can be used to
 CC combat infection at the site of wounds, surgical implants and other in-
 CC dwelling devices (such as catheters), and as antiadherent agents in oral
 CC hygiene. They can also be used in the manufacture of a medicament for the
 CC prevention of adhesion of bacteria to extracellular matrix proteins
 CC present on in-dwelling devices or in wounds, or of oral pathogens to
 CC similar proteins on surfaces in the oral cavity

XX Sequence 113 AA;

Query Match 95.0%; Score 57; DB 2; Length 113;
 Best Local Similarity 90.0%; Pred. No. 0.027;
 Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy	1 DKPSYQFGH 10
Db	75 DKENVQFGH 84

Search completed: October 25, 2005, 21:29:12
 Job time : 69.7126 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using BW model

Run on: October 22, 2005, 07:41:53 ; Search time 17.2989 Seconds
(without alignments)
43.153 Million cell updates/sec

Title: US-10-731-238-95
Perfect score: 60
Sequence: 1 DKPSYQFGH 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: /cgn2_6/ptodata/1/1aa/5A.COMB.pep:*
2: /cgn2_6/ptodata/1/1aa/5B.COMB.pep:*
3: /cgn2_6/ptodata/1/1aa/6A.COMB.pep:*
4: /cgn2_6/ptodata/1/1aa/6B.COMB.pep:*
5: /cgn2_6/ptodata/1/1aa/PCTUS.COMB.pep:*
6: /cgn2_6/ptodata/1/1aa/backfltest.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	length	DB ID	Description
1	60	100.0	10	4	US-09-010-317-95
2	60	100.0	37	1	US-08-234-622A-4
3	60	100.0	38	1	US-08-294-189-8
4	60	100.0	38	1	US-08-729-767-5
5	60	100.0	114	1	US-08-259-000-3
6	60	100.0	139	3	US-08-856-253-8
7	60	100.0	178	2	US-08-459-135A-12
8	60	100.0	178	3	US-08-495-559-12
9	60	100.0	1027	4	US-08-956-171E-5254
10	60	100.0	1027	4	US-08-781-986A-5254
11	57	95.0	130	2	US-08-459-135A-7
12	57	95.0	130	2	US-08-459-135A-8
13	57	95.0	130	3	US-08-495-559-7
14	57	95.0	130	3	US-08-495-559-8
15	57	95.0	174	2	US-08-459-135A-10
16	57	95.0	174	2	US-08-459-135A-13
17	57	95.0	174	3	US-08-495-559-10
18	57	95.0	174	3	US-08-495-559-13
19	57	95.0	176	3	US-08-495-559-6
20	57	95.0	181	2	US-08-459-135A-6
21	57	95.0	559	4	US-08-956-171E-5251
22	57	95.0	559	4	US-08-781-986A-5251
23	54	90.0	21	4	US-09-010-317-9
24	54	90.0	21	4	US-09-010-317-22
25	54	90.0	21	4	US-09-010-317-23
26	54	90.0	21	4	US-09-010-317-24
27	54	90.0	21	4	US-09-010-317-25

28	54	90.0	21	4	US-09-010-317-26	Sequence 26, Appl
29	54	90.0	21	4	US-09-010-317-27	Sequence 27, Appl
30	54	90.0	21	4	US-09-010-317-28	Sequence 28, Appl
31	54	90.0	21	4	US-09-010-317-29	Sequence 29, Appl
32	54	90.0	21	4	US-09-010-317-30	Sequence 30, Appl
33	54	90.0	21	4	US-09-010-317-31	Sequence 31, Appl
34	54	90.0	21	4	US-09-010-317-32	Sequence 32, Appl
35	54	90.0	21	4	US-09-010-317-33	Sequence 33, Appl
36	49	81.7	10	4	US-09-010-317-96	Sequence 96, Appl
37	49	81.7	19	1	US-08-234-622A-1	Sequence 1, Appl
38	49	81.7	21	4	US-09-010-317-14	Sequence 14, Appl
39	49	81.7	21	4	US-09-010-317-16	Sequence 16, Appl
40	48	80.0	21	4	US-09-010-317-18	Sequence 18, Appl
41	46	76.7	10	4	US-09-010-317-94	Sequence 94, Appl
42	46	76.7	21	4	US-09-010-317-10	Sequence 10, Appl
43	46	76.7	21	4	US-09-010-317-15	Sequence 15, Appl
44	46	76.7	21	4	US-09-010-317-20	Sequence 20, Appl
45	46	76.7	21	4	US-09-010-317-21	Sequence 21, Appl

ALIGNMENTS

```
RESULT 1
US-09-010-317-95
; Sequence 95, Application US/09010317
; Patent No. 6685943
; GENERAL INFORMATION:
; APPLICANT: Hook, Magnus
; APPLICANT: Patti, Joseph M.
; APPLICANT: House-Pompeo, Karen L.
; APPLICANT: Speziale, Pietro
; APPLICANT: Joh, Danny
; APPLICANT: McGavin, Martin J.
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
; TITLE OF INVENTION: AND METHODS OF USE
; NUMBER OF SEQUENCES: 105
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: TX
; COUNTRY: USA
; ZIP: 77210-4433
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/010.317
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/036,139
; FILING DATE: 21-JAN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Hibler, David W.
; REGISTRATION NUMBER: 41,071
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 512-474-7577
; TELEFAX: 512-474-7577
; INFORMATION FOR SEQ ID NO: 95:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; US-09-010-317-95
; Query Match 100.0%; Score 60; DB 4; Length 10;
; Best Local Similarity 100.0%; Pred. No. 0.00011;
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Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DKPSYQFGH 10
| | | | | | | | | |
Db 1 DKPSYQFGH 10

RESULT 2

US-08-234-622A-4
; Sequence 4, Application US/08234622A
; Patent No. 540014
; GENERAL INFORMATION:
; APPLICANT: HOOK, Magnus
; APPLICANT: MCGAVIN, Martin
; APPLICANT: RAUCCI, Giuseppe
; TITLE OF INVENTION: A FIBRONECTIN BINDING PEPTIDE
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Doane, Swecker & Mathis
; STREET: P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/234,622A
; FILING DATE: 28-APR-1994
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: SE 9002617-0
; FILING DATE: 10-AUG-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/SE91/00534
; FILING DATE: 09-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Meuth, Donna M
; REGISTRATION NUMBER: 36,607
; REFERENCE/DOCKET NUMBER: 012885-044
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 37 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-234-622A-4

Query Match 100.0%; Score 60; DB 1; Length 37;
Best Local Similarity 100.0%; Pred. No. 0.00042;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DKPSYQFGH 10
| | | | | | | | | |
Db 15 DKPSYQFGH 24

RESULT 3

US-08-294-189-8
; Sequence 8, Application US/08294189
; Patent No. 5707822
; GENERAL INFORMATION:
; APPLICANT: Fieschetti, Vincent A.
; APPLICANT: Rakonjac, Jasna
; APPLICANT: Robbins, John
; TITLE OF INVENTION: GENE SERUM OPACITY FACTOR

NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack Avenue
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
ZIP: 07601

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/294,189
FILING DATE: 22-AUG-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-118
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 487-5800
TELEFAX: 201 343-1684
TELEX: 133521
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
ORGANISM: Streptococcus pyogenes
STRAIN: D734
INDIVIDUAL ISOLATE: 22
IMMEDIATE SOURCE:
CLONE: BAU3a
US-08-294-189-8

Query Match 100.0%; Score 60; DB 1; Length 38;
Best Local Similarity 100.0%; Pred. No. 0.00043;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DKPSYQFGH 10
| | | | | | | | | |
Db 9 DKPSYQFGH 18

RESULT 4
US-08-729-767-5
; Sequence 5, Application US/08729767
; Patent No. 5770702
; GENERAL INFORMATION:
; APPLICANT: HOOK, Magnus
; APPLICANT: LINDBERG, Martin Kjell
; APPLICANT: SIGNAS, Lars Christer
; APPLICANT: MADSTROM, Torkel Mikael
; APPLICANT: FROMAN, Gunnar

; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN AS WELL AS
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Doane, Swecker & Mathis, L.L.P.
; STREET: P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/729,767
FILING DATE: 07-OCT-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/259,000
FILING DATE: 13-JUN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/007,817
FILING DATE: 22-JAN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/201,028
FILING DATE: 01-JUN-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: SE 8702272-9
FILING DATE: 01-JUN-1987
ATTORNEY/AGENT INFORMATION:
NAME: McGowan, Malcolm K.
REGISTRATION NUMBER: 39,300
REFERENCE/DOCKET NUMBER: 012889-036
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-729-767-5

Query Match 100.0%; Score 60; DB 1; Length 38;
Best Local Similarity 100.0%; Pred. No. 0.00043;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DKPSYQFGGH 10
|||
Db 16 DKPSYQFGGH 25

RESULT 5
US-08-259-000-3
Sequence 3, Application US/08259000
Patent No. 5571514
GENERAL INFORMATION:
APPLICANT: HOOK, Magnus
APPLICANT: LINDBERG, Martin Kjell
APPLICANT: SIGNAS, Lars Christer
APPLICANT: WADSTROM, Torkel Mikael
APPLICANT: FROMAN, Gunnar
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN AS WELL AS
NUMBER OF SEQUENCES: 4
TITLE OF INVENTION: ITS PREPARATION
CORRESPONDENCE ADDRESS:
ADDRESSEE: Burns, Doane, Swecker & Mathis
STREET: P.O. Box 1404
CITY: Alexandria
STATE: Virginia
COUNTRY: United States
ZIP: 2213-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/259,000
FILING DATE: 13-JUN-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: SE 8702272-9

FILING DATE: 01-JUN-1987
ATTORNEY/AGENT INFORMATION:
NAME: Meuth, Donna M
REGISTRATION NUMBER: 36,607
REFERENCE/DOCKET NUMBER: 012885-062
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 114 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-259-000-3

Query Match 100.0%; Score 60; DB 1; Length 114;
Best Local Similarity 100.0%; Pred. No. 0.0013;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DKPSYQFGGH 10
|||
Db 92 DKPSYQFGGH 101

RESULT 6
US-08-856-253-8
Sequence 8, Application US/08856253
Patent No. 6288214
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
APPLICANT: Patli, Joseph M.
APPLICANT: House-Pompeo, Karen
APPLICANT: Sthanam, Narayana
APPLICANT: Symersky, Jindrich
TITLE OF INVENTION: AND METHODS OF USE
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: Texas
COUNTRY: U.S.
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/856,253
FILING DATE: Concurrently Herewith
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/017,678
FILING DATE: 16-MAY-1996
ATTORNEY/AGENT INFORMATION:
NAME: Kitchell, Barbara S.
REGISTRATION NUMBER: 33,928
REFERENCE/DOCKET NUMBER: TMK1193
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
TELEFAX: (512) 474-7577
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 139 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-08-856-253-8

Query Match 100.0%; Score 60; DB 3; Length 139;
Best Local Similarity 100.0%; Pred. No. 0.0017;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DKPSYQFGH 10
|||||
Db 106 DKPSYQFGH 115

RESULT 7

US-08-459-135A-12
; Sequence 12, Application US/08459135A
; Patent No. 5955078

GENERAL INFORMATION:

APPLICANT: BURHAM, Martin Karl Russel

APPLICANT: CHOPRA, Ian

APPLICANT: CRITCHLEY, Ian Alfred

APPLICANT: KNOWLES, David Justin Charles

TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN: MONOCLONAL ANTIBODY AND THEIR US

NUMBER OF SEQUENCES: 15

CORRESPONDENCE ADDRESS:

ADDRESSEE: SmithKline Beecham Corporation

STREET: 709 Swedeland Road

CITY: King of Prussia

STATE: PA

COUNTRY: U.S.A.

ZIP: 19406-0939

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: Fastseq, Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/459,135A

FILING DATE: 02-JUN-1995

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/GB/94/00215

FILING DATE: 04-Feb-1994

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Gimmil, Edward R

REGISTRATION NUMBER: 38,891

REFERENCE/DOCKET NUMBER: P30591C2

TELECOMMUNICATION INFORMATION:

TELEPHONE: 610-270-4478

TELEFAX: 610-270-5090

TELEX:

INFORMATION FOR SEQ ID NO: 12:

SEQUENCE CHARACTERISTICS:

LENGTH: 178 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: Protein

US-08-459-135A-12

Query Match 100.0%; Score 60; DB 2; Length 178;
Best Local Similarity 100.0%; Pred. No. 0.0021;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DKPSYQFGH 10
|||||
Db 92 DKPSYQFGH 101

RESULT 8

US-08-495-559-12
; Sequence 12, Application US/08495559A
; Patent No. 6054572
; GENERAL INFORMATION:
; APPLICANT: BURHAM, Martin Karl Russel
; APPLICANT: CHOPRA, Ian

APPLICANT: CRITCHLEY, Ian Alfred
APPLICANT: KNOWLES, David Justin Charles
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN: MONOCLONAL
TITLE OF INVENTION: ANTIBODY AND THEIR USE IN PREVENTING BACTERIAL ADHESION
FILE REFERENCE: P30591
CURRENT APPLICATION NUMBER: US/08/495,559A
CURRENT FILING DATE: 1995-08-03
EARLIER APPLICATION NUMBER: GB 9302289.5
EARLIER FILING DATE: 1993-02-05
EARLIER APPLICATION NUMBER: GB 9321592.9
EARLIER FILING DATE: 1993-10-20
NUMBER OF SEQ ID NOS: 13
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 12
LENGTH: 178
TYPE: PRT
ORGANISM: Staphylococcus aureus
US-08-495-559-12

Query Match 100.0%; Score 60; DB 3; Length 178;
Best Local Similarity 100.0%; Pred. No. 0.0021;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DKPSYQFGH 10
|||||
Db 92 DKPSYQFGH 101

RESULT 9

US-08-956-171E-5254
; Sequence 5254, Application US/08956171E
; Patent No. 6593114

GENERAL INFORMATION:

APPLICANT: Charles Kunsch

Patrick S. Dillon

Craig A. Rosen

Steven C. Barash

Michael R. Fannon

TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences

NUMBER OF SEQUENCES: 5256

CORRESPONDENCE ADDRESS:

ADDRESSEE: Human Genome Sciences, Inc.

STREET: 9410 Key West Avenue

CITY: Rockville

STATE: Maryland

COUNTRY: USA

ZIP: 20850

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.50 inch, 1.4mb storage

COMPUTER: HP Vectra 486/33

OPERATING SYSTEM: MSDOS version 6.2

SOFTWARE: ASCII Text

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/956,171E

FILING DATE: 20-Oct-1997

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 60/009,861

FILING DATE: January 5, 1996

APPLICATION NUMBER: 08/781,986

FILING DATE: January 3, 1997

ATTORNEY/AGENT INFORMATION:

NAME: Mark J. Hyman

REGISTRATION NUMBER: 46,789

REFERENCE/DOCKET NUMBER: PB248P1

TELECOMMUNICATION INFORMATION:

TELEPHONE: (240) 314-1224

TELEFAX: (301) 309-8439

INFORMATION FOR SEQ ID NO: 5254:

SEQUENCE CHARACTERISTICS:

LENGTH: 1027 amino acids

TYPE: amino acid

STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 5254:
US-08-956-171E-5254

Query Match 100.0%; Score 60; DB 4; Length 1027;
Best Local Similarity 100.0%; Pred. No. 0.013;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DKPSYQFGGH 10
|||||
Db 845 DKPSYQFGGH 854

RESULT 10
US-08-781-986A-5254
Sequence 5254, Application US/08781986A
Patent No. 6737248
GENERAL INFORMATION:
APPLICANT: Charles Kunech
TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
NUMBER OF SEQUENCES: 5255
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COUNTRY: USA
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/781,986A
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION NUMBER:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Benson, Bob
REGISTRATION NUMBER: 30,446
REFERENCE/DOCKET NUMBER: PB248PP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 5254:
SEQUENCE CHARACTERISTICS:
LENGTH: 1027 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-781-986A-5254

Query Match 100.0%; Score 60; DB 4; Length 1027;
Best Local Similarity 100.0%; Pred. No. 0.013;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DKPSYQFGGH 10
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Db 845 DKPSYQFGGH 854

RESULT 11
US-08-459-135A-7
Sequence 7, Application US/08459135A
Patent No. 5955078
GENERAL INFORMATION:
APPLICANT: BURHAM, Martin Karl Russel

APPLICANT: CHOPRA, Ian
APPLICANT: CRITCHLEY, Ian Alfred
APPLICANT: KNOWLES, David Justin Charles
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN: MONOCLONAL ANTIBODY AND THEIR US
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
STATE: PA
COUNTRY: U.S.A.
ZIP: 19406-0939

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: Fastseq, Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/459,135A
FILING DATE: 02-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB/94/00215
FILING DATE: 04-Feb-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Gimm, Edward R
REGISTRATION NUMBER: 38,891
REFERENCE/DOCKET NUMBER: P30591C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-4478
TELEFAX: 610-270-5090
TELEX:
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 130 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-459-135A-7

Query Match 95.0%; Score 57; DB 2; Length 130;
Best Local Similarity 90.0%; Pred. No. 0.0054;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DKPSYQFGGH 10
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Db 92 DKPSYQFGGH 101

RESULT 12
US-08-459-135A-8
Sequence 8, Application US/08459135A
Patent No. 5955078
GENERAL INFORMATION:
APPLICANT: BURHAM, Martin Karl Russel
APPLICANT: CHOPRA, Ian
APPLICANT: CRITCHLEY, Ian Alfred
APPLICANT: KNOWLES, David Justin Charles
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN: MONOCLONAL ANTIBODY AND THEIR U
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
STATE: PA
COUNTRY: U.S.A.
ZIP: 19406-0939
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: Fastseq, Version 2.0

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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/459,135A
; FILING DATE: 02-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB/94/00215
; FILING DATE: 04-Feb-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Gimmil, Edward R
; REGISTRATION NUMBER: 38,891
; REFERENCE/DOCKET NUMBER: P30591C2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-270-4478
; TELEFAX: 610-270-5090
; TELEX:
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 130 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
;
US-08-459-135A-8
;
Query Match          95.0%; Score 57; DB 2; Length 130;
Best Local Similarity 90.0%; Pred. No. 0.0054;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 DKPSYQFGGH 10
DB      92 DKPNYQFGGH 101

RESULT 13
US-08-495-559-7
; Sequence 7, Application US/08495559A
; Patent No. 6054572
; GENERAL INFORMATION:
; APPLICANT: BURHAM, Martin Karl Russel
; APPLICANT: CHOPRA, Ian
; APPLICANT: CRITCHLEY, Ian Alfred
; APPLICANT: KNOWLES, David Justin Charles
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN: MONOCLONAL
; FILE REFERENCE: P30591
; CURRENT APPLICATION NUMBER: US/08/495,559A
; EARLIER FILING DATE: 1995-08-03
; EARLIER APPLICATION NUMBER: GB 9302289.5
; EARLIER FILING DATE: 1993-02-05
; EARLIER APPLICATION NUMBER: GB 9321592.9
; EARLIER FILING DATE: 1993-10-20
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 7
; LENGTH: 130
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
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US-08-495-559-7
;
Query Match          95.0%; Score 57; DB 3; Length 130;
Best Local Similarity 90.0%; Pred. No. 0.0054;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 DKPSYQFGGH 10
DB      92 DKPNYQFGGH 101

RESULT 14
US-08-495-559-8
; Sequence 8, Application US/08495559A
; Patent No. 6054572
; GENERAL INFORMATION:
; APPLICANT: BURHAM, Martin Karl Russel
; APPLICANT: CHOPRA, Ian
; APPLICANT: CRITCHLEY, Ian Alfred
; APPLICANT: KNOWLES, David Justin Charles
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN: MONOCLONAL
; FILE REFERENCE: P30591
; CURRENT APPLICATION NUMBER: US/08/495,559A
; EARLIER FILING DATE: 1995-08-03
; EARLIER APPLICATION NUMBER: GB 9302289.5
; EARLIER FILING DATE: 1993-02-05
; EARLIER APPLICATION NUMBER: GB 9321592.9
; EARLIER FILING DATE: 1993-10-20
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 8
; LENGTH: 130
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
;
US-08-495-559-8
;
Query Match          95.0%; Score 57; DB 3; Length 130;
Best Local Similarity 90.0%; Pred. No. 0.0054;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 DKPSYQFGGH 10
DB      92 DKPNYQFGGH 101

RESULT 15
US-08-459-135A-10
; Sequence 10, Application US/08459135A
; Patent No. 5955078
; GENERAL INFORMATION:
; APPLICANT: BURHAM, Martin Karl Russel
; APPLICANT: CHOPRA, Ian
; APPLICANT: CRITCHLEY, Ian Alfred
; APPLICANT: KNOWLES, David Justin Charles
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN: MONOCLONAL ANTIBODY AND THEIR US
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corporation
; STREET: 709 Swedeland Road
; CITY: King of Prussia
; STATE: PA
; COUNTRY: U.S.A.
; ZIP: 19406-0939
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: Fastseq, Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/459,135A
; FILING DATE: 02-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB/94/00215
; FILING DATE: 04-Feb-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Gimmil, Edward R
; REGISTRATION NUMBER: 38,891
; REFERENCE/DOCKET NUMBER: P30591C2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-270-4478
; TELEFAX: 610-270-5090
; TELEX:
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 174 amino acids
; TYPE: amino acid
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! TOPOLOGY: linear
! MOLECULE TYPE: Protein
US-08-459-135A-10

Query Match 95.0%; Score 57; DB 2; Length 174;
Best Local Similarity 90.0%; Pred. NO. 0.0073;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DKPSYQFGGH 10
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Db 92 DKPNYQFGGH 101

Search completed: October 22, 2005, 09:35:45
Job time : 17.2989 secs

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GenCore version 5.1.6
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OM protein - protein search, using SW model

Run on: October 22, 2005, 12:39:57 ; Search time 56.1494 Seconds
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Title: US-10-731-238-95
Perfect score: 60
Sequence: 1 DKPSYQFGCH 10

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 1862951 seqs, 417491010 residues

Total number of hits satisfying chosen parameters: 1862951

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	60	100.0	10	US-10-731-238-95	Sequence 95, Appl
2	60	100.0	37	US-11-066-697-1134	Sequence 1134, Ap
3	60	100.0	139	US-09-813-820-8	Sequence 8, Appl
4	60	100.0	1018	US-09-815-242-5797	Sequence 5797, Ap
5	60	100.0	1018	US-09-815-242-12838	Sequence 12838, A
6	60	100.0	1018	US-10-470-048B-68	Sequence 68, Appl
7	60	100.0	1027	US-08-781-986A-5254	Sequence 5254, Ap
8	60	100.0	1027	US-10-329-624-5254	Sequence 5254, Ap
9	57	95.0	388	US-08-901-062-1	Sequence 1, Appl
10	57	95.0	559	US-08-781-986A-5251	Sequence 5251, Ap
11	57	95.0	559	US-10-329-624-5251	Sequence 5251, Ap

12	57	95.0	940	17	US-10-470-048B-424	Sequence 424, App
13	57 <td>95.0</td> <td>948</td> <td>17<td>US-10-470-048B-69</td><td>Sequence 69, Appl</td></td>	95.0	948	17 <td>US-10-470-048B-69</td> <td>Sequence 69, Appl</td>	US-10-470-048B-69	Sequence 69, Appl
14	57 <td>95.0</td> <td>961</td> <td>15<td>US-10-282-122A-43778</td><td>Sequence 43778, A</td></td>	95.0	961	15 <td>US-10-282-122A-43778</td> <td>Sequence 43778, A</td>	US-10-282-122A-43778	Sequence 43778, A
15	57 <td>95.0</td> <td>978</td> <td>9<td>US-09-815-242-5456</td><td>Sequence 5456, Ap</td></td>	95.0	978	9 <td>US-09-815-242-5456</td> <td>Sequence 5456, Ap</td>	US-09-815-242-5456	Sequence 5456, Ap
16	57 <td>95.0</td> <td>1001</td> <td>9<td>US-09-815-242-12686</td><td>Sequence 12686, A</td></td>	95.0	1001	9 <td>US-09-815-242-12686</td> <td>Sequence 12686, A</td>	US-09-815-242-12686	Sequence 12686, A
17	57 <td>95.0</td> <td>1038</td> <td>15<td>US-10-282-122A-43827</td><td>Sequence 43827, A</td></td>	95.0	1038	15 <td>US-10-282-122A-43827</td> <td>Sequence 43827, A</td>	US-10-282-122A-43827	Sequence 43827, A
18	54	90.0	21	18 <td>US-10-731-238-9</td> <td>Sequence 9, Appl</td>	US-10-731-238-9	Sequence 9, Appl
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20	54	90.0	21	18 <td>US-10-731-238-23</td> <td>Sequence 23, Appl</td>	US-10-731-238-23	Sequence 23, Appl
21	54	90.0	21	18 <td>US-10-731-238-24</td> <td>Sequence 24, Appl</td>	US-10-731-238-24	Sequence 24, Appl
22	54	90.0	21	18 <td>US-10-731-238-25</td> <td>Sequence 25, Appl</td>	US-10-731-238-25	Sequence 25, Appl
23	54	90.0	21	18 <td>US-10-731-238-26</td> <td>Sequence 26, Appl</td>	US-10-731-238-26	Sequence 26, Appl
24	54	90.0	21	18 <td>US-10-731-238-27</td> <td>Sequence 27, Appl</td>	US-10-731-238-27	Sequence 27, Appl
25	54	90.0	21	18 <td>US-10-731-238-28</td> <td>Sequence 28, Appl</td>	US-10-731-238-28	Sequence 28, Appl
26	54	90.0	21	18 <td>US-10-731-238-29</td> <td>Sequence 29, Appl</td>	US-10-731-238-29	Sequence 29, Appl
27	54	90.0	21	18 <td>US-10-731-238-30</td> <td>Sequence 30, Appl</td>	US-10-731-238-30	Sequence 30, Appl
28	54	90.0	21	18 <td>US-10-731-238-31</td> <td>Sequence 31, Appl</td>	US-10-731-238-31	Sequence 31, Appl
29	54	90.0	21	18 <td>US-10-731-238-32</td> <td>Sequence 32, Appl</td>	US-10-731-238-32	Sequence 32, Appl
30	54	90.0	21	18 <td>US-10-731-238-33</td> <td>Sequence 33, Appl</td>	US-10-731-238-33	Sequence 33, Appl
31	49	81.7	21	18 <td>US-10-731-238-96</td> <td>Sequence 96, Appl</td>	US-10-731-238-96	Sequence 96, Appl
32	49	81.7	21	18 <td>US-10-731-238-14</td> <td>Sequence 14, Appl</td>	US-10-731-238-14	Sequence 14, Appl
33	49	81.7	21	18 <td>US-10-731-238-16</td> <td>Sequence 16, Appl</td>	US-10-731-238-16	Sequence 16, Appl
34	48	80.0	21	18 <td>US-10-731-238-18</td> <td>Sequence 18, Appl</td>	US-10-731-238-18	Sequence 18, Appl
35	46	76.7	21	18 <td>US-10-731-238-94</td> <td>Sequence 94, Appl</td>	US-10-731-238-94	Sequence 94, Appl
36	46	76.7	21	18 <td>US-10-731-238-10</td> <td>Sequence 10, Appl</td>	US-10-731-238-10	Sequence 10, Appl
37	46	76.7	21	18 <td>US-10-731-238-15</td> <td>Sequence 15, Appl</td>	US-10-731-238-15	Sequence 15, Appl
38	46	76.7	21	18 <td>US-10-731-238-20</td> <td>Sequence 20, Appl</td>	US-10-731-238-20	Sequence 20, Appl
39	46	76.7	21	18 <td>US-10-731-238-21</td> <td>Sequence 21, Appl</td>	US-10-731-238-21	Sequence 21, Appl
40	46	76.7	22	18 <td>US-10-731-238-13</td> <td>Sequence 13, Appl</td>	US-10-731-238-13	Sequence 13, Appl
41	44	73.3	21	18 <td>US-10-731-238-17</td> <td>Sequence 17, Appl</td>	US-10-731-238-17	Sequence 17, Appl
42	44	73.3	21	18 <td>US-10-731-238-19</td> <td>Sequence 19, Appl</td>	US-10-731-238-19	Sequence 19, Appl
43	41	68.3	117	15 <td>US-10-425-114-42791</td> <td>Sequence 42791, A</td>	US-10-425-114-42791	Sequence 42791, A
44	41	68.3	335	18 <td>US-10-450-763-59542</td> <td>Sequence 59542, A</td>	US-10-450-763-59542	Sequence 59542, A
45	41	68.3	782	18 <td>US-10-450-763-59546</td> <td>Sequence 59546, A</td>	US-10-450-763-59546	Sequence 59546, A

ALIGNMENTS

RESULT 1
US-10-731-238-95
Sequence 95, Application US/10731238
Publication No. US20050123552A1
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
Patel, Joseph M.
House-Pompeo, Karen L.
Speziale, Pietro
John, Danny
McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/731, 238
FILING DATE: 10-Dec-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/010, 317
FILING DATE: 21-Jan-1998
APPLICATION NUMBER: US 60/036,139

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/ FILING DATE: 21-JAN-1997
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Hibler, David W.
/ REGISTRATION NUMBER: 41,071
/ REFERENCE/DOCKET NUMBER: TAMK:189
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 512-418-3000
/ TELEFAX: 512-474-7577
/ INFORMATION FOR SEQ ID NO: 95:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 10 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: <Unknown>
/ TOPOLOGY: linear
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/ SEQUENCE DESCRIPTION: SEQ ID NO: 95:
US-10-731-238-95

Query Match      100.0%; Score 60; DB 18; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.00048;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 DKPSYQFGGH 10
Db      1 DKPSYQFGGH 10

RESULT 2
US-11-066-697-1134
/ Sequence 1134, Application US/11066697
/ Publication No. US20050187159A1
/ GENERAL INFORMATION:
/ APPLICANT: Bidon, Dominique P.
/ APPLICANT: Ezrin, Alan M.
/ APPLICANT: Holmer, Peter G.
/ APPLICANT: Holmes, Darren L.
/ APPLICANT: Thibaudau, Karen
/ TITLE OF INVENTION: PROTECTION OF ENDOGENOUS THERAPEUTIC PEPTIDES FROM
/ TITLE OF INVENTION: PEPTIDASE ACTIVITY THROUGH COMUGATION TO BLOOD
/ FILE REFERENCE: 500862002301
/ CURRENT APPLICATION NUMBER: US/11/066,697
/ CURRENT FILING DATE: 2005-02-25
/ PRIOR APPLICATION NUMBER: 09/657,276
/ PRIOR FILING DATE: 2000-09-07
/ PRIOR APPLICATION NUMBER: 60/153,406
/ PRIOR FILING DATE: 1999-09-10
/ PRIOR APPLICATION NUMBER: 60/159,783
/ PRIOR FILING DATE: 1999-10-15
/ NUMBER OF SEQ ID NOS: 1617
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 1134
/ LENGTH: 37
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURES:
/ OTHER INFORMATION: Description of Artificial Sequence: Synthetic
/ OTHER INFORMATION: Peptide
US-11-066-697-1134

Query Match      100.0%; Score 60; DB 20; Length 37;
Best Local Similarity 100.0%; Pred. No. 0.0018;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 DKPSYQFGGH 10
Db      15 DKPSYQFGGH 24

RESULT 3
US-09-813-820-8
/ Sequence 8, Application US/09813820
/ Patent No. US20020102262A1
/ GENERAL INFORMATION:
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/ APPLICANT: Hook, Magnus
/ Patti, Joseph M.
/ House-Pompeo, Karen
/ Sthanam, Narayana
/ Syneraky, Jindrich
/ TITLE OF INVENTION: COLLAGEN BINDING PROTEIN COMPOSITIONS
/ AND METHODS OF USE
/
/ NUMBER OF SEQUENCES: 8
/ CORRESPONDENCE ADDRESS:
/ ADDRESSER: Arnold, White & Durkee
/ STREET: P.O. Box 4433
/ CITY: Houston
/ STATE: Texas
/ COUNTRY: U.S.
/ ZIP: 77210
/
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.30
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/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/813,820
/ FILING DATE: 22-Mar-2001
/ CLASSIFICATION: <Unknown>
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/856,253
/ FILING DATE: <Unknown>
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Kitchell, Barbara S.
/ REGISTRATION NUMBER: 33,928
/ REFERENCE/DOCKET NUMBER: TAMK:193
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (512) 418-3000
/ TELEFAX: (512) 474-7577
/ INFORMATION FOR SEQ ID NO: 8:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 139 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: <Unknown>
/ TOPOLOGY: linear
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/ SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-09-813-820-8

Query Match      100.0%; Score 60; DB 9; Length 139;
Best Local Similarity 100.0%; Pred. No. 0.0066;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 DKPSYQFGGH 10
Db      106 DKPSYQFGGH 115

RESULT 4
US-09-815-242-5797
/ Sequence 5797, Application US/09815242
/ Patent No. US2002061569A1
/ GENERAL INFORMATION:
/ APPLICANT: Haselbeck, Robert
/ APPLICANT: Ohlsen, Karl L.
/ APPLICANT: Zyskind, Judith W.
/ APPLICANT: Wall, Daniel
/ APPLICANT: Trawick, John D.
/ APPLICANT: Carr, Grant J.
/ APPLICANT: Yamamoto, Robert T.
/ APPLICANT: Xu, H. Howard
/ TITLE OF INVENTION: Identification of Essential Genes in
/ TITLE OF INVENTION: Prokaryotes
/ FILE REFERENCE: ELITRA.011A
/ CURRENT APPLICATION NUMBER: US/09/815,242
/ CURRENT FILING DATE: 2001-03-21
/ PRIOR APPLICATION NUMBER: 60/191,078
/ PRIOR FILING DATE: 2000-03-21
/ PRIOR APPLICATION NUMBER: 60/206,848
```

;; PRIOR FILING DATE: 2000-05-23
;; PRIOR APPLICATION NUMBER: 60/207,727
;; PRIOR FILING DATE: 2000-05-26
;; PRIOR APPLICATION NUMBER: 60/242,578
;; PRIOR FILING DATE: 2000-10-23
;; PRIOR APPLICATION NUMBER: 60/253,625
;; PRIOR FILING DATE: 2000-11-27
;; PRIOR APPLICATION NUMBER: 60/257,931
;; PRIOR FILING DATE: 2000-12-22
;; PRIOR APPLICATION NUMBER: 60/269,308
;; PRIOR FILING DATE: 2001-02-16
;; NUMBER OF SEQ ID NOS: 14110
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 5797
;; LENGTH: 1018
;; TYPE: PRT
;; ORGANISM: Staphylococcus aureus
US-09-815-242-5797

Query Match 100.0%; Score 60; DB 9; Length 1018;
Best Local Similarity 100.0%; Pred. No. 0.048;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DKPSYQFGGH 10
Db 836 DKPSYQFGGH 845

RESULT 5
US-09-815-242-12838
;; Sequence 12838, Application US/09815242
;; Patent No. US20020061569A1
;; GENERAL INFORMATION:
;; APPLICANT: Haselbeck, Robert
;; APPLICANT: Ohlsen, Kari L.
;; APPLICANT: Zyekind, Judith W.
;; APPLICANT: Wall, Daniel
;; APPLICANT: Trawick, John D.
;; APPLICANT: Carr, Grant J.
;; APPLICANT: Yamamoto, Robert T.
;; APPLICANT: Xu, H. Howard
;; TITLE OF INVENTION: Identification of Essential Genes in
;; FILE REFERENCE: ELITRA.011A
;; CURRENT APPLICATION NUMBER: US/09/815,242
;; PRIOR FILING DATE: 2001-03-21
;; PRIOR APPLICATION NUMBER: 60/191,078
;; PRIOR FILING DATE: 2000-03-21
;; PRIOR APPLICATION NUMBER: 60/206,848
;; PRIOR FILING DATE: 2000-05-23
;; PRIOR APPLICATION NUMBER: 60/207,727
;; PRIOR FILING DATE: 2000-05-26
;; PRIOR APPLICATION NUMBER: 60/242,578
;; PRIOR FILING DATE: 2000-10-23
;; PRIOR APPLICATION NUMBER: 60/253,625
;; PRIOR FILING DATE: 2000-11-27
;; PRIOR APPLICATION NUMBER: 60/257,931
;; PRIOR FILING DATE: 2000-12-22
;; PRIOR APPLICATION NUMBER: 60/269,308
;; PRIOR FILING DATE: 2001-02-16
;; NUMBER OF SEQ ID NOS: 14110
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 12838
;; LENGTH: 1018
;; TYPE: PRT
;; ORGANISM: Staphylococcus aureus
US-09-815-242-12838

Query Match 100.0%; Score 60; DB 9; Length 1018;
Best Local Similarity 100.0%; Pred. No. 0.048;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 DKPSYQFGGH 10

Db 836 DKPSYQFGGH 845

RESULT 6
US-10-470-048B-68
;; Sequence 68, Application US/10470048B
;; Publication No. US2005003744A1
;; GENERAL INFORMATION:
;; APPLICANT: MEINKE ET AL.
;; TITLE OF INVENTION: A METHOD FOR IDENTIFICATION, ISOLATION AND PRODUCTION OF
;; FILE REFERENCE: SOMN-035US
;; CURRENT APPLICATION NUMBER: US/10/470,048B
;; CURRENT FILING DATE: 2003-07-25
;; NUMBER OF SEQ ID NOS: 603
;; SOFTWARE: PatentIn version 3.1
;; SEQ ID NO 68
;; LENGTH: 1018
;; TYPE: PRT
;; ORGANISM: Staphylococcus aureus
US-10-470-048B-68

Query Match 100.0%; Score 60; DB 17; Length 1018;
Best Local Similarity 100.0%; Pred. No. 0.048;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DKPSYQFGGH 10
Db 836 DKPSYQFGGH 845

RESULT 7
US-08-781-986A-5254
;; Sequence 5254, Application US/08781986A
;; Publication No. US20030054436A1
;; GENERAL INFORMATION:
;; APPLICANT: Charles Kunsch
;; TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
;; NUMBER OF SEQUENCES: 5255
;; CORRESPONDENCE ADDRESSES:
;; ADDRESSEE: Human Genome Sciences, Inc.
;; STREET: 9410 Key West Avenue
;; CITY: Rockville
;; STATE: Maryland
;; COUNTRY: USA
;; ZIP: 20850
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Diskette, 3.50 inch, 1.4mb storage
;; COMPUTER: HP Vectra 486/33
;; OPERATING SYSTEM: MSDOS version 6.2
;; SOFTWARE: ASCII Text
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/781,986A
;; FILING DATE:
;; CLASSIFICATION: 435
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER:
;; FILING DATE:
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Benson, Bob
;; REGISTRATION NUMBER: 30,446
;; REFERENCE/DOCKET NUMBER: PB248PP
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (301) 309-8504
;; TELEFAX: (301) 309-8512
;; INFORMATION FOR SEQ ID NO: 5254:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 1027 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein

FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Benson, Bob
REGISTRATION NUMBER: 30,446
REFERENCE/DOCKET NUMBER: PB248PP
TELEPHONE: (301) 309-8504
TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 5251:
SEQUENCE CHARACTERISTICS:
LENGTH: 559 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-781-986A-5251

Query Match 95.0%; Score 57; DB 8; Length 559;
Best Local Similarity 90.0%; Pred. No. 0.092;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DKPSYQFGH 10
|||:|||||
Db 391 DKPNYQFGH 400

RESULT 11
US-10-329-624-5251
Sequence 5251, Application US/10329624
Publication No. US20040043037A1
GENERAL INFORMATION:
APPLICANT: Charles Kunsch
Gill H. Choi
Patrick S. Dillon
Craig A. Rosen
Steven C. Barash
Michael R. Fannon
TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
NUMBER OF SEQUENCES: 5256
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COUNTRY: USA
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/329,624
FILING DATE: 27-Dec-2002
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/956,171
FILING DATE: October 20, 1997
APPLICATION NUMBER: 60/009,861
FILING DATE: January 5, 1996
APPLICATION NUMBER: 08/781,986
FILING DATE: January 3, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Mark J. Hyman
REGISTRATION NUMBER: 46,789
REFERENCE/DOCKET NUMBER: PB248P1D1
TELEPHONE: (240) 314-1224
TELEFAX: (301) 309-8439
INFORMATION FOR SEQ ID NO: 5251:

SEQUENCE CHARACTERISTICS:
LENGTH: 559 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 5251:
US-10-329-624-5251

Query Match 95.0%; Score 57; DB 15; Length 559;
Best Local Similarity 90.0%; Pred. No. 0.092;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DKPSYQFGH 10
|||:|||||
Db 391 DKPNYQFGH 400

RESULT 12
US-10-470-048B-424
Sequence 424, Application US/10470048B
Publication No. US20050037444A1
GENERAL INFORMATION:
APPLICANT: MEINKE ET AL.
TITLE OF INVENTION: A METHOD FOR IDENTIFICATION, ISOLATION AND PRODUCTION OF
FILE REFERENCE: SONN:035US
CURRENT APPLICATION NUMBER: US/10/470,048B
CURRENT FILING DATE: 2003-07-25
NUMBER OF SEQ ID NOS: 603
SOFTWARE: PatentIn version 3.1
SEQ ID NO: 424
LENGTH: 940
TYPE: PRT
ORGANISM: Staphylococcus aureus
US-10-470-048B-424

Query Match 95.0%; Score 57; DB 17; Length 940;
Best Local Similarity 90.0%; Pred. No. 0.15;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DKPSYQFGH 10
|||:|||||
Db 772 DKPNYQFGH 781

RESULT 13
US-10-470-048B-69
Sequence 69, Application US/10470048B
Publication No. US20050037444A1
GENERAL INFORMATION:
APPLICANT: MEINKE ET AL.
TITLE OF INVENTION: A METHOD FOR IDENTIFICATION, ISOLATION AND PRODUCTION OF
FILE REFERENCE: SONN:035US
CURRENT APPLICATION NUMBER: US/10/470,048B
CURRENT FILING DATE: 2003-07-25
NUMBER OF SEQ ID NOS: 603
SOFTWARE: PatentIn version 3.1
SEQ ID NO: 69
LENGTH: 948
TYPE: PRT
ORGANISM: Staphylococcus aureus
US-10-470-048B-69

Query Match 95.0%; Score 57; DB 17; Length 948;
Best Local Similarity 90.0%; Pred. No. 0.16;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DKPSYQFGH 10
|||:|||||
Db 780 DKPNYQFGH 789

RESULT 14

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US-10-282-122A-43778
; Sequence 43778, Application US/10282122A
; Publication No. US2004029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Karl
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 43778
; LENGTH: 961
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-10-282-122A-43778

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Query Match

95.0%; Score 57; DB 15; Length 961;

Best Local Similarity 90.0%; Pred. No. 0.16; Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DKPSYQFGH 10

Db 783 DKPNYQFGH 792

RESULT 15

```

US-09-815-242-5456
; Sequence 5456, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Karl L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard

```

; TITLE OF INVENTION: Identification of Essential Genes in Prokaryotes

; FILE REFERENCE: ELITRA.011A

; CURRENT APPLICATION NUMBER: US/09/815,242

; CURRENT FILING DATE: 2001-03-21

; PRIOR APPLICATION NUMBER: 60/191,078

; PRIOR FILING DATE: 2000-03-21

; PRIOR APPLICATION NUMBER: 60/206,848

; PRIOR FILING DATE: 2000-05-23

; PRIOR APPLICATION NUMBER: 60/207,727

; PRIOR FILING DATE: 2000-05-26

; PRIOR APPLICATION NUMBER: 60/242,578

; PRIOR FILING DATE: 2000-10-23

; PRIOR APPLICATION NUMBER: 60/253,625

; PRIOR FILING DATE: 2000-11-27

; PRIOR APPLICATION NUMBER: 60/257,931

; PRIOR FILING DATE: 2000-12-22

; PRIOR APPLICATION NUMBER: 60/269,308

; PRIOR FILING DATE: 2001-02-16

; NUMBER OF SEQ ID NOS: 14110

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 5456

; LENGTH: 978

; TYPE: PRT

; ORGANISM: Staphylococcus aureus

US-09-815-242-5456

Query Match

95.0%; Score 57; DB 9; Length 978;

Best Local Similarity 90.0%; Pred. No. 0.16; Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DKPSYQFGH 10

Db 814 DKPNYQFGH 823

Search completed: October 22, 2005, 12:56:28
Job time : 56.1494 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 22, 2005, 08:04:46 ; Search time 11.6092 Seconds
(without alignments)
82.880 Million cell updates/sec

Title: US-10-731-238-95
Perfect score: 60
Sequence: 1 DKPSYQFGCH 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	60	100.0	1018	2	A32192
2	57	95.0	940	2	S19702
3	57	95.0	961	2	G90053
4	57	95.0	1038	2	H90053
5	41	68.3	206	2	AH0259
6	41	68.3	1322	2	A59288
7	40	66.7	379	2	B82083
8	40	66.7	382	1	S01319
9	40	66.7	382	1	SYCCS
10	40	66.7	382	2	AD0510
11	40	66.7	382	2	B85484
12	38	66.7	382	2	G90633
13	38	63.3	291	2	T08557
14	38	63.3	295	2	S56302
15	38	63.3	327	2	S53305
16	37	61.7	378	1	T03758
17	37	61.7	378	1	T02977
18	37	61.7	831	2	C87372
19	37	61.7	962	2	T01688
20	36.5	60.8	525	2	A99557
21	36	60.0	177	2	T07286
22	36	60.0	830	2	T07824
23	36	60.0	861	1	S34730
24	35	58.3	163	1	MMV8M
25	35	58.3	163	1	S39662
26	35	58.3	200	2	A83566
27	35	58.3	289	2	A69405
28	35	58.3	327	2	S25071
29	35	58.3	380	2	H95129

30	35	58.3	380	2	P98000
31	35	58.3	391	2	F71702
32	35	58.3	332	2	A69474
33	35	58.3	399	2	H84087
34	35	58.3	427	1	S63615
35	35	58.3	433	2	T01405
36	35	58.3	652	2	S71753
37	35	58.3	676	1	A39379
38	35	58.3	813	2	A40601
39	35	58.3	815	2	H83345
40	35	58.3	820	2	C81252
41	35	58.3	826	2	G90283
42	35	58.3	1079	2	F84946
43	35	58.3	1790	1	S27772
44	35	58.3	2586	2	T21676
45	34.5	57.5	663	2	H83346

ALIGNMENTS

RESULT 1
A32192
fibronectin-binding protein - Staphylococcus aureus
C:Species: Staphylococcus aureus
C:Date: 31-Jul-1989 #sequence_revision 31-Jul-1989 #text_change 16-Feb-1997
C:Accession: A32192
R:Signaes, C.; Raucci, G.; Joensen, K.; Lindgren, P.E.; Anantharamaiah, G.M.; Heeok,
Proc. Natl. Acad. Sci. U.S.A. 86, 699-703, 1989
A:Title: Nucleotide sequence of the gene for a fibronectin-binding protein from Staphy]
A:Reference number: A32192; MUID:8908998; PMID:2521391
A:Accession: A32192
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1018 <SIG>
A:Cross-references: GB:J04151
C:Keywords: fibronectin binding

Query Match 100.0%; Score 60; DB 2; Length 1018;
Best Local Similarity 100.0%; Pred. No. 0.0034;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DKPSYQFGCH 10
Db 836 DKPSYQFGCH 845

RESULT 2

S19702
fibronectin-binding protein B - Staphylococcus aureus
C:Species: Staphylococcus aureus
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
R:Joensen, K.; Signaes, C.; Mueller, H.P.; Lindberg, M.
Eur. J. Biochem. 202, 1041-1048, 1991
A:Title: Two different genes encode fibronectin binding proteins in Staphylococcus aure
A:Reference number: S19702; MUID:9211475; PMID:1837266
A:Accession: S19702
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-940 <JOB>
A:Cross-references: UNIPROT:Q53682; EMBL:X62992; NID:949040; PIDN:CAA44726.1; PID:G5815
C:Keywords: fibronectin binding

Query Match 95.0%; Score 57; DB 2; Length 940;
Best Local Similarity 90.0%; Pred. No. 0.012;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DKPSYQFGCH 10
Db 772 DKPSYQFGCH 781

glucose-1-phosphat
hypothetical prote
myo-inositol-1-pho
hypothetical prote
male protein homol
vesicle-associated
repellent protein
hatching-supprese
ferritoverdine re
ferritoverdine re
probable NADH2 de
hypothetical prote
carbamoyl-phosphat
vitellinogenin precu
hypothetical prote
probable ATP-bind

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RESULT 3
G90053
hypothetical protein fnbB [imported] - Staphylococcus aureus (strain N315)
C/Species: Staphylococcus aureus
C/Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C/Accession: G90053
R/Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguc
ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.;
C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
A/Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.
A/Reference number: A89758; PMID:21311952; PMID:11418146
A/Accession: G90053
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-961 <KUR>
A/Cross-references: UNIPROT:Q99RD3; GB:BA000018; PID:g13702452; PIDN:BAB43593.1; GSPDB:C
A/Experimental source: strain N315
C/Genetics:
A/Gene: fnbB

Query Match 95.0%; Score 57; DB 2; Length 961;
Best Local Similarity 90.0%; Pred. No. 0.012; Mismatches 0; Indels 0; Gaps 0;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DKPSYQFGGH 10
|||:|||||
Db 783 DKPNYQFGGH 792

RESULT 4
H90053
hypothetical protein fnb [imported] - Staphylococcus aureus (strain N315)
C/Species: Staphylococcus aureus
C/Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C/Accession: H90053
R/Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguc
ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.;
C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
A/Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.
A/Reference number: A89758; PMID:21311952; PMID:11418146
A/Accession: H90053
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-1038 <KUR>
A/Cross-references: UNIPROT:Q99RD2; GB:BA000018; PID:g13702453; PIDN:BAB43594.1; GSPDB:C
A/Experimental source: strain N315
C/Genetics:
A/Gene: fnb

Query Match 95.0%; Score 57; DB 2; Length 1038;
Best Local Similarity 90.0%; Pred. No. 0.013; Mismatches 0; Indels 0; Gaps 0;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DKPSYQFGGH 10
|||:|||||
Db 832 DKPNYQFGGH 841

RESULT 5
AH0259
probable phage tail assembly protein YPO2129 [imported] - Yersinia pestis (strain CO92)
C/Species: Yersinia pestis
C/Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Jul-2004
C/Accession: AH0259
R/Perkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B.;
deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.;
11, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrrell,
Nature 413, 523-527, 2001
A/Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A/Reference number: AB0001; MUID:21470413; PMID:11586360
A/Accession: AH0259

A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-206 <KUR>
A/Cross-references: UNIPROT:Q8ZEN2; GB:AL590842; PIDN:CAC90940.1; PID:g15980136; GSPDB:C
C/Genetics:
A/Gene: YPO2129
C/Superfamily: phage lambda tail assembly protein I

Query Match 68.3%; Score 41; DB 2; Length 206;
Best Local Similarity 77.8%; Pred. No. 2.6; Mismatches 1; Indels 0; Gaps 0;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 DKPSYQFGG 9
|||:|||||
Db 163 NKPSYAFGG 171

RESULT 6
A59288
myosin heavy chain Myr 8 - rat
C/Species: Rattus norvegicus (Norway rat)
C/Date: 09-Jun-2000 #sequence_revision 09-Jun-2000 #text_change 09-Jul-2004
C/Accession: A59288
R/Patel, K.G.; Liu, C.; Cameron, P.L.; Cameron, R.S.
Submitted to Genbank, November 1999
A/Description: Identification of a Novel Mammalian Myosin Class, XVI, in Developing Brai
A/Reference number: A59288
A/Accession: A59288
A/Status: preliminary; not compared with conceptual translation
A/Molecule type: mRNA
A/Residues: 1-1322 <PAT>
A/Cross-references: UNIPROT:Q9QX10; GB:AF209114; PIDN:AAF20150.1
A/Experimental source: strain Sprague-Dawley; clone KP4; cell type type 1 astrocyte
F/404-1132/Domain: myosin motor domain homology <MMO>

Query Match 68.3%; Score 41; DB 2; Length 1322;
Best Local Similarity 75.0%; Pred. No. 19; Mismatches 0; Indels 0; Gaps 0;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PSYQFGGH 10
|||:|||||
Db 961 PSFKFGGH 968

RESULT 7
E82083
carbamoyl-phosphate synthase, small chain VC2390 [imported] - Vibrio cholerae (strain N1
C/Species: Vibrio cholerae
C/Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
C/Accession: E82083
R/Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwin, M.L.; Dodson, R.J.;
chardson, D.; Erskolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragol, I.; Sellers, E
1, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
A/Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A/Reference number: A82035; MUID:20406833; PMID:10952301
A/Accession: E82083
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-379 <HEI>
A/Cross-references: UNIPROT:Q9KPH8; GB:AE004309; GB:AE003852; NID:g9656954; PIDN:AAF9552
A/Experimental source: serogroup O1; strain N16961; biotype El Tor
C/Genetics:
A/Gene: VC2390
A/Map position: 1
C/Superfamily: carbamoyl-phosphate synthase (glutamine-hydrolyzing) small chain; carbam

Query Match 66.7%; Score 40; DB 2; Length 379;
Best Local Similarity 60.0%; Pred. No. 7.8; Mismatches 2; Indels 0; Gaps 0;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 DKPSYQFGGH 10
|||:|||||
```


F;52-312/Domain: cytochrome-b5 reductase homology <CBR>
F;176-327/Domain: NADP binding #statue predicted <NADP>

Query Match 63.3%; Score 38; DB 2; Length 327;
Best Local Similarity 66.7%; Pred. No. 16;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 DKPSYQFGG 9
| | | | |
| | | | |
Db 202 DVPTVRRFGG 210

Search completed: October 22, 2005, 09:55:46
Job time : 12.6092 secs

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GenCore version 5.1.6
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OM protein - protein search, using SW model

Run on: October 22, 2005, 08:01:06 ; Search time 56.2069 Seconds
(without alignments)
91.106 Million cell updates/sec

Title: US-10-731-238-95
Perfect score: 60
Sequence: 1 DKPSYQFGCH 10

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_03.*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	60	100.0	152 2 Q9AEP9	Q9AEP9 staphylococ
2	60	100.0	1018 1 FNBA STAAU	P14738 staphylococ
3	57	95.0	940 2 OS36B2	OS36B2 staphylococ
4	57	95.0	943 2 Q8NUU8	Q8NUU8 staphylococ
5	57	95.0	957 2 Q6G6H4	Q6G6H4 staphylococ
6	57	95.0	961 2 Q99RD3	Q99RD3 staphylococ
7	57	95.0	961 2 Q7A3J8	Q7A3J8 staphylococ
8	57	95.0	965 2 Q6GDU5	Q6GDU5 staphylococ
9	57	95.0	1015 2 Q8NUU7	Q8NUU7 staphylococ
10	57	95.0	1015 2 Q6G6H3	Q6G6H3 staphylococ
11	57	95.0	1038 2 Q99RD2	Q99RD2 staphylococ
12	57	95.0	1038 2 Q7A3J7	Q7A3J7 staphylococ
13	41	68.3	199 2 Q6XQCO	Q6XQCO enterobacte
14	41	68.3	206 2 Q8ZENZ	Q8ZENZ yersinia pe
15	41	68.3	251 2 Q6EM68	Q6EM68 debaryomyce
16	41	68.3	993 2 Q8BUV4	Q8BUV4 mus musculu
17	41	68.3	1322 2 Q9GX10	Q9GX10 rattus norv
18	41	68.3	1912 2 Q9ERCI	Q9ERCI rattus norv
19	40	66.7	155 2 Q7H5Q4	Q7H5Q4 photorhabdu
20	40	66.7	169 2 Q9HFP3	Q9HFP3 cladoporti
21	40	66.7	243 1 S112 ARATH	S112 ARATH arabis
22	40	66.7	280 1 Q8STZ5	Q8STZ5 encaphalito
23	40	66.7	379 1 Q9RPH8	Q9RPH8 vibrio chol
24	40	66.7	379 1 Q87Bf4	Q87Bf4 vibrio para
25	40	66.7	379 1 Q87Bf4	Q87Bf4 vibrio para
26	40	66.7	379 1 Q6F8M7	Q6F8M7 acinetobact
27	40	66.7	379 2 Q7MNU1	Q7MNU1 vibrio vuln
28	40	66.7	382 1 CARA_ECOL6	CARA_ECOL6 escherichia
29	40	66.7	382 1 CARA_ECOL6	CARA_ECOL6 escherichia
30	40	66.7	382 1 CARA_SALTI	CARA_SALTI salmonella
31	40	66.7	382 1 CARA_SALTY	CARA_SALTY salmonella

32	40	66.7	382 2 Q7UDT7	Q7UDT7 shigella fl
33	40	66.7	382 2 Q6D0C8	Q6D0C8 erwania car
34	40	66.7	384 2 Q6LTK6	Q6LTK6 photobacter
35	40	66.7	386 1 CARA_SHEON	Q8E86 shewanella
36	40	66.7	387 2 Q7N8W2	Q7N8W2 photorhabdu
37	40	66.7	391 2 Q83MNS	Q83MNS shigella fl
38	40	66.7	403 2 Q9SER3	Q9SER3 medicago sa
39	40	66.7	482 2 Q7S4C9	Q7S4C9 neurospora
40	39	65.0	375 2 Q6F0S6	Q6F0S6 candida gla
41	39	65.0	654 2 Q9FUD3	Q9FUD3 arabidopsis
42	39	65.0	1032 2 Q967D4	Q967D4 dirosophila
43	38	63.3	170 2 Q8EON1	Q8EON1 oceanobacil
44	38	63.3	252 1 RCEL_ACTICV	Q6E137 acidiphilum
45	38	63.3	254 1 RCEL_ACTOR	Q6E141 acidiphilum

ALIGNMENTS

RESULT 1

ID	Q9AEP9	PRELIMINARY;	PRT;	152 AA.
AC	Q9AEP9;			
DT	01-JUN-2001 (TrEMBL:rel. 17, Created)			
DT	01-JUN-2001 (TrEMBL:rel. 17, Last sequence update)			
DT	01-DEC-2001 (TrEMBL:rel. 19, Last annotation update)			
DE	Fibronectin-binding protein (fragment).			
GN	Name=fnb;			
OS	Staphylococcus aureus.			
OC	Bacteria; Firmicutes; Bacillales; Staphylococcus.			
OX	NCBI_TaxID=1280;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=CMRSA-1;			
RX	MEDLINE=21246681; PubMed=11349044;			
RX	DOI=10.1128/IAI.69.6.3791-3799.2001.			
RA	Rice K., Huebner M., Var D., McGavin M.J.,			
RT	"Variance in fibronectin binding and fimb locus polymorphisms in			
RT	Staphylococcus aureus: identification of antigenic variation in a			
RT	fibronectin binding protein adhesion of the epidemic CMRSA-1 strain of			
RT	methicillin-resistant S. aureus."			
RL	Infect. Immun. 69:3791-3799(2001).			
DR	EMBL; AY029184; AKK31508.1; -.			
FT	NON_TER			
FT	NON_TER			
FT	NON_TER			
SQ	SEQUENCE	152 AA;	17193 MW;	CFA3913C2B11C025 CRC64;

Query Match 100.0%; Score 60; DB 2; Length 152;
Best Local Similarity 100.0%; Pred. NO. 0.0048; Mismatches 0; Indels 0;
Matches 10; Conservative 0; Mismatches 0; Indels 0;

QY 1 DKPSYQFGCH 10
|||
Db 129 DKPSYQFGCH 138

RESULT 2

ID	FNBA STAAU	STANDARD;	PRT;	1018 AA.
AC	P14738;			
DT	01-APR-1990 (Rel. 14, Created)			
DT	01-APR-1990 (Rel. 14, Last sequence update)			
DT	25-OCT-2004 (Rel. 45, Last annotation update)			
DE	Fibronectin-binding protein precursor (FNBP).			
GN	Name=fmba;			
OS	Staphylococcus aureus.			
OC	Bacteria; Firmicutes; Bacillales; Staphylococcus.			
OX	NCBI_TaxID=1280;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=NCRC 8325-4;			
RX	MEDLINE=89098998; PubMed=2521391;			
RA	Stignaes C., Kaucsi G., Joensen K., Lindgren P.-E.,			

```

RA  Anantharamiah G.M., Hoeck M., Lindberg M.;
RT  "Nucleotide sequence of the gene for a fibronectin-binding protein
RT  from Staphylococcus aureus: use of this peptide sequence in the
RL  synthesis of biologically active peptides";
RN  Proc. Natl. Acad. Sci. U.S.A. 86:699-703(1989).
CC  -1- FUNCTION: The ability of bacteria to bind fibronectin has been
CC  proposed as a virulence factor enabling bacteria to colonize wound
CC  tissues and blood clots. Binding of plasma fibronectin to the
CC  bacterial surface might block adhesion receptors on S. aureus, thus
CC  representing an important defense mechanism against tissue
CC  invasion.
CC  -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC  an amide bond (potential).
CC  -----
CC  This SWISS-PROT entry is copyright. It is produced through a collaboration
CC  between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC  the European Bioinformatics Institute. There are no restrictions on its
CC  use by non-profit institutions as long as its content is in no way
CC  modified and this statement is not removed. Usage by and for commercial
CC  entities requires a license agreement (See http://www.ebi.ac.uk/announcement/
CC  or send an email to license@ebi.ac.uk).
CC  -----
DR  EMBL, J04151; AAA2632.1; -.
DR  InterPro: IPR004237; Fm_bind.
DR  InterPro: IPR005877; Gpos_YsIRK.
DR  InterPro: IPR001899; Gram_pos_anchor.
DR  Pfam: PF02986; Fm_bind_1.
DR  Pfam: PF00746; Gram_pos_anchor_1.
DR  Pfam: PF04650; YsIRK_signal_1.
DR  TIGRfams: TIGR01167; LpXTG_anchor_1.
DR  TIGRfams: TIGR01168; YsIRK_signal_1.
DR  PROSITE: PS50847; GRAM_POS_ANCHORING_1.
KM  Cell adhesion; Cell wall; Peptidoglycan-anchor; Repeat; Signal;
KW  virulence.
FT  SIGNAL 1 36
FT  CHAIN 1 985
FT  PROPEP 986 1018
FT  REPEAT 545 574
FT  REPEAT 575 604
FT  DOMAIN 745 878
FT  REPEAT 745 782
FT  REPEAT 783 820
FT  REPEAT 821 859
FT  REPEAT 860 878
FT  DOMAIN 879 948
FT  REPEAT 879 892
FT  REPEAT 893 906
FT  REPEAT 907 920
FT  REPEAT 921 934
FT  REPEAT 935 948
FT  SITE 982 985
FT  MOD_RS 985 985
SQ  SEQUENCE 1018 AA; 111780 MW; 58175E0020E81F1F CRC64;
Query Match 100.0%; Score 60; DB 1; Length 1018;
Best Local Similarity 100.0%; Pred. No. 0.036;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 DKPSYQFGGH 10
DB 836 DKPSYQFGGH 845

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GN  Name=fnbB;
OS  Staphylococcus aureus.
OC  Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX  NCBI_TaxID=1280;
RN  [1]
RP  SEQUENCE FROM N.A.
RC  STRAIN=8325-4;
RX  MEDLINE=92111475; PubMed=1837266;
RA  Jonsson K., Signas C., Muller H.P., Lindberg M.;
RT  "Two different genes encode fibronectin binding proteins in
RT  Staphylococcus aureus. The complete nucleotide sequence and
RT  characterization of the second gene."
RL  Eur. J. Biochem. 202:1041-1048(1991).
CC  -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC  an amide bond (By similarity).
CC  EMBL: X62992; CAA44726.1; -.
DR  PIR, S19702; S19702.
DR  HSSP, Q53653; 1N67.
DR  GO: GO:0009986; C:cell surface; IEA.
DR  GO: GO:0005618; C:cell wall; IEA.
DR  GO: GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR  GO: GO:0016020; C:membrane; IEA.
DR  GO: GO:0007155; P:cell adhesion; IEA.
DR  InterPro: IPR008966; Adhes_Bact.
DR  InterPro: IPR004237; Fm_bind.
DR  InterPro: IPR005877; Gpos_YsIRK.
DR  InterPro: IPR001899; Gram_pos_anchor.
DR  Pfam: PF02986; Fm_bind_2.
DR  Pfam: PF00746; Gram_pos_anchor_1.
DR  Pfam: PF04650; YsIRK_signal_1.
DR  TIGRfams: TIGR01167; LpXTG_anchor_1.
DR  TIGRfams: TIGR01168; YsIRK_signal_1.
DR  PROSITE: PS50847; GRAM_POS_ANCHORING_1.
KM  Cell wall; Peptidoglycan-anchor.
SQ  SEQUENCE 940 AA; 103555 MW; E35FBBCA907AE345 CRC64;
Query Match 95.0%; Score 57; DB 2; Length 940;
Best Local Similarity 90.0%; Pred. No. 0.12;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 DKPSYQFGGH 10
DB 772 DKPSYQFGGH 781

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RESULT 4
Q8NTU8
ID  Q8NTU8      PRELIMINARY;      PRT;      943 AA.
AC  Q8NTU8;
DT  01-OCT-2002 (TREMblrel. 22, Created)
DT  01-OCT-2002 (TREMblrel. 22, Last sequence update)
DT  01-OCT-2003 (TREMblrel. 25, Last annotation update)
DE  FnbB protein.
GN  Name=fnbB; Ordered locus Names=MW2420;
OS  Staphylococcus aureus (strain MW2).
OC  Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX  NCBI_TaxID=196620;
RN  [1]
RP  SEQUENCE FROM N.A.
RC  STRAIN=MW2;
RX  MEDLINE=22040717; PubMed=12044378; DOI=10.1016/S0140-6736(02)08713-5;
RA  Baba T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Oguchi A.,
RA  Nagai Y., Iwama N., Asano K., Naimi T., Kuroda H., Cui L.,
RA  Yamamoto K., Hiramatsu K.;
RT  "Genome and virulence determinants of high virulence community-
RT  acquired MRSA."
RL  Lancet 359:1819-1827(2002).
CC  -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC  an amide bond (By similarity).
DR  EMBL, AP004830; BAB96285.1; -.
DR  HSSP, Q53653; 1N67.
DR  GO: GO:0009986; C:cell surface; IEA.
DR  GO: GO:0005618; C:cell wall; IEA.

```

DR GO: GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
 DR GO: GO:0016020; C:membrane; IEA.
 DR GO: GO:0007155; P:cell adhesion; IEA.
 DR InterPro: IPR008966; Adhes_bact.
 DR InterPro: IPR004237; Fn_bind.
 DR InterPro: IPR005877; Gpos_YsIRK.
 DR InterPro: IPR001899; Gram_pos_anchor.
 DR Pfam: PF02986; Fn_bind; 1.
 DR Pfam: PF00746; Gram_pos_anchor; 1.
 DR Pfam: PF06650; YsIRK_signal; 1.
 DR TIGRfams; TIGR01167; LpxTG_anchor; 1.
 DR TIGRfams; TIGR01168; YsIRK_signal; 1.
 DR PROSITE; PS50847; GRAM_POS_ANCHORING; 1.
 DR Cell wall; Complete proteome; Peptidoglycan-anchor.
 SQ SEQUENCE 943 AA; 104537 MW; DA8A5F31947E1B6A CRC64;

Query Match 95.0%; Score 57; DB 2; Length 943;
 Best Local Similarity 90.0%; Pred. No. 0.12;
 Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DKPSYQFGH 10
 Db 779 DKPNYQFGH 788

RESULT 5
 ID 06G6H4 PRELIMINARY; PRT; 957 AA.
 AC 06G6H4;
 DT 05-JUL-2004 (TREMBLrel. 27, Created)
 DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
 DE Fibronectin-binding protein.
 DE Name=fnbb; OrderedLocustNames=SA52387;
 OS Staphylococcus aureus (strain MSSA476).
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 OX NCBI_TaxID=282459;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX PubMed:15213324; DOI=10.1073/pnas.0402521101;
 RA Holden M.T.G., Fell E.U., Lindsay J.A., Peacock S.J., Day N.P.J.,
 RA Enright M.C., Foster T.J., Moore C.E., Hurst L., Alkin R., Barton A.,
 RA Baeson N., Bentley S.D., Chillingworth C., Chillingworth T.,
 RA Churcher C., Clark L., Corson C., Doggett J., Dowd L.,
 RA Feltwell T., Hance Z., Harris B., Hauser H., Holtroyd S., Jagels K.,
 RA James K.D., Leonard N., Line A., Mayes R., Moule S., Mungall K.,
 RA Ormond D., Quail M.A., Rabinowitch E., Rutherford K.M., Sanders M.,
 RA Sharp S., Simmonds M., Stevens K., Whitehead S., Barrall B.G.,
 RA Spratt B.G., Parkhill J.;
 RT "Complete genomes of two clinical Staphylococcus aureus strains:
 RT evidence for the rapid evolution of virulence and drug resistance.";
 RT Proc. Natl. Acad. Sci. U.S.A. 101:9786-9791(2004).
 CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
 CC an amide bond (By similarity).
 DR EMBL; BX571857; CAG4201.1; -;
 DR GO: GO:0009986; C:cell surface; IEA.
 DR GO: GO:0005618; C:cell wall; IEA.
 DR GO: GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
 DR GO: GO:0016020; C:membrane; IEA.
 DR GO: GO:0007155; P:cell adhesion; IEA.
 DR InterPro: IPR008966; Adhes_bact.
 DR InterPro: IPR004237; Fn_bind.
 DR InterPro: IPR005877; Gpos_YsIRK.
 DR InterPro: IPR001899; Gram_pos_anchor.
 DR Pfam; PF02986; Fn_bind; 1.
 DR Pfam; PF00746; Gram_pos_anchor; 1.
 DR Pfam; PF06650; YsIRK_signal; 1.
 DR TIGRfams; TIGR01167; LpxTG_anchor; 1.
 DR TIGRfams; TIGR01168; YsIRK_signal; 1.
 DR PROSITE; PS50847; GRAM_POS_ANCHORING; 1.
 DR Cell wall; Complete proteome; Peptidoglycan-anchor.
 KW SEQUENCE 957 AA; 105980 MW; 28F8BA7FFDF03EAF CRC64;

Query Match 95.0%; Score 57; DB 2; Length 957;
 Best Local Similarity 90.0%; Pred. No. 0.12;
 Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DKPSYQFGH 10
 Db 779 DKPNYQFGH 788

RESULT 6
 ID 099RD3 PRELIMINARY; PRT; 961 AA.
 AC 099RD3;
 DT 01-JUN-2001 (TREMBLrel. 17, Created)
 DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
 DT 01-JUN-2001 (TREMBLrel. 24, Last annotation update)
 DE Fibronectin-binding protein homolog.
 DE Name=fnbb; OrderedLocustNames=SAV2502;
 OS Staphylococcus aureus (strain Mu50 / ATCC 700699).
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 OX NCBI_TaxID=158878;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX STRAIN=Mu50 / ATCC 700699;
 RX MEDLINE=21311952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2;
 RX Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
 RX Cui L., Oguchi A., Aoki K.-I., Nagai Y., Iian J.-Q., Ito T.,
 RX Kanamori M., Matsunaru H., Maruyama A., Murakami H., Hoshoyama A.,
 RX Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
 RX Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
 RX Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
 RA Hattori M., Ogasawara N., Hayashi H., Hiratake K.;
 RT "Whole genome sequencing of methicillin-resistant Staphylococcus
 RT aureus.";
 RL Lancet 357:1225-1240(2001).
 CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
 CC an amide bond (By similarity).
 DR EMBL; AP003365; BAB58664.1; -;
 DR PIR; G90053; G90053.
 DR HSSP; Q53653; 1N67.
 DR GO: GO:0009986; C:cell surface; IEA.
 DR GO: GO:0005618; C:cell wall; IEA.
 DR GO: GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
 DR GO: GO:0016020; C:membrane; IEA.
 DR GO: GO:0007155; P:cell adhesion; IEA.
 DR InterPro: IPR008966; Adhes_bact.
 DR InterPro: IPR004237; Fn_bind.
 DR InterPro: IPR005877; Gpos_YsIRK.
 DR InterPro: IPR001899; Gram_pos_anchor.
 DR Pfam; PF02986; Fn_bind; 1.
 DR Pfam; PF00746; Gram_pos_anchor; 1.
 DR Pfam; PF06650; YsIRK_signal; 1.
 DR TIGRfams; TIGR01167; LpxTG_anchor; 1.
 DR TIGRfams; TIGR01168; YsIRK_signal; 1.
 DR PROSITE; PS50847; GRAM_POS_ANCHORING; 1.
 DR Cell wall; Complete proteome; Peptidoglycan-anchor.
 KW SEQUENCE 961 AA; 106010 MW; 364940F884BA4101 CRC64;

Query Match 95.0%; Score 57; DB 2; Length 961;
 Best Local Similarity 90.0%; Pred. No. 0.12;
 Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DKPSYQFGH 10
 Db 783 DKPNYQFGH 792

RESULT 7
 ID 07A3J8 PRELIMINARY; PRT; 961 AA.
 AC 07A3J8;
 DT 05-JUL-2004 (TREMBLrel. 27, Created)
 DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)

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DT 05-JUL-2004 (TReMBLrel. 27, Last annotation update)
DE FnbB protein.
GN Name=fnbB: OrderedlocusNames=SA2290;
OS Staphylococcus aureus (strain N315);
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=158879;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21311952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2;
RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Iian J.-Q., Ito T.,
RA Kanamori M., Matsunaru H., Maruyama A., Motokami H., Hoshoyama A.,
RA Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
RA Sakimizu K., Hiraoka H., Kubara S., Goto S., Yabuzaki J.,
RA Kanesha M., Yamashita A., Ohshima K., Furuya K., Yoshino C., Shiba T.,
RA Hattori M., Ogasawara N., Hayashi H., Hiratazu K.;
RT "Whole genome sequencing of methicillin-resistant Staphylococcus
RT aureus."
RL Lancet 357:1225-1240(2001).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC an amide bond (By similarity).
DR EMBL: AP003137; BAB43593.1; -.
DR GO: GO:0009986; C:cell surface; IEA.
DR GO: GO:0005518; C:cell wall; IEA.
DR GO: GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO: GO:0016020; C:membrane; IEA.
DR GO: GO:0007155; P:cell adhesion; IEA.
DR InterPro: IPR008966; Adhes_bact.
DR InterPro: IPR004237; Fn_bind.
DR InterPro: IPR005877; Gpos_YsIRK.
DR InterPro: IPR001899; Gram_pos_anchor.
DR Pfam: PF02986; Fn_bind. 1.
DR Pfam: PF0746; Gram_pos_anchor. 1.
DR Pfam: PF04650; YsIRK_signal. 1.
DR TIGRPFAMs: TIGR01167; LPXTG_anchor. 1.
DR TIGRPFAMs: TIGR01168; YsIRK_signal. 1.
DR PROSITE: PS50847; GRAM_POS_ANCHORING. 1.
KM Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ SEQUENCE 961 AA; 106010 MW; 364940F884EA4101 CRC64;

Query Match 95.0%; Score 57; DB 2; Length 961;
Best Local Similarity 90.0%; Pred. No. 0.12;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Cy 1 DKPSYQFGGH 10
Db 783 DKPNYQFGGH 792

RESULT 8
ID 06GDU5 PRELIMINARY; PRT; 965 AA.
AC 06GDU5;
DT 05-JUL-2004 (TReMBLrel. 27, Created)
DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update)
DE Fibronectin-binding protein.
GN Name=fnbA: OrderedlocusNames=SA2580;
OS Staphylococcus aureus (strain MRSA252).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=282458;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=1521324; DOI=10.1073/pnas.0402521101;
RA Holden M.T.G., Fell E.J., Lindsey J.A., Peacock S.J., Day N.P.J.,
RA Bright M.C., Foster T.J., Moore C.E., Hurst L., Atkin R., Barron A.,
RA Bason N., Bentley S.D., Chillingworth C., Chillingworth T.,
RA Churcher C., Clark L., Cotton C., Cronin A., Doggett J., Dowd L.,
RA Feltwell T., Hance Z., Harris B., Hauser H., Holtroyd S., Jagsels K.,
RA James K.D., Lennard N., Line A., Mayes R., Moule S., Mungall K.,
RA Ormond D., Quail M.A., Rabinowitsch E., Rutherford K.M., Sanders M.,
RA Sharp S., Simmonds M., Stevens K., Whitehead S., Barrell B.G.,
RA Spratt B.G., Parkhill J.;
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RT "Complete genomes of two clinical Staphylococcus aureus strains:
RT evidence for the rapid evolution of virulence and drug resistance.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:9786-9791(2004).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC an amide bond (By similarity).
DR EMBL: BX571856; CAG41560.1; -.
DR GO: GO:0009986; C:cell surface; IEA.
DR GO: GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO: GO:0016020; C:membrane; IEA.
DR GO: GO:0007155; P:cell adhesion; IEA.
DR InterPro: IPR008966; Adhes_bact.
DR InterPro: IPR004237; Fn_bind.
DR InterPro: IPR005877; Gpos_YsIRK.
DR InterPro: IPR001899; Gram_pos_anchor.
DR Pfam: PF02986; Fn_bind. 1.
DR Pfam: PF0746; Gram_pos_anchor. 1.
DR Pfam: PF04650; YsIRK_signal. 1.
DR TIGRPFAMs: TIGR01167; LPXTG_anchor. 1.
DR TIGRPFAMs: TIGR01168; YsIRK_signal. 1.
DR PROSITE: PS50847; GRAM_POS_ANCHORING. 1.
KM Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ SEQUENCE 965 AA; 105691 MW; 2982E132164D0551 CRC64;

Query Match 95.0%; Score 57; DB 2; Length 965;
Best Local Similarity 90.0%; Pred. No. 0.12;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Cy 1 DKPSYQFGGH 10
Db 801 DKPNYQFGGH 810

RESULT 9
ID 08NUU7 PRELIMINARY; PRT; 1015 AA.
AC 08NUU7;
DT 01-OCT-2002 (TReMBLrel. 22, Created)
DT 01-OCT-2002 (TReMBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE Fnb protein.
GN Name=fnb: OrderedlocusNames=MM2421;
OS Staphylococcus aureus (strain MM2).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=196620;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=MM2;
RX MEDLINE=22040717; PubMed=12044378; DOI=10.1016/S0140-6736(02)08713-5;
RA Baba T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Oguchi A.,
RA Nagai Y., Iwama N., Abeo K., Naimi T., Kuroda H., Cui L.,
RA Yamamoto K., Hiratazu K.;
RT "Genome and virulence determinants of high virulence community-
RT acquired MRSA.";
RL Lancet 359:1819-1827(2002).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC an amide bond (By similarity).
DR EMBL: AP004830; BAB96286.1; -.
DR GO: GO:0009986; C:cell surface; IEA.
DR GO: GO:0005518; C:cell wall; IEA.
DR GO: GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO: GO:0016020; C:membrane; IEA.
DR GO: GO:0007155; P:cell adhesion; IEA.
DR InterPro: IPR008966; Adhes_bact.
DR InterPro: IPR004237; Fn_bind.
DR InterPro: IPR005877; Gpos_YsIRK.
DR InterPro: IPR001899; Gram_pos_anchor.
DR Pfam: PF02986; Fn_bind. 1.
DR Pfam: PF0746; Gram_pos_anchor. 1.
DR Pfam: PF04650; YsIRK_signal. 1.
DR TIGRPFAMs: TIGR01167; LPXTG_anchor. 1.
DR TIGRPFAMs: TIGR01168; YsIRK_signal. 1.
DR PROSITE: PS50847; GRAM_POS_ANCHORING. 1.
KM Cell wall; Complete proteome; Peptidoglycan-anchor.
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SQ SEQUENCE 1015 AA; 111145 MW; D0F9281BB64D44D2 CRC64;
 Query Match 95.0%; Score 57; DB 2; Length 1015;
 Best Local Similarity 90.0%; Pred. No. 0.13;
 Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DKPSYQFGGH 10
 |||:|||||
 DB 837 DKPNYQFGGH 846

RESULT 10
 Q6G6H3 PRELIMINARY; PRT; 1015 AA.
 AC Q6G6H3;
 DT 05-JUL-2004 (TREMBLrel. 27, Created)
 DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
 DE Fibronectin-binding protein.
 GN OrderedLocustNames=SA5238;
 OS Staphylococcus aureus (strain MSSA476).
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 NC NCB1_TaxID=282459;
 RX SEQUENCE FROM N.A.
 RP PubMed=15213324; DOI=10.1073/pnae.0402521101;
 RA Holden M.T.G., Fell E.J., Lindsey J.A., Peacock S.J., Day N.P.J.,
 RA Entignt M.C., Foster T.J., Moore C.E., Hurst L., Atkin R., Barton A.,
 RA Baeson N., Bentley S.D., Chillingworth C., Chillingworth T.,
 RA Churcher C., Clark L., Cotton C., Cronin A., Doggett J., Dowd L.,
 RA Feltham T., Hance Z., Harris B., Hauser H., Holtroyd S., Jagels K.,
 RA James K.D., Lennard N., Line A., Mayes R., Moulie S., Mungall K.,
 RA Ommond D., Quail M.A., Rabinowitch E., Rutherford K.M., Sanders M.,
 RA Sharp S., Simmonds M., Stevens K., Whitehead S., Barrell B.G.,
 RA Spratt B.G., Parkhill J.;
 RT "Complete genomes of two clinical Staphylococcus aureus strains:
 RT evidence for the rapid evolution of virulence and drug resistance.";
 RL Proc. Natl. Acad. Sci. U.S.A. 101:9786-9791(2004).
 CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
 CC an amide bond (by similarity).
 DR EMBL; BX571857; CAG44202.1; -;
 DR GO; GO:0009986; C:cell surface; IEA.
 DR GO; GO:0005618; C:cell wall; IEA.
 DR GO; GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0007155; P:cell adhesion; IEA.
 DR InterPro; IPR008966; Adhes_bact.
 DR InterPro; IPR004237; Fn_bind.
 DR InterPro; IPR005877; Gpos_YsIRK.
 DR InterPro; IPR001899; Gram_pos_anchor.
 DR Pfam; PF02986; Fn_bind; 1.
 DR Pfam; PF00746; Gram_pos_anchor; 1.
 DR Pfam; PF04650; YsIRK_signal; 1.
 DR TIGRFAMs; TIGR01167; LpxTG_anchor; 1.
 DR TIGRFAMs; TIGR01168; YsIRK_signal; 1.
 DR PROSITE; PS50847; GRAM_POS_ANCHORING; 1.
 KW Cell wall, Complete proteome; Peptidoglycan-anchor.
 SQ SEQUENCE 1015 AA; 111145 MW; D0F9281BB64D44D2 CRC64;

Query Match 95.0%; Score 57; DB 2; Length 1015;
 Best Local Similarity 90.0%; Pred. No. 0.13;
 Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DKPSYQFGGH 10
 |||:|||||
 DB 837 DKPNYQFGGH 846

RESULT 11
 Q99RD2 PRELIMINARY; PRT; 1038 AA.
 AC Q99RD2;
 DT 01-JUN-2001 (TREMBLrel. 17, Created)

DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
 DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
 DE Fibronectin-binding protein homolog.
 GN Name=fnb; OrderedLocustNames=SAV2503;
 OS Staphylococcus aureus (strain Mu50 / ATCC 700699).
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 NC NCB1_TaxID=158878;
 RX SEQUENCE FROM N.A.
 RP STRAIN=Mu50 / ATCC 700699;
 RC MEDLINE=21311952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2;
 RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
 RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Iian J.-O., Ito T.,
 RA Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hoshiyama A.,
 RA Mizutani U. Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
 RA Sekimizu K., Hirakawa H., Kihara S., Goto S., Yabuzaki J.,
 RA Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
 RA Hattori M., Ogasawara N., Hayashi H., Hiratake K.;
 RT "Whole genome sequencing of methicillin-resistant Staphylococcus
 RT aureus.";
 RL Lancet 357:1225-1240(2001).
 CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
 CC an amide bond (By similarity).
 DR EMBL; AP003365; BAB58665.1; -;
 DR PIR; H90053; H90053.
 DR GO; GO:0009986; C:cell surface; IEA.
 DR GO; GO:0005618; C:cell wall; IEA.
 DR GO; GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0007155; P:cell adhesion; IEA.
 DR InterPro; IPR008966; Adhes_bact.
 DR InterPro; IPR004237; Fn_bind.
 DR InterPro; IPR005877; Gpos_YsIRK.
 DR InterPro; IPR001899; Gram_pos_anchor.
 DR Pfam; PF02986; Fn_bind; 1.
 DR Pfam; PF00746; Gram_pos_anchor; 1.
 DR Pfam; PF04650; YsIRK_signal; 1.
 DR TIGRFAMs; TIGR01167; LpxTG_anchor; 1.
 DR TIGRFAMs; TIGR01168; YsIRK_signal; 1.
 DR PROSITE; PS50847; GRAM_POS_ANCHORING; 1.
 KW Cell wall, Complete proteome; Peptidoglycan-anchor.
 SQ SEQUENCE 1038 AA; 113618 MW; 6656F6F2FBBE12 CRC64;

Query Match 95.0%; Score 57; DB 2; Length 1038;
 Best Local Similarity 90.0%; Pred. No. 0.13;
 Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DKPSYQFGGH 10
 |||:|||||
 DB 832 DKPNYQFGGH 841

RESULT 12
 Q7A3J7 PRELIMINARY; PRT; 1038 AA.
 AC Q7A3J7;
 DT 05-JUL-2004 (TREMBLrel. 27, Created)
 DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
 DE Fnb protein.
 GN Name=fnb; OrderedLocustNames=SA2291;
 OS Staphylococcus aureus (strain N315).
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 NC NCB1_TaxID=158879;
 RX SEQUENCE FROM N.A.
 RP MEDLINE=21311952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2;
 RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
 RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Iian J.-O., Ito T.,
 RA Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hoshiyama A.,
 RA Mizutani U. Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
 RA Sekimizu K., Hirakawa H., Kihara S., Goto S., Yabuzaki J.,
 RA Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,

RA Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
 RT "Whole genome sequencing of methicillin-resistant *Staphylococcus aureus*."
 CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by an amide bond (By similarity).
 DR EMBL: AP003137; BAB43594.1; -;
 DR GO: GO:0009986; C:cell surface; IEA.
 DR GO: GO:0005618; C:cell wall; IEA.
 DR GO: GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
 DR GO: GO:0016020; C:membrane; IEA.
 DR GO: GO:0007155; P:cell adhesion; IEA.
 DR InterPro: IPR008966; Adhes_bact.
 DR InterPro: IPR004237; Fn_bind.
 DR InterPro: IPR005877; Gram_pos_anchor.
 DR InterPro: IPR001899; Gram_pos_anchor.
 DR Pfam: PF02986; Fn_bind_1.
 DR Pfam: PF00746; Gram_pos_anchor_1.
 DR Pfam: PF04650; YSIRK_signal_1.
 DR TIGRFAMs: TIGR01167; LPXTG_anchor_1.
 DR TIGRFAMs: TIGR01168; YSIRK_signal_1.
 DR PROSITE: PSS0847; GRAM_POS_ANCHORING_1.
 DR Cgil wall; Complete proteome; Peptidoglycan-anchor.
 KW SEQUENCE 1038 AA; 113618 MW; 666BFBFBFBEB12 CRC64;
 SQ

Query Match 95.0%; Score 57; DB 2; Length 1038;
 Best Local Similarity 90.0%; Pred. No. 0.13;
 Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DKPSYQFGH 10
 Db 832 DKPNYQFGH 841

RESULT 13
 Q6XQCO
 ID Q6XQCO PRELIMINARY; PRT; 199 AA.
 AC Q6XQCO;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Putative tail assembly protein.
 GN ORFNames=34;
 OS Enterobacteria phage T1.
 OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae;
 OC T1-like viruses.
 NC NCBI_TaxID=12355;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX PubMed=14972552; DOI=10.1016/j.virol.2003.09.020;
 RA Robertes M.D., Martin N.L., Kropinski A.M.;
 RT "The genome and proteome of coliphage T1."
 RL Virology 318:245-266(2004).
 DR EMBL: AY216660; AAP49965.1; -;
 DR InterPro: IPR010654; Lambda_tail_1.
 DR Pfam: PF06805; Lambda_tail_1;
 SO SEQUENCE 199 AA; 20897 MW; 6DB4FA2C1914E53B CRC64;
 SQ

Query Match 68.3%; Score 41; DB 2; Length 199;
 Best Local Similarity 77.8%; Pred. No. 20;
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 DKPSYQFG 9
 Db 156 NKPSYAFGC 164

RESULT 14
 Q8ZENZ
 ID Q8ZENZ PRELIMINARY; PRT; 206 AA.
 AC Q8ZENZ; Q7C1F9;
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)

DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
 DE Putative phage tail assembly protein (Putative phage tail protein).
 GN OrderedLocustNames=YPO2129, y2189;
 OS Yersinia pestis.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Yersinia.
 NC NCBI_TaxID=632;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CO-92 / Bivovar Orientalis;
 RX MEDLINE=21470413; PubMed=11586360; DOI=10.1038/75097083;
 RA Parkhill J., Wren B.W., Thomson N.R., Tibball R.W., Holden M.T.G.,
 RA Prentice M.B., Sebahinia M., James K.D., Churcher C.M., Mungall K.L.,
 RA Baker S., Basham D., Bentley S.D., Brooks K., Cerdono-Tarraga A.-M.,
 RA Chillingworth T., Cronin A., Davies R.M., Davis P., Dougan G.,
 RA Felwell T., Hamlin N., Holroyd S., Jagels K., Karlyshev A.V.,
 RA Leather S., Moule S., Oyston P.C.F., Quail M.A., Rutherford K.M.,
 RA Simmonds M., Skelton J., Stevens K., Whitehead S., Barrall B.G.;
 RT "Genome sequence of *Yersinia pestis*, the causative agent of plague."
 RL Nature 413:523-527(2001).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=KIMS / Bivovar Mediaevalis;
 RX MEDLINE=22137863; PubMed=12142430;
 RX DOI=10.1128/JB.184.16.4601-4611.2002;
 RA Deng W., Burland V., Plunkett G., III, Boutin A., Mayhew G.F., Liss P.,
 RA Perna N.T., Rose D.J., Mau B., Zhou S., Schwartz D.C.,
 RA Rutherford J.D., Lindler L.E., Brubaker R.R., Plano G.V.,
 RA Straley S.C., McDonough K.A., Nilles M.L., Matson J.S., Blattner F.R.,
 RA Perry R.D.;
 RT "Genome sequence of *Yersinia pestis* KIM."
 RL J. Bacteriol. 184:4601-4611(2002).
 DR EMBL: AJ41451; CAC90940.1; -;
 DR EMBL: AE013823; AAM85750.1; -;
 DR DR PF06805; Lambda_tail_1;
 DR PROSITE: PS00583; PF06805; PF06805; PF06805; PF06805;
 KW Complete proteome.
 SO SEQUENCE 206 AA; 21448 MW; 5E480DF74EFDCE CRC64;
 SQ

Query Match 68.3%; Score 41; DB 2; Length 206;
 Best Local Similarity 77.8%; Pred. No. 21;
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 DKPSYQFG 9
 Db 163 NKPSYAFGC 171

RESULT 15
 Q6BW68
 ID Q6BW68 PRELIMINARY; PRT; 251 AA.
 AC Q6BW68;
 DT 25-OCT-2004 (TrEMBLrel. 28, Created)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
 DE Similar to CA34771|IPF3229 *Candida albicans* IPF3229.
 GN ORFNames=DEHAOF087899;
 OS *Debaryomyces hansenii* CBS767.
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Saccharomycetaceae; Debaryomycetes.
 NC NCBI_TaxID=284592;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CBS767;
 RG Genolevures;
 RA Dujon B., Sherman D., Fischer G., Durrens P., Casaregola S.,
 RA Lafontaine I., de Montigny J., Marck C., Neuvéglise C., Talla E.,
 RA Goffard N., Frangeul L., Aigle M., Anhouard V., Babour A., Barbe V.,
 RA Barney S., Blanchin S., Beckerich J.M., Beyne E., Bleykasten C.,
 RA Boistrame A., Boyer J., Catolico L., Confanioli F., de Daruvar A.,
 RA Despons V., Fabre E., Fairhead C., Ferry-Dumazet H., Groppe A.,

RA Hantaye F., Hennequin C., Jauniaux N., Joyet P., Kachouri R.,
 RA Kerrest A., Koszul R., Lemaire M., Lesur I., Ma L., Muller H.,
 RA Nicaud J.M., Nikolski M., Ozias S., Ozier-Kalogeropoulos O.,
 RA Pellenz S., Potter S., Richard G.F., Straub M.L., Suleau A.,
 RA Svennevik D., Tekala F., Wesolowski-Louvel M., Westhof E., Wirth B.,
 RA Zenlou-Meyer M., Zivanovic I., Bolotin-Fukuhara M., Thierry A.,
 RA Bouchier C., Caudron B., Scarpelli C., Gallardin C., Weissenbach J.,
 RA Wincker P., Souciet J.L.;
 RT "Genome evolution in yeast.";
 RL Nature 430:35-44(2004).
 RN (2)
 RP SEQUENCE FROM N.A.
 RC STRAIN=CB5767;
 RA Genoscope;
 RL Submitted (JUL-2004) to the EMBL/Genbank/DBJ databases.
 DR EMBL: CR382138; CAC89043.1; -;
 DR GO: GO:0008757; F:S-adenosylmethionine-dependent methyltransf. . .; IEA.
 DR InterPro: IPR000051; SAM_bind.
 SQ SEQUENCE 251 AA; 28557 MW; 1D2AB5136F10E6E4 CRC64;

Query Match 68.3%; Score 41; DB 2; Length 251;
 Best Local Similarity 77.8%; Pred. No. 26;
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 DKPSYQFCG 9
 | | | | |
 | | | | |
 Db 229 DYPSFQFCG 237

Search completed: October 22, 2005, 09:52:21
 Job time : 57.2069 secs

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OM protein - protein search, using bw model

Run on: October 25, 2005, 20:58:51 ; Search time 69.7126 Seconds
(without alignments)
55.479 Million cell updates/sec

Title: US-10-731-238-96
Perfect score: 59
Sequence: 1 PSYQFGGHNS 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: Genesegp16Dec04:*
2: Genesegp1980s:*
3: Genesegp1990s:*
4: Genesegp2000s:*
5: Genesegp2001s:*
6: Genesegp2002s:*
7: Genesegp2003as:*
8: Genesegp2003bs:*
9: Genesegp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	59	100.0	10	2	AAW65752
2	59	100.0	21	2	AAW65670
3	59	100.0	21	2	AAW65680
4	59	100.0	21	2	AAW65683
5	59	100.0	21	2	AAW65689
6	59	100.0	21	2	AAW65684
7	59	100.0	21	2	AAW65685
8	59	100.0	21	2	AAW65682
9	59	100.0	21	2	AAW65688
10	59	100.0	21	2	AAW65687
11	59	100.0	21	2	AAW65686
12	59	100.0	21	2	AAW65681
13	59	100.0	21	2	AAW65665
14	59	100.0	22	2	AAW65662
15	59	100.0	37	4	AAW65662
16	59	100.0	38	1	AAW65662
17	59	100.0	134	1	AAW65662
18	59	100.0	139	2	AAW65662
19	59	100.0	1018	1	AAW65662
20	59	100.0	1018	4	AAW65662
21	59	100.0	1018	4	AAW65662
22	59	100.0	1018	6	AAW65662
23	59	100.0	1018	6	AAW65662
24	59	100.0	1027	6	AAW65662
25	56	94.9	77	2	AAW65662

26	56	94.9	101	2	AAW65662
27	56	94.9	113	2	AAW65662
28	56	94.9	124	2	AAW65662
29	56	94.9	128	2	AAW65662
30	56	94.9	130	2	AAW65662
31	56	94.9	130	2	AAW65662
32	56	94.9	130	2	AAW65662
33	56	94.9	130	2	AAW65662
34	56	94.9	134	2	AAW65662
35	56	94.9	162	2	AAW65662
36	56	94.9	164	2	AAW65662
37	56	94.9	174	2	AAW65662
38	56	94.9	174	2	AAW65662
39	56	94.9	181	2	AAW65662
40	56	94.9	181	2	AAW65662
41	56	94.9	559	2	AAW65662
42	56	94.9	940	2	AAW65662
43	56	94.9	940	6	AAW65662
44	56	94.9	948	6	AAW65662
45	56	94.9	948	6	AAW65662

ALIGNMENTS

RESULT 1
AAW65752 standard; peptide; 10 AA.

AAW65752;

16-OCT-1998 (first entry)

Fibronectin binding protein-derived peptide #96.

microbial surface components recognising adhesive matrix molecule;
MSGRAM; fibronectin; fibronectin-binding protein; antibody; epitope;
KW Anticlotic; bacterial infection; antibiotic-resistant strain.

OS Synthetic.

Staphylococcus aureus.

WO9831389-A2.

23-JUL-1998.

21-JAN-1998; 98WO-US001222.

21-JAN-1997; 97US-0036139P.

(TEXA) UNIV TEXAS A & M SYSTEM.

Hooeek M, Patil JM, House-Pompeo KL, Speziale P, Joh D;

McGavin M;

WPI; 1998-413816/35.

Antibody that binds to fibronectin-binding protein, preventing its binding to fibronectin - used to treat or prevent bacterial infection, especially by Staphylococci and Streptococci.

Example 9; Page 111; 201P; English.

The invention relates to antibodies that bind to a fibronectin-binding domain of a fibronectin-binding protein, and inhibit binding of the protein to fibronectin. Also claimed are: (1) isolated peptides of a fibronectin-binding protein that do not bind to fibronectin; (2) fusion protein containing at least one peptide of a fibronectin-binding protein linked to a second amino acid sequence; (3) nucleic acid encoding the isolated peptide of (1). Antibodies, the isolated peptides of (1) and the nucleic acid are all useful for immunisation (active or passive) and (by inhibiting binding of bacteria to fibronectin) for preventing or creating infection in humans or other animals, particularly by staphylococci or

CC streptococci, e.g. meningitis, otitis media, pneumonia, endocarditis,
 CC mastitis in cattle, abortion in horses and many others. Since the
 CC antibodies block binding of bacteria, they should be effective against
 CC antibiotic-resistant strains, and may replace antibiotic therapy or
 CC increase its effectiveness. Sequences AAM6574-58 represent peptides
 CC which were synthesised to span the D3 motif of *S. aureus* fibronectin
 CC binding protein A
 CC
 XX
 SO Sequence 10 AA;

Query Match 100.0%; Score 59; DB 2; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.00061;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PSYQFGGHS 10
 |||||
 1 PSYQFGGHS 10

RESULT 2
 ID AAM65670 standard; peptide; 21 AA.
 XX
 AC AAM65670;
 XX
 DT 16-OCT-1998 (first entry)
 XX

DE Fibronectin binding protein-derived peptide #14.

XX microbial surface components recognising adhesive matrix molecule;
 KW MSCRAMM; fibronectin; fibronectin-binding protein; antibody; epitope;
 KW antibiotic; bacterial infection; antibiotic-resistant strain.

XX Synthetic.
 OS Staphylococcus aureus.

XX WO9831389-A2.

XX 23-JUL-1998.

XX 21-JAN-1998; 98WO-US001222.

XX 21-JAN-1997; 97US-0036139P.

XX (TEXA) UNIV TEXAS A & M SYSTEM.

PI Hoeoek M, Patti JM, House-Pompeo KL, Speziale P, Joh D;
 PI Megavlin MJ;

XX WPI; 1998-413816/35.

PT Antibody that binds to fibronectin-binding protein, preventing its
 binding to fibronectin - used to treat or prevent bacterial infection,
 PT especially by Staphylococci and Streptococci.

XX Example 8; Page 100; 201pp; English.

XX The invention relates to antibodies that bind to a fibronectin-binding
 CC domain of a fibronectin-binding protein, and inhibit binding of the
 CC protein to fibronectin. Also claimed are: (1) isolated peptides of a
 CC fibronectin-binding protein that do not bind to fibronectin; (2) fusion
 CC protein containing at least one peptide of a fibronectin-binding protein
 CC linked to a second amino acid sequence; (3) nucleic acid encoding the
 CC isolated peptide of (1). Antibodies, the isolated peptides of (1) and the
 CC nucleic acids are all useful for immunisation (active or passive) and (by
 CC inhibiting binding of bacteria to fibronectin) for preventing or treating
 CC infection in humans or other animals, particularly by staphylococci or
 CC streptococci, e.g. meningitis, otitis media, pneumonia, endocarditis,
 CC mastitis in cattle, abortion in horses and many others. Since the
 CC antibodies block binding of bacteria, they should be effective against
 CC antibiotic-resistant strains, and may replace antibiotic therapy or
 CC increase its effectiveness. Sequences AAM65670-90 represent a series of
 CC synthetic peptides based on the D3 repeat of *S. aureus* fibronectin

CC binding protein A. They were synthesised to contain a proline residue at
 CC each position throughout the sequence (ie a proline scan)
 CC
 XX
 SO Sequence 21 AA;

Query Match 100.0%; Score 59; DB 2; Length 21;
 Best Local Similarity 100.0%; Pred. No. 0.0013;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PSYQFGGHS 10
 |||||
 2 PSYQFGGHS 11

RESULT 3
 ID AAM65680 standard; peptide; 21 AA.
 XX
 AC AAM65680;
 XX
 DT 16-OCT-1998 (first entry)
 XX

DE Fibronectin binding protein-derived peptide #24.

XX microbial surface components recognising adhesive matrix molecule;
 KW MSCRAMM; fibronectin; fibronectin-binding protein; antibody; epitope;
 KW antibiotic; bacterial infection; antibiotic-resistant strain.

XX Synthetic.
 OS Staphylococcus aureus.

XX WO9831389-A2.

XX 23-JUL-1998.

XX 21-JAN-1998; 98WO-US001222.

XX 21-JAN-1997; 97US-0036139P.

XX (TEXA) UNIV TEXAS A & M SYSTEM.

PI Hoeoek M, Patti JM, House-Pompeo KL, Speziale P, Joh D;
 PI Megavlin MJ;

XX WPI; 1998-413816/35.

PT Antibody that binds to fibronectin-binding protein, preventing its
 binding to fibronectin - used to treat or prevent bacterial infection,
 PT especially by Staphylococci and Streptococci.

XX Example 8; Page 100; 201pp; English.

XX The invention relates to antibodies that bind to a fibronectin-binding
 CC domain of a fibronectin-binding protein, and inhibit binding of the
 CC protein to fibronectin. Also claimed are: (1) isolated peptides of a
 CC fibronectin-binding protein that do not bind to fibronectin; (2) fusion
 CC protein containing at least one peptide of a fibronectin-binding protein
 CC linked to a second amino acid sequence; (3) nucleic acid encoding the
 CC isolated peptide of (1). Antibodies, the isolated peptides of (1) and the
 CC nucleic acids are all useful for immunisation (active or passive) and (by
 CC inhibiting binding of bacteria to fibronectin) for preventing or treating
 CC infection in humans or other animals, particularly by staphylococci or
 CC streptococci, e.g. meningitis, otitis media, pneumonia, endocarditis,
 CC mastitis in cattle, abortion in horses and many others. Since the
 CC antibodies block binding of bacteria, they should be effective against
 CC antibiotic-resistant strains, and may replace antibiotic therapy or
 CC increase its effectiveness. Sequences AAM65670-90 represent a series of
 CC synthetic peptides based on the D3 repeat of *S. aureus* fibronectin
 CC binding protein A. They were synthesised to contain a proline residue at
 CC each position throughout the sequence (ie a proline scan)

XX Sequence 21 AA;

Query Match 100.0%; Score 59; DB 2; Length 21;
 Best Local Similarity 100.0%; Pred. No. 0.0013;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PSYQFGHNS 10
 |||||
 DB 2 PSYQFGHNS 11

RESULT 4

AAW65683 ID AAW65683 standard; peptide; 21 AA.

AAW65683;

16-OCT-1998 (first entry)

Fibronectin binding protein-derived peptide #27.

microbial surface components recognising adhesive matrix molecule;
 MSCRAMM; fibronectin; fibronectin-binding protein; antibody; epitope;
 antibiotic; bacterial infection; antibiotic-resistant strain.

Synthetic.

Staphylococcus aureus.

MO9831389-A2.

23-JUL-1998.

21-JAN-1998; 98WO-US001222.

21-JAN-1997; 97US-0036139P.

(TEXA) UNIV TEXAS A & M SYSTEM.

Hoseok M, Patti JM, House-Pompeo KL, Speziale P, Joh D;
 Mcgavin MJ;

WPI; 1998-413816/35.

Antibody that binds to fibronectin-binding protein, preventing its
 binding to fibronectin - used to treat or prevent bacterial infection,
 especially by Staphylococci and Streptococci.

Example 8; Page 101; 201pp; English.

The invention relates to antibodies that bind to a fibronectin-binding
 domain of a fibronectin-binding protein, and inhibit binding of the
 protein to fibronectin. Also claimed are: (1) isolated peptides of a
 fibronectin-binding protein that do not bind to fibronectin; (2) fusion
 protein containing at least one peptide of a fibronectin-binding protein
 linked to a second amino acid sequence; (3) nucleic acid encoding the
 isolated peptide of (1). Antibodies, the isolated peptides of (1) and the
 nucleic acids are all useful for immunisation (active or passive) and (by
 inhibiting binding of bacteria to fibronectin) for preventing or treating
 infection in humans or other animals, particularly by staphylococci or
 streptococci, e.g. meningitis, otitis media, pneumonia, endocarditis,
 mastitis in cattle, abortion in horses and many others. Since the
 antibodies block binding of bacteria, they should be effective against
 antibiotic-resistant strains, and may replace antibiotic therapy or
 increase its effectiveness. Sequences AAW65670-90 represent a series of
 synthetic peptides based on the D3 repeat of S. aureus fibronectin
 binding protein A. They were synthesised to contain a proline residue at
 each position through the sequence (ie a proline scan)

Sequence 21 AA;

Query Match 100.0%; Score 59; DB 2; Length 21;
 Best Local Similarity 100.0%; Pred. No. 0.0013;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PSYQFGHNS 10

DB 2 PSYQFGHNS 11
 |||||

RESULT 5

AAW65689 ID AAW65689 standard; peptide; 21 AA.

AAW65689;

16-OCT-1998 (first entry)

Fibronectin binding protein-derived peptide #23.

microbial surface components recognising adhesive matrix molecule;
 MSCRAMM; fibronectin; fibronectin-binding protein; antibody; epitope;
 antibiotic; bacterial infection; antibiotic-resistant strain.

Synthetic.

Staphylococcus aureus.

MO9831389-A2.

23-JUL-1998.

21-JAN-1998; 98WO-US001222.

21-JAN-1997; 97US-0036139P.

(TEXA) UNIV TEXAS A & M SYSTEM.

Hoseok M, Patti JM, House-Pompeo KL, Speziale P, Joh D;
 Mcgavin MJ;

WPI; 1998-413816/35.

Antibody that binds to fibronectin-binding protein, preventing its
 binding to fibronectin - used to treat or prevent bacterial infection,
 especially by Staphylococci and Streptococci.

Example 8; Page 101; 201pp; English.

The invention relates to antibodies that bind to a fibronectin-binding
 domain of a fibronectin-binding protein, and inhibit binding of the
 protein to fibronectin. Also claimed are: (1) isolated peptides of a
 fibronectin-binding protein that do not bind to fibronectin; (2) fusion
 protein containing at least one peptide of a fibronectin-binding protein
 linked to a second amino acid sequence; (3) nucleic acid encoding the
 isolated peptide of (1). Antibodies, the isolated peptides of (1) and the
 nucleic acids are all useful for immunisation (active or passive) and (by
 inhibiting binding of bacteria to fibronectin) for preventing or treating
 infection in humans or other animals, particularly by staphylococci or
 streptococci, e.g. meningitis, otitis media, pneumonia, endocarditis,
 mastitis in cattle, abortion in horses and many others. Since the
 antibodies block binding of bacteria, they should be effective against
 antibiotic-resistant strains, and may replace antibiotic therapy or
 increase its effectiveness. Sequences AAW65670-90 represent a series of
 synthetic peptides based on the D3 repeat of S. aureus fibronectin
 binding protein A. They were synthesised to contain a proline residue at
 each position through the sequence (ie a proline scan)

Sequence 21 AA;

Query Match 100.0%; Score 59; DB 2; Length 21;
 Best Local Similarity 100.0%; Pred. No. 0.0013;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PSYQFGHNS 10
 |||||
 DB 2 PSYQFGHNS 11

RESULT 6

```
AAW65684
ID AAW65684 standard; peptide; 21 AA.
XX
AC AAW65684;
XX
DE 16-OCT-1998 (first entry)
XX
DE Fibronectin binding protein-derived peptide #28.
XX
KM microbial surface components recognising adhesive matrix molecule;
KM MSCRAMM; fibronectin; fibronectin-binding protein; antibody; epitope;
KM antibiotic; bacterial infection; antibiotic-resistant strain.
XX
OS Synthetic.
OS Staphylococcus aureus.
XX
PN WO9831389-A2.
XX
PD 23-JUL-1998.
XX
PF 21-JAN-1998; 98WO-US001222.
XX
PR 21-JAN-1997; 97US-0036139P.
XX
PA (TEXA ) UNIV TEXAS A & M SYSTEM.
XX
PI Hoeek M, Patli JM, House-Pompeo KL, Speziale P, Joh D;
PI Megavlin MJ;
XX
DR WPI; 1998-413816/35.
XX
PT Antibody that binds to fibronectin-binding protein, preventing its
PT binding to fibronectin - used to treat or prevent bacterial infection,
PT especially by Staphylococci and Streptococci.
XX
PS Example 8; Page 101; 201pp; English.
XX
DE The invention relates to antibodies that bind to a fibronectin-binding
DE domain of a fibronectin-binding protein, and inhibit binding of the
DE protein to fibronectin. Also claimed are: (1) isolated peptides of a
DE fibronectin-binding protein that do not bind to fibronectin; (2) fusion
DE protein containing at least one peptide of a fibronectin-binding protein
DE linked to a second amino acid sequence; (3) nucleic acid encoding the
DE isolated peptide of (1). Antibodies, the isolated peptides of (1) and the
DE nucleic acids are all useful for immunisation (active or passive) and (by
DE inhibiting binding of bacteria to fibronectin) for preventing or treating
DE infection in humans or other animals, particularly by staphylococci or
DE streptococci, e.g. meningitis, otitis media, pneumonia, endocarditis,
DE mastitis in cattle, abortion in horses and many others. Since the
DE antibodies block binding of bacteria, they should be effective against
DE antibiotic-resistant strains, and may replace antibiotic therapy or
DE increase its effectiveness. Sequences AAW65670-90 represent a series of
DE synthetic peptides based on the D3 repeat of S. aureus fibronectin
DE binding protein A. They were synthesised to contain a proline residue at
DE each position through the sequence (ie a proline scan)
XX
SQ Sequence 21 AA;
XX
Query Match 100.0%; Score 59; DB 2; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.0013;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 PSYQFGHNS 10
DB 2 PSYQFGHNS 11
XX
RESULT 7
ID AAW65685 standard; peptide; 21 AA.
XX
AC AAW65685;
XX
```

```
DT 16-OCT-1998 (first entry)
XX
DE Fibronectin binding protein-derived peptide #29.
XX
DE microbial surface components recognising adhesive matrix molecule;
KM MSCRAMM; fibronectin; fibronectin-binding protein; antibody; epitope;
KM antibiotic; bacterial infection; antibiotic-resistant strain.
XX
OS Synthetic.
OS Staphylococcus aureus.
XX
PN WO9831389-A2.
XX
PD 23-JUL-1998.
XX
PF 21-JAN-1998; 98WO-US001222.
XX
PR 21-JAN-1997; 97US-0036139P.
XX
PA (TEXA ) UNIV TEXAS A & M SYSTEM.
XX
PI Hoeek M, Patli JM, House-Pompeo KL, Speziale P, Joh D;
PI Megavlin MJ;
XX
DR WPI; 1998-413816/35.
XX
PT Antibody that binds to fibronectin-binding protein, preventing its
PT binding to fibronectin - used to treat or prevent bacterial infection,
PT especially by Staphylococci and Streptococci.
XX
PS Example 8; Page 101; 201pp; English.
XX
DE The invention relates to antibodies that bind to a fibronectin-binding
DE domain of a fibronectin-binding protein, and inhibit binding of the
DE protein to fibronectin. Also claimed are: (1) isolated peptides of a
DE fibronectin-binding protein that do not bind to fibronectin; (2) fusion
DE protein containing at least one peptide of a fibronectin-binding protein
DE linked to a second amino acid sequence; (3) nucleic acid encoding the
DE isolated peptide of (1). Antibodies, the isolated peptides of (1) and the
DE nucleic acids are all useful for immunisation (active or passive) and (by
DE inhibiting binding of bacteria to fibronectin) for preventing or treating
DE infection in humans or other animals, particularly by staphylococci or
DE streptococci, e.g. meningitis, otitis media, pneumonia, endocarditis,
DE mastitis in cattle, abortion in horses and many others. Since the
DE antibodies block binding of bacteria, they should be effective against
DE antibiotic-resistant strains, and may replace antibiotic therapy or
DE increase its effectiveness. Sequences AAW65670-90 represent a series of
DE synthetic peptides based on the D3 repeat of S. aureus fibronectin
DE binding protein A. They were synthesised to contain a proline residue at
DE each position through the sequence (ie a proline scan)
XX
SQ Sequence 21 AA;
XX
Query Match 100.0%; Score 59; DB 2; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.0013;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 PSYQFGHNS 10
DB 2 PSYQFGHNS 11
XX
RESULT 8
ID AAW65682 standard; peptide; 21 AA.
XX
AC AAW65682;
XX
DE 16-OCT-1998 (first entry)
XX
DE Fibronectin binding protein-derived peptide #26.
XX
KM microbial surface components recognising adhesive matrix molecule;
XX
```

KM MSCRAMM; fibronectin; fibronectin-binding protein; antibody; epitope;
 KM antibiotic; bacterial infection; antibiotic-resistant strain.
 XX
 OS Synthetic.
 OS Staphylococcus aureus.
 PN WO9831389-A2.
 XX
 PD 23-JUL-1998.
 XX
 PF 21-JAN-1998; 98MO-US001222.
 XX
 PR 21-JAN-1997; 97US-0036139P.
 XX
 PA (TEXA) UNIV TEXAS A & M SYSTEM.
 PI Hoeoek M, Patti JM, House-Pompeo KL, Speziale P, Joh D;
 PI McGavin MJ;
 DR WPI; 1998-413816/35.
 XX
 PT Antibody that binds to fibronectin-binding protein, preventing its
 PT binding to fibronectin - used to treat or prevent bacterial infection,
 PT especially by Staphylococci and Streptococci.
 XX
 PS Example 8; Page 101; 201pp; English.
 XX
 CC The invention relates to antibodies that bind to a fibronectin-binding
 CC domain of a fibronectin-binding protein, and inhibit binding of the
 CC protein to fibronectin. Also claimed are: (1) isolated peptides of a
 CC fibronectin-binding protein that do not bind to fibronectin; (2) fusion
 CC protein containing at least one peptide of a fibronectin-binding protein
 CC linked to a second amino acid sequence; (3) nucleic acid encoding the
 CC isolated peptide of (1). Antibodies, the isolated peptides of (1) and the
 CC nucleic acids are all useful for immunisation (active or passive) and (by
 CC inhibiting binding of bacteria to fibronectin) for preventing or treating
 CC infection in humans or other animals, particularly by staphylococci or
 CC streptococci, e.g. meningitis, otitis media, pneumonia, endocarditis,
 CC mastitis in cattle, abortion in horses and many others. Since the
 CC antibodies block binding of bacteria, they should be effective against
 CC antibiotic-resistant strains, and may replace antibiotic therapy or
 CC increase its effectiveness. Sequences AAW65670-90 represent a series of
 CC synthetic peptides based on the D3 repeat of S. aureus fibronectin
 CC binding protein A. They were synthesised to contain a proline residue at
 CC each position through the sequence (ie a proline scan)
 XX
 SQ Sequence 21 AA;
 Query Match 100.0%; Score 59; DB 2; Length 21;
 Best Local Similarity 100.0%; Pred. No. 0.0013;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PSYQFGGHS 10
 |||||
 Db 2 PSYQFGGHS 11

RESULT 9
 AAW65688
 ID AAW65688 standard; peptide; 21 AA.
 XX
 AC AAW65688;
 XX
 DT 16-OCT-1998 (first entry)
 XX
 DE Fibronectin binding protein-derived peptide #32.
 XX
 KM microbial surface components recognising adhesive matrix molecule;
 KM MSCRAMM; fibronectin; fibronectin-binding protein; antibody; epitope;
 KM antibiotic; bacterial infection; antibiotic-resistant strain.
 XX
 OS Synthetic.
 OS Staphylococcus aureus.

XX
 PN WO9831389-A2.
 XX
 PD 23-JUL-1998.
 XX
 PF 21-JAN-1998; 98MO-US001222.
 XX
 PR 21-JAN-1997; 97US-0036139P.
 XX
 PA (TEXA) UNIV TEXAS A & M SYSTEM.
 PI Hoeoek M, Patti JM, House-Pompeo KL, Speziale P, Joh D;
 PI McGavin MJ;
 DR WPI; 1998-413816/35.
 XX
 PT Antibody that binds to fibronectin-binding protein, preventing its
 PT binding to fibronectin - used to treat or prevent bacterial infection,
 PT especially by Staphylococci and Streptococci.
 XX
 PS Example 8; Page 101; 201pp; English.
 XX
 CC The invention relates to antibodies that bind to a fibronectin-binding
 CC domain of a fibronectin-binding protein, and inhibit binding of the
 CC protein to fibronectin. Also claimed are: (1) isolated peptides of a
 CC fibronectin-binding protein that do not bind to fibronectin; (2) fusion
 CC protein containing at least one peptide of a fibronectin-binding protein
 CC linked to a second amino acid sequence; (3) nucleic acid encoding the
 CC isolated peptide of (1). Antibodies, the isolated peptides of (1) and the
 CC nucleic acids are all useful for immunisation (active or passive) and (by
 CC inhibiting binding of bacteria to fibronectin) for preventing or treating
 CC infection in humans or other animals, particularly by staphylococci or
 CC streptococci, e.g. meningitis, otitis media, pneumonia, endocarditis,
 CC mastitis in cattle, abortion in horses and many others. Since the
 CC antibodies block binding of bacteria, they should be effective against
 CC antibiotic-resistant strains, and may replace antibiotic therapy or
 CC increase its effectiveness. Sequences AAW65670-90 represent a series of
 CC synthetic peptides based on the D3 repeat of S. aureus fibronectin
 CC binding protein A. They were synthesised to contain a proline residue at
 CC each position through the sequence (ie a proline scan)
 XX
 SQ Sequence 21 AA;
 Query Match 100.0%; Score 59; DB 2; Length 21;
 Best Local Similarity 100.0%; Pred. No. 0.0013;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PSYQFGGHS 10
 |||||
 Db 2 PSYQFGGHS 11

RESULT 10
 AAW65687
 ID AAW65687 standard; peptide; 21 AA.
 XX
 AC AAW65687;
 XX
 DT 16-OCT-1998 (first entry)
 XX
 DE Fibronectin binding protein-derived peptide #31.
 XX
 KM microbial surface components recognising adhesive matrix molecule;
 KM MSCRAMM; fibronectin; fibronectin-binding protein; antibody; epitope;
 KM antibiotic; bacterial infection; antibiotic-resistant strain.
 XX
 OS Synthetic.
 OS Staphylococcus aureus.
 XX
 PN WO9831389-A2.
 XX
 PD 23-JUL-1998.

XX Antibody that binds to fibronectin-binding protein, preventing its
 PT binding to fibronectin - used to treat or prevent bacterial infection,
 PT especially by Staphylococci and Streptococci.

XX Example 8; Page 101; 201pp; English.

XX The invention relates to antibodies that bind to a fibronectin-binding
 CC domain of a fibronectin-binding protein, and inhibit binding of the
 CC protein to fibronectin. Also claimed are: (1) isolated peptides of a
 CC fibronectin-binding protein that do not bind to fibronectin; (2) fusion
 CC protein containing at least one peptide of a fibronectin-binding protein
 CC linked to a second amino acid sequence; (3) nucleic acid encoding the
 CC isolated peptide of (1). Antibodies, the isolated peptides of (1) and the
 CC nucleic acids are all useful for immunisation (active or passive) and (by
 CC inhibiting binding of bacteria to fibronectin) for preventing or treating
 CC infection in humans or other animals, particularly by staphylococci or
 CC streptococci, e.g. meningitis, otitis media, pneumonia, endocarditis,
 CC mastitis in cattle, abortion in horses and many others. Since the
 CC antibodies block binding of bacteria, they should be effective against
 CC antibiotic-resistant strains, and may replace antibiotic therapy or
 CC increase its effectiveness. Sequences AAW65670-90 represent a series of
 CC synthetic peptides based on the D3 repeat of S. aureus fibronectin
 CC binding protein A. They were synthesised to contain a proline residue at
 CC each position throughout the sequence (ie a proline scan)

XX Sequence 21 AA;

Query Match 100.0%; Score 59; DB 2; Length 21;
 Best Local Similarity 100.0%; Pred. No. 0.0013;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PSYQFGHNS 10
 |||||
 Db 2 PSYQFGHNS 11

RESULT 13

AAW65665
 ID AAW65665 standard; peptide; 21 AA.

XX AAW65665;

XX 16-OCT-1998 (first entry)

XX Fibronectin binding protein-derived peptide #9.

XX microbial surface components recognising adhesive matrix molecule;

XX MSCRAMM; fibronectin; fibronectin-binding protein; antibody; epitope;

XX antibiotic; bacterial infection; antibiotic-resistant strain.

XX Synthetic.

XX Staphylococcus aureus.

XX WO9831389-A2.

XX 23-JUL-1998.

XX 21-JAN-1998; 98WO-US001222.

XX 21-JAN-1997; 97US-0036139P.

XX (TEXA) UNIV TEXAS A & M SYSTEM.

XX Hoecek M, Patti JM, House-Pompeo KL, Speciale P, Joh D;

XX MPI; 1998-413816/35.

XX Antibody that binds to fibronectin-binding protein, preventing its
 PT binding to fibronectin - used to treat or prevent bacterial infection,
 PT especially by Staphylococci and Streptococci.

PS Example 2; Page 92; 201pp; English.

XX The invention relates to antibodies that bind to a fibronectin-binding
 CC domain of a fibronectin-binding protein, and inhibit binding of the
 CC protein to fibronectin. Also claimed are: (1) isolated peptides of a
 CC fibronectin-binding protein that do not bind to fibronectin; (2) fusion
 CC protein containing at least one peptide of a fibronectin-binding protein
 CC linked to a second amino acid sequence; (3) nucleic acid encoding the
 CC isolated peptide of (1). Antibodies, the isolated peptides of (1) and the
 CC nucleic acids are all useful for immunisation (active or passive) and (by
 CC inhibiting binding of bacteria to fibronectin) for preventing or treating
 CC infection in humans or other animals, particularly by staphylococci or
 CC streptococci, e.g. meningitis, otitis media, pneumonia, endocarditis,
 CC mastitis in cattle, abortion in horses and many others. Since the
 CC antibodies block binding of bacteria, they should be effective against
 CC antibiotic-resistant strains, and may replace antibiotic therapy or
 CC increase its effectiveness. Sequences AAW65659-68 represent synthetic
 CC epitopes from the fibronectin binding domains DU and D1-D4 of the S.
 CC aureus fnbA gene

XX Sequence 21 AA;

Query Match 100.0%; Score 59; DB 2; Length 21;
 Best Local Similarity 100.0%; Pred. No. 0.0013;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PSYQFGHNS 10
 |||||
 Db 2 PSYQFGHNS 11

RESULT 14

AAAR21340
 ID AAR21340 standard; peptide; 22 AA.

XX AAR21340;

XX 25-MAR-2003 (revised)

XX 15-JUN-1992 (first entry)

XX Fibronectin binding protein.

XX FNBp; wound infection reduction; vaccination; mastitis;

XX Staphylococcal infections; D3.

XX Synthetic.

XX WO9202555-A.

XX 20-FEB-1992.

XX 10-AUG-1990; 90SE-00002617.

XX 10-AUG-1990; 90SE-00002617.

XX (ALFA) ALFA LAVAL AGRIC INT AB.

XX Hook M, McGavin M, Raucel G;

XX MPI; 1992-080035/10.

XX New fibronectin binding peptide - combines with fusion peptide to form
 PT large antigen, used in immunisation, diagnosis and for treating wounds.

XX Claim 1; Page 22; 33pp; English.

XX The sequence comprises amino acids 17-33 of a tandem repeat, designated
 CC D3 of the fibronectin binding site of Staphylococcus aureus 8325-4 FNBp.
 CC The N-terminal DK may be replaced with H or K, and the C-terminal LKP may
 CC be replaced by either L, LP, or OH. The peptides were synthesised using
 CC standard methods and purified using reverse phase HPLC. The appropriate
 CC fractions were dialysed and lyophilised. Peptide sequencing was performed
 CC and the peptides digested and chemically modified by dihydroxypropylation

CC of the amino side chain of lysine. The carboxylic side chains were
 CC converted to glycine methyl esters. The phenyl side chains of tyrosine
 CC residues were oxidised. Chemically modified peptide D3 was compared to
 CC unmodified D3. Lysine and tyrosine modifications only partially
 CC diminished its activity whereas modification of aspartic/glutamic
 CC residues resulted in complete loss of activity. The peptide can be used
 CC for the prevention or reduction of the risk of wound infection. The
 CC peptide can be used to create a large antigen for vaccinating ruminants
 CC against mastitis caused by Staphylococcal infections. It can also be used
 CC to diagnose Staphylococcal infections using ELISA or DNA probes. (Updated
 CC on 25-MAR-2003 to correct PA field.)
 XX

SQ Sequence 22 AA;

Query Match 100.0%; Score 59; DB 2; Length 22;
 Best Local Similarity 100.0%; Pred. No. 0.0014;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PSYQFGGHNS 10
 |||||
 Db 3 PSYQFGGHNS 12

RESULT 15

AAB91958 AAB91958 standard; peptide; 37 AA.

XX AAB91958;

XX 22-JUN-2001 (first entry)

XX Fibronectin fragment and fibrin related peptide SEQ ID NO:1134.

KM Protection; endogenous therapeutic peptide; peptidase; conjugation;
 KM blood component; modification; succinimidy; maleimido group; amino;
 KW hydroxyl; thiol; hormone; growth factor; neurotransmitter.

XX Homo sapiens.
 OS Synthetic.

PN WO200069900-A2.

XX 23-NOV-2000.

XX 17-MAY-2000; 2000WO-US013576.

XX 17-MAY-1999; 99US-0134406P.

XX 10-SEP-1999; 99US-0153406P.

XX 15-OCT-1999; 99US-0159783P.

XX (CONJ-) CONJUCHEM INC.

PI Bridon DP, Ezrin AM, Milner PG, Holmes DL, Thibaudau K;

XX WPI; 2001-112059/12.

PT Modifying and attaching therapeutic peptides to albumin prevents
 PT peptidase degradation, useful for increasing length of in vivo activity.

XX Disclosure; Page 566; 733pp; English.

XX The present invention describes a modified therapeutic peptide (I)
 CC comprising a therapeutically active amino acid region (II) and a
 CC reactive group (III) (e.g. succinimidy and maleimido groups) attached to
 CC a less therapeutically active amino acid region (IV), which covalently
 CC bonds with amino/hydroxyl/thiol groups on blood components to form a
 CC peptidase stabilised therapeutic peptide composed of 3-50 amino acids.
 CC (I) are useful for modifying therapeutic peptides e.g. hormones, growth
 CC factors and neurotransmitters, to protect them from peptidase activity in
 CC vivo for the treatment of various disorders. Endogenous therapeutic
 CC peptides are not suitable as drug candidates as they require frequent
 CC administration due to rapid degradation by peptidases in the body.
 CC Modifying and attaching therapeutic peptides to albumin prevents or

CC reduces the action of peptidases to increase length of activity (half
 CC life) and specificity as bonding to large molecules decreases
 CC intracellular uptake and interference with physiological processes.
 CC AAB90829 to AAB92441 represent peptides which can be used in the
 CC exemplification of the present invention
 XX

SQ Sequence 37 AA;

Query Match 100.0%; Score 59; DB 4; Length 37;
 Best Local Similarity 100.0%; Pred. No. 0.0024;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PSYQFGGHNS 10
 |||||
 Db 17 PSYQFGGHNS 26

Search completed: October 25, 2005, 21:29:13
 Job time : 70.7126 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 22, 2005, 07:41:53 ; Search time 17.2989 Seconds
(without alignments)
43.153 Million cell updates/sec

Title: US-10-731-238-96
Sequence: 1 PSYQFGHNS 10

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*

- 1: /cgn2_6/ptodata/1/1aa/5A.COMB.pep:*
- 2: /cgn2_6/ptodata/1/1aa/5B.COMB.pep:*
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- 6: /cgn2_6/ptodata/1/1aa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	59	100.0	10	4	US-09-010-317-96
2	59	100.0	19	1	US-08-234-622A-1
3	59	100.0	21	4	US-09-010-317-9
4	59	100.0	21	4	US-09-010-317-14
5	59	100.0	21	4	US-09-010-317-24
6	59	100.0	21	4	US-09-010-317-25
7	59	100.0	21	4	US-09-010-317-26
8	59	100.0	21	4	US-09-010-317-27
9	59	100.0	21	4	US-09-010-317-28
10	59	100.0	21	4	US-09-010-317-29
11	59	100.0	21	4	US-09-010-317-30
12	59	100.0	21	4	US-09-010-317-31
13	59	100.0	21	4	US-09-010-317-32
14	59	100.0	21	4	US-09-010-317-33
15	59	100.0	37	1	US-08-234-622A-4
16	59	100.0	38	1	US-08-294-189-8
17	59	100.0	38	1	US-08-729-767-5
18	59	100.0	114	1	US-08-259-000-3
19	59	100.0	139	3	US-08-856-253-8
20	59	100.0	178	2	US-08-459-135A-12
21	59	100.0	178	2	US-08-495-559-12
22	59	100.0	1027	4	US-08-956-171E-5254
23	59	100.0	1027	4	US-08-781-986A-5254
24	56	94.9	130	2	US-08-459-135A-7
25	56	94.9	130	2	US-08-459-135A-8
26	56	94.9	130	3	US-08-495-559-7
27	56	94.9	130	3	US-08-495-559-8

28	56	94.9	174	2	US-08-459-135A-10	Sequence 10, Appl
29	56	94.9	174	2	US-08-459-135A-13	Sequence 13, Appl
30	56	94.9	174	3	US-08-495-559-10	Sequence 10, Appl
31	56	94.9	174	3	US-08-495-559-13	Sequence 13, Appl
32	56	94.9	176	3	US-08-495-559-6	Sequence 6, Appl
33	56	94.9	181	2	US-08-459-135A-6	Sequence 6, Appl
34	56	94.9	559	4	US-08-956-171E-5251	Sequence 5251, Ap
35	56	94.9	559	4	US-08-781-986A-5251	Sequence 5251, Ap
36	55	93.2	21	4	US-09-010-317-23	Sequence 23, Appl
37	54	91.5	21	4	US-09-010-317-16	Sequence 16, Appl
38	53	89.8	21	4	US-09-010-317-18	Sequence 18, Appl
39	52	88.1	21	4	US-09-010-317-15	Sequence 15, Appl
40	51	86.4	21	4	US-09-010-317-20	Sequence 20, Appl
41	51	86.4	21	4	US-09-010-317-22	Sequence 22, Appl
42	51	86.4	21	4	US-09-010-317-13	Sequence 13, Appl
43	51	86.4	22	4	US-09-010-317-95	Sequence 95, Appl
44	49	83.1	10	4	US-09-010-317-95	Sequence 95, Appl
45	49	83.1	21	4	US-09-010-317-17	Sequence 17, Appl

ALIGNMENTS

RESULT 1
US-09-010-317-96
Sequence 96, Application US/09010317
Patent No. 6685943
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
APPLICANT: Patti, Joseph M.
APPLICANT: House-Pompeo, Karen L.
APPLICANT: Speziale, Pietro
APPLICANT: Joh, Danny
APPLICANT: McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
TITLE OF INVENTION: AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/010.317
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TMMK.189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 96:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-09-010-317-96
Query Match 100.0%; Score 59; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.00013;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PSYFGGSHS 10
Db 1 PSYFGGSHS 10

RESULT 2
US-08-234-622A-1
; Sequence 1, Application US/08234622A
; Patent No. 544014
; GENERAL INFORMATION:
; APPLICANT: HOOK, Magnus
; APPLICANT: MCGAVIN, Martin
; APPLICANT: RAUCCI, Giuseppe
; TITLE OF INVENTION: A FIBRONECTIN BINDING PEPTIDE
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Doane, Swecker & Mathis
; STREET: P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/234,622A
; FILING DATE: 28-APR-1994
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: SE 9002617-0
; FILING DATE: 10-AUG-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/SE91/00534
; FILING DATE: 09-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Meuth, Donna M
; REGISTRATION NUMBER: 36,607
; REFERENCE/DOCKET NUMBER: 012885-044
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 19 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1
; OTHER INFORMATION: /note= "Amino acid 1 is R' wherein
; OTHER INFORMATION: R' is hydrogen, K or DK."
; NAME/KEY: Peptide
; LOCATION: 19
; OTHER INFORMATION: /note= "Amino acid 19 is R2 wherein
; OTHER INFORMATION: R2 is hydroxy, L, LP or LPK."
US-08-234-622A-1

Query Match 100.0%; Score 59; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. NO. 0.00026; Indels 0; Gaps 0;
Matches 10; Conservative 0; Mismatches 0;

Qy 1 PSYFGGSHS 10
Db 2 PSYFGGSHS 11

RESULT 3

US-09-010-317-9
; Sequence 9, Application US/09010317
; Patent No. 6685943
; GENERAL INFORMATION:
; APPLICANT: HOOK, Magnus
; APPLICANT: Patti, Joseph M.
; APPLICANT: House-Pompeo, Karen L.
; APPLICANT: Speciale, Pietro
; APPLICANT: Joh, Danny
; APPLICANT: McGavin, Martin J.
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
; NUMBER OF SEQUENCES: 105
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: TX
; COUNTRY: USA
; ZIP: 77210-4433
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/010,317
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/036,139
; FILING DATE: 21-JAN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Hibler, David W.
; REGISTRATION NUMBER: 41,071
; REFERENCE/DOCKET NUMBER: TANK:189
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 512-418-3000
; TELEFAX: 512-474-7577
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
US-09-010-317-9

Query Match 100.0%; Score 59; DB 4; Length 21;
Best Local Similarity 100.0%; Pred. NO. 0.00029; Indels 0; Gaps 0;
Matches 10; Conservative 0; Mismatches 0;

Qy 1 PSYFGGSHS 10
Db 2 PSYFGGSHS 11

RESULT 4
US-09-010-317-14
; Sequence 14, Application US/09010317
; Patent No. 6685943
; GENERAL INFORMATION:
; APPLICANT: Hook, Magnus
; APPLICANT: Patti, Joseph M.
; APPLICANT: House-Pompeo, Karen L.
; APPLICANT: Speciale, Pietro
; APPLICANT: Joh, Danny
; APPLICANT: McGavin, Martin J.
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
; NUMBER OF SEQUENCES: 105
; CORRESPONDENCE ADDRESS:

ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAMK.189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-09-010-317-14

Query Match 100.0%; Score 59; DB 4; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.00029;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PSYQFGHNS 10
|||
Db 2 PSYQFGHNS 11

RESULT 5
US-09-010-317-24
Sequence 24, Application US/09010317
Patent No. 6685943
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
APPLICANT: Patti, Joseph M.
APPLICANT: House-Pompeo, Karen L.
APPLICANT: Speziale, Pietro
APPLICANT: Joh, Danny
APPLICANT: McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAMK.189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-09-010-317-24

Query Match 100.0%; Score 59; DB 4; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.00029;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PSYQFGHNS 10
|||
Db 2 PSYQFGHNS 11

RESULT 6
US-09-010-317-25
Sequence 25, Application US/09010317
Patent No. 6685943
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
APPLICANT: Patti, Joseph M.
APPLICANT: House-Pompeo, Karen L.
APPLICANT: Speziale, Pietro
APPLICANT: Joh, Danny
APPLICANT: McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAMK.189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-09-010-317-25

Query Match	100.0%;	Score 59;	DB 4;	Length 21;
Best Local Similarity	100.0%;	Pred. No. 0.00029;		
Matches 10;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

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QY      1 PSYQFGGHS 10
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Db      2 PSYQFGGHS 11

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RESULT 7
US-09-010-317-26
; Sequence 26, Application US/09010317
; Patent No. 6685943
; GENERAL INFORMATION:
; APPLICANT: Hook, Magnus
; APPLICANT: Patti, Joseph M.
; APPLICANT: House-Pompeo, Karen L.
; APPLICANT: Speziale, Pietro
; APPLICANT: Joh, Danny
; APPLICANT: McGavin, Martin J.
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
; TITLE OF INVENTION: AND METHODS OF USE
; NUMBER OF SEQUENCES: 105
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: TX
; COUNTRY: USA
; ZIP: 77210-4433
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/010,317
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/036,139
; FILING DATE: 21-JAN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Hibley, David W.
; REGISTRATION NUMBER: 41,071
; REFERENCE/DOCKET NUMBER: TAMK:189
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 512-418-3000
; TELEFAX: 512-474-7577
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: 1linear
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US-09-010-317-26
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; Query Match 100.0%; Score 59; DB 4; Length 21;
; Best Local Similarity 100.0%; Pred. No. 0.00029;
; Matches 10; Conservative 0; Mismatches 0; Indels 0
;
OY 1 PSYFGGHNH 10
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| | | | | | | |
Db 2 PSYFGGHNH 11

```

```

1  APPLICANT: Patti, Joseph M.
2  APPLICANT: House-Pompeo, Karen L.
3  APPLICANT: Speciale, Pietro
4  APPLICANT: Joh, Danny
5  APPLICANT: McGeavin, Martin J.
6  TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
7  TITLE OF INVENTION: AND METHODS OF USE
8  NUMBER OF SEQUENCES: 105
9  CORRESPONDENCE ADDRESS:
10 ADDRESS: Arnold, White & Durkee
11 STREET: P.O. Box 4433
12 CITY: Houston
13 STATE: TX
14 COUNTRY: USA
15 ZIP: 77210-4433
16 COMPUTER READABLE FORM:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/010.317
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TANK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-09-010-317-28

Query Match 100.0%; Score 59; DB 4; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.00029;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PSYOGGSHNS 10
Db 2 PSYOGGSHNS 11

RESULT 10
US-09-010-317-29
Sequence 29, Application US/09010317
Patent No. 6685943
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
APPLICANT: Patil, Joseph M.
APPLICANT: House-Pompeo, Karen L.
APPLICANT: Speziale, Pietro
APPLICANT: Job, Danny
APPLICANT: McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
TITLE OF INVENTION: AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/010.317
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TANK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-09-010-317-30

TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 29:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-09-010-317-29

Query Match 100.0%; Score 59; DB 4; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.00029;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PSYOGGSHNS 10
Db 2 PSYOGGSHNS 11

RESULT 11
US-09-010-317-30
Sequence 30, Application US/09010317
Patent No. 6685943
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
APPLICANT: Patil, Joseph M.
APPLICANT: House-Pompeo, Karen L.
APPLICANT: Speziale, Pietro
APPLICANT: Job, Danny
APPLICANT: McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
TITLE OF INVENTION: AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/010.317
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TANK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-09-010-317-30

Query Match 100.0%; Score 59; DB 4; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.00029;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PSYOGGSHNS 10
Db 2 PSYOGGSHNS 11

Db 2 PSYQFGHNS 11

RESULT 12

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US-09-010-317-31
; Sequence 31, Application US/09010317
; Patent No. 6685943
; GENERAL INFORMATION:
; APPLICANT: Hook, Magnus
; APPLICANT: Patti, Joseph M.
; APPLICANT: House-Pompeo, Karen L.
; APPLICANT: Speciale, Pietro
; APPLICANT: Joh, Danny
; APPLICANT: McGavin, Martin J.
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
; TITLE OF INVENTION: AND METHODS OF USE
; NUMBER OF SEQUENCES: 105
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: TX
; COUNTRY: USA
; ZIP: 77210-4433
; COMPUTER READABLE FORM:
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; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
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; APPLICATION NUMBER: US/09/010,317
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/036,139
; FILING DATE: 21-JAN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Hibler, David W.
; REGISTRATION NUMBER: 41,071
; REFERENCE/DOCKET NUMBER: TANK:189
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 512-418-3000
; TELEFAX: 512-474-7577
; INFORMATION FOR SEQ ID NO: 31:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; US-09-010-317-31

Query Match 100.0%; Score 59; DB 4; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.00029;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 1 PSYQFGHNS 10
Db 2 PSYQFGHNS 11

RESULT 13

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US-09-010-317-32
; Sequence 32, Application US/09010317
; Patent No. 6685943
; GENERAL INFORMATION:
; APPLICANT: Hook, Magnus
; APPLICANT: Patti, Joseph M.
; APPLICANT: House-Pompeo, Karen L.
; APPLICANT: Speciale, Pietro
; APPLICANT: Joh, Danny
; APPLICANT: McGavin, Martin J.
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
; TITLE OF INVENTION: AND METHODS OF USE
```

NUMBER OF SEQUENCES: 105

CORRESPONDENCE ADDRESS:

ADDRESSEE: Arnold, White & Durkee

STREET: P.O. Box 4433

CITY: Houston

STATE: TX

COUNTRY: USA

ZIP: 77210-4433

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/010,317

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 60/036,139

FILING DATE: 21-JAN-1997

ATTORNEY/AGENT INFORMATION:

NAME: Hibler, David W.

REGISTRATION NUMBER: 41,071

REFERENCE/DOCKET NUMBER: TANK:189

TELECOMMUNICATION INFORMATION:

TELEPHONE: 512-418-3000

TELEFAX: 512-474-7577

INFORMATION FOR SEQ ID NO: 32:

SEQUENCE CHARACTERISTICS:

LENGTH: 21 amino acids

TYPE: amino acid

STRANDEDNESS:

TOPOLOGY: linear

Qy 1 PSYQFGHNS 10
Db 2 PSYQFGHNS 11

RESULT 14

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US-09-010-317-33
; Sequence 33, Application US/09010317
; Patent No. 6685943
; GENERAL INFORMATION:
; APPLICANT: Hook, Magnus
; APPLICANT: Patti, Joseph M.
; APPLICANT: House-Pompeo, Karen L.
; APPLICANT: Speciale, Pietro
; APPLICANT: Joh, Danny
; APPLICANT: McGavin, Martin J.
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
; TITLE OF INVENTION: AND METHODS OF USE
; NUMBER OF SEQUENCES: 105
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: TX
; COUNTRY: USA
; ZIP: 77210-4433
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/010,317
; FILING DATE:
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CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAMK.189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-09-010-317-33

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Query Match      100.0%; Score 59; DB 4; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.00029;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      1 PSYQFGGHNS 10
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        2 PSYQFGGHNS 11

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RESULT 15
US-08-234-622A-4
Sequence 4, Application US/08234622A
Patent No. 5440014
GENERAL INFORMATION:
APPLICANT: HOOK, Magnus
APPLICANT: MCGAVIN, Martin
APPLICANT: RAUCCI, Giuseppe
TITLE OF INVENTION: A FIBRONECTIN BINDING PEPTIDE
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Burns, Doane, Swecker & Mathis
STREET: P.O. Box 1404
CITY: Alexandria
STATE: Virginia
COUNTRY: United States
ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/234,622A
FILING DATE: 28-APR-1994
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: SE 9002617-0
FILING DATE: 10-AUG-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/SE91/00534
FILING DATE: 09-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: Meuth, Donna M
REGISTRATION NUMBER: 36,607
REFERENCE/DOCKET NUMBER: 012885-044
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 37 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear

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MOLECULE TYPE: peptide
US-08-234-622A-4

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Query Match      100.0%; Score 59; DB 1; Length 37;
Best Local Similarity 100.0%; Pred. No. 0.00052;
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Job time : 18.2989 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 22, 2005, 12:39:57 ; Search time 56.1494 Seconds
(without alignments)
74.354 Million cell updates/sec

Title: US-10-731-238-96
Perfect score: 59
Sequence: 1 PSYQFGGHS 10

Scoring table: BIOSM62
Gapop 10.0 , Gapext 0.5

Searched: 1862951 seqs, 417491010 residues
Total number of hits satisfying chosen parameters: 1862951

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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22: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	59	100.0	21	US-10-731-238-9	Sequence 9, Appl
3	59	100.0	21	US-10-731-238-14	Sequence 14, Appl
4	59	100.0	21	US-10-731-238-24	Sequence 24, Appl
5	59	100.0	21	US-10-731-238-25	Sequence 25, Appl
6	59	100.0	21	US-10-731-238-26	Sequence 26, Appl
7	59	100.0	21	US-10-731-238-27	Sequence 27, Appl
8	59	100.0	21	US-10-731-238-28	Sequence 28, Appl
9	59	100.0	21	US-10-731-238-29	Sequence 29, Appl
10	59	100.0	21	US-10-731-238-30	Sequence 30, Appl
11	59	100.0	21	US-10-731-238-31	Sequence 31, Appl

12	59	100.0	21	US-10-731-238-32	Sequence 32, Appl
13	59	100.0	21	US-10-731-238-33	Sequence 33, Appl
14	59	100.0	37	US-11-066-697-1134	Sequence 1134, Ap
15	59	100.0	139	US-09-813-820-8	Sequence 8, Appl
16	59	100.0	1018	US-09-815-242-5797	Sequence 5797, Ap
17	59	100.0	1018	US-09-815-242-12838	Sequence 12838, A
18	59	100.0	1018	US-10-470-048B-68	Sequence 68, Appl
19	59	100.0	1027	US-08-781-986A-5254	Sequence 5254, Ap
20	59	100.0	1027	US-10-329-624-5254	Sequence 5254, Ap
21	56	94.9	388	US-08-901-062-1	Sequence 1, Appl
22	56	94.9	559	US-08-781-986A-5251	Sequence 5251, Ap
23	56	94.9	559	US-10-329-624-5251	Sequence 5251, Ap
24	56	94.9	940	US-10-470-048B-424	Sequence 424, Ap
25	56	94.9	948	US-10-470-048B-69	Sequence 69, Appl
26	56	94.9	961	US-10-282-122A-43778	Sequence 43778, A
27	56	94.9	978	US-09-815-242-5456	Sequence 5456, Ap
28	56	94.9	1001	US-09-815-242-12686	Sequence 12686, A
29	56	94.9	1038	US-10-282-122A-43827	Sequence 43827, A
30	55	93.2	21	US-10-731-238-23	Sequence 23, Appl
31	54	91.5	21	US-10-731-238-16	Sequence 16, Appl
32	53	89.8	21	US-10-731-238-18	Sequence 18, Appl
33	52	88.1	21	US-10-731-238-15	Sequence 15, Appl
34	51	86.4	21	US-10-731-238-10	Sequence 10, Appl
35	51	86.4	21	US-10-731-238-20	Sequence 20, Appl
36	51	86.4	21	US-10-731-238-22	Sequence 22, Appl
37	51	86.4	22	US-10-731-238-13	Sequence 13, Appl
38	49	83.1	10	US-10-731-238-95	Sequence 95, Appl
39	49	83.1	21	US-10-731-238-17	Sequence 17, Appl
40	49	83.1	21	US-10-731-238-19	Sequence 19, Appl
41	49	83.1	21	US-10-731-238-21	Sequence 21, Appl
42	48	81.4	10	US-10-731-238-97	Sequence 97, Appl
43	46	78.0	244	US-10-424-599-180746	Sequence 180746
44	41	69.5	14	US-10-731-238-61	Sequence 61, Appl
45	41	69.5	15	US-10-425-114-57258	Sequence 57258, A

ALIGNMENTS

RESULT 1
US-10-731-238-96
; Sequence 96, Application US/10731238
; Publication No. US2005012552A1
;
; GENERAL INFORMATION:
; APPLICANT: Hook, Magnus
; Patci, Joseph M.
; House-Pompeo, Karen L.
; Speziale, Pietro
; Joh, Danny
; McGavin, Martin J
; TITLE OF INVENTION: FIBROECTIN BINDING PROTEIN COMPOSITIONS
; AND METHODS OF USE
; NUMBER OF SEQUENCES: 105
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: TX
; COUNTRY: USA
; ZIP: 77210-4433
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/731,238
; FILING DATE: 10-Dec-2003
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/010,317
; FILING DATE: 21-Jan-1998
; APPLICATION NUMBER: US 60/036,139

```

1      FILING DATE: 21-JAN-1997
2      ATTORNEY/AGENT INFORMATION:
3      NAME: Hibler, David W.
4      REGISTRATION NUMBER: 41,071
5      REFERENCE/DOCKET NUMBER: TANK:189
6      TELECOMMUNICATION INFORMATION:
7      TELEPHONE: 512-418-3000
8      TELEFAX: 512-474-7577
9      INFORMATION FOR SEQ ID NO: 96:
10     SEQUENCE CHARACTERISTICS:
11     LENGTH: 10 amino acids
12     TYPE: amino acid
13     STRANDEDNESS: <Unknown>
14     TOPOLOGY: linear
15     US-10-731-238-96
16
17     SEQUENCE DESCRIPTION: SEQ ID NO: 96:
18
19     Query Match      100.0%; Score 59; DB 18; Length 10;
20     Best Local Similarity 100.0%; Pred. No. 0.00088;
21     Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0.
22
23
24     Oy      1 PSYOGGCHNS 10
25             |||||
26     Db      1 PSYOGGCHNS 10
27
28
29 RESULT 2
30 US-10-731-238-9
31 Sequence 9, Application US/10731238
32 Publication No. US20050123552A1
33 GENERAL INFORMATION:
34 APPLICANT: Hook, Magnus
35          Pati, Joseph M.
36          House-Pompeo, Karen L.
37          Speziale, Pietro
38          Joh, Danny
39          McGarlin, Martin J.
40 TITLE OF INVENTION: FIBROBLAST BINDING PROTEIN COMPOSITIONS
41 AND METHODS OF USE
42 NUMBER OF SEQUENCES: 105
43 CORRESPONDENCE ADDRESS:
44 ADDRESSEE: Arnold, White & Durkee
45 STREET: P.O. Box 4433
46 CITY: Houston
47 STATE: TX
48 COUNTRY: USA
49 ZIP: 77210-4433
50 COMPUTER READABLE FORM:
51 MEDIUM TYPE: floppy disk
52 COMPUTER: IBM PC compatible
53 OPERATING SYSTEM: PC-DOS/MS-DOS
54 SOFTWARE: PatentIn Release #1.0, Version #1.30
55 CURRENT APPLICATION DATA:
56 APPLICATION NUMBER: US/10/731,238
57 FILING DATE: 10-Dec-2003
58 CLASSIFICATION: <Unknown>
59 PRIOR APPLICATION DATA:
60 APPLICATION NUMBER: US/09/010,317
61 FILING DATE: 21-Jan-1998
62 APPLICATION NUMBER: US 60/036,139
63 FILING DATE: 21-JAN-1997
64 ATTORNEY/AGENT INFORMATION:
65 NAME: Hibler, David W.
66 REGISTRATION NUMBER: 41,071
67 REFERENCE/DOCKET NUMBER: TANK:189
68 TELECOMMUNICATION INFORMATION:
69 TELEPHONE: 512-418-3000
70 TELEFAX: 512-474-7577
71 INFORMATION FOR SEQ ID NO: 9:
72 SEQUENCE CHARACTERISTICS:
73 LENGTH: 21 amino acids
74 TYPE: amino acid
75 STRANDEDNESS: <Unknown>

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?          TOPOLOGY: linear
?          SEQUENCE DESCRIPTION: SEQ ID NO: 9:
US-10-731-238-9

Query Match      100.0%; Score 59; DB 18; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.0018;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      1 PSYOGGCHNS 10
        |||||
        2 PSYOGGCHNS 11

Db

RESULT 3
US-10-731-238-14
: Sequence 14, Application US/10731238
: Publication No. US20050123552A1
: GENERAL INFORMATION:
: APPLICANT: Hook, Magnus
:       Patti, Joseph M.
:       House-Pompeo, Karen L.
:       Speziale, Pietro
:       Joh, Danny
:       McGavin, Martin J.
: TITLE OF INVENTION: FIBROECTIN BINDING PROTEIN COMPOSITIONS
: AND METHODS OF USE
: NUMBER OF SEQUENCES: 105
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Arnold, White & Durkee
: STREET: P.O. Box 4433
: CITY: Houston
: STATE: TX
: COUNTRY: USA
: ZIP: 77210-4433
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/10/731,238
: FILING DATE: 10-Dec-2003
: CLASSIFICATION: <Unknown>
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US/09/010,317
: FILING DATE: 21-Jan-1998
: APPLICATION NUMBER: US 60/036,139
: FILING DATE: 21-JAN-1997
: ATTORNEY/AGENT INFORMATION:
: NAME: Hihler, David W.
: REGISTRATION NUMBER: 41,071
: REFERENCE/DOCKET NUMBER: TMMK:189
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 512-474-3000
: TELEFAX: 512-474-7577
: INFORMATION FOR SEQ ID NO: 14:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 21 amino acids
: TYPE: amino acid
: STRANDEDNESS: <Unknown>
: TOPOLOGY: linear
: SEQUENCE DESCRIPTION: SEQ ID NO: 14:
US-10-731-238-14

Query Match      100.0%; Score 59; DB 18; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.0018;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      1 PSYOGGCHNS 10
        |||||
        2 PSYOGGCHNS 11

Db

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RESULT 4
US-10-731-238-24
; Sequence 24, Application US/10731238
; Publication No. US20050123552A1
; GENERAL INFORMATION:
; APPLICANT: Hook, Magnus
;             Patti, Joseph M.
;             House-Pompeo, Karen L.
;             Speziale, Pietro
;             Joh, Danny
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
; AND METHODS OF USE
; NUMBER OF SEQUENCES: 105
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: TX
; COUNTRY: USA
; ZIP: 77210-4433
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/731,238
; FILING DATE: 10-Dec-2003
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/010,317
; FILING DATE: 21-Jan-1998
; APPLICATION NUMBER: US 60/036,139
; FILING DATE: 21-Jan-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Hibler, David W.
; REGISTRATION NUMBER: 41,071
; REFERENCE/DOCKET NUMBER: TANK:189
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 512-418-3000
; TELEFAX: 512-474-7577
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 24:
US-10-731-238-24

Query Match      100.0%; Score 59; DB 18; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.0018;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      1 PSYOGGHNS 10
        |||||
        2 PSYOGGHNS 11

Db

RESULT 5
US-10-731-238-25
; Sequence 25, Application US/10731238
; Publication No. US20050123552A1
; GENERAL INFORMATION:
; APPLICANT: Hook, Magnus
;             Patti, Joseph M.
;             House-Pompeo, Karen L.
;             Speziale, Pietro
;             Joh, Danny
;             McGavin, Martin J.
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
; AND METHODS OF USE
```

```
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/731,238
FILING DATE: 10-Dec-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE: 21-Jan-1998
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-Jan-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TANK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 25:
US-10-731-238-25

Query Match      100.0%; Score 59; DB 18; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.0018;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      1 PSYOGGHNS 10
        |||||
        2 PSYOGGHNS 11

Db

RESULT 6
US-10-731-238-26
; Sequence 26, Application US/10731238
; Publication No. US20050123552A1
; GENERAL INFORMATION:
; APPLICANT: Hook, Magnus
;             Patti, Joseph M.
;             House-Pompeo, Karen L.
;             Speziale, Pietro
;             Joh, Danny
;             McGavin, Martin J.
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
; AND METHODS OF USE
; NUMBER OF SEQUENCES: 105
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: TX
; COUNTRY: USA
; ZIP: 77210-4433
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
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;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/731.238
; FILING DATE: 10-Dec-2003
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/010.317
; FILING DATE: 21-Jan-1998
; APPLICATION NUMBER: US 60/036.139
; FILING DATE: 21-JAN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Hibler, David W.
; REGISTRATION NUMBER: 41,071
; REFERENCE/DOCKET NUMBER: TAMK:189
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 512-418-3000
; TELEFAX: 512-474-7577
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 26:
US-10-731-238-26

Query Match      100.0%; Score 59; DB 18; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.0018;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 PSYQFGGHS 10
        |||||
        2 PSYQFGGHS 11

RESULT 7
US-10-731-238-27
; Sequence 27, Application US/10731238
; Publication No. US20050123552A1
; GENERAL INFORMATION:
; APPLICANT: Hook, Magnus
;          Patti, Joseph M.
;          House-Pompeo, Karen L.
;          Speciale, Pietro
;          Joh, Danny
;          McGavin, Martin J.
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
; NUMBER OF SEQUENCES: 105
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: TX
; COUNTRY: USA
; ZIP: 77210-4433
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/731.238
; FILING DATE: 10-Dec-2003
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/010.317
; FILING DATE: 21-Jan-1998
; APPLICATION NUMBER: US 60/036.139
; FILING DATE: 21-JAN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Hibler, David W.
; REGISTRATION NUMBER: 41,071
; REFERENCE/DOCKET NUMBER: TAMK:189
```

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;
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 512-418-3000
; TELEFAX: 512-474-7577
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 27:
US-10-731-238-27

Query Match      100.0%; Score 59; DB 18; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.0018;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 PSYQFGGHS 10
        |||||
        2 PSYQFGGHS 11

Db

RESULT 8
US-10-731-238-28
; Sequence 28, Application US/10731238
; Publication No. US20050123552A1
; GENERAL INFORMATION:
; APPLICANT: Hook, Magnus
;          Patti, Joseph M.
;          House-Pompeo, Karen L.
;          Speciale, Pietro
;          Joh, Danny
;          McGavin, Martin J.
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
; AND METHODS OF USE
; NUMBER OF SEQUENCES: 105
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: TX
; COUNTRY: USA
; ZIP: 77210-4433
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/731.238
; FILING DATE: 10-Dec-2003
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/010.317
; FILING DATE: 21-Jan-1998
; APPLICATION NUMBER: US 60/036.139
; FILING DATE: 21-JAN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Hibler, David W.
; REGISTRATION NUMBER: 41,071
; REFERENCE/DOCKET NUMBER: TAMK:189
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 512-418-3000
; TELEFAX: 512-474-7577
; INFORMATION FOR SEQ ID NO: 28:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 28:
US-10-731-238-28

Query Match      100.0%; Score 59; DB 18; Length 21;
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Best Local Similarity 100.0%; Pred. No. 0.0018;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PSYQFGHNS 10
Db 2 PSYQFGHNS 11

RESULT 9

US-10-731-238-29

; Sequence 29, Application US/10731238
; Publication No. US20050123552A1
; GENERAL INFORMATION:

APPLICANT: Hook, Magnus

Patti, Joseph M.
House-Pompeo, Karen L.
Speziale, PietroJohn, Danny
McGavin, Martin J.TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
AND METHODS OF USE

NUMBER OF SEQUENCES: 105

CORRESPONDENCE ADDRESS:

ADDRESSEE: Arnold, White & Durkee

STREET: P.O. Box 4433

CITY: Houston

STATE: TX

COUNTRY: USA

ZIP: 77210-4433

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/731,238

FILING DATE: 10-Dec-2003

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/010,317

FILING DATE: 21-Jan-1998

APPLICATION NUMBER: US 60/036,139

FILING DATE: 21-JAN-1997

ATTORNEY/AGENT INFORMATION:

NAME: Hibler, David W.

REGISTRATION NUMBER: 41,071

REFERENCE/DOCKET NUMBER: TANK:189

TELECOMMUNICATION INFORMATION:

TELEPHONE: 512-418-3000

TELEFAX: 512-474-7577

INFORMATION FOR SEQ ID NO: 29:

SEQUENCE CHARACTERISTICS:

LENGTH: 21 amino acids

TYPE: amino acid

STRANDEDNESS: <Unknown>

TOPOLOGY: linear

SEQUENCE DESCRIPTION: SEQ ID NO: 29:

Query Match 100.0%; Score 59; DB 18; Length 21;

Best Local Similarity 100.0%; Pred. No. 0.0018;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PSYQFGHNS 10

Db 2 PSYQFGHNS 11

RESULT 10

US-10-731-238-30

; Sequence 30, Application US/10731238
; Publication No. US20050123552A1
; GENERAL INFORMATION:

APPLICANT: Hook, Magnus

Patti, Joseph M.
House-Pompeo, Karen L.
Speziale, PietroJohn, Danny
McGavin, Martin J.TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
AND METHODS OF USE

NUMBER OF SEQUENCES: 105

CORRESPONDENCE ADDRESS:

ADDRESSEE: Arnold, White & Durkee

STREET: P.O. Box 4433

CITY: Houston

STATE: TX

COUNTRY: USA

ZIP: 77210-4433

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/731,238

FILING DATE: 10-Dec-2003

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/010,317

FILING DATE: 21-Jan-1998

APPLICATION NUMBER: US 60/036,139

FILING DATE: 21-JAN-1997

ATTORNEY/AGENT INFORMATION:

NAME: Hibler, David W.

REGISTRATION NUMBER: 41,071

REFERENCE/DOCKET NUMBER: TANK:189

TELECOMMUNICATION INFORMATION:

TELEPHONE: 512-418-3000

TELEFAX: 512-474-7577

INFORMATION FOR SEQ ID NO: 30:

SEQUENCE CHARACTERISTICS:

LENGTH: 21 amino acids

TYPE: amino acid

STRANDEDNESS: <Unknown>

TOPOLOGY: linear

SEQUENCE DESCRIPTION: SEQ ID NO: 30:

Query Match 100.0%; Score 59; DB 18; Length 21;

Best Local Similarity 100.0%; Pred. No. 0.0018;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PSYQFGHNS 10

Db 2 PSYQFGHNS 11

RESULT 11

US-10-731-238-31

; Sequence 31, Application US/10731238
; Publication No. US20050123552A1
; GENERAL INFORMATION:

APPLICANT: Hook, Magnus

Patti, Joseph M.
House-Pompeo, Karen L.
Speziale, PietroJohn, Danny
McGavin, Martin J.TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
AND METHODS OF USE

NUMBER OF SEQUENCES: 105

CORRESPONDENCE ADDRESS:

ADDRESSEE: Arnold, White & Durkee

STREET: P.O. Box 4433

CITY: Houston

STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/731,238
FILING DATE: 10-Dec-2003
CLASSIFICATION: <Unknown>
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE: 21-Jan-1998
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAMK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 31:
US-10-731-238-31
Query Match 100.0%; Score 59; DB 18; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.0018;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 PSYQFGHNS 10
Db 2 PSYQFGHNS 11
RESULT 12
US-10-731-238-32
Sequence 32, Application US/10731238
Publication No. US20050123552A1
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
Patli, Joseph M.
House-Pompeo, Karen L.
Speziale, Pietro
Joh, Danny
McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/731,238
FILING DATE: 10-Dec-2003
CLASSIFICATION: <Unknown>
PRIORITY APPLICATION DATA:

APPLICATION NUMBER: US/09/010,317
FILING DATE: 21-Jan-1998
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAMK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 32:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 32:
US-10-731-238-32
Query Match 100.0%; Score 59; DB 18; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.0018;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 PSYQFGHNS 10
Db 2 PSYQFGHNS 11
RESULT 13
US-10-731-238-33
Sequence 33, Application US/10731238
Publication No. US20050123552A1
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
Patli, Joseph M.
House-Pompeo, Karen L.
Speziale, Pietro
Joh, Danny
McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/731,238
FILING DATE: 10-Dec-2003
CLASSIFICATION: <Unknown>
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE: 21-Jan-1998
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAMK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:

LENGTH: 21 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 33:
US-10-731-238-33

Query Match 100.0%; Score 59; DB 18; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.0018;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PSYQFGGHS 10
DB 2 PSYQFGGHS 11

RESULT 14
US-11-066-697-1134
Sequence 1134, Application US/11066697
Publication No. US20050187159A1
GENERAL INFORMATION:
APPLICANT: Bridon, Dominique P.
APPLICANT: Ezrin, Alan M.
APPLICANT: Milner, Peter G.
APPLICANT: Holmes, Darren L.
APPLICANT: Thibadeau, Karen
TITLE OF INVENTION: PROTECTION OF ENDOGENOUS THERAPEUTIC PEPTIDES FROM
TITLE OF INVENTION: PEPTIDASE ACTIVITY THROUGH CONJUGATION TO BLOOD
TITLE OF INVENTION: COMPONENTS
FILE REFERENCE: 500862002301
CURRENT APPLICATION NUMBER: US/11/066,697
CURRENT FILING DATE: 2005-02-25
PRIOR APPLICATION NUMBER: 09/657,276
PRIOR FILING DATE: 2000-09-07
PRIOR APPLICATION NUMBER: 60/153,406
PRIOR FILING DATE: 1999-09-10
PRIOR APPLICATION NUMBER: 60/159,783
PRIOR FILING DATE: 1999-10-15
NUMBER OF SEQ ID NOS: 1617
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1134
LENGTH: 37
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
OTHER INFORMATION: Peptide
US-11-066-697-1134

Query Match 100.0%; Score 59; DB 20; Length 37;
Best Local Similarity 100.0%; Pred. No. 0.0032;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PSYQFGGHS 10
DB 17 PSYQFGGHS 26

RESULT 15
US-09-813-820-8
Sequence 8, Application US/09813820
Patent No. US20020102262A1
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
Patel, Joseph M.
House-Pompeo, Karen
Schanam, Narayana
Symerky, Jindrich
TITLE OF INVENTION: COLLAGEN BINDING PROTEIN COMPOSITIONS
AND METHODS OF USE
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Arnold, White & Durkee

STREET: P.O. Box 4433
CITY: Houston
STATE: Texas
COUNTRY: U.S.
ZIP: 77210
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/813,820
FILING DATE: 22-Mar-2001
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/856,253
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Kirchell, Barbara S.
REGISTRATION NUMBER: 33,928
REFERENCE/DOCKET NUMBER: TAWK:193
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
TELEFAX: (512) 474-7577
INFORMATION FOR SEQ ID NO: 8:

SEQUENCE CHARACTERISTICS:
LENGTH: 139 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-09-813-820-8

Query Match 100.0%; Score 59; DB 9; Length 139;
Best Local Similarity 100.0%; Pred. No. 0.012;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PSYQFGGHS 10
DB 108 PSYQFGGHS 117

Search completed: October 22, 2005, 12:56:28
Job time : 56.1494 secs

This Page Blank (uspto)

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 22, 2005, 08:04:46 ; Search time 11.6092 Seconds
(without alignments)
82.880 Million cell updates/sec

Title: US-10-731-238-96

Perfect score: 59

Sequence: 1 PSYQFGHNS 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	59	100.0	1018	2	A32192 fibronectin-binding
2	56	94.9	940	2	S19702 fibronectin-binding
3	56	94.9	961	2	G90053 hypothetical prote
4	56	94.9	1038	2	H90053 hypothetical prote
5	45	76.3	1322	2	A59288 myosin heavy chain
6	41	69.5	416	2	C72020 3-oxoacyl-(acyl)-ca
7	41	69.5	416	2	B86605 acyl carrier prote
8	41	69.5	418	2	G81735 3-oxoacyl-(acyl)-ca
9	41	69.5	418	2	E71473 probable acyl carr
10	41	69.5	462	1	A39356 3-oxoacyl-[acyl]-ca
11	41	69.5	469	2	T10061 3-oxoacyl-[acyl]-ca
12	41	69.5	489	1	S47076 3-oxoacyl-[acyl]-ca
13	41	69.5	495	1	S47074 3-oxoacyl-[acyl]-ca
14	41	69.5	535	2	T10055 probable 3-oxoacyl
15	41	69.5	541	2	D96779 probable 3-ketoacy
16	39	66.1	402	2	S74525 hypothetical prote
17	38	64.4	291	2	T08557 hypothetical prote
18	38	64.4	406	2	D97147 3-oxoacyl-(acyl)-ca
19	38	64.4	413	2	A11349 3-oxoacyl-(acyl)-car
20	38	64.4	413	2	A01720 3-oxoacyl-(acyl)-car
21	37	62.7	40	2	P00533 3-oxoacyl-[acyl]-ca
22	37	62.7	407	2	A60524 conserved hypotnet
23	37	62.7	412	2	C72335 3-oxoacyl-(acyl) ca
24	37	62.7	414	2	T44711 beta-ketoacyl-ACP
25	37	62.7	416	2	S74664 3-oxoacyl-[acyl]-ca
26	37	62.7	416	2	A87116 3-oxoacyl-[acyl]-ca
27	37	62.7	416	2	A70779 probable kasa prot
28	37	62.7	416	2	AH2223 3-oxoacyl-[acyl]-ca
29	37	62.7	423	2	T11214 3-oxoacyl-[acyl]-ca

30	37	62.7	425	2	T44710 beta-ketoacyl-ACP
31	37	62.7	438	2	B70779 probable kasa prot
32	37	62.7	362	2	T01688 starch debranching
33	36	61.0	391	2	F71702 hypothetical prote
34	36	61.0	764	2	3-oxoacyl-(acyl)-ca
35	36	61.0	921	2	F84593 hypothetical prote
36	36	61.0	1274	2	I40813 neurotoxin type F
37	35	59.3	151	2	S70788 curlin protein csg
38	35	59.3	152	2	D90806 curlin major subun
39	35	59.3	152	2	H85665 hypothetical prote
40	35	59.3	162	2	C89838 conserved hypotnet
41	35	59.3	200	2	A83566 probable bacteriop
42	35	59.3	206	2	AH0259 probable phage tail
43	35	59.3	287	2	S42144 ribosomal protein
44	35	59.3	392	2	A69474 myo-inositol-1-pho
45	35	59.3	411	2	H95048 3-oxoacyl-(acyl)-ca

ALIGNMENTS

RESULT 1
A32192
fibronectin-binding protein B - Staphylococcus aureus
C:Species: Staphylococcus aureus
C:Date: 31-Jul-1989 #sequence_revision 31-Jul-1989 #text_change 16-Feb-1997
C:Accession: A32192
R:Signaes, C.; Raucel, G.; Joensson, K.; Lindgren, P.E.; Anantharamaiah, G.M.; Hoeoek,
Proc. Natl. Acad. Sci. U.S.A. 86, 699-703, 1989
A:Title: Nucleotide sequence of the gene for a fibronectin-binding protein from Staphy
A:Reference number: A32192; MUID:8908998; PMID:2521391
A:Accession: A32192
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1018 <SIG>
A:Cross-references: GB:J04151
C:Keywords: Fibronectin binding

Query Match 100.0%; Score 59; DB 2; Length 1018;
Best Local Similarity 100.0%; Pred. No. 0.0072;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PSYQFGHNS 10
DB 838 PSYQFGHNS 847

RESULT 2
S19702
fibronectin-binding protein B - Staphylococcus aureus
C:Species: Staphylococcus aureus
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
C:Accession: S19702
R:Joensson, K.; Signaes, C.; Mueller, H.P.; Lindberg, M.
Eur. J. Biochem. 202, 1041-1048, 1991
A:Title: Two different genes encode fibronectin binding proteins in Staphylococcus aure
A:Reference number: S19702; MUID:9211475; PMID:1837266
A:Accession: S19702
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-940 <JOB>
A:Cross-references: UNIPROT:Q53682; EMBL:X62992; NID:949040; PIDD:CAAA4726.1; PID:95815
C:Keywords: fibronectin binding

Query Match 94.9%; Score 56; DB 2; Length 940;
Best Local Similarity 90.0%; Pred. No. 0.024;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 PSYQFGHNS 10
DB 774 PSYQFGHNS 783

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RESULT 3
G90053
hypothetical protein fnbB [imported] - Staphylococcus aureus (strain N315)
C/Species: Staphylococcus aureus
C/Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C/Accession: G90053
R/Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguc
ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.;
C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
A/Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.
A/Reference number: A89758; PMID:21311952; PMID:11418146
A/Accession: G90053
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-961 <RUR>
A/Cross-references: UNIPROT:Q99RD3; GB:BA000018; PID:g13702452; PIDN:BA843593.1; GSPDB:G
A/Experimental source: strain N315
C/Genetics:
A/Gene: fnbB

Query Match          94.9%; Score 56; DB 2; Length 961;
Best Local Similarity 90.0%; Pred. No. 0.025;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 PSYQFGGHS 10
|:|||||
Db 785 PNYQFGGHS 794

RESULT 4
H90053
hypothetical protein fnb [imported] - Staphylococcus aureus (strain N315)
C/Species: Staphylococcus aureus
C/Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C/Accession: H90053
R/Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguc
ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.;
C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
A/Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.
A/Reference number: A89758; PMID:21311952; PMID:11418146
A/Accession: H90053
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-1038 <KUR>
A/Cross-references: UNIPROT:Q99RD3; GB:BA000018; PID:g13702453; PIDN:BA843594.1; GSPDB:G
A/Experimental source: strain N315
C/Genetics:
A/Gene: fnbB

Query Match          94.9%; Score 56; DB 2; Length 1038;
Best Local Similarity 90.0%; Pred. No. 0.027;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 PSYQFGGHS 10
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Db 834 PNYQFGGHS 843

RESULT 5
A59288
myosin heavy chain Myr 8 - rat
C/Species: Rattus norvegicus (Norway rat)
C/Date: 09-Jun-2000 #sequence_revision 09-Jun-2000 #text_change 09-Jul-2004
C/Accession: A59288
R/Patel, K.G.; Liu, C.; Cameron, P.L.; Cameron, R.S.
submitted to GenBank, November 1999
A/Description: Identification of a Novel Mammalian Myosin Class, XVI, in Developing Brain
A/Reference number: A59288
A/Accession: A59288
A/Status: preliminary; not compared with conceptual translation
A/Gene: fabp
A/Molecule type: mRNA

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A/Residues: 1-1322 <PAT>
A/Cross-references: UNIPROT:Q9OXI0; GB:AF209114; PIDN:AAF20150.1
A/Experimental source: strain Sprague-Dawley; clone KP4; cell type type 1 astrocyte
F:404-1132/Domain: myosin motor domain homology <MMO>

Query Match          76.3%; Score 45; DB 2; Length 1322;
Best Local Similarity 70.0%; Pred. No. 3.9;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 PSYQFGGHS 10
|:|||||
Db 961 PSFKGGGHS 970

RESULT 6
C72020
3-oxoacyl-[acyl-carrier-protein] synthase II CP0950 [imported] - Chlamydia pneumoniae
C/Species: Chlamydia pneumoniae
C/Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004
C/Accession: C72020; G81519
R/Kalman, S.; Mitchell, W.; Marathe, R.; Lammel, C.; Fan, J.; Olinger, L.; Grimwood, J.;
Nature Genet. 21, 385-389, 1999
A/Title: Comparative genomes of Chlamydia pneumoniae and C. trachomatis.
A/Reference number: A72000; PMID:99206606; PMID:10192388
A/Accession: C72020
A/Molecule type: DNA
A/Residues: 1-416 <ARN>
A/Cross-references: UNIPROT:Q9Z6Z0; GB:AE001671; GB:AE001363; NID:g4377226; PIDN:AAD1905
A/Experimental source: strain CW029
R/Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hickey,
C.; Dodson, R.; Gwinn, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salzberg,
Nucleic Acids Res. 28, 1397-1406, 2000
A/Title: Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39.
A/Reference number: A81500; PMID:20150255; PMID:10684935
A/Accession: G81519
A/Molecule type: DNA
A/Residues: 1-416 <REA>
A/Cross-references: GB:AE002253; GB:AE002161; NID:g7189859; PIDN:AAF38732.1; PID:g718986
A/Experimental source: strain AR39, HL cells
C/Genetics:
A/Gene: fabP, CP0950
C/Superfamily: 3-oxoacyl-[acyl-carrier-protein] synthase I; 3-oxoacyl-[acyl-carrier-prot
F:24-411/Domain: 3-oxoacyl-[acyl-carrier-protein] synthase I homology <ONS>

Query Match          69.5%; Score 41; DB 2; Length 416;
Best Local Similarity 77.8%; Pred. No. 6.5;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 SYQFGGHS 10
|:|||||
Db 399 SFGGGS 407

RESULT 7
B86605
acyl carrier protein synthase [imported] - Chlamydia pneumoniae (strain J138)
C/Species: Chlamydia pneumoniae
C/Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C/Accession: B86605
R/Shirai, M.; Hirakawa, H.; Kimoto, M.; Tabuchi, M.; Kishii, F.; Ouchi, K.; Shiba, T.; Is
Nucleic Acids Res. 28, 2311-2314, 2000
A/Title: Comparison of whole genome sequences of chlamydia pneumoniae J138.
A/Reference number: A86491; PMID:20330349; PMID:10871362
A/Accession: B86605
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-416 <STO>
A/Cross-references: UNIPROT:Q9Z6Z0; GB:BA000008; NID:g8579290; PIDN:BA89124.1; GSPDB:GN
A/Experimental source: strain J138
C/Genetics:
A/Gene: fabP
C/Superfamily: 3-oxoacyl-[acyl-carrier-protein] synthase I; 3-oxoacyl-[acyl-carrier-prot

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Query Match 69.5%; Score 41; DB 2; Length 416;
Best Local Similarity 77.8%; Pred. No. 6.5;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 2 SYOFGCHNS 10
|:|||||
Db 399 SFGFGCHNS 407

RESULT 8

G81735
3-oxoacyl-[acyl-carrier-protein] synthase II TC0151 [imported] - Chlamydia muridarum (at
C:Species: Chlamydia muridarum, Chlamydia trachomatis Mopn
C:Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004
C:Accession: G81735
R:Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hickey,
C.; Dodson, R.; Gwinn, M.; Nelson, W.; Deboy, R.; Kolonay, J.; McClarty, G.; Salzberg,
Nucleic Acids Res. 28, 1397-1406, 2000
A:Title: Genome sequences of Chlamydia trachomatis Mopn and Chlamydia pneumoniae AR39.
A:Reference number: A81500; MUID:20150255; PMID:10684935
A:Accession: G81735
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-418 <TET>
A:Cross-references: UNIPROT:Q9PLF3; GB:AE002282; GB:AE002160; NID:97190182; PIDN:AAF3902
A:Experimental source: strain Nigg (MOPn)
C:Genetics:
A:Gene: TC0151
C:Superfamily: 3-oxoacyl-[acyl-carrier-protein] synthase I; 3-oxoacyl-[acyl-carrier-prot
F:24-411/Domain: 3-oxoacyl-[acyl-carrier-protein] synthase I homology <OAS>

Query Match 69.5%; Score 41; DB 2; Length 418;
Best Local Similarity 77.8%; Pred. No. 6.5;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 2 SYOFGCHNS 10
|:|||||
Db 399 SFGFGCHNS 407

RESULT 9
E71473
Probable acyl carrier protein synthase - Chlamydia trachomatis (serotype D, strain UW3/C
C:Species: Chlamydia trachomatis
C:Date: 13-Sep-1998 #sequence_revision 13-Sep-1998 #text_change 09-Jul-2004
C:Accession: E71473
R:Stephens, R.S.; Kalman, S.; Lammel, C.J.; Fan, J.; Marathe, R.; Aravind, L.; Mitchell,
Science 282, 754-759, 1998
A:Title: Genome sequence of an obligate intracellular pathogen of humans: Chlamydia trac
A:Reference number: A71570; MUID:99000809; PMID:9784136
A:Accession: E71473
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-418 <ARN>
A:Cross-references: UNIPROT:O84775; GB:AE001349; GB:AE001273; NID:93329226; PIDN:AA6836
A:Experimental source: serotype D, strain UW-3/Cx
C:Genetics:
A:Gene: FabP
C:Superfamily: 3-oxoacyl-[acyl-carrier-protein] synthase I; 3-oxoacyl-[acyl-carrier-prot
F:24-411/Domain: 3-oxoacyl-[acyl-carrier-protein] synthase I homology <OAS>

Query Match 69.5%; Score 41; DB 2; Length 418;
Best Local Similarity 77.8%; Pred. No. 6.5;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 2 SYOFGCHNS 10
|:|||||
Db 399 SFGFGCHNS 407

RESULT 10
A39356
3-oxoacyl-[acyl-carrier-protein] synthase (EC 2.3.1.41) I beta chain precursor, chlorop

N:Alternate names: beta-ketoacyl-[acyl carrier protein] synthase I
C:Species: Hordeum vulgare (barley)
C:Date: 06-Mar-1992 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
C:Accession: A39356; A45129
R:Siggaard-Andersen, M.; Kauppinen, S.; von Wettstein-Knowles, P.
Proc Natl Acad Sci U S A 88, 4114-4118, 1991
A:Title: Primary structure of a centromere-binding beta-ketoacyl-[acyl carrier protein] (

A:Reference number: A39356; MUID:91239517; PMID:2034657
A:Accession: A39356
A:Molecule type: mRNA
A:Residues: 1-462 <SIG>
A:Cross-references: UNIPROT:P23902; GB:M60410; NID:9167064; PIDN:AAA2968.1; PID:916706;

A:Experimental source: cv. Bonus, leaf
A:Note: parts of this sequence, including the amino end of the mature protein, were con
J. Kauppinen, S.
R. Biol. Chem. 267, 23999-24006, 1992

A:Title: Structure and expression of the Kae12 gene encoding a beta-ketoacyl-acyl carri
A:Reference number: A45129; MUID:93054767; PMID:1429736

A:Accession: A45129
A:Molecule type: DNA
A:Residues: 1-395,397-414,'T',415-462 <KAU>

A:Experimental source: cv. Bonus
A:Note: sequence inconsistent with the nucleotide translation; translation agrees with

A:Note: sequence extracted from NCBI backbone (NCBIP.118934)
C:Genetics:
A:Gene: Kae12
A:Map position: 2
A:Intons: 144/3; 288/3; 346/3; 384/3; 418/3; 441/1

C:Complex: homodimer or heterodimer with alpha chain
C:Superfamily: 3-oxoacyl-[acyl-carrier-protein] synthase I; 3-oxoacyl-[acyl-carrier-pro
C:Keywords: acyltransferase; chloroplast; fatty acid biosynthesis; heterodimer; homodim

F:1-36/Domain: transist peptide (chloroplast) #status predicted <TNP>
F:36-462/Product: 3-oxoacyl-[acyl-carrier-protein] synthase I beta chain #status experi
F:68-457/Domain: 3-oxoacyl-[acyl-carrier-protein] synthase I homology <OAS>

F:213/Active site: Cys #status experimental

Query Match 69.5%; Score 41; DB 1; Length 462;
Best Local Similarity 77.8%; Pred. No. 7.2;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 2 SYOFGCHNS 10
|:|||||
Db 445 SFGFGCHNS 453

RESULT 11

T10061
3-oxoacyl-[acyl-carrier-protein] synthase (EC 2.3.1.41) precursor, chloroplast - castor
N:Alternate names: beta-ketoacyl-[acyl carrier protein] synthase
C:Species: Ricinus communis (castor bean)
C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004
C:Accession: T10061
R:Gene: A.L.
Submitted to the EMBL Data Library, April 1993

A:Description: Cloning and molecular characterisation of B-ketoacyl-ACP synthases from e
A:Reference number: Z16924
A:Accession: T10061

A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: mRNA
A:Residues: 1-469 <GEN>

A:Cross-references: UNIPROT:Q41135; EMBL:L13242; NID:9294667; PID:9294668
C:Genetics:
A:Gene: nuclear

A:Genome: nuclear
C:Function:

A:Pathway: fatty acid biosynthesis
C:Superfamily: 3-oxoacyl-[acyl-carrier-protein] synthase I; 3-oxoacyl-[acyl-carrier-pro
C:Keywords: acyltransferase; chloroplast; fatty acid biosynthesis

F:1-42/Domain: transist peptide (chloroplast) #status predicted <TNP>
F:43-469/Product: 3-oxoacyl-[acyl-carrier-protein] synthase #status predicted <MAT>
F:77-464/Domain: 3-oxoacyl-[acyl-carrier-protein] synthase I homology <OAS>

Query Match 69.5%; Score 41; DB 2; Length 469;
Best Local Similarity 77.8%; Pred. No. 7.3;

Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 2 SYFGGCHNS 10
|:|||||
Db 452 SFGFGCHNS 460

RESULT 12
S47076
3-oxoacyl-[acyl-carrier-protein] synthase (EC 2.3.1.41) precursor [similarity] - barley
C/Species: Hordeum vulgare (barley)
C/Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 09-Jul-2004
C/Accession: S47076
R/Miesenbach, M.
Submitted to the EMBL Data Library, June 1994
A/Description: New members of the barley beta-ketoacyl-ACP synthase (KAS) gene family.
A/Reference number: S47075
A/Accession: S47076
A/Molecule type: mRNA
A/Residues: 1-489 <MIS>
A/Cross-references: UNIPROT:Q40028; EMBL:Z34269; NID:g498741; PIDN:CAA84023.1; PID:g4987
C/Superfamily: 3-oxoacyl-[acyl-carrier-protein] synthase I; 3-oxoacyl-[acyl-carrier-prot
C/Keywords: acyltransferase
F/117-535/Product: probable 3-oxoacyl-[acyl-carrier-protein] synthase I homology <OAS>
F/144-531/Dominant: 3-oxoacyl-[acyl-carrier-protein] synthase I homology <OAS>

Query Match 69.5%; Score 41; DB 1; Length 489;
Best Local Similarity 77.8%; Pred. No. 7.6;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 SYFGGCHNS 10
|:|||||
Db 474 SFGFGCHNS 482

RESULT 13
S47074
3-oxoacyl-[acyl-carrier-protein] synthase (EC 2.3.1.41) precursor [similarity] - barley
C/Species: Hordeum vulgare (barley)
C/Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 09-Jul-2004
C/Accession: S47074; S47075; S47092
R/Miesenbach, M.
Submitted to the EMBL Data Library, June 1994
A/Description: New members of the barley Kae gene family encoding beta-ketoacyl-acyl car
A/Reference number: S47074
A/Accession: S47074
A/Molecule type: mRNA
A/Residues: 1-495 <MIS>
A/Cross-references: UNIPROT:Q40027; EMBL:Z34268; NID:g498739; PIDN:CAA84022.1; PID:g4987
A/Accession: S47075
A/Molecule type: mRNA
A/Residues: 1-416 <M12>
A/Cross-references: EMBL:Z34266
A/Accession: S47092
A/Molecule type: mRNA
A/Residues: 103-495 <M13>
A/Cross-references: EMBL:Z34267
C/Superfamily: 3-oxoacyl-[acyl-carrier-protein] synthase I; 3-oxoacyl-[acyl-carrier-pro
C/Keywords: acyltransferase
F/104-491/Dominant: 3-oxoacyl-[acyl-carrier-protein] synthase I homology <OAS>

Query Match 69.5%; Score 41; DB 1; Length 495;
Best Local Similarity 77.8%; Pred. No. 7.7;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 SYFGGCHNS 10
|:|||||
Db 479 SFGFGCHNS 487

RESULT 14
T10055
probable 3-oxoacyl-[acyl-carrier-protein] synthase (EC 2.3.1.41) precursor, chloroplast
N/Alternate names: beta-ketoacyl-[acyl carrier protein] synthase

C/Species: Ricinus communis (castor bean)
C/Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004
C/Accession: T10055
R/Genez, A.L.
Submitted to the EMBL Data Library, April 1993
A/Description: Cloning and molecular characterisation of B-ketoacyl-ACP synthases from en
A/Reference number: Z16924
A/Accession: T10055
A/Status: translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-535 <GEN>

A/Cross-references: UNIPROT:Q41134; EMBL:L13241; NID:g294665; PID:g294666
C/Function:
A/Pathway: fatty acid biosynthesis
C/Superfamily: 3-oxoacyl-[acyl-carrier-protein] synthase I; 3-oxoacyl-[acyl-carrier-prot
C/Keywords: acyltransferase; chloroplast; fatty acid biosynthesis
F/116/Dominant: transit peptide (chloroplast) #status predicted <TNP>
F/117-535/Product: probable 3-oxoacyl-[acyl-carrier-protein] synthase #status predicted
F/144-531/Dominant: 3-oxoacyl-[acyl-carrier-protein] synthase I homology <OAS>

Query Match 69.5%; Score 41; DB 2; Length 535;
Best Local Similarity 77.8%; Pred. No. 8.4;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 SYFGGCHNS 10
|:|||||
Db 519 SFGFGCHNS 527

RESULT 15
D96779
probable 3-ketoacyl-ACP synthase P9E10.19 [imported] - Arabidopsis thaliana
C/Species: Arabidopsis thaliana (mouse-ear cress)
C/Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C/Accession: D96779
R/Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
Chlin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewart, K.;
ansen, N.F.; Hughes, B.; Hultzar, L.
Nature 408, 816-820, 2000
A/Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
C.A.; Li, J.H.; Li, Y.; Liu, X.; Liu, S.X.; Liu, Z.A.; Luro, J.S.; Malt, R.; Martell,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A/Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A/Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A/Reference number: A66141; MUID:21016719; PMID:11130712
A/Accession: D96779
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-541 <STO>
A/Cross-references: UNIPROT:Q9C9P4; GB:AE005173; NID:g6646768; PIDN:AAF21080.1; GSPDB:GN
C/Genetics:
A/Map position: 1
C/Superfamily: 3-oxoacyl-[acyl-carrier-protein] synthase I; 3-oxoacyl-[acyl-carrier-prot

Query Match 69.5%; Score 41; DB 2; Length 541;
Best Local Similarity 77.8%; Pred. No. 8.5;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 SYFGGCHNS 10
|:|||||
Db 525 SFGFGCHNS 533

Search completed: October 22, 2005, 09:55:47
JDB time : 12.6092 secs

GenCore version 5.1.6
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OM protein - protein search, using SW model

Run on: October 22, 2005, 08:01:06 ; Search time 56.2069 Seconds
(without alignments)
91.106 Million cell updates/sec

Title: US-10-731-238-96
Perfect score: 59
Sequence: 1 PSYQFGGHS 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_03: *
1: uniprot_sprot: *
2: uniprot_trembl: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	59	100.0	1018	1	FNBA STAAU
2	56	94.9	940	2	Q53682 staphylococ
3	56	94.9	943	2	Q8NU8 staphylococ
4	56	94.9	957	2	Q6G6H4 staphylococ
5	56	94.9	961	2	Q99RD3 staphylococ
6	56	94.9	961	2	Q7A3U8 staphylococ
7	56	94.9	965	2	Q6GDU5 staphylococ
8	56	94.9	1015	2	Q8NU7 staphylococ
9	56	94.9	1015	2	Q6G6H3 staphylococ
10	56	94.9	1038	2	Q99RD2 staphylococ
11	56	94.9	1038	2	Q7A3J7 staphylococ
12	55	93.2	152	2	Q9AEP9 staphylococ
13	45	76.3	993	2	Q8BUV4 mus musculu
14	45	76.3	1322	2	Q9QX10 ratius norv
15	45	76.3	1912	2	Q9ERC1 ratius norv
16	41	69.5	169	2	Q9HFP3
17	41	69.5	243	1	S112_ARATH
18	41	69.5	416	2	Q820E2
19	41	69.5	416	2	Q9Z6Z0
20	41	69.5	418	2	Q84775 chlamydia t
21	41	69.5	418	2	Q9PLF3 chlamydia m
22	41	69.5	433	2	Q9M4Z6 brassica na
23	41	69.5	442	2	Q7XUM9
24	41	69.5	456	2	Q94G70
25	41	69.5	462	1	FABB_HORVU
26	41	69.5	465	2	Q69YAZ
27	41	69.5	469	2	Q41135 ricinus com
28	41	69.5	469	2	Q9M507
29	41	69.5	469	2	Q9M508 glycine max
30	41	69.5	473	1	FABB_ARATH
31	41	69.5	474	2	Q48942

ALIGNMENTS

32	41	69.5	488	2	Q82520	082520 capsicum ch
33	41	69.5	488	2	Q9M4Z8	09M4Z8 glycine max
34	41	69.5	489	2	Q40028	Q40028 hordeum vul
35	41	69.5	495	2	Q40027	Q40027 hordeum vul
36	41	69.5	507	2	Q8H3I6	Q8H3I6 oryza sativ
37	41	69.5	517	2	P93117	P93117 cuphea wri
38	41	69.5	530	2	Q48943	Q48943 perilla fru
39	41	69.5	534	2	Q9ZRG4	Q9ZRG4 cuphea hook
40	41	69.5	535	2	Q41134	Q41134 ricinus com
41	41	69.5	538	2	Q949J2	Q949J2 cuphea lanc
42	41	69.5	540	2	P93118	P93118 cuphea wri
43	41	69.5	541	2	Q8RXF5	Q8RXF5 arabidopsis
44	41	69.5	541	2	Q9C9P4	Q9C9P4 arabidopsis
45	41	69.5	546	2	Q9ZRG5	Q9ZRG5 cuphea pulc

RESULT 1
FNBA STAAU STANDARD; PRT; 1018 AA.
ID FNBA STAAU
AC P14738;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Fibronectin-binding protein precursor (FNBP).
GN Name=fnba;
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1280;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NCCTC 8325-4;
RX MEDLINE=89038998; PubMed=2521391;
RA Signaes C., Raucel G., Joensen K., Lindgren P.-E.,
R Mantzarmas G.M., Hoeck M., Lindberg M.;
RT "Nucleotide sequence of the gene for a fibronectin-binding protein
from Staphylococcus aureus: use of this peptide sequence in the
synthesis of biologically active peptides."
RL Proc. Natl. Acad. Sci. U.S.A. 86:699-703(1989).
CC -!- FUNCTION: The ability of bacteria to bind fibronectin has been
proposed as a virulence factor enabling bacteria to colonize wound
tissues and blood clots. Binding of plasma fibronectin to the
bacterial surface might block adhesion receptors on S.aureus, thus
representing an important defense mechanism against tissue
invasion.
CC -!- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
an amide bond (Potential).
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL Outstation -
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See <http://www.ebi.ac.uk/announcements> or
send an email to license@ebi.ac.uk).
CC EMBL: J04151; AAA26632.1; -;
DR InterPro: IPR004237; Fn_bind.
DR InterPro: IPR005877; GPOB_XSIRK.
DR InterPro: IPR001899; Gram_pos_anchor.
DR Pfam: PF02986; Fn_bind. 1.
DR Pfam: PF00746; Gram_pos_anchor. 1.
DR Pfam: PF04650; XSIRK_signal. 1.
DR TIGRfam: TIGR01167; LPXG_anchor. 1.
DR TIGRfam: TIGR01168; XSIRK_signal. 1.
DR PROSITE: PS50847; GRAM_POS_ANCHORING. 1.
KW Cell adhesion; Cell wall; Peptidoglycan-anchor; Repeat; Signal;
FT SIGNAL 1 36
FT CHAIN 37 985
FT PROPEP 986 1018
FT FIBRONECTIN-binding protein.
FT Removed by sortase (Potential).

```

FT REPEAT 545 574 B-1.
FT REPEAT 575 604 B-2.
FT DOMAIN 745 878 4 X approximate tandem repeats,
  fibronectin-binding domain.
FT REPEAT 745 782 D-1.
FT REPEAT 783 820 D-2.
FT REPEAT 821 859 D-3.
FT REPEAT 860 878 D-4 (incomplete).
FT DOMAIN 879 948 5 X tandem repeats, Pro-rich (WR).
FT REPEAT 879 892 WR 1.
FT REPEAT 893 906 WR 2.
FT REPEAT 907 920 WR 3.
FT REPEAT 921 934 WR 4.
FT REPEAT 935 948 WR 5.
FT SITE 982 986 LPXTG sorting signal (potential).
FT MOD_RES 985 985 Pentaglycyl murein peptidoglycan amidated
  threonine (potential).
SQ SEQUENCE 1018 AA; 111780 MW; 58175E020E81F1F CRC64;

Query Match 100.0%; Score 59; DB 1; Length 1018;
Best Local Similarity 100.0%; Pred. No. 0.039;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PSYOGGSHNS 10
Db 838 PSYOGGSHNS 847

RESULT 2
ID Q53682 PRELIMINARY; PRT; 940 AA.
AC Q53682;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Fibronectin binding protein B.
GN Name=fnbB;
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
NCBI_TaxID=1280;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=8325-4;
RA MEDLINE=92111475; PubMed=1837266;
RX Johnson K., Sigas C., Muller H.P., Lindberg M.;
RT "Two different genes encode fibronectin binding proteins in
  Staphylococcus aureus. The complete nucleotide sequence and
  characterization of the second gene."
RL Eur. J. Biochem. 202:1041-1048 (1991).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
  an amide bond (By similarity).
DR EMBL: X62992; CAA44726.1; -.
DR PIR: S19702; S19702.
DR HSSP: Q53653; IN67.
DR GO: GO:0009986; C:cell surface; IEA.
DR GO: GO:0005618; C:cell wall; IEA.
DR GO: GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO: GO:0016020; C:membrane; IEA.
DR GO: GO:007155; P:cell adhesion; IEA.
DR InterPro: IPR008966; Adhes_bact.
DR InterPro: IPR004237; Fn_bind.
DR InterPro: IPR005877; Gpos_YsIRK.
DR Pfam: PF02986; Fn_bind_2.
DR Pfam: PF00746; Gram_pos_anchor; 1.
DR Pfam: PF04650; YsIRK_signal; 1.
DR TIGRfams: TIGR01167; LPXTG_anchor; 1.
DR TIGRfams: TIGR01168; YsIRK_signal; 1.
DR PROSITE: PS50847; GRAM_POS_ANCHORING; 1.
KW Cell wall; Peptidoglycan-anchor.
SQ SEQUENCE 940 AA; 103555 MW; E35FBBCA907AB345 CRC64;
OX NCBI_TaxID=282439;

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Best Local Similarity 90.0%; Pred. No. 0.13;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PSYOGGSHNS 10
Db 774 PSYOGGSHNS 783

RESULT 3
ID Q8NU8 PRELIMINARY; PRT; 943 AA.
AC Q8NU8;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE FnbB protein.
GN Name=fnbB; Ordered locus names=MW2420;
OS Staphylococcus aureus (strain MW2).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
NCBI_TaxID=196620;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MW2;
RX MEDLINE=22040717; PubMed=12044378; DOI=10.1016/S0140-6736(02)08713-5;
RA Baba T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Oguchi A.,
  Nagai Y., Iwama N., Asano K., Naito T., Kuroda H., Cui L.,
  Yamamoto K., Hiramoto K.;
RT "Genome and virulence determinants of high virulence community-
  acquired MRSA."
RL Lancet 359:1819-1827 (2002).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
  an amide bond (By similarity).
DR EMBL: AP004830; BAB96285.1; -.
DR HSSP: Q53653; IN67.
DR GO: GO:0009986; C:cell surface; IEA.
DR GO: GO:0005618; C:cell wall; IEA.
DR GO: GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO: GO:0016020; C:membrane; IEA.
DR GO: GO:007155; P:cell adhesion; IEA.
DR InterPro: IPR008966; Adhes_bact.
DR InterPro: IPR004237; Fn_bind.
DR InterPro: IPR005877; Gpos_YsIRK.
DR InterPro: IPR001899; Gram_pos_anchor.
DR Pfam: PF02986; Fn_bind_1.
DR Pfam: PF00746; Gram_pos_anchor; 1.
DR Pfam: PF04650; YsIRK_signal; 1.
DR TIGRfams: TIGR01167; LPXTG_anchor; 1.
DR TIGRfams: TIGR01168; YsIRK_signal; 1.
DR PROSITE: PS50847; GRAM_POS_ANCHORING; 1.
KW Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ SEQUENCE 943 AA; 104537 MW; DA8A5F3194781B64 CRC64;

Query Match 94.9%; Score 56; DB 2; Length 943;
Best Local Similarity 90.0%; Pred. No. 0.13;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PSYOGGSHNS 10
Db 781 PSYOGGSHNS 790

RESULT 4
ID Q6G6H4 PRELIMINARY; PRT; 957 AA.
AC Q6G6H4;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 01-OCT-2004 (TrEMBLrel. 27, Last annotation update)
DE Fibronectin-binding protein.
GN Name=fnbB; Ordered locus names=SA52387;
OS Staphylococcus aureus (strain MSSA476).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
NCBI_TaxID=282439;

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RN [1]
RP SEQUENCE FROM N.A.
RX Pubmed=15213324; DOI=10.1073/pnas.0402521101;
RA Halden M.T.G., Fell E.J., Lindsay J.A., Peacock S.J., Day N.P.J.,
RA Errington M.C., Foster T.J., Moore C.E., Hurst L., Atlin R., Barron A.,
RA Bason N., Bentley S.D., Chillingworth C., Cronin A., Doggett J., Dowd L.,
RA Churcher C., Clark L., Cotton C., Cronin A., Duggan G., Edwards J.,
RA Felwell T., Hance Z., Harris B., Hauser H., Holtroyd S., Jørgensen K.,
RA James K.D., Lennard N., Line A., Mayes R., Moule S., Mungall K.,
RA Ormond S., Quail M.A., Rabinowitsch E., Rutherford K.M., Sanders M.,
RA Sharp S., Simmonds M., Stevens K., Whitehead S., Barrett B.G.,
RA Spratt B.G., Parkhill J.;
RT "Complete genomes of two clinical Staphylococcus aureus strains:
RT evidence for the rapid evolution of virulence and drug resistance."
RL Proc. Natl. Acad. Sci. U.S.A. 101:9786-9791(2004).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC an amide bond (By similarity).
DR EMBL; BX571857; CAC44201.1; -.
DR GO; GO:0009986; C:cell surface; IEA.
DR GO; GO:0005618; C:cell wall; IEA.
DR GO; GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0007155; P:cell adhesion; IEA.
DR InterPro; IPR008966; Adhes_bact.
DR InterPro; IPR004237; Fn_bind.
DR InterPro; IPR005877; Gpos_YsIRK.
DR InterPro; IPR001899; Gram_pos_anchor.
DR Pfam; PF02986; Fn_bind_1.
DR Pfam; PF00746; Gram_pos_anchor; 1.
DR Pfam; PF04650; YsIRK_signal; 1.
DR TIGRFAMs; TIGR01167; LPXTG_anchor; 1.
DR TIGRFAMs; TIGR01168; YsIRK_signal; 1.
DR PROSITE; PS50847; GRAM_POS_ANCHORING; 1.
KM Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ SEQUENCE 957 AA; 105980 MW; 28F8BA7FFDD3DEAF CRC64;

Query Match 94.9%; Score 56; DB 2; Length 957;
Best Local Similarity 90.0%; Pred. No. 0.13;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 PSYQFGGHNS 10
Db 781 PNYQFGGHNS 790

RESULT 5
AC O99RD3; PRELIMINARY; PRT; 961 AA.
ID O99RD3
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Fibronectin-binding protein homolog.
GN Name=fnbB; OrderedLocustNames=SAV502;
OS Staphylococcus aureus (strain Mu50 / ATCC 700699).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
CC NCBI_TaxID=158879;

RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=Mu50 / ATCC 700699;
RX MEDLINE=21311952; Pubmed=11418146; DOI=10.1016/S0140-6736(00)04403-2;
RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Iian J.-Q., Ito T.,
RA Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hoshoyama A.,
RA Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
RA Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
RA Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
RA Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
RT "Whole genome sequencing of methicillin-resistant Staphylococcus aureus."
RL Lancet 357:1225-1240(2001).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC an amide bond (By similarity).
```

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DR EMBL; AP003365; BAB58664.1; -.
DR FTR; G90053; G90053.
DR HSSP; Q53653; IN67.
DR GO; GO:0009986; C:cell surface; IEA.
DR GO; GO:0005618; C:cell wall; IEA.
DR GO; GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0007155; P:cell adhesion; IEA.
DR InterPro; IPR008966; Adhes_bact.
DR InterPro; IPR004237; Fn_bind.
DR InterPro; IPR005877; Gpos_YsIRK.
DR InterPro; IPR001899; Gram_pos_anchor.
DR Pfam; PF02986; Fn_bind_1.
DR Pfam; PF00746; Gram_pos_anchor; 1.
DR Pfam; PF04650; YsIRK_signal; 1.
DR TIGRFAMs; TIGR01167; LPXTG_anchor; 1.
DR TIGRFAMs; TIGR01168; YsIRK_signal; 1.
DR PROSITE; PS50847; GRAM_POS_ANCHORING; 1.
KM Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ SEQUENCE 961 AA; 106010 MW; 364940F884E8A101 CRC64;

Query Match 94.9%; Score 56; DB 2; Length 961;
Best Local Similarity 90.0%; Pred. No. 0.13;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 PSYQFGGHNS 10
Db 785 PNYQFGGHNS 794

RESULT 6
AC O7A3J8; PRELIMINARY; PRT; 961 AA.
ID O7A3J8
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE FnbB protein.
GN Name=fnbB; OrderedLocustNames=SA2290;
OS Staphylococcus aureus (strain N315).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
CC NCBI_TaxID=158879;

RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21311952; Pubmed=11418146; DOI=10.1016/S0140-6736(00)04403-2;
RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Iian J.-Q., Ito T.,
RA Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hoshoyama A.,
RA Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
RA Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
RA Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
RA Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
RT "Whole genome sequencing of methicillin-resistant Staphylococcus aureus."
RL Lancet 357:1225-1240(2001).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC an amide bond (By similarity).
DR EMBL; AP003137; BAB43593.1; -.
DR GO; GO:0009986; C:cell surface; IEA.
DR GO; GO:0005618; C:cell wall; IEA.
DR GO; GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0007155; P:cell adhesion; IEA.
DR InterPro; IPR008966; Adhes_bact.
DR InterPro; IPR004237; Fn_bind.
DR InterPro; IPR005877; Gpos_YsIRK.
DR InterPro; IPR001899; Gram_pos_anchor.
DR Pfam; PF02986; Fn_bind_1.
DR Pfam; PF00746; Gram_pos_anchor; 1.
DR Pfam; PF04650; YsIRK_signal; 1.
DR TIGRFAMs; TIGR01167; LPXTG_anchor; 1.
DR TIGRFAMs; TIGR01168; YsIRK_signal; 1.
DR PROSITE; PS50847; GRAM_POS_ANCHORING; 1.
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KW Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ SEQUENCE 961 AA; 106010 MW; 364940F84EA4101 CRC64;

Query Match 94.9%; Score 56; DB 2; Length 961;
Best Local Similarity 90.0%; Pred. No. 0.13;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 PSYOGGSHNS 10
DB 785 PNYQFGSHNS 794

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RESULT 7
O6G6D5 PRELIMINARY; PRT; 965 AA.
ID O6G6D5;
AC O6G6D5;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DE Fibronectin-binding protein.
GN Name:fnbA; OrderedLocuNames=SAR2580;
OS Staphylococcus aureus (strain MSA252).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=282458;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=15213324; DOI=10.1073/pnas.0402521101;
RA Holden M.T.G., Fell E.J., Lindsay J.A., Peacock S.J., Day N.P.J.,
RA Errington M.C., Foster T.J., Moore C.E., Hurst L., Atkin R., Barron A.,
RA Bason N., Bentley S.D., Chillingworth C., Chillingworth T.,
RA Churcher C., Clark L., Cotton C., Cronin A., Doggett J., Dowd L.,
RA Felwell T., Hance Z., Harris B., Hauser H., Holtroyd S., Jagels K.,
RA James K.D., Lennard N., Line A., Mayes R., Moule S., Mungall K.,
RA Omond D., Quail M.A., Rabinowitsch E., Rutherford K.M., Sanders M.,
RA Sharp S., Simmonds M., Stevens K., Whitehead S., Barrett B.G.,
RA Spratt B.G., Parkhill J.;
RT "Complete genomes of two clinical Staphylococcus aureus strains:
RT evidence for the rapid evolution of virulence and drug resistance.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:9786-9791(2004).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC an amide bond (By similarity).
DR EMBL: BX571856; CAC41560.1; -.
DR GO: GO:0009986; C:cell surface; IEA.
DR GO: GO:0009375; C:cell wall (senu Gram-positive Bacteria); IEA.
DR GO: GO:0016020; C:membrane; IEA.
DR GO: GO:0007155; P:cell adhesion; IEA.
DR InterPro: IPR008966; Adhes_bact.
DR InterPro: IPR004237; Fn_bind.
DR InterPro: IPR005877; Gpos_YsIRK.
DR InterPro: IPR001899; Gram_pos_anchor.
DR Pfam: PF02986; Fn_bind.1.
DR Pfam: PF00746; Gram_pos_anchor.1.
DR TIGRFAMs: TIGR01167; LPXTG_anchor.1.
DR TIGRFAMs: TIGR01168; YsIRK_signal.1.
DR PROSITE: PS50847; GRAM_POS_ANCHORING.1.
KW Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ SEQUENCE 965 AA; 105691 MW; 2982E132164D0551 CRC64;

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Query Match 94.9%; Score 56; DB 2; Length 965;
Best Local Similarity 90.0%; Pred. No. 0.14;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 PSYOGGSHNS 10
DB 803 PNYQFGSHNS 812

RESULT 8
O6NUU7 PRELIMINARY; PRT; 1015 AA.
AC O6NUU7;
DT 01-OCT-2002 (TREMBlrel. 22, Created)

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DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Fnb protein.
GN Name:fnb; OrderedLocuNames=MW2421;
OS Staphylococcus aureus (strain MW2).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=196620;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MW2;
RX MEDLINE=22040717; PubMed=12044378; DOI=10.1016/S0140-6736(02)08713-5;
RA Baba T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Oguchi A.,
RA Nagai Y., Iwama N., Asano K., Naim T., Kuroda H., Cui L.,
RA Yamamoto K., Hiratake K.;
RT "Genome and virulence determinants of high virulence community-
RT acquired MRSA.";
RL Lancet 359:1819-1827(2002).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC an amide bond (By similarity).
DR EMBL: AP004830; BAB96286.1; -.
DR GO: GO:0009986; C:cell surface; IEA.
DR GO: GO:0005618; C:cell wall; IEA.
DR GO: GO:0009375; C:cell wall (senu Gram-positive Bacteria); IEA.
DR GO: GO:0016020; C:membrane; IEA.
DR GO: GO:007155; P:cell adhesion; IEA.
DR InterPro: IPR008966; Adhes_bact.
DR InterPro: IPR004237; Fn_bind.
DR InterPro: IPR005877; Gpos_YsIRK.
DR InterPro: IPR001899; Gram_pos_anchor.
DR Pfam: PF02986; Fn_bind.1.
DR Pfam: PF00746; Gram_pos_anchor.1.
DR TIGRFAMs: TIGR01167; LPXTG_anchor.1.
DR TIGRFAMs: TIGR01168; YsIRK_signal.1.
DR PROSITE: PS50847; GRAM_POS_ANCHORING.1.
KW Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ SEQUENCE 1015 AA; 111145 MW; D0F9281BB64D4D2 CRC64;

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Query Match 94.9%; Score 56; DB 2; Length 1015;
Best Local Similarity 90.0%; Pred. No. 0.14;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 PSYOGGSHNS 10
DB 839 PNYQFGSHNS 848

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RESULT 9
O6G6H3 PRELIMINARY; PRT; 1015 AA.
ID O6G6H3;
AC O6G6H3;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DE Fibronectin-binding protein.
GN OrderedLocuNames=SA52386;
OS Staphylococcus aureus (strain MSA476).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=282459;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=15213324; DOI=10.1073/pnas.0402521101;
RA Holden M.T.G., Fell E.J., Lindsay J.A., Peacock S.J., Day N.P.J.,
RA Errington M.C., Foster T.J., Moore C.E., Hurst L., Atkin R., Barron A.,
RA Bason N., Bentley S.D., Chillingworth C., Chillingworth T.,
RA Churcher C., Clark L., Cotton C., Cronin A., Doggett J., Dowd L.,
RA Felwell T., Hance Z., Harris B., Hauser H., Holtroyd S., Jagels K.,
RA James K.D., Lennard N., Line A., Mayes R., Moule S., Mungall K.,
RA Omond D., Quail M.A., Rabinowitsch E., Rutherford K.M., Sanders M.,
RA Sharp S., Simmonds M., Stevens K., Whitehead S., Barrett B.G.,
RA Spratt B.G., Parkhill J.;
RT "Complete genomes of two clinical Staphylococcus aureus strains:
RT evidence for the rapid evolution of virulence and drug resistance.";

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RL Proc. Natl. Acad. Sci. U.S.A. 101:9786-9791(2004).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC an amide bond (By similarity).
DR EMBL: BX571857; CNG4202.1; -.
DR GO: GO:0009986; C:cell surface; IEA.
DR GO: GO:0005618; C:cell wall; IEA.
DR GO: GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO: GO:0016020; C:membrane; IEA.
DR GO: GO:0007155; P:cell adhesion; IEA.
DR InterPro: IPR008965; Adhes_bact.
DR InterPro: IPR004237; Fn_bind.
DR InterPro: IPR005877; Gpos_YsIRK.
DR InterPro: IPR001899; Gram_pos_anchor.
DR Pfam: PF02986; Fn_bind.1.
DR Pfam: PF00746; Gram_pos_anchor.1.
DR TIGRFAMs: TIGR01167; LPXTG_anchor.1.
DR TIGRFAMs: TIGR01168; YsIRK_signal.1.
DR PROSITE: PS50847; GRAM_POS_ANCHORING.1.
KM Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ SEQUENCE 1015 AA; 11145 MW; D0F9261BB64D4D2 CRC64;

Query Match 94.9%; Score 56; DB 2; Length 1015;
Best Local Similarity 90.0%; Pred. No. 0.14;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 PSYOGGHNS 10
DB 839 PNYOFGHNS 848

RESULT 10
O99RD2 PRELIMINARY; PRT; 1038 AA.
ID O99RD2;
AC O99RD2;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Fibronectin-binding protein homolog.
GN Name-fnb; OrderedLocustNames=SV2503;
OS Staphylococcus aureus (strain Mu50 / ATCC 700699).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=158879;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Mu50 / ATCC 700699;
RX MEDLINE=21311952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2;
RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Iian J.-Q., Ito T.,
RA Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,
RA Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
RA Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
RA Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
RA Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
RT "Whole genome sequencing of methicillin-resistant Staphylococcus
RT aureus."
RL Lancel 357:1225-1240(2001).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC an amide bond (By similarity).
DR EMBL: AP003365; BAB58665.1; -.
DR PIR: H90053; H90053.
DR GO: GO:0009986; C:cell surface; IEA.
DR GO: GO:0005618; C:cell wall; IEA.
DR GO: GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO: GO:0016020; C:membrane; IEA.
DR GO: GO:0007155; P:cell adhesion; IEA.
DR InterPro: IPR008966; Adhes_bact.
DR InterPro: IPR004237; Fn_bind.
DR InterPro: IPR005877; Gpos_YsIRK.
DR InterPro: IPR001899; Gram_pos_anchor.
DR Pfam: PF02986; Fn_bind.1.
DR Pfam: PF00746; Gram_pos_anchor.1.
DR TIGRFAMs: TIGR01167; LPXTG_anchor.1.
DR TIGRFAMs: TIGR01168; YsIRK_signal.1.
DR PROSITE: PS50847; GRAM_POS_ANCHORING.1.
KM Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ SEQUENCE 1038 AA; 113618 MW; 666BF6BF2FBEB12 CRC64;

Query Match 94.9%; Score 56; DB 2; Length 1038;
Best Local Similarity 90.0%; Pred. No. 0.15;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 PSYOGGHNS 10
DB 834 PNYOFGHNS 843

RESULT 12
O9AEP9 PRELIMINARY; PRT; 152 AA.
ID O9AEP9

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DR TIGRFAMs: TIGR01167; LPXTG_anchor.1.
DR TIGRFAMs: TIGR01168; YsIRK_signal.1.
DR PROSITE: PS50847; GRAM_POS_ANCHORING.1.
KM Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ SEQUENCE 1038 AA; 113618 MW; 666BF6BF2FBEB12 CRC64;

Query Match 94.9%; Score 56; DB 2; Length 1038;
Best Local Similarity 90.0%; Pred. No. 0.15;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 PSYOGGHNS 10
DB 834 PNYOFGHNS 843

RESULT 11
O7A3J7 PRELIMINARY; PRT; 1038 AA.
ID O7A3J7;
AC O7A3J7;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Fnb protein.
GN Name-fnb; OrderedLocustNames=SA2291;
OS Staphylococcus aureus (strain N315).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=158879;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21311952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2;
RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Iian J.-Q., Ito T.,
RA Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,
RA Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
RA Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
RA Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
RA Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
RT "Whole genome sequencing of methicillin-resistant Staphylococcus
RT aureus."
RL Lancel 357:1225-1240(2001).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC an amide bond (By similarity).
DR EMBL: AP003377; BAB43594.1; -.
DR GO: GO:0009986; C:cell surface; IEA.
DR GO: GO:0005618; C:cell wall; IEA.
DR GO: GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO: GO:0016020; C:membrane; IEA.
DR GO: GO:0007155; P:cell adhesion; IEA.
DR InterPro: IPR008966; Adhes_bact.
DR InterPro: IPR004237; Fn_bind.
DR InterPro: IPR005877; Gpos_YsIRK.
DR InterPro: IPR001899; Gram_pos_anchor.
DR Pfam: PF02986; Fn_bind.1.
DR Pfam: PF00746; Gram_pos_anchor.1.
DR TIGRFAMs: TIGR01167; LPXTG_anchor.1.
DR TIGRFAMs: TIGR01168; YsIRK_signal.1.
DR PROSITE: PS50847; GRAM_POS_ANCHORING.1.
KM Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ SEQUENCE 1038 AA; 113618 MW; 666BF6BF2FBEB12 CRC64;

Query Match 94.9%; Score 56; DB 2; Length 1038;
Best Local Similarity 90.0%; Pred. No. 0.15;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 PSYOGGHNS 10
DB 834 PNYOFGHNS 843

RESULT 12
O9AEP9 PRELIMINARY; PRT; 152 AA.
ID O9AEP9

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AC Q9AEP9;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Fibronectin-binding protein (Fragment).
GN Name=fnb;
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
NCBI_TaxID=1280;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CMSA-1;
RX MEDLINE=21246681; PubMed=11349044;
DOI=10.1128/IAI.69.6.3791-3799.2001;
RA Rice K., Huesca M., Vaz D., McGavin M.J.;
RT "variance in fibronectin binding and fnb locus polymorphisms in
RT Staphylococcus aureus: identification of antigenic variation in a
RT fibronectin binding protein adhesin of the epidemic CMSA-1 strain of
RT methicillin-resistant S. aureus.";
RL Infect. Immun. 69:3791-3799(2001).
DR EMBL; AY029184; AKK31588.1; -.
FT NON_TER 1
SQ SEQUENCE 152 AA; 17193 MW; CPA3913C2B11C025 CRC64;

Query Match 93.2%; Score 55; DB 2; Length 152;
Best Local Similarity 100.0%; Pred. No. 0.027;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PSYFGGHN 9
DB 131 PSYFGGHN 139

RESULT 13
Q8BV4 PRELIMINARY; PRT; 993 AA.
ID Q8BV4;
AC Q8BV4;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Mus musculus 0 day neonate cerebellum cDNA, RIKEN full-length enriched
DE library, clone: C230040D10 product: MYOSIN HEAVY CHAIN MTR 8 homolog
DE (fragment).
GN Name=C230040D10R1k;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Cerebellum;
RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Mech. Enzymol. 303:19-44(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Cerebellum;
RX MEDLINE=21055660; PubMed=11217851; DOI=10.1038/35055500;
RA RIKEN FANTOM Consortium;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Cerebellum;
RA The FANTOM Consortium;
RT the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
RN [4]
RP SEQUENCE FROM N.A.

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RC STRAIN=C57BL/6J; TISSUE=Cerebellum;
RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata Y., Hayatsu M., Sugahara Y., Shibata K., Itoh M.,
RA Kono H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630(2000).
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Cerebellum;
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Saeki N., Carninci P.,
RA Kono H., Akiyama U., Nishi K., Katsunari T., Teshiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishino T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwaka S., Inoue K., Togawa Y., Izawa Y., Ohara E., Watabiki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai U.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system: 384-format
RT sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771(2000).
RN [6]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Cerebellum;
RA Adachi U., Aizawa K., Akimura T., Arikawa T., Bono H., Carninci P.,
RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
RA Katoh H., Kawai U., Kojima Y., Kondo S., Kono H., Konda M., Koya S.,
RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
RA Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
RA Tomaru A., Taya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
RL Submitted (Apr-2002) to the EMBL/Genbank/DBJ databases.
DR EMBL; AK082350; BAC38475.1; -.
DR HSSP; P08799; 1MD.
DR MGD; MGI:268591; C230040D10R1k.
DR GO; GO:0016459; C:myosin, IEA.
DR GO; GO:0005524; P:ATP binding, IEA.
DR GO; GO:0003774; P:motor activity, IEA.
DR InterPro; IPR002110; ANK.
DR InterPro; IPR001609; Myosin_head.
DR InterPro; IPR000169; Pept_cys_acsite.
DR Pfam; PF00023; Ank; 6.
DR Pfam; PF00063; Myosin_head; 3.
DR PRINTS; PR01415; ANKYRIN.
DR PRINTS; PR00193; MYOSINHEAVY.
DR ProDom; PD000355; Myosin_head; 1.
DR SMART; SM00248; ANK; 5.
DR SMART; SM00242; MYSC; 1.
DR PROSITE; PS00088; ANK_REPEAT; 4.
DR PROSITE; PS00297; ANK_REPEAT_REGION; 1.
DR PROSITE; PS00659; THIOL_PROTEASE_HIS; UNKNOWN_1.
KW ANK repeat.
FT NON_TER 993
SQ SEQUENCE 993 AA; 111027 MW; 95A98B7CA05676F5 CRC64;

Query Match 76.3%; Score 45; DB 2; Length 993;
Best Local Similarity 70.0%; Pred. No. 16;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 PSYFGGHN 10
DB 960 PSYFGGHN 969

RESULT 14
Q9OX10 PRELIMINARY; PRT; 1322 AA.
ID Q9OX10;
AC Q9OX10;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)

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DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Myosin heavy chain Myr 8.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
CX NCBI_TaxId=10116;
RN [1]
RN SEQUENCE FROM N.A.
RP STRAIN=Sprague-Dawley;
RC MEDLINE=21472394; PubMed=11588169;
RX Patel K.G., Liu C., Cameron P.L., Cameron R.S.;
RA "Myr 8, a novel unconventional myosin expressed during brain
RT development associates with the protein phosphatase catalytic subunits
RT 1alpha and 1gamma.";
RL J. Neurosci. 21:7954-7968(2001).
RR EMBL; AF209114; AAF20150.1; -.
DR PIR; A59288; A59288.
DR HSSP; P08799; 1MND.
DR GO; GO:0016459; C:myosin; IEA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0003774; F:motor activity; IEA.
DR InterPro; IPR002110; ANK.
DR InterPro; IPR000048; IQ_region.
DR InterPro; IPR001609; Myosin_head.
DR InterPro; IPR000169; Pept_cys_acsite.
DR Pfam; PF00612; IQ; 1.
DR Pfam; PF00623; Ank; 6.
DR Pfam; PF00663; Myosin_head; 2.
DR PRINTS; PR01415; ANKYRIN.
DR PRINTS; PR00193; MYOSINHEAVY.
DR ProDom; PD000355; Myosin_head; 1.
DR SMART; SM00248; ANK; 5.
DR SMART; SM00242; MYSC; 1.
DR SMART; SM00015; IQ; 1.
DR PROSITE; PS00088; ANK_REPEAT; 4.
DR PROSITE; PS00297; ANK_REPEAT_REGION; 1.
DR PROSITE; PS00096; IQ; 1.
DR PROSITE; PS00639; THIOL_PROTEASE_HIS; UNKNOWN_1.
DR ANK repeat.
KW SEQUENCE
SQ 1322 AA; 147841 MW; 2554F7AAC222DB66 CRC64;

Query Match 76.3%; Score 45; DB 2; Length 1322;
Best Local Similarity 70.0%; Pred. No. 22;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0.

Cy 1 PSYRGGHNS 10
Db 961 PSFKFGHKS 970

RESULT 15
Q9ERC1 PRELIMINARY; PRT; 1912 AA.
AC Q9ERC1;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Myosin heavy chain Myr 8b.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
CX NCBI_TaxId=10116;
RN [1]
RN SEQUENCE FROM N.A.
RP STRAIN=Sprague-Dawley;
RC MEDLINE=21472394; PubMed=11588169;
RX Patel K.G., Liu C., Cameron P.L., Cameron R.S.;
RA "Myr 8, a novel unconventional myosin expressed during brain
RT development associates with the protein phosphatase catalytic subunits
RT 1alpha and 1gamma.";
RL J. Neurosci. 21:7954-7968(2001).
RR EMBL; AV004215; AAG23288.1; -.

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DR HSSP; P08799; IMND.
DR GO; GO:0016459; C:myosin; IEA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0003774; F:motor activity; IEA.
DR InterPro; IPR002110; ANK.
DR InterPro; IPR000048; IQ_region.
DR InterPro; IPR001609; Myosin_head.
DR InterPro; IPR00169; Pept_cys_acetate.
DR Pfam; PF00023; Ank; 6.
DR Pfam; PF00612; IQ; 1.
DR Pfam; PF00063; Myosin_head; 2.
DR PRINTS; PR01415; ANKYRIN.
DR PRINTS; PR00193; MYOSINHEAVY.
DR ProDom; PD000355; Myosin_head; 1.
DR SMART; SM00248; ANK; 5.
DR SMART; SM00015; IQ; 1.
DR SMART; SM00242; MYSC; 1.
DR PROSITE; PSS00088; ANK_REPEAT; 4.
DR PROSITE; PSS0297; ANK_REPEAT_REGION; 1.
DR PROSITE; PSS0096; IQ; 1.
DR PROSITE; PSS0639; THIOL_PROTEASE_HIS; UNKNOWN_1.
DR KW repeat.
SQ SEQUENCE 1912 AA; 210689 MW; 7C15014A1A83C9C3 CRC64;

Query Match 76.3%; Score 45; DB 2; Length 1912;
Best Local Similarity 70.0%; Pred. No. 33;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0,
QY 1 PSYQFGGHS 10
|:::|||||
Db 961 PSFKFGGHS 970

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 25, 2005, 20:58:51 ; Search time 69.7126 Seconds
(without alignments)
55.479 Million cell updates/sec

Title: US-10-731-238-97
Perfect score: 58
Sequence: 1 YQFGHNSVD 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :
1: A_Geneseq_16Dec04:*
2: geneseqp1980s:*
3: geneseqp1990s:*
4: geneseqp2000s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	58	100.0	10	2	AAW65753 Fibronec
2	58	100.0	21	2	AAW65670 Fibronec
3	58	100.0	21	2	AAW65683 Fibronec
4	58	100.0	21	2	AAW65689 Fibronec
5	58	100.0	21	2	AAW65684 Fibronec
6	58	100.0	21	2	AAW65685 Fibronec
7	58	100.0	21	2	AAW65671 Fibronec
8	58	100.0	21	2	AAW65682 Fibronec
9	58	100.0	21	2	AAW65688 Fibronec
10	58	100.0	21	2	AAW65672 Fibronec
11	58	100.0	21	2	AAW65687 Fibronec
12	58	100.0	21	2	AAW65686 Fibronec
13	58	100.0	21	2	AAW65665 Fibronec
14	58	100.0	22	2	AAW65665 Fibronec
15	58	100.0	37	4	AAW65665 Fibronec
16	58	100.0	38	1	AAW65662 Protein w
17	58	100.0	77	2	AAW65662 Protein w
18	58	100.0	101	2	AAW65662 Protein w
19	58	100.0	113	2	AAW65662 Protein w
20	58	100.0	124	2	AAW65662 Protein w
21	58	100.0	124	2	AAW65662 Protein w
22	58	100.0	130	2	AAW65662 Protein w
23	58	100.0	130	2	AAW65662 Protein w
24	58	100.0	130	2	AAW65662 Protein w
25	58	100.0	130	2	AAW65662 Protein w

26	58	100.0	134	2	AAW65753 Fibronec
27	58	100.0	134	2	AAW65753 Fibronec
28	58	100.0	139	2	AAW65753 Fibronec
29	58	100.0	162	2	AAW65753 Fibronec
30	58	100.0	164	2	AAW65753 Fibronec
31	58	100.0	174	2	AAW65753 Fibronec
32	58	100.0	174	2	AAW65753 Fibronec
33	58	100.0	181	2	AAW65753 Fibronec
34	58	100.0	181	2	AAW65753 Fibronec
35	58	100.0	559	2	AAW65753 Fibronec
36	58	100.0	940	2	AAW65753 Fibronec
37	58	100.0	940	2	AAW65753 Fibronec
38	58	100.0	948	6	AAW65753 Fibronec
39	58	100.0	948	6	AAW65753 Fibronec
40	58	100.0	961	6	AAW65753 Fibronec
41	58	100.0	978	6	AAW65753 Fibronec
42	58	100.0	1001	4	AAW65753 Fibronec
43	58	100.0	1018	1	AAW65753 Fibronec
44	58	100.0	1018	1	AAW65753 Fibronec
45	58	100.0	1018	4	AAW65753 Fibronec

ALIGNMENTS

RESULT 1
AAW65753 standard; peptide; 10 AA.

AAW65753:

16-OCT-1998 (first entry)

Fibronec binding protein-derived peptide #97.

microbial surface components recognising adhesive matrix molecule;
MGRAM, fibronec, fibronec binding protein; antibody; epitope;
antibiotic; bacterial infection; antibiotic-resistant strain.

Synthetic.

Staphylococcus aureus.

23-JUL-1998.

21-JAN-1998; 98WO-US001222.

21-JAN-1997; 97US-0036139P.

(TEXA) UNIV TEXAS A & M SYSTEM.

Hosook M, Patti JM, House-Pompeo KL, Speziale P, Joh D;

McGavin M;

WPI; 1998-413816/35.

Antibody that binds to fibronec binding protein, preventing its

binding to fibronec - used to treat or prevent bacterial infection,

especially by Staphylococci and Streptococci.

Example 9; Page 111; 201p; English.

The invention relates to antibodies that bind to a fibronec binding domain of a fibronec binding protein, and inhibit binding of a protein to a fibronec binding protein. Also claimed are: (1) isolated peptides of a fibronec binding protein that do not bind to fibronec; (2) fusion protein containing at least one peptide of a fibronec binding protein linked to a second amino acid sequence; (3) nucleic acid encoding the isolated peptide of (1). Antibodies, the isolated peptides of (1) and the nucleic acids are all useful for immunisation (active or passive) and (by inhibiting binding of bacteria to fibronec) for preventing or treating infection in humans or other animals, particularly by staphylococci or

CC streptococci, e.g. meningitis, otitis media, pneumonia, endocarditis,
CC mastitis in cattle, abortion in horses and many others. Since the
CC antibodies block binding of bacteria, they should be effective against
CC antibiotic-resistant strains, and may replace antibiotic therapy or
CC increase its effectiveness. Sequences AAM65744-58 represent peptides
CC which were synthesised to span the D3 motif of *S. aureus* fibronectin
CC binding protein A
CC
XX
SQ Sequence 10 AA;

Query Match 100.0%; Score 58; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.00092;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YQFGHNSVD 10
Db 1 YQFGHNSVD 10

RESULT 2
ID AAM65670 standard; peptide; 21 AA.
XX
AC AAM65670;
XX
DT 16-OCT-1998 (first entry)
XX
DE Fibronectin binding protein-derived peptide #14.
XX
KM microbial surface components recognising adhesive matrix molecule;
KM MSCRAMM; fibronectin; fibronectin-binding protein; antibody; epitope;
KW antibiotic; bacterial infection; antibiotic-resistant strain.
XX
OS Synthetic.
OS *Staphylococcus aureus*.
XX
PN W09831389-A2.
XX
PD 23-JUL-1998.
XX
PF 21-JAN-1998; 98WO-US001222.
XX
PR 21-JAN-1997; 97US-0036139P.
XX
PA (TEXA) UNIV TEXAS A & M SYSTEM.
XX
PI Hoeck M, Patti JM, House-Pompeo KL, Speziale P, Joh D;
PI McGavin MJ;
DR WPI; 1998-413816/35.
XX
PT Antibody that binds to fibronectin-binding protein, preventing its
PT binding to fibronectin - used to treat or prevent bacterial infection,
PT especially by *Staphylococci* and *Streptococci*.
XX
PS Example 8; Page 100; 201pp; English.
XX
CC The invention relates to antibodies that bind to a fibronectin-binding
CC domain of a fibronectin-binding protein, and inhibit binding of the
CC protein to fibronectin. Also claimed are: (1) isolated peptides of a
CC fibronectin-binding protein that do not bind to fibronectin; (2) fusion
CC protein containing at least one peptide of a fibronectin-binding protein
CC linked to a second amino acid sequence; (3) nucleic acid encoding the
CC isolated peptide of (1). Antibodies, the isolated peptides of (1) and the
CC nucleic acids are all useful for immunisation (active or passive) and (by
CC inhibiting binding of bacteria to fibronectin) for preventing or treating
CC infection in humans or other animals, particularly by *Staphylococci* or
CC streptococci, e.g. meningitis, otitis media, pneumonia, endocarditis,
CC mastitis in cattle, abortion in horses and many others. Since the
CC antibodies block binding of bacteria, they should be effective against
CC antibiotic-resistant strains, and may replace antibiotic therapy or
CC increase its effectiveness. Sequences AAM65670-90 represent a series of
CC synthetic peptides based on the D3 repeat of *S. aureus* fibronectin

CC binding protein A. They were synthesised to contain a proline residue at
CC each position through the sequence (1e a proline scan)
XX
SQ Sequence 21 AA;

Query Match 100.0%; Score 58; DB 2; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.002;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YQFGHNSVD 10
Db 4 YQFGHNSVD 13

RESULT 3
ID AAM65683 standard; peptide; 21 AA.
XX
AC AAM65683;
XX
DT 16-OCT-1998 (first entry)
XX
DE Fibronectin binding protein-derived peptide #27.
XX
KM microbial surface components recognising adhesive matrix molecule;
KM MSCRAMM; fibronectin; fibronectin-binding protein; antibody; epitope;
KW antibiotic; bacterial infection; antibiotic-resistant strain.
XX
OS Synthetic.
OS *Staphylococcus aureus*.
XX
PN W09831389-A2.
XX
PD 23-JUL-1998.
XX
PF 21-JAN-1998; 98WO-US001222.
XX
PR 21-JAN-1997; 97US-0036139P.
XX
PA (TEXA) UNIV TEXAS A & M SYSTEM.
XX
PI Hoeck M, Patti JM, House-Pompeo KL, Speziale P, Joh D;
PI McGavin MJ;
DR WPI; 1998-413816/35.
XX
PT Antibody that binds to fibronectin-binding protein, preventing its
PT binding to fibronectin - used to treat or prevent bacterial infection,
PT especially by *Staphylococci* and *Streptococci*.
XX
PS Example 8; Page 101; 201pp; English.
XX
CC The invention relates to antibodies that bind to a fibronectin-binding
CC domain of a fibronectin-binding protein, and inhibit binding of the
CC protein to fibronectin. Also claimed are: (1) isolated peptides of a
CC fibronectin-binding protein that do not bind to fibronectin; (2) fusion
CC protein containing at least one peptide of a fibronectin-binding protein
CC linked to a second amino acid sequence; (3) nucleic acid encoding the
CC isolated peptide of (1). Antibodies, the isolated peptides of (1) and the
CC nucleic acids are all useful for immunisation (active or passive) and (by
CC inhibiting binding of bacteria to fibronectin) for preventing or treating
CC infection in humans or other animals, particularly by *Staphylococci* or
CC streptococci, e.g. meningitis, otitis media, pneumonia, endocarditis,
CC mastitis in cattle, abortion in horses and many others. Since the
CC antibodies block binding of bacteria, they should be effective against
CC antibiotic-resistant strains, and may replace antibiotic therapy or
CC increase its effectiveness. Sequences AAM65670-90 represent a series of
CC synthetic peptides based on the D3 repeat of *S. aureus* fibronectin
CC binding protein A. They were synthesised to contain a proline residue at
CC each position through the sequence (1e a proline scan)
XX
SQ Sequence 21 AA;

Query Match 100.0%; Score 58; DB 2; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.002;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YQFGHNSVD 10
DB 4 YQFGHNSVD 13

RESULT 4
AAW65689 standard; peptide; 21 AA.

AC AAW65689;
XX
DT 16-OCT-1998 (first entry)
XX
DE Fibronectin binding protein-derived peptide #33.

XX microbial surface components recognising adhesive matrix molecule;
KM MSCRAMM; fibronectin; fibronectin-binding protein; antibody; epitope;
XX antibiotic; bacterial infection; antibiotic-resistant strain.

XX Synthetic.
OS Staphylococcus aureus.

XX MO9831389-A2.

XX 23-JUL-1998.

XX 21-JAN-1998; 98WO-US001222.

XX 21-JAN-1997; 97US-0036139P.

XX (TEXA) UNIV TEXAS A & M SYSTEM.

XX Hoeek M, Patti JM, House-Pompeo KL, Speciale P, Joh D;
PI McGavin MJ;

XX WPI; 1998-413816/35.

XX Antibody that binds to fibronectin-binding protein, preventing its
PT binding to fibronectin - used to treat or prevent bacterial infection,
PT especially by Staphylococci and Streptococci.

XX Example 8; Page 101; 201pp; English.

XX The invention relates to antibodies that bind to a fibronectin-binding
CC domain of a fibronectin-binding protein, and inhibit binding of the
CC protein to fibronectin. Also claimed are: (1) isolated peptides of a
CC fibronectin-binding protein that do not bind to fibronectin; (2) fusion
CC protein containing at least one peptide of a fibronectin-binding protein
CC linked to a second amino acid sequence; (3) nucleic acid encoding the
CC isolated peptide of (1). Antibodies, the isolated peptides of (1) and the
CC nucleic acids are all useful for immunisation (active or passive) and (by
CC inhibiting binding of bacteria to fibronectin) for preventing or treating
CC infection in humans or other animals, particularly by staphylococci or
CC streptococci, e.g. meningitis, otitis media, pneumonia, endocarditis,
CC mastitis in cattle, abortion in horses and many others. Since the
CC antibodies block binding of bacteria, they should be effective against
CC antibiotic-resistant strains, and may replace antibiotic therapy or
CC increase its effectiveness. Sequences AAW65670-90 represent a series of
CC synthetic peptides based on the D3 repeat of S. aureus fibronectin
CC binding protein A. They were synthesised to contain a proline residue at
CC each position through the sequence (ie a proline scan)

XX Sequence 21 AA;

QY Query Match 100.0%; Score 58; DB 2; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.002;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YQFGHNSVD 10

DB 4 YQFGHNSVD 13

RESULT 5
AAW65684 standard; peptide; 21 AA.

AC AAW65684;
XX
DT 16-OCT-1998 (first entry)
XX

DE Fibronectin binding protein-derived peptide #28.

XX microbial surface components recognising adhesive matrix molecule;
KM MSCRAMM; fibronectin; fibronectin-binding protein; antibody; epitope;
XX antibiotic; bacterial infection; antibiotic-resistant strain.

XX Synthetic.
OS Staphylococcus aureus.

XX MO9831389-A2.

XX 23-JUL-1998.

XX 21-JAN-1998; 98WO-US001222.

XX 21-JAN-1997; 97US-0036139P.

XX (TEXA) UNIV TEXAS A & M SYSTEM.

XX Hoeek M, Patti JM, House-Pompeo KL, Speciale P, Joh D;
PI McGavin MJ;

XX WPI; 1998-413816/35.

XX Antibody that binds to fibronectin-binding protein, preventing its
PT binding to fibronectin - used to treat or prevent bacterial infection,
PT especially by Staphylococci and Streptococci.

XX Example 8; Page 101; 201pp; English.

XX The invention relates to antibodies that bind to a fibronectin-binding
CC domain of a fibronectin-binding protein, and inhibit binding of the
CC protein to fibronectin. Also claimed are: (1) isolated peptides of a
CC fibronectin-binding protein that do not bind to fibronectin; (2) fusion
CC protein containing at least one peptide of a fibronectin-binding protein
CC linked to a second amino acid sequence; (3) nucleic acid encoding the
CC isolated peptide of (1). Antibodies, the isolated peptides of (1) and the
CC nucleic acids are all useful for immunisation (active or passive) and (by
CC inhibiting binding of bacteria to fibronectin) for preventing or treating
CC infection in humans or other animals, particularly by staphylococci or
CC streptococci, e.g. meningitis, otitis media, pneumonia, endocarditis,
CC mastitis in cattle, abortion in horses and many others. Since the
CC antibodies block binding of bacteria, they should be effective against
CC antibiotic-resistant strains, and may replace antibiotic therapy or
CC increase its effectiveness. Sequences AAW65670-90 represent a series of
CC synthetic peptides based on the D3 repeat of S. aureus fibronectin
CC binding protein A. They were synthesised to contain a proline residue at
CC each position through the sequence (ie a proline scan)

XX Sequence 21 AA;

QY Query Match 100.0%; Score 58; DB 2; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.002;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YQFGHNSVD 10
DB 4 YQFGHNSVD 13

RESULT 6

AAW65685
 ID AAW65685 standard; peptide; 21 AA.
 XX
 AC AAW65685;
 XX
 DT 16-OCT-1998 (first entry)
 XX
 DE Fibronectin binding protein-derived peptide #29.
 XX
 KM microbial surface components recognising adhesive matrix molecule;
 KM MSCRAMM; fibronectin; fibronectin-binding protein; antibody; epitope;
 KM antibiotic; bacterial infection; antibiotic-resistant strain.
 XX
 OS Synthetic.
 OS Staphylococcus aureus.
 XX
 PN WO9831389-A2.
 PD
 PD 23-JUL-1998.
 XX
 PF 21-JAN-1998; 98WO-US001222.
 XX
 PR 21-JAN-1997; 97US-0036139P.
 XX
 PA (TEXA) UNIV TEXAS A & M SYSTEM.
 XX
 PI Hoeoek M, Patti JM, House-Pompeo KL, Speziale P, Joh D;
 PI McGavin MJ;
 DR WPI; 1998-413816/35.
 XX
 PT Antibody that binds to fibronectin-binding protein, preventing its
 PT binding to fibronectin - used to treat or prevent bacterial infection,
 PT especially by Staphylococci and Streptococci.
 PS Example 8; Page 101; 201pp; English.
 XX
 CC The invention relates to antibodies that bind to a fibronectin-binding
 CC domain of a fibronectin-binding protein, and inhibit binding of the
 CC protein to fibronectin. Also claimed are: (1) isolated peptides of a
 CC fibronectin-binding protein that do not bind to fibronectin; (2) fusion
 CC protein containing at least one peptide of a fibronectin-binding protein
 CC linked to a second amino acid sequence; (3) nucleic acid encoding the
 CC isolated peptide of (1). Antibodies, the isolated peptides of (1) and the
 CC nucleic acids are all useful for immunisation (active or passive) and (by
 CC inhibiting binding of bacteria to fibronectin) for preventing or treating
 CC infection in humans or other animals, particularly by staphylococci or
 CC streptococci, e.g. meningitis, otitis media, pneumonia, endocarditis,
 CC mastitis in cattle, abortion in horses and many others. Since the
 CC antibodies block binding of bacteria, they should be effective against
 CC antibiotic-resistant strains, and may replace antibiotic therapy or
 CC increase its effectiveness. Sequences AAW65670-90 represent a series of
 CC synthetic peptides based on the D3 repeat of S. aureus fibronectin
 CC binding protein A. They were synthesised to contain a proline residue at
 CC each position through the sequence (ie a proline scan)
 XX
 SQ Sequence 21 AA;
 QY
 Query Match 100.0%; Score 58; DB 2; Length 21;
 Best Local Similarity 100.0%; Pred. No. 0.002;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 DB 1 YQFGHNSVD 10
 4 YQFGHNSVD 13
 RESULT 7
 AAW65671
 ID AAW65671 standard; peptide; 21 AA.
 XX
 AC AAW65671;
 XX

DT 16-OCT-1998 (first entry)
 XX
 DE Fibronectin binding protein-derived peptide #15.
 XX
 KM microbial surface components recognising adhesive matrix molecule;
 KM MSCRAMM; fibronectin; fibronectin-binding protein; antibody; epitope;
 KM antibiotic; bacterial infection; antibiotic-resistant strain.
 XX
 OS Synthetic.
 OS Staphylococcus aureus.
 XX
 PN WO9831389-A2.
 PD
 PD 23-JUL-1998.
 XX
 PF 21-JAN-1998; 98WO-US001222.
 XX
 PR 21-JAN-1997; 97US-0036139P.
 XX
 PA (TEXA) UNIV TEXAS A & M SYSTEM.
 XX
 PI Hoeoek M, Patti JM, House-Pompeo KL, Speziale P, Joh D;
 PI McGavin MJ;
 DR WPI; 1998-413816/35.
 XX
 PT Antibody that binds to fibronectin-binding protein, preventing its
 PT binding to fibronectin - used to treat or prevent bacterial infection,
 PT especially by Staphylococci and Streptococci.
 PS Example 8; Page 100; 201pp; English.
 XX
 CC The invention relates to antibodies that bind to a fibronectin-binding
 CC domain of a fibronectin-binding protein, and inhibit binding of the
 CC protein to fibronectin. Also claimed are: (1) isolated peptides of a
 CC fibronectin-binding protein that do not bind to fibronectin; (2) fusion
 CC protein containing at least one peptide of a fibronectin-binding protein
 CC linked to a second amino acid sequence; (3) nucleic acid encoding the
 CC isolated peptide of (1). Antibodies, the isolated peptides of (1) and the
 CC nucleic acids are all useful for immunisation (active or passive) and (by
 CC inhibiting binding of bacteria to fibronectin) for preventing or treating
 CC infection in humans or other animals, particularly by staphylococci or
 CC streptococci, e.g. meningitis, otitis media, pneumonia, endocarditis,
 CC mastitis in cattle, abortion in horses and many others. Since the
 CC antibodies block binding of bacteria, they should be effective against
 CC antibiotic-resistant strains, and may replace antibiotic therapy or
 CC increase its effectiveness. Sequences AAW65670-90 represent a series of
 CC synthetic peptides based on the D3 repeat of S. aureus fibronectin
 CC binding protein A. They were synthesised to contain a proline residue at
 CC each position through the sequence (ie a proline scan)
 XX
 SQ Sequence 21 AA;
 QY
 Query Match 100.0%; Score 58; DB 2; Length 21;
 Best Local Similarity 100.0%; Pred. No. 0.002;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 DB 1 YQFGHNSVD 10
 4 YQFGHNSVD 13
 RESULT 8
 AAW65682
 ID AAW65682 standard; peptide; 21 AA.
 XX
 AC AAW65682;
 XX
 DT 16-OCT-1998 (first entry)
 XX
 DE Fibronectin binding protein-derived peptide #26.
 XX
 KM microbial surface components recognising adhesive matrix molecule;
 KM

KW MSCRAMM; fibronectin; fibronectin-binding protein; antibody; epitope;
 XX antibiotic; bacterial infection; antibiotic-resistant strain.
 OS Synthetic.
 PN Staphylococcus aureus.
 PD WO9831389-A2.
 XX 23-JUL-1998.
 PF 21-JAN-1998; 98MO-US001222.
 XX 21-JAN-1997; 97US-0036139P.
 XX (TEXA) UNIV TEXAS A & M SYSTEM.
 PA Hoeoek M, Patti JM, House-Pompeo KL, Speziale P, Joh D;
 PI Mcgavin MJ;
 XX WPI; 1998-413816/35.
 DR
 XX
 PT Antibody that binds to fibronectin-binding protein, preventing its
 PT binding to fibronectin - used to treat or prevent bacterial infection,
 PT especially by Staphylococci and Streptococci.
 XX
 PS Example 8; Page 101; 201pp; English.
 XX The invention relates to antibodies that bind to a fibronectin-binding
 CC domain of a fibronectin-binding protein, and inhibit binding of the
 CC protein to fibronectin. Also claimed are: (1) isolated peptides of a
 CC fibronectin-binding protein that do not bind to fibronectin; (2) fusion
 CC protein containing at least one peptide of a fibronectin-binding protein
 CC linked to a second amino acid sequence; (3) nucleic acid encoding the
 CC isolated peptide of (1). Antibodies, the isolated peptides of (1) and the
 CC nucleic acids are all useful for immunisation (active or passive) or treating
 CC infection in humans or other animals, particularly by staphylococci or
 CC streptococci, e.g. meningitis, otitis media, pneumonia, endocarditis,
 CC mastitis in cattle, abortion in horses and many others. Since the
 CC antibodies block binding of bacteria, they should be effective against
 CC antibiotic-resistant strains, and may replace antibiotic therapy or
 CC increase its effectiveness. Sequences AAW65670-90 represent a series of
 CC synthetic peptides based on the D3 repeat of S. aureus fibronectin
 CC binding protein A. They were synthesised to contain a proline residue at
 CC each position through the sequence (ie a proline scan)
 XX
 SQ Sequence 21 AA;
 Query Match 100.0%; Score 58; DB 2; Length 21;
 Best Local Similarity 100.0%; Pred. No. 0.002;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 YQFGHNSVD 10
 |||||
 DB 4 YQFGHNSVD 13
 RESULT 9
 ID AAW65688 standard; peptide; 21 AA.
 AC AAW65688;
 XX 16-OCT-1998 (first entry)
 XX Fibronectin binding protein-derived peptide #32.
 DE microbial surface components recognising adhesive matrix molecule;
 KW MSCRAMM; fibronectin; fibronectin-binding protein; antibody; epitope;
 KW antibiotic; bacterial infection; antibiotic-resistant strain.
 XX Synthetic.
 OS Staphylococcus aureus.

XX
 PN WO9831389-A2.
 XX 23-JUL-1998.
 PD WO9831389-A2.
 XX 23-JUL-1998.
 PF 21-JAN-1998; 98MO-US001222.
 XX 21-JAN-1997; 97US-0036139P.
 XX (TEXA) UNIV TEXAS A & M SYSTEM.
 PA Hoeoek M, Patti JM, House-Pompeo KL, Speziale P, Joh D;
 PI Mcgavin MJ;
 XX WPI; 1998-413816/35.
 DR
 XX
 PT Antibody that binds to fibronectin-binding protein, preventing its
 PT binding to fibronectin - used to treat or prevent bacterial infection,
 PT especially by Staphylococci and Streptococci.
 XX
 PS Example 8; Page 101; 201pp; English.
 XX The invention relates to antibodies that bind to a fibronectin-binding
 CC domain of a fibronectin-binding protein, and inhibit binding of the
 CC protein to fibronectin. Also claimed are: (1) isolated peptides of a
 CC fibronectin-binding protein that do not bind to fibronectin; (2) fusion
 CC protein containing at least one peptide of a fibronectin-binding protein
 CC linked to a second amino acid sequence; (3) nucleic acid encoding the
 CC isolated peptide of (1). Antibodies, the isolated peptides of (1) and the
 CC nucleic acids are all useful for immunisation (active or passive) or treating
 CC infection in humans or other animals, particularly by staphylococci or
 CC streptococci, e.g. meningitis, otitis media, pneumonia, endocarditis,
 CC mastitis in cattle, abortion in horses and many others. Since the
 CC antibodies block binding of bacteria, they should be effective against
 CC antibiotic-resistant strains, and may replace antibiotic therapy or
 CC increase its effectiveness. Sequences AAW65670-90 represent a series of
 CC synthetic peptides based on the D3 repeat of S. aureus fibronectin
 CC binding protein A. They were synthesised to contain a proline residue at
 CC each position through the sequence (ie a proline scan)
 XX
 SQ Sequence 21 AA;
 Query Match 100.0%; Score 58; DB 2; Length 21;
 Best Local Similarity 100.0%; Pred. No. 0.002;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 YQFGHNSVD 10
 |||||
 DB 4 YQFGHNSVD 13
 RESULT 10
 ID AAW65672 standard; peptide; 21 AA.
 AC AAW65672;
 XX 16-OCT-1998 (first entry)
 XX Fibronectin binding protein-derived peptide #16.
 DE microbial surface components recognising adhesive matrix molecule;
 KW MSCRAMM; fibronectin; fibronectin-binding protein; antibody; epitope;
 KW antibiotic; bacterial infection; antibiotic-resistant strain.
 XX Synthetic.
 OS Staphylococcus aureus.
 PN WO9831389-A2.
 XX 23-JUL-1998.

PF 21-JAN-1998; 98WO-US001222.
 XX
 PR 21-JAN-1997; 97US-0036139P.
 XX
 PA (TEXA) UNIV TEXAS A & M SYSTEM.
 XX
 PI Hoeoek M, Patti JM, House-Pompeo KL, Speziale P, Joh D;
 PI McGavin MJ;
 XX
 DR WPI; 1998-413816/35.
 XX
 PT Antibody that binds to fibronectin-binding protein, preventing its
 PT binding to fibronectin - used to treat or prevent bacterial infection,
 PT especially by Staphylococci and Streptococci.
 XX
 PS Example 8; Page 100; 201pp; English.
 XX
 CC The invention relates to antibodies that bind to a fibronectin-binding
 CC domain of a fibronectin-binding protein, and inhibit binding of the
 CC protein to fibronectin. Also claimed are: (1) isolated peptides of a
 CC fibronectin-binding protein that do not bind to fibronectin; (2) fusion
 CC protein containing at least one peptide of a fibronectin-binding protein
 CC linked to a second amino acid sequence; (3) nucleic acid encoding the
 CC isolated peptide of (1). Antibodies, the isolated peptides of (1) and the
 CC nucleic acids are all useful for immunisation (active or passive) and (by
 CC inhibiting binding of bacteria to fibronectin) for preventing or treating
 CC infection in humans or other animals, particularly by staphylococci or
 CC streptococci, e.g. meningitis, otitis media, pneumonia, endocarditis,
 CC mastitis in cattle, abortion in horses and many others. Since the
 CC antibodies block binding of bacteria, they should be effective against
 CC antibiotic-resistant strains, and may replace antibiotic therapy or
 CC increase its effectiveness. Sequences AAW65670-90 represent a series of
 CC binding peptides based on the D3 repeat of S. aureus fibronectin
 CC binding protein A. They were synthesised to contain a proline residue at
 CC each position through the sequence (ie a proline scan)
 XX
 SQ Sequence 21 AA;
 XX
 QY
 Db 1 YQFGHNSVD 10
 4 YQFGHNSVD 13
 Query Match 100.0%; Score 58; DB 2; Length 21;
 Best Local Similarity 100.0%; Pred. No. 0.002;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 11
 AAW65687 standard; peptide; 21 AA.
 XX
 AC AAW65687;
 XX
 DT 16-OCT-1998 (first entry)
 XX
 DE Fibronectin binding protein-derived peptide #31.
 XX
 KM microbial surface components recognising adhesive matrix molecule;
 KM MSCRAMM; fibronectin; fibronectin-binding protein; antibody; epitope;
 KM antibiotic; bacterial infection; antibiotic-resistant strain.
 XX
 OS Synthetic.
 OS Staphylococcus aureus.
 XX
 PN WO981389-A2.
 XX
 PD 23-JUL-1998.
 XX
 PF 21-JAN-1998; 98WO-US001222.
 XX
 PR 21-JAN-1997; 97US-0036139P.
 XX
 PA (TEXA) UNIV TEXAS A & M SYSTEM.

XX
 PI Hoeoek M, Patti JM, House-Pompeo KL, Speziale P, Joh D;
 PI McGavin MJ;
 XX
 DR WPI; 1998-413816/35.
 XX
 PT Antibody that binds to fibronectin-binding protein, preventing its
 PT binding to fibronectin - used to treat or prevent bacterial infection,
 PT especially by Staphylococci and Streptococci.
 XX
 PS Example 8; Page 101; 201pp; English.
 XX
 CC The invention relates to antibodies that bind to a fibronectin-binding
 CC domain of a fibronectin-binding protein, and inhibit binding of the
 CC protein to fibronectin. Also claimed are: (1) isolated peptides of a
 CC fibronectin-binding protein that do not bind to fibronectin; (2) fusion
 CC protein containing at least one peptide of a fibronectin-binding protein
 CC linked to a second amino acid sequence; (3) nucleic acid encoding the
 CC isolated peptide of (1). Antibodies, the isolated peptides of (1) and the
 CC nucleic acids are all useful for immunisation (active or passive) and (by
 CC inhibiting binding of bacteria to fibronectin) for preventing or treating
 CC infection in humans or other animals, particularly by staphylococci or
 CC streptococci, e.g. meningitis, otitis media, pneumonia, endocarditis,
 CC mastitis in cattle, abortion in horses and many others. Since the
 CC antibodies block binding of bacteria, they should be effective against
 CC antibiotic-resistant strains, and may replace antibiotic therapy or
 CC increase its effectiveness. Sequences AAW65670-90 represent a series of
 CC synthetic peptides based on the D3 repeat of S. aureus fibronectin
 CC binding protein A. They were synthesised to contain a proline residue at
 CC each position through the sequence (ie a proline scan)
 XX
 SQ Sequence 21 AA;
 XX
 QY
 Db 1 YQFGHNSVD 10
 4 YQFGHNSVD 13
 Query Match 100.0%; Score 58; DB 2; Length 21;
 Best Local Similarity 100.0%; Pred. No. 0.002;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 12
 AAW65686 standard; peptide; 21 AA.
 XX
 AC AAW65686;
 XX
 DT 16-OCT-1998 (first entry)
 XX
 DE Fibronectin binding protein-derived peptide #30.
 XX
 KM microbial surface components recognising adhesive matrix molecule;
 KM MSCRAMM; fibronectin; fibronectin-binding protein; antibody; epitope;
 KM antibiotic; bacterial infection; antibiotic-resistant strain.
 XX
 OS Synthetic.
 OS Staphylococcus aureus.
 XX
 PN WO981389-A2.
 XX
 PD 23-JUL-1998.
 XX
 PF 21-JAN-1998; 98WO-US001222.
 XX
 PR 21-JAN-1997; 97US-0036139P.
 XX
 PA (TEXA) UNIV TEXAS A & M SYSTEM.
 XX
 PI Hoeoek M, Patti JM, House-Pompeo KL, Speziale P, Joh D;
 PI McGavin MJ;
 XX
 DR WPI; 1998-413816/35.

XX Antibody that binds to fibronectin-binding protein, preventing its
 PT binding to fibronectin - used to treat or prevent bacterial infection,
 PT especially by Staphylococci and Streptococci.

XX Example 8; Page 101; 201pp; English.

PS The invention relates to antibodies that bind to a fibronectin-binding
 CC domain of a fibronectin-binding protein, and inhibit binding of the
 CC protein to fibronectin. Also claimed are: (1) isolated peptides of a
 CC fibronectin-binding protein that do not bind to fibronectin; (2) fusion
 CC protein containing at least one peptide of a fibronectin-binding protein
 CC linked to a second amino acid sequence; (3) nucleic acid encoding the
 CC isolated peptide of (1). Antibodies, the isolated peptides of (1) and the
 CC nucleic acids are all useful for immunisation (active or passive) and (by
 CC inhibiting binding of bacteria to fibronectin) for preventing or treating
 CC infection in humans or other animals, particularly by staphylococci or
 CC streptococci, e.g. meningitis, otitis media, pneumonia, endocarditis,
 CC mastitis in cattle, abortion in horses and many others. Since the
 CC antibodies block binding of bacteria, they should be effective against
 CC antibiotic-resistant strains, and may replace antibiotic therapy or
 CC increase its effectiveness. Sequences AAM65670-90 represent a series of
 CC synthetic peptides based on the D3 repeat of S. aureus fibronectin
 CC binding protein A. They were synthesised to contain a proline residue at
 CC each position throughout the sequence (ie a proline scan)

XX Sequence 21 AA;

Query Match 100.0%; Score 58; DB 2; Length 21;
 Best Local Similarity 100.0%; Pred. No. 0.002;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YQFGHNSVD 10
 |||||
 Db 4 YQFGHNSVD 13

RESULT 13

AAM65665
 ID AAM65665 standard; peptide; 21 AA.

XX AAM65665;
 AC
 XX
 DT 16-OCT-1998 (first entry)
 XX

DE Fibronectin binding protein-derived peptide #9.

XX microbial surface components recognising adhesive matrix molecule;
 KM MSCRAMM; fibronectin; fibronectin-binding protein; antibody; epitope;
 KM antibiotic; bacterial infection; antibiotic-resistant strain.

XX Synthetic.
 OS Staphylococcus aureus.

XX WO9831389-A2.

XX 23-JUL-1998.

XX 21-JAN-1998; 98WO-US001222.

XX 21-JAN-1997; 97US-0036139P.

XX (TEXA) UNIV TEXAS A & M SYSTEM.

XX Hosoe M, Patti JM, House-Pompeo KI, Speciale P, Joh D;
 PI Mcgavin M;

XX WPI, 1998-413016/35.

PT Antibody that binds to fibronectin-binding protein, preventing its
 PT binding to fibronectin - used to treat or prevent bacterial infection,
 PT especially by Staphylococci and Streptococci.

PS Example 2; Page 92; 201pp; English.

XX The invention relates to antibodies that bind to a fibronectin-binding
 CC domain of a fibronectin-binding protein, and inhibit binding of the
 CC protein to fibronectin. Also claimed are: (1) isolated peptides of a
 CC fibronectin-binding protein that do not bind to fibronectin; (2) fusion
 CC protein containing at least one peptide of a fibronectin-binding protein
 CC linked to a second amino acid sequence; (3) nucleic acid encoding the
 CC isolated peptide of (1). Antibodies, the isolated peptides of (1) and the
 CC nucleic acids are all useful for immunisation (active or passive) and (by
 CC inhibiting binding of bacteria to fibronectin) for preventing or treating
 CC infection in humans or other animals, particularly by staphylococci or
 CC streptococci, e.g. meningitis, otitis media, pneumonia, endocarditis,
 CC mastitis in cattle, abortion in horses and many others. Since the
 CC antibodies block binding of bacteria, they should be effective against
 CC antibiotic-resistant strains, and may replace antibiotic therapy or
 CC increase its effectiveness. Sequences AAM65659-68 represent synthetic
 CC epitopes from the fibronectin binding domains DU and D1-D4 of the S.
 CC aureus fnbA gene

XX Sequence 21 AA;

Query Match 100.0%; Score 58; DB 2; Length 21;
 Best Local Similarity 100.0%; Pred. No. 0.002;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YQFGHNSVD 10
 |||||
 Db 4 YQFGHNSVD 13

RESULT 14

AAR21340
 ID AAR21340 standard; peptide; 22 AA.

XX AAR21340;

XX 25-MAR-2003 (revised)
 DT 15-JUN-1992 (first entry)
 XX

DE Fibronectin binding protein.

XX FMBP; wound infection reduction; vaccination; mastitis;
 KM Staphylococcal infections; D3.

XX Synthetic.

XX WO9202555-A.

XX 20-FEB-1992.

XX 10-AUG-1990; 90SE-00002617.

XX 10-AUG-1990; 90SE-00002617.

XX (ALFA) ALFA LAVAL AGRIC INT AB.

XX Hook M, McGavin M, Raucel G;

XX WPI, 1992-080035/10.

PT New fibronectin binding peptide - combines with fusion peptide to form
 PT large antigen, used in immunisation, diagnosis and for treating wounds.

XX Claim 1; Page 22; 33pp; English.

XX The sequence comprises amino acids 17-33 of a tandem repeat, designated
 CC D3 of the fibronectin binding site of Staphylococcus aureus 8325-4 FMBP.
 CC The N-terminal DK may be replaced with H or K, and the C-terminal LKP may
 CC be replaced by either L, LP, or OH. The peptides were synthesised using
 CC standard methods and purified using reverse phase HPLC. The appropriate
 CC fractions were dialysed and lyophilised. Peptide sequencing was performed
 CC and the peptides digested and chemically modified by dihydroxypropylation

CC of the amino side chain of lysine. The carboxylic side chains were
 CC converted to glycine methyl esters. The phenyl side chains of tyrosine
 CC residues were oxidised. Chemically modified peptide D3 was compared to
 CC unmodified D3. Lysine and tyrosine modifications only partially
 CC diminished its activity whereas modification of aspartic/glutamic
 CC residues resulted in complete loss of activity. The peptide can be used
 CC for the prevention or reduction of the risk of wound infection. The
 CC peptide can be used to create a large antigen for vaccinating ruminants
 CC against mastitis caused by Staphylococcal infections. It can also be used
 CC to diagnose Staphylococcal infections using ELISA or DNA probes. (Updated
 CC on 25-MAR-2003 to correct PA field.)
 XX

SQ Sequence 22 AA;

Query Match 100.0%; Score 58; DB 2; Length 22;
 Best Local Similarity 100.0%; Pred. No. 0.0021;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YQFGHNSVD 10
 |||||
 Db 5 YQFGHNSVD 14

RESULT 15

AAB91958
 ID AAB91958 standard; peptide; 37 AA.

XX AAB91958;

XX 22-JUN-2001 (first entry)

XX Fibronectin fragment and fibrin related peptide SEQ ID NO:1134.

XX Protection; endogenous therapeutic peptide; peptidase; conjugation;
 KM blood component; modification; succinimidyl; maleimido group; amino;
 KW hydroxyl; thiol; hormone; growth factor; neurotransmitter.

XX Homo sapiens.
 OS Synthetic.

XX MO200069900-A2.

XX 23-NOV-2000.

XX 17-MAY-2000; 2000MO-US013576.

XX 17-MAY-1999; 99US-0134406P.

XX 10-SEP-1999; 99US-0153406P.

XX 15-OCT-1999; 99US-0159783P.

XX (CONF-) CONTUCHEM INC.

XX Bridon DP, Ezrin AM, Milner PG, Holmes DL, Thibaudau K;

XX MPI; 2001-112059/12.

XX Modifying and attaching therapeutic peptides to albumin prevents
 PT peptidase degradation, useful for increasing length of in vivo activity.

XX Disclosure, Page 566, 733pp, English.

XX The present invention describes a modified therapeutic peptide (I)
 CC comprising a therapeutically active amino acid region (III) and a
 CC reactive group (II) (e.g. succinimidyl and maleimido groups) attached to
 CC a less therapeutically active amino acid region (IV), which covalently
 CC bonds with amino/hydroxyl/thiol groups on blood components to form a
 CC peptidase stabilised therapeutic peptide composed of 3-50 amino acids.
 CC (I) are useful for modifying therapeutic peptides e.g. hormones, growth
 CC factors and neurotransmitters, to protect them from peptidase activity in
 CC vivo for the treatment of various disorders. Endogenous therapeutic
 CC peptides are not suitable as drug candidates as they require frequent
 CC administration due to rapid degradation by peptidases in the body.
 CC Modifying and attaching therapeutic peptides to albumin prevents or

CC reduces the action of peptidases to increase length of activity (half
 CC life) and specificity as bonding to large molecules decreases
 CC intracellular uptake and interference with physiological processes.
 CC AAB90829 to AAB92441 represent peptides which can be used in the
 CC exemplification of the present invention
 XX

SQ Sequence 37 AA;

Query Match 100.0%; Score 58; DB 4; Length 37;
 Best Local Similarity 100.0%; Pred. No. 0.0037;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YQFGHNSVD 10
 |||||
 Db 19 YQFGHNSVD 28

Search completed: October 25, 2005, 21:29:13
 Job time : 69.7126 secs

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OM protein - protein search, using sw model

Run on: October 22, 2005, 07:41:53 ; Search time 17.2989 Seconds
(without alignments)
43.153 Million cell updates/sec

Title: US-10-731-238-97

Sequence: 1 YQFGHNSVD 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :
1: /cgn2_6/ptodata/1/iaa/5A.COMB.pep.*
2: /cgn2_6/ptodata/1/iaa/5B.COMB.pep.*
3: /cgn2_6/ptodata/1/iaa/6A.COMB.pep.*
4: /cgn2_6/ptodata/1/iaa/6B.COMB.pep.*
5: /cgn2_6/ptodata/1/iaa/PCTUS.COMB.pep.*
6: /cgn2_6/ptodata/1/iaa/backfile1.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	58	100.0	10	4	US-09-010-317-97
2	58	100.0	19	1	US-08-234-622A-1
3	58	100.0	21	4	US-09-010-317-9
4	58	100.0	21	4	US-09-010-317-14
5	58	100.0	21	4	US-09-010-317-15
6	58	100.0	21	4	US-09-010-317-16
7	58	100.0	21	4	US-09-010-317-26
8	58	100.0	21	4	US-09-010-317-27
9	58	100.0	21	4	US-09-010-317-28
10	58	100.0	21	4	US-09-010-317-29
11	58	100.0	21	4	US-09-010-317-30
12	58	100.0	21	4	US-09-010-317-31
13	58	100.0	21	4	US-09-010-317-32
14	58	100.0	21	4	US-09-010-317-33
15	58	100.0	37	1	US-08-234-622A-4
16	58	100.0	38	1	US-08-294-189-8
17	58	100.0	38	1	US-08-729-767-5
18	58	100.0	114	1	US-08-259-000-3
19	58	100.0	130	2	US-08-459-135A-7
20	58	100.0	130	2	US-08-459-135A-8
21	58	100.0	130	3	US-08-495-559-7
22	58	100.0	130	3	US-08-495-559-8
23	58	100.0	139	3	US-08-856-253-8
24	58	100.0	174	2	US-08-459-135A-10
25	58	100.0	174	2	US-08-459-135A-13
26	58	100.0	174	3	US-08-495-559-10
27	58	100.0	174	3	US-08-495-559-13

28	58	100.0	176	3	US-08-495-559-6	Sequence 6, Appl
29	58	100.0	178	2	US-08-459-135A-12	Sequence 12, Appl
30	58	100.0	178	3	US-08-495-559-12	Sequence 12, Appl
31	58	100.0	181	2	US-08-459-135A-6	Sequence 6, Appl
32	58	100.0	559	4	US-08-956-171E-5251	Sequence 5251, Ap
33	58	100.0	559	4	US-08-781-986A-5251	Sequence 5251, Ap
34	58	100.0	1027	4	US-08-956-171E-5254	Sequence 5254, Ap
35	58	100.0	1027	4	US-08-781-986A-5254	Sequence 5254, Ap
36	53	91.4	21	4	US-09-010-317-23	Sequence 23, Appl
37	52	89.7	21	4	US-09-010-317-18	Sequence 18, Appl
38	52	89.7	21	4	US-09-010-317-24	Sequence 24, Appl
39	52	89.7	21	4	US-09-010-317-25	Sequence 25, Appl
40	51	87.9	14	4	US-09-010-317-61	Sequence 61, Appl
41	51	87.9	21	4	US-09-010-317-17	Sequence 17, Appl
42	50	86.2	21	4	US-09-010-317-10	Sequence 10, Appl
43	50	86.2	21	4	US-09-010-317-20	Sequence 20, Appl
44	50	86.2	21	4	US-09-010-317-22	Sequence 22, Appl
45	50	86.2	22	4	US-09-010-317-13	Sequence 13, Appl

ALIGNMENTS

RESULT 1
US-09-010-317-97
Sequence 97, Application US/09010317
Patent No. 6685943
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
APPLICANT: Patti, Joseph M.
APPLICANT: House, Pompeo, Karen L.
APPLICANT: Speziale, Pietro
APPLICANT: Job, Danny
APPLICANT: Mcgavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
TITLE OF INVENTION: AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAMK:189
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 97:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-09-010-317-97
Query Match 100.0%; Score 58; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.00018;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YORFGHNSVD 10
1 YORFGHNSVD 10

RESULT 2

US-08-234-622A-1
; Sequence 1, Application US/08234622A
; Patent No. 5440014
; GENERAL INFORMATION:
; APPLICANT: HOOK, Magnus
; APPLICANT: MCGAVIN, Martin
; APPLICANT: RAUCCI, Giuseppe
; TITLE OF INVENTION: A FIBRONECTIN BINDING PEPTIDE
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Doane, Swecker & Mathis
; STREET: P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-POS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/234,622A
; FILING DATE: 28-APR-1994
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: SE 9002617-0
; FILING DATE: 10-AUG-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/SE91/00534
; FILING DATE: 09-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Meuth, Donna M
; REGISTRATION NUMBER: 36,607
; REFERENCE/DOCKET NUMBER: 012885-044
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ. ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 19 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1
; OTHER INFORMATION: /note= "Amino acid 1 is R' wherein
; OTHER INFORMATION: R' is hydrogen, K or DK."
; NAME/KEY: Peptide
; LOCATION: 19
; OTHER INFORMATION: /note= "Amino acid 19 is R2 wherein
; OTHER INFORMATION: R2 is hydroxy, L, LP or LPK."
US-08-234-622A-1

Query Match 100.0%; Score 58; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 0.00035;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YORFGHNSVD 10
4 YORFGHNSVD 13

RESULT 3

US-09-010-317-9
; Sequence 9, Application US/09010317
; Patent No. 6685943
; GENERAL INFORMATION:
; APPLICANT: Hook, Magnus
; APPLICANT: Patil, Joseph M.
; APPLICANT: House-Pompeo, Karen L.
; APPLICANT: Speziale, Pietro
; APPLICANT: Joh, Danny
; APPLICANT: McGavin, Martin J.
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
; NUMBER OF SEQUENCES: 105
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: TX
; COUNTRY: USA
; ZIP: 77210-4433
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/010,317
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/036,139
; FILING DATE: 21-JAN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Hibler, David W.
; REGISTRATION NUMBER: 41,071
; REFERENCE/DOCKET NUMBER: TANK:189
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 512-418-3000
; TELEFAX: 512-474-7577
; INFORMATION FOR SEQ. ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
US-09-010-317-9

Query Match 100.0%; Score 58; DB 4; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.00039;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YORFGHNSVD 10
4 YORFGHNSVD 13

RESULT 4

US-09-010-317-14
; Sequence 14, Application US/09010317
; Patent No. 6685943
; GENERAL INFORMATION:
; APPLICANT: Hook, Magnus
; APPLICANT: Patil, Joseph M.
; APPLICANT: House-Pompeo, Karen L.
; APPLICANT: Speziale, Pietro
; APPLICANT: Joh, Danny
; APPLICANT: McGavin, Martin J.
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
; NUMBER OF SEQUENCES: 105
; CORRESPONDENCE ADDRESS:

ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-09-010-317-14

Query Match 100.0%; Score 58; DB 4; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.00039;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 YQFGHNSVD 10
|||
Db 4 YQFGHNSVD 13

RESULT 5
US-09-010-317-15
Sequence 15, Application US/09010317
Patent No. 6685943
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
APPLICANT: Patti, Joseph M.
APPLICANT: House-Pompeo, Karen L.
APPLICANT: Speziale, Pietro
APPLICANT: John, Danny
APPLICANT: McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-09-010-317-15

Query Match 100.0%; Score 58; DB 4; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.00039;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 YQFGHNSVD 10
|||
Db 4 YQFGHNSVD 13

RESULT 6
US-09-010-317-16
Sequence 16, Application US/09010317
Patent No. 6685943
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
APPLICANT: Patti, Joseph M.
APPLICANT: House-Pompeo, Karen L.
APPLICANT: Speziale, Pietro
APPLICANT: John, Danny
APPLICANT: McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-09-010-317-16

Query Match 100.0%; Score 58; DB 4; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.00039;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YQFGHNSVD 10
| | | | | | | | | |
| | | | | | | | | |
Db 4 YQFGHNSVD 13

RESULT 7
US-09-010-317-26
; Sequence 26, Application US/09010317
; Patent No. 6685943
; GENERAL INFORMATION:
; APPLICANT: Hook, Magnus
; APPLICANT: Patti, Joseph M.
; APPLICANT: House-Pompeo, Karen L.
; APPLICANT: Speziale, Pietro
; APPLICANT: John, Danny
; APPLICANT: McGavin, Martin J.
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
; NUMBER OF SEQUENCES: 105
; TITLE OF INVENTION: AND METHODS OF USE
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: TX
; COUNTRY: USA
; ZIP: 77210-4433
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Releasee #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/010,317
; FILING DATE:
; STRANDEDNESS:
; TOPOLOGY: linear
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/036,139
; FILING DATE: 21-JAN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Hibler, David W.
; REGISTRATION NUMBER: 41,071
; REFERENCE/DOCKET NUMBER: TAMK:189
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 512-418-3000
; TELEFAX: 512-474-7577
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
US-09-010-317-26

Query Match 100.0%; Score 58; DB 4; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.00039;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YQFGHNSVD 10
| | | | | | | | | |
| | | | | | | | | |
Db 4 YQFGHNSVD 13

RESULT 8
US-09-010-317-27
; Sequence 27, Application US/09010317
; Patent No. 6685943
; GENERAL INFORMATION:
; APPLICANT: Hook, Magnus

; APPLICANT: Patti, Joseph M.
; APPLICANT: House-Pompeo, Karen L.
; APPLICANT: Speziale, Pietro
; APPLICANT: John, Danny
; APPLICANT: McGavin, Martin J.
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
; NUMBER OF SEQUENCES: 105
; TITLE OF INVENTION: AND METHODS OF USE
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: TX
; COUNTRY: USA
; ZIP: 77210-4433

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Releasee #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE:
STRANDEDNESS:
TOPOLOGY: linear

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAMK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577

INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-09-010-317-27

Query Match 100.0%; Score 58; DB 4; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.00039;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YQFGHNSVD 10
| | | | | | | | | |
| | | | | | | | | |
Db 4 YQFGHNSVD 13

RESULT 9
US-09-010-317-28
; Sequence 28, Application US/09010317
; Patent No. 6685943
; GENERAL INFORMATION:
; APPLICANT: Hook, Magnus
; APPLICANT: Patti, Joseph M.
; APPLICANT: House-Pompeo, Karen L.
; APPLICANT: Speziale, Pietro
; APPLICANT: John, Danny
; APPLICANT: McGavin, Martin J.
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
; NUMBER OF SEQUENCES: 105
; TITLE OF INVENTION: AND METHODS OF USE
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: TX
; COUNTRY: USA
; ZIP: 77210-4433
COMPUTER READABLE FORM:

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Releasee #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE:
STRANDEDNESS:
TOPOLOGY: linear

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAMK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/010.317
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-09-010-317-28

Query Match 100.0%; Score 58; DB 4; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.00039;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YQFGHNSVD 10
Db 4 YQFGHNSVD 13

RESULT 10
US-09-010-317-29
Sequence 29, Application US/09010317
Patent No. 6685943
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
APPLICANT: Patti, Joseph M.
APPLICANT: House-Pompeo, Karen L.
APPLICANT: Speziale, Pietro
APPLICANT: Joh, Danny
APPLICANT: McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
TITLE OF INVENTION: AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/010.317
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAWK:189
TELECOMMUNICATION INFORMATION:

TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 29:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-09-010-317-29

Query Match 100.0%; Score 58; DB 4; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.00039;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YQFGHNSVD 10
Db 4 YQFGHNSVD 13

RESULT 11
US-09-010-317-30
Sequence 30, Application US/09010317
Patent No. 6685943
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
APPLICANT: Patti, Joseph M.
APPLICANT: House-Pompeo, Karen L.
APPLICANT: Speziale, Pietro
APPLICANT: Joh, Danny
APPLICANT: McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
TITLE OF INVENTION: AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/010.317
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAWK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-09-010-317-30

Query Match 100.0%; Score 58; DB 4; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.00039;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YQFGHNSVD 10
Db 4 YQFGHNSVD 13

Db 4 YQFGHNSVD 13

RESULT 12

US-09-010-317-31

; Sequence 31, Application US/09010317
; Patent No. 6685943

GENERAL INFORMATION:

APPLICANT: Hook, Magnus

APPLICANT: Patti, Joseph M.

APPLICANT: House-Pompeo, Karen L.

APPLICANT: Speziale, Pietro

APPLICANT: McGavin, Martin J.

TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS

TITLE OF INVENTION: AND METHODS OF USE

NUMBER OF SEQUENCES: 105

CORRESPONDENCE ADDRESS:

ADDRESSEE: Arnold, White & Durkee

STREET: P.O. Box 4433

CITY: Houston

STATE: TX

COUNTRY: USA

ZIP: 77210-4433

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/010,317

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 60/036,139

FILING DATE: 21-JAN-1997

ATTORNEY/AGENT INFORMATION:

NAME: Hibler, David W.

REGISTRATION NUMBER: 41,071

REFERENCE/DOCKET NUMBER: TANK:189

TELECOMMUNICATION INFORMATION:

TELEPHONE: 512-418-3000

TELEFAX: 512-474-7577

INFORMATION FOR SEQ ID NO: 31:

SEQUENCE CHARACTERISTICS:

LENGTH: 21 amino acids

TYPE: amino acid

STRANDEDNESS:

TOPOLOGY: linear

US-09-010-317-31

Query Match 100.0%; Score 58; DB 4; Length 21;

Best Local Similarity 100.0%; Pred. No. 0.00039;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YQFGHNSVD 10

Db 4 YQFGHNSVD 13

RESULT 13

US-09-010-317-32

; Sequence 32, Application US/09010317
; Patent No. 6685943

GENERAL INFORMATION:

APPLICANT: Hook, Magnus

APPLICANT: Patti, Joseph M.

APPLICANT: House-Pompeo, Karen L.

APPLICANT: Speziale, Pietro

APPLICANT: McGavin, Martin J.

TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS

TITLE OF INVENTION: AND METHODS OF USE

NUMBER OF SEQUENCES: 105

CORRESPONDENCE ADDRESS:

ADDRESSEE: Arnold, White & Durkee

STREET: P.O. Box 4433

CITY: Houston

STATE: TX

COUNTRY: USA

ZIP: 77210-4433

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/010,317

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 60/036,139

FILING DATE: 21-JAN-1997

ATTORNEY/AGENT INFORMATION:

NAME: Hibler, David W.

REGISTRATION NUMBER: 41,071

REFERENCE/DOCKET NUMBER: TANK:189

TELECOMMUNICATION INFORMATION:

TELEPHONE: 512-418-3000

TELEFAX: 512-474-7577

INFORMATION FOR SEQ ID NO: 32:

SEQUENCE CHARACTERISTICS:

LENGTH: 21 amino acids

TYPE: amino acid

STRANDEDNESS:

TOPOLOGY: linear

US-09-010-317-32

Query Match 100.0%; Score 58; DB 4; Length 21;

Best Local Similarity 100.0%; Pred. No. 0.00039;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YQFGHNSVD 10

Db 4 YQFGHNSVD 13

RESULT 14

US-09-010-317-33

; Sequence 33, Application US/09010317
; Patent No. 6685943

GENERAL INFORMATION:

APPLICANT: Hook, Magnus

APPLICANT: Patti, Joseph M.

APPLICANT: House-Pompeo, Karen L.

APPLICANT: Speziale, Pietro

APPLICANT: McGavin, Martin J.

TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS

TITLE OF INVENTION: AND METHODS OF USE

NUMBER OF SEQUENCES: 105

CORRESPONDENCE ADDRESS:

ADDRESSEE: Arnold, White & Durkee

STREET: P.O. Box 4433

CITY: Houston

STATE: TX

COUNTRY: USA

ZIP: 77210-4433

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/010,317

FILING DATE:

CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAMR:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-09-010-317-33

Query Match 100.0%; Score 58; DB 4; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.00039;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YQFGHNSVD 10
Db 4 YQFGHNSVD 13

RESULT 15
US-08-234-622A-4
Sequence 4, Application US/08234622A
Patent No. 5440014
GENERAL INFORMATION:
APPLICANT: HOOK, Magnus
APPLICANT: MCGAVIN, Martin
APPLICANT: RAUCCI, Giuseppe
TITLE OF INVENTION: A FIBRONECTIN BINDING PEPTIDE
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Burns, Doane, Swecker & Mathis
STREET: P.O. Box 1404
CITY: Alexandria
STATE: Virginia
COUNTRY: United States
ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/234,622A
FILING DATE: 28-APR-1994
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: SE 9002617-0
FILING DATE: 10-AUG-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/SE91/00534
FILING DATE: 09-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: Meuch, Donna M
REGISTRATION NUMBER: 36,607
REFERENCE/DOCKET NUMBER: 012885-044
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 37 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear

MOLECULE TYPE: peptide
US-08-234-622A-4

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Best Local Similarity 100.0%; Pred. No. 0.00072;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YQFGHNSVD 10
Db 19 YQFGHNSVD 28

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Job time: 17.2989 secs

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OM protein - protein search, using sw model

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Searched: 1862951 seqs, 417491010 residues

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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	58	100.0	21	US-10-731-238-9	Sequence 9, Appl
3	58	100.0	21	US-10-731-238-14	Sequence 14, Appl
4	58	100.0	21	US-10-731-238-15	Sequence 15, Appl
5	58	100.0	21	US-10-731-238-16	Sequence 16, Appl
6	58	100.0	21	US-10-731-238-26	Sequence 26, Appl
7	58	100.0	21	US-10-731-238-27	Sequence 27, Appl
8	58	100.0	21	US-10-731-238-28	Sequence 28, Appl
9	58	100.0	21	US-10-731-238-29	Sequence 29, Appl
10	58	100.0	21	US-10-731-238-30	Sequence 30, Appl
11	58	100.0	21	US-10-731-238-31	Sequence 31, Appl

12	58	100.0	21	18	US-10-731-238-32	Sequence 32, Appl
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32	52	89.7	21	18 <td>US-10-731-238-24</td> <td>Sequence 24, Appl</td>	US-10-731-238-24	Sequence 24, Appl
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34	51	87.9	14	18 <td>US-10-731-238-61</td> <td>Sequence 61, Appl</td>	US-10-731-238-61	Sequence 61, Appl
35	51	87.9	21	18 <td>US-10-731-238-17</td> <td>Sequence 17, Appl</td>	US-10-731-238-17	Sequence 17, Appl
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ALIGNMENTS

RESULT 1
US-10-731-238-97
Sequence 97, Application US/10731238
Publication No. US20050123552A1
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
Patel, Joseph M.
House-Pompeo, Karen L.
Speziale, Pietro
Joh, Danny
McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/731, 238
FILING DATE: 10-Dec-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/010, 317
FILING DATE: 21-Jan-1998
APPLICATION NUMBER: US 60/036, 139

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; FILING DATE: 21-JAN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Hibler, David W.
; REGISTRATION NUMBER: 41,071
; REFERENCE/DOCKET NUMBER: TAMK:189
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 512-418-3000
; TELEFAX: 512-474-7577
; INFORMATION FOR SEQ ID NO: 97:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 97:
US-10-731-238-97

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Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db       1 YQFGGHSVD 10

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; GENERAL INFORMATION:
; APPLICANT: Hook, Magnus
; Patti, Joseph M.
; House-Pompeo, Karen L.
; Speziale, Pietro
; John, Danny
; McGavin, Martin J.
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
; AND METHODS OF USE
; NUMBER OF SEQUENCES: 105
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: TX
; COUNTRY: USA
; ZIP: 77210-4433
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/731,238
; FILING DATE: 10-Dec-2003
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; APPLICATION NUMBER: US/09/010,317
; FILING DATE: 21-Jan-1998
; APPLICATION NUMBER: US 60/036,139
; FILING DATE: 21-JAN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Hibler, David W.
; REGISTRATION NUMBER: 41,071
; REFERENCE/DOCKET NUMBER: TAMK:189
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 512-418-3000
; TELEFAX: 512-474-7577
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; STRANDEDNESS: <Unknown>
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; TOPOLOGY: linear
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Db       4 YQFGGHSVD 13

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; GENERAL INFORMATION:
; APPLICANT: Hook, Magnus
; Patti, Joseph M.
; House-Pompeo, Karen L.
; Speziale, Pietro
; John, Danny
; McGavin, Martin J.
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
; AND METHODS OF USE
; NUMBER OF SEQUENCES: 105
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: TX
; COUNTRY: USA
; ZIP: 77210-4433
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
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; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
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; FILING DATE: 10-Dec-2003
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/010,317
; FILING DATE: 21-Jan-1998
; APPLICATION NUMBER: US 60/036,139
; FILING DATE: 21-JAN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Hibler, David W.
; REGISTRATION NUMBER: 41,071
; REFERENCE/DOCKET NUMBER: TAMK:189
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 512-418-3000
; TELEFAX: 512-474-7577
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 14:
US-10-731-238-14

Query Match      100.0%; Score 58; DB 18; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.0025;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 YQFGGHSVD 10
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Db       4 YQFGGHSVD 13
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RESULT 4
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; Sequence 15, Application US/10731238
; Publication No. US20050123552A1
; GENERAL INFORMATION:
;   APPLICANT: Hook, Magnus
;             Patti, Joseph M.
;             House-Pompeo, Karen L.
;             Speziale, Pietro
;             Joh, Danny
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
; AND METHODS OF USE
; NUMBER OF SEQUENCES: 105
; CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Arnold, White & Durkee
;   STREET: P.O. Box 4433
;   CITY: Houston
;   STATE: TX
;   COUNTRY: USA
;   ZIP: 77210-4433
; COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/10/731,238
;   FILING DATE: 10-Dec-2003
;   CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US/09/010,317
;   FILING DATE: 21-Jan-1998
;   APPLICATION NUMBER: US 60/036,139
;   FILING DATE: 21-Jan-1997
; ATTORNEY/AGENT INFORMATION:
;   NAME: Hibler, David W.
;   REGISTRATION NUMBER: 41,071
;   REFERENCE/DOCKET NUMBER: TANK:189
; TELECOMMUNICATION INFORMATION:
;   TELEPHONE: 512-418-3000
;   TELEFAX: 512-474-7577
; INFORMATION FOR SEQ ID NO: 15:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH: 21 amino acids
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;     STRANDEDNESS: <Unknown>
;     TOPOLOGY: linear
;   SEQUENCE DESCRIPTION: SEQ ID NO: 15:
US-10-731-238-15

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Best Local Similarity 100.0%; Pred. No. 0.0025;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 YQFGGHSVD 10
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        4 YQFGGHSVD 13

Db

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; Sequence 16, Application US/10731238
; Publication No. US20050123552A1
; GENERAL INFORMATION:
;   APPLICANT: Hook, Magnus
;             Patti, Joseph M.
;             House-Pompeo, Karen L.
;             Speziale, Pietro
;             Joh, Danny
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
; AND METHODS OF USE
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NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
  ADDRESSEE: Arnold, White & Durkee
  STREET: P.O. Box 4433
  CITY: Houston
  STATE: TX
  COUNTRY: USA
  ZIP: 77210-4433
COMPUTER READABLE FORM:
  MEDIUM TYPE: Floppy disk
  OPERATING SYSTEM: PC-DOS/MS-DOS
  SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
  APPLICATION NUMBER: US/10/731,238
  FILING DATE: 10-Dec-2003
  CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
  APPLICATION NUMBER: US/09/010,317
  FILING DATE: 21-Jan-1998
  APPLICATION NUMBER: US 60/036,139
  FILING DATE: 21-Jan-1997
ATTORNEY/AGENT INFORMATION:
  NAME: Hibler, David W.
  REGISTRATION NUMBER: 41,071
  REFERENCE/DOCKET NUMBER: TANK:189
TELECOMMUNICATION INFORMATION:
  TELEPHONE: 512-418-3000
  TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 16:
  SEQUENCE CHARACTERISTICS:
    LENGTH: 21 amino acids
    TYPE: amino acid
    STRANDEDNESS: <Unknown>
    TOPOLOGY: linear
  SEQUENCE DESCRIPTION: SEQ ID NO: 16:
US-10-731-238-16

Query Match      100.0%; Score 58; DB 18; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.0025;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 YQFGGHSVD 10
        |||||
        4 YQFGGHSVD 13

Db

RESULT 6
US-10-731-238-26
; Sequence 26, Application US/10731238
; Publication No. US20050123552A1
; GENERAL INFORMATION:
;   APPLICANT: Hook, Magnus
;             Patti, Joseph M.
;             House-Pompeo, Karen L.
;             Speziale, Pietro
;             Joh, Danny
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
; AND METHODS OF USE
; NUMBER OF SEQUENCES: 105
; CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Arnold, White & Durkee
;   STREET: P.O. Box 4433
;   CITY: Houston
;   STATE: TX
;   COUNTRY: USA
;   ZIP: 77210-4433
; COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: Patentin Release #1.0, Version #1.30
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;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/731,238
; FILING DATE: 10-Dec-2003
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/010,317
; FILING DATE: 21-Jan-1998
; APPLICATION NUMBER: US 60/036,139
; FILING DATE: 21-JAN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Hibler, David W.
; REGISTRATION NUMBER: 41,071
; REFERENCE/DOCKET NUMBER: TAMK:189
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 512-418-3000
; TELEFAX: 512-474-7577
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 26:
US-10-731-238-26

Query Match      100.0%; Score 58; DB 18; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.0025;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 YQFGGHSVD 10
        |||||
        4 YQFGGHSVD 13

RESULT 7
US-10-731-238-27
; Sequence 27, Application US/10731238
; Publication No. US20050123552A1
; GENERAL INFORMATION:
; APPLICANT: Hook, Magnus
;          Patti, Joseph M.
;          House-Pompeo, Karen L.
;          Speziale, Pietro
;          Jon, Danny
;          McGavin, Martin J.
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
; AND METHODS OF USE
; NUMBER OF SEQUENCES: 105
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: TX
; COUNTRY: USA
; ZIP: 77210-4433
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/731,238
; FILING DATE: 10-Dec-2003
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/010,317
; FILING DATE: 21-Jan-1998
; APPLICATION NUMBER: US 60/036,139
; FILING DATE: 21-JAN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Hibler, David W.
; REGISTRATION NUMBER: 41,071
; REFERENCE/DOCKET NUMBER: TAMK:189
```

```

;
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 512-418-3000
; TELEFAX: 512-474-7577
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 27:
US-10-731-238-27

Query Match      100.0%; Score 58; DB 18; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.0025;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 YQFGGHSVD 10
        |||||
        4 YQFGGHSVD 13

RESULT 8
US-10-731-238-28
; Sequence 28, Application US/10731238
; Publication No. US20050123552A1
; GENERAL INFORMATION:
; APPLICANT: Hook, Magnus
;          Patti, Joseph M.
;          House-Pompeo, Karen L.
;          Speziale, Pietro
;          Jon, Danny
;          McGavin, Martin J.
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
; AND METHODS OF USE
; NUMBER OF SEQUENCES: 105
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: TX
; COUNTRY: USA
; ZIP: 77210-4433
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/731,238
; FILING DATE: 10-Dec-2003
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/010,317
; FILING DATE: 21-Jan-1998
; APPLICATION NUMBER: US 60/036,139
; FILING DATE: 21-JAN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Hibler, David W.
; REGISTRATION NUMBER: 41,071
; REFERENCE/DOCKET NUMBER: TAMK:189
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 512-418-3000
; TELEFAX: 512-474-7577
; INFORMATION FOR SEQ ID NO: 28:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 28:
US-10-731-238-28

Query Match      100.0%; Score 58; DB 18; Length 21;
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Best Local Similarity 100.0%; Pred. No. 0.0025;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YQFGHNSVD 10
DB 4 YQFGHNSVD 13

RESULT 9

US-10-731-238-29

Sequence 29, Application US/10731238
Publication No. US20050123552A1

GENERAL INFORMATION:

APPLICANT: Hook, Magnus
Patl, Joseph M.
House-Pompeo, Karen L.
Speziale, Pietro
Joh, Danny
McGavin, Martin J.

TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
AND METHODS OF USE

NUMBER OF SEQUENCES: 105

CORRESPONDENCE ADDRESS:

ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/731,238
FILING DATE: 10-Dec-2003
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE: 21-Jan-1998
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-Jan-1997

ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAWK:189

TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577

INFORMATION FOR SEQ ID NO: 29:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear

SEQUENCE DESCRIPTION: SEQ ID NO: 29:
US-10-731-238-29

Query Match 100.0%; Score 58; DB 18; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.0025;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YQFGHNSVD 10
DB 4 YQFGHNSVD 13

RESULT 10

US-10-731-238-30

Sequence 30, Application US/10731238
Publication No. US20050123552A1

GENERAL INFORMATION:

APPLICANT: Hook, Magnus

Patl, Joseph M.
House-Pompeo, Karen L.
Speziale, Pietro
Joh, Danny
McGavin, Martin J.

TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
AND METHODS OF USE

NUMBER OF SEQUENCES: 105

CORRESPONDENCE ADDRESS:

ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/731,238
FILING DATE: 10-Dec-2003
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/010,317
FILING DATE: 21-Jan-1998
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-Jan-1997

ATTORNEY/AGENT INFORMATION:

NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAWK:189

TELECOMMUNICATION INFORMATION:

TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577

INFORMATION FOR SEQ ID NO: 30:

SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear

SEQUENCE DESCRIPTION: SEQ ID NO: 30:
US-10-731-238-30

Query Match 100.0%; Score 58; DB 18; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.0025;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YQFGHNSVD 10
DB 4 YQFGHNSVD 13

RESULT 11

US-10-731-238-31

Sequence 31, Application US/10731238
Publication No. US20050123552A1

GENERAL INFORMATION:

APPLICANT: Hook, Magnus
Patl, Joseph M.
House-Pompeo, Karen L.
Speziale, Pietro
Joh, Danny
McGavin, Martin J.

TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
AND METHODS OF USE

NUMBER OF SEQUENCES: 105

CORRESPONDENCE ADDRESS:

ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston

STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/731,238
FILING DATE: 10-Dec-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE: 21-Jan-1998
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAMK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 31:
US-10-731-238-31
Query Match 100.0%; Score 58; DB 18; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.0025;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 YQFGHNSVD 10
Db 4 YQFGHNSVD 13
RESULT 12
US-10-731-238-32
; Sequence 32, Application US/10731238
; Publication No. US20050123552A1
; GENERAL INFORMATION:
; APPLICANT: Hook, Magnus
; Patti, Joseph M.
; House-Pompeo, Karen L.
; Speziale, Pietro
; John, Danny
; McGavin, Martin J.
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
; AND METHODS OF USE
; NUMBER OF SEQUENCES: 105
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: TX
; COUNTRY: USA
; ZIP: 77210-4433
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/731,238
; FILING DATE: 10-Dec-2003
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/010,317
FILING DATE: 21-Jan-1998
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAMK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 32:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 32:
US-10-731-238-32
Query Match 100.0%; Score 58; DB 18; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.0025;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 YQFGHNSVD 10
Db 4 YQFGHNSVD 13
RESULT 13
US-10-731-238-33
; Sequence 33, Application US/10731238
; Publication No. US20050123552A1
; GENERAL INFORMATION:
; APPLICANT: Hook, Magnus
; Patti, Joseph M.
; House-Pompeo, Karen L.
; Speziale, Pietro
; John, Danny
; McGavin, Martin J.
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
; AND METHODS OF USE
; NUMBER OF SEQUENCES: 105
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: TX
; COUNTRY: USA
; ZIP: 77210-4433
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/731,238
; FILING DATE: 10-Dec-2003
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/010,317
; FILING DATE: 21-Jan-1998
; APPLICATION NUMBER: US 60/036,139
; FILING DATE: 21-JAN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Hibler, David W.
; REGISTRATION NUMBER: 41,071
; REFERENCE/DOCKET NUMBER: TAMK:189
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 512-418-3000
; TELEFAX: 512-474-7577
; INFORMATION FOR SEQ ID NO: 33:
; SEQUENCE CHARACTERISTICS:

LENGTH: 21 amino acids
 TYPE: amino acid
 STRANDEDNESS: <Unknown>
 TOPOLOGY: linear
 SEQUENCE DESCRIPTION: SEQ ID NO: 33:
 US-10-731-238-33

Query Match 100.0%; Score 58; DB 18; Length 21;
 Best Local Similarity 100.0%; Pred. No. 0.0025;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YQFGGHSVD 10
 |||||
 Db 4 YQFGGHSVD 13

RESULT 14
 US-11-066-697-1134
 ; Sequence 1134, Application US/11066697
 ; Publication No. US20050187159A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Bridon, Dominique P.
 ; APPLICANT: Ezrin, Alan M.
 ; APPLICANT: Milner, Peter G.
 ; APPLICANT: Holmes, Darren L.
 ; APPLICANT: Thibaudau, Karen
 ; TITLE OF INVENTION: PROTECTION OF ENDOGENOUS THERAPEUTIC PEPTIDES FROM
 ; TITLE OF INVENTION: PEPTIDASE ACTIVITY THROUGH CONJUGATION TO BLOOD
 ; TITLE OF INVENTION: COMPONENTS
 ; FILE REFERENCE: 500862002301
 ; CURRENT APPLICATION NUMBER: US/11/066,697
 ; PRIOR FILING DATE: 2005-02-25
 ; PRIOR APPLICATION NUMBER: 09/657,276
 ; PRIOR FILING DATE: 2000-09-07
 ; PRIOR APPLICATION NUMBER: 60/153,406
 ; PRIOR FILING DATE: 1999-09-10
 ; PRIOR APPLICATION NUMBER: 60/159,783
 ; PRIOR FILING DATE: 1999-10-15
 ; NUMBER OF SEQ ID NOS: 1617
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 1134
 ; LENGTH: 37
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURES:
 ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
 ; OTHER INFORMATION: Peptide
 US-11-066-697-1134

Query Match 100.0%; Score 58; DB 20; Length 37;
 Best Local Similarity 100.0%; Pred. No. 0.0045;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YQFGGHSVD 10
 |||||
 Db 19 YQFGGHSVD 28

RESULT 15
 US-09-813-820-8
 ; Sequence 8, Application US/09813820
 ; Patent No. US20020102262A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Hook, Magnus
 ; Patil, Joseph M.
 ; House-Pompeo, Karen
 ; Schanam, Narayana
 ; Symerky, Jindrich
 ; TITLE OF INVENTION: COLLAGEN BINDING PROTEIN COMPOSITIONS
 ; AND METHODS OF USE
 ; NUMBER OF SEQUENCES: 8
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Arnold, White & Durkee

STREET: P.O. Box 4433
 CITY: Houston
 STATE: Texas
 COUNTRY: U.S.
 ZIP: 77210
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/813,820
 FILING DATE: 22-Mar-2001
 CLASSIFICATION: <Unknown>
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/856,253
 FILING DATE: <Unknown>
 ATTORNEY/AGENT INFORMATION:
 NAME: Kitchell, Barbara S.
 REGISTRATION NUMBER: 33,928
 REFERENCE/DOCKET NUMBER: TAMK:193
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (512) 418-3000
 TELEFAX: (512) 474-7577
 INFORMATION FOR SEQ ID NO: 8:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 139 amino acids
 TYPE: amino acid
 STRANDEDNESS: <Unknown>
 TOPOLOGY: linear
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 8:
 ; US-09-813-820-8
 Query Match 100.0%; Score 58; DB 9; Length 139;
 Best Local Similarity 100.0%; Pred. No. 0.017;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YQFGGHSVD 10
 |||||
 Db 110 YQFGGHSVD 119

Search completed: October 22, 2005, 12:56:29
 Job time : 57.1494 secs

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OM protein - protein search, using sw model

Run on: October 22, 2005, 08:04:46 ; Search time 11.6092 Seconds
(without alignments)
82.880 Million cell updates/sec

Title: US-10-731-238-97

Perfect score: 58

Sequence: 1 YQFGHNSVD 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	58	100.0	940	2	S19702 fibronectin-binding
2	58	100.0	961	2	G90053 fibronectin-binding
3	58	100.0	1018	2	A32192 fibronectin-binding
4	58	100.0	1038	2	H90053 fibronectin-binding
5	42	72.4	427	2	D95159 3-phosphoshikimate
6	42	72.4	431	2	D98025 3-phosphoshikimate
7	41	70.7	462	1	A39356 3-oxoacyl-(acyl)-ca
8	41	70.7	469	2	T10061 3-oxoacyl-(acyl)-ca
9	41	70.7	681	2	T24426 3-oxoacyl-(acyl)-ca
10	38	65.5	409	2	G86721 3-oxoacyl-(acyl)-ca
11	38	65.5	411	2	H95048 3-oxoacyl-(acyl)-ca
12	38	65.5	414	2	F97919 3-oxoacyl-(acyl)-ca
13	38	65.5	417	2	T34930 3-oxoacyl-(acyl)-ca
14	38	63.8	198	2	F71702 3-oxoacyl-(acyl)-ca
15	37	63.8	391	2	F71702 3-oxoacyl-(acyl)-ca
16	37	63.8	414	2	A89866 3-oxoacyl-(acyl)-ca
17	37	63.8	416	2	C72020 3-oxoacyl-(acyl)-ca
18	37	63.8	416	2	B86605 3-oxoacyl-(acyl)-ca
19	37	63.8	418	2	G81735 3-oxoacyl-(acyl)-ca
20	37	63.8	418	2	E71473 3-oxoacyl-(acyl)-ca
21	37	63.8	427	1	ZRBP4 gene F protein - p
22	37	63.8	457	2	I73636 neuronal olfactome
23	37	63.8	485	2	I73637 neuronal olfactome
24	37	63.8	489	1	S47076 3-oxoacyl-(acyl)-ca
25	37	63.8	495	1	S47074 3-oxoacyl-(acyl)-ca
26	37	63.8	535	2	T10055 probable 3-oxoacyl
27	37	63.8	541	2	D66779 probable 3-oxoacyl
28	37	63.8	704	1	S50448 1,4-alpha-glucan b
29	37	63.8	777	2	S58162 probable Rho GTPas

30	37	63.8	830	2	S50810
31	37	63.8	1042	2	G84332
32	36	62.1	367	2	A84714
33	36	62.1	764	2	H83879
34	35	60.3	151	2	S70788
35	35	60.3	152	2	D90806
36	35	60.3	152	2	H85665
37	35	60.3	161	2	S78002
38	35	60.3	162	2	C89838
39	35	60.3	227	2	D69296
40	35	60.3	368	2	T44305
41	35	60.3	374	2	D83328
42	35	60.3	377	2	T16985
43	35	60.3	377	2	T04086
44	35	60.3	377	2	T04089
45	35	60.3	377	2	T07376

ALIGNMENTS

RESULT 1

S19702 fibronectin-binding protein B - Staphylococcus aureus

C/Species: Staphylococcus aureus

C/Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004

C/Accession: S19702

R/Joenson, K.; Signaes, C.; Mueller, H.P.; Lindberg, M.

Eur. J. Biochem. 202, 1041-1048, 1991

A/Title: Two different genes encode fibronectin binding proteins in Staphylococcus aureus

A/Reference number: S19702; PMID:92111475; PMID:1837266

A/Accession: S19702

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-940 <JOB>

A/Cross-references: UNIPROT:Q53682; EMBL:X62992; NID:G49040; PIDN:CA44726.1; PID:G5815

C/Keywords: fibronectin binding

Query Match 100.0%; Score 58; DB 2; Length 940;
Best Local Similarity 100.0%; Pred. No. 0.01;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YQFGHNSVD 10
|||||

Db 776 YQFGHNSVD 785

RESULT 2

G90053 hypothetical protein fnbB [imported] - Staphylococcus aureus (strain N315)

C/Species: Staphylococcus aureus

C/Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004

C/Accession: G90053

R/Kuroda, M.; Ohba, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguni, A.; Mizutani, U.; Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.;

C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hizumatsu, K.

Lancet 357, 1225-1240, 2001

A/Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.

A/Reference number: A89758; PMID:11418146

A/Accession: G90053

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-961 <KUR>

A/Cross-references: UNIPROT:Q99RD3; GB:BA000018; PID:G13702452; PIDN:BA43593.1; GSPDB:

A/Experimental source: strain N315

C/Genetics:

A/Gene: fnbB

Query Match 100.0%; Score 58; DB 2; Length 961;
Best Local Similarity 100.0%; Pred. No. 0.011;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 YQFGHNSVD 10

|||||
Db 787 YQFGHNSVD 796

RESULT 3

A32192
fibronectin-binding protein - Staphylococcus aureus
C:Species: Staphylococcus aureus
C>Date: 31-Jul-1989 #sequence_revision 31-Jul-1989 #ext_change 16-Feb-1997
C:Accession: A32192
R:Signaas, C.; Kaucci, G.; Joensson, K.; Lindgren, P.E.; Anantharamiah, G.M.; Hoeoek, M.
Proc. Natl. Acad. Sci. U.S.A. 86, 699-703, 1989
A>Title: Nucleotide sequence of the gene for a fibronectin-binding protein from Staphylo
A:Reference number: A32192; MUID:89098998; PMID:2521391
A:Accession: A32192
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1018 <SIG>
A:Cross-references: GB:J04151
C:Keywords: fibronectin binding

Query Match 100.0%; Score 58; DB 2; Length 1018;
Best Local Similarity 100.0%; Pred. No. 0.011;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

YQ 1 YQFGHNSVD 10
|||||
Db 840 YQFGHNSVD 849

RESULT 4

H90053
hypothetical protein fnb [imported] - Staphylococcus aureus (strain N315)
C:Species: Staphylococcus aureus
C>Date: 10-May-2001 #sequence_revision 10-May-2001 #ext_change 09-Jul-2004
C:Accession: H90053
R:Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguc
ma, A.; Mizutani-Uli, Y.; Kobayashi, N.; Savano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.;
C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiratsutsu, K.
Lancet 357, 1225-1240, 2001
A>Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.
A:Reference number: A89758; MUID:21311952; PMID:11418146
A:Accession: H90053
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1038 <KUB>
A:Cross-references: UNIPROT:Q99RP2; GB:BA000018; PID:g13702453; PIDN:BA843594.1; GSPDB:C
A:Experimental source: strain N315
C:Genetics:
A:Gene: fnb

Query Match 100.0%; Score 58; DB 2; Length 1038;
Best Local Similarity 100.0%; Pred. No. 0.012;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

YQ 1 YQFGHNSVD 10
|||||
Db 836 YQFGHNSVD 845

RESULT 5

D95159
3-phosphohikimate 1-carboxyvinyltransferase [imported] - Streptococcus pneumoniae (stra
C:Species: Streptococcus pneumoniae
C>Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #ext_change 09-Jul-2004
C:Accession: D95159
R:Jettelein, H.; Nelson, K.E.; Paulsen, I.T.; Eissen, J.A.; Read, T.D.; Peterson, S.; Heid
on, J.D.; Unayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzaple,
son, T.; Hickey, E.K.; Holt, I.E.
Science 293, 498-506, 2001
A:Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison,
A>Title: Complete Sequence of a Virulent Isolate of Streptococcus pneumoniae.
A:Reference number: A95000; MUID:21357209; PMID:11463916

A:Accession: D95159
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-427 <KUB>
A:Cross-references: UNIPROT:Q9S400; GB:AE005672; PIDN:AAK75469.1; PID:g14972856; GSPDB:C
A:Experimental source: strain TIGRA
C:Genetics:
A:Gene: SPI371
C:Superfamily: 3-phosphohikimate 1-carboxyvinyltransferase; 3-phosphohikimate 1-carbox

Query Match 72.4%; Score 42; DB 2; Length 427;
Best Local Similarity 88.9%; Pred. No. 4.4;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

YQ 2 QFGHNSVD 10
|||||
Db 202 QFGHNSVD 210

RESULT 6

D98025
3-phosphohikimate 1-carboxyvinyltransferase (EC 2.5.1.19) [imported] - Streptococcus pn
C:Species: Streptococcus pneumoniae
C>Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #ext_change 02-Nov-2001
C:Accession: D98025
R:Hoskins, J.A.; Alborn Jr., W.; Arnold, J.; Blaszcak, L.; Burgett, S.; DeHoff, B.S.; E
e, R.; LeBlanc, D.J.; Lee, L.N.; Lefkowitz, E.J.; Lu, J.; Matsushima, P.; McAhren, S.; M
y, P.; Sun, P.M.; Winkler, M.E.
J. Bacteriol. 183, 5709-5717, 2001
A:Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaaknaas, S.R.;
A>Title: Genome of the Bacterium Streptococcus pneumoniae Strain R6.
A:Reference number: A97872; MUID:21429245; PMID:11544234
A:Accession: D98025
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-431 <KUB>
A:Cross-references: GB:AE007317; PIDN:AAL00033.1; PID:g15458865; GSPDB:GN00174
C:Genetics:
A:Gene: arca
C:Superfamily: 3-phosphohikimate 1-carboxyvinyltransferase; 3-phosphohikimate 1-carbox
C:Keywords: transferase

Query Match 72.4%; Score 42; DB 2; Length 431;
Best Local Similarity 88.9%; Pred. No. 4.5;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

YQ 2 QFGHNSVD 10
|||||
Db 206 QFGHNSVD 214

RESULT 7

A39356
3-oxoacyl-[acyl-carrier-protein] synthase (EC 2.3.1.41) I beta chain precursor, chloropl
N:Alternate names: beta-ketoacyl-[acyl carrier protein] synthase I
C:Species: Hordeum vulgare (barley)
C>Date: 06-Mar-1992 #sequence_revision 13-Jan-1995 #ext_change 09-Jul-2004
C:Accession: A39356; A45129
R:Siggaard-Andersen, M.; Kauppinen, S.; von Wettstein-Knowles, P.
Proc. Natl. Acad. Sci. U.S.A. 88, 4114-4118, 1991
A>Title: Primary structure of a cerulenin-binding beta-ketoacyl-[acyl carrier protein] s
A:Reference number: A39356; MUID:91239517; PMID:2034657
A:Accession: A39356
A:Molecule type: mRNA
A:Residues: 1-462 <SIG>
A:Cross-references: UNIPROT:P23902; GB:M60410; NID:9167064; PIDN:AAA2968.1; PID:g167065
A:Experimental source: cv. Bonus, leaf
A>Note: parts of this sequence, including the amino end of the mature protein, were conf
R:Kauppinen, S.
J. Biol. Chem. 267, 23999-24006, 1992
A>Title: Structure and expression of the Kas12 gene encoding a beta-ketoacyl-acyl carrie
A:Reference number: A45129; MUID:93054767; PMID:1429736
A:Accession: A45129

A/Molecule type: DNA
A/Residues: 1-395,397-414, 'T', 415-462 <XAU>
A/Experimental source: cv. Bonus
A/Note: sequence inconsistent with the nucleotide translation; translation agrees with s
A/Note: sequence extracted from NCBI backbone (NCBI:P.118934)
C/Genetics:
A/Gene: Kae12
A/Map position: 2
A/Intons: 144/3; 346/3; 384/3; 418/3; 441/1
C/Complex: homodimer or heterodimer with alpha chain
C/Suprafamily: 3-oxoacyl-[acyl-carrier-protein] synthase I; 3-oxoacyl-[acyl-carrier-prot
C/Keywords: acyltransferase; chloroplast; fatty acid biosynthesis; heterodimer; homodimer
F/1-36/Domain: transit peptide (chloroplast) #status predicted <TNP>
F/36-462/Product: 3-oxoacyl-[acyl-carrier-protein] synthase I beta chain #status experim
F/68-457/Domain: 3-oxoacyl-[acyl-carrier-protein] synthase I homology <OAS>
F/213/Active site: Cys #status experimental

Query Match 70.7%; Score 41; DB 1; Length 462;
Best Local Similarity 77.8%; Pred. No. 7.4;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 YORGHNSV 9
:|||||:
446 FGFGRHNSV 454

RESULT 8
T10061
3-oxoacyl-[acyl-carrier-protein] synthase (EC 2.3.1.41) precursor, chloroplast - caator
N/Alternate names: beta-ketoacyl-[acyl carrier protein] synthase
C/Species: Ricinus communis (castor bean)
C/Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004
C/Accession: T10061
R/Gene: A.L.
Submitted to the EMBL Data Library, April 1993
A/Description: Cloning and molecular characterisation of B-ketoacyl-ACP synthases from er
A/Reference number: Z16924
A/Accession: T10061
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-469 <GEN>
A/Cross-references: UNIPROT:Q41135; EMBL:L13242; NID:G294667; PID:G294668
C/Genetics:
A/Genome: nuclear
C/Function:
A/Pathway: fatty acid biosynthesis
C/Suprafamily: 3-oxoacyl-[acyl-carrier-protein] synthase I; 3-oxoacyl-[acyl-carrier-prot
C/Keywords: acyltransferase; chloroplast; fatty acid biosynthesis
F/1-42/Domain: transit peptide (chloroplast) #status predicted <TNP>
F/43-469/Product: 3-oxoacyl-[acyl-carrier-protein] synthase I homology <OAS>
F/77-464/Domain: 3-oxoacyl-[acyl-carrier-protein] synthase I homology <OAS>

Query Match 70.7%; Score 41; DB 2; Length 469;
Best Local Similarity 77.8%; Pred. No. 7.5;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 YORGHNSV 9
:|||||:
453 FGFGRHNSV 461

RESULT 9
T24426
hypothetical protein T04A8.7 - Caenorhabditis elegans
C/Species: Caenorhabditis elegans
C/Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C/Accession: T24426
R/Palmer, S.
Submitted to the EMBL Data Library, August 1994
A/Reference number: Z19889
A/Accession: T24426
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA

A/Residues: 1-681 <MLL>
A/Cross-references: UNIPROT:Q22137; EMBL:Z35663; PIDN:CAA84727.1; GSPDB:GN00021; CESP:T0
A/Experimental source: clone T04A8
C/Genetics:
A/Gene: CESP:T04A8.7
A/Map position: 3
A/Intons: 85/1; 312/2; 351/1; 512/1; 626/2
C/Suprafamily: 1,4-alpha-glucan branching enzyme

Query Match 70.7%; Score 41; DB 2; Length 681;
Best Local Similarity 66.7%; Pred. No. 11;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 ORGHNSVD 10
:|||||:
637 KFGGRHNSV 645

RESULT 10
G86721
hypothetical protein fabF [imported] - Lactococcus lactis subsp. lactis (strain IL1403)
C/Species: Lactococcus lactis subsp. lactis
C/Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 09-Jul-2004
C/Accession: G86721
R/Bolotin, A.; Wincker, P.; Manger, S.; Jallion, O.; Malarme, K.; Weissenbach, J.; Ehrlich
Genome Res. 11, 731-753, 2001
A/Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis ss
A/Reference number: A86625; MUID:21235186; PMID:11337471
A/Accession: G86721
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-409 <STO>
A/Cross-references: UNIPROT:Q9CHF6; GB:AE005116; PID:G12723594; PIDN:AAK04873.1; GSPDB:C
C/Genetics:
A/Gene: fabF
C/Suprafamily: 3-oxoacyl-[acyl-carrier-protein] synthase I; 3-oxoacyl-[acyl-carrier-prot

Query Match 65.5%; Score 38; DB 2; Length 409;
Best Local Similarity 66.7%; Pred. No. 24;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 YORGHNSV 9
:|||||:
392 FGFGRHNSV 400

RESULT 11
H95048
3-oxoacyl-[acyl-carrier-protein] synthase II [imported] - Streptococcus pneumoniae (str
C/Species: Streptococcus pneumoniae
C/Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 09-Jul-2004
C/Accession: H95048
R/Fretzelin, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Helc
on, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtapple,
nson, T.; Hickey, E.K.; Holt, I.E.
Science 293, 498-506, 2001
A/Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison
A/Title: Complete Genome Sequence of a virulent isolate of Streptococcus pneumoniae.
A/Reference number: A95000; MUID:21357209; PMID:11463916
A/Accession: H95048
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-411 <KUR>
A/Cross-references: UNIPROT:Q9FBC2; GB:AE005672; PIDN:AAK74585.1; PID:G14971892; GSPDB:C
A/Experimental source: strain T1064
C/Genetics:
A/Gene: SP0422
C/Suprafamily: 3-oxoacyl-[acyl-carrier-protein] synthase I; 3-oxoacyl-[acyl-carrier-prot

Query Match 65.5%; Score 38; DB 2; Length 411;
Best Local Similarity 66.7%; Pred. No. 24;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 YQFGGNSV 9
: |||||:
Db 394 FQFGGNAV 402

RESULT 12

3-oxoacyl-[acyl-carrier-protein] synthase (EC 2.3.1.41) [imported] - Streptococcus pneumoniae
C:Species: Streptococcus pneumoniae
C:Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 09-Jul-2004
C:Accession: F97919
R:Hoising, J.A.; Alborn Jr., W.; Arnold, J.; Blaszcak, L.; Burgett, S.; Dehoff, B.S.; E
e, R.; Leblanc, D.J.; Lee, L.N.; Lefkowitz, E.J.; Lu, J.; Matsushima, P.; McAhren, S.; M
y, P.; Sun, P.M.; Winkler, M.E.
J: Bacteriol. 183, 5709-5717, 2001
A:Author: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaakunas, S.R.;
A:Title: Genome of the Bacterium Streptococcus pneumoniae Strain R6.
A:Reference number: A97872; MUID:21429245; PMID:11544234
A:Accession: F97919
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-414 <RUR>
A:Cross-references: UNIPROT:Q9DR14; GB:AE007317; PIDN:AAK99186.1; PID:G15457943; GSPDB:C
C:Genetics: FabP
A:Gene family: 3-oxoacyl-[acyl-carrier-protein] synthase I; 3-oxoacyl-[acyl-carrier-prod
C:Keyword: acyltransferase

Query Match 65.5%; Score 38; DB 2; Length 414;
Best Local Similarity 66.7%; Pred. No. 24;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 YQFGGNSV 9
: |||||:
Db 397 FQFGGNAV 405

RESULT 13

T34930
probable secreted protein - Streptomyces coelicolor
C:Species: Streptomyces coelicolor
C:Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 09-Jul-2004
C:Accession: T34930
R:Seeger, K.J.; Harris, D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
submitted to the EMBL Data Library, June 1998
A:Reference number: Z21562
A:Accession: T34930
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-417 <SEE>
A:Cross-references: UNIPROT:Q69948; EMBL:AL023862; PIDN:CAA19631.1; GSPDB:GNO0070; SCOE
A:Experimental source: strain A3(2)
C:Genetics:
A:Gene: SCOEDB:SC3P9.08
C:Superfamily: myo-inositol-1-phosphate synthase

Query Match 65.5%; Score 38; DB 2; Length 417;
Best Local Similarity 75.0%; Pred. No. 24;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 FQGHNSVD 10
|||:|:
Db 66 FQGHTRVD 73

RESULT 14

T28191
hypothetical protein ORF30 - Melanoplus sanguinipes entomopoxvirus
N:Alternate names: ORF MSV030 hypothetical protein
C:Species: Melanoplus sanguinipes entomopoxvirus
C:Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 09-Jul-2004
C:Accession: T28191

R:Afonso, C.L.; Tulman, E.R.; Lu, Z.; Oma, E.; Kutlich, G.F.; Rock, D.L.
J. Virol. 73, 533-552, 1999
A:Title: The genome of Melanoplus sanguinipes entomopoxvirus.
A:Reference number: Z20484; MUID:99102612; PMID:9847359
A:Accession: T28191
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-198 <APO>
A:Cross-references: UNIPROT:Q9YW62; EMBL:AF063866; NID:94049647; PIDN:AAK97842.1; PID:94
C:Experimental source: isolate Tuscon
C:Genetics:
A:Note: MSV030

Query Match 63.8%; Score 37; DB 2; Length 198;
Best Local Similarity 77.8%; Pred. No. 17;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 YQFGGNSV 9
|||:|:
Db 175 YQFVGNSV 183

RESULT 15

F71702
hypothetical protein RP439 - Rickettsia prowazekii
C:Species: Rickettsia prowazekii
C:Date: 21-Nov-1998 #sequence_revision 21-Nov-1998 #text_change 09-Jul-2004
C:Accession: F71702
R:Anderson, S.G.E.; Zomorodipour, A.; Anderson, J.O.; Slichteritz-Porten, T.; Alsmark, U
Nature 396, 133-140, 1998
A:Title: The genome sequence of Rickettsia prowazekii and the origin of mitochondria.
A:Reference number: A71630; MUID:99039499; PMID:9823893
A:Accession: F71702
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-391 <AND>
A:Cross-references: UNIPROT:Q9ZDA3; GB:AJ235271; GB:AJ235269; NID:93868717; PIDN:CAA1489
A:Experimental source: strain Madrid E
C:Genetics:
A:Gene: RP439
C:Superfamily: Rickettsia prowazekii hypothetical protein RP439

Query Match 63.8%; Score 37; DB 2; Length 391;
Best Local Similarity 50.0%; Pred. No. 35;
Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 YQFGGNSVD 10
|||:|:
Db 208 YQFGHRTPE 217

Search completed: October 22, 2005, 09:55:48
Job time : 12.6092 secs

GenCore version 5.1.6
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OM protein - protease search, using sw model

Run on: October 22, 2005, 08:01:06 : Search time 56.2069 Seconds
(without alignments)
91.106 Million cell updates/sec

Title: US-10-731-238-97
Perfect score: 58
Sequence: 1 Y0FGHNSVD 10

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: 1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	58	100.0	940	2	Q53682 staphylococ
2	58	100.0	943	2	Q8NUT8 staphylococ
3	58	100.0	957	2	Q6G6H4 staphylococ
4	58	100.0	961	2	Q99RD3 staphylococ
5	58	100.0	961	2	Q7A3J8 staphylococ
6	58	100.0	965	2	Q6GD05 staphylococ
7	58	100.0	1015	2	Q8NUT7 staphylococ
8	58	100.0	1015	2	Q6G6H3 staphylococ
9	58	100.0	1018	1	FNBA STAU
10	58	100.0	1038	2	Q99RD2 staphylococ
11	58	100.0	1038	2	Q7A3J7 staphylococ
12	53	91.4	152	2	Q9AEP9 staphylococ
13	42	72.4	427	1	AROA STRPN
14	42	72.4	427	1	AROA STRR6
15	42	72.4	705	2	Q6FJ70 staphylococ
16	42	72.4	1190	2	Q6SLA2 staphylococ
17	41	70.7	442	2	Q7XUM9 staphylococ
18	41	70.7	456	2	Q9AG70 staphylococ
19	41	70.7	462	1	FABH HORVU
20	41	70.7	465	2	Q69YA2 staphylococ
21	41	70.7	469	2	Q9M507 staphylococ
22	41	70.7	469	2	Q9M508 staphylococ
23	41	70.7	469	2	Q9M509 staphylococ
24	41	70.7	474	1	FABH ARATH
25	41	70.7	474	1	Q8A942 staphylococ
26	41	70.7	488	2	Q8A942 staphylococ
27	41	70.7	488	2	Q8A942 staphylococ
28	41	70.7	681	2	Q22137 staphylococ
29	40	69.0	131	2	Q7P3T8 staphylococ
30	40	69.0	406	2	Q8R230 staphylococ
31	40	69.0	413	2	Q8RGX4 staphylococ

32	40	69.0	413	2	Q7RPP5 mus musculu
33	40	69.0	424	2	Q81IK3 mus musculu
34	40	69.0	426	2	Q96NU7 homo sapien
35	40	69.0	426	2	Q96NU7 mus musculu
36	40	69.0	446	2	Q68C18 homo sapien
37	40	69.0	463	2	Q8T0H4 drosophila
38	40	69.0	463	2	Q8T0H4 drosophila
39	40	69.0	885	2	Q9V6K7 drosophila
40	40	69.0	836	2	Q6BL30 drosophila
41	39	67.2	873	2	Q8PDE2 drosophila
42	39	67.2	408	2	Q7S1C5 drosophila
43	39	67.2	432	2	Q68EP2 drosophila
44	39	67.2	447	2	Q7SKX5 drosophila
45	39	67.2	558	2	Q749H5 drosophila

ALIGNMENTS

RESULT 1			
ID	Q53682	PRELIMINARY;	PRT; 940 AA.
AC	Q53682;		
DT	01-NOV-1996 (TrEMBLrel. 01, Created)		
DT	01-MAR-2004 (TrEMBLrel. 26, Last annotation update)		
DE	Fibronectin binding protein B.		
GN	Name=fnb1;		
OS	Staphylococcus aureus.		
OC	Bacteria; Firmicutes; Bacillales; Staphylococcus.		
OX	NCBI_TaxID=1280;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=8325-4;		
RX	MEDLINE=9211475; PubMed=1837266;		
RA	Johnson K., Signas C., Muller H.P., Lindberg M.;		
RT	"Two different genes encode fibronectin binding proteins in Staphylococcus aureus. The complete nucleotide sequence and characterization of the second gene.";		
RL	Eur. J. Biochem. 202:1041-1048 (1991).		
CC	-1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by an amide bond (By similarity).		
DR	EMBL: X62992; CAA44726.1; -.		
DR	PIR: S19702; S19702.		
DR	HSP; Q53653; IN67.		
DR	GO: GO:0009986; C:cell surface; IEA.		
DR	GO: GO:0005618; C:cell wall; IEA.		
DR	GO: GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.		
DR	GO: GO:0016020; C:membrane; IEA.		
DR	GO: GO:0007155; P:cell adhesion; IEA.		
DR	InterPro: IPR008966; Adhes_Bact.		
DR	InterPro: IPR004237; Fb_bind.		
DR	InterPro: IPR005877; Gpoc_YsIRK.		
DR	InterPro: IPR001899; Gram_pos_anchor.		
DR	Pfam: PF02986; Fb_bind; 2.		
DR	Pfam: PF00746; Gram_pos_anchor; 1.		
DR	Pfam: PF04650; YsIRK_signal; 1.		
DR	TIGRFAMS: TIGR01167; LPXTG_anchor; 1.		
DR	TIGRFAMS: TIGR01168; YsIRK_signal; 1.		
DR	PROSITE: PSS0847; GRAM_POS_ANCHORING; 1.		
KW	Cell wall; Peptidoglycan-anchor.		
SQ	SEQUENCE 940 AA; 10355 MW; E35FBBCA907AE345 CRC64;		
QY	1 YQFGHNSVD 10		
DB	776 YQFGHNSVD 785		
Query Match	100.0%;	Score 58;	DB 2; Length 940;
Best Local Similarity	100.0%;	Pred. No. 0.034;	
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
RESULT 2			

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Q8NUU8
ID Q8NUU8      PRELIMINARY;      PRT;      943 AA.
AC Q8NUU8;
DT 01-OCT-2002 (TReMBLrel. 22, Created)
DT 01-OCT-2002 (TReMBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE FnbA protein.
GN Name=fNB; OrderedLocustNames=SAS2420;
OS Staphylococcus aureus (strain MW2).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=196620;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=MW2;
RX MEDLINE=22040717; PubMed=12044378; DOI=10.1016/S0140-6736(02)08713-5;
RA Baba T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Oguchi A.,
RA Nagai Y., Iwama N., Asano K., Naimi T., Kuroda H., Cui L.,
RA Yamamoto K., Hiratsugu K.;
RA "Genome and virulence determinants of high virulence community-
RT acquired MRSA."
RL Lancet 359.1819-1827(2002).
CC -I- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
an amide bond (By similarity).
DR EMBL; AP004830; BAB96285.1; -.
DR HSSP; Q53653; 1N67.
DR GO; GO:0009986; C:cell surface; IEA.
DR GO; GO:0005618; C:cell wall; IEA.
DR GO; GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0007155; P:cell adhesion; IEA.
DR InterPro; IPR008966; Adhes_bact.
DR InterPro; IPR004237; Fb_bind.
DR InterPro; IPR005877; Gpos_YsIRK.
DR InterPro; IPR001899; Gram_pos_anchor.
DR Pfam; PF02986; Fb_bind_1.
DR Pfam; PF00746; Gram_pos_anchor; 1.
DR Pfam; PF04650; YsIRK_signal; 1.
DR TIGRFAMs; TIGR01167; LPXTG_anchor; 1.
DR TIGRFAMs; TIGR01168; YsIRK_signal; 1.
DR PROSITE; PS50847; GRAM_POS_ANCHORING; 1.
KW Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ
SEQUENCE 943 AA; 104537 MW; DABASF531947E1B6A CR64;

Query Match      100.0%; Score 58; DB 2; Length 943;
Best Local Similarity 100.0%; Pred. No. 0.034;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 YQFGHNSVD 10
DB      783 YQFGHNSVD 792

RESULT 3
ID Q6G6H4      PRELIMINARY;      PRT;      957 AA.
AC Q6G6H4;
DT 05-JUL-2004 (TReMBLrel. 27, Created)
DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TReMBLrel. 27, Last annotation update)
DE Fibronectin-binding protein.
GN Name=fNB; OrderedLocustNames=SAS2387;
OS Staphylococcus aureus (strain MSSA476).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=282459;
RN (1)
RP SEQUENCE FROM N.A.
RC PubMed=15213324; DOI=10.1073/pnas.0403521101;
RX Holden M.T.G., Fell E.J., Lindsay J.A., Peacock S.J., Day N.P.J.,
RA Holten M.T.G., Foster T.J., Moore C.E., Hurst L., Atkin R., Barron A.,
RA Bason N., Bentley S.D., Chillingworth C., Chillingworth T.,
RA Churcher C., Clark L., Cotton C., Cronin A., Doggett J., Dowd L.,
RA Felwell T., Hance Z., Harris B., Hauser H., Holtroyd S., Jagsels K.,
RA James K.D., Lennard N., Line A., Mayes R., Moule S., Mungall K.,

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RA Ormond D., Quail M.A., Rabinowitch E., Rabinford K.M., Sanders M.,
RA Sharp S., Simmonds M., Stevens K., Whitehead S., Barrett B.G.,
RA Spratt B.G., Parhill J.;
RT "Complete genomes of two clinical Staphylococcus aureus strains:
RT evidence for the rapid evolution of virulence and drug resistance."
RT Proc. Natl. Acad. Sci. U.S.A. 101:9786-9791(2004).
CC -I- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
an amide bond (By similarity).
DR EMBL; BX571857; CAG44201.1; -.
DR GO; GO:0009986; C:cell surface; IEA.
DR GO; GO:0005618; C:cell wall; IEA.
DR GO; GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0007155; P:cell adhesion; IEA.
DR InterPro; IPR008966; Adhes_bact.
DR InterPro; IPR004237; Fb_bind.
DR InterPro; IPR005877; Gpos_YsIRK.
DR InterPro; IPR001899; Gram_pos_anchor.
DR Pfam; PF02986; Fb_bind_1.
DR Pfam; PF00746; Gram_pos_anchor; 1.
DR Pfam; PF04650; YsIRK_signal; 1.
DR TIGRFAMs; TIGR01167; LPXTG_anchor; 1.
DR TIGRFAMs; TIGR01168; YsIRK_signal; 1.
DR PROSITE; PS50847; GRAM_POS_ANCHORING; 1.
KW Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ
SEQUENCE 957 AA; 105980 MW; 28F8BA7FFDFD3EAF CR64;

Query Match      100.0%; Score 58; DB 2; Length 957;
Best Local Similarity 100.0%; Pred. No. 0.035;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 YQFGHNSVD 10
DB      783 YQFGHNSVD 792

RESULT 4
ID Q99RD3      PRELIMINARY;      PRT;      961 AA.
AC Q99RD3;
DT 01-JUN-2001 (TReMBLrel. 17, Created)
DT 01-JUN-2001 (TReMBLrel. 17, Last sequence update)
DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)
DE Fibronectin-binding protein homolog.
GN Name=fNB; OrderedLocustNames=SAV2502;
OS Staphylococcus aureus (strain Mu50 / ATCC 700699).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=158878;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=Mu50 / ATCC 700699;
RX MEDLINE=21311952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2;
RA Kuroda M., Ohba T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Iian J.-Q., Ito T.,
RA Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,
RA Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
RA Kanahisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
RA Hattori M., Ogasawara N., Hayashi H., Hiratsugu K.;
RT "Whole genome sequencing of methicillin-resistant Staphylococcus
RT aureus."
RL Lancet 357.1225-1240(2001).
CC -I- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
an amide bond (By similarity).
DR EMBL; AP003365; BAB58664.1; -.
DR PIR; G90053; G90053.
DR HSSP; Q53653; 1N67.
DR GO; GO:0009986; C:cell surface; IEA.
DR GO; GO:0005618; C:cell wall; IEA.
DR GO; GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0007155; P:cell adhesion; IEA.
DR InterPro; IPR008966; Adhes_bact.

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DR InterPro: IPR004237; Fn_bind.
 DR InterPro: IPR005877; Gpos_YsIRK.
 DR InterPro: IPR001899; Gram_pos_anchor.
 DR Pfam: PF02986; Fn_bind_1.
 DR Pfam: PF00746; Gram_pos_anchor; 1.
 DR Pfam: PF04650; YsIRK_signal; 1.
 DR TIGRFAMs: TIGR01167; LpxTG_anchor; 1.
 DR TIGRFAMs: TIGR01168; YsIRK_signal; 1.
 DR PROSITE: PS50847; GRAM_POS_ANCHORING; 1.
 KM Cell wall; Complete proteome; Peptidoglycan-anchor.
 SQ SEQUENCE 961 AA; 106010 MW; 364940884EA4101 CRC64;

Query Match 100.0%; Score 58; DB 2; Length 961;
 Best Local Similarity 100.0%; Pred. No. 0.035;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YORGCHNSVD 10
 DB 787 YORGCHNSVD 796

RESULT 5
 ID Q7A3J8 PRELIMINARY; PRT; 961 AA.

AC Q7A3J8; 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE FndB protein.
 GN Name=fndB; OrderedLocusNames=SA2290;
 OS Staphylococcus aureus (strain N315).
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 OX NCBI_TaxID=158879;
 RN [1]

SEQUENCE FROM N.A.
 RP MEDLINE=21311952; Pubmed=11418146; DOI=10.1016/S0140-6736(00)04403-2;
 RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
 RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Iian J.-O., Ito T.,
 RA Kanamori M., Matsunaru H., Maruyama A., Murakami H., Hosoyama A.,
 RA Mizumori U. Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
 RA Sekimizu K., Hirakawa H., Kihara S., Goto S., Yabuzaki J.,
 RA Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
 RA Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
 RT "Whole genome sequencing of methicillin-resistant Staphylococcus
 aureus";
 RL Lancet 357:1225-1240(2001).
 CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
 an amide bond (By similarity).
 DR EMBL: AP003137; BAB43593.1; -;
 DR GO: GO:0009986; C:cell surface; IEA.
 DR GO: GO:0005618; C:cell wall; IEA.
 DR GO: GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
 DR GO: GO:0016020; C:membrane; IEA.
 DR GO: GO:0007155; P:cell adhesion; IEA.
 DR InterPro: IPR008966; Adhes_bact.
 DR InterPro: IPR004237; Fn_bind.
 DR InterPro: IPR005877; Gpos_YsIRK.
 DR InterPro: IPR001899; Gram_pos_anchor.
 DR Pfam: PF02986; Fn_bind_1.
 DR Pfam: PF00746; Gram_pos_anchor; 1.
 DR Pfam: PF04650; YsIRK_signal; 1.
 DR TIGRFAMs: TIGR01167; LpxTG_anchor; 1.
 DR TIGRFAMs: TIGR01168; YsIRK_signal; 1.
 DR PROSITE: PS50847; GRAM_POS_ANCHORING; 1.
 KM Cell wall; Complete proteome; Peptidoglycan-anchor.
 SQ SEQUENCE 961 AA; 106010 MW; 364940884EA4101 CRC64;

Query Match 100.0%; Score 58; DB 2; Length 961;
 Best Local Similarity 100.0%; Pred. No. 0.035;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YORGCHNSVD 10
 DB 787 YORGCHNSVD 796

DB 787 YORGCHNSVD 796

RESULT 6
 ID Q6GDU5 PRELIMINARY; PRT; 965 AA.
 AC Q6GDU5; 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Fibronectin-binding protein.
 GN Name=fndB; OrderedLocusNames=SA2580;
 OS Staphylococcus aureus (strain MRSA252).
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 OX NCBI_TaxID=282458;
 RN [1]

SEQUENCE FROM N.A.
 RP Pubmed=15213324; DOI=10.1073/pnas.0402521101;
 RA Holden M.T.G., Fell E.J., Lindsay J.A., Peacock S.J., Day N.P.J.,
 RA Enright M.C., Foster T.J., Moore C.E., Hurst L., Atkin R., Barron A.,
 RA Bason N., Bentley S.D., Chillingworth C., Chillingworth T., Dowd L.,
 RA Churcher C., Clark L., Corton C., Cronin A., Doggett J., Dowd L.,
 RA Felwell T., Hance Z., Harris B., Hauser H., Holtroyd S., Jagsels K.,
 RA James K.D., Lennard N., Line A., Mayes R., Moul S., Mungall K.,
 RA Omond S., Stimmings M., Stevens K., Whitehead S., Barrell B.G.,
 RA Sharp S., Spratt B.G., Parkhill J.;
 RT "Complete genomes of two clinical Staphylococcus aureus strains:
 evidence for the rapid evolution of virulence and drug resistance";
 RL Proc. Natl. Acad. Sci. U.S.A. 101:9786-9791(2004).
 CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
 an amide bond (By similarity).
 DR EMBL: BX571856; CAG41560.1; -;
 DR GO: GO:0009986; C:cell surface; IEA.
 DR GO: GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
 DR GO: GO:0016020; C:membrane; IEA.
 DR GO: GO:0007155; P:cell adhesion; IEA.
 DR InterPro: IPR008966; Adhes_bact.
 DR InterPro: IPR004237; Fn_bind.
 DR InterPro: IPR005877; Gpos_YsIRK.
 DR InterPro: IPR001899; Gram_pos_anchor.
 DR Pfam: PF02986; Fn_bind_1.
 DR Pfam: PF00746; Gram_pos_anchor; 1.
 DR Pfam: PF04650; YsIRK_signal; 1.
 DR TIGRFAMs: TIGR01167; LpxTG_anchor; 1.
 DR TIGRFAMs: TIGR01168; YsIRK_signal; 1.
 DR PROSITE: PS50847; GRAM_POS_ANCHORING; 1.
 KM Cell wall; Complete proteome; Peptidoglycan-anchor.
 SQ SEQUENCE 965 AA; 105691 MW; 2982E132164D0551 CRC64;

Query Match 100.0%; Score 58; DB 2; Length 965;
 Best Local Similarity 100.0%; Pred. No. 0.035;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YORGCHNSVD 10
 DB 805 YORGCHNSVD 814

RESULT 7
 ID Q8NUU7 PRELIMINARY; PRT; 1015 AA.

AC Q8NUU7; 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Fnd protein.
 GN Name=fndB; OrderedLocusNames=MM2421;
 OS Staphylococcus aureus (strain MM2).
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 OX NCBI_TaxID=196620;
 RN [1]
 RP SEQUENCE FROM N.A.

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RC STRAIN=MM2;
RX MEDLINE=22040717; PubMed=12044378; DOI=10.1016/S0140-6736(02)08713-5;
RA Baba T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Ogunchi A.,
RA Nagai Y., Iwama N., Asano K., Naimi T., Kuroda H., Cui L.,
RA Yamamoto K., Hiratake K.,
RT Genome and virulence determinants of high virulence community-
RT acquired MRSA."
RL Lancet 359:1819-1827(2002).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC an amide bond (By similarity).
DR EMBL, AF04830, BAB96286.1, -.
DR GO, GO:0009986, C:cell surface, IEA.
DR GO, GO:0005618, C:cell wall, IEA.
DR GO, GO:0009275, C:cell wall (sensu Gram-positive Bacteria), IEA.
DR GO, GO:0016020, C:membrane, IEA.
DR GO, GO:0007155, P:cell adhesion, IEA.
DR InterPro, IPR008966, Adhes_bact.
DR InterPro, IPR004237, Fn_bind.
DR InterPro, IPR005877, Gpos_YsIRK.
DR InterPro, IPR001899, Gram_pos_anchor.
DR Pfam, PF02986, Fn_bind, 1.
DR Pfam, PF00746, Gram_pos_anchor, 1.
DR TIGRfams, TIGR01167, LpxTG_anchor, 1.
DR TIGRfams, TIGR01168, YsIRK_signal, 1.
DR PROSITE, PS50847, GRAM_POS_ANCHORING, 1.
DR Cell wall, Complete proteome; Peptidoglycan-anchor.
SQ SEQUENCE 1015 AA; 11145 MW; D0F9281BB64D4D2 CRC64;

Query Match 100.0%; Score 58; DB 2; Length 1015;
Best Local Similarity 100.0%; Pred. No. 0.037;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YQFGHNSVD 10
DB 841 YQFGHNSVD 850

RESULT 8
06G6H3 PRELIMINARY; PRT; 1015 AA.
ID 06G6H3
AC 06G6H3
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Fibronectin-binding protein.
GN OrderedlocusNames=SA52388;
OS Staphylococcus aureus (Strain MSSA476).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=282459;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=15213324; DOI=10.1073/pnas.0402521101;
RA Holden M.T.G., Fell E.J., Lindsey J.A., Peacock S.J., Day N.P.J.,
RA Enright M.C., Foster T.U., Moore C.E., Hurst L., Atkin R., Barron A.,
RA Bason N., Bentley S.D., Chillingworth C., Chillingworth T.,
RA Churcher C., Clark L., Cotton C., Cronin A., Doggett J., Dowd L.,
RA Felwell T., Hance Z., Harris B., Hauber H., Holtroyd S., Jagsels K.,
RA James K.D., Lennard N., Line A., Mayes R., Moule S., Mungall K.,
RA Ormond D., Quail M.A., Rabbittowitch R., Rutherford K.M., Sanders M.,
RA Sharp S., Simmonds M., Stevens K., Whithead S., Barrett B.G.,
RA Spratt B.G., Parkhill J.
RT "Complete genomes of two clinical Staphylococcus aureus strains:
RT evidence for the rapid evolution of virulence and drug resistance."
RL Proc. Natl. Acad. Sci. U.S.A. 101:9786-9791(2004).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC an amide bond (By similarity).
DR EMBL, BX571857, CAG44202.1, -.
DR GO, GO:0009986, C:cell surface, IEA.
DR GO, GO:0005618, C:cell wall, IEA.
DR GO, GO:0009275, C:cell wall (sensu Gram-positive Bacteria), IEA.
DR GO, GO:0016020, C:membrane, IEA.
DR GO, GO:0007155, P:cell adhesion, IEA.

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DR InterPro, IPR008966, Adhes_bact.
DR InterPro, IPR004237, Fn_bind.
DR InterPro, IPR005877, Gpos_YsIRK.
DR InterPro, IPR001899, Gram_pos_anchor.
DR Pfam, PF02986, Fn_bind, 1.
DR Pfam, PF00746, Gram_pos_anchor, 1.
DR Pfam, PF04650, YsIRK_signal, 1.
DR TIGRfams, TIGR01167, LpxTG_anchor, 1.
DR TIGRfams, TIGR01168, YsIRK_signal, 1.
DR PROSITE, PS50847, GRAM_POS_ANCHORING, 1.
DR Cell wall, Complete proteome; Peptidoglycan-anchor.
SQ SEQUENCE 1015 AA; 11145 MW; D0F9281BB64D4D2 CRC64;

Query Match 100.0%; Score 58; DB 2; Length 1015;
Best Local Similarity 100.0%; Pred. No. 0.037;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YQFGHNSVD 10
DB 841 YQFGHNSVD 850

RESULT 9
FNBA_STAU STANDARD; PRT; 1018 AA.
ID FNBA_STAU
AC P14738;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Fibronectin-binding protein precursor (FNBP).
GN Name=FNBA;
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1280;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=NCTC 8325-4;
RX MEDLINE=8908998; PubMed=2521391;
RA Signaes C., Raucel G., Joensson K., Lindgren P.-E.,
RA Anantharamaiah G.M., Hoeoek M., Lindberg M.;
RT "Nucleotide sequence of the gene for a fibronectin-binding protein
RT from Staphylococcus aureus: use of this peptide sequence in the
RT synthesis of biologically active peptides."
RL Proc. Natl. Acad. Sci. U.S.A. 86:699-703(1989).
CC -1- FUNCTION: The ability of bacteria to bind fibronectin has been
CC proposed as a virulence factor enabling bacteria to colonize wound
CC tissues and blood clots. Binding of plasma fibronectin to the
CC bacterial surface might block adhesion receptors on S.aureus, thus
CC representing an important defense mechanism against tissue
CC invasion.
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC an amide bond (Potential).
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (see http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL, J04151, AAA26632.1, -.
DR InterPro, IPR004237, Fn_bind.
DR InterPro, IPR005877, Gpos_YsIRK.
DR InterPro, IPR001899, Gram_pos_anchor.
DR Pfam, PF02986, Fn_bind, 1.
DR Pfam, PF00746, Gram_pos_anchor, 1.
DR Pfam, PF04650, YsIRK_signal, 1.
DR TIGRfams, TIGR01167, LpxTG_anchor, 1.
DR TIGRfams, TIGR01168, YsIRK_signal, 1.
DR PROSITE, PS50847, GRAM_POS_ANCHORING, 1.
DR Cell adhesion, Cell wall, Peptidoglycan-anchor; Repeat; Signal;
KW Virulence.

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FT SIGNAL 1 36
FT CHAIN 37 985 Fibronectin-binding protein.
FT PROPE 986 1018 Removed by sortase (Potential).
FT REPEAT 545 574 B-1.
FT REPEAT 575 604 B-2.
FT DOMAIN 745 878 4 X approximate tandem repeats,
  fibronectin-binding domain.
FT REPEAT 745 782 D-1.
FT REPEAT 783 820 D-2.
FT REPEAT 821 859 D-3.
FT DOMAIN 860 878 D-4 (incomplete).
FT REPEAT 879 948 5 X tandem repeats, Pro-rich (WR).
FT REPEAT 893 906 WR 1.
FT REPEAT 907 920 WR 2.
FT REPEAT 921 934 WR 3.
FT REPEAT 935 948 WR 4.
FT SITE 982 986 WR 5.
FT MOD_RES 985 985 LeuTg sorting signal (potential).
  Pentaglycyl murein peptidoglycan amidated
  chreonine (potential).
SQ SEQUENCE 1018 AA; 111780 MW; 581758020E81F1F CRC64;

Query Match 100.0%; Score 58; DB 1; Length 1018;
Best Local Similarity 100.0%; Pred. No. 0.037;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YORGHNSVD 10
Db 840 YORGHNSVD 849

RESULT 10
Q99RD2 PRELIMINARY; PRT; 1038 AA.
ID Q99RD2;
AC Q99RD2;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Fibronectin-binding protein homolog.
OS Name=fnd; Orderedlocusnames=SAV2503;
GN Staphylococcus aureus (strain Mu50 / ATCC 700699).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=158878;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MU50 / ATCC 700699;
RA MEDLINE=21311952; Pubmed=11418146; DOI=10.1016/S0140-6736(00)04403-2;
RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
  Cui L., Oguchi A., Aoki K.-I., Nagai Y., Iian J.-O., Ito T.,
  Kanamori M., Matsunaru H., Maruyama A., Murakami H., Hosoyama A.,
  Mizutani U. Y., Takahashi N. K., Sawano T., Inoue R.-I., Kaito C.,
  Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
  Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
  Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
RT "Whole genome sequencing of methicillin-resistant Staphylococcus
  aureus.";
RL Lancet 357:1225-1240(2001).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
  an amide bond (by similarity).
EMBL AP003365; BAB58665.1; -.
DR GO; GO:0009986; C:cell surface; IEA.
DR GO; GO:0005618; C:cell wall; IEA.
DR GO; GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0007155; P:cell adhesion; IEA.
DR InterPro; IPR008966; Adhes_bact.
DR InterPro; IPR004237; Fn_bind.
DR InterPro; IPR005877; Gpos_YSIRK.
DR Pfam; PF02986; Fn_bind; 1.
DR Pfam; PF00746; Gram_pos_anchor; 1.
DR Pfam; PF04650; YSIRK_signal; 1.

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DR TIGRFAMs; TIGR01167; LpXTG_anchor; 1.
DR TIGRFAMs; TIGR01168; YSIRK_signal; 1.
DR PROSITE; PS50847; GRAM_POS_ANCHORING; 1.
DR Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ SEQUENCE 1038 AA; 113618 MW; 666BF6BF2BFEB12 CRC64;

Query Match 100.0%; Score 58; DB 2; Length 1038;
Best Local Similarity 100.0%; Pred. No. 0.038;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YORGHNSVD 10
Db 836 YORGHNSVD 845

RESULT 11
Q7A3J7 PRELIMINARY; PRT; 1038 AA.
ID Q7A3J7;
AC Q7A3J7;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Fnb protein.
OS Name=fnb; Orderedlocusnames=SA2291;
GN Staphylococcus aureus (strain N315).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=158879;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=21311952; Pubmed=11418146; DOI=10.1016/S0140-6736(00)04403-2;
RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
  Cui L., Oguchi A., Aoki K.-I., Nagai Y., Iian J.-O., Ito T.,
  Kanamori M., Matsunaru H., Maruyama A., Murakami H., Hosoyama A.,
  Mizutani U. Y., Takahashi N. K., Sawano T., Inoue R.-I., Kaito C.,
  Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
  Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
  Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
RT "Whole genome sequencing of methicillin-resistant Staphylococcus
  aureus.";
RL Lancet 357:1225-1240(2001).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
  an amide bond (by similarity).
EMBL AP003377; BAB3594.1; -.
DR GO; GO:0009986; C:cell surface; IEA.
DR GO; GO:0005618; C:cell wall; IEA.
DR GO; GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0007155; P:cell adhesion; IEA.
DR InterPro; IPR008966; Adhes_bact.
DR InterPro; IPR004237; Fn_bind.
DR InterPro; IPR005877; Gpos_YSIRK.
DR InterPro; IPR001899; Gram_pos_anchor.
DR Pfam; PF02986; Fn_bind; 1.
DR Pfam; PF00746; Gram_pos_anchor; 1.
DR Pfam; PF04650; YSIRK_signal; 1.
DR TIGRFAMs; TIGR01167; LpXTG_anchor; 1.
DR TIGRFAMs; TIGR01168; YSIRK_signal; 1.
DR PROSITE; PS50847; GRAM_POS_ANCHORING; 1.
DR Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ SEQUENCE 1038 AA; 113618 MW; 666BF6BF2BFEB12 CRC64;

Query Match 100.0%; Score 58; DB 2; Length 1038;
Best Local Similarity 100.0%; Pred. No. 0.038;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YORGHNSVD 10
Db 836 YORGHNSVD 845

RESULT 12
Q9AEP9 PRELIMINARY; PRT; 152 AA.
ID Q9AEP9

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AC Q9AEP9;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Fibronectin-binding protein (Fragment).
GN Name=fnb;
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1280;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CMRSA-1;
RX MEDLINE=21246681; PubMed=11339044;
DOI=10.1128/IAI.69.6.3791-3799.2001;
RA Rice K., Huesca M., Vaz D., McGavin M.J.;
RT "Variance in fibronectin binding and fnb locus polymorphisms in
RT Staphylococcus aureus: identification of antigenic variation in a
RT fibronectin binding protein adhesin of the epidemic CMRSA-1 strain of
RT methicillin-resistant S. aureus."
RL Infect. Immun. 69:3791-3799(2001).
DR EMBL; AY029184; AAK31588.1; -
FT NON TER 152 152
FT SEQUENCE 152 AA; 17193 MW; CFA3913C2B1C025 CRC64;
SQ

Query Match 91.4%; Score 53; DB 2; Length 152;
Best Local Similarity 80.0%; Pred. No. 0.044;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 YORGCHNSVD 10
Db 133 YORGCHNSVD 142

RESULT 13
AROA_STRPN STANDARD; PRT; 427 AA.
ID AROA_STRPN
AC Q9S400;
DT 30-MAY-2000 (Rel. 39, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE 3-phosphoshikimate 1-carboxyvinyltransferase (EC 2.5.1.19) (5-
DE enolpyruvylshikimate-3-phosphate synthase) (EPSP synthase).
GN Name=aroA; OrderedLocNames=SPI371;
OS Streptococcus pneumoniae.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1313;
RN [1]
RP SEQUENCE FROM N.A., AND CHARACTERIZATION.
RC STRAIN=NCIMB 40794 / 0100993;
RX MEDLINE=20069365; PubMed=10601870;
RA Du W., Wallis N.G., Mazulla M.J., Chalker A.F., Zhang L., Liu W.-S.,
RA Kallender H., Payne D.J.;
RT "Characterization of Streptococcus pneumoniae 5-enolpyruvylshikimate
RT 3-phosphate synthase and its activation by univalent cations."
RT Eur. J. Biochem. 267:222-227(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC BAA-334 / TIGR4;
RX MEDLINE=21357209; PubMed=1163916; DOI=10.1126/science.1061217;
RA Tettein H., Nelson K.E., Paulsen I.T., Eisen J.A., Read T.D.,
RA Peterson S.N., Heidelberg J.F., DeBoy R.T., Haft D.H., Dodson R.J.,
RA Durkin A.S., Gilm M.L., Kolonay J.F., Nelson W.C., Peterson J.D.,
RA Umayam L.A., White O., Salzberg S.L., Lewis M.R., Radune D.,
RA Holtzapfel E.K., Khouri H.M., Wolf A.M., Uitterback T.R., Hansen C.L.,
RA McDonald L.A., Feldblyum T.V., Angiuoli S.V., Dickinson T.,
RA Hickey E.K., Holt I.E., Loftus B.J., Yang F., Smith H.O., Venter J.C.,
RA Dougherty B.K., Morrison D.A., Hollingshead S.K., Fraser C.M.;
RT "Complete genome sequence of a virulent isolate of Streptococcus
RT pneumoniae."
RL Science 293:498-506(2001).
-1- CATALYTIC ACTIVITY: Phosphoenolpyruvate + 3-phosphoshikimate =

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CC phosphate + 5-O-(1-carboxyvinyl)-3-phosphoshikimate.
CC -1- PATHWAY: Aromatic amino acids biosynthesis; shikimate pathway;
CC sixth step.
CC -1- SUBUNIT: Monomer (By similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (Probable).
CC -1- SIMILARITY: Belongs to the EPSP synthase family.
CC -----
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CC -----
DR EMBL; AF169483; AAD45819.1; -
DR EMBL; AE007434; AAK75469.1; -
DR PIR; D95159; D95159
DR PDB; 1RP4; X-ray; A/B/C/D=1-427.
DR TIGR; SP1371; -
DR HAMAP; MF_00210; -; 1.
DR InterPro; IPR006264; AroA.
DR InterPro; IPR001986; EPSP synth.
DR Pfam; PF00275; EPSP_synthase; 1.
DR ProDom; PD001867; EPSP_synth; 1.
DR TIGRFAMs; TIGR01356; aroA; 1.
DR PROSITE; PS00104; EPSP_SYNTHASE_1; 1.
DR PROSITE; PS00885; EPSP_SYNTHASE_2; 1.
KW 3D-structure; Aromatic amino acid biosynthesis; Complete proteome;
KW Transferase.
FT CONFLICT 13 13 S -> I (in Ref. 1).
FT CONFLICT 71 71 I -> V (in Ref. 1).
FT CONFLICT 201 201 K -> Q (in Ref. 1).
FT CONFLICT 303 303 G -> C (in Ref. 1).
SQ SEQUENCE 427 AA; 45766 MW; 45CE6F4DD0D1C7B70 CRC64;

Query Match 72.4%; Score 42; DB 1; Length 427;
Best Local Similarity 88.9%; Pred. No. 17;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 OFGCHLSVD 10
Db 202 OFGCHLSVD 210

RESULT 14
AROA_STRPN STANDARD; PRT; 427 AA.
ID AROA_STRPN
AC Q8CW07;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE 3-phosphoshikimate 1-carboxyvinyltransferase (EC 2.5.1.19) (5-
DE enolpyruvylshikimate-3-phosphate synthase) (EPSP synthase) (EPSPS).
GN Name=aroA; OrderedLocNames=SPI229;
OS Streptococcus pneumoniae (strain ATCC BAA-295 / R6).
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=171101;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=21429245; PubMed=11544234;
RX DOI=10.1128/JB.183.19.5709-5717.2001;
RA Hoskins J., Alborn W.E. Jr., Arnold J., Blaszczak L.C., Burgett S.,
RA Gehoff B.S., Bateman S.T., Fritz L., Fu D.-J., Fuller W., Geringer C.,
RA Gilmour R., Glass J.S., Khoja H., Kraft A.R., Lagace R.E.,
RA LeBlanc D.J., Lee L.N., Letkowitz B.J., Lu J., Matsushima P.,
RA McArthur S.M., McHenry M., McLeaster K., Mundy C.W., Nicas T.I.,
RA Norris F.H., O'Gara M., Peery R.B., Robertson G.T., Rocky P.,
RA Sun P.-M., Winkler M.E., Yang Y., Young-Bellido M., Zhao G.,
RA Zook C.A., Baltz R.H., Jaskunas S.R., Rostock P.R. Jr., Skatrud P.L.,
RA Glass J.I.;
RT "Genome of the bacterium Streptococcus pneumoniae strain R6."

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RL J. Bacteriol. 183:5709-5717(2001).
CC -1- CATALYTIC ACTIVITY: Phosphoenolpyruvate + 3-phosphoshikimate =
CC PHOSPHATE + 5-O-(1-carboxyvinyl)-3-phosphoshikimate.
CC -1- PATHWAY: Aromatic amino acids biosynthesis; shikimate pathway;
CC sixth step.
CC -1- SUBUNIT: Monomer (By similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (Probable).
CC -1- SIMILARITY: Belongs to the EPSP synthase family.
-----
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CC or send an email to license@isb-sib.ch).
-----
CC EMBL; AB008494; ALA00033.1; ALT_INIT.
DR HAMAP; MF_00210; -; 1.
DR InterPro; IPR006264; AroA.
DR InterPro; IPR001986; EPSP_synth.
DR Pfam; PF00275; EPSP_synthase; 1.
DR ProDom; PD001867; EPSP_synth; 1.
DR TIGRPFAM; TIGR01356; aroA; 1.
DR PROSITE; PS00104; EPSP SYNTHASE 1; 1.
DR PROSITE; PS00885; EPSP SYNTHASE 2; 1.
KM Aromatic amino acid biosynthesis; Complete proteome; Transferase.
SQ SEQUENCE 427 AA; 45719 MW; D48A60F44B5018 CRC64;

Query Match 72.4%; Score 42; DB 1; Length 427;
Best Local Similarity 88.9%; Pred. No. 17;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 QFGHNSVD 10
Db 202 QFGHLSVD 210

RESULT 15
Q6FJV0 PRELIMINARY; PRT; 706 AA.
ID Q6FJV0
AC Q6FJV0;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Similar to EP132775 Saccharomyces cerevisiae YEL011w GUC3.
GN ORFNames=CAGL0M033779;
OS Candida glabrata CBS138.
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; mitosporic Saccharomycetales; Candida.
OX NCBI_TaxID=284593;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CBS138;
RG Genolevures;
RA Dujon B., Sherman D., Fischer G., Durrens P., Casaregola S.,
RA Lafontaine I., de Montigny J., Marc C., Neuvéglise C., Talla E.,
RA Goffard N., Frangeul L., Aigle M., Anthonard V., Babour A., Barde V.,
RA Barnay S., Blanchin S., Beckrich J.M., Beyne E., Bleykasten C.,
RA Boissarie A., Boyer J., Catolico L., Confantolero F., de Daruvar A.,
RA Despons L., Fabre E., Fairhead C., Ferry-Dumazet H., Groppi A.,
RA Hantreya F., Hennequin C., Jauniaux N., Joyet P., Kachouri R.,
RA Kerrest A., Koszul R., Lemaire M., Lesur I., Ma L., Muller H.,
RA Nicoud J.M., Nikolaki M., Ozias S., Ozier-Kalogeropoulos O.,
RA Pellenz S., Potier S., Richard G.P., Straub M.U., Suleau A.,
RA Swenne D., Tekala F., Wesolowski-Louvel M., Westhof E., Wirth B.,
RA Zenlou-Meyer M., Zivanovic I., Bolotin-Fukuhara M., Thierry A.,
RA Bouchier C., Caudron B., Scarpelli C., Gallardin C., Weissenbach J.,
RA Wincker P., Souciet J.L.;
RT "Genome evolution in yeasts.";
RL EMBL; CR380959; CAG62470.1; -.
DR GO; GO:0004556; F:alpha-amylase activity; IEA.

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DR GO; GO:0004553; F:hydrolyase activity, hydrolyzing O-glycosyl . . .; IEA.
DR GO; GO:0005975; F:carbohydrate metabolism; IEA.
DR InterPro; IPR006047; Alpha_amyl_cat.
DR InterPro; IPR006589; Alp_amyl_cat_sub.
DR InterPro; IPR004193; Glyco_hydro_13N.
DR Pfam; PF00128; Alpha-amylase; 1.
DR Pfam; PF02822; Isoamylase_N; 1.
DR SMART; SM00642; Amy; 1.
SQ SEQUENCE 706 AA; 81044 MW; 18872CNADECD2A87 CRC64;

Query Match 72.4%; Score 42; DB 2; Length 706;
Best Local Similarity 66.7%; Pred. No. 30;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 QFGHNSVD 10
Db 663 EFGHNRID 671

Search completed: October 22, 2005, 09:52:23
Job time : 57.2069 secs

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OW protein - protein search, using sw model

Run on: October 25, 2005, 20:58:51 ; Search time 69.7126 Seconds
(without alignments)
55.479 Million cell updates/sec

Title: US-10-731-238-98
Sequence: 1 FCGHNSVDPE 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:.*
1: geneseqp1980s:.*
2: geneseqp1990s:.*
3: geneseqp2000s:.*
4: geneseqp2001s:.*
5: geneseqp2002s:.*
6: geneseqp2003as:.*
7: geneseqp2003bs:.*
8: geneseqp2004s:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	57	100.0	10	2	AAW65754 F1Dronect
2	57	100.0	14	2	AAW65717 F1Dronect
3	57	100.0	21	2	AAW65670 F1Dronect
4	57	100.0	21	2	AAW65689 F1Dronect
5	57	100.0	21	2	AAW65673 F1Dronect
6	57	100.0	21	2	AAW65684 F1Dronect
7	57	100.0	21	2	AAW65685 F1Dronect
8	57	100.0	21	2	AAW65671 F1Dronect
9	57	100.0	21	2	AAW65688 F1Dronect
10	57	100.0	21	2	AAW65672 F1Dronect
11	57	100.0	21	2	AAW65687 F1Dronect
12	57	100.0	21	2	AAW65686 F1Dronect
13	57	100.0	21	2	AAW65665 F1Dronect
14	57	100.0	21	2	AAW65674 F1Dronect
15	57	100.0	22	2	AAW65674 F1Dronect
16	57	100.0	37	1	AAW65674 F1Dronect
17	57	100.0	37	4	AAW65674 F1Dronect
18	57	100.0	38	1	AAW65674 F1Dronect
19	57	100.0	77	2	AAW65674 F1Dronect
20	57	100.0	101	2	AAW65674 F1Dronect
21	57	100.0	113	2	AAW65674 F1Dronect
22	57	100.0	124	2	AAW65674 F1Dronect
23	57	100.0	128	2	AAW65674 F1Dronect
24	57	100.0	130	2	AAW65674 F1Dronect
25	57	100.0	130	2	AAW65674 F1Dronect

26	57	100.0	130	2	AAW65754	AAW65754 standard; peptide; 10 AA.
27	57	100.0	130	2	AAW65754	AAW65754 standard; peptide; 10 AA.
28	57	100.0	134	2	AAW65754	AAW65754 standard; peptide; 10 AA.
29	57	100.0	134	2	AAW65754	AAW65754 standard; peptide; 10 AA.
30	57	100.0	139	2	AAW65754	AAW65754 standard; peptide; 10 AA.
31	57	100.0	162	2	AAW65754	AAW65754 standard; peptide; 10 AA.
32	57	100.0	164	2	AAW65754	AAW65754 standard; peptide; 10 AA.
33	57	100.0	174	2	AAW65754	AAW65754 standard; peptide; 10 AA.
34	57	100.0	174	2	AAW65754	AAW65754 standard; peptide; 10 AA.
35	57	100.0	181	2	AAW65754	AAW65754 standard; peptide; 10 AA.
36	57	100.0	181	2	AAW65754	AAW65754 standard; peptide; 10 AA.
37	57	100.0	559	2	AAW65754	AAW65754 standard; peptide; 10 AA.
38	57	100.0	940	2	AAW65754	AAW65754 standard; peptide; 10 AA.
39	57	100.0	940	6	AAW65754	AAW65754 standard; peptide; 10 AA.
40	57	100.0	948	6	AAW65754	AAW65754 standard; peptide; 10 AA.
41	57	100.0	948	6	AAW65754	AAW65754 standard; peptide; 10 AA.
42	57	100.0	948	6	AAW65754	AAW65754 standard; peptide; 10 AA.
43	57	100.0	961	6	AAW65754	AAW65754 standard; peptide; 10 AA.
44	57	100.0	978	4	AAW65754	AAW65754 standard; peptide; 10 AA.
45	57	100.0	1001	4	AAW65754	AAW65754 standard; peptide; 10 AA.

ALIGNMENTS

RESULT 1
ID AAW65754 standard; peptide; 10 AA.
AC AAW65754:
XX
XX 16-OCT-1998 (first entry)
XX
XX Fibronectin binding protein-derived peptide #98.
DE
XX
XX microbial surface components recognising adhesive matrix molecule;
KW MCRAMM, fibronectin, fibronectin-binding protein; antibody; epitope;
KW antibiotic; bacterial infection; antibiotic-resistant strain.
XX
XX Synthetic.
OS Staphylococcus aureus.
XX
XX
XX W09831389-A2.
XX
XX 23-JUL-1998.
XX
XX 21-JAN-1998; 98MO-US001222.
XX
XX 21-JAN-1997; 97US-0036139P.
XX
XX (TEXA) UNIV TEXAS A & M SYSTEM.
XX
XX Hoeoek M; Patti JM, House-Pompeo KL, Speziale P, Joh D;
PI Mcgavin MJ;
XX WPI; 1998-413816/35.
XX
XX
XX Antibody that binds to fibronectin-binding protein, preventing its
PT binding to fibronectin - used to treat or prevent bacterial infection,
PT especially by Staphylococci and Streptococci.
XX
XX
XX Example 9, Page 111; 201P; English.
XX
XX The invention relates to antibodies that bind to a fibronectin-binding
XX domain of a fibronectin-binding protein, and inhibit binding of a
XX protein to fibronectin. Also claimed are: (1) isolated peptides of a
XX fibronectin-binding protein that do not bind to fibronectin; (2) fusion
XX protein containing at least one peptide of a fibronectin-binding protein
XX linked to a second amino acid sequence; (3) nucleic acid encoding the
XX isolated peptide of (1). Antibodies, the isolated peptides of (1) and the
XX nucleic acids are all useful for immunisation (active or passive) and (by
XX inhibiting binding of bacteria to fibronectin) for preventing or treating
XX infection in humans or other animals, particularly by staphylococci or

```

CC streptococci, e.g. meningitis, otitis media, pneumonia, endocarditis,
CC mastitis in cattle, abortion in horses and many others. Since the
CC antibodies block binding of bacteria, they should be effective against
CC antibiotic-resistant strains and may replace antibiotic therapy or
CC increase its effectiveness. Sequences AAW65744-58 represent peptides
CC which were synthesised to span the D3 motif of S. aureus fibronectin
CC binding protein A
XX
XX
SQ Sequence 10 AA;

Query Match      100.0%; Score 57; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0029;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FCGHNSVDPE 10
   |||||
DB 1 FCGHNSVDPE 10

RESULT 2
AAW65717 standard; peptide; 14 AA.
XX
XX AAW65717;
AC
XX
XX
XX 16-OCT-1998 (first entry)
DE Fibronectin binding protein fragment (residues 20-33 of D3 motif).
XX
XX microbial surface components recognising adhesive matrix molecule;
KW MSCRAMM; fibronectin; fibronectin-binding protein; antibody; epitope;
XX antibiotic; bacterial infection; antibiotic-resistant strain.
XX
OS Synthetic.
OS Staphylococcus aureus.
XX
XX WO9811389-A2.
XX
XX 23-JUL-1998.
PD
XX
XX 21-JAN-1998; 98WO-US001222.
PF
XX
XX 21-JAN-1997; 97US-0036139P.
PR
XX
XX (TEXA ) UNIV TEXAS A & M SYSTEM.
PA
XX Hoecek M, Patti JM, House-Pompeo KL, Speziale P, Joh D;
PI Mcgavin MJ;
XX
XX WPI; 1998-413816/35.
DR
XX
XX Antibody that binds to fibronectin-binding protein, preventing its
PT binding to fibronectin - used to treat or prevent bacterial infection,
PT especially by Staphylococci and Streptococci.
XX
XX Claim 42; Page 105; 201pp; English.
XX
XX The invention relates to antibodies that bind to a fibronectin-binding
XX domain of a fibronectin-binding protein, and inhibit binding of the
XX protein to fibronectin. Also claimed are: (1) isolated peptides of a
XX fibronectin-binding protein that do not bind to fibronectin; (2) fusion
XX protein containing at least one peptide of a fibronectin-binding protein
XX linked to a second amino acid sequence; (3) nucleic acid encoding the
XX isolated peptide of (1). Antibodies, the isolated peptides of (1) and the
XX nucleic acids are all useful for immunisation (active or passive) and (by
XX inhibiting binding of bacteria to fibronectin) for preventing or treating
XX infection in humans or other animals, particularly by staphylococci or
XX streptococci, e.g. meningitis, otitis media, pneumonia, endocarditis,
XX mastitis in cattle, abortion in horses and many others. Since the
XX antibodies block binding of bacteria, they should be effective against
XX antibiotic-resistant strains, and may replace antibiotic therapy or
XX increase its effectiveness. Sequences AAW65744-58 represent a series of
XX synthetic peptides based on the D3 repeat of S. aureus fibronectin
XX binding protein A. They were synthesised to contain a proline residue at
XX each position throughout the sequence (ie a proline scan)
XX
XX Sequence 21 AA;
SQ
Query Match      100.0%; Score 57; DB 2; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.0063;

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XX
XX Sequence 14 AA;
SQ
Query Match      100.0%; Score 57; DB 2; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.0042;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FCGHNSVDPE 10
   |||||
DB 2 FCGHNSVDPE 11

RESULT 3
AAW65670 standard; peptide; 21 AA.
XX
XX AAW65670;
AC
XX
XX 16-OCT-1998 (first entry)
DT
XX
XX Fibronectin binding protein-derived peptide #14.
DE
XX
XX microbial surface components recognising adhesive matrix molecule;
KW MSCRAMM; fibronectin; fibronectin-binding protein; antibody; epitope;
KW antibiotic; bacterial infection; antibiotic-resistant strain.
XX
XX Synthetic.
OS Staphylococcus aureus.
XX
XX WO9811389-A2.
XX
XX 23-JUL-1998.
PD
XX
XX 21-JAN-1998; 98WO-US001222.
PF
XX
XX 21-JAN-1997; 97US-0036139P.
PR
XX
XX (TEXA ) UNIV TEXAS A & M SYSTEM.
PA
XX Hoecek M, Patti JM, House-Pompeo KL, Speziale P, Joh D;
PI Mcgavin MJ;
XX
XX WPI; 1998-413816/35.
DR
XX
XX Antibody that binds to fibronectin-binding protein, preventing its
PT binding to fibronectin - used to treat or prevent bacterial infection,
PT especially by Staphylococci and Streptococci.
XX
XX Example 8; Page 100; 201pp; English.
XX
XX The invention relates to antibodies that bind to a fibronectin-binding
XX domain of a fibronectin-binding protein, and inhibit binding of the
XX protein to fibronectin. Also claimed are: (1) isolated peptides of a
XX fibronectin-binding protein that do not bind to fibronectin; (2) fusion
XX protein containing at least one peptide of a fibronectin-binding protein
XX linked to a second amino acid sequence; (3) nucleic acid encoding the
XX isolated peptide of (1). Antibodies, the isolated peptides of (1) and the
XX nucleic acids are all useful for immunisation (active or passive) and (by
XX inhibiting binding of bacteria to fibronectin) for preventing or treating
XX infection in humans or other animals, particularly by staphylococci or
XX streptococci, e.g. meningitis, otitis media, pneumonia, endocarditis,
XX mastitis in cattle, abortion in horses and many others. Since the
XX antibodies block binding of bacteria, they should be effective against
XX antibiotic-resistant strains, and may replace antibiotic therapy or
XX increase its effectiveness. Sequences AAW65670-90 represent a series of
XX synthetic peptides based on the D3 repeat of S. aureus fibronectin
XX binding protein A. They were synthesised to contain a proline residue at
XX each position throughout the sequence (ie a proline scan)
XX
XX Sequence 21 AA;
SQ
Query Match      100.0%; Score 57; DB 2; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.0063;

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XX AAW65684;
XX
XX 16-OCT-1998 (first entry)
XX
XX Fibronectin binding protein-derived peptide #28.
XX
XX MSCRAMM; fibronectin; fibronectin-binding protein; antibody; epitope;
XX antibiotic; bacterial infection; antibiotic-resistant strain.
XX
XX Synthetic.
XX Staphylococcus aureus.
XX
XX MO9831389-A2.
XX
XX 23-JUL-1998.
XX
XX 21-JAN-1998; 98WO-US001222.
XX
XX 21-JAN-1997; 97US-0036139P.
XX
XX (TEXA ) UNIV TEXAS A & M SYSTEM.
XX
XX Hoegek M, Patti JM, House-Pompeo KL, Speziale P, Joh D;
XX Mcgavin MJ;
XX
XX WPI, 1998-413816/35.
XX
XX Antibody that binds to fibronectin-binding protein, preventing its
XX binding to fibronectin - used to treat or prevent bacterial infection,
XX especially by Staphylococci and Streptococci.
XX
XX Example 8; Page 101; 201pp; English.
XX
XX The invention relates to antibodies that bind to a fibronectin-binding
XX domain of a fibronectin-binding protein, and inhibit binding of the
XX protein to fibronectin. Also claimed are: (1) isolated peptides of a
XX fibronectin-binding protein that do not bind to fibronectin; (2) fusion
XX protein containing at least one peptide of a fibronectin-binding protein
XX linked to a second amino acid sequence; (3) nucleic acid encoding the
XX isolated peptide of (1). Antibodies, the isolated peptides of (1) and the
XX nucleic acids are all useful for immunisation (active or passive) and (by
XX inhibiting binding of bacteria to fibronectin) for preventing or treating
XX infection in humans or other animals, particularly by staphylococci or
XX streptococci, e.g. meningitis, otitis media, pneumonia, endocarditis,
XX mastitis in cattle, abortion in horses and many others. Since the
XX antibodies block binding of bacteria, they should be effective against
XX antibiotic-resistant strains, and may replace antibiotic therapy or
XX increase its effectiveness. Sequences AAW65670-90 represent a series of
XX synthetic peptides based on the D3 repeat of S. aureus fibronectin
XX binding protein A. They were synthesised to contain a proline residue at
XX each position through the sequence (ie a proline scan)
XX
XX Sequence 21 AA;
XX
XX Query Match 100.0%; Score 57; DB 2; Length 21;
XX Best Local Similarity 100.0%; Pred. No. 0.0063;
XX Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 FCGHNSVDPE 10
XX |||||
XX DB 6 FCGHNSVDPE 15
XX
XX RESULT 7
XX AAW65685
XX ID AAW65685 standard; peptide; 21 AA.
XX
XX AC AAW65685;
XX
XX DT 16-OCT-1998 (first entry)
XX
XX

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DE Fibronectin binding protein-derived peptide #29.
XX
XX MSCRAMM; fibronectin; fibronectin-binding protein; antibody; epitope;
XX antibiotic; bacterial infection; antibiotic-resistant strain.
XX
XX Synthetic.
XX Staphylococcus aureus.
XX
XX MO9831389-A2.
XX
XX 23-JUL-1998.
XX
XX 21-JAN-1998; 98WO-US001222.
XX
XX 21-JAN-1997; 97US-0036139P.
XX
XX (TEXA ) UNIV TEXAS A & M SYSTEM.
XX
XX Hoegek M, Patti JM, House-Pompeo KL, Speziale P, Joh D;
XX Mcgavin MJ;
XX
XX WPI, 1998-413816/35.
XX
XX Antibody that binds to fibronectin-binding protein, preventing its
XX binding to fibronectin - used to treat or prevent bacterial infection,
XX especially by Staphylococci and Streptococci.
XX
XX Example 8; Page 101; 201pp; English.
XX
XX The invention relates to antibodies that bind to a fibronectin-binding
XX domain of a fibronectin-binding protein, and inhibit binding of the
XX protein to fibronectin. Also claimed are: (1) isolated peptides of a
XX fibronectin-binding protein that do not bind to fibronectin; (2) fusion
XX protein containing at least one peptide of a fibronectin-binding protein
XX linked to a second amino acid sequence; (3) nucleic acid encoding the
XX isolated peptide of (1). Antibodies, the isolated peptides of (1) and the
XX nucleic acids are all useful for immunisation (active or passive) and (by
XX inhibiting binding of bacteria to fibronectin) for preventing or treating
XX infection in humans or other animals, particularly by staphylococci or
XX streptococci, e.g. meningitis, otitis media, pneumonia, endocarditis,
XX mastitis in cattle, abortion in horses and many others. Since the
XX antibodies block binding of bacteria, they should be effective against
XX antibiotic-resistant strains, and may replace antibiotic therapy or
XX increase its effectiveness. Sequences AAW65670-90 represent a series of
XX synthetic peptides based on the D3 repeat of S. aureus fibronectin
XX binding protein A. They were synthesised to contain a proline residue at
XX each position through the sequence (ie a proline scan)
XX
XX Sequence 21 AA;
XX
XX Query Match 100.0%; Score 57; DB 2; Length 21;
XX Best Local Similarity 100.0%; Pred. No. 0.0063;
XX Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 FCGHNSVDPE 10
XX |||||
XX DB 6 FCGHNSVDPE 15
XX
XX RESULT 8
XX AAW65671
XX ID AAW65671 standard; peptide; 21 AA.
XX
XX AC AAW65671;
XX
XX DT 16-OCT-1998 (first entry)
XX
XX Fibronectin binding protein-derived peptide #15.
XX
XX MSCRAMM; fibronectin; fibronectin-binding protein; antibody; epitope;
XX antibiotic; bacterial infection; antibiotic-resistant strain.
XX
XX

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XX OS Synthetic.
XX OS Staphylococcus aureus.
XX PN WO9831389-A2.
XX PD 23-JUL-1998.
XX PF 21-JAN-1998; 98WO-US001222.
XX PR 21-JAN-1997; 97US-0036139P.
XX PA (TEXA ) UNIV TEXAS A & M SYSTEM.
XX PI Hoeoek M, Patti JM, House-Pompeo KL, Speziale P, Joh D;
XX PI McGavin MJ;
XX DR WPI; 1998-413816/35.
XX PT Antibody that binds to fibronectin-binding protein, preventing its
XX PT binding to fibronectin - used to treat or prevent bacterial infection,
XX PT especially by Staphylococci and Streptococci.
XX PS Example 8; Page 100; 201pp; English.
XX CC The invention relates to antibodies that bind to a fibronectin-binding
XX CC domain of a fibronectin-binding protein, and inhibit binding of the
XX CC protein to fibronectin. Also claimed are: (1) isolated peptides of a
XX CC fibronectin-binding protein that do not bind to fibronectin; (2) fusion
XX CC protein containing at least one peptide of a fibronectin-binding protein
XX CC linked to a second amino acid sequence; (3) nucleic acid encoding the
XX CC isolated peptide of (1). Antibodies, the isolated peptides of (1) and the
XX CC nucleic acids are all useful for immunisation (active or passive) and (by
XX CC inhibiting binding of bacteria to fibronectin) for preventing or treating
XX CC infection in humans or other animals, particularly by staphylococci or
XX CC streptococci, e.g. meningitis, otitis media, pneumonia, endocarditis,
XX CC mastitis in cattle, abortion in horses and many others. Since the
XX CC antibodies block binding of bacteria, they should be effective against
XX CC antibiotic-resistant strains, and may replace antibiotic therapy or
XX CC increase its effectiveness. Sequences AAW65670-90 represent a series of
XX CC synthetic peptides based on the D3 repeat of S. aureus fibronectin
XX CC binding protein A. They were synthesised to contain a proline residue at
XX CC each position through the sequence (ie a proline scan)
XX SQ Sequence 21 AA;
XX
XX Query Match 100.0%; Score 57; DB 2; Length 21;
XX Best Local Similarity 100.0%; Pred. No. 0.0063;
XX Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 FGGHNSVDPE 10
XX DB 6 FGGHNSVDPE 15
XX
XX RESULT 9
XX ID AAW65688 standard; peptide; 21 AA.
XX AC AAW65688;
XX XX
XX DT 16-OCT-1998 (first entry)
XX DE Fibronectin binding protein-derived peptide #32.
XX XX
XX KM microbial surface components recognising adhesive matrix molecule;
XX KM MSCRAMM; fibronectin; fibronectin-binding protein; antibody; epitope;
XX KM antibiotic; bacterial infection; antibiotic-resistant strain.
XX OS Synthetic.
XX OS Staphylococcus aureus.
XX PN WO9831389-A2.

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XX PD 23-JUL-1998.
XX PF 21-JAN-1998; 98WO-US001222.
XX PR 21-JAN-1997; 97US-0036139P.
XX PA (TEXA ) UNIV TEXAS A & M SYSTEM.
XX PI Hoeoek M, Patti JM, House-Pompeo KL, Speziale P, Joh D;
XX PI McGavin MJ;
XX DR WPI; 1998-413816/35.
XX PT Antibody that binds to fibronectin-binding protein, preventing its
XX PT binding to fibronectin - used to treat or prevent bacterial infection,
XX PT especially by Staphylococci and Streptococci.
XX PS Example 8; Page 101; 201pp; English.
XX CC The invention relates to antibodies that bind to a fibronectin-binding
XX CC domain of a fibronectin-binding protein, and inhibit binding of the
XX CC protein to fibronectin. Also claimed are: (1) isolated peptides of a
XX CC fibronectin-binding protein that do not bind to fibronectin; (2) fusion
XX CC protein containing at least one peptide of a fibronectin-binding protein
XX CC linked to a second amino acid sequence; (3) nucleic acid encoding the
XX CC isolated peptide of (1). Antibodies, the isolated peptides of (1) and the
XX CC nucleic acids are all useful for immunisation (active or passive) and (by
XX CC inhibiting binding of bacteria to fibronectin) for preventing or treating
XX CC infection in humans or other animals, particularly by staphylococci or
XX CC streptococci, e.g. meningitis, otitis media, pneumonia, endocarditis,
XX CC mastitis in cattle, abortion in horses and many others. Since the
XX CC antibodies block binding of bacteria, they should be effective against
XX CC antibiotic-resistant strains, and may replace antibiotic therapy or
XX CC increase its effectiveness. Sequences AAW65670-90 represent a series of
XX CC synthetic peptides based on the D3 repeat of S. aureus fibronectin
XX CC binding protein A. They were synthesised to contain a proline residue at
XX CC each position through the sequence (ie a proline scan)
XX SQ Sequence 21 AA;
XX
XX Query Match 100.0%; Score 57; DB 2; Length 21;
XX Best Local Similarity 100.0%; Pred. No. 0.0063;
XX Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 FGGHNSVDPE 10
XX DB 6 FGGHNSVDPE 15
XX
XX RESULT 10
XX ID AAW65672 standard; peptide; 21 AA.
XX AC AAW65672;
XX XX
XX DT 16-OCT-1998 (first entry)
XX DE Fibronectin binding protein-derived peptide #16.
XX XX
XX KM microbial surface components recognising adhesive matrix molecule;
XX KM MSCRAMM; fibronectin; fibronectin-binding protein; antibody; epitope;
XX KM antibiotic; bacterial infection; antibiotic-resistant strain.
XX OS Synthetic.
XX OS Staphylococcus aureus.
XX PN WO9831389-A2.
XX PD 23-JUL-1998.
XX PF 21-JAN-1998; 98WO-US001222.

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PR 21-JAN-1997; 97US-0036139P.
XX
XX (TEXA ) UNIV TEXAS A & M SYSTEM.
XX
XX Hoeoek M, Patti JM, House-Pompeo KL, Speziale P, Joh D;
PI Mcgavin MJ;
XX
XX WPI; 1998-413816/35.
XX
XX
XX Antibody that binds to fibronectin-binding protein, preventing its
PT binding to fibronectin - used to treat or prevent bacterial infection,
PT especially by Staphylococci and Streptococci.
XX
XX Example 8; Page 100; 201pp; English.
XX
XX The invention relates to antibodies that bind to a fibronectin-binding
CC domain of a fibronectin-binding protein, and inhibit binding of the
CC protein to fibronectin. Also claimed are: (1) isolated peptides of a
CC fibronectin-binding protein that do not bind to fibronectin; (2) fusion
CC protein containing at least one peptide of a fibronectin-binding protein
CC linked to a second amino acid sequence; (3) nucleic acid encoding the
CC isolated peptide of (1). Antibodies, the isolated peptides of (1) and the
CC nucleic acids are all useful for immunisation (active or passive) and (by
CC inhibiting binding of bacteria to fibronectin) for preventing or treating
CC infection in humans or other animals, particularly by staphylococci or
CC streptococci, e.g. meningitis, otitis media, pneumonia, endocarditis,
CC mastitis in cattle, abortion in horses and many others. Since the
CC antibodies block binding of bacteria, they should be effective against
CC antibiotic-resistant strains, and may replace antibiotic therapy or
CC increase its effectiveness. Sequences AAW65670-90 represent a series of
CC synthetic peptides based on the D3 repeat of S. aureus fibronectin
CC binding protein A. They were synthesised to contain a proline residue at
CC each position through the sequence (ie a proline scan)
XX
XX Sequence 21 AA:
SQ
Query Match 100.0%; Score 57; DB 2; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.0063;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 FGGHNSVDFE 10
DB 6 FGGHNSVDFE 15
RESULT 11
AAW65687 standard; peptide; 21 AA.
XX
XX AAW65687;
XX
XX 16-OCT-1998 (first entry)
XX
XX Fibronectin binding protein-derived peptide #31.
XX
XX Microbial surface components recognising adhesive matrix molecule;
KM MSCRAMM; fibronectin; fibronectin-binding protein; antibody; epitope;
KM antibiotic; bacterial infection; antibiotic-resistant strain.
XX
XX Synthetic.
OS Staphylococcus aureus.
XX
XX WO9831389-A2.
XX
XX 23-JUL-1998.
XX
XX 21-JAN-1998; 98WO-US001222.
XX
XX 21-JAN-1997; 97US-0036139P.
XX
XX (TEXA ) UNIV TEXAS A & M SYSTEM.
XX
XX Hoeoek M, Patti JM, House-Pompeo KL, Speziale P, Joh D;
PI

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PI Mcgavin MJ;
XX
XX WPI; 1998-413816/35.
XX
XX
XX Antibody that binds to fibronectin-binding protein, preventing its
PT binding to fibronectin - used to treat or prevent bacterial infection,
PT especially by Staphylococci and Streptococci.
XX
XX Example 8; Page 101; 201pp; English.
XX
XX The invention relates to antibodies that bind to a fibronectin-binding
CC domain of a fibronectin-binding protein, and inhibit binding of the
CC protein to fibronectin. Also claimed are: (1) isolated peptides of a
CC fibronectin-binding protein that do not bind to fibronectin; (2) fusion
CC protein containing at least one peptide of a fibronectin-binding protein
CC linked to a second amino acid sequence; (3) nucleic acid encoding the
CC isolated peptide of (1). Antibodies, the isolated peptides of (1) and the
CC nucleic acids are all useful for immunisation (active or passive) and (by
CC inhibiting binding of bacteria to fibronectin) for preventing or treating
CC infection in humans or other animals, particularly by staphylococci or
CC streptococci, e.g. meningitis, otitis media, pneumonia, endocarditis,
CC mastitis in cattle, abortion in horses and many others. Since the
CC antibodies block binding of bacteria, they should be effective against
CC antibiotic-resistant strains, and may replace antibiotic therapy or
CC increase its effectiveness. Sequences AAW65670-90 represent a series of
CC synthetic peptides based on the D3 repeat of S. aureus fibronectin
CC binding protein A. They were synthesised to contain a proline residue at
CC each position through the sequence (ie a proline scan)
XX
XX Sequence 21 AA:
SQ
Query Match 100.0%; Score 57; DB 2; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.0063;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 FGGHNSVDFE 10
DB 6 FGGHNSVDFE 15
RESULT 12
AAW65686 standard; peptide; 21 AA.
XX
XX AAW65686;
XX
XX 16-OCT-1998 (first entry)
XX
XX Fibronectin binding protein-derived peptide #30.
XX
XX Microbial surface components recognising adhesive matrix molecule;
KM MSCRAMM; fibronectin; fibronectin-binding protein; antibody; epitope;
KM antibiotic; bacterial infection; antibiotic-resistant strain.
XX
XX Synthetic.
OS Staphylococcus aureus.
XX
XX WO9831389-A2.
XX
XX 23-JUL-1998.
XX
XX 21-JAN-1998; 98WO-US001222.
XX
XX 21-JAN-1997; 97US-0036139P.
XX
XX (TEXA ) UNIV TEXAS A & M SYSTEM.
XX
XX Hoeoek M, Patti JM, House-Pompeo KL, Speziale P, Joh D;
PI Mcgavin MJ;
XX
XX WPI; 1998-413816/35.
XX
XX Antibody that binds to fibronectin-binding protein, preventing its
PT

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PT binding to fibronectin - used to treat or prevent bacterial infection,
 PT especially by Staphylococci and Streptococci.

PS Example 8; Page 101; 201pp; English.

XX The invention relates to antibodies that bind to a fibronectin-binding
 CC domain of a fibronectin-binding protein, and inhibit binding of the
 CC protein to fibronectin. Also claimed are: (1) isolated peptides of a
 CC fibronectin-binding protein that do not bind to fibronectin; (2) fusion
 CC protein containing at least one peptide of a fibronectin-binding protein
 CC linked to a second amino acid sequence; (3) nucleic acid encoding the
 CC isolated peptide of (1). Antibodies, the isolated peptides of (1) and the
 CC nucleic acids are all useful for immunisation (active or passive) and (by
 CC inhibiting binding of bacteria to fibronectin) for preventing or treating
 CC infection in humans or other animals, particularly by staphylococci or
 CC streptococci, e.g. meningitis, otitis media, pneumonia, endocarditis,
 CC mastitis in cattle, abortion in horses and many others. Since the
 CC antibodies block binding of bacteria, they should be effective against
 CC antibiotic-resistant strains, and may replace antibiotic therapy or
 CC increase its effectiveness. Sequences AAW65670-90 represent a series of
 CC synthetic peptides based on the D3 repeat of S. aureus fibronectin
 CC binding protein A. They were synthesised to contain a proline residue at
 CC each position through the sequence (ie a proline scan)

XX Sequence 21 AA;

Query Match 100.0%; Score 57; DB 2; Length 21;

Best Local Similarity 100.0%; Pred. No. 0.0063; Indels 0; Gaps 0;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FCGHNSVDPE 10
 |||||
 6 FCGHNSVDPE 15

Db

RESULT 13

AAW65665 ID AAW65665 standard; peptide; 21 AA.

XX AAW65665;

XX 16-OCT-1998 (first entry)

XX Fibronectin binding protein-derived peptide #9.

XX microbial surface components recognising adhesive matrix molecule;

KW MSCRAMM; fibronectin; fibronectin-binding protein; antibody; epitope;

KW antibiotic; bacterial infection; antibiotic-resistant strain.

XX Synthetic.

OS Staphylococcus aureus.

XX WO9831389-A2.

XX 23-JUL-1998.

XX 21-JAN-1998; 98WO-US001222.

XX 21-JAN-1997; 97US-0036139P.

XX (TEXA) UNIV TEXAS A & M SYSTEM.

XX Hooeok M, Patti JM, House-Pompeo KL, Speziale P, Joh D;

XX Mcgavin MJ;

XX WPI; 1998-413816/35.

XX Antibody that binds to fibronectin-binding protein, preventing its
 PT binding to fibronectin - used to treat or prevent bacterial infection,
 PT especially by Staphylococci and Streptococci.

XX Example 2; Page 92; 201pp; English.

CC The invention relates to antibodies that bind to a fibronectin-binding
 CC domain of a fibronectin-binding protein, and inhibit binding of the
 CC protein to fibronectin. Also claimed are: (1) isolated peptides of a
 CC fibronectin-binding protein that do not bind to fibronectin; (2) fusion
 CC protein containing at least one peptide of a fibronectin-binding protein
 CC linked to a second amino acid sequence; (3) nucleic acid encoding the
 CC isolated peptide of (1). Antibodies, the isolated peptides of (1) and the
 CC nucleic acids are all useful for immunisation (active or passive) and (by
 CC inhibiting binding of bacteria to fibronectin) for preventing or treating
 CC infection in humans or other animals, particularly by staphylococci or
 CC streptococci, e.g. meningitis, otitis media, pneumonia, endocarditis,
 CC mastitis in cattle, abortion in horses and many others. Since the
 CC antibodies block binding of bacteria, they should be effective against
 CC antibiotic-resistant strains, and may replace antibiotic therapy or
 CC increase its effectiveness. Sequences AAW65659-68 represent synthetic
 CC epitopes from the fibronectin binding domains DU and DI-D4 of the S.
 CC aureus fnba gene

XX Sequence 21 AA;

Query Match 100.0%; Score 57; DB 2; Length 21;

Best Local Similarity 100.0%; Pred. No. 0.0063; Indels 0; Gaps 0;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FCGHNSVDPE 10
 |||||
 6 FCGHNSVDPE 15

Db

RESULT 14

AAW65674 ID AAW65674 standard; peptide; 21 AA.

XX AAW65674;

XX 16-OCT-1998 (first entry)

XX Fibronectin binding protein-derived peptide #18.

XX microbial surface components recognising adhesive matrix molecule;

KW MSCRAMM; fibronectin; fibronectin-binding protein; antibody; epitope;

KW antibiotic; bacterial infection; antibiotic-resistant strain.

XX Synthetic.

OS Staphylococcus aureus.

XX WO9831389-A2.

XX 23-JUL-1998.

XX 21-JAN-1998; 98WO-US001222.

XX 21-JAN-1997; 97US-0036139P.

XX (TEXA) UNIV TEXAS A & M SYSTEM.

XX Hooeok M, Patti JM, House-Pompeo KL, Speziale P, Joh D;

XX Mcgavin MJ;

XX WPI; 1998-413816/35.

XX Antibody that binds to fibronectin-binding protein, preventing its
 PT binding to fibronectin - used to treat or prevent bacterial infection,
 PT especially by Staphylococci and Streptococci.

XX Example 8; Page 100; 201pp; English.

XX The invention relates to antibodies that bind to a fibronectin-binding
 CC domain of a fibronectin-binding protein, and inhibit binding of the
 CC protein to fibronectin. Also claimed are: (1) isolated peptides of a
 CC fibronectin-binding protein that do not bind to fibronectin; (2) fusion
 CC protein containing at least one peptide of a fibronectin-binding protein
 CC linked to a second amino acid sequence; (3) nucleic acid encoding the

XX linked to a second amino acid sequence; (3) nucleic acid encoding the

CC isolated peptide of (1). Antibodies, the isolated peptides of (1) and the
CC nucleic acids are all useful for immunisation (active or passive) and (by
CC inhibiting binding of bacteria to fibronectin) for preventing or treating
CC infection in humans or other animals, particularly by staphylococci or
CC streptococci, e.g. meningitis, otitis media, pneumonia, endocarditis,
CC mastitis in cattle, abortion in horses and many others. Since the
CC antibodies block binding of bacteria, they should be effective against
CC antibiotic-resistant strains, and may replace antibiotic therapy or
CC increase its effectiveness. Sequences AAW65670-90 represent a series of
CC synthetic peptides based on the D3 repeat of *S. aureus* fibronectin
CC binding protein A. They were synthesised to contain a proline residue at
CC each position through the sequence (ie a proline scan)
XX
SQ Sequence 21 AA;

Query Match 100.0%; Score 57; DB 2; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.0063;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 FGGHNSVDPE 10
DB 6 FGGHNSVDPE 15

RESULT 15
AAR21340
ID AAR21340 standard; peptide; 22 AA.
XX

AC AAR21340;

DT 25-MAR-2003 (revised)

DT 15-JUN-1992 (first entry)

DE Fibronectin binding protein.

KM FNBp; wound infection reduction; vaccination; mastitis;
KW Staphylococcal infections; D3.

OS Synthetic.

PN WO9202555-A.

PD 20-FEB-1992.

PF 10-AUG-1990; 90SE-00002617.

PR 10-AUG-1990; 90SE-00002617.

PA (ALFA) ALFA LAVAL AGRIC INT AB.

PI Hook M, McGavin M, Raucel G;

DR MPI; 1992-080035/10.

PT New fibronectin binding peptide - combines with fusion peptide to form
PT large antigen, used in immunisation, diagnosis and for treating wounds.

PS Claim 1; Page 22; 33pp; English.

CC The sequence comprises amino acids 17-33 of a tandem repeat, designated
CC D3 of the fibronectin binding site of *Staphylococcus aureus* 8325-4 FNBp.
CC The N-terminal DK may be replaced with H or K, and the C-terminal LKP may
CC be replaced by either L, IP, or OH. The peptides were synthesised using
CC standard methods and purified using reverse phase HPLC. The appropriate
CC fractions were dialysed and lyophilised. Peptide sequencing was performed
CC and the peptides digested and chemically modified by dihydroxypropylation
CC of the amino side chain of lysine. The carboxylic side chains were
CC converted to glycine methyl esters. The phenyl side chains of tyrosine
CC residues were oxidised. Chemically modified peptide D3 was compared to
CC unmodified D3. Lysine and tyrosine modifications only partially
CC diminished its activity whereas modification of aspartic/glutamic
CC residues resulted in complete loss of activity. The peptide can be used
CC for the prevention or reduction of the risk of wound infection. The

CC peptide can be used to create a large antigen for vaccinating ruminants
CC against mastitis caused by *Staphylococcal* infections. It can also be used
CC to diagnose *Staphylococcal* infections using ELISA or DNA probes. (Updated
CC on 25-MAR-2003 to correct PA field.)
XX

SQ Sequence 22 AA;

Query Match 100.0%; Score 57; DB 2; Length 22;
Best Local Similarity 100.0%; Pred. No. 0.0066;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 FGGHNSVDPE 10
DB 7 FGGHNSVDPE 16

Search completed: October 25, 2005, 21:29:13
JOB time : 69.7126 secs

GenCore version 5.1.6
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OM protein - protein search, using SW model

Run on: October 22, 2005, 07:41:53 ; Search time 17.2989 Seconds
(without alignments)
43.153 Million cell updates/sec

Title: US-10-731-238-98
Perfect score: 57
Sequence: 1 FCGHNSVDPE 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents_AA:*
1: /cgn2_6/prodata/1/iaa/5A.COMB.pep.*
2: /cgn2_6/prodata/1/iaa/5B.COMB.pep.*
3: /cgn2_6/prodata/1/iaa/5A.COMB.pep.*
4: /cgn2_6/prodata/1/iaa/6B.COMB.pep.*
5: /cgn2_6/prodata/1/iaa/PCTUS.COMB.pep.*
6: /cgn2_6/prodata/1/iaa/backfile1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	57	100.0	10	US-09-010-317-98	Sequence 98, Appl
2	57	100.0	14	US-09-010-317-61	Sequence 61, Appl
3	57	100.0	19	US-08-234-622A-1	Sequence 1, Appl
4	57	100.0	21	US-09-010-317-9	Sequence 9, Appl
5	57	100.0	21	US-09-010-317-14	Sequence 14, Appl
6	57	100.0	21	US-09-010-317-15	Sequence 15, Appl
7	57	100.0	21	US-09-010-317-16	Sequence 16, Appl
8	57	100.0	21	US-09-010-317-17	Sequence 17, Appl
9	57	100.0	21	US-09-010-317-18	Sequence 18, Appl
10	57	100.0	21	US-09-010-317-28	Sequence 28, Appl
11	57	100.0	21	US-09-010-317-29	Sequence 29, Appl
12	57	100.0	21	US-09-010-317-30	Sequence 30, Appl
13	57	100.0	21	US-09-010-317-31	Sequence 31, Appl
14	57	100.0	21	US-09-010-317-32	Sequence 32, Appl
15	57	100.0	21	US-09-010-317-33	Sequence 33, Appl
16	57	100.0	37	US-08-234-622A-4	Sequence 4, Appl
17	57	100.0	38	US-08-294-189-8	Sequence 8, Appl
18	57	100.0	38	US-08-729-767-5	Sequence 5, Appl
19	57	100.0	114	US-08-259-000-3	Sequence 3, Appl
20	57	100.0	130	US-08-459-135A-7	Sequence 8, Appl
21	57	100.0	130	US-08-459-135A-8	Sequence 8, Appl
22	57	100.0	130	US-08-495-559-7	Sequence 8, Appl
23	57	100.0	130	US-08-495-559-8	Sequence 8, Appl
24	57	100.0	139	US-08-856-253-8	Sequence 8, Appl
25	57	100.0	174	US-08-459-135A-10	Sequence 10, Appl
26	57	100.0	174	US-08-459-135A-13	Sequence 13, Appl
27	57	100.0	174	US-08-495-559-10	Sequence 10, Appl

28	57	100.0	174	US-08-495-559-13	Sequence 13, Appl
29	57	100.0	176	US-08-495-559-6	Sequence 6, Appl
30	57	100.0	178	US-08-459-135A-12	Sequence 12, Appl
31	57	100.0	178	US-08-495-559-12	Sequence 12, Appl
32	57	100.0	181	US-08-459-135A-6	Sequence 6, Appl
33	57	100.0	559	US-08-956-171E-5251	Sequence 5251, Ap
34	57	100.0	559	US-08-781-986A-5251	Sequence 5251, Ap
35	57	100.0	1027	US-08-956-171E-5254	Sequence 5254, Ap
36	57	100.0	1027	US-08-781-986A-5254	Sequence 5254, Ap
37	52	91.2	21	US-09-010-317-23	Sequence 23, Appl
38	52	91.2	21	US-09-010-317-27	Sequence 27, Appl
39	51	89.5	21	US-09-010-317-19	Sequence 19, Appl
40	51	89.5	21	US-09-010-317-24	Sequence 24, Appl
41	50	87.7	21	US-09-010-317-25	Sequence 25, Appl
42	49	86.0	21	US-09-010-317-10	Sequence 10, Appl
43	49	86.0	21	US-09-010-317-20	Sequence 20, Appl
44	49	86.0	21	US-09-010-317-22	Sequence 22, Appl
45	49	86.0	22	US-09-010-317-13	Sequence 13, Appl

ALIGNMENTS

RESULT 1
US-09-010-317-98
Sequence 98, Application US/09010317
Patent No. 6685943
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
APPLICANT: Patti, Joseph M.
APPLICANT: House-Pompeo, Karen L.
APPLICANT: Speziale, Pietro
APPLICANT: Joh, Danny
APPLICANT: McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
TITLE OF INVENTION: AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
City: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAMK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 98:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-09-010-317-98
Query Match 100.0%; Score 57; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.00039;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FGGHNSVDPE 10
| | | | | | | | | |
Db 1 FGGHNSVDPE 10

RESULT 2

US-09-010-317-61
; Sequence 61, Application US/09010317
; Patent No. 6685943
; GENERAL INFORMATION:
; APPLICANT: Hook, Magnus
; APPLICANT: Patil, Joseph M.
; APPLICANT: House-Pompeo, Karen L.
; APPLICANT: Speziale, Pietro
; APPLICANT: Joh, Danny
; APPLICANT: McGavin, Martin J.
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
; NUMBER OF SEQUENCES: 105
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: TX
; COUNTRY: USA
; ZIP: 77210-4433
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/010,317
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/036,139
; FILING DATE: 21-JAN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Hibler, David W.
; REGISTRATION NUMBER: 41,071
; REFERENCE/DOCKET NUMBER: TANK:189
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 512-418-3000
; TELEFAX: 512-474-7577
; INFORMATION FOR SEQ ID NO: 61:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; US-09-010-317-61

Query Match 100.0%; Score 57; DB 4; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.00056;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FGGHNSVDPE 10
| | | | | | | | | |
Db 2 FGGHNSVDPE 11

RESULT 3

US-08-234-622A-1
; Sequence 1, Application US/08234622A
; Patent No. 5440014
; GENERAL INFORMATION:
; APPLICANT: Hook, Magnus
; APPLICANT: McGavin, Martin
; APPLICANT: RAUCCI, Giuseppe
; TITLE OF INVENTION: A FIBRONECTIN BINDING PEPTIDE

; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Doane, Swecker & Mathis
; STREET: P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22113-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/234,622A
; FILING DATE: 28-APR-1994
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: SE 9002617-0
; FILING DATE: 10-AUG-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/SE91/00534
; FILING DATE: 09-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Neuth, Donna M.
; REGISTRATION NUMBER: 36,607
; REFERENCE/DOCKET NUMBER: 012885-044
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 19 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1
; OTHER INFORMATION: /note= "Amino acid 1 is R' wherein
; OTHER INFORMATION: R' is hydrogen, K or DK."
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 19
; OTHER INFORMATION: /note= "Amino acid 19 is R2 wherein
; OTHER INFORMATION: R2 is hydroxy, L, LP or LPK."

US-08-234-622A-1

Query Match 100.0%; Score 57; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 0.00077;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FGGHNSVDPE 10
| | | | | | | | | |
Db 6 FGGHNSVDPE 15

RESULT 4

US-09-010-317-9
; Sequence 9, Application US/09010317
; Patent No. 6685943
; GENERAL INFORMATION:
; APPLICANT: Hook, Magnus
; APPLICANT: Patil, Joseph M.
; APPLICANT: House-Pompeo, Karen L.
; APPLICANT: Speziale, Pietro
; APPLICANT: Joh, Danny
; APPLICANT: McGavin, Martin J.
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
; NUMBER OF SEQUENCES: 105
; CORRESPONDENCE ADDRESS:

ADDRESSER: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TANK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-09-010-317-9

Query Match 100.0%; Score 57; DB 4; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.00086;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FGGHNSVDFE 10
| | | | | | | | | |
Db 6 FGGHNSVDFE 15

RESULT 5
US-09-010-317-14
Sequence 14, Application US/09010317
Patent No. 6685943
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
APPLICANT: Patil, Joseph M.
APPLICANT: House-Pompeo, Karen L.
APPLICANT: Speziale, Pietro
APPLICANT: Job, Danny
APPLICANT: McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSER: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TANK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-09-010-317-14

Query Match 100.0%; Score 57; DB 4; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.00086;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FGGHNSVDFE 10
| | | | | | | | | |
Db 6 FGGHNSVDFE 15

RESULT 6
US-09-010-317-15
Sequence 15, Application US/09010317
Patent No. 6685943
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
APPLICANT: Patil, Joseph M.
APPLICANT: House-Pompeo, Karen L.
APPLICANT: Speziale, Pietro
APPLICANT: Job, Danny
APPLICANT: McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSER: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TANK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-09-010-317-15

Query Match 100.0%; Score 57; DB 4; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.00086;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FCGHNSVDFE 10
| | | | | | | | | |
DB 6 FCGHNSVDFE 15

RESULT 7

US-09-010-317-16
; Sequence 16, Application US/09010317
; Patent No. 6685943
; GENERAL INFORMATION:
; APPLICANT: Hook, Magnus
; APPLICANT: Patti, Joseph M.
; APPLICANT: House-Pompeo, Karen L.
; APPLICANT: Speziale, Pietro
; APPLICANT: Joh, Danny
; APPLICANT: McGavin, Martin J.
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
; NUMBER OF SEQUENCES: 105
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P. O. Box 4433
; CITY: Houston
; STATE: TX
; COUNTRY: USA
; ZIP: 77210-4433
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/010,317
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/036,139
; FILING DATE: 21-JAN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Hibler, David W.
; REGISTRATION NUMBER: 41,071
; REFERENCE/DOCKET NUMBER: TANK:189
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 512-418-3000
; TELEFAX: 512-474-7577
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
US-09-010-317-16

Query Match 100.0%; Score 57; DB 4; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.00086;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FCGHNSVDFE 10
| | | | | | | | | |
DB 6 FCGHNSVDFE 15

RESULT 8

US-09-010-317-17
; Sequence 17, Application US/09010317
; Patent No. 6685943
; GENERAL INFORMATION:
; APPLICANT: Hook, Magnus

; APPLICANT: Patti, Joseph M.
; APPLICANT: House-Pompeo, Karen L.
; APPLICANT: Speziale, Pietro
; APPLICANT: Joh, Danny
; APPLICANT: McGavin, Martin J.
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
; NUMBER OF SEQUENCES: 105
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P. O. Box 4433
; CITY: Houston
; STATE: TX
; COUNTRY: USA
; ZIP: 77210-4433
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/010,317
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/036,139
; FILING DATE: 21-JAN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Hibler, David W.
; REGISTRATION NUMBER: 41,071
; REFERENCE/DOCKET NUMBER: TANK:189
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 512-418-3000
; TELEFAX: 512-474-7577
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
US-09-010-317-17

Query Match 100.0%; Score 57; DB 4; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.00086;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FCGHNSVDFE 10
| | | | | | | | | |
DB 6 FCGHNSVDFE 15

RESULT 9

US-09-010-317-18
; Sequence 18, Application US/09010317
; Patent No. 6685943
; GENERAL INFORMATION:
; APPLICANT: Hook, Magnus
; APPLICANT: Patti, Joseph M.
; APPLICANT: House-Pompeo, Karen L.
; APPLICANT: Speziale, Pietro
; APPLICANT: Joh, Danny
; APPLICANT: McGavin, Martin J.
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
; NUMBER OF SEQUENCES: 105
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P. O. Box 4433
; CITY: Houston
; STATE: TX
; COUNTRY: USA
; ZIP: 77210-4433
; COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAMK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-09-010-317-18

Query Match 100.0%; Score 57; DB 4; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.00086;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FGCHNSVDPE 10
Db 6 FGCHNSVDPE 15

RESULT 10
US-09-010-317-28
Sequence 28, Application US/09010317
Patent No. 6685943
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
APPLICANT: Patli, Joseph M.
APPLICANT: House-Pompeo, Karen L.
APPLICANT: Speziale, Pietro
APPLICANT: Joh, Danny
APPLICANT: McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
TITLE OF INVENTION: AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAMK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 29:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-09-010-317-29

TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-09-010-317-28

Query Match 100.0%; Score 57; DB 4; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.00086;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FGCHNSVDPE 10
Db 6 FGCHNSVDPE 15

RESULT 11
US-09-010-317-29
Sequence 29, Application US/09010317
Patent No. 6685943
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
APPLICANT: Patli, Joseph M.
APPLICANT: House-Pompeo, Karen L.
APPLICANT: Speziale, Pietro
APPLICANT: Joh, Danny
APPLICANT: McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
TITLE OF INVENTION: AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAMK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 29:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-09-010-317-29

Query Match 100.0%; Score 57; DB 4; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.00086;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FGCHNSVDPE 10
Db 6 FGCHNSVDPE 15

Db 6 FCGHNSVDPE 15

RESULT 12

US-09-010-317-30

; Sequence 30, Application US/09010317
; Patent No. 6685943

GENERAL INFORMATION:

APPLICANT: Hook, Magnus

APPLICANT: Patti, Joseph M.

APPLICANT: House-Pompeo, Karen L.

APPLICANT: Speziale, Pietro

APPLICANT: Joh, Danny

APPLICANT: McGavin, Martin J.

TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS

TITLE OF INVENTION: AND METHODS OF USE

NUMBER OF SEQUENCES: 105

CORRESPONDENCE ADDRESS:

ADDRESSEE: Arnold, White & Durkee

STREET: P.O. Box 4433

CITY: Houston

STATE: TX

COUNTRY: USA

ZIP: 77210-4433

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/010,317

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 60/036,139

FILING DATE: 21-JAN-1997

ATTORNEY/AGENT INFORMATION:

NAME: Hibler, David W.

REGISTRATION NUMBER: 41,071

REFERENCE/DOCKET NUMBER: TANK:189

TELECOMMUNICATION INFORMATION:

TELEPHONE: 512-418-3000

TELEFAX: 512-474-7577

INFORMATION FOR SEQ ID NO: 30:

SEQUENCE CHARACTERISTICS:

LENGTH: 21 amino acids

TYPE: amino acid

STRANDEDNESS:

TOPOLOGY: linear

US-09-010-317-30

Query Match 100.0%; Score 57; DB 4; Length 21;

Best Local Similarity 100.0%; Pred. No. 0.00086;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FCGHNSVDPE 10

Db 6 FCGHNSVDPE 15

RESULT 13

US-09-010-317-31

; Sequence 31, Application US/09010317
; Patent No. 6685943

GENERAL INFORMATION:

APPLICANT: Hook, Magnus

APPLICANT: Patti, Joseph M.

APPLICANT: House-Pompeo, Karen L.

APPLICANT: Speziale, Pietro

APPLICANT: Joh, Danny

APPLICANT: McGavin, Martin J.

TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS

TITLE OF INVENTION: AND METHODS OF USE

NUMBER OF SEQUENCES: 105

CORRESPONDENCE ADDRESS:

ADDRESSEE: Arnold, White & Durkee

STREET: P.O. Box 4433

CITY: Houston

STATE: TX

COUNTRY: USA

ZIP: 77210-4433

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/010,317

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 60/036,139

FILING DATE: 21-JAN-1997

ATTORNEY/AGENT INFORMATION:

NAME: Hibler, David W.

REGISTRATION NUMBER: 41,071

REFERENCE/DOCKET NUMBER: TANK:189

TELECOMMUNICATION INFORMATION:

TELEPHONE: 512-418-3000

TELEFAX: 512-474-7577

INFORMATION FOR SEQ ID NO: 31:

SEQUENCE CHARACTERISTICS:

LENGTH: 21 amino acids

TYPE: amino acid

STRANDEDNESS:

TOPOLOGY: linear

US-09-010-317-31

Query Match 100.0%; Score 57; DB 4; Length 21;

Best Local Similarity 100.0%; Pred. No. 0.00086;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FCGHNSVDPE 10

Db 6 FCGHNSVDPE 15

RESULT 14

US-09-010-317-32

; Sequence 32, Application US/09010317
; Patent No. 6685943

GENERAL INFORMATION:

APPLICANT: Hook, Magnus

APPLICANT: Patti, Joseph M.

APPLICANT: House-Pompeo, Karen L.

APPLICANT: Speziale, Pietro

APPLICANT: Joh, Danny

APPLICANT: McGavin, Martin J.

TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS

TITLE OF INVENTION: AND METHODS OF USE

NUMBER OF SEQUENCES: 105

CORRESPONDENCE ADDRESS:

ADDRESSEE: Arnold, White & Durkee

STREET: P.O. Box 4433

CITY: Houston

STATE: TX

COUNTRY: USA

ZIP: 77210-4433

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/010,317

FILING DATE:

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; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/036,139
; FILING DATE: 21-JAN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Hibler, David W.
; REGISTRATION NUMBER: 41,071
; REFERENCE/DOCKET NUMBER: TAMK:189
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 512-418-3000
; TELEFAX: 512-474-7577
; INFORMATION FOR SEQ ID NO: 32:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
;
US-09-010-317-32

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Query Match      100.0%; Score 57; DB 4; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.00086;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      1 FGGHNSVDPE 10
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Db      6 FGGHNSVDPE 15

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RESULT 15
US-09-010-317-33
; Sequence 33, Application US/09010317
; Patent No. 6685943
; GENERAL INFORMATION:
; APPLICANT: Hook, Magnus
; APPLICANT: Patti, Joseph M.
; APPLICANT: House-Pompeo, Karen L.
; APPLICANT: Speziale, Pietro
; APPLICANT: Joh, Danny
; APPLICANT: McGavin, Martin J.
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
; TITLE OF INVENTION: AND METHODS OF USE
; NUMBER OF SEQUENCES: 105
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: TX
; COUNTRY: USA
; ZIP: 77210-4433
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/010,317
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/036,139
; FILING DATE: 21-JAN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Hibler, David W.
; REGISTRATION NUMBER: 41,071
; REFERENCE/DOCKET NUMBER: TAMK:189
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 512-418-3000
; TELEFAX: 512-474-7577
; INFORMATION FOR SEQ ID NO: 33:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21 amino acids
; TYPE: amino acid
; STRANDEDNESS:
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; TOPOLOGY: linear
;
US-09-010-317-33
Query Match      100.0%; Score 57; DB 4; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.00086;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      1 FGGHNSVDPE 10
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Db      6 FGGHNSVDPE 15

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Job time : 17.2989 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 22, 2005, 12:39:57 ; Search time 56.1494 Seconds
(without alignments)
74.354 Million cell updates/sec

Title: US-10-731-238-98

Perfect score: 57
Sequence: 1 FCGHNSVDPE 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1862951 seqs, 417491010 residues

Total number of hits satisfying chosen parameters: 1862951

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

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2:	/cgnt2_6/prodata/2/pubppa/PCT_NEW_PUB.pep.*
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19:	/cgnt2_6/prodata/2/pubppa/US11_PUBCOMB.pep.*
20:	/cgnt2_6/prodata/2/pubppa/US11_NEW_PUB.pep.*
21:	/cgnt2_6/prodata/2/pubppa/US60_NEW_PUB.pep.*
22:	/cgnt2_6/prodata/2/pubppa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	57	100.0	10	US-10-731-238-98	Sequence 98, Appl
2	57	100.0	14	US-10-731-238-61	Sequence 61, Appl
3	57	100.0	21	US-10-731-238-9	Sequence 9, Appl
4	57	100.0	21	US-10-731-238-14	Sequence 14, Appl
5	57	100.0	21	US-10-731-238-15	Sequence 15, Appl
6	57	100.0	21	US-10-731-238-16	Sequence 16, Appl
7	57	100.0	21	US-10-731-238-17	Sequence 17, Appl
8	57	100.0	21	US-10-731-238-18	Sequence 18, Appl
9	57	100.0	21	US-10-731-238-28	Sequence 28, Appl
10	57	100.0	21	US-10-731-238-29	Sequence 29, Appl
11	57	100.0	21	US-10-731-238-30	Sequence 30, Appl

12	57	100.0	21	US-10-731-238-31	Sequence 31, Appl
13	57	100.0	21	US-10-731-238-32	Sequence 32, Appl
14	57	100.0	21	US-10-731-238-33	Sequence 33, Appl
15	57	100.0	37	US-11-066-697-1134	Sequence 1134, Ap
16	57	100.0	139	US-09-813-820-8	Sequence 8, Appl
17	57	100.0	38	US-08-901-062-1	Sequence 1, Appl
18	57	100.0	559	US-08-781-986A-5251	Sequence 5251, Ap
19	57	100.0	559	US-10-329-624-5251	Sequence 5251, Ap
20	57	100.0	940	US-10-470-048B-424	Sequence 424, Ap
21	57	100.0	948	US-10-470-048B-69	Sequence 69, Appl
22	57	100.0	961	US-10-282-122A-43778	Sequence 43778, A
23	57	100.0	978	US-09-815-242-5456	Sequence 5456, Ap
24	57	100.0	1001	US-09-815-242-12686	Sequence 12686, A
25	57	100.0	1018	US-09-815-242-5797	Sequence 5797, Ap
26	57	100.0	1018	US-09-815-242-12838	Sequence 12838, A
27	57	100.0	1018	US-10-470-048B-68	Sequence 68, Appl
28	57	100.0	1027	US-08-781-986A-5254	Sequence 5254, Ap
29	57	100.0	1027	US-10-329-624-5254	Sequence 5254, Ap
30	57	100.0	1038	US-10-282-122A-43827	Sequence 43827, A
31	52	91.2	21	US-10-731-238-23	Sequence 23, Appl
32	52	91.2	21	US-10-731-238-27	Sequence 27, Appl
33	51	89.5	21	US-10-731-238-19	Sequence 19, Appl
34	51	89.5	21	US-10-731-238-24	Sequence 24, Appl
35	50	87.7	21	US-10-731-238-25	Sequence 25, Appl
36	49	86.0	21	US-10-731-238-10	Sequence 10, Appl
37	49	86.0	21	US-10-731-238-20	Sequence 20, Appl
38	49	86.0	21	US-10-731-238-22	Sequence 22, Appl
39	49	86.0	22	US-10-731-238-13	Sequence 13, Appl
40	47	82.5	21	US-10-731-238-21	Sequence 21, Appl
41	47	82.5	21	US-10-731-238-26	Sequence 26, Appl
42	46	80.7	10	US-10-731-238-97	Sequence 97, Appl
43	45	78.9	10	US-10-731-238-99	Sequence 99, Appl
44	41	71.9	21	US-10-731-238-34	Sequence 34, Appl
45	40	70.2	15	US-10-425-114-57258	Sequence 57258, A

ALIGNMENTS

RESULT 1
US-10-731-238-98
; Sequence 98, Application US/10731238
; Publication No. US20050123552A1
; GENERAL INFORMATION:
; APPLICANT: Hook, Magnus
; House-Pompeo, Karen L.
; Speziale, Pietro
; John, Danny
; Mcgavin, Martin J.
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
; AND METHODS OF USE
; NUMBER OF SEQUENCES: 105
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: TX
; COUNTRY: USA
; ZIP: 77210-4433
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/731.238
; FILING DATE: 10-Dec-2003
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/010.317
; FILING DATE: 21-Jan-1998
; APPLICATION NUMBER: US 60/036.139

```
/
/ FILING DATE: 21-JAN-1997
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Hibler, David W.
/ REGISTRATION NUMBER: 41,071
/ REFERENCE/DOCKET NUMBER: TAMK:189
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 512-418-3000
/ TELEFAX: 512-474-7577
/ INFORMATION FOR SEQ ID NO: 98:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 10 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: <Unknown>
/ TOPOLOGY: linear
/
/ SEQUENCE DESCRIPTION: SEQ ID NO: 98:
US-10-731-238-98

Query Match      100.0%; Score 57; DB 18; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0016;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 FGHNSVDPE 10
Db      1 FGHNSVDPE 10

RESULT 2
US-10-731-238-61
/ Sequence 61, Application US/10731238
/ Publication No. US20050123552A1
/ GENERAL INFORMATION:
/ APPLICANT: Hook, Magnus
/          Patti, Joseph M.
/          House-Pompeo, Karen L.
/          Speziale, Pietro
/          John, Danny
/          McGavin, Martin J.
/ TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
/ AND METHODS OF USE
/ NUMBER OF SEQUENCES: 105
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Arnold, White & Durkee
/ STREET: P.O. Box 4433
/ CITY: Houston
/ STATE: TX
/ COUNTRY: USA
/ ZIP: 77210-4433
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patentin Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/10/731,238
/ FILING DATE: 10-Dec-2003
/ CLASSIFICATION: <Unknown>
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US/09/010,317
/ FILING DATE: 21-Jan-1998
/ APPLICATION NUMBER: US 60/036,139
/ FILING DATE: 21-JAN-1997
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Hibler, David W.
/ REGISTRATION NUMBER: 41,071
/ REFERENCE/DOCKET NUMBER: TAMK:189
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 512-418-3000
/ TELEFAX: 512-474-7577
/ INFORMATION FOR SEQ ID NO: 61:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 14 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: <Unknown>
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/ TOPOLOGY: linear
/ SEQUENCE DESCRIPTION: SEQ ID NO: 61:
US-10-731-238-61

Query Match      100.0%; Score 57; DB 18; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.0022;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 FGHNSVDPE 10
Db      2 FGHNSVDPE 11

RESULT 3
US-10-731-238-9
/ Sequence 9, Application US/10731238
/ Publication No. US20050123552A1
/ GENERAL INFORMATION:
/ APPLICANT: Hook, Magnus
/          Patti, Joseph M.
/          House-Pompeo, Karen L.
/          Speziale, Pietro
/          John, Danny
/          McGavin, Martin J.
/ TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
/ AND METHODS OF USE
/ NUMBER OF SEQUENCES: 105
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Arnold, White & Durkee
/ STREET: P.O. Box 4433
/ CITY: Houston
/ STATE: TX
/ COUNTRY: USA
/ ZIP: 77210-4433
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patentin Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/10/731,238
/ FILING DATE: 10-Dec-2003
/ CLASSIFICATION: <Unknown>
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US/09/010,317
/ FILING DATE: 21-Jan-1998
/ APPLICATION NUMBER: US 60/036,139
/ FILING DATE: 21-JAN-1997
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Hibler, David W.
/ REGISTRATION NUMBER: 41,071
/ REFERENCE/DOCKET NUMBER: TAMK:189
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 512-418-3000
/ TELEFAX: 512-474-7577
/ INFORMATION FOR SEQ ID NO: 9:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 21 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: <Unknown>
/ TOPOLOGY: linear
/
/ SEQUENCE DESCRIPTION: SEQ ID NO: 9:
US-10-731-238-9

Query Match      100.0%; Score 57; DB 18; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.0034;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 FGHNSVDPE 10
Db      6 FGHNSVDPE 15
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RESULT 4
US-10-731-238-14
; Sequence 14, Application US/10731238
; Publication No. US20050123552A1
; GENERAL INFORMATION:
; APPLICANT: Hook, Magnus
; Patti, Joseph M.
; House-Pompeo, Karen L.
; Speziale, Pietro
; Joh, Danny
; McGavin, Martin J.
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
; AND METHODS OF USE
; NUMBER OF SEQUENCES: 105
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: TX
; COUNTRY: USA
; ZIP: 77210-4433
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/731,238
; FILING DATE: 10-Dec-2003
; CLASSIFICATION: <Unknown>
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: US/09/010,317
; FILING DATE: 21-Jan-1998
; APPLICATION NUMBER: US 60/036,139
; FILING DATE: 21-Jan-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Hibler, David W.
; REGISTRATION NUMBER: 41,071
; REFERENCE/DOCKET NUMBER: TWMK:189
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 512-418-3000
; TELEFAX: 512-474-7577
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 14:
US-10-731-238-14
Query Match 100.0%; Score 57; DB 18; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.0034;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 FGGHNSVDPE 10
Db 6 FGGHNSVDPE 15
RESULT 5
US-10-731-238-15
; Sequence 15, Application US/10731238
; Publication No. US20050123552A1
; GENERAL INFORMATION:
; APPLICANT: Hook, Magnus
; Patti, Joseph M.
; House-Pompeo, Karen L.
; Speziale, Pietro
; Joh, Danny
; McGavin, Martin J.
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
; AND METHODS OF USE

NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/731,238
FILING DATE: 10-Dec-2003
CLASSIFICATION: <Unknown>
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE: 21-Jan-1998
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-Jan-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TWMK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 15:
US-10-731-238-15
Query Match 100.0%; Score 57; DB 18; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.0034;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 FGGHNSVDPE 10
Db 6 FGGHNSVDPE 15
RESULT 6
US-10-731-238-16
; Sequence 16, Application US/10731238
; Publication No. US20050123552A1
; GENERAL INFORMATION:
; APPLICANT: Hook, Magnus
; Patti, Joseph M.
; House-Pompeo, Karen L.
; Speziale, Pietro
; Joh, Danny
; McGavin, Martin J.
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
; AND METHODS OF USE
; NUMBER OF SEQUENCES: 105
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: TX
; COUNTRY: USA
; ZIP: 77210-4433
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30

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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/731,238
FILING DATE: 10-Dec-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE: 21-Jan-1998
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAMK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 16:
US-10-731-238-16
Query Match 100.0%; Score 57; DB 18; Length 21;
Best Local Similarity 100.0%; Pred.No. 0.0034;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0
Ct 1 FGHNSTDPE 10
Db 6 FGHNSTDPE 15
RESULT 7
US-10-731-238-17
Sequence 17, Application US/10731238
Publication No. US20050123552A1
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
Pattl, Joseph M.
House-Pompeo, Karen L.
Speziale, Pietro
Job, Danny
McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/731,238
FILING DATE: 10-Dec-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE: 21-Jan-1998
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAMK:189

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TELKOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
US-10-731-238-17
SEQUENCE DESCRIPTION: SEQ ID NO: 17:
Query Match      100.0%; Score 57; DB 18; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.0034;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 FGGHNSVDFF 10
Db       6 FGGHNSVDFF 15

RESULT 8
US-10-731-238-18
Sequence 18, Application US/10731.238
Publication No. US20050123552n1
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
Patl, Joseph M.
House-Pompeo, Karen L.
Speziale, Pietro
Joh, Danny
McGavin, Martin J.
TITLE OF INVENTION: FIBROBLAST BINDING PROTEIN COMPOSITIONS
AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESSES:
ADDRESS: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/731.238
FILING DATE: 10-Dec-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/010.317
FILING DATE: 21-Jan-1998
APPLICATION NUMBER: US 60/036.139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TMWK.189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-474-7577
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 18:
US-10-731-238-18
Query Match      100.0%; Score 57; DB 18; Length 21;

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Best Local Similarity 100.0%; Pred. No. 0.0034;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 FGGHNSVDFE 10
100.0%
Db 6 FGGHNSVDFE 15

RESULT 9

US-10-731-238-28
Sequence 28, Application US/10731238
Publication No. US20050123552A1
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
Patti, Joseph M.
House-Pompeo, Karen L.
Speziale, Pietro
John, Danny
McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/731,238
FILING DATE: 10-Dec-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE: 21-Jan-1998
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TWMK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 28:
US-10-731-238-28
Query Match 100.0%; Score 57; DB 18; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.0034;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 FGGHNSVDFE 10
100.0%
Db 6 FGGHNSVDFE 15

RESULT 10

US-10-731-238-29
Sequence 29, Application US/10731238
Publication No. US20050123552A1
GENERAL INFORMATION:

APPLICANT: Hook, Magnus

Patti, Joseph M.
House-Pompeo, Karen L.
Speziale, Pietro
John, Danny
McGavin, Martin J.

TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
AND METHODS OF USE
NUMBER OF SEQUENCES: 105

CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/731,238
FILING DATE: 10-Dec-2003
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE: 21-Jan-1998

APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997

ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.

REGISTRATION NUMBER: 41,071

REFERENCE/DOCKET NUMBER: TWMK:189

TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577

INFORMATION FOR SEQ ID NO: 29:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear

SEQUENCE DESCRIPTION: SEQ ID NO: 29:
US-10-731-238-29

Query Match 100.0%; Score 57; DB 18; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.0034;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 FGGHNSVDFE 10
100.0%
Db 6 FGGHNSVDFE 15

RESULT 11

US-10-731-238-30
Sequence 30, Application US/10731238
Publication No. US20050123552A1
GENERAL INFORMATION:

APPLICANT: Hook, Magnus

Patti, Joseph M.
House-Pompeo, Karen L.
Speziale, Pietro
John, Danny
McGavin, Martin J.

TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
AND METHODS OF USE
NUMBER OF SEQUENCES: 105

CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston

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/ STATE: TX
/ COUNTRY: USA
/ ZIP: 77210-4433
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patentin Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/10/731,238
/ FILING DATE: 10-Dec-2003
/ CLASSIFICATION: <Unknown>
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US/09/010,317
/ FILING DATE: 21-Jan-1998
/ APPLICATION NUMBER: US 60/036,139
/ FILING DATE: 21-JAN-1997
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Hibler, David W.
/ REGISTRATION NUMBER: 41,071
/ REFERENCE/DOCKET NUMBER: TAMK:189
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 512-418-3000
/ TELEFAX: 512-474-7577
/ INFORMATION FOR SEQ ID NO: 30:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 21 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: <Unknown>
/ TOPOLOGY: linear
/ SEQUENCE DESCRIPTION: SEQ ID NO: 30:
/
/ US-10-731-238-30
/
Query Match          100.0%; Score 57; DB 18; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.0034;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 FCGHNSVDPE 10
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        6 FCGHNSVDPE 15

RESULT 12
US-10-731-238-31
/ Sequence 31, Application US/10731238
/ Publication No. US20050123552A1
/ GENERAL INFORMATION:
/ APPLICANT: Hook, Magnus
/      Patti, Joseph M.
/      House-Pompeo, Karen L.
/      Speziale, Pietro
/      Joh, Danny
/      McGavin, Martin J.
/ TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
/ NUMBER OF SEQUENCES: 105
/ CORRESPONDENCE ADDRESSES:
/ ADDRESSER: Arnold, White & Durkee
/ STREET: P.O. Box 4433
/ CITY: Houston
/ STATE: TX
/ COUNTRY: USA
/ ZIP: 77210-4433
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patentin Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/10/731,238
/ FILING DATE: 10-Dec-2003
/ CLASSIFICATION: <Unknown>
/ PRIOR APPLICATION DATA:
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/ APPLICATION NUMBER: US/09/010,317
/ FILING DATE: 21-Jan-1998
/ APPLICATION NUMBER: US 60/036,139
/ FILING DATE: 21-JAN-1997
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Hibler, David W.
/ REGISTRATION NUMBER: 41,071
/ REFERENCE/DOCKET NUMBER: TAMK:189
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 512-418-3000
/ TELEFAX: 512-474-7577
/ INFORMATION FOR SEQ ID NO: 31:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 21 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: <Unknown>
/ TOPOLOGY: linear
/ SEQUENCE DESCRIPTION: SEQ ID NO: 31:
/
/ US-10-731-238-31
/
Query Match          100.0%; Score 57; DB 18; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.0034;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 FCGHNSVDPE 10
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        6 FCGHNSVDPE 15

RESULT 13
US-10-731-238-32
/ Sequence 32, Application US/10731238
/ Publication No. US20050123552A1
/ GENERAL INFORMATION:
/ APPLICANT: Hook, Magnus
/      Patti, Joseph M.
/      House-Pompeo, Karen L.
/      Speziale, Pietro
/      Joh, Danny
/      McGavin, Martin J.
/ TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
/ NUMBER OF SEQUENCES: 105
/ CORRESPONDENCE ADDRESSES:
/ ADDRESSER: Arnold, White & Durkee
/ STREET: P.O. Box 4433
/ CITY: Houston
/ STATE: TX
/ COUNTRY: USA
/ ZIP: 77210-4433
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patentin Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/10/731,238
/ FILING DATE: 10-Dec-2003
/ CLASSIFICATION: <Unknown>
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US/09/010,317
/ FILING DATE: 21-Jan-1998
/ APPLICATION NUMBER: US 60/036,139
/ FILING DATE: 21-JAN-1997
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Hibler, David W.
/ REGISTRATION NUMBER: 41,071
/ REFERENCE/DOCKET NUMBER: TAMK:189
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 512-418-3000
/ TELEFAX: 512-474-7577
/ INFORMATION FOR SEQ ID NO: 32:
/ SEQUENCE CHARACTERISTICS:
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LENGTH: 21 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 32:
US-10-731-238-32

Query Match 100.0%; Score 57; DB 18; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.0034;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FGCHNSVDPE 10
| | | | | | | | | |
Db 6 FGCHNSVDPE 15

RESULT 14
US-10-731-238-33
Sequence 33, Application US/107311238
Publication No. US20050123552A1
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
Pactl, Joseph M.
House-Pompeo, Karen L.
Speziale, Pietro
John, Danny
McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/731,238
FILING DATE: 10-Dec-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE: 21-Jan-1998
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-Jan-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAMK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 33:
US-10-731-238-33

Query Match 100.0%; Score 57; DB 18; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.0034;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 FGCHNSVDPE 10
| | | | | | | | | |

Db 6 FGCHNSVDPE 15

RESULT 15
US-11-066-697-1134
Sequence 1134, Application US/11066697
Publication No. US20050187159A1
GENERAL INFORMATION:
APPLICANT: Bridon, Dominique P.
APPLICANT: Ezrin, Alan M.
APPLICANT: Milner, Peter G.
APPLICANT: Holmes, Darren L.
APPLICANT: Thibaudau, Karen
TITLE OF INVENTION: PROTECTION OF ENDOGENOUS THERAPEUTIC PEPTIDES FROM
PEPTIDASE ACTIVITY THROUGH CONJUGATION TO BLOOD
COMPONENTS
FILE REFERENCE: 500862002301
CURRENT APPLICATION NUMBER: US/11/066,697
CURRENT FILING DATE: 2005-02-25
PRIOR APPLICATION NUMBER: 09/657,276
PRIOR FILING DATE: 2000-09-07
PRIOR APPLICATION NUMBER: 60/153,406
PRIOR FILING DATE: 1999-09-10
PRIOR APPLICATION NUMBER: 60/159,783
PRIOR FILING DATE: 1999-10-15
NUMBER OF SEQ ID NOS: 1617
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 1134
LENGTH: 37
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-11-066-697-1134

Query Match 100.0%; Score 57; DB 20; Length 37;
Best Local Similarity 100.0%; Pred. No. 0.0061;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FGCHNSVDPE 10
| | | | | | | | | |
Db 21 FGCHNSVDPE 30

Search completed: October 22, 2005, 12:56:29
Job time : 56.1494 secs

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OM protein - protein search, using sw model

Run on: October 22, 2005, 08:04:46 ; Search time 11.6092 Seconds
(without alignments)
82.880 Million cell updates/sec

Title: US-10-731-238-98
Perfect score: 57
Sequence: 1 FCGHNSVDPE 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	57	100.0	940	2 S19702	fibronectin-binding
2	57	100.0	961	2 G90053	hypothetical prote
3	57	100.0	1018	2 A32192	fibronectin-binding
4	57	100.0	1038	2 H90053	hypothetical prote
5	41	71.9	429	2 D8414	ribonuclease II fa
6	40	70.2	356	2 T51480	hypothetical prote
7	40	70.2	462	1 A39356	3-oxoacyl-[acyl]-ca
8	40	70.2	469	2 T10061	3-oxoacyl-[acyl]-ca
9	40	70.2	681	2 T24426	hypothetical prote
10	39	68.4	443	1 QOBYPT	hypothetical prote
11	38	66.7	417	2 T34930	probable secreted
12	37	64.9	409	2 G86721	hypothetical prote
13	37	64.9	411	2 H95048	3-oxoacyl-[acyl]-ca
14	37	64.9	414	2 A89866	3-oxoacyl-[acyl]-ca
15	37	64.9	414	2 F97919	3-phosphoshikimate
16	37	64.9	427	2 D95159	3-oxoacyl-[acyl]-ca
17	37	64.9	431	2 D98025	3-phosphoshikimate
18	37	64.9	431	2 D95912	probable membrane
19	37	64.9	449	2 B81963	Iga-specific serin
20	37	64.9	1457	2 D81019	adhesion and penet
21	36	63.2	291	2 A82000	hypothetical prote
22	36	63.2	341	2 A64383	hypothetical prote
23	36	63.2	364	2 AE1591	B. subtilis PBSX p
24	36	63.2	416	2 C72020	3-oxoacyl-[acyl]-ca
25	36	63.2	416	2 B86605	acyl carrier prote
26	36	63.2	418	2 G81735	3-oxoacyl-[acyl]-ca
27	36	63.2	426	2 E71473	probable acyl car
28	36	63.2	426	2 C96804	hypothetical prote
29	36	63.2	489	1 S47076	3-oxoacyl-[acyl]-ca

30	36	63.2	495	1 S47074	3-oxoacyl-[acyl]-ca
31	36	63.2	535	2 T10055	probable 3-oxoacyl
32	36	63.2	541	2 D96779	probable 3-ketocacyl
33	36	63.2	645	2 F70825	probable PPE prote
34	36	63.2	709	2 C64057	Iga-specific metal
35	36	63.2	747	2 D75436	ATP-dependent Clp
36	36	63.2	764	2 H83879	3-oxoacyl-[acyl]-ca
37	35	61.4	193	2 A85658	robable tellurium
38	35	61.4	193	2 G90797	probable tellurium
39	35	61.4	287	2 S57770	xyloglucan endo-1,
40	35	61.4	289	2 S49812	xyloglucan endo-1,
41	35	61.4	360	2 S06287	fragmin - slime mo
42	35	61.4	391	2 D69462	pyruvate synthase
43	35	61.4	427	1 ZFBP64	gene F protein - p
44	35	61.4	453	2 H70333	conserved hypochet
45	35	61.4	471	2 F64213	hypothetical prote

ALIGNMENTS

RESULT 1
S19702
fibronectin-binding protein B - Staphylococcus aureus
C:Species: Staphylococcus aureus
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
R:Accession: S19702
R:Jensen, K.; Signaes, C.; Mueller, H.P.; Lindberg, M.
Eur. J. Biochem. 202, 1041-1048, 1991
A:Title: Two different genes encode fibronectin binding proteins in Staphylococcus aureus
A:Reference number: S19702; MUID:92111475; PMID:1837266
A:Accession: S19702
A:Status: Preliminary
A:Molecule type: DNA
A:Residues: 1-940 <JOB>
A:Cross-references: UNIPROT:Q53682; EMBL:X62992; NID:G49040; PIDN:CAA44726.1; PID:G58156;
C:Keywords: fibronectin binding

Query Match
Best Local Similarity 100.0%; Score 57; DB 2; Length 940;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FCGHNSVDPE 10
Db 778 FCGHNSVDPE 787

RESULT 2

G90053
hypothetical protein fnbB [imported] - Staphylococcus aureus (strain N315)
C:Species: Staphylococcus aureus
C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
R:Kuroda, M.; Ohts, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Og
ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.
C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
A:Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.
A:Reference number: A89758; MUID:21311952; PMID:11418146
A:Accession: G90053
A:Status: Preliminary
A:Molecule type: DNA
A:Residues: 1-961 <KUR>
A:Cross-references: UNIPROT:Q99RD3; GB:BA000018; PID:G13702452; PIDN:BA843593.1; GS
A:Experimental source: strain N315
C:Genetics:
A:Gene: fnbB

Query Match
Best Local Similarity 100.0%; Score 57; DB 2; Length 961;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FCGHNSVDPE 10

Db 789 FCGHNSVDPE 798
|||||

RESULT 3

A32192

A:Species: Staphylococcus aureus

C/Date: 31-Jul-1989 #sequence_revision 31-Jul-1989 #text_change 16-Feb-1997

C/Species: Staphylococcus aureus

C/Date: 31-Jul-1989 #sequence_revision 31-Jul-1989 #text_change 16-Feb-1997

R/Signer: C. Raucet, G. Joensen, K. Lindgren, P.E. Anantharamiah, G.M. Hoeck, M.

Proc. Natl. Acad. Sci. U.S.A. 86, 699-703, 1989

A/Title: Nucleotide sequence of the gene for a fibronectin-binding protein from Staphylo-

A/Reference number: A32192; MUID:89098998; PMID:2521391

A/Accession: A32192

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-1018 <SIG>

A/Cross-references: GB:J04151

C/Keywords: fibronectin binding

Query Match 100.0%; Score 57; DB 2; Length 1018;

Best Local Similarity 100.0%; Pred. No. 0.017;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FCGHNSVDPE 10
|||||

Db 842 FCGHNSVDPE 851

RESULT 4

H90053

A:Species: Staphylococcus aureus

C/Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004

C/Accession: H90053

R/Kuroda, M.; Ohca, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguc

ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kato, C.; Sekimizu, K.;

C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.

Lancet 357, 1225-1240, 2001

A/Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.

A/Reference number: A89758; MUID:21311952; PMID:11418146

A/Accession: H90053

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-1038 <NR>

A/Cross-references: UNIPROT:Q99RD2; GB:BA000018; PID:g13702453; PIDN:BA843594.1; GSPDB:C

A/Experimental source: strain N315

C/Genetics:

A/Gene: fnb

Query Match 100.0%; Score 57; DB 2; Length 1038;

Best Local Similarity 100.0%; Pred. No. 0.018;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FCGHNSVDPE 10
|||||

Db 838 FCGHNSVDPE 847

RESULT 5

D84414

A:Species: Halobacterium sp. NRC-1

C/Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004

C/Accession: D84414

R/M, W.V.; Kennedy, S.P.; Maharis, G.G.; Bergstedt, B.; Pan, M.; Shukla, H.D.; Lasfy, S.

Leitauer, B.; Keller, K.; Cruz, R.; Danon, M.J.; Hough, D.W.; Maddocks, D.G.; Jabb

Jung, K.H.; Alam, M.; Freitas, T.

Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000

A/Authors: Hou, S.; Danels, C.J.; Dennis, P.P.; Omer, A.D.; Ebhardt, H.; Lowe, T.M.; Li

A/Title: Genome sequence of Halobacterium species NRC-1.

A/Reference number: A84160; MUID:20504483; PMID:11016950

A/Accession: D84414
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-429 <STO>
A/Cross-references: UNIPROT:Q9HM91; GB:AE004437; NID:g10582029; PIDN:AA320680.1; GSP
A/Genetics:
A/Gene: vacB

Query Match 71.9%; Score 41; DB 2; Length 429;

Best Local Similarity 60.0%; Pred. No. 7;

Matches 6; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 FCGHNSVDPE 10
|||||

Db 340 FCGHNSVDPE 349

RESULT 6

T51480

A:Species: Arabidopsis thaliana

C/Date: 18-Aug-2000 #sequence_revision 18-Aug-2000 #text_change 09-Jul-2004

C/Accession: T51480

R/Sato, S.; Nakamura, Y.; Kaneko, T.; Kato, T.; Asamizu, E.; Kotani, H.; Tabata, S.; Mew

submitted to the Protein Sequence Database, August 2000

A/Reference number: Z25394

A/Accession: T51480

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-356 <SAT>

A/Cross-references: UNIPROT:Q9LF18; EMBL:AL391148

A/Experimental source: cultivar Columbia; BAC clone T21H9

A/Map position: 5

A/Intons: 191/1

A/Note: T21H9_20

Query Match 70.2%; Score 40; DB 2; Length 356;

Best Local Similarity 70.0%; Pred. No. 8.9;

Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 FCGHNSVDPE 10
|||||

Db 146 FCGHNSVDPE 155

RESULT 7

A39356

A:Species: Hordeum vulgare (barley)

C/Date: 06-Mar-1992 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004

C/Accession: A39356; A45129

R/Sigvard-Andersen, M.; Kauppinen, S.; von Wettstein-Knowles, P.

Proc. Natl. Acad. Sci. U.S.A. 88, 4114-4118, 1991

A/Title: Primary structure of a cerulenin-binding beta-ketoacyl-[acyl carrier protein] b

A/Reference number: A39356; MUID:9129517; PMID:2034657

A/Accession: A39356

A/Molecule type: mRNA

A/Residues: 1-462 <SIG>

A/Cross-references: UNIPROT:P23902; GB:M60410; NID:g167064; PIDN:AAA32968.1; PID:g167065

A/Experimental source: cv. Bonus, leaf

A/Note: parts of this sequence, including the amino end of the mature protein, were confi

R/Kauppinen, S.

J. Biol. Chem. 267, 23999-24006, 1992

A/Title: Structure and expression of the Kas12 gene encoding a beta-ketoacyl-acyl carrier

A/Reference number: A45129; MUID:93054767; PMID:1429736

A/Accession: A45129

A/Molecule type: DNA

A/Residues: 1-395, 397-414, 'T', 415-462 <KAU>

A/Experimental source: cv. Bonus

A/Note: sequence inconsistent with the nucleotide translation; translation agrees with s

```

C:Genetics:
A:Gene: Kas12
A:Map position: 2
A:Introns: 144/3; 288/3; 346/3; 384/3; 418/3; 441/1
C:Complex: homodimer or heterodimer with alpha chain
C:Superfamily: 3-oxoacyl-[acyl-carrier-protein] synthase I; 3-oxoacyl-[acyl-carrier-pro]
C:Keywords: acyltransferase; chloroplast; fatty acid biosynthesis; heterodimer; homodime
F:1-36/Domain: transit peptide (chloroplast) #status predicted <TMP>
F:36-46/Domain: transit peptide (chloroplast) #status predicted <TMP>
F:46-45/Domain: 3-oxoacyl-[acyl-carrier-protein] synthase I beta chain #status experit
F:213/Active site: Cys #status experimental

Query Match      70.2%; Score 40; DB 1; Length 462;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 FCGHNSV 7
    |||||
    |||||
Db 448 FCGHNSV 454

RESULT 8
T10061
3-oxoacyl-[acyl-carrier-protein] synthase (EC 2.3.1.41) precursor, chloroplast - castor
N:Alternate names: beta-ketoacyl-[acyl carrier protein] synthase
C:Species: Ricinus communis (castor bean)
C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004
C:Accession: T10061
R:GeneZ, A.L.
submitted to the EMBL Data Library, April 1993
A:Description: Cloning and molecular characterisation of B-ketoacyl-ACP synthases from er
A:Reference number: Z16924
A:Accession: T10061
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-469 <GEN>
A:Cross-references: UNIPROT:Q41135; EMBL:L13242; NID:G294667; PID:G294668
C:Genetics:
A:Genome: nuclear
C:Function:
A:Pathway: fatty acid biosynthesis
C:Superfamily: 3-oxoacyl-[acyl-carrier-protein] synthase I; 3-oxoacyl-[acyl-carrier-pro]
C:Keywords: acyltransferase; chloroplast; fatty acid biosynthesis
F:1-42/Domain: transit peptide (chloroplast) #status predicted <TMP>
F:43-46/Domain: 3-oxoacyl-[acyl-carrier-protein] synthase I beta chain #status predicted <MAT>
F:77-464/Domain: 3-oxoacyl-[acyl-carrier-protein] synthase I homology <ONS>

Query Match      70.2%; Score 40; DB 2; Length 469;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 FCGHNSV 7
    |||||
    |||||
Db 455 FCGHNSV 461

RESULT 9
T24426
hypothetical protein T04A8.7 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T24426
R:Palmer, S.
submitted to the EMBL Data Library, August 1994
A:Reference number: Z19889
A:Accession: T24426
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-681 <WIL>
A:Cross-references: UNIPROT:Q22117; EMBL:Z35661; PID:CAA64727.1; GSPDB:GN00021; CESP:T0
C:Genetics:
A:Gene: CESP.T04A8.7

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A:Map position: 3
A:Introns: 85/1; 312/2; 351/1; 512/1; 626/2
C:Superfamily: 1,4-alpha-glucan branching enzyme

Query Match      70.2%; Score 40; DB 2; Length 681;
Best Local Similarity 75.0%; Pred. No. 18;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Oy 1 FCGHNSVD 8
    |||||
    |||||
Db 638 FCGHNSVD 645

RESULT 10
Q08YPT
hypothetical protein YER152c - yeast (Saccharomyces cerevisiae)
C:Species: Saccharomyces cerevisiae
C:Date: 30-Jun-1991 #sequence_revision 12-May-1995 #text_change 09-Jul-2004
C:Accession: S50655; C36328; S05725; S12290
R:Dieckrich, F.S.
submitted to the EMBL Data Library, December 1994
A:Description: The sequence of S. cerevisiae cosmid 8229, 9115, 9132, 9981, and lambda
A:Reference number: S50430
A:Accession: S50655
A:Molecule type: DNA
A:Residues: 1-443 <DIE>
A:Cross-references: UNIPROT:P10356; EMBL:U18917; NID:G603377; PID:AA64679.1; PID:G6033
R:Ohmen, J.D.; Burke, K.A.; McEwen, J.E.
Mol. Cell. Biol. 10, 3027-3035, 1990
A:Title: Divergent overlapping transcripts at the PET122 locus in Saccharomyces cerevisi
A:Reference number: A36328; MUID:90258894; PMID:2160592
A:Accession: C36328
A:Molecule type: DNA
A:Residues: 1-230 <OHM>
A:Cross-references: GB:X07558; NID:G4127; PID:CAA30440.1; PID:G4129
R:Ohmen, J.D.; Kloeckner-Gruissem, B.; McEwen, J.E.
Nucleic Acids Res. 16, 10783-10802, 1988
A:Title: Molecular cloning and nucleotide sequence of the nuclear PET122 gene required f
A:Reference number: S05724; MUID:89083497; PMID:2849752
A:Accession: S05725
A:Molecule type: DNA
A:Residues: 1-56, 'CGA', 60-61, 63-66, 'V', 68-72, 'T', 74-76, 'R', 78-86, 'V', 88-122, 'SDQC', 128-1
A:Cross-references: EMBL:X07558
A>Note: this sequence has been revised in reference A36328
C:Genetics:
A:Gene: MIPS:YER152c
A:Cross-references: SGD:S0000954
A:Map position: 5R
C:Superfamily: yeast hypothetical protein YER152c

Query Match      68.4%; Score 39; DB 1; Length 443;
Best Local Similarity 75.0%; Pred. No. 17;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Oy 3 GHSVDPE 10
    ||:|:|
    ||:|:|
Db 145 GHSVDPE 152

RESULT 11
T34930
probable secreted protein - Streptomyces coelicolor
C:Species: Streptomyces coelicolor
C:Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 09-Jul-2004
C:Accession: T34930
R:Seeger, K.J.; Harris, D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
submitted to the EMBL Data Library, June 1998
A:Reference number: Z21562
A:Accession: T34930
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-417 <SEE>
A:Cross-references: UNIPROT:O69948; EMBL:AL023862; PID:CAA19631.1; GSPDB:GN00070; SCOD

```

A:Experimental source: strain A3 (2)

C:Genetics:

A:Gene: SCOPDB:SC3F9.08
C:Superfamily: myo-inositol-1-phosphate synthase

Query Match

Best Local Similarity 66.7%; Score 38; DB 2; Length 417;

Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 FCGHNSVD 8

Db 66 FCGHDTVD 73

RESULT 12

G86721

hypothetical protein fabp [imported] - Lactococcus lactis subsp. lactis (strain IL1403)

C:Species: Lactococcus lactis subsp. lactis
C:Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 09-Jul-2004

C:Accession: G86721

R:Botolin, A.; Winkler, P.; Manger, S.; Dailion, O.; Malarme, K.; Weissenbach, J.; Ehrlich

Genome Res. 11, 731-753, 2001

A:Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis s

A:Reference number: A86625; MUID:21235186; PMID:11337471

A:Accession: G86721

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-409 <STD>

A:Cross-references: UNIPROT:O9CHF6; GB:AE005176; PID:g12723694; PIDN:AAK04873.1; GSPDB:C

A:Experimental source: strain IL1403

C:Genetics:

A:Gene: fabp
C:Superfamily: 3-oxoacyl-[acyl-carrier-protein] synthase I; 3-oxoacyl-[acyl-carrier-pro

Query Match

Best Local Similarity 64.9%; Score 37; DB 2; Length 409;

Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 FCGHNSV 7

Db 394 FCGHNAV 400

RESULT 13

H93048

3-oxoacyl-[acyl-carrier-protein] synthase II [imported] - Streptococcus pneumoniae (stra

C:Species: Streptococcus pneumoniae

C:Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 09-Jul-2004

C:Accession: H93048

R:Teretlin, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Heid

on, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapfel,

neon, T.; Hickay, E.K.; Holt, I.E.

Science 293, 498-506, 2001

A:Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison,

A:Title: Complete Genome Sequence of a virulent isolate of Streptococcus pneumoniae.

A:Reference number: A95000; MUID:21357209; PMID:11463916

A:Accession: H93048

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-411 <KUR>

A:Cross-references: UNIPROT:O9FPC2; GB:AE005672; PIDN:AAK74585.1; PID:g14971892; GSPDB:C

C:Genetics:

A:Gene: SP0422

C:Superfamily: 3-oxoacyl-[acyl-carrier-protein] synthase I; 3-oxoacyl-[acyl-carrier-pro

Query Match

Best Local Similarity 64.9%; Score 37; DB 2; Length 411;

Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 FCGHNSV 7

Db 396 FCGHNAV 402

RESULT 14

A89866

3-oxoacyl-[acyl-carrier-protein] synthase [imported] - Staphylococcus aureus (strain N31;

C:Species: Staphylococcus aureus

C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004

C:Accession: A89866

R:Kuroda, M.; Onota, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguci

ma, A.; Mizutani-Uji, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.; i

C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.

Lancet 357, 1225-1240, 2001

A:Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.

A:Reference number: A89758; MUID:21311952; PMID:11418146

A:Accession: A89866

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-414 <KUR>

A:Cross-references: UNIPROT:Q99VA6; GB:BA000018; PID:g13700788; PIDN:BA842084.1; GSPDB:C

A:Experimental source: strain N315

C:Genetics:

A:Gene: fab

C:Superfamily: 3-oxoacyl-[acyl-carrier-protein] synthase I; 3-oxoacyl-[acyl-carrier-pro

Query Match

Best Local Similarity 64.9%; Score 37; DB 2; Length 414;

Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 FCGHNSV 7

Db 400 FCGHNAV 406

RESULT 15

F97919

3-oxoacyl-[acyl-carrier-protein] synthase (BC 2.3.1.41) [imported] - Streptococcus pneum

C:Species: Streptococcus pneumoniae

C:Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 09-Jul-2004

C:Accession: F97919

R:Hoskins, J.A.; Alborn Jr., W.; Arnold, J.; Blaszcak, L.; Buxett, S.; Dehoff, B.S.; B

e, R.; LeBlanc, D.J.; Lee, L.N.; Lefkowitz, E.J.; Lu, J.; Matsushima, P.; McAhren, S.; M

Y, P.; Sun, P.M.; Winkler, M.B.

J. Bacteriol. 183, 5709-5717, 2001

A:Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, S.R.;

A:Title: Genome of the Bacterium Streptococcus pneumoniae Strain R6.

A:Reference number: A97872; MUID:21429245; PMID:11544234

A:Accession: F97919

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-414 <KUR>

A:Cross-references: UNIPROT:Q8DR14; GB:AE007317; PIDN:AAK99186.1; PID:g15457943; GSPDB:GI

C:Genetics:

A:Gene: fabp

C:Superfamily: 3-oxoacyl-[acyl-carrier-protein] synthase I; 3-oxoacyl-[acyl-carrier-pro

Query Match

Best Local Similarity 64.9%; Score 37; DB 2; Length 414;

Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 FCGHNSV 7

Db 399 FCGHNAV 405

Search completed: October 22, 2005, 09:55:49

job time : 12.6092 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 22, 2005, 08:01:06 ; Search time 56.2069 Seconds
(without alignments)
91.106 Million cell updates/sec

Title: US-10-731-238-98
Perfect score: 57
Sequence: 1 FGHNSVDPE 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Uniprot_03: *
1: uniprot_sprot: *
2: uniprot_trembl: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	57	100.0	940	2	Q53682 staphylococ
2	57	100.0	943	2	Q8NUH8 staphylococ
3	57	100.0	957	2	Q6G6H4 staphylococ
4	57	100.0	961	2	Q99RD3 staphylococ
5	57	100.0	961	2	Q7A3J8 staphylococ
6	57	100.0	965	2	Q6GDU5 staphylococ
7	57	100.0	1015	2	Q8NUU7 staphylococ
8	57	100.0	1015	2	Q6G6H3 staphylococ
9	57	100.0	1018	1	FNBA STRAU
10	57	100.0	1038	2	Q99RD2 staphylococ
11	57	100.0	1038	2	Q7A3J7 staphylococ
12	47	82.5	152	2	Q9AEP9 staphylococ
13	41	71.9	290	1	XTX3 ARATH
14	41	71.9	290	1	Q9HMS1
15	40	70.2	114	2	Q74CG1
16	40	70.2	131	2	Q7EPT8
17	40	70.2	194	2	Q9S406
18	40	70.2	356	2	Q9LF18
19	40	70.2	366	2	Q6N4J1
20	40	70.2	413	2	Q8RGX4
21	40	70.2	442	2	Q7XUM9
22	40	70.2	456	2	Q94G70
23	40	70.2	462	1	FAB8 HORVU
24	40	70.2	463	2	Q870H4
25	40	70.2	465	2	Q69YA2
26	40	70.2	469	2	Q41135
27	40	70.2	469	2	Q9MS07
28	40	70.2	469	2	Q9MS08
29	40	70.2	473	1	FAB8 ARATH
30	40	70.2	474	2	Q48942
31	40	70.2	488	2	Q82520

32	40	70.2	523	2	Q8KIB7	Q8KIB7 haemophilus
33	40	70.2	523	2	Q8KSC1	Q8KSC1 haemophilus
34	40	70.2	526	2	Q8KSB9	Q8KSB9 haemophilus
35	40	70.2	606	2	Q8G692	Q8G692 caenorhabdi
36	40	70.2	681	2	Q22137	Q22137 caenorhabdi
37	40	70.2	685	2	Q9V6K7	Q9V6K7 drosophila
38	40	70.2	706	2	Q6FJV0	Q6FJV0 candida gla
39	40	70.2	1436	2	Q8G0P3	Q8G0P3 haemophilus
40	39	68.4	443	1	Y5Y2_YEAST	P10356 saccharomyc
41	38	66.7	140	2	Q6NFQ5	Q6NFQ5 corynebacte
42	38	66.7	253	2	Q8D943	Q8D943 vibrio vuln
43	38	66.7	255	2	Q7NMC7	Q7NMC7 gloeobacter
44	38	66.7	271	2	Q7MLC8	Q7MLC8 vibrio vuln
45	38	66.7	275	2	Q7XTB5	Q7XTB5 oryza sativ

ALIGNMENTS

```

RESULT 1
Q53682 ID Q53682 PRELIMINARY; PRT; 940 AA.
AC Q53682;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Fibronectin binding protein B.
GN Name=fnbB;
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxId=1280;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=8325-4;
RX MEDLINE=9211475; PubMed=1837266;
RA Jonson K., Signas C., Muller H.P., Lindberg M.;
RT "Two different genes encode fibronectin binding proteins in
RT Staphylococcus aureus. The complete nucleotide sequence and
RT characterization of the second gene."
RL Eur. J. Biochem. 202:1041-1048 (1991).
CC -! SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC an amide bond (By similarity).
DR EMBL: X62992; CAA44726.1; -.
DR PIR: S19702; S19702.
DR HSSP: Q53653; IN67.
DR GO: GO:0009986; C:cell surface; IEA.
DR GO: GO:0005618; C:cell wall; IEA.
DR GO: GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO: GO:0016020; C:membrane; IEA.
DR GO: GO:007155; P:cell adhesion; IEA.
DR InterPro: IPR008966; Adhes_bact.
DR InterPro: IPR004237; Fn_bind.
DR InterPro: IPR005877; Gpos_YsIRK.
DR InterPro: IPR001899; Gram_pos_anchor.
DR Pfam: PF02986; Fn_bind; 2.
DR Pfam: PF00746; Gram_pos_anchor; 1.
DR Pfam: PF04650; YsIRK_signal; 1.
DR TIGRFAMs: TIGR01167; LPXTG_anchor; 1.
DR TIGRFAMs: TIGR01168; YsIRK_signal; 1.
DR PROSITE: PS50647; GRAM_POS_ANCHORING; 1.
KW Cell wall; Peptidoglycan-anchor.
SQ SEQUENCE 940 AA; 10355 MW; E35FBBCA907AE345 CRC64;

Query Match 100.0%; Score 57; DB 2; Length 940;
Best local similarity 100.0%; Pred. No. 0.097;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FGHNSVDPE 10
Db 778 FGHNSVDPE 787

RESULT 2

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```
08NUT8
ID 08NUT8      PRELIMINARY;      PRT;      943 AA.
AC 08NUT8;
DT 01-OCT-2002 (TREMBlrel. 22, Created)
DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Fndb protein.
GN Name=fndb; OrderedLocusNames=MM2420;
OS Staphylococcus aureus (strain MM2).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=196620;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=2204017; PubMed=1204378; DOI=10.1016/S0140-6736(02)08713-5;
RA Baba T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Oguchi A.,
RA Yamamoto K., Hiramatsu K.,
RT "Genome and virulence determinants of high virulence community-
RT acquired MRSA.";
RL Lancet 359:1819-1827(2002).
CC -I- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC an amide bond (By similarity).
DR EMBL; AP004830; BAB96285.1; -.
DR HSSP; Q53653; IN67.
DR GO; GO:0009986; C:cell surface; IEA.
DR GO; GO:0005618; C:cell wall; IEA.
DR GO; GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0007155; P:cell adhesion; IEA.
DR InterPro; IPR008966; Adhes_bact.
DR InterPro; IPR004237; Fn_bind.
DR InterPro; IPR005877; Gpos_YsIRK.
DR InterPro; IPR001899; Gram_pos_anchor.
DR Pfam; PF02986; Fn_bind.1.
DR Pfam; PF00746; Gram_pos_anchor.1.
DR TIGRFAMs; TIGR01167; LpxTG_anchor.1.
DR TIGRFAMs; TIGR01168; YsIRK_signal.1.
DR PROSITE; PS50847; GRAM_POS_ANCHORING.1.
KW Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ SEQUENCE 943 AA; 104537 MW; DA8AF531947E1B6A CRC64;

Query Match      100.0%; Score 57; DB 2; Length 943;
Best Local Similarity 100.0%; Pred. No. 0.097;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FCGHNSVDPE 10
   |||||
Db 785 FCGHNSVDPE 794

RESULT 3
ID 06G6H4      PRELIMINARY;      PRT;      957 AA.
AC 06G6H4;
DT 05-JUN-2004 (TREMBlrel. 27, Created)
DT 05-JUN-2004 (TREMBlrel. 27, Last sequence update)
DT 05-JUN-2004 (TREMBlrel. 27, Last annotation update)
DE Fibronectin-binding protein.
GN Name=fndb; OrderedLocusNames=SA52387;
OS Staphylococcus aureus (strain MSS4476).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=282459;
RN [1]
RP SEQUENCE FROM N.A.
RC PubMed=15213324; DOI=10.1073/pnas.040251101;
RA Holden M.T.G., Fell E.J., Lindsay J.A., Peacock S.J., Day N.P.J.,
RA Enright M.C., Foster T.J., Moore C.E., Hurst L., Atkin R., Barron A.,
RA Baon N., Bentley S.D., Chillingworth C., Chillingworth T.,
RA Churcher C., Clark L., Cotton C., Cronin A., Doggett J., Dowd L.,
RA Felwell T., Hance Z., Harris B., Hauser H., Holtroyd S., Jagele K.,
RA James K.D., Lennard N., Line A., Mayes R., Moule S., Mungall K.,
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RA Ormond D., Quail M.A., Rabinowitsch E., Rutherford K.M., Sanders M.,
RA Sharp S., Simmonds M., Stevens K., Whitehead S., Barrell B.G.,
RA Spratt B.G., Parkhill J.;
RT "Complete genomes of two clinical Staphylococcus aureus strains:
RT evidence for the rapid evolution of virulence and drug resistance.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:9786-9791(2004).
CC -I- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC an amide bond (By similarity).
DR EMBL; BX51857; CAG4201.1; -.
DR GO; GO:0009986; C:cell surface; IEA.
DR GO; GO:0005618; C:cell wall; IEA.
DR GO; GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0007155; P:cell adhesion; IEA.
DR InterPro; IPR008966; Adhes_bact.
DR InterPro; IPR004237; Fn_bind.
DR InterPro; IPR005877; Gpos_YsIRK.
DR InterPro; IPR001899; Gram_pos_anchor.
DR Pfam; PF02986; Fn_bind.1.
DR Pfam; PF00746; Gram_pos_anchor.1.
DR TIGRFAMs; TIGR01167; LpxTG_anchor.1.
DR TIGRFAMs; TIGR01168; YsIRK_signal.1.
DR PROSITE; PS50847; GRAM_POS_ANCHORING.1.
KW Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ SEQUENCE 957 AA; 105980 MW; 28F8BA7FDFD3AF CRC64;

Query Match      100.0%; Score 57; DB 2; Length 957;
Best Local Similarity 100.0%; Pred. No. 0.098;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FCGHNSVDPE 10
   |||||
Db 785 FCGHNSVDPE 794

RESULT 4
ID 099RD3      PRELIMINARY;      PRT;      961 AA.
AC 099RD3;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE Fibronectin-binding protein homolog.
GN Name=fndb; OrderedLocusNames=SAV2502;
OS Staphylococcus aureus (strain Mu50 / ATCC 700699).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=158878;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Mu50 / ATCC 700699;
RA MEDLINE=21311952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2;
RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Iian J.-O., Ito T.,
RA Kanamori M., Matsunaru H., Maruyama A., Murakami H., Hosoyama A.,
RA Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
RA Sekizuka K., Hirakawa H., Kuhara S., Goto S., Yanuzaki J.,
RA Kanehisa M., Yamaishi A., Oshima K., Furuya K., Yoshino C., Shiba T.,
RA Hattori M., Ogasawara N., Hayaishi H., Hiramatsu K.;
RT "Whole genome sequencing of methicillin-resistant Staphylococcus
RT aureus.";
RL Lancet 357:1225-1240(2001).
CC -I- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC an amide bond (By similarity).
DR EMBL; AP003365; BAB58664.1; -.
DR PIR; G90053; G90053.
DR HSSP; Q53653; IN67.
DR GO; GO:0009986; C:cell surface; IEA.
DR GO; GO:0005618; C:cell wall; IEA.
DR GO; GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0007155; P:cell adhesion; IEA.
DR InterPro; IPR008966; Adhes_bact.
```

DR InterPro: IPR004237; Fn_bind.
 DR InterPro: IPR005877; Gpos_YsIRK.
 DR InterPro: IPR001899; Gram_pos_anchor.
 DR Pfam: PF02986; Fn_bind; 1.
 DR Pfam: PF00746; Gram_pos_anchor; 1.
 DR Pfam: PF04650; YsIRK_signal; 1.
 DR TIGRFAMs: TIGR01167; LpxTG_anchor; 1.
 DR TIGRFAMs: TIGR01168; YsIRK_signal; 1.
 DR PROSITE: PS50847; GRAM_POS_ANCHORING; 1.
 DR Cell wall; Complete proteome; Peptidoglycan-anchor.
 KW Cell wall; Complete proteome; Peptidoglycan-anchor.
 SQ SEQUENCE 961 AA; 106010 MW; 364940F884EA4101 CRC64;

Query Match 100.0%; Score 57; DB 2; Length 961;
 Best Local Similarity 100.0%; Pred. No. 0.099;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FGGHNSVDPE 10
 |||||
 Db 789 FGGHNSVDPE 798

RESULT 5
 Q7A3J8 PRELIMINARY; PRT; 961 AA.
 ID Q7A3J8
 AC Q7A3J8
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Fnb protein.
 GN Name=fnb; OrderedLocustNames=SA2290;
 OS Staphylococcus aureus (strain N315).
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 NC NCB1_TaxID=158879;
 RX MEDLINE=21311952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2;
 RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
 RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Iino T., Ito T.,
 RA Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,
 RA Mizutani-Uji Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
 RA Sekimizu K., Hiraoka H., Kihara S., Goto S., Yabuaki J.,
 RA Kanehisa M., Yamashita A., Oshika K., Furuya K., Yoshino C., Shiba T.,
 RA Hatori M., Ogasawara N., Hayashi H., Hiramatsu K.;
 RT "Whole genome sequencing of methicillin-resistant Staphylococcus
 aureus.";
 RL Lancet 357:1225-1240(2001).
 CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
 an amide bond (By similarity).
 DR EMBL: AP003137; BAB43593.1; -;
 DR GO: GO:0009986; C:cell surface; IEA.
 DR GO: GO:0005618; C:cell wall; IEA.
 DR GO: GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
 DR GO: GO:0016020; C:membrane; IEA.
 DR GO: GO:0007155; P:cell adhesion; IEA.
 DR InterPro: IPR008966; Adhes_bact.
 DR InterPro: IPR004237; Fn_bind.
 DR InterPro: IPR005877; Gpos_YsIRK.
 DR InterPro: IPR001899; Gram_pos_anchor.
 DR Pfam: PF02986; Fn_bind; 1.
 DR Pfam: PF00746; Gram_pos_anchor; 1.
 DR Pfam: PF04650; YsIRK_signal; 1.
 DR TIGRFAMs: TIGR01167; LpxTG_anchor; 1.
 DR TIGRFAMs: TIGR01168; YsIRK_signal; 1.
 DR PROSITE: PS50847; GRAM_POS_ANCHORING; 1.
 KW Cell wall; Complete proteome; Peptidoglycan-anchor.
 SQ SEQUENCE 961 AA; 106010 MW; 364940F884EA4101 CRC64;

Query Match 100.0%; Score 57; DB 2; Length 961;
 Best Local Similarity 100.0%; Pred. No. 0.099;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 FGGHNSVDPE 10
 |||||

Db 789 FGGHNSVDPE 798

RESULT 6
 Q6GDUS PRELIMINARY; PRT; 965 AA.
 ID Q6GDUS
 AC Q6GDUS
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Fibronectin-binding protein.
 GN Name=fnb; OrderedLocustNames=SA2580;
 OS Staphylococcus aureus (strain MRSA252).
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 NC NCB1_TaxID=282458;
 RX PubMed=15213324; DOI=10.1073/pnas.0402521101;
 RA Holden M.T.G., Feil E.J., Lindsey J.A., Peacock S.J., Day N.P.J.,
 RA Enright M.C., Foster T.J., Moore C.E., Huret L., Atkin R., Barron A.,
 RA Baason N., Bentley S.D., Chillingworth C., Chillingworth T.,
 RA Churcher C., Clark L., Corton C., Cronin A., Doggett J., Dowd L.,
 RA Fellwell T., Hance Z., Harris B., Hauser H., Holroyd S., Jagels K.,
 RA James K.D., Leonard N., Line A., Mayes R., Moule S., Mungall K.,
 RA Ormond D., Quail M.A., Rabinowitch E., Rutherford K.M., Sanders M.,
 RA Sharp S., Simmonds M., Stevens K., Whitehead S., Barrett B.G.,
 RA Spratt B.G., Parkhill J.;
 RT "Complete genomes of two clinical Staphylococcus aureus strains:
 evidence for the rapid evolution of virulence and drug resistance.";
 RL Proc. Natl. Acad. Sci. U.S.A. 101:9786-9791(2004).
 CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
 an amide bond (by similarity).
 DR EMBL: BX571856; CAG41560.1; -;
 DR GO: GO:0009986; C:cell surface; IEA.
 DR GO: GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
 DR GO: GO:0016020; C:membrane; IEA.
 DR GO: GO:0007155; P:cell adhesion; IEA.
 DR InterPro: IPR008966; Adhes_bact.
 DR InterPro: IPR004237; Fn_bind.
 DR InterPro: IPR005877; Gpos_YsIRK.
 DR InterPro: IPR001899; Gram_pos_anchor.
 DR Pfam: PF02986; Fn_bind; 1.
 DR Pfam: PF00746; Gram_pos_anchor; 1.
 DR Pfam: PF04650; YsIRK_signal; 1.
 DR TIGRFAMs: TIGR01167; LpxTG_anchor; 1.
 DR TIGRFAMs: TIGR01168; YsIRK_signal; 1.
 DR PROSITE: PS50847; GRAM_POS_ANCHORING; 1.
 KW Cell wall; Complete proteome; Peptidoglycan-anchor.
 SQ SEQUENCE 965 AA; 105691 MW; 2982513216400551 CRC64;

Query Match 100.0%; Score 57; DB 2; Length 965;
 Best Local Similarity 100.0%; Pred. No. 0.099;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FGGHNSVDPE 10
 |||||
 Db 807 FGGHNSVDPE 816

RESULT 7
 Q8NUU7 PRELIMINARY; PRT; 1015 AA.
 ID Q8NUU7
 AC Q8NUU7
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Fnb protein.
 GN Name=fnb; OrderedLocustNames=MM2421;
 OS Staphylococcus aureus (strain MM2).
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 NC NCB1_TaxID=196620;
 RX [1]
 RP SEQUENCE FROM N.A.


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DR InterPro: IPR008966; Adhes_bact.
DR InterPro: IPR004237; Fn_bind.
DR InterPro: IPR005877; Gpos_YsIRK.
DR InterPro: IPR001899; Gram_pos_anchor.
DR Pfam: PF02986; Fn_bind; 1.
DR Pfam: PF00746; Gram_pos_anchor; 1.
DR TIGRFAMs: TIGR01167; LPTXG_anchor; 1.
DR TIGRFAMs: TIGR01168; YsIRK_signal; 1.
DR PROSITE: PS50847; GRAM_POS_ANCHORING; 1.
KW Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ SEQUENCE 1015 AA; 111145 MW; D0F9281B864D44D2 CRC64;

Query Match 100.0%; Score 57; DB 2; Length 1015;
Best Local Similarity 100.0%; Pred. No. 0.1;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FGGHNSVDFE 10
Db 843 FGGHNSVDFE 852

RESULT 9
FNBA_STAAU STANDARD; PRT; 1018 AA.
ID FNBA_STAAU
AC P14738;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Fibronectin-binding protein precursor (FNBP).
GN Name:fnba;
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1280;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NCCTC 8325-4;
RX MEDLINE=8909898; PubMed=2521391;
RA Sjognaas C., Kaucci G., Joensson K., Lindgren P.-E.,
  Anantharamaiah G.M., Hoecel M., Lindberg M.;
RT "Nucleotide sequence of the gene for a fibronectin-binding protein
  from Staphylococcus aureus: use of this peptide sequence in the
  synthesis of biologically active peptides.";
RT Proc. Natl. Acad. Sci. U.S.A. 86:699-703(1989).
RL
CC -!- FUNCTION: The ability of bacteria to bind fibronectin has been
CC proposed as a virulence factor enabling bacteria to colonize wound
CC tissues and blood clots. Binding of plasma fibronectin to the
CC bacterial surface might block adhesion receptors on S.aureus, thus
CC representing an important defense mechanism against tissue
CC invasion.
CC -!- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC an amide bond (Potential).
CC -----
CC This SWISS-PROT entry is copyrighted. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: J04151; AAA2632.1; -.
CC InterPro: IPR004237; Fn_bind.
CC InterPro: IPR005877; Gpos_YsIRK.
CC InterPro: IPR001899; Gram_pos_anchor.
CC Pfam: PF02986; Fn_bind; 1.
CC Pfam: PF00746; Gram_pos_anchor; 1.
CC TIGRFAMs: TIGR01167; LPTXG_anchor; 1.
CC TIGRFAMs: TIGR01168; YsIRK_signal; 1.
CC PROSITE: PS50847; GRAM_POS_ANCHORING; 1.
KW Cell adhesion; Cell wall; Peptidoglycan-anchor; Repeat; Signal;
KW Virulence.

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FT SIGNAL 1 36
FT CHAIN 37 985 Fibronectin-binding protein.
FT PROPEP 986 1018 Removed by sortase (potential).
FT REPEAT 545 574 B-1.
FT REPEAT 575 604 B-2.
FT DOMAIN 745 878 4 X approximate tandem repeats,
FT REPEAT 745 878 fibronectin-binding domain.
FT REPEAT 745 878 D-1.
FT REPEAT 783 820 D-2.
FT REPEAT 821 859 D-3.
FT REPEAT 860 878 D-4 (incomplete).
FT DOMAIN 879 948 5 X tandem repeats, Pro-rich (WR).
FT REPEAT 879 892 WR 1.
FT REPEAT 893 906 WR 2.
FT REPEAT 907 920 WR 3.
FT REPEAT 921 934 WR 4.
FT REPEAT 935 948 WR 5.
FT SITE 982 986 LPTXG sorting signal (potential).
FT MOD_RES 985 985 Pentaglycyl murein peptidoglycan amidated
SQ SEQUENCE 1018 AA; 111780 MW; 58175E0020B81F1F CRC64;

Query Match 100.0%; Score 57; DB 1; Length 1018;
Best Local Similarity 100.0%; Pred. No. 0.1;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FCGHNSVDPE 10
DB 842 FCGHNSVDPE 851

RESULT 10
Q99RD2 PRELIMINARY; PRT; 1038 AA.
AC Q99RD2;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Fibronectin-binding protein homolog.
GN Name=fnb; OrderedlocusNames=SAV2503;
OS Staphylococcus aureus (strain Mu50 / ATCC 700699).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=158878;
[1]
RN SEQUENCE FROM N.A.
RC STRAIN=Mu50 / ATCC 700699;
RA MEDLINE=21311952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2;
RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Lian J.-Q., Ito T.,
RA Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyma A.,
RA Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
RA Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
RA Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
RA Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
RT "Whole genome sequencing of methicillin-resistant Staphylococcus
aureus."
RL Lancet 357:1225-1240(2001).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
an amide bond (By similarity).
EMBL AP003365; BAB58665.1; -.
CC DR PIR; H90053;
DR GO; GO:0009986; C:cell surface; IEA.
DR GO; GO:0005618; C:cell wall; IEA.
DR GO; GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0007155; P:cell adhesion; IEA.
DR InterPro; IPR008966; Adhes_Dact.
DR InterPro; IPR004237; Gpos_YsIRK.
DR InterPro; IPR005877; Gpos_YsIRK.
DR InterPro; IPR001899; Gram_pos_anchor.
DR Pfam; PF02986; Fn_bind; 1.
DR Pfam; PF02986; Fn_bind; 1.
DR Pfam; PF00746; Gram_pos_anchor; 1.
DR Pfam; PF00746; Gram_pos_anchor; 1.
DR Pfam; PF04650; YsIRK_signal; 1.

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DR TIGRFAMS; TIGR01167; LPTXG anchor; 1.
DR TIGRFAMS; TIGR01168; YsIRK_signal; 1.
DR PROSITE; PS50847; GRAM_POS_ANCHORING; 1.
DR Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ SEQUENCE 1038 AA; 113618 MW; 666BF6BF2BFBB12 CRC64;

Query Match 100.0%; Score 57; DB 2; Length 1038;
Best Local Similarity 100.0%; Pred. No. 0.11;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FCGHNSVDPE 10
DB 838 FCGHNSVDPE 847

RESULT 11
Q7A3J7 PRELIMINARY; PRT; 1038 AA.
AC Q7A3J7;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Fnb protein.
GN Name=fnb; OrderedlocusNames=SA2291;
OS Staphylococcus aureus (strain N315).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=158879;
[1]
RN SEQUENCE FROM N.A.
RC MEDLINE=21311952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2;
RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Lian J.-Q., Ito T.,
RA Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyma A.,
RA Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
RA Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
RA Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
RA Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
RT "Whole genome sequencing of methicillin-resistant Staphylococcus
aureus."
RL Lancet 357:1225-1240(2001).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
an amide bond (By similarity).
EMBL AP003373; BAB3594.1; -.
CC DR GO; GO:0009986; C:cell surface; IEA.
DR GO; GO:0005618; C:cell wall; IEA.
DR GO; GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0007155; P:cell adhesion; IEA.
DR InterPro; IPR008966; Adhes_Dact.
DR InterPro; IPR004237; Gpos_YsIRK.
DR InterPro; IPR005877; Gpos_YsIRK.
DR InterPro; IPR001899; Gram_pos_anchor.
DR Pfam; PF02986; Fn_bind; 1.
DR Pfam; PF00746; Gram_pos_anchor; 1.
DR Pfam; PF04650; YsIRK_signal; 1.
DR TIGRFAMS; TIGR01167; LPTXG anchor; 1.
DR TIGRFAMS; TIGR01168; YsIRK_signal; 1.
DR PROSITE; PS50847; GRAM_POS_ANCHORING; 1.
DR Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ SEQUENCE 1038 AA; 113618 MW; 666BF6BF2BFBB12 CRC64;

Query Match 100.0%; Score 57; DB 2; Length 1038;
Best Local Similarity 100.0%; Pred. No. 0.11;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FCGHNSVDPE 10
DB 838 FCGHNSVDPE 847

RESULT 12
Q9AEP9 PRELIMINARY; PRT; 152 AA.

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AC O9A99;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE Fibronectin-binding protein (Fragment).
GN Name-fnb;
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1280;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CMRSA-1;
RX DOI=10.1128/JAI.69.6.3791-3799.2001;
RA Rice K., Huesca M., Vaz D., McGavin M.J.;
RT "Variance in fibronectin binding and fnb locus polymorphisms in
RT Staphylococcus aureus: identification of antigenic variation in a
RT fibronectin binding protein adhesion of the epidemic CMRSA-1 strain of
RT methicillin-resistant S. aureus";
RL Infect.Immun. 69:3791-3799(2001).
DR EMBL; AY029184; AAKJ1588.1; -.
FT NON_TER 1 152
FT TER 1 152
SQ SEQUENCE 152 AA; 17193 MW; CFA3913C2B11C025 CRC64;

Query Match 82.5%; Score 47; DB 2; Length 152;
Best Local Similarity 77.8%; Pred. No. 1.1;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Oy 1 FGHNSVDF 9
Db 135 FGHNGIDF 143

RESULT 13
XTH3_ARATH STANDARD; PRT; 290 AA.
ID XTH3_ARATH
AC Q9LUR7;
DT 29-MAR-2004 (Rel. 43, Created)
DT 29-MAR-2004 (Rel. 43, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Probable xyloglucan endotransglucosylase/hydrolase protein 3 precursor
DE (EC 2.4.1.207) (At-XTH3) (XTH-3).
GN Name:XTH3; OrderedLocuNames=At3g25050; ORFNames=X3G3.6;
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosoids II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Columbia;
RX MEDLINE=20363099; PubMed=10907853;
RA Kaneke T., Katoh T., Sato S., Nakamura Y., Asamizu E., Tabata S.;
RT "Structural analysis of Arabidopsis thaliana chromosome 3. II.
RT Sequence features of the 4,251,695 bp regions covered by 90 Pl. TAC
RT and BAC clones.";
RL DNA Res. 7:217-221(2000).
RN [2]
RP TISSUE SPECIFICITY, AND INDUCTION.
RX MEDLINE=21530286; PubMed=11673616;
RA Yokoyama R., Nishitani K.;
RT "A comprehensive expression analysis of all members of a gene family
RT encoding cell-wall enzymes allowed us to predict cis-regulatory
RT regions involved in cell-wall construction in specific organs of
RT Arabidopsis.";
RL Plant Cell Physiol. 42:1025-1033(2001).
RN [3]
RP Nomenclature.
RX MEDLINE=22402747; PubMed=12514239;
RA Rose J.K.C., Braam J., Fry S.C., Nishitani K.;
RT "The XTH family of enzymes involved in xyloglucan
RT endotransglucosylation and endohydrolysis: current perspectives and a

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RT new unifying nomenclature.";
RL Plant Cell Physiol. 43:1421-1435(2002).
CC -1- FUNCTION: Catalyzes xyloglucan endohydrolysis (XEH) and/or
CC endotransglucosylation (XET). Cleaves and religates xyloglucan
CC polymers, an essential constituent of the primary cell wall, and
CC thereby participates in cell wall construction of growing tissues
CC (By similarity).
CC -1- CATALYTIC ACTIVITY: Breaks a beta-(1-24) bond in the backbone of a
CC xyloglucan and transfers the xyloglucanyl segment on to O-4 of the
CC non-reducing terminal glucose residue of an acceptor, which can be
CC a xyloglucan or an oligosaccharide of xyloglucan.
CC -1- SUBCELLULAR LOCATION: Apoplast (Probable).
CC -1- TISSUE SPECIFICITY: Predominantly expressed in flower buds.
CC -1- INDUCTION: By auxin and brassinolide.
CC -1- PTM: Contains at least one intrachain disulfide bond essential for
CC its enzymatic activity (By similarity).
CC -1- SIMILARITY: Belongs to the glycosyl hydrolase 16 family. XTH group
CC 1 subfamily.
CC -1- DATABASE: NAME=XTH-world;
CC WWW="http://www.plantbio.cornell.edu/XTH".
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AP000412; BAB01890.1; -.
DR HSSP; P23904; 1AJK.
DR InterPro; IPR008264; Beta glucanase.
DR InterPro; IPR008985; ConA_like_1ec.g1.
DR InterPro; IPR008263; Glyco_hydro_16.
DR InterPro; IPR000757; Glyco_hydro_16.
DR InterPro; IPR010713; XET_C.
DR Pfam; PF00722; Glyco_hydro_16; 1.
DR Pfam; PF06955; XET_C_1.
DR PRINTS; PR00737; GLHYDRLASE16.
DR PROSITE; PS01034; GLYCOSYL_HYDROL_F16; FALSE_NEG.
DR Apolplast; Cell wall; Glycosylase; Hydrolase; Multigene family; Signal;
KW Transferrase.
FT SIGNAL 1 21
FT CHAIN 22 290
FT FT Probable xyloglucan
FT ACT_SITE 109 109 endotransglucosylase/hydrolase protein 3.
FT ACT_SITE 113 113 Nucleophile (By similarity).
FT CARBOHYD 210 210 Proton donor (By similarity).
FT N-linked (GlcNAc...) (Potential).
SQ SEQUENCE 290 AA; 33259 MW; 5139594737955AF0 CRC64;

Query Match 71.9%; Score 41; DB 1; Length 290;
Best Local Similarity 66.7%; Pred. No. 27;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Oy 2 GGHNSVDF 10
Db 105 GGHDEIDF 113

RESULT 14
O9HM91 PRELIMINARY; PRT; 429 AA.
AC O9HM91;
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE Ribonuclease II family protein.
GN Name=vacB; OrderedLocuNames=VNC2647G;
OS Halobacterium sp. (strain NRC-1 / ATCC 700922 / JCM 11081).
OC Archaea; Euryarchaeota; Halobacteriales; Halobacteriales;
OC Halobacteriaceae; Halobacterium.
OX NCBI_TaxID=64091;
RN [1]

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RP  SEQUENCE FROM N.A.
RX  MEDLINE=20504483; PubMed=11016950; DOI=10.1073/pnas.190337797;
RA  Ng W.V., Kennedy S.P., Mahairas G.G., Bergquist B., Pan M.,
RA  Shukla H.D., Laasy S.R., Baliga N.S., Thorsson V., Shrogha J.,
RA  Swartzell S., Weir D., Hall J., Dahl T.A., Welti R., Goo Y.A.,
RA  Leithauser B., Keller K., Cruz R., Danson M.J., Hough D.W.,
RA  Maddocks D.G., Jablonski P.E., Krebs M.P., Angewine C.M., Dale H.,
RA  Isenbarger T.A., Peck R.F., Pohlschroder M., Spudich J.L., Jung K.-H.,
RA  Alam M., Freitas T., Hou S., Daniels C.J., Dennis P.P., Omer A.D.,
RA  Ehardt H., Lowe T.M., Liang P., Riley M., Hood L., Dassarma S.;
RT  "Genome sequence of Halobacterium species NRC-1."
RL  Proc. Natl. Acad. Sci. U.S.A. 97:12176-12181(2000).
DR  EMBL; AE005137; AAG20680.1; -.
DR  PIR; D84414; D84414.
DR  GO; GO:0004540; P:ribonuclease activity; IEA.
DR  GO; GO:0003723; P:RNA binding; IEA.
DR  InterPro; IPR001900; Ribonuclease_I1.
DR  Pfam; PF00773; RNB; 1.
KW  Complete proteome.
SQ  SEQUENCE 429 AA; 48953 MW; 655CA63B84279D57 CRC64;

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Query Match          71.9%; Score 41; DB 2; Length 429;
Best Local Similarity 60.0%; Pred. No. 41;
Matches 6; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

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QY  1 GGHNSVDPE 10
    |||:::|
DB  340 PGGHNLNPE 349

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RESULT 15
O74CG1 PRELIMINARY; PRT; 114 AA.
AC  O74CG1:

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DT  05-JUL-2004 (TrEMBLrel. 27, Created)
DT  05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT  05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE  Conserved hypothetical protein, truncation.
GN  Ordered locus names=GSU1713;
OS  Geobacter sulfurreducens.
OC  Bacteria; Proteobacteria; Deltaproteobacteria; Desulfuromonadales;
OC  Geodacteraceae; Geodacter.
OX  NCBI_TaxID=35554;
RN  [1]
RP  SEQUENCE FROM N.A.
RX  STRAIN=PCA / ATCC 51573;
RX  PubMed=14671304; DOI=10.1126/science.1089727;
RA  Wetne B.A., Nelson K.E., Eisen J.A., Paulsen I.T., Nelson W.C.,
RA  Heidelberg J.F., Wu D., Wu M., Ward N.L., Beanan M.J., Dodson R.J.,
RA  Madupu R., Brinkac L.M., Daugherty S.C., DeBoy R.T., Durkin A.S.,
RA  Gwinn M.L., Kolonay J.F., Sullivan S.A., Haft D.H., Selengut J.,
RA  Davidson T.M., Zafar N., White O., Tran B., Romero C., Forberger H.A.,
RA  Weidman J.F., Khouri H.M., Feldblyum T.V., Utterback T.R.,
RA  Van Aken S.E., Lovley D.R., Fraser C.M.;
RT  "Genome of Geobacter sulfurreducens: metal reduction in subsurface
RT  environments."
RL  Science 302:1967-1969(2003).
DR  EMBL; AR017180; AAR35090.1; -.
DR  TIGR; GSU1713; -.
KW  Complete proteome.
SQ  SEQUENCE 114 AA; 12964 MW; 9A0CF9B6EC7096A CRC64;

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Query Match          70.2%; Score 40; DB 2; Length 114;
Best Local Similarity 66.7%; Pred. No. 16;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

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QY  2 GGHNSVDPE 10
    |||:::|
DB  97 GGHNRLDYE 105

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 25, 2005, 20:58:51 ; Search time 69.7126 Seconds
(without alignments)
55.479 Million cell updates/sec

Title: US-10-731-238-99

Perfect score: 56

Sequence: 1 GHSVDFRED 10

Scoring table: GAPDP 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:*
1: geneseqp19808:*
2: geneseqp19908:*
3: geneseqp20008:*
4: geneseqp20018:*
5: geneseqp20028:*
6: geneseqp20038:*
7: geneseqp20038:*
8: geneseqp20048:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	56	100.0	10	2	AAW65755 Fibronec
2	56	100.0	14	2	AAW65717 Fibronec
3	56	100.0	21	2	AAW65670 Fibronec
4	56	100.0	21	2	AAW65689 Fibronec
5	56	100.0	21	2	AAW65673 Fibronec
6	56	100.0	21	2	AAW65671 Fibronec
7	56	100.0	21	2	AAW65675 Fibronec
8	56	100.0	21	2	AAW65666 Fibronec
9	56	100.0	21	2	AAW65688 Fibronec
10	56	100.0	21	2	AAW65672 Fibronec
11	56	100.0	21	2	AAW65687 Fibronec
12	56	100.0	21	2	AAW65686 Fibronec
13	56	100.0	21	2	AAW65665 Fibronec
14	56	100.0	21	2	AAW65674 Fibronec
15	56	100.0	22	2	AAW65674 Fibronec
16	56	100.0	22	2	AAW65669 Fibronec
17	56	100.0	37	1	AAW65618 Fibronec
18	56	100.0	37	1	AAW65618 Fibronec
19	56	100.0	38	1	AAW65662 Fibronec
20	56	100.0	77	2	AAW65662 Fibronec
21	56	100.0	101	2	AAW65662 Fibronec
22	56	100.0	113	2	AAW65662 Fibronec
23	56	100.0	124	2	AAW65662 Fibronec
24	56	100.0	128	2	AAW65662 Fibronec
25	56	100.0	130	2	AAW65662 Fibronec

26	56	100.0	130	2	AAW656807	AAW656807 Fibronec
27	56	100.0	130	2	AAW656807	AAW656807 Fibronec
28	56	100.0	130	2	AAW656807	AAW656807 Fibronec
29	56	100.0	134	2	AAW656807	AAW656807 Fibronec
30	56	100.0	134	2	AAW656807	AAW656807 Fibronec
31	56	100.0	139	2	AAW656807	AAW656807 Fibronec
32	56	100.0	162	2	AAW656807	AAW656807 Fibronec
33	56	100.0	164	2	AAW656807	AAW656807 Fibronec
34	56	100.0	174	2	AAW656807	AAW656807 Fibronec
35	56	100.0	174	2	AAW656807	AAW656807 Fibronec
36	56	100.0	181	2	AAW656807	AAW656807 Fibronec
37	56	100.0	181	2	AAW656807	AAW656807 Fibronec
38	56	100.0	559	2	AAW656807	AAW656807 Fibronec
39	56	100.0	940	2	AAW656807	AAW656807 Fibronec
40	56	100.0	940	2	AAW656807	AAW656807 Fibronec
41	56	100.0	948	6	AAW656807	AAW656807 Fibronec
42	56	100.0	948	6	AAW656807	AAW656807 Fibronec
43	56	100.0	948	6	AAW656807	AAW656807 Fibronec
44	56	100.0	961	6	AAW656807	AAW656807 Fibronec
45	56	100.0	978	4	AAW656807	AAW656807 Fibronec

ALIGNMENTS

RESULT 1
AAW65755 standard; peptide, 10 AA.
ID AAW65755 standard; peptide, 10 AA.

AAW65755;

16-OCT-1998 (first entry)

Fibronec binding protein-derived peptide #99.

microbial surface components recognizing adhesive matrix molecule;

MSCRAMM; fibronec binding protein; antibody; epitope;

antibiotic; bacterial infection; antibiotic-resistant strain.

Synthetic.

Staphylococcus aureus.

MO9831389-A2.

23-JUL-1998.

21-JAN-1998; 98WO-US001222.

21-JAN-1997; 97US-0036139P.

(TEXA) UNIT TEXAS A & M SYSTEM.

Hoeek M, Patti JM, House-Pompeo KL, Speziale P, Joh D;

McGavin MJ;

WPI; 1998-413816/35.

Antibody that binds to fibronec binding protein, preventing its

binding to fibronec - used to treat or prevent bacterial infection,

especially by Staphylococci and Streptococci.

Example 9; Page 111; 201P; English.

The invention relates to antibodies that bind to a fibronec binding domain of a fibronec binding protein, and inhibit binding of the protein to fibronec. Also claimed are: (1) isolated peptides of a fibronec binding protein that do not bind to fibronec; (2) fusion protein containing at least one peptide of a fibronec binding protein linked to a second amino acid sequence; (3) nucleic acid encoding the isolated peptide of (1). Antibodies, the isolated peptides of (1) and the nucleic acids are all useful for immunisation (active or passive) and (by inhibiting binding of bacteria to fibronec) for preventing or treating infection in humans or other animals, particularly by staphylococci or

CC streptococci, e.g. meningitis, otitis media, pneumonia, endocarditis,
 CC mastitis in cattle, abortion in horses and many others. Since the
 CC antibodies block binding of bacteria, they should be effective against
 CC antibiotic-resistant strains, and may replace antibiotic therapy or
 CC increase its effectiveness. Sequences AAW65744-58 represent peptides
 CC which were synthesised to span the D3 motif of *S. aureus* fibronectin
 CC binding protein A
 XX
 SQ Sequence 10 AA;
 Query Match 100.0%; Score 56; DB 2; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.00091;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GHSVDPEED 10
 DB 1 GHSVDPEED 10
 RESULT 2
 AAW65717
 ID AAW65717 standard; peptide; 14 AA.
 XX
 AC AAW65717;
 XX
 DT 16-OCT-1998 (first entry)
 XX
 DE Fibronectin binding protein fragment (residues 20-33 of D3 motif).
 XX
 KW microbial surface components recognising adhesive matrix molecule;
 KW MSCRAMM; fibronectin; fibronectin-binding protein; antibody; epitope;
 KW antibiotic; bacterial infection; antibiotic-resistant strain.
 XX
 OS Synthetic.
 OS Staphylococcus aureus.
 XX
 PN WO9831389-A2.
 XX
 PD 23-JUL-1998.
 XX
 PF 21-JAN-1998; 98WO-US001222.
 XX
 PR 21-JAN-1997; 97US-0036139P.
 XX
 PA (TEXA) UNIV TEXAS A & M SYSTEM.
 PI Hoeoek M, Patti JM, House-Pompeo KL, Speziale P, Joh D;
 PI McGavin MJ;
 XX
 DR WPI; 1998-413816/35.
 XX
 PT Antibody that binds to fibronectin-binding protein, preventing its
 PT binding to fibronectin - used to treat or prevent bacterial infection,
 PT especially by Staphylococci and Streptococci.
 XX
 PS Claim 42; Page 105; 201pp; English.
 XX
 CC The invention relates to antibodies that bind to a fibronectin-binding
 CC domain of a fibronectin-binding protein, and inhibit binding of the
 CC protein to fibronectin. Also claimed are: (1) isolated peptides of a
 CC fibronectin-binding protein that do not bind to fibronectin; (2) fusion
 CC protein containing at least one peptide of a fibronectin-binding protein
 CC linked to a second amino acid sequence; (3) nucleic acid encoding the
 CC isolated peptide of (1). Antibodies, the isolated peptides of (1) and the
 CC nucleic acids are all useful for immunisation (active or passive) and (by
 CC inhibiting binding of bacteria to fibronectin) for preventing or treating
 CC infection in humans or other animals, particularly by streptococci or
 CC streptococci, e.g. meningitis, otitis media, pneumonia, endocarditis,
 CC mastitis in cattle, abortion in horses and many others. Since the
 CC antibodies block binding of bacteria, they should be effective against
 CC antibiotic-resistant strains, and may replace antibiotic therapy or
 CC increase its effectiveness. The present sequence represents a
 CC specifically claimed peptide

XX
 SQ Sequence 14 AA;
 Query Match 100.0%; Score 56; DB 2; Length 14;
 Best Local Similarity 100.0%; Pred. No. 0.0013;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GHSVDPEED 10
 DB 4 GHSVDPEED 13
 RESULT 3
 AAW65670
 ID AAW65670 standard; peptide; 21 AA.
 XX
 AC AAW65670;
 XX
 DT 16-OCT-1998 (first entry)
 XX
 DE Fibronectin binding protein-derived peptide #14.
 XX
 KW microbial surface components recognising adhesive matrix molecule;
 KW MSCRAMM; fibronectin; fibronectin-binding protein; antibody; epitope;
 KW antibiotic; bacterial infection; antibiotic-resistant strain.
 XX
 OS Synthetic.
 OS Staphylococcus aureus.
 XX
 PN WO9831389-A2.
 XX
 PD 23-JUL-1998.
 XX
 PF 21-JAN-1998; 98WO-US001222.
 XX
 PR 21-JAN-1997; 97US-0036139P.
 XX
 PA (TEXA) UNIV TEXAS A & M SYSTEM.
 PI Hoeoek M, Patti JM, House-Pompeo KL, Speziale P, Joh D;
 PI McGavin MJ;
 XX
 DR WPI; 1998-413816/35.
 XX
 PT Antibody that binds to fibronectin-binding protein, preventing its
 PT binding to fibronectin - used to treat or prevent bacterial infection,
 PT especially by Staphylococci and Streptococci.
 XX
 PS Example 8; Page 100; 201pp; English.
 XX
 CC The invention relates to antibodies that bind to a fibronectin-binding
 CC domain of a fibronectin-binding protein, and inhibit binding of the
 CC protein to fibronectin. Also claimed are: (1) isolated peptides of a
 CC fibronectin-binding protein that do not bind to fibronectin; (2) fusion
 CC protein containing at least one peptide of a fibronectin-binding protein
 CC linked to a second amino acid sequence; (3) nucleic acid encoding the
 CC isolated peptide of (1). Antibodies, the isolated peptides of (1) and the
 CC nucleic acids are all useful for immunisation (active or passive) and (by
 CC inhibiting binding of bacteria to fibronectin) for preventing or treating
 CC infection in humans or other animals, particularly by streptococci or
 CC streptococci, e.g. meningitis, otitis media, pneumonia, endocarditis,
 CC mastitis in cattle, abortion in horses and many others. Since the
 CC antibodies block binding of bacteria, they should be effective against
 CC antibiotic-resistant strains, and may replace antibiotic therapy or
 CC increase its effectiveness. Sequences AAW65670-90 represent a series of
 CC synthetic peptides based on the D3 repeat of *S. aureus* fibronectin
 CC binding protein A. They were synthesised to contain a proline residue at
 CC each position through the sequence (ie a proline scan)
 XX
 SQ Sequence 21 AA;
 Query Match 100.0%; Score 56; DB 2; Length 21;
 Best Local Similarity 100.0%; Pred. No. 0.0021;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GHNSVDFEED 10
 |||||
 Db 8 GHNSVDFEED 17

RESULT 4

AAW65689 standard; peptide; 21 AA.

AC AAW65689;
 DT 16-OCT-1998 (first entry)
 DE Fibronectin binding protein-derived peptide #33.
 XX
 XX microbial surface components recognising adhesive matrix molecule;
 KM MSCRAMM; fibronectin; fibronectin-binding protein; antibody; epitope;
 KM antibiotic; bacterial infection; antibiotic-resistant strain.
 XX

OS Synthetic.
 OS Staphylococcus aureus.

PN WO9831389-A2.

PD 23-JUL-1998.

PF 21-JAN-1998; 98WO-US001222.

PR 21-JAN-1997; 97US-0036139P.

XX (TEXA) UNIV TEXAS A & M SYSTEM.

XX Hoeoek M, Patti JM, House-Pompeo KL, Speziale P, Joh D;
 PI Mcgavin MJ;

DR WPI; 1998-413816/35.

PT Antibody that binds to fibronectin-binding protein, preventing its
 binding to fibronectin - used to treat or prevent bacterial infection,
 PT especially by Staphylococci and Streptococci.

PS Example 8; Page 101; 201pp; English.

XX The invention relates to antibodies that bind to a fibronectin-binding
 CC domain of a fibronectin-binding protein, and inhibit binding of the
 CC protein to fibronectin. Also claimed are: (1) isolated peptides of a
 CC fibronectin-binding protein that do not bind to fibronectin; (2) fusion
 CC protein containing at least one peptide of a fibronectin-binding protein
 CC linked to a second amino acid sequence; (3) nucleic acid encoding the
 CC isolated peptide of (1). Antibodies, the isolated peptides of (1) and the
 CC nucleic acids are all useful for immunisation (active or passive) and (by
 CC inhibiting binding of bacteria to fibronectin) for preventing or treating
 CC infection in humans or other animals, particularly by staphylococci or
 CC streptococci, e.g. meningitis, otitis media, pneumonia, endocarditis,
 CC mastitis in cattle, abortion in horses and many others. Since the
 CC antibodies block binding of bacteria, they should be effective against
 CC antibiotic-resistant strains, and may replace antibiotic therapy or
 CC increase its effectiveness. Sequences AAW65670-90 represent a series of
 CC synthetic peptides based on the D3 repeat of S. aureus fibronectin
 CC binding protein A. They were synthesised to contain a proline residue at
 CC each position through the sequence (ie a proline scan)

XX Sequence 21 AA;

Query Match 100.0%; Score 56; DB 2; Length 21;

Best Local Similarity 100.0%; Pred. No. 0.0021;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GHNSVDFEED 10
 |||||
 Db 8 GHNSVDFEED 17

AAW65673 standard; peptide; 21 AA.

AC AAW65673;
 DT 16-OCT-1998 (first entry)
 DE Fibronectin binding protein-derived peptide #17.

XX
 XX microbial surface components recognising adhesive matrix molecule;
 KM MSCRAMM; fibronectin; fibronectin-binding protein; antibody; epitope;
 KM antibiotic; bacterial infection; antibiotic-resistant strain.
 XX

OS Synthetic.
 OS Staphylococcus aureus.

PN WO9831389-A2.

PD 23-JUL-1998.

PF 21-JAN-1998; 98WO-US001222.

PR 21-JAN-1997; 97US-0036139P.

XX (TEXA) UNIV TEXAS A & M SYSTEM.

XX Hoeoek M, Patti JM, House-Pompeo KL, Speziale P, Joh D;
 PI Mcgavin MJ;

DR WPI; 1998-413816/35.

PT Antibody that binds to fibronectin-binding protein, preventing its
 binding to fibronectin - used to treat or prevent bacterial infection,
 PT especially by Staphylococci and Streptococci.

PS Example 8; Page 100; 201pp; English.

XX The invention relates to antibodies that bind to a fibronectin-binding
 CC domain of a fibronectin-binding protein, and inhibit binding of the
 CC protein to fibronectin. Also claimed are: (1) isolated peptides of a
 CC fibronectin-binding protein that do not bind to fibronectin; (2) fusion
 CC protein containing at least one peptide of a fibronectin-binding protein
 CC linked to a second amino acid sequence; (3) nucleic acid encoding the
 CC isolated peptide of (1). Antibodies, the isolated peptides of (1) and the
 CC nucleic acids are all useful for immunisation (active or passive) and (by
 CC inhibiting binding of bacteria to fibronectin) for preventing or treating
 CC infection in humans or other animals, particularly by staphylococci or
 CC streptococci, e.g. meningitis, otitis media, pneumonia, endocarditis,
 CC mastitis in cattle, abortion in horses and many others. Since the
 CC antibodies block binding of bacteria, they should be effective against
 CC antibiotic-resistant strains, and may replace antibiotic therapy or
 CC increase its effectiveness. Sequences AAW65670-90 represent a series of
 CC synthetic peptides based on the D3 repeat of S. aureus fibronectin
 CC binding protein A. They were synthesised to contain a proline residue at
 CC each position through the sequence (ie a proline scan)

XX Sequence 21 AA;

Query Match 100.0%; Score 56; DB 2; Length 21;

Best Local Similarity 100.0%; Pred. No. 0.0021;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GHNSVDFEED 10
 |||||
 Db 8 GHNSVDFEED 17

RESULT 6

AAW65671 standard; peptide; 21 AA.


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XX AC AAW65671;
XX XX 16-OCT-1998 (first entry)
XX DT
XX DE Fibronectin binding protein-derived peptide #15.
XX KM microbial surface components recognising adhesive matrix molecule;
XX KM MSCRAMM; fibronectin; fibronectin-binding protein; antibody; epitope;
XX KM antibiotic; bacterial infection; antibiotic-resistant strain.
XX OS Synthetic.
XX OS Staphylococcus aureus.
XX PN MO9831389-A2.
XX PD 23-JUL-1998.
XX PR 21-JAN-1998; 98WO-US001222.
XX PF 21-JAN-1997; 97US-0036139P.
XX PR 21-JAN-1997; 97US-0036139P.
XX PA (TEXA ) UNIV TEXAS A & M SYSTEM.
XX PI Hoeoek M, Patti JM, House-Pompeo KL, Speziale P, Joh D;
XX PI Megavlin MJ;
XX DR WPI; 1998-413816/35.
XX XX
XX PT Antibody that binds to fibronectin-binding protein, preventing its
XX PT binding to fibronectin - used to treat or prevent bacterial infection,
XX PT especially by Staphylococci and Streptococci.
XX PS Example 8; Page 100; 201pp; English.
XX XX
XX CC The invention relates to antibodies that bind to a fibronectin-binding
XX CC domain of a fibronectin-binding protein, and inhibit binding of the
XX CC protein to fibronectin. Also claimed are: (1) isolated peptides of a
XX CC fibronectin-binding protein that do not bind to fibronectin; (2) fusion
XX CC protein containing at least one peptide of a fibronectin-binding protein
XX CC linked to a second amino acid sequence; (3) nucleic acid encoding the
XX CC isolated peptide of (1). Antibodies, the isolated peptides of (1) and the
XX CC nucleic acids are all useful for immunisation (active or passive) and (by
XX CC inhibiting binding of bacteria to fibronectin) for preventing or treating
XX CC infection in humans or other animals, particularly by staphylococci or
XX CC streptococci, e.g. meningitis, otitis media, pneumonia, endocarditis,
XX CC mastitis in cattle, abortion in horses and many others. Since the
XX CC antibodies block binding of bacteria, they should be effective against
XX CC antibiotic-resistant strains, and may replace antibiotic therapy or
XX CC increase its effectiveness. Sequences AAW65670-90 represent a series of
XX CC synthetic peptides based on the D3 repeat of S. aureus fibronectin
XX CC binding protein A. They were synthesised to contain a proline residue at
XX CC each position through the sequence (ie a proline scan)
XX SO Sequence 21 AA;

Query Match 100.0%; Score 56; DB 2; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.0021;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GHNSVDFEED 10
DB 8 GHNSVDFEED 17

RESULT 7
AAW65675
ID AAW65675 standard; peptide; 21 AA.
XX AC AAW65675;
XX XX
XX DT 16-OCT-1998 (first entry)
XX XX

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DE DE Fibronectin binding protein-derived peptide #19.
XX KM microbial surface components recognising adhesive matrix molecule;
XX KM MSCRAMM; fibronectin; fibronectin-binding protein; antibody; epitope;
XX KM antibiotic; bacterial infection; antibiotic-resistant strain.
XX OS Synthetic.
XX OS Staphylococcus aureus.
XX PN MO9831389-A2.
XX PD 23-JUL-1998.
XX PR 21-JAN-1998; 98WO-US001222.
XX PF 21-JAN-1997; 97US-0036139P.
XX PR 21-JAN-1997; 97US-0036139P.
XX PA (TEXA ) UNIV TEXAS A & M SYSTEM.
XX PI Hoeoek M, Patti JM, House-Pompeo KL, Speziale P, Joh D;
XX PI Megavlin MJ;
XX DR WPI; 1998-413816/35.
XX XX
XX PT Antibody that binds to fibronectin-binding protein, preventing its
XX PT binding to fibronectin - used to treat or prevent bacterial infection,
XX PT especially by Staphylococci and Streptococci.
XX PS Example 8; Page 100; 201pp; English.
XX XX
XX CC The invention relates to antibodies that bind to a fibronectin-binding
XX CC domain of a fibronectin-binding protein, and inhibit binding of the
XX CC protein to fibronectin. Also claimed are: (1) isolated peptides of a
XX CC fibronectin-binding protein that do not bind to fibronectin; (2) fusion
XX CC protein containing at least one peptide of a fibronectin-binding protein
XX CC linked to a second amino acid sequence; (3) nucleic acid encoding the
XX CC isolated peptide of (1). Antibodies, the isolated peptides of (1) and the
XX CC nucleic acids are all useful for immunisation (active or passive) and (by
XX CC inhibiting binding of bacteria to fibronectin) for preventing or treating
XX CC infection in humans or other animals, particularly by staphylococci or
XX CC streptococci, e.g. meningitis, otitis media, pneumonia, endocarditis,
XX CC mastitis in cattle, abortion in horses and many others. Since the
XX CC antibodies block binding of bacteria, they should be effective against
XX CC antibiotic-resistant strains, and may replace antibiotic therapy or
XX CC increase its effectiveness. Sequences AAW65670-90 represent a series of
XX CC synthetic peptides based on the D3 repeat of S. aureus fibronectin
XX CC binding protein A. They were synthesised to contain a proline residue at
XX CC each position through the sequence (ie a proline scan)
XX SO Sequence 21 AA;

Query Match 100.0%; Score 56; DB 2; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.0021;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GHNSVDFEED 10
DB 8 GHNSVDFEED 17

RESULT 8
AAW65666
ID AAW65666 standard; peptide; 21 AA.
XX AC AAW65666;
XX XX
XX DT 16-OCT-1998 (first entry)
XX XX
XX DE Fibronectin binding protein-derived peptide #10.
XX KM microbial surface components recognising adhesive matrix molecule;
XX KM MSCRAMM; fibronectin; fibronectin-binding protein; antibody; epitope;
XX KM antibiotic; bacterial infection; antibiotic-resistant strain.

```

XX OS Synthetic.
 OS Staphylococcus aureus.
 XX
 XX MO9831389-A2.
 XX
 XX 23-JUL-1998.
 XX
 XX 21-JAN-1998; 98WO-US001222.
 XX
 XX 21-JAN-1997; 97US-0036139P.
 XX
 XX (TEXA) UNIV TEXAS A & M SYSTEM.
 XX
 XX Hoecek M, Patti JM, House-Pompeo KL, Speziale P, Joh D;
 XX Mcgavin MJ;
 XX WPI; 1998-413816/35.
 XX
 XX Antibody that binds to fibronectin-binding protein, preventing its
 XX binding to fibronectin - used to treat or prevent bacterial infection,
 XX especially by Staphylococci and Streptococci.
 XX
 XX Example 2; Page 92; 201pp; English.
 XX
 XX The invention relates to antibodies that bind to a fibronectin-binding
 XX domain of a fibronectin-binding protein, and inhibit binding of the
 XX protein to fibronectin. Also claimed are: (1) isolated peptides of a
 XX fibronectin-binding protein that do not bind to fibronectin; (2) fusion
 XX protein containing at least one peptide of a nucleic acid encoding the
 XX isolated peptide of (1). Antibodies, the isolated peptides of (1) and (2)
 XX nucleic acids are all useful for immunisation (active or passive) and (by
 XX inhibiting binding of bacteria to fibronectin) for preventing or treating
 XX infection in humans or other animals, particularly by staphylococci or
 XX streptococci, e.g. meningitis, otitis media, pneumonia, endocarditis,
 XX mastitis in cattle, abortion in horses and many others. Since the
 XX antibodies block binding of bacteria, they should be effective against
 XX antibiotic-resistant strains, and may replace antibiotic therapy or
 XX increase its effectiveness. Sequences AAW65659-68 represent synthetic
 XX epitopes from the fibronectin binding domains DU and DI-D4 of the S.
 XX aureus fnda gene
 XX
 XX Sequence 21 AA;
 XX
 XX Query Match 100.0%; Score 56; DB 2; Length 21;
 XX Best Local Similarity 100.0%; Pred. No. 0.0021;
 XX Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX
 XX QY 1 GHNSVDFFED 10
 XX |||||
 XX Db 8 GHNSVDFFED 17
 XX
 XX RESULT 9
 XX AAW65688
 XX ID AAW65688 standard; peptide; 21 AA.
 XX
 XX AC AAW65688;
 XX
 XX DT 16-OCT-1998 (first entry)
 XX
 XX DE Fibronectin binding protein-derived peptide #32.
 XX
 XX OS microbial surface components recognising adhesive matrix molecule;
 XX KM MSCRAMM; fibronectin; fibronectin-binding protein; antibody; epitope;
 XX KW antibiotic; bacterial infection; antibiotic-resistant strain.
 XX
 XX OS Synthetic.
 XX OS Staphylococcus aureus.
 XX
 XX PN MO9831389-A2.

PD 23-JUL-1998.
 XX
 XX 21-JAN-1998; 98WO-US001222.
 XX
 XX 21-JAN-1997; 97US-0036139P.
 XX
 XX (TEXA) UNIV TEXAS A & M SYSTEM.
 XX
 XX Hoecek M, Patti JM, House-Pompeo KL, Speziale P, Joh D;
 XX Mcgavin MJ;
 XX WPI; 1998-413816/35.
 XX
 XX Antibody that binds to fibronectin-binding protein, preventing its
 XX binding to fibronectin - used to treat or prevent bacterial infection,
 XX especially by Staphylococci and Streptococci.
 XX
 XX Example 8; Page 101; 201pp; English.
 XX
 XX The invention relates to antibodies that bind to a fibronectin-binding
 XX domain of a fibronectin-binding protein, and inhibit binding of the
 XX protein to fibronectin. Also claimed are: (1) isolated peptides of a
 XX fibronectin-binding protein that do not bind to fibronectin; (2) fusion
 XX protein containing at least one peptide of a fibronectin-binding protein
 XX linked to a second amino acid sequence; (3) nucleic acid encoding the
 XX isolated peptide of (1). Antibodies, the isolated peptides of (1) and (2)
 XX nucleic acids are all useful for immunisation (active or passive) and (by
 XX inhibiting binding of bacteria to fibronectin) for preventing or treating
 XX infection in humans or other animals, particularly by staphylococci or
 XX streptococci, e.g. meningitis, otitis media, pneumonia, endocarditis,
 XX mastitis in cattle, abortion in horses and many others. Since the
 XX antibodies block binding of bacteria, they should be effective against
 XX antibiotic-resistant strains, and may replace antibiotic therapy or
 XX increase its effectiveness. Sequences AAW65670-90 represent a series of
 XX synthetic peptides based on the D3 repeat of S. aureus fibronectin
 XX binding protein A. They were synthesised to contain a proline residue at
 XX each position through the sequence (1e a proline scan)
 XX
 XX Sequence 21 AA;
 XX
 XX Query Match 100.0%; Score 56; DB 2; Length 21;
 XX Best Local Similarity 100.0%; Pred. No. 0.0021;
 XX Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX
 XX QY 1 GHNSVDFFED 10
 XX |||||
 XX Db 8 GHNSVDFFED 17
 XX
 XX RESULT 10
 XX AAW65672
 XX ID AAW65672 standard; peptide; 21 AA.
 XX
 XX AC AAW65672;
 XX
 XX DT 16-OCT-1998 (first entry)
 XX
 XX DE Fibronectin binding protein-derived peptide #16.
 XX
 XX OS microbial surface components recognising adhesive matrix molecule;
 XX KM MSCRAMM; fibronectin; fibronectin-binding protein; antibody; epitope;
 XX KW antibiotic; bacterial infection; antibiotic-resistant strain.
 XX
 XX OS Synthetic.
 XX OS Staphylococcus aureus.
 XX
 XX PN MO9831389-A2.
 XX
 XX XX 23-JUL-1998.
 XX
 XX 21-JAN-1998; 98WO-US001222.
 XX
 XX 21-JAN-1997; 97US-0036139P.

XX (TEXA) UNIV TEXAS A & M SYSTEM.
XX Hoeoek M, Patti JM, House-Pompeo KL, Speciale P, Joh D;
XX Mcgavin MJ;
XX WPI: 1998-413816/35.
XX
XX Antibody that binds to fibronectin-binding protein, preventing its
XX binding to fibronectin - used to treat or prevent bacterial infection,
XX especially by Staphylococci and Streptococci.
XX
XX Example 8; Page 100; 201pp; English.
XX
XX The invention relates to antibodies that bind to a fibronectin-binding
XX domain of a fibronectin-binding protein, and inhibit binding of the
XX protein to fibronectin. Also claimed are: (1) isolated peptides of a
XX fibronectin-binding protein that do not bind to fibronectin; (2) fusion
XX protein containing at least one peptide of a fibronectin-binding protein
XX linked to a second amino acid sequence; (3) nucleic acid encoding the
XX isolated peptide of (1). Antibodies, the isolated peptides of (1) and the
XX nucleic acids are all useful for immunisation (active or passive) and (by
XX inhibiting binding of bacteria to fibronectin) for preventing or treating
XX infection in humans or other animals, particularly by staphylococci or
XX streptococci, e.g. meningitis, otitis media, pneumonia, endocarditis,
XX mastitis in cattle, abortion in horses and many others. Since the
XX antibodies block binding of bacteria, they should be effective against
XX antibiotic-resistant strains, and may replace antibiotic therapy or
XX increase its effectiveness. Sequences AAW65670-90 represent a series of
XX synthetic peptides based on the D3 repeat of S. aureus fibronectin
XX binding protein A. They were synthesised to contain a proline residue at
XX each position throughout the sequence (ie a proline scan)
SQ Sequence 21 AA;

Query March 100.0%; Score 56; DB 2; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.0021;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GHNSVDFEED 10
|||
DB 8 GHNSVDFEED 17

RESULT 11
AAW65687
ID AAW65687 standard; peptide; 21 AA.
XX AAW65687;
AC
XX 16-OCT-1998 (first entry)
DT
XX
DE Fibronectin binding protein-derived peptide #31.
XX
XX
KW microbial surface components recognising adhesive matrix molecule;
KW MSCRAMM; fibronectin; fibronectin-binding protein; antibody; epitope;
KW antibiotic; bacterial infection; antibiotic-resistant strain.
XX
XX Synthetic.
OS Staphylococcus aureus.
XX
XX W09831389-A2.
PN
XX 23-JUL-1998.
PD
XX 21-JAN-1998; 98WO-US001222.
PF
XX 21-JAN-1997; 97US-0036139P.
PR
XX (TEXA) UNIV TEXAS A & M SYSTEM.
PA
XX Hoeoek M, Patti JM, House-Pompeo KL, Speciale P, Joh D;
PI Mcgavin MJ;

XX WPI: 1998-413816/35.
XX
XX Antibody that binds to fibronectin-binding protein, preventing its
XX binding to fibronectin - used to treat or prevent bacterial infection,
XX especially by Staphylococci and Streptococci.
XX
XX Example 8; Page 101; 201pp; English.
XX

XX The invention relates to antibodies that bind to a fibronectin-binding
XX domain of a fibronectin-binding protein, and inhibit binding of the
XX protein to fibronectin. Also claimed are: (1) isolated peptides of a
XX fibronectin-binding protein that do not bind to fibronectin; (2) fusion
XX protein containing at least one peptide of a fibronectin-binding protein
XX linked to a second amino acid sequence; (3) nucleic acid encoding the
XX isolated peptide of (1). Antibodies, the isolated peptides of (1) and the
XX nucleic acids are all useful for immunisation (active or passive) and (by
XX inhibiting binding of bacteria to fibronectin) for preventing or treating
XX infection in humans or other animals, particularly by staphylococci or
XX streptococci, e.g. meningitis, otitis media, pneumonia, endocarditis,
XX mastitis in cattle, abortion in horses and many others. Since the
XX antibodies block binding of bacteria, they should be effective against
XX antibiotic-resistant strains, and may replace antibiotic therapy or
XX increase its effectiveness. Sequences AAW65670-90 represent a series of
XX synthetic peptides based on the D3 repeat of S. aureus fibronectin
XX binding protein A. They were synthesised to contain a proline residue at
XX each position throughout the sequence (ie a proline scan)
SQ Sequence 21 AA;

Query March 100.0%; Score 56; DB 2; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.0021;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GHNSVDFEED 10
|||
DB 8 GHNSVDFEED 17

RESULT 12
AAW65686
ID AAW65686 standard; peptide; 21 AA.
XX AAW65686;
AC
XX 16-OCT-1998 (first entry)
DT
XX
DE Fibronectin binding protein-derived peptide #30.
XX
XX
KW microbial surface components recognising adhesive matrix molecule;
KW MSCRAMM; fibronectin; fibronectin-binding protein; antibody; epitope;
KW antibiotic; bacterial infection; antibiotic-resistant strain.
XX
XX Synthetic.
OS Staphylococcus aureus.
XX
XX W09831389-A2.
PN
XX 23-JUL-1998.
PD
XX 21-JAN-1998; 98WO-US001222.
PF
XX 21-JAN-1997; 97US-0036139P.
PR
XX (TEXA) UNIV TEXAS A & M SYSTEM.
PA
XX Hoeoek M, Patti JM, House-Pompeo KL, Speciale P, Joh D;
PI Mcgavin MJ;
XX WPI: 1998-413816/35.
XX
XX Antibody that binds to fibronectin-binding protein, preventing its
XX binding to fibronectin - used to treat or prevent bacterial infection,
XX

PT especially by Staphylococci and Streptococci.
 XX
 PS Example 8; Page 101; 201pp; English.
 CC The invention relates to antibodies that bind to a fibronectin-binding
 CC domain of a fibronectin-binding protein, and inhibit binding of the
 CC protein to fibronectin. Also claimed are: (1) isolated peptides of a
 CC fibronectin-binding protein that do not bind to fibronectin; (2) fusion
 CC protein containing at least one peptide of a fibronectin-binding protein
 CC linked to a second amino acid sequence; (3) nucleic acid encoding the
 CC isolated peptide of (1). Antibodies, the isolated peptides of (1) and the
 CC nucleic acids are all useful for immunisation (active or passive) and (by
 CC inhibiting binding of bacteria to fibronectin) for preventing or treating
 CC infection in humans or other animals, particularly by staphylococci or
 CC streptococci, e.g. meningitis, otitis media, pneumonia, endocarditis,
 CC mastitis in cattle, abortion in horses and many others. Since the
 CC antibodies block binding of bacteria, they should be effective against
 CC antibiotic-resistant strains, and may replace antibiotic therapy or
 CC increase its effectiveness. Sequences AAW65670-90 represent a series of
 CC synthetic peptides based on the D3 repeat of *S. aureus* fibronectin
 CC binding protein A. They were synthesised to contain a proline residue at
 CC each position throughout the sequence (ie a proline scan)
 CC
 XX Sequence 21 AA;
 SQ
 Query Match Score 56; DB 2; Length 21;
 Best Local Similarity 100.0%; Pred. No. 0.0021;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GHNSVDPEED 10
 DB 8 GHNSVDPEED 17
 RESULT 13
 AAW65665
 ID AAW65665 standard; peptide; 21 AA.
 XX
 AC AAW65665;
 XX
 DT 16-OCT-1998 (first entry)
 XX
 DE Fibronectin binding protein-derived peptide #9.
 XX
 OS microbial surface components recognising adhesive matrix molecule;
 KM MSCRAMM; fibronectin; fibronectin-binding protein; antibody; epitope;
 KW antibiotic; bacterial infection; antibiotic-resistant strain.
 XX
 OS Synthetic.
 OS Staphylococcus aureus.
 XX
 PN WO9831389-A2.
 XX
 PD 23-JUL-1998.
 XX
 PF 21-JAN-1996; 98WO-US001222.
 XX
 PR 21-JAN-1997; 97US-0036139P.
 XX
 PA (TEXA) UNIV TEXAS A & M SYSTEM.
 XX
 PI Hoeoek M, Patti JM, House-Pompeo KL, Speziale P, Joh D;
 PT Mcgavin MJ;
 DR MPI; 1998-413816/35.
 XX
 XX Antibody that binds to fibronectin-binding protein, preventing its
 PT binding to fibronectin - used to treat or prevent bacterial infection,
 PT especially by Staphylococci and Streptococci.
 XX
 XX Example 2; Page 92; 201pp; English.
 PS
 CC The invention relates to antibodies that bind to a fibronectin-binding

CC domain of a fibronectin-binding protein, and inhibit binding of the
 CC protein to fibronectin. Also claimed are: (1) isolated peptides of a
 CC fibronectin-binding protein that do not bind to fibronectin; (2) fusion
 CC protein containing at least one peptide of a fibronectin-binding protein
 CC linked to a second amino acid sequence; (3) nucleic acid encoding the
 CC isolated peptide of (1). Antibodies, the isolated peptides of (1) and the
 CC nucleic acids are all useful for immunisation (active or passive) and (by
 CC inhibiting binding of bacteria to fibronectin) for preventing or treating
 CC infection in humans or other animals, particularly by staphylococci or
 CC streptococci, e.g. meningitis, otitis media, pneumonia, endocarditis,
 CC mastitis in cattle, abortion in horses and many others. Since the
 CC antibodies block binding of bacteria, they should be effective against
 CC antibiotic-resistant strains, and may replace antibiotic therapy or
 CC increase its effectiveness. Sequences AAW65659-68 represent synthetic
 CC epitopes from the fibronectin binding domains DU and D1-D4 of the *S.*
 CC aureus fmbA gene
 CC
 XX Sequence 21 AA;
 SQ
 Query Match Score 56; DB 2; Length 21;
 Best Local Similarity 100.0%; Pred. No. 0.0021;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GHNSVDPEED 10
 DB 8 GHNSVDPEED 17
 RESULT 14
 AAW65674
 ID AAW65674 standard; peptide; 21 AA.
 XX
 AC AAW65674;
 XX
 DT 16-OCT-1998 (first entry)
 XX
 DE Fibronectin binding protein-derived peptide #18.
 XX
 OS microbial surface components recognising adhesive matrix molecule;
 KM MSCRAMM; fibronectin; fibronectin-binding protein; antibody; epitope;
 KW antibiotic; bacterial infection; antibiotic-resistant strain.
 XX
 OS Synthetic.
 OS Staphylococcus aureus.
 XX
 PN WO9831389-A2.
 XX
 PD 23-JUL-1998.
 XX
 PF 21-JAN-1996; 98WO-US001222.
 XX
 PR 21-JAN-1997; 97US-0036139P.
 XX
 PA (TEXA) UNIV TEXAS A & M SYSTEM.
 XX
 PI Hoeoek M, Patti JM, House-Pompeo KL, Speziale P, Joh D;
 PT Mcgavin MJ;
 DR MPI; 1998-413816/35.
 XX
 XX Antibody that binds to fibronectin-binding protein, preventing its
 PT binding to fibronectin - used to treat or prevent bacterial infection,
 PT especially by Staphylococci and Streptococci.
 XX
 XX Example 8; Page 100; 201pp; English.
 PS
 CC The invention relates to antibodies that bind to a fibronectin-binding
 CC domain of a fibronectin-binding protein, and inhibit binding of the
 CC protein to fibronectin. Also claimed are: (1) isolated peptides of a
 CC fibronectin-binding protein that do not bind to fibronectin; (2) fusion
 CC protein containing at least one peptide of a fibronectin-binding protein
 CC linked to a second amino acid sequence; (3) nucleic acid encoding the
 CC isolated peptide of (1). Antibodies, the isolated peptides of (1) and the

CC nucleic acids are all useful for immunisation (active or passive) and (by
CC inhibiting binding of bacteria to fibronection) for preventing or treating
CC infection in humans or other animals, particularly by staphylococci or
CC streptococci, e.g. meningitis, otitis media, pneumonia, endocarditis,
CC mastitis in cattle, abortion in horses and many others. Since the
CC antibodies block binding of bacteria, they should be effective against
CC antibiotic-resistant strains, and may replace antibiotic therapy or
CC increase its effectiveness. Sequences AA65670-90 represent a series of
CC synthetic peptides based on the D3 repeat of S. aureus fibronection
CC binding protein A. They were synthesised to contain a proline residue at
CC each position throughout the sequence (ie a proline scan)
XX
SQ Sequence 21 AA;

Query Match 100.0%; Score 56; DB 2; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.0021;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Gy 1 GHNSVDPEED 10
Db 8 GHNSVDPEED 17

RESULT 15

AA21340
ID AAR21340 standard; peptide; 22 AA.

XX AAR21340;

XX 25-MAR-2003 (revised)
XX 15-JUN-1992 (first entry)

XX Fibronection binding protein.

XX FmBP; wound infection reduction; vaccination; mastitis;
XX Staphylococcal infections; D3.

XX Synthetic.

XX MO9202555-A.

XX 20-FEB-1992.

XX 10-AUG-1990; 90SE-00002617.

XX 10-AUG-1990; 90SE-00002617.

XX (ALFA) ALFA LAVAL AGRIC INT AB.

XX Hook M, McGavin M, Raucel G;

XX WPI; 1992-080035/10.

XX New fibronection binding peptide - combines with fusion peptide to form
XX large antigen, used in immunisation, diagnosis and for treating wounds.

XX Claim 1; Page 22; 33pp; English.

XX The sequence comprises amino acids 17-33 of a tandem repeat, designated
CC D3 of the fibronection binding site of Staphylococcus aureus 8325-4 FmBP.
CC The N-terminal DK may be replaced with H or K, and the C-terminal LKP may
CC be replaced by either L, LP, or OH. The peptides were synthesised using
CC standard methods and purified using reverse phase HPLC. The appropriate
CC fractions were dialysed and lyophilised. Peptide sequencing was performed
CC and the peptides digested and chemically modified by dinitropropylation
CC of the amino side chain of lysine. The carboxylic side chains were
CC converted to glycine methyl esters. The phenyl side chains of tyrosine
CC residues were oxidised. Chemically modified peptide D3 was compared to
CC unmodified D3. Lysine and tyrosine modifications only partially
CC diminished its activity whereas modification of aspartic/glutamic
CC residues resulted in complete loss of activity. The peptide can be used
CC for the prevention or reduction of the risk of wound infection. The
CC peptide can be used to create a large antigen for vaccinating ruminants

CC against mastitis caused by Staphylococcal infections. It can also be used
CC to diagnose Staphylococcal infections using ELISA or DNA probes. (Updated
CC on 25-MAR-2003 to correct PA field.)
XX

SQ Sequence 22 AA;

Query Match 100.0%; Score 56; DB 2; Length 22;
Best Local Similarity 100.0%; Pred. No. 0.0022;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Gy 1 GHNSVDPEED 10
Db 9 GHNSVDPEED 18

Search completed: October 25, 2005, 21:29:14
Job time : 70.7126 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 22, 2005, 07:41:53 ; Search time 17.2989 Seconds
(without alignments)
43.153 Million cell updates/sec

Title: US-10-731-238-99
Perfect score: 56
Sequence: 1 GHNSVDFEED 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:
1: /cgn2_6/ptodata/1/1aa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/1aa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/1aa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/1aa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/1aa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/1aa/Backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	56	100.0	10	4	US-09-010-317-99
2	56	100.0	14	4	US-09-010-317-61
3	56	100.0	19	1	US-08-234-622A-1
4	56	100.0	21	4	US-09-010-317-9
5	56	100.0	21	4	US-09-010-317-10
6	56	100.0	21	4	US-09-010-317-14
7	56	100.0	21	4	US-09-010-317-15
8	56	100.0	21	4	US-09-010-317-16
9	56	100.0	21	4	US-09-010-317-17
10	56	100.0	21	4	US-09-010-317-18
11	56	100.0	21	4	US-09-010-317-19
12	56	100.0	21	4	US-09-010-317-30
13	56	100.0	21	4	US-09-010-317-31
14	56	100.0	21	4	US-09-010-317-32
15	56	100.0	21	4	US-09-010-317-33
16	56	100.0	22	4	US-09-010-317-13
17	56	100.0	37	1	US-08-234-622A-4
18	56	100.0	38	1	US-08-294-189-8
19	56	100.0	38	1	US-08-729-767-5
20	56	100.0	114	1	US-08-259-000-3
21	56	100.0	130	2	US-08-459-135A-7
22	56	100.0	130	2	US-08-459-135A-8
23	56	100.0	130	3	US-08-495-559-7
24	56	100.0	130	3	US-08-495-559-8
25	56	100.0	139	3	US-08-856-253-8
26	56	100.0	174	2	US-08-459-135A-10
27	56	100.0	174	2	US-08-459-135A-13

28	56	100.0	174	3	US-08-495-559-10	Sequence 10, Appl
29	56	100.0	174	3	US-08-495-559-13	Sequence 13, Appl
30	56	100.0	176	3	US-08-495-559-6	Sequence 6, Appl
31	56	100.0	178	2	US-08-459-135A-12	Sequence 12, Appl
32	56	100.0	178	3	US-08-495-559-12	Sequence 6, Appl
33	56	100.0	181	2	US-08-459-135A-6	Sequence 6, Appl
34	56	100.0	559	4	US-08-956-171E-5251	Sequence 5251, Ap
35	56	100.0	559	4	US-08-781-986A-5251	Sequence 5251, Ap
36	56	100.0	1027	4	US-08-956-171E-5254	Sequence 5254, Ap
37	56	100.0	1027	4	US-08-781-986A-5254	Sequence 5254, Ap
38	51	91.1	21	4	US-09-010-317-23	Sequence 23, Appl
39	50	89.3	21	4	US-09-010-317-20	Sequence 20, Appl
40	50	89.3	21	4	US-09-010-317-24	Sequence 24, Appl
41	50	89.3	21	4	US-09-010-317-27	Sequence 27, Appl
42	50	89.3	21	4	US-09-010-317-28	Sequence 28, Appl
43	50	89.3	21	4	US-09-010-317-29	Sequence 29, Appl
44	50	89.3	21	4	US-09-010-317-34	Sequence 34, Appl
45	49	87.5	21	4	US-09-010-317-25	Sequence 25, Appl

ALIGNMENTS

RESULT 1
US-09-010-317-99
Sequence 99, Application US/09010317
Patent No. 6685943
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
APPLICANT: Patti, Joseph M.
APPLICANT: House-Pompeo, Karen L.
APPLICANT: Speziale, Pietro
APPLICANT: Joh, Danny
APPLICANT: McGavin, Martin J.
TITLE OF INVENTION: FIBROBLAST BINDING PROTEIN COMPOSITIONS
TITLE OF INVENTION: AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/010.317
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 99:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-09-010-317-99
Query Match 100.0%; Score 56; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.00059;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GHSVDPEED 10
|||||
Db 1 GHSVDPEED 10

RESULT 2

US-09-010-317-61
Sequence 61, Application US/09010317
Patent No. 6685943
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
APPLICANT: Patti, Joseph M.
APPLICANT: House-Pompeo, Karen L.
APPLICANT: Speziale, Pietro
APPLICANT: McGavin, Martin J.
APPLICANT: McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
TITLE OF INVENTION: AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/010.317
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hieber, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TMK.189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 61:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-09-010-317-61

Query Match 100.0%; Score 56; DB 4; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.00065;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GHSVDPEED 10
|||||
Db 4 GHSVDPEED 13

RESULT 3
US-08-234-622A-1
Sequence 1, Application US/08234622A
Patent No. 5440014
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
APPLICANT: Patti, Joseph M.
APPLICANT: House-Pompeo, Karen L.
APPLICANT: Speziale, Pietro
APPLICANT: McGavin, Martin J.
APPLICANT: McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
TITLE OF INVENTION: AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:

NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:

ADDRESSEE: Burns, Doane, Swecker & Mathis
STREET: P.O. Box 1404
CITY: Alexandria
STATE: Virginia
COUNTRY: United States
ZIP: 22313-1404

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/234,622A

FILING DATE: 28-APR-1994

CLASSIFICATION: 530

PRIOR APPLICATION DATA:

APPLICATION NUMBER: SE 9002617-0

FILING DATE: 10-AUG-1990

PRIOR APPLICATION DATA:

APPLICATION NUMBER: WO PCT/SE91/00534

FILING DATE: 09-AUG-1991

ATTORNEY/AGENT INFORMATION:

NAME: Meuth, Donna M

REGISTRATION NUMBER: 36,607

REFERENCE/DOCKET NUMBER: 012885-044

TELECOMMUNICATION INFORMATION:

TELEPHONE: (703) 836-6620

TELEFAX: (703) 836-2021

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 19 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

FEATURE:

NAME/KEY: Peptide

LOCATION: 1

OTHER INFORMATION: /note= "Amino acid 1 is R' wherein

OTHER INFORMATION: R' is hydroxy, K or DK."

FEATURE:

NAME/KEY: Peptide

LOCATION: 19

OTHER INFORMATION: /note= "Amino acid 19 is R2 wherein

OTHER INFORMATION: R2 is hydroxy, L, LP or LPK."

US-08-234-622A-1

Query Match 100.0%; Score 56; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 0.0012;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GHSVDPEED 10
|||||
Db 8 GHSVDPEED 17

RESULT 4
US-09-010-317-9
Sequence 9, Application US/09010317
Patent No. 6685943
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
APPLICANT: Patti, Joseph M.
APPLICANT: House-Pompeo, Karen L.
APPLICANT: Speziale, Pietro
APPLICANT: McGavin, Martin J.
APPLICANT: McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
TITLE OF INVENTION: AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:

ADDRESSER: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TANK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-09-010-317-9

Query Match 100.0%; Score 56; DB 4; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.0013;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GHSVDFFED 10
|||||
Db 8 GHSVDFFED 17

RESULT 5
US-09-010-317-10
Sequence 10, Application US/09010317
Patent No. 6685943
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
APPLICANT: Patti, Joseph M.
APPLICANT: House-Pompeo, Karen L.
APPLICANT: Speziale, Pietro
APPLICANT: John, Danny
APPLICANT: McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSER: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TANK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-09-010-317-10

Query Match 100.0%; Score 56; DB 4; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.0013;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GHSVDFFED 10
|||||
Db 8 GHSVDFFED 17

RESULT 6
US-09-010-317-14
Sequence 14, Application US/09010317
Patent No. 6685943
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
APPLICANT: Patti, Joseph M.
APPLICANT: House-Pompeo, Karen L.
APPLICANT: Speziale, Pietro
APPLICANT: John, Danny
APPLICANT: McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSER: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TANK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-09-010-317-14

Query Match 100.0%; Score 56; DB 4; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.0013;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GHSVDFFED 10
|||||
Db 8 GHSVDFFED 17

RESULT 7
US-09-010-317-15
; Sequence 15, Application US/09010317
; Patent No. 6685943
; GENERAL INFORMATION:
; APPLICANT: Hook, Magnus
; APPLICANT: Patti, Joseph M.
; APPLICANT: House-Pompeo, Karen L.
; APPLICANT: Speziale, Pietro
; APPLICANT: John, Danny
; APPLICANT: McGavin, Martin J.
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
; NUMBER OF SEQUENCES: 105
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: TX
; COUNTRY: USA
; ZIP: 77210-4433
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/010,317
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/036,139
; FILING DATE: 21-JAN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Hibler, David W.
; REGISTRATION NUMBER: 41,071
; REFERENCE/DOCKET NUMBER: TAMK:189
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 512-418-3000
; TELEFAX: 512-474-7577
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
US-09-010-317-15

Query Match 100.0%; Score 56; DB 4; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.0013;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GHSVDFFED 10
|||||
Db 8 GHSVDFFED 17

RESULT 8
US-09-010-317-16
; Sequence 16, Application US/09010317
; Patent No. 6685943
; GENERAL INFORMATION:
; APPLICANT: Hook, Magnus

APPLICANT: Patti, Joseph M.
; APPLICANT: House-Pompeo, Karen L.
; APPLICANT: Speziale, Pietro
; APPLICANT: John, Danny
; APPLICANT: McGavin, Martin J.
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
; NUMBER OF SEQUENCES: 105
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: TX
; COUNTRY: USA
; ZIP: 77210-4433
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/010,317
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/036,139
; FILING DATE: 21-JAN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Hibler, David W.
; REGISTRATION NUMBER: 41,071
; REFERENCE/DOCKET NUMBER: TAMK:189
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 512-418-3000
; TELEFAX: 512-474-7577
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
US-09-010-317-16

Query Match 100.0%; Score 56; DB 4; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.0013;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GHSVDFFED 10
|||||
Db 8 GHSVDFFED 17

RESULT 9
US-09-010-317-17
; Sequence 17, Application US/09010317
; Patent No. 6685943
; GENERAL INFORMATION:
; APPLICANT: Hook, Magnus
; APPLICANT: Patti, Joseph M.
; APPLICANT: House-Pompeo, Karen L.
; APPLICANT: Speziale, Pietro
; APPLICANT: John, Danny
; APPLICANT: McGavin, Martin J.
; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
; NUMBER OF SEQUENCES: 105
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: TX
; COUNTRY: USA
; ZIP: 77210-4433
; COMPUTER READABLE FORM:

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/
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patentin Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/010,317
/ FILING DATE:
/ CLASSIFICATION:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 60/036,139
/ FILING DATE: 21-JAN-1997
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Hibler, David W.
/ REGISTRATION NUMBER: 41,071
/ REFERENCE/DOCKET NUMBER: TANK:189
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 512-418-3000
/ TELEFAX: 512-474-7577
/ INFORMATION FOR SEQ ID NO: 17:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 21 amino acids
/ TYPE: amino acid
/ STRANDEDNESS:
/ TOPOLOGY: linear
/
US-09-010-317-17

Query Match      100.0%; Score 56; DB 4; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.0013;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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      8 GHSVD FEED 17

Db

RESULT 10
US-09-010-317-18
/ Sequence 18, Application US/09010317
/ Patent No. 6685943
/ GENERAL INFORMATION:
/ APPLICANT: Hook, Magnus
/ APPLICANT: Patil, Joseph M.
/ APPLICANT: House-Pompeo, Karen L.
/ APPLICANT: Speziale, Pietro
/ APPLICANT: Joh, Danny
/ APPLICANT: McGavin, Martin J.
/ TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
/ NUMBER OF SEQUENCES: 105
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Arnold, White & Durkee
/ STREET: P.O. Box 4433
/ CITY: Houston
/ STATE: TX
/ COUNTRY: USA
/ ZIP: 77210-4433
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patentin Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/010,317
/ FILING DATE:
/ CLASSIFICATION:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 60/036,139
/ FILING DATE: 21-JAN-1997
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Hibler, David W.
/ REGISTRATION NUMBER: 41,071
/ REFERENCE/DOCKET NUMBER: TANK:189
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 512-418-3000
/ TELEFAX: 512-474-7577
/ INFORMATION FOR SEQ ID NO: 17:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 21 amino acids
/ TYPE: amino acid
/ STRANDEDNESS:
/ TOPOLOGY: linear
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US-09-010-317-19
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/
/ TELEPHONE: 512-418-3000
/ TELEFAX: 512-474-7577
/ INFORMATION FOR SEQ ID NO: 18:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 21 amino acids
/ TYPE: amino acid
/ STRANDEDNESS:
/ TOPOLOGY: linear
/
US-09-010-317-18

Query Match      100.0%; Score 56; DB 4; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.0013;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GHSVD FEED 10
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      8 GHSVD FEED 17

Db

RESULT 11
US-09-010-317-19
/ Sequence 19, Application US/09010317
/ Patent No. 6685943
/ GENERAL INFORMATION:
/ APPLICANT: Hook, Magnus
/ APPLICANT: Patil, Joseph M.
/ APPLICANT: House-Pompeo, Karen L.
/ APPLICANT: Speziale, Pietro
/ APPLICANT: Joh, Danny
/ APPLICANT: McGavin, Martin J.
/ TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
/ NUMBER OF SEQUENCES: 105
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Arnold, White & Durkee
/ STREET: P.O. Box 4433
/ CITY: Houston
/ STATE: TX
/ COUNTRY: USA
/ ZIP: 77210-4433
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patentin Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/010,317
/ FILING DATE:
/ CLASSIFICATION:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 60/036,139
/ FILING DATE: 21-JAN-1997
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Hibler, David W.
/ REGISTRATION NUMBER: 41,071
/ REFERENCE/DOCKET NUMBER: TANK:189
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 512-418-3000
/ TELEFAX: 512-474-7577
/ INFORMATION FOR SEQ ID NO: 19:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 21 amino acids
/ TYPE: amino acid
/ STRANDEDNESS:
/ TOPOLOGY: linear
/
US-09-010-317-19

Query Match      100.0%; Score 56; DB 4; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.0013;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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      8 GHSVD FEED 17
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Db 8 GHNSVDFFED 17

RESULT 12

US-09-010-317-30

Sequence 30, Application US/09010317

Patent No. 6685943

GENERAL INFORMATION:

APPLICANT: Hook, Magnus

APPLICANT: Patti, Joseph M.

APPLICANT: House-Pompeo, Karen L.

APPLICANT: Speziale, Pietro

APPLICANT: Joh, Danny

APPLICANT: McGavin, Martin J.

TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS

TITLE OF INVENTION: AND METHODS OF USE

NUMBER OF SEQUENCES: 105

CORRESPONDENCE ADDRESS:

ADDRESSEE: Arnold, White & Durkee

STREET: P.O. Box 4433

CITY: Houston

STATE: TX

COUNTRY: USA

ZIP: 77210-4433

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/010,317

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 60/036,139

FILING DATE: 21-JAN-1997

ATTORNEY/AGENT INFORMATION:

NAME: Hibler, David W.

REGISTRATION NUMBER: 41,071

REFERENCE/DOCKET NUMBER: TANK:189

TELECOMMUNICATION INFORMATION:

TELEPHONE: 512-418-3000

TELEFAX: 512-474-7577

INFORMATION FOR SEQ ID NO: 30:

SEQUENCE CHARACTERISTICS:

LENGTH: 21 amino acids

TYPE: amino acid

STRANDEDNESS:

TOPOLOGY: linear

US-09-010-317-30

Query Match 100.0%; Score 56; DB 4; Length 21;

Best Local Similarity 100.0%; Pred. No. 0.0013;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GHNSVDFFED 10

Db 8 GHNSVDFFED 17

RESULT 13

US-09-010-317-31

Sequence 31, Application US/09010317

Patent No. 6685943

GENERAL INFORMATION:

APPLICANT: Hook, Magnus

APPLICANT: Patti, Joseph M.

APPLICANT: House-Pompeo, Karen L.

APPLICANT: Speziale, Pietro

APPLICANT: Joh, Danny

APPLICANT: McGavin, Martin J.

TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS

TITLE OF INVENTION: AND METHODS OF USE

NUMBER OF SEQUENCES: 105

CORRESPONDENCE ADDRESS:

ADDRESSEE: Arnold, White & Durkee

STREET: P.O. Box 4433

CITY: Houston

STATE: TX

COUNTRY: USA

ZIP: 77210-4433

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/010,317

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 60/036,139

FILING DATE: 21-JAN-1997

ATTORNEY/AGENT INFORMATION:

NAME: Hibler, David W.

REGISTRATION NUMBER: 41,071

REFERENCE/DOCKET NUMBER: TANK:189

TELECOMMUNICATION INFORMATION:

TELEPHONE: 512-418-3000

TELEFAX: 512-474-7577

INFORMATION FOR SEQ ID NO: 31:

SEQUENCE CHARACTERISTICS:

LENGTH: 21 amino acids

TYPE: amino acid

STRANDEDNESS:

TOPOLOGY: linear

US-09-010-317-31

Query Match 100.0%; Score 56; DB 4; Length 21;

Best Local Similarity 100.0%; Pred. No. 0.0013;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GHNSVDFFED 10

Db 8 GHNSVDFFED 17

RESULT 14

US-09-010-317-32

Sequence 32, Application US/09010317

Patent No. 6685943

GENERAL INFORMATION:

APPLICANT: Hook, Magnus

APPLICANT: Patti, Joseph M.

APPLICANT: House-Pompeo, Karen L.

APPLICANT: Speziale, Pietro

APPLICANT: Joh, Danny

APPLICANT: McGavin, Martin J.

TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS

TITLE OF INVENTION: AND METHODS OF USE

NUMBER OF SEQUENCES: 105

CORRESPONDENCE ADDRESS:

ADDRESSEE: Arnold, White & Durkee

STREET: P.O. Box 4433

CITY: Houston

STATE: TX

COUNTRY: USA

ZIP: 77210-4433

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/010,317

FILING DATE:

CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAMK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 32:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-09-010-317-32

Query Match 100.0%; Score 56; DB 4; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.0013;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GHSVDFFED 10
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DB 8 GHSVDFFED 17

RESULT 15
US-09-010-317-33
Sequence 33, Application US/09010317
Patent No. 6685943
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
APPLICANT: Patti, Joseph M.
APPLICANT: House-Pompeo, Karen L.
APPLICANT: Speziale, Pietro
APPLICANT: Job, Danny
APPLICANT: McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
TITLE OF INVENTION: AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAMK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: amino acid
STRANDEDNESS:

TOPOLOGY: linear
US-09-010-317-33

Query Match 100.0%; Score 56; DB 4; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.0013;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GHSVDFFED 10
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DB 8 GHSVDFFED 17

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Job time : 17.2989 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 22, 2005, 12:39:57 (Search time 56.1494 Seconds
(without alignments)
74.354 Million cell updates/sec

Title: US-10-731-238-99

Perfect score: 56
Sequence: 1 GHNSVDFEED 10

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 1862951 seqs, 417491010 residues

Total number of hits satisfying chosen parameters: 1862951

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA.*

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10: /cgn2_6/ptodata/2/pubppa/US09C_PUBCOMB.pep.*
11: /cgn2_6/ptodata/2/pubppa/US09_NEW_PUB.pep.*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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2	56	100.0	14	US-10-731-238-61	Sequence 61, Appl
3	56	100.0	21	US-10-731-238-9	Sequence 9, Appl
4	56	100.0	21	US-10-731-238-10	Sequence 10, Appl
5	56	100.0	21	US-10-731-238-14	Sequence 14, Appl
6	56	100.0	21	US-10-731-238-15	Sequence 15, Appl
7	56	100.0	21	US-10-731-238-16	Sequence 16, Appl
8	56	100.0	21	US-10-731-238-17	Sequence 17, Appl
9	56	100.0	21	US-10-731-238-18	Sequence 18, Appl
10	56	100.0	21	US-10-731-238-19	Sequence 19, Appl
11	56	100.0	21	US-10-731-238-30	Sequence 30, Appl

12	56	100.0	21	18	US-10-731-238-31	Sequence 31, Appl
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14	56 <td>100.0</td> <td>21</td> <td>18<td>US-10-731-238-33</td><td>Sequence 33, Appl</td></td>	100.0	21	18 <td>US-10-731-238-33</td> <td>Sequence 33, Appl</td>	US-10-731-238-33	Sequence 33, Appl
15	56 <td>100.0</td> <td>22</td> <td>18<td>US-10-731-238-13</td><td>Sequence 13, Appl</td></td>	100.0	22	18 <td>US-10-731-238-13</td> <td>Sequence 13, Appl</td>	US-10-731-238-13	Sequence 13, Appl
16	56 <td>100.0</td> <td>37</td> <td>20<td>US-11-066-697-1134</td><td>Sequence 1134, Ap</td></td>	100.0	37	20 <td>US-11-066-697-1134</td> <td>Sequence 1134, Ap</td>	US-11-066-697-1134	Sequence 1134, Ap
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18	56 <td>100.0</td> <td>388</td> <td>8<td>US-08-901-062-1</td><td>Sequence 1, Appl</td></td>	100.0	388	8 <td>US-08-901-062-1</td> <td>Sequence 1, Appl</td>	US-08-901-062-1	Sequence 1, Appl
19	56 <td>100.0</td> <td>559</td> <td>8<td>US-08-781-986A-5251</td><td>Sequence 5251, Ap</td></td>	100.0	559	8 <td>US-08-781-986A-5251</td> <td>Sequence 5251, Ap</td>	US-08-781-986A-5251	Sequence 5251, Ap
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43	45	80.4	10	18 <td>US-10-731-238-98</td> <td>Sequence 98, Appl</td>	US-10-731-238-98	Sequence 98, Appl
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ALIGNMENTS

RESULT 1
US-10-731-238-99
Sequence 99, Application US/10731238
Publication No. US20050123552A1
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
Patti, Joseph M.
House-Pompeo, Karen L.
Speziale, Pietro
Joh, Danny
McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSER: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/731,238
FILING DATE: 10-Dec-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE: 21-Jan-1998
APPLICATION NUMBER: US 60/036,139

```

;
; FILING DATE: 21-JAN-1997
; ATTORNEY/AGENT INFORMATION:
;   NAME: Hibler, David W.
;   REGISTRATION NUMBER: 41,071
;   REFERENCE/DOCKET NUMBER: TAMK:189
; TELECOMMUNICATION INFORMATION:
;   TELEPHONE: 512-418-3000
;   TELEFAX: 512-474-7577
; INFORMATION FOR SEQ ID NO: 99:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH: 10 amino acids
;     TYPE: amino acid
;     STRANDEDNESS: <Unknown>
;   TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 99:
US-10-731-238-99

Query Match      100.0%; Score 56; DB 18; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0022;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 GHSVDFEED 10
        |||||
        1 GHSVDFEED 10

Db
1 GHSVDFEED 10

RESULT 2
US-10-731-238-61
; Sequence 61, Application US/10731238
; Publication No. US20050123552A1
; GENERAL INFORMATION:
;   APPLICANT: Hook, Magnus
;               Patti, Joseph M.
;               House-Pompeo, Karen L.
;               Speziale, Pietro
;               Joh, Danny
;               McGavin, Martin J.
; TITLE OF INVENTION: FIBROECTIN BINDING PROTEIN COMPOSITIONS
; AND METHODS OF USE
; NUMBER OF SEQUENCES: 105
; CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Arnold, White & Durkee
;   STREET: P.O. Box 4433
;   CITY: Houston
;   STATE: TX
;   COUNTRY: USA
;   ZIP: 77210-4433
; COMPUTER READABLE FORM:
;   MEDIUM TYPE: floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/10/731,238
;   FILING DATE: 10-Dec-2003
;   CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US/09/010,317
;   FILING DATE: 21-Jan-1998
;   APPLICATION NUMBER: US 60/036,139
;   FILING DATE: 21-JAN-1997
; ATTORNEY/AGENT INFORMATION:
;   NAME: Hibler, David W.
;   REGISTRATION NUMBER: 41,071
;   REFERENCE/DOCKET NUMBER: TAMK:189
; TELECOMMUNICATION INFORMATION:
;   TELEPHONE: 512-418-3000
;   TELEFAX: 512-474-7577
; INFORMATION FOR SEQ ID NO: 61:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH: 14 amino acids
;     TYPE: amino acid
;     STRANDEDNESS: <Unknown>
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```

;
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 61:
US-10-731-238-61

Query Match      100.0%; Score 56; DB 18; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.0031;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 GHSVDFEED 10
        |||||
        4 GHSVDFEED 13

Db
4 GHSVDFEED 13

RESULT 3
US-10-731-238-9
; Sequence 9, Application US/10731238
; Publication No. US20050123552A1
; GENERAL INFORMATION:
;   APPLICANT: Hook, Magnus
;               Patti, Joseph M.
;               House-Pompeo, Karen L.
;               Speziale, Pietro
;               Joh, Danny
;               McGavin, Martin J.
; TITLE OF INVENTION: FIBROECTIN BINDING PROTEIN COMPOSITIONS
; AND METHODS OF USE
; NUMBER OF SEQUENCES: 105
; CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Arnold, White & Durkee
;   STREET: P.O. Box 4433
;   CITY: Houston
;   STATE: TX
;   COUNTRY: USA
;   ZIP: 77210-4433
; COMPUTER READABLE FORM:
;   MEDIUM TYPE: floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/10/731,238
;   FILING DATE: 10-Dec-2003
;   CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US/09/010,317
;   FILING DATE: 21-Jan-1998
;   APPLICATION NUMBER: US 60/036,139
;   FILING DATE: 21-JAN-1997
; ATTORNEY/AGENT INFORMATION:
;   NAME: Hibler, David W.
;   REGISTRATION NUMBER: 41,071
;   REFERENCE/DOCKET NUMBER: TAMK:189
; TELECOMMUNICATION INFORMATION:
;   TELEPHONE: 512-418-3000
;   TELEFAX: 512-474-7577
; INFORMATION FOR SEQ ID NO: 9:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH: 21 amino acids
;     TYPE: amino acid
;     STRANDEDNESS: <Unknown>
;   TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 9:
US-10-731-238-9

Query Match      100.0%; Score 56; DB 18; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.0048;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 GHSVDFEED 10
        |||||
        8 GHSVDFEED 17

Db
8 GHSVDFEED 17
```

RESULT 4
US-10-731-238-10
Sequence 10, Application US/10731238
Publication No. US20050123552A1
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
Patti, Joseph M.
House-Pompeo, Karen L.
Speziale, Pietro
Joh, Danny
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/731,238
FILING DATE: 10-Dec-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE: 21-Jan-1998
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-Jan-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAMK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 10:
US-10-731-238-10
Query Match 100.0%; Score 56; DB 18; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.0048;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GHNSVDFEED 10
Db 8 GHNSVDFEED 17
RESULT 5
US-10-731-238-14
Sequence 14, Application US/10731238
Publication No. US20050123552A1
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
Patti, Joseph M.
House-Pompeo, Karen L.
Speziale, Pietro
Joh, Danny
McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
AND METHODS OF USE

NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/731,238
FILING DATE: 10-Dec-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE: 21-Jan-1998
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-Jan-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAMK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 14:
US-10-731-238-14
Query Match 100.0%; Score 56; DB 18; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.0048;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GHNSVDFEED 10
Db 8 GHNSVDFEED 17
RESULT 6
US-10-731-238-15
Sequence 15, Application US/10731238
Publication No. US20050123552A1
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
Patti, Joseph M.
House-Pompeo, Karen L.
Speziale, Pietro
Joh, Danny
McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/731,238
FILING DATE: 10-Dec-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE: 21-Jan-1998
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-Jan-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibiier, David W.
REGISTRATION NUMBER: 41,071
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 15:
US-10-731-238-15

Query Match 100.0%; Score 56; DB 18; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.0048;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GHSVDPEED 10
|||
Db 8 GHSVDPEED 17

RESULT 7
US-10-731-238-16
Sequence 16, Application US/10731238
Publication No. US20050123552A1
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
Patli, Joseph M.
House-Pompeo, Karen L.
Speziale, Pietro
Joh, Danny
McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/731,238
FILING DATE: 10-Dec-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE: 21-Jan-1998
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-Jan-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibiier, David W.
REGISTRATION NUMBER: 41,071
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 17:
US-10-731-238-17

Query Match 100.0%; Score 56; DB 18; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.0048;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GHSVDPEED 10
|||
Db 8 GHSVDPEED 17

TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 16:
US-10-731-238-16

Query Match 100.0%; Score 56; DB 18; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.0048;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GHSVDPEED 10
|||
Db 8 GHSVDPEED 17

RESULT 8
US-10-731-238-17
Sequence 17, Application US/10731238
Publication No. US20050123552A1
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
Patli, Joseph M.
House-Pompeo, Karen L.
Speziale, Pietro
Joh, Danny
McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/731,238
FILING DATE: 10-Dec-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE: 21-Jan-1998
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-Jan-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibiier, David W.
REGISTRATION NUMBER: 41,071
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 17:
US-10-731-238-17

Query Match 100.0%; Score 56; DB 18; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.0048;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GHSVDPEED 10
|||
Db 8 GHSVDPEED 17

Best Local Similarity 100.0%; Pred. No. 0.0048;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GHNSVDFFED 10
|||||
DB 8 GHNSVDFFED 17

RESULT 9

US-10-731-238-18

; Sequence 18, Application US/10731238

; Publication No. US20050123552A1

; GENERAL INFORMATION:

; APPLICANT: Hook, Magnus

; Patti, Joseph M.

; House-Pompeo, Karen L.

; Speziale, Pietro

; John, Danny

; McGavin, Martin J.

; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS

; AND METHODS OF USE

; NUMBER OF SEQUENCES: 105

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Arnold, White & Durkee

; STREET: P.O. Box 4433

; CITY: Houston

; STATE: TX

; COUNTRY: USA

; ZIP: 77210-4433

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/10/731,238

; FILING DATE: 10-Dec-2003

; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US/09/010,317

; FILING DATE: 21-Jan-1998

; APPLICATION NUMBER: US 60/036,139

; FILING DATE: 21-Jan-1997

; ATTORNEY/AGENT INFORMATION:

; NAME: Hibler, David W.

; REGISTRATION NUMBER: 41,071

; REFERENCE/DOCKET NUMBER: TAMK:189

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 512-418-3000

; TELEFAX: 512-474-7577

; INFORMATION FOR SEQ ID NO: 18:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 21 amino acids

; TYPE: amino acid

; STRANDEDNESS: <Unknown>

; TOPOLOGY: linear

; SEQUENCE DESCRIPTION: SEQ ID NO: 18:

US-10-731-238-18

Query Match 100.0%; Score 56; DB 18; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.0048;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GHNSVDFFED 10
|||||
DB 8 GHNSVDFFED 17

RESULT 10

US-10-731-238-19

; Sequence 19, Application US/10731238

; Publication No. US20050123552A1

; GENERAL INFORMATION:

; APPLICANT: Hook, Magnus

; Patti, Joseph M.

; House-Pompeo, Karen L.

; Speziale, Pietro

; John, Danny

; McGavin, Martin J.

; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS

; AND METHODS OF USE

; NUMBER OF SEQUENCES: 105

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Arnold, White & Durkee

; STREET: P.O. Box 4433

; CITY: Houston

; STATE: TX

; COUNTRY: USA

; ZIP: 77210-4433

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/10/731,238

; FILING DATE: 10-Dec-2003

; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US/09/010,317

; FILING DATE: 21-Jan-1998

; APPLICATION NUMBER: US 60/036,139

; FILING DATE: 21-Jan-1997

; ATTORNEY/AGENT INFORMATION:

; NAME: Hibler, David W.

; REGISTRATION NUMBER: 41,071

; REFERENCE/DOCKET NUMBER: TAMK:189

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 512-418-3000

; TELEFAX: 512-474-7577

; INFORMATION FOR SEQ ID NO: 19:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 21 amino acids

; TYPE: amino acid

; STRANDEDNESS: <Unknown>

; TOPOLOGY: linear

; SEQUENCE DESCRIPTION: SEQ ID NO: 19:

US-10-731-238-19

Query Match 100.0%; Score 56; DB 18; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.0048;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GHNSVDFFED 10
|||||
DB 8 GHNSVDFFED 17

RESULT 11

US-10-731-238-30

; Sequence 30, Application US/10731238

; Publication No. US20050123552A1

; GENERAL INFORMATION:

; APPLICANT: Hook, Magnus

; Patti, Joseph M.

; House-Pompeo, Karen L.

; Speziale, Pietro

; John, Danny

; McGavin, Martin J.

; TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS

; AND METHODS OF USE

; NUMBER OF SEQUENCES: 105

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Arnold, White & Durkee

; STREET: P.O. Box 4433

; CITY: Houston

STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/731,238
FILING DATE: 10-Dec-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE: 21-Jan-1998
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-Jan-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAMK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 30:
US-10-731-238-30

Query Match 100.0%; Score 56; DB 18; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.0048;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 |||||
8 GHSVDPEED 17

RESULT 12
US-10-731-238-31
Sequence 31, Application US/10731238
Publication No. US20050123552A1
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
Patil, Joseph M.
House-Pompeo, Karen L.
Speziale, Pietro
Joh, Danny
McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/731,238
FILING DATE: 10-Dec-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/010,317
FILING DATE: 21-Jan-1998
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-Jan-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAMK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 31:
US-10-731-238-31

Query Match 100.0%; Score 56; DB 18; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.0048;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 |||||
8 GHSVDPEED 17

RESULT 13
US-10-731-238-32
Sequence 32, Application US/10731238
Publication No. US20050123552A1
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
Patil, Joseph M.
House-Pompeo, Karen L.
Speziale, Pietro
Joh, Danny
McGavin, Martin J.
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
AND METHODS OF USE
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/731,238
FILING DATE: 10-Dec-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE: 21-Jan-1998
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-Jan-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAMK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 32:
SEQUENCE CHARACTERISTICS:

LENGTH: 21 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 32:
US-10-731-238-32

Query Match 100.0%; Score 56; DB 18; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.0048;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GHSVDFFED 10
|||||
DB 8 GHSVDFFED 17

RESULT 14
US-10-731-238-33
Sequence 33, Application US/10731238
Publication No. US20050123552A1
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
Patti, Joseph M.
House-Pompeo, Karen L.
Speziale, Pietro
Joh, Danny
McGavin, Martin J.

TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
AND METHODS OF USE

NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX

COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/731,238
FILING DATE: 10-Dec-2003
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE: 21-Jan-1998
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-Jan-1997

ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAMK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577

INFORMATION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear

SEQUENCE DESCRIPTION: SEQ ID NO: 33:
US-10-731-238-33

Query Match 100.0%; Score 56; DB 18; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.0048;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GHSVDFFED 10
|||||

DB 8 GHSVDFFED 17

RESULT 15
US-10-731-238-13
Sequence 13, Application US/10731238
Publication No. US20050123552A1
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
Patti, Joseph M.
House-Pompeo, Karen L.
Speziale, Pietro
Joh, Danny
McGavin, Martin J.

TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
AND METHODS OF USE

NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX

COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/731,238
FILING DATE: 10-Dec-2003
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/010,317
FILING DATE: 21-Jan-1998
APPLICATION NUMBER: US 60/036,139
FILING DATE: 21-Jan-1997

ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAMK:189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577

INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 22 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear

SEQUENCE DESCRIPTION: SEQ ID NO: 13:
US-10-731-238-13

Query Match 100.0%; Score 56; DB 18; Length 22;
Best Local Similarity 100.0%; Pred. No. 0.0051;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GHSVDFFED 10
|||||
DB 8 GHSVDFFED 17

Search completed: October 22, 2005, 12:56:29
Job time : 56.1494 secs

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GenCore version 5.1.6
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OM protein - protein search, using SW model

Run on: October 22, 2005, 08:04:46 ; Search time 11.6092 Seconds
(without alignments)
82.880 Million cell updates/sec

Title: US-10-731-238-99
Perfect score: 56
Sequence: 1 GHSNVDPEED 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapexc 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	56	100.0	940	2	S19702 fibronectin-binding
2	56	100.0	961	2	G90053 hypothetical prote
3	56	100.0	1018	2	A32192 fibronectin-binding
4	56	100.0	1038	2	H90053 hypothetical prote
5	39	69.6	443	1	Q08YPT hypothetical prote
6	38	67.9	747	2	D75436 ATP-dependent Clp
7	37	66.1	201	2	D83852 hypothetical prote
8	37	66.1	331	2	T51419 CARBONIC ANHYDRASE
9	37	66.1	336	1	S28412 carbonate dehydrat
10	37	66.1	364	2	A31591 B. subtilis PBSX P
11	37	66.1	949	2	D90803 Aldh-I adhesin-lik
12	37	66.1	1005	2	H85611 probable adhesin z
13	37	66.1	1091	2	G64964 hypothetical prote
14	37	66.1	1227	2	B96673 hypothetical prote
15	36	64.3	31	2	PC4276 dentin phosphophor
16	36	64.3	241	2	T27917 hypothetical prote
17	36	64.3	399	1	S41787 xylase repressor x
18	36	64.3	471	2	F64213 hypothetical prote
19	35	62.5	287	2	S57770 xyloglucan endo-1,
20	35	62.5	289	2	S49812 xyloglucan endo-1,
21	35	62.5	341	2	G89986 hypothetical prote
22	35	62.5	347	1	HPMS haptoglobin precur
23	35	62.5	385	2	G89956 metalloproteinase
24	35	62.5	478	2	JN0892 metalloproteinase
25	35	62.5	479	2	JN0891 metalloproteinase
26	35	62.5	481	2	A33712 metalloproteinase
27	35	62.5	687	2	T02459 probable beta-amy1
28	35	62.5	743	2	T26102 hypothetical prote
29	35	62.5	743	2	T26102

30	35	62.5	871	2	T32275 hypothetical prote
31	35	62.5	916	2	B84473 copii-like retroel
32	35	62.5	928	1	VGBEMC glycoprotein B pre
33	35	62.5	1871	2	D96796 probable heat shoc
34	35	62.5	3796	2	T18514 lysosomal traffick
35	35	61.6	626	2	A41284 transfection initia
36	34	60.7	722	2	A37417 thrombin inhibitor
37	34	60.7	118	2	AB1186 negative regulatio
38	34	60.7	118	2	A11543 negative regulatio
39	34	60.7	192	2	S60226 cyclokine IGF - mo
40	34	60.7	218	2	H83512 probable short-cha
41	34	60.7	249	2	G82808 toluene tolerance
42	34	60.7	324	2	T22580 hypothetical prote
43	34	60.7	326	1	B64547 nitrogen fixation
44	34	60.7	326	2	B71960 nitrogen fixation
45	34	60.7	387	2	E90533

ALIGNMENTS

RESULT 1

S19702
fibronectin-binding protein B - Staphylococcus aureus
C:Species: Staphylococcus aureus
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
C:Accession: S19702
R:Jensen, K.; Signaes, C.; Mueller, H.P.; Lindberg, M.
Eur. J. Biochem. 202, 1041-1048, 1991
A:Title: Two different genes encode fibronectin binding proteins in Staphylococcus aureu
A:Reference number: S19702; MUID:92111475; PMID:1837266
A:Accession: S19702
A:Status: Preliminary
A:Molecule type: DNA
A:Residues: 1-940 <JOB>
A:Cross-references: UNIPROT:Q53682; EMBL:X62992; NID:g49040; PIDN:CAA44726.1; PID:g58156
C:Keywords: fibronectin binding

Query Match 100.0%; Score 56; DB 2; Length 940;
Best Local Similarity 100.0%; Pred. No. 0.02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GHSNVDPEED 10
|||||
DB 780 GHSNVDPEED 789

RESULT 2
G90053
hypothetical protein fnb [imported] - Staphylococcus aureus (strain N315)

C:Species: Staphylococcus aureus
C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C:Accession: G90053
R:Kurita, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguc
ma, A.; Mizutani-Uji, Y.; Kobayashi, N.; Swano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.;
C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
A:Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.
A:Reference number: A89758; MUID:21311952; PMID:11418146
A:Accession: G90053
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-961 <KUR>
A:Cross-references: UNIPROT:Q99RD3; GB:BA000018; PID:g13702452; PIDN:BA843593.1; GSPDB:G
A:Experimental source: strain N315
C:Genetics:
A:Gene: fnb3

Query Match 100.0%; Score 56; DB 2; Length 961;
Best Local Similarity 100.0%; Pred. No. 0.02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GHSNVDPEED 10

Db |||||
791 GHNSVDFEED 800

RESULT 3

A32192
fibronectin-binding protein - Staphylococcus aureus
C/Species: Staphylococcus aureus
C/Date: 31-Jul-1989 #sequence_revision 31-Jul-1989 #text_change 16-Feb-1997
C/Accession: A32192
R/Stnaes, C.; Raucel, G.; Joensen, K.; Lindgren, P.E.; Anantharamiah, G.M.; Hoeoek, M.
Proc. Natl. Acad. Sci. U.S.A. 86, 699-703, 1989
A/Title: Nucleotide sequence of the gene for a fibronectin-binding protein from Staphylo
A/Reference number: A32192; MUID:89089898; PMID:2521391
A/Accession: A32192
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-1018 <SIG>
A/Cross-references: GB:J04151
C/Keywords: fibronectin binding

Query Match 100.0%; Score 56; DB 2; Length 1018;
Best Local Similarity 100.0%; Pred. No. 0.022;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GHNSVDFEED 10
Db 844 GHNSVDFEED 853

RESULT 4

H90053
hypothetical protein fnb [imported] - Staphylococcus aureus (strain N315)
C/Species: Staphylococcus aureus
C/Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C/Accession: H90053
R/Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Ogu
ma, A.; Mizutani-Hi, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.;
C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hirata, K.;
Lancet 357, 1225-1240, 2001
A/Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.
A/Reference number: A89758; MUID:21311952; PMID:11418146
A/Accession: H90053
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-1038 <KUR>
A/Cross-references: UNIPROT:Q9PRD2; GB:BA000018; PID:g13702453; PIDN:BA843594.1; GSPDB:C
A/Experimental source: strain N315
C/Genetics:
A/Gene: fnb

Query Match 100.0%; Score 56; DB 2; Length 1038;
Best Local Similarity 100.0%; Pred. No. 0.022;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GHNSVDFEED 10
Db 840 GHNSVDFEED 849

RESULT 5

COBYP1
hypothetical protein YER152c - Yeast (Saccharomyces cerevisiae)
C/Species: Saccharomyces cerevisiae
C/Date: 30-Jun-1991 #sequence_revision 12-May-1995 #text_change 09-Jul-2004
C/Accession: S50655; C36328; S05725; S12290
R/Dietrich, F.S.
Submitted to the EMBL Data Library, December 1994
A/Description: The sequence of S. cerevisiae cosmid 8229, 9115, 9132, 9981, and lambda
A/Accession: S50655
A/Reference number: S50430
A/Molecule type: DNA
A/Residues: 1-443 <DIE>

A/Cross-references: UNIPROT:P10356; EMBL:U18917; NID:9603377; PIDN:AA864679.1; PID:96033;
R/Omen, J.D.; Burke, K.A.; McEwen, J.E.
Mol. Cell. Biol. 10, 3027-3035, 1990
A/Title: Divergent overlapping transcripts at the PET122 locus in Saccharomyces cerevisiae
A/Reference number: A36328; MUID:90258894; PMID:2160592
A/Accession: C36328
A/Molecule type: DNA

A/Residues: 1-230 <OHM>
A/Cross-references: GB:X07558; NID:g4127; PIDN:CA30440.1; PID:g4129
R/Omen, J.D.; Kloeckner-Gruissem, B.; McEwen, J.E.
Nucleic Acids Res. 16, 10783-10802, 1988
A/Title: Molecular cloning and nucleotide sequence of the nuclear PET122 gene required for
A/Reference number: S05724; MUID:89083497; PMID:2849752
A/Accession: S05725
A/Molecule type: DNA
A/Residues: 1-56, 'CGA', 60-61, 63-66, 'V', 68-72, 'T', 74-76, 'R', 78-86, 'V', 88-122, 'SDQQ', 128-1;
A/Cross-references: EMBL:X07558
A/Note: this sequence has been revised in reference A36328
C/Genetics:
A/Gene: MIP5:YER152C
A/Cross-references: SGD:S0000954
A/Map position: 5R
C/Superfamily: yeast hypothetical protein YER152c

Query Match 69.6%; Score 39; DB 1; Length 443;
Best Local Similarity 75.0%; Pred. No. 15;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GHNSVDFE 8
Db 145 GHNSIDFE 152

RESULT 6

D75436
ATP-dependent Clp protease, ATP-binding subunit ClpC - Deinococcus radiodurans (strain
C/Species: Deinococcus radiodurans
C/Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C/Accession: D75436
R/White, O.; Bisen, J.A.; Heideberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;
M.; Shen, M.; Vamathavan, J.J.; Lam, P.; McDonald, L.; Uterback, T.; Zalewski, C.; Ma
S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999
A/Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
A/Reference number: A75250; MUID:20036896; PMID:10567266
A/Accession: D75436
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-747 <WHI>
A/Cross-references: UNIPROT:Q9RVE2; GB:AE001961; GB:AE000513; NID:g6458843; PIDN:AAF1068
A/Experimental source: strain R1
C/Genetics:
A/Gene: DR1117
A/Map position: 1
C/Superfamily: endopeptidase Clp ATP-binding chain
C/Keywords: ATP; molecular chaperone; nucleotide binding; P-loop
F:203-210/Region: nucleotide-binding motif A (P-loop)
F:269-274/Region: nucleotide-binding motif B
F:486-493/Region: nucleotide-binding motif A (P-loop)
F:554-559/Region: nucleotide-binding motif B
F:209/Binding site: ATP (Lys) #status predicted
F:492/Binding site: ATP (Lys) #status predicted

Query Match 67.9%; Score 38; DB 2; Length 747;
Best Local Similarity 66.7%; Pred. No. 42;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GHNSVDFE 9
Db 728 GHNSIDFEQ 736

RESULT 7

D83852
 hypoheterical protein BH1620 [imported] - *Bacillus halodurans* (strain C-125)
 C/Species: *Bacillus halodurans*
 C/Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004
 C/Accession: D83852
 R/Takami, H.; Nakasono, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, F.; Hira
 Nucleic Acids Res. 28, 4317-4331, 2000
 A/Title: Complete genome sequence of the alkaliphilic bacterium *Bacillus halodurans* and
 A/Reference number: AB3650; MUID:20512582; PMID:11058132
 A/Accession: D83852
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-201 <STO>
 A/Cross-references: UNIPROT:Q9KCP1; GB:AP001512; GB:BA000004; NID:G10174030; PIDN:BA8053
 A/Experimental source: strain C-125
 C/Genetics:
 A/Gene: BH1620

Query Match 66.1%; Score 37; DB 2; Length 201;
 Best Local Similarity 60.0%; Pred. No. 15;
 Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 GHSNVDFFED 10
 |||||
 DB 79 GHQSDFFED 88

RESULT 8
 T51419
 CARBONIC ANHYDRASE 2 - *Arabidopsis thaliana*
 N/Alternate names: protein T9L3 40
 C/Species: *Arabidopsis thaliana* (mouse-ear cress)
 C/Date: 18-Aug-2000 #sequence_revision 18-Aug-2000 #text_change 17-Nov-2000
 C/Accession: T51419
 R/Sato, S.; Nakamura, Y.; Kaneko, T.; Kato, T.; Asamizu, E.; Kotani, H.; Tabata, S.; Men
 submitted to the Protein Sequence Database, August 2000
 A/Reference number: Z25394
 A/Accession: T51419
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-331 <SAT>
 A/Cross-references: EMBL:AL391149
 A/Experimental source: cultivar Columbia; BAC clone T9L3
 C/Genetics:
 A/Map position: 5
 A/Introns: 29/3; 69/1; 90/2; 140/2; 156/3; 195/3; 213/3; 242/2; 277/3
 A/Note: T9L3_40
 C/Superfamily: Escherichia coli carbonate dehydratase

Query Match 66.1%; Score 37; DB 2; Length 331;
 Best Local Similarity 70.0%; Pred. No. 26;
 Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 GHSNVDFFED 10
 |||||
 DB 238 GNSSTDFED 247

RESULT 9
 S28412
 carbonate dehydratase (EC 4.2.1.1) precursor, chloroplast - *Arabidopsis thaliana*
 N/Alternate names: carbonic anhydrase
 C/Species: *Arabidopsis thaliana* (mouse-ear cress)
 C/Date: 21-Nov-1998 #sequence_revision 21-Nov-1998 #text_change 09-Jul-2004
 C/Accession: S28412; S21379
 R/Raines, C.A.; Horneill, P.R.; Holder, C.; Lloyd, J.C.
 Plant Mol. Biol. 20, 1143-1148, 1992
 A/Title: *Arabidopsis thaliana* carbonic anhydrase: cDNA sequence and effect of CO(2) on P
 A/Reference number: S28412; MUID:9309264; PMID:1463847
 A/Accession: S28412
 A/Status: preliminary
 A/Molecule type: mRNA
 A/Residues: 1-336 <RAI>
 A/Cross-references: UNIPROT:P27140; EMBL:X65541; NID:G14342; PIDN:CAA46508.1; PID:G14343

C/Genetics:
 A/Genome: nuclear
 C/Complex: homohexamer
 C/Function:
 A/Description: catalyzes the reversible hydration of carbon dioxide
 C/Species: *Escherichia coli* carbonate dehydratase
 C/KeyWords: carbon-oxygen lyase, chloroplast, homohexamer, hydro-lyase, zinc
 F.1-78/Domains: transit peptide (chloroplast) #status predicted <TNP>
 F.79-336/Product: carbonate dehydratase, long form #status predicted <MATL>
 F.117-336/Product: carbonate dehydratase, short form #status predicted <MATL>

Query Match 66.1%; Score 37; DB 1; Length 336;
 Best Local Similarity 70.0%; Pred. No. 27;
 Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 GHSNVDFFED 10
 |||||
 DB 243 GNSSTDFED 252

RESULT 10
 AE1591
 B. subtilis PBX phage protein homolog lin1270 [imported] - *Listeria innocua* (strain CI
 C/Species: *Listeria innocua*
 C/Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
 C/Accession: AE1591
 R/Glaeser, P.; Frangoul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloeker
 ; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurgey, O.; Entian, K.D.; Fehli, H.
 D.; Jones, L.M.; Karst, U.
 Science 294, 849-852, 2001
 A/Authors: Krete, U.; Kunz, M.; Kunst, F.; Kurapat, G.; Madueno, E.; Maitournam, A.; Ma
 ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehlend,
 A/Title: Comparative genomics of *Listeria* species.
 A/Reference number: AB1077; MUID:21537279; PMID:11679669
 A/Accession: AE1591
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-364 <GLA>
 A/Cross-references: UNIPROT:Q92CB9; GB:AL592022; PIDN:CAC96501.1; PID:G16413744; GSPDB:G
 A/Experimental source: strain Clijp11262
 C/Genetics:
 A/Gene: lin1270

Query Match 66.1%; Score 37; DB 2; Length 364;
 Best Local Similarity 75.0%; Pred. No. 29;
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 HNSVDFEE 9
 |||||
 DB 214 HNSVDFOK 221

RESULT 11
 D90803
 AIDA-1 adhesin-like protein [imported] - *Escherichia coli* (strain O157:H7, substrain RIM
 C/Species: *Escherichia coli*
 C/Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 09-Jul-2004
 C/Accession: D90803
 R/Hayashi, T.; Makino, K.; Onishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G
 gatawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
 DNA Res. 8, 11-22, 2001
 A/Title: Complete genome sequence of enterohemorrhagic *Escherichia coli* O157:H7 and gene
 A/Reference number: A99629; MUID:21156231; PMID:11258796
 A/Accession: D90803
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-949 <RAY>
 A/Cross-references: UNIPROT:Q8X914; GB:BA000007; PIDN:BA834819.1; PID:G13360856; GSPDB:G
 A/Experimental source: strain O157:H7, substrain RIMD 0509952
 C/Genetics:
 A/Gene: ECa1396

Query Match 66.1%; Score 37; DB 2; Length 949;

Best Local Similarity 60.0%; Pred. No. 85;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Oy 1 GHNSVDPEED 10
||:||||:|
Db 711 GHSSVDVKDD 720

RESULT 12

H85611
probable adhesin Z1211 [imported] - Escherichia coli (strain O157:H7, substrain EDL933)
C/Species: Escherichia coli
C/Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
C/Accession: H85611; B85663
R/Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glaesner, J.D.; Rose, D.J.; Mayhew
Miller, L.; Grobeck, E.J.; Davis, N.W.; Lam, A.; Dimalanta, E.; Potamoudis, K.; Apodaca,
Nature 409, 529-533, 2001
A/Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A/Reference number: A85480; MUID:21074935; PMID:11206551
A/Accession: H85611
A/Status: Preliminary
A/Molecule type: DNA
A/Residues: 1-1005 <STO>
A/Cross-references: UNIPROT:Q8X9L4; GB:AE005174; NID:G12514025; PIDN:AAG5356.1; GSPDB:G
A/Experimental source: strain O157:H7, substrain EDL933
A/Accession: B85663
A/Status: Preliminary
A/Molecule type: DNA
A/Residues: 1-1005 <ST2>
A/Cross-references: GB:AE005174; NID:G12514546; PIDN:AAG55766.1; GSPDB:GN00145; UWGP:Z16
A/Experimental source: strain O157:H7, substrain EDL933
C/Genetics:
A/Gene: Z1211; Z1651

Query Match 66.1%; Score 37; DB 2; Length 1005;
Best Local Similarity 60.0%; Pred. No. 91;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Oy 1 GHNSVDPEED 10
||:||||:|
Db 767 GHSSVDVKDD 776

RESULT 13

G64964
hypothetical protein b2000 - Escherichia coli (strain K-12)
C/Species: Escherichia coli
C/Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 01-Mar-2002
C/Accession: G64964
R/Baltner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; CC
Science 277, 1453-1462, 1997
A/Title: The complete genome sequence of Escherichia coli K-12.
A/Reference number: A64720; MUID:97426617; PMID:9278503
A/Accession: G64964
A/Status: nucleic acid sequence not shown; translation not shown
A/Molecule type: DNA
A/Residues: 1-1091 <BLAT>
A/Cross-references: GB:U00096; NID:G1788298; PIDN:AACT5061.1; PID:G1788309;
A/Experimental source: strain K-12, substrain MG1655
C/Keywords: nucleotide binding; P-loop
F/683-690/Region: nucleotide-binding motif A (P-loop)

Query Match 66.1%; Score 37; DB 2; Length 1091;
Best Local Similarity 60.0%; Pred. No. 1e+02;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Oy 1 GHNSVDPEED 10
||:||||:|
Db 853 GHSSVDVKDD 862

RESULT 14

B96673
hypothetical protein F13011.26 [imported] - Arabidopsis thaliana

C/Species: Arabidopsis thaliana (mouse-ear cress)
C/Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C/Accession: B96673
R/Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;
ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A/Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.,
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziani,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A/Authors: Salberg, S.L.; Schwartz, J.R.; Shim, P.; Southwick, A.M.; Sun, H.; Tallon,
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A/Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A/Reference number: A86141; MUID:21016719; PMID:11130712
A/Accession: B96673
A/Status: Preliminary
A/Molecule type: DNA
A/Residues: 1-1227 <STO>
A/Cross-references: UNIPROT:Q9X1Q0; GB:AE005173; NID:G5042431; PIDN:AAJ38270.1; GSPDB:GK
C/Genetics:
A/Gene: F13011.26
A/Map position: 1

Query Match 66.1%; Score 37; DB 2; Length 1227;
Best Local Similarity 60.0%; Pred. No. 1.1e+02;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Oy 1 GHNSVDPEED 10
||:||||:|
Db 758 GKNAISFEED 767

RESULT 15

PC4276
dentin phosphophoryn precursor - rat (fragment)
C/Species: Rattus norvegicus (Norway rat)
C/Date: 28-May-1997 #sequence_revision 17-Sep-1997 #text_change 09-Jul-2004
C/Accession: PC4276
R/Ritche, H.; Wang, L.H.
Biochem. Biophys. Res. Commun. 231, 425-428, 1997
A/Title: A mammalian bicistronic transcript encoding two dentin-specific proteins.
A/Reference number: PC4275; MUID:97223472; PMID:9070293
A/Accession: PC4276
A/Molecule type: mRNA
A/Residues: 1-31 <RT>
A/Cross-references: UNIPROT:Q8VBY1
A/Note: the authors translated the codon AGG for residue 5 as Ser
C/Comment: This protein plays a central role in the mineralization process leading to mat
F/1-27/Domain: signal sequence #status predicted <SIG>

Query Match 64.3%; Score 36; DB 2; Length 31;
Best Local Similarity 50.0%; Pred. No. 2.8;
Matches 5; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Oy 1 GHNSVDPEED 10
||:||||:|
Db 14 GHDSYDFDE 23

Search completed: October 22, 2005, 09:55:50
Job time : 12.6092 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 22, 2005, 08:01:06 ; Search time 56.2069 Seconds
(without alignments)
91.106 Million cell updates/sec

Title: US-10-731-238-99
Perfect score: 56
Sequence: 1 GHSNVDFFED 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues
Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 200000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Uniprot_03: *
1: uniprot_sprot: *
2: uniprot_trembl: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	56	100.0	940	2 Q53682	Q53682 staphylococ
2	56	100.0	943	2 Q8NUU8	Q8NUU8 staphylococ
3	56	100.0	957	2 Q6G6H4	Q6G6H4 staphylococ
4	56	100.0	961	2 Q998D3	Q998D3 staphylococ
5	56	100.0	961	2 Q7A3U8	Q7A3U8 staphylococ
6	56	100.0	965	2 Q6GDU5	Q6GDU5 staphylococ
7	56	100.0	1015	2 Q8NUU7	Q8NUU7 staphylococ
8	56	100.0	1015	2 Q6G6H3	Q6G6H3 staphylococ
9	56	100.0	1038	1 FNBA SPAAU	P14738 staphylococ
10	56	100.0	1038	2 Q998D2	Q998D2 staphylococ
11	56	100.0	1038	2 Q7A3U7	Q7A3U7 staphylococ
12	44	78.6	152	2 Q9AEP9	Q9AEP9 staphylococ
13	40	71.4	387	2 Q8C5I1	Q8C5I1 staphylococ
14	40	71.4	443	2 Q6BRP9	Q6BRP9 debaryomyce
15	39	69.6	782	1 YERY YEAST	P10356 saccharomyce
16	39	69.6	580	2 Q701S6	Q701S6 anopheles g
17	38	67.9	86	2 Q7UW19	Q7UW19 rhodospirell
18	38	67.9	168	2 Q81U07	Q81U07 plasmidium
19	38	67.9	168	2 Q7R9A1	Q7R9A1 plasmidium
20	38	67.9	255	2 Q93261	Q93261 protopetereus
21	38	67.9	255	2 Q9PMN1	Q9PMN1 protopetereus
22	38	67.9	281	2 Q9LS15	Q9LS15 arabidopsis
23	38	67.9	747	2 Q9RVB2	Q9RVB2 deinococcus
24	38	67.9	1463	2 Q703J0	Q703J0 cavia porce
25	37.5	67.0	410	2 Q9VXS4	Q9VXS4 drosophila
26	37	66.1	201	1 MEAL BACHD	Q9KCF1 bacillus ha
27	37	66.1	255	2 Q7NNC7	Q7NNC7 glaucobacter
28	37	66.1	259	1 CAH2 ARATH	P42737 arabidopsis
29	37	66.1	319	2 Q9STW6	Q9STW6 gossypium h
30	37	66.1	322	2 Q9XFE9	Q9XFE9 gossypium h
31	37	66.1	326	2 Q8LSC8	Q8LSC8 gossypium h

32	37	66.1	336	2 Q6Q9W7	Q6Q9W7 thlaspi cae
33	37	66.1	347	1 CAHC ARATH	P27140 arabidopsis
34	37	66.1	364	2 Q92CE9	Q92CE9 listeria in
35	37	66.1	404	2 Q7QWU8	Q7QWU8 giardia lam
36	37	66.1	492	2 Q6SD73	Q6SD73 bacillus il
37	37	66.1	529	2 Q6BWP3	Q6BWP3 debaryomyce
38	37	66.1	680	2 Q75BD2	Q75BD2 ashbya goss
39	37	66.1	706	2 Q7UBU5	Q7UBU5 shigella fl
40	37	66.1	718	2 Q6FUG7	Q6FUG7 candida gl
41	37	66.1	799	2 Q7FAB7	Q7FAB7 oryza sativ
42	37	66.1	949	2 Q7AFC7	Q7AFC7 escherichia
43	37	66.1	973	2 Q707F8	Q707F8 escherichia
44	37	66.1	1005	2 Q8X9L4	Q8X9L4 escherichia
45	37	66.1	1039	1 AG43_ECOLI	P39180 escherichia

ALIGNMENTS

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RESULT 1
Q53682 PRELIMINARY; PRT; 940 AA.
ID Q53682;
AC Q53682;
DT 01-NOV-1996 (TREMblrel. 01, Created)
DT 01-NOV-1996 (TREMblrel. 01, Last sequence update)
DT 01-MAR-2004 (TREMblrel. 26, Last annotation update)
DE Fibronectin binding protein B.
GN Name=fnbB;
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1280;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=8325-4;
RX MEDLINE=92111475; PubMed=1837266;
RA Jonsson K., Signas C., Muller H.P., Lindberg M.;
RT "Two different genes encode fibronectin binding proteins in
RT staphylococcus aureus. The complete nucleotide sequence and
RT characterization of the second gene."
RL Eur. J. Biochem. 202:1041-1048(1991).
CC -! SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC an amide bond (By similarity).
DR EMBL: X62992; CAA44726.1; -.
DR PIR: S19702; S19702.
DR HSP: Q53653; IN67.
DR GO: GO:0009986; C:cell surface; IEA.
DR GO: GO:0005618; C:cell wall; IEA.
DR GO: GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO: GO:0016020; C:membrane; IEA.
DR GO: GO:007155; P:cell adhesion; IEA.
DR InterPro: IPR008966; Adhes_Bact.
DR InterPro: IPR004237; Fn_bind.
DR InterPro: IPR005877; Gpos_YsIRK.
DR InterPro: IPR001899; Gram_pos_anchor.
DR Pfam: PF02986; Fn_bind; 2.
DR Pfam: PF00746; Gram_pos_anchor; 1.
DR Pfam: PF04650; YsIRK_signal; 1.
DR TIGRPFAM: TIGR01167; LpYTG_anchor; 1.
DR TIGRPFAM: TIGR01168; YsIRK_signal; 1.
DR PROSITE: PSS0847; GRAM_POS_ANCHORING; 1.
KW Cell wall; Peptidoglycan-anchor.
SQ
SEQUENCE 940 AA; 10355 MW; E35FBCA907AE345 CRC64;

Query Match 100.0%; Score 56; DB 2; Length 940;
Best local similarity 100.0%; Pred. No. 0.22;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GHSNVDFFED 10
DB 780 GHSNVDFFED 789

RESULT 2

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Q8NU8      PRELIMINARY;      PRT;      943 AA.
ID Q8NU8
AC Q8NU8;
DT 01-OCT-2002 (TREMBlrel. 22, Created)
DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE FmbB protein.
GN Name=fmbB; OrderedLocustNames=MM2420;
OS Staphylococcus aureus (strain MSS4476).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=196620;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MM2;
RX MEDLINE=22040717; PubMed=12044378; DOI=10.1016/S0140-6736(02)08713-5;
RA Baba T., Takuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Oguchi A.,
RA Nagai Y., Iwama N., Asano K., Naimi T., Kuroda H., Cui L.,
RA Yamamoto K., Hiramatsu K.;
"Genome and virulence determinants of high virulence community-
RT acquired MRSA."
RL Lancet 359:1819-1827(2002).
CC -I- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
an amide bond (By similarity).
DR EMBL; AP004830; BAB96285.1; -.
DR HSSP; Q53653; IN67.
DR GO; GO:0009986; C:cell surface; IEA.
DR GO; GO:0005618; C:cell wall; IEA.
DR GO; GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0007155; P:cell adhesion; IEA.
DR InterPro; IPR008966; Adhes_Bact.
DR InterPro; IPR004237; Gpos_YsIRK.
DR InterPro; IPR001899; Gram_pos_anchor.
DR Pfam; PF02986; Fb_bind.1.
DR Pfam; PF00746; Gram_pos_anchor.1.
DR Pfam; PF04650; YsIRK_signal.1.
DR TIGRFAMs; TIGR01167; LpxTG_anchor.1.
DR TIGRFAMs; TIGR01168; YsIRK_signal.1.
DR PROSITE; PS50847; GRAM_POS_ANCHORING.1.
KW Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ SEQUENCE 943 AA; 104537 MW; DA8A5F31947B1BA CRC64;

Query Match      100.0%; Score 56; DB 2; Length 943;
Best Local Similarity 100.0%; Pred. No. 0.23;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GHSNVDFEED 10
DB 787 GHSNVDFEED 796

RESULT 3
ID Q6G6H4      PRELIMINARY;      PRT;      957 AA.
AC Q6G6H4;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE Fibronectin-binding protein.
GN Name=fnbB; OrderedLocustNames=SAS2387;
OS Staphylococcus aureus (strain MSS4476).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=282459;
RN [1]
RP SEQUENCE FROM N.A.
RC PubMed=15213324; DOI=10.1073/pnas.0402521101;
RA Holden M.T.G., Peil E.U., Lindsay J.A., Peacock S.J., Day N.P.U.,
RA Enright M.C., Foster T.J., Moore C.E., Hurst L., Atkin R., Barron A.,
RA Baon N., Bentley S.D., Chillingworth T., Chillingworth T.,
RA Churcher C., Clark L., Cronin C., Cronin A., Doggett J., Dowd L.,
RA Feltwell T., Hance Z., Harris B., Hauser H., Holtrold S., Jagele K.,
RA James K.D., Lennard N., Line A., Mayes R., Moulé S., Mungall K.,

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RA Ormond D., Quail M.A., Rabinowitz E., Rutherford K.M., Sanders M.,
RA Sharp S., Simmonds M., Stevens K., Whitehead S., Barrell B.G.,
RA Spratt B.G., Parkhill J.;
"Complete genomes of two clinical Staphylococcus aureus strains:
RT evidence for the rapid evolution of virulence and drug resistance."
Proc. Natl. Acad. Sci. U.S.A. 101:9786-9791(2004).
CC -I- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
an amide bond (By similarity).
DR EMBL; BX571857; CA644201.1; -.
DR GO; GO:0009986; C:cell surface; IEA.
DR GO; GO:0005618; C:cell wall; IEA.
DR GO; GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0007155; P:cell adhesion; IEA.
DR InterPro; IPR008966; Adhes_Bact.
DR InterPro; IPR004237; Fb_bind.
DR InterPro; IPR005877; Gpos_YsIRK.
DR InterPro; IPR001899; Gram_pos_anchor.
DR Pfam; PF02986; Fb_bind.1.
DR Pfam; PF00746; Gram_pos_anchor.1.
DR Pfam; PF04650; YsIRK_signal.1.
DR TIGRFAMs; TIGR01167; LpxTG_anchor.1.
DR TIGRFAMs; TIGR01168; YsIRK_signal.1.
DR PROSITE; PS50847; GRAM_POS_ANCHORING.1.
KW Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ SEQUENCE 957 AA; 105980 MW; 28F8BA7FDPD3AFAF CRC64;

Query Match      100.0%; Score 56; DB 2; Length 957;
Best Local Similarity 100.0%; Pred. No. 0.23;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GHSNVDFEED 10
DB 787 GHSNVDFEED 796

RESULT 4
ID Q99RD3      PRELIMINARY;      PRT;      961 AA.
AC Q99RD3;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE Fibronectin-binding protein homolog.
GN Name=fnbB; OrderedLocustNames=SAV2502;
OS Staphylococcus aureus (strain Mu50 / ATCC 700699).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=158878;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Mu50 / ATCC 700699;
RX MEDLINE=21311952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2;
RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Iian J.-Q., Ito T.,
RA Kanamori M., Matsunaru H., Maruyama A., Murakami H., Hoshoyama A.,
RA Mizutani U.I., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
RA Sekimizu K., Hiraoka H., Kuhnra S., Goto S., Yabuzaki J.,
RA Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
RA Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
"Whole genome sequencing of methicillin-resistant Staphylococcus
RT aureus."
RL Lancet 357:1225-1240(2001).
CC -I- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
an amide bond (By similarity).
DR EMBL; AP003365; BAB58664.1; -.
DR PIR; G90053; G90053.
DR HSSP; Q53653; IN67.
DR GO; GO:0009986; C:cell surface; IEA.
DR GO; GO:0005618; C:cell wall; IEA.
DR GO; GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0007155; P:cell adhesion; IEA.
DR InterPro; IPR008966; Adhes_Bact.

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DR InterPro: IPR004237; Fn_bind.
DR InterPro: IPR005877; Gpos_YsIRK.
DR InterPro: IPR001899; Gram_pos_anchor.
DR Pfam: PF02986; Fn_bind; 1.
DR Pfam: PF00746; Gram_pos_anchor; 1.
DR Pfam: PF04650; YsIRK_signal; 1.
DR TIGRFAMs: TIGR01167; LpxTG_anchor; 1.
DR TIGRFAMs: TIGR01168; YsIRK_signal; 1.
DR PROSITE: PS50847; GRAM_POS_ANCHORING; 1.
KW Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ SEQUENCE 961 AA; 106010 MW; 364940F884EA4101 CRC64;

Query Match 100.0%; Score 56; DB 2; Length 961;
Best Local Similarity 100.0%; Pred. No. 0.23;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GHSVDFFED 10
    |||||
Db 791 GHSVDFFED 800

RESULT 5
ID Q7A3J8 PRELIMINARY; PRT; 961 AA.
AC Q7A3J8;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Fnb protein.
GN Name=fnb; OrderedLocustNames=SA2290;
OS Staphylococcus aureus (strain N315).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
NCBI_TaxID=158879;
[1]
RN SEQUENCE FROM N.A.
RP MEDLINE=21311952; PubMed=1418146; DOI=10.1016/S0140-6736(00)04403-2;
RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Itoh Y., Ito T.,
RA Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,
RA Mizutani Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
RA Sekizawa K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
RA Kaneshita M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
RA Hattori M., Ogasawara N., Hayaishi H., Hiramatsu K.;
RT "Whole genome sequencing of methicillin-resistant Staphylococcus
RT aureus ";
RL Lancet 357;1225-1240(2001).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC an amide bond (By similarity).
DR EMBL: AP003137; BAB43593.1; -.
DR GO: GO:0009986; C:cell surface; IEA.
DR GO: GO:0005618; C:cell wall; IEA.
DR GO: GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO: GO:0016020; C:membrane; IEA.
DR GO: GO:0007155; P:cell adhesion; IEA.
DR InterPro: IPR008966; Adhes_bact.
DR InterPro: IPR004237; Fn_bind.
DR InterPro: IPR005877; Gpos_YsIRK.
DR InterPro: IPR001899; Gram_pos_anchor.
DR Pfam: PF02986; Fn_bind; 1.
DR Pfam: PF00746; Gram_pos_anchor; 1.
DR Pfam: PF04650; YsIRK_signal; 1.
DR TIGRFAMs: TIGR01167; LpxTG_anchor; 1.
DR TIGRFAMs: TIGR01168; YsIRK_signal; 1.
DR PROSITE: PS50847; GRAM_POS_ANCHORING; 1.
KW Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ SEQUENCE 961 AA; 106010 MW; 364940F884EA4101 CRC64;

Query Match 100.0%; Score 56; DB 2; Length 961;
Best Local Similarity 100.0%; Pred. No. 0.23;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GHSVDFFED 10
    |||||
Db 791 GHSVDFFED 800

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Db 791 GHSVDFFED 800

..
RESULT 6
ID Q6GDUS PRELIMINARY; PRT; 965 AA.
AC Q6GDUS;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Fibronectin-binding protein.
GN Name=fnbA; OrderedLocustNames=SA2580;
OS Staphylococcus aureus (strain MRSA252).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
NCBI_TaxID=282458;
[1]
RN SEQUENCE FROM N.A.
RP PubMed=15213324; DOI=10.1073/pnas.0402521101;
RA Holden M.T.G., Feil E.J., Lindsay J.A., Peacock S.J., Day N.P.J.,
RA Enright M.C., Foster T.J., Moore C.E., Hurst L., Atkin R., Barron A.,
RA Baason N., Bentley S.D., Chillingworth C., Chillingworth T.,
RA Churcher C., Clark L., Corton C., Cronin A., Doggett J., Dowd L.,
RA Feltwell T., Hance Z., Harris B., Hauser H., Holroyd S., Jagels K.,
RA James K.D., Leonard N., Line A., Mayes R., Moule S., Mungall K.,
RA Ormond D., Quail M.A., Rabinowitch E., Rutherford K.M., Sanders M.,
RA Sharp S., Simmonds M., Stevens K., Whitehead S., Barrett B.G.,
RA Spratt B.G., Parkhill J.;
RT "Complete genomes of two clinical Staphylococcus aureus strains:
RT evidence for the rapid evolution of virulence and drug resistance.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:9786-9791(2004).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC an amide bond (By similarity).
DR EMBL: BX571856; CAG41560.1; -.
DR GO: GO:0009986; C:cell surface; IEA.
DR GO: GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO: GO:0016020; C:membrane; IEA.
DR GO: GO:0007155; P:cell adhesion; IEA.
DR InterPro: IPR008966; Adhes_bact.
DR InterPro: IPR004237; Fn_bind.
DR InterPro: IPR005877; Gpos_YsIRK.
DR InterPro: IPR001899; Gram_pos_anchor.
DR Pfam: PF02986; Fn_bind; 1.
DR Pfam: PF00746; Gram_pos_anchor; 1.
DR Pfam: PF04650; YsIRK_signal; 1.
DR TIGRFAMs: TIGR01167; LpxTG_anchor; 1.
DR TIGRFAMs: TIGR01168; YsIRK_signal; 1.
DR PROSITE: PS50847; GRAM_POS_ANCHORING; 1.
KW Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ SEQUENCE 965 AA; 105691 MW; 2982E132164D0551 CRC64;

Query Match 100.0%; Score 56; DB 2; Length 965;
Best Local Similarity 100.0%; Pred. No. 0.23;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GHSVDFFED 10
    |||||
Db 809 GHSVDFFED 818

RESULT 7
ID Q8NUU7 PRELIMINARY; PRT; 1015 AA.
AC Q8NUU7;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Fnb protein.
GN Name=fnb; OrderedLocustNames=MM2421;
OS Staphylococcus aureus (strain MM2).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
NCBI_TaxID=196620;
[1]
RN SEQUENCE FROM N.A.
RP

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RC STRAIN=MM2;
RX MEDLINE=22040717; PubMed=12044378; DOI=10.1016/S0140-6736(02)08713-5;
RA Baba T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Oguchi A.,
RA Nagai Y., Ikawa N., Amano K., Naimi T., Kuroda H., Cui L.,
RA Yamamoto K., Hiramatsu K.;
RT "Genome and virulence determinants of high virulence community-
RT acquired MRSA.";
RU Lancet 359:1819-1827(2002).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC an amide bond (By similarity).
EMBL: AP004830; BAB96286.1; -.
DR GO: GO:0009986; C:cell surface; IEA.
DR GO: GO:0005618; C:cell wall; IEA.
DR GO: GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO: GO:0016020; C:membrane; IEA.
DR GO: GO:0007155; P:cell adhesion; IEA.
DR InterPro: IPR008966; Adhes_bact.
DR InterPro: IPR004237; Fn_bind.
DR InterPro: IPR005877; Gpos_YsIRK.
DR Pfam: PF02986; Fn_bind; 1.
DR Pfam: PF04650; YsIRK_signal; 1.
DR TIGRFAMs: TIGR01167; LpxTG_anchor; 1.
DR TIGRFAMs: TIGR01168; YsIRK_signal; 1.
DR PROSITE: PS50847; GRAM_POS_ANCHORING; 1.
KM Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ SEQUENCE 1015 AA; 11145 MW; D0F9281BB64D4D2 CRC64;

Query Match 100.0%; Score 56; DB 2; Length 1015;
Best Local Similarity 100.0%; Pred. No. 0.24;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GHNSVDFEED 10
DB 845 GHNSVDFEED 854
|||||

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DR InterPro: IPR008966; Adhes_bact.
DR InterPro: IPR004237; Fn_bind.
DR InterPro: IPR005877; Gpos_YsIRK.
DR InterPro: IPR001899; Gram_pos_anchor.
DR Pfam: PF02986; Fn_bind; 1.
DR Pfam: PF00746; Gram_pos_anchor; 1.
DR Pfam: PF04650; YsIRK_signal; 1.
DR TIGRFAMs: TIGR01167; LpxTG_anchor; 1.
DR TIGRFAMs: TIGR01168; YsIRK_signal; 1.
DR PROSITE: PS50847; GRAM_POS_ANCHORING; 1.
KM Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ SEQUENCE 1015 AA; 11145 MW; D0F9281BB64D4D2 CRC64;

Query Match 100.0%; Score 56; DB 2; Length 1015;
Best Local Similarity 100.0%; Pred. No. 0.24;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GHNSVDFEED 10
DB 845 GHNSVDFEED 854
|||||

RESULT 9
FNBA_STAU STANDARD; PRT; 1018 AA.
ID FNBA_STAU
AC P14738;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Fibronectin-binding protein precursor (FNBP).
GN Name:fnba;
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
ON NCBI_TaxID=1280;
RX MEDLINE=89098998; PubMed=2521391;
RA Anantharamaiah G.M., Hoecek M., Lindberg M.,
RA Signes C., Raucel G., Joensson K., Lindgren P.-E.,
RT "Nucleotide sequence of the gene for a fibronectin-binding protein
RT from Staphylococcus aureus: use of this peptide sequence in the
RT synthesis of biologically active peptides.";
RU Proc. Natl. Acad. Sci. U.S.A. 86:699-703(1989).
CC -1- FUNCTION: The ability of bacteria to bind fibronectin has been
CC proposed as a virulence factor enabling bacteria to colonize wound
CC tissues and blood clots. Binding of plasma fibronectin to the
CC bacterial surface might block adhesion receptors on S.aureus, thus
CC representing an important defense mechanism against tissue
CC invasion.
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC an amide bond (Potential).
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CC -----
EMBL: J04151; AAA26632.1; -.
DR InterPro: IPR004237; Fn_bind.
DR InterPro: IPR005877; Gpos_YsIRK.
DR InterPro: IPR001899; Gram_pos_anchor.
DR Pfam: PF02986; Fn_bind; 1.
DR Pfam: PF00746; Gram_pos_anchor; 1.
DR Pfam: PF04650; YsIRK_signal; 1.
DR TIGRFAMs: TIGR01167; LpxTG_anchor; 1.
DR TIGRFAMs: TIGR01168; YsIRK_signal; 1.
DR PROSITE: PS50847; GRAM_POS_ANCHORING; 1.
KM Cell adhesion; Cell wall; Peptidoglycan-anchor; Repeat; Signal;
KM Virulence.

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FT SIGNAL 1 36
FT CHAIN 37 985 Fibronectin-binding protein.
FT PROPE 986 1018 Removed by sortase (potential).
FT REPEAT 545 574 B-1.
FT REPEAT 575 604 B-2.
FT DOMAIN 745 878 4 X approximate tandem repeats,
  fibronectin-binding domain.
FT REPEAT 745 782 D-1.
FT REPEAT 783 820 D-2.
FT REPEAT 821 859 D-3.
FT REPEAT 860 878 D-4 (incomplete).
FT DOMAIN 879 948 5 X tandem repeats, Pro-rich (WR).
FT REPEAT 879 892 WR 1.
FT REPEAT 893 906 WR 2.
FT REPEAT 907 920 WR 3.
FT REPEAT 921 934 WR 4.
FT REPEAT 935 948 WR 5.
FT SITE 982 986 Pentaglycyl murein peptidoglycan amidated
  threonine (Potential).
FT MOD_RES 985 985
SQ SEQUENCE 1018 AA; 111780 MW; 58175E0020E81F1F CRC64;

Query Match 100.0%; Score 56; DB 1; Length 1018;
Best Local Similarity 100.0%; Pred. No. 0.24;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GHSVDFFED 10
DB 844 GHSVDFFED 853

RESULT 10
Q99RD2 PRELIMINARY; PRT; 1038 AA.
ID 099RD2;
AC 01-JUN-2001 (TREMblrel. 17, Created)
DT 01-JUN-2001 (TREMblrel. 17, Last sequence update)
DT 01-MAR-2004 (TREMblrel. 26, Last annotation update)
DE Fibronectin-binding protein homolog.
GN Name=fib; OrderedLocustNames=SAV2503;
OS Staphylococcus aureus (strain Mu50 / ATCC 700699).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=158878;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Mu50 / ATCC 700699;
RX MEDLINE=21311952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2;
RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
  Cui L., Oguchi A., Aoki K.-I., Nagai Y., Iano J.-O., Ito T.,
  Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,
  Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
  Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
  Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
  Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
RT "Whole genome sequencing of methicillin-resistant Staphylococcus
  aureus."
RL Lancet 357:1225-1240(2001).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
  an amide bond (By similarity).
EMBL: AP003365; BAB58665.1; -
DR GO: 0009986; C:cell surface; IEA.
DR GO: 0005618; C:cell wall; IEA.
DR GO: 0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO: 0016020; C:membrane; IEA.
DR GO: 0007155; P:cell adhesion; IEA.
DR InterPro: IPR008966; Adhes_bact.
DR InterPro: IPR004237; Fn_bind.
DR InterPro: IPR005877; Gpos_YsIRK.
DR InterPro: IPR001899; Gram_pos_anchor.
DR Pfam: PF02986; Fn_bind.1.
DR Pfam: PF02946; Gram_pos_anchor.1.
DR Pfam: PF04650; YsIRK_signal.1.

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DR TIGRFAMs: TIGR01167; LPXTG anchor; 1.
DR TIGRFAMs: TIGR01168; YsIRK_signal; 1.
DR PROSITE: PS50847; GRAM_POS_ANCHORING; 1.
DR Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ SEQUENCE 1038 AA; 113618 MW; 666BF6BF2BFBB12 CRC64;

Query Match 100.0%; Score 56; DB 2; Length 1038;
Best Local Similarity 100.0%; Pred. No. 0.25;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GHSVDFFED 10
DB 840 GHSVDFFED 849

RESULT 11
Q7A3J7 PRELIMINARY; PRT; 1038 AA.
ID Q7A3J7;
AC Q7A3J7;
DT 05-JUL-2004 (TREMblrel. 27, Created)
DT 05-JUL-2004 (TREMblrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMblrel. 27, Last annotation update)
DE Fnb protein.
GN Name=fnb; OrderedLocustNames=SA2291;
OS Staphylococcus aureus (strain N315).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=158879;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=21311952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2;
RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
  Cui L., Oguchi A., Aoki K.-I., Nagai Y., Iano J.-O., Ito T.,
  Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,
  Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
  Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
  Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
  Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
RT "Whole genome sequencing of methicillin-resistant Staphylococcus
  aureus."
RL Lancet 357:1225-1240(2001).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
  an amide bond (By similarity).
EMBL: AP003137; BAB43594.1; -
DR GO: 0009986; C:cell surface; IEA.
DR GO: 0005618; C:cell wall; IEA.
DR GO: 0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO: 0016020; C:membrane; IEA.
DR GO: 0007155; P:cell adhesion; IEA.
DR InterPro: IPR008966; Adhes_bact.
DR InterPro: IPR004237; Fn_bind.
DR InterPro: IPR005877; Gpos_YsIRK.
DR InterPro: IPR001899; Gram_pos_anchor.
DR Pfam: PF02986; Fn_bind.1.
DR Pfam: PF02946; Gram_pos_anchor.1.
DR Pfam: PF04650; YsIRK_signal.1.
DR TIGRFAMs: TIGR01167; LPXTG anchor; 1.
DR TIGRFAMs: TIGR01168; YsIRK_signal; 1.
DR PROSITE: PS50847; GRAM_POS_ANCHORING; 1.
DR Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ SEQUENCE 1038 AA; 113618 MW; 666BF6BF2BFBB12 CRC64;

Query Match 100.0%; Score 56; DB 2; Length 1038;
Best Local Similarity 100.0%; Pred. No. 0.25;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GHSVDFFED 10
DB 840 GHSVDFFED 849

RESULT 12
Q9AEP9 PRELIMINARY; PRT; 152 AA.
ID Q9AEP9

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AC 09AEP9:
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Fibronectin-binding protein (Fragment).
GN Name=fnb;
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1280;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CMRSA-1;
RX DOI=10.1128/IAI.69.6.3791-3799.2001;
RA Rice K., Huesca M., Vaz D., McGavin M.J.;
RT "Variance in fibronectin binding and fnb locus polymorphisms in
RT Staphylococcus aureus: identification of antigenic variation in a
RT fibronectin binding protein adhesin of the epidemic CMRSA-1 strain of
RT methicillin-resistant S. aureus.";
RL Infect.Immun. 69:3791-3799(2001).
DR EMBL; AY029184; AAK31588.1; -.
FT NON TER 1
FT TER 152
SQ SEQUENCE 152 AA; 17193 MW; CFA3913C2B11C025 CRC64;

Query Match
Best Local Similarity 78.6%; Score 44; DB 2; Length 152;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GHNSVDPEED 10
Db 137 GHNGIDPVED 146

RESULT 13
ID 08CS51 PRELIMINARY; PRT; 387 AA.
AC 08CS51.
DT 01-MAR-2003 (TREMBLrel. 23, Created)
DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Hypothetical protein.
GN OrderedLocustNames=SE1400;
OS Staphylococcus epidermidis.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1282;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 12228;
RX PubMed=12950922;
RA Zhang Y.-Q., Ren S.-X., Li H.-L., Wang Y.-X., Fu G., Yang J.,
RA Qiu Z.-Q., Miao Y.-G., Wang W.-Y., Chen R.-S., Shen Y., Chen Z.,
RA Yuan Z.-H., Zhao G.-P., Qu D., Danchin A., Wen Y.-M.;
RT "Genome-based analysis of virulence genes in a non-biofilm-forming
RT Staphylococcus epidermidis strain (ATCC 12228).";
RL Mol. Microbiol. 49:1577-1593(2003).
DR EMBL; AB016748; AA004999.1; -.
DR HSSP; P21549; 1H0C.
DR GO; GO:0008463; F:transaminase activity; IEA.
DR InterPro: IPR000192; Anticodons_V.
DR Pfam; PF00266; Anticodon_5_1.
DR PROSITE; PS00595; AA_TRANSFER_CLASS_5; 1.
KM Complete proteome; Hypothetical protein.
SQ SEQUENCE 387 AA; 42800 MW; DCC08239C9BC0409 CRC64;

Query Match
Best Local Similarity 71.4%; Score 40; DB 2; Length 387;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GHNSVDPEED 9
Db 30 GHSTDFEE 38

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RESULT 14
ID 06BKP9 PRELIMINARY; PRT; 782 AA.
AC 06BKP9.
DT 25-OCT-2004 (TREMBLrel. 28, Created)
DT 25-OCT-2004 (TREMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TREMBLrel. 28, Last annotation update)
DE Similar to CA3918|CAVTC2 Candida albicans CAVTC2 putative
DE polyphosphate synthetase.
GN ORFNames=DEHA0F214289;
OS Debaryomyces hanseoli CBS767.
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Debaryomyces.
OX NCBI_TaxID=284592;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CBS767;
RG Genolevures;
RA Dujon B., Sherman D., Fischer G., Durrens P., Casaregola S.,
RA Lafontaine I., de Montigny J., Marck C., Neveglisse C., Talla E.,
RA Goffard N., Frangeul L., Aigle M., Anthouard V., Babour A., Barbe V.,
RA Barnay S., Blanchin S., Beckerich J.M., Bayne E., Bleykasten C.,
RA Boistrume A., Boyer J., Carrolico L., Confanioleri F., de Danvar A.,
RA Despons L., Fabre E., Fairhead C., Ferry-Dumazet H., Groppi A.,
RA Hantreaye F., Hennequin C., Jauniaux N., Joyet P., Kachouri R.,
RA Kerrest A., Koszul R., Lemaire M., Lesur I., Ma L., Muller H.,
RA Niclaud J.M., Nikolski M., Oztas S., Ozier-Kalogeropoulos O.,
RA Pellenz S., Porter S., Richard G.F., Straub M.L., Suleau A.,
RA Swennene D., Tekala F., Wesolowski-Jouvet M., Westhof E., Wirth B.,
RA Zeniou-Meyer M., Zivanovic I., Bolotin-Fukuhara M., Thierry A.,
RA Bouchier C., Caudron B., Scarpelli C., Galliardin C., Weissendach J.,
RA Wincker P., Souciet J.L.;
RT "Genome evolution in yeasts.";
RL Nature 430:35-44(2004).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=CBS767;
RA Genoscope;
RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; CR382138; CAG89610.1; -.
DR InterPro: IPR004331; SPX_N.
DR Pfam; PF03105; SPX; 1.
SQ SEQUENCE 782 AA; 90196 MW; 04915B5DFB448B5 CRC64;

Query Match
Best Local Similarity 71.4%; Score 40; DB 2; Length 782;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GHNSVDPEED 10
Db 578 GHSSDPEER 587

RESULT 15
ID YEY2 YEAST STANDARD; PRT; 443 AA.
AC P10356;
DT 01-MAR-1989 (Rel. 10, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 25-JAN-2005 (Rel. 46, Last annotation update)
DE Hypothetical 49.5 kDa protein in UBP3-PET122 intergenic region.
GN OrderedLocustNames=YER152C;
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=S288C / AB972;
RX MEDLINE=97313264; PubMed=9169868;
RA Dietrich F.S., Mulligan J.T., Hennessy K.M., Yelton M.A., Allen E.,

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RA Araujo R., Aviles E., Berno A., Brennan T., Carpenter J., Chen E.,
 RA Cherry J.M., Chung E., Duncan M., Guzman E., Hartzell G.,
 RA Hunticke-Smith S., Hyman R.W., Kayser A., Komp C., Lashkari D., Lew H.,
 RA Lin D., Mosedale D., Nakahara K., Namath A., Norgren R., Oefner P.,
 RA Oh C., Petel F.X., Roberts D., Sehl P., Schramm S., Shogren T.,
 RA Smith V., Taylor P., Wei Y., Botstein D., Davis R.W.,
 RT "The nucleotide sequence of Saccharomyces cerevisiae chromosome V.",
 RL Nature 387:78-81(1997).

[2]
 RN SEQUENCE OF 1-230 FROM N.A.
 RP STRAIN-AB320;

RC MEDLINE=89083497; PubMed=2849752;
 RX Ohmen J.D., Kloeckener-Grussem B., McEwen J.E.;

RA "Molecular cloning and nucleotide sequence of the nuclear PET122 gene
 RT required for expression of the mitochondrial COX3 gene in S.
 RT cerevisiae.";

RL Nucleic Acids Res. 16:10783-10802(1988).

[3]
 RN SEQUENCE OF 1-230 FROM N.A., AND REVISIONS.

RX MEDLINE=90258894; PubMed=2160592;

RA Ohmen J.D., Burke K.A., McEwen J.E.;

RT "Divergent overlapping transcripts at the PET122 locus in
 RT Mol. Cell. Biol. 10:3027-3035(1990).

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CC -----
 DR EMBL; U18917; AAB64679.1; -
 DR EMBL; X07558; CAA30440.1; -;

DR PIR; S50655; Q0BYPT.

DR GeneOnline; 139230; -;

DR SGD; S000000954; YER152C.

DR GO; GO:0005737; C:cytoplasm; IDA.

DR GO; GO:0005634; C:nucleus; IDA.

KW Hypothetical protein.

SQ SEQUENCE 443 AA; 49490 MW; BCA67A4D3B9D7A14 CRC64;

QY 1 GHNSVDFE 8
 DB 145 GHDSIDFE 152

Search completed: October 22, 2005, 09:52:26
 Job time : 58.2069 secs

Query Match 69.6%; Score 39; DB 1; Length 443;
 Best Local Similarity 75.0%; Pred. No. 1.3e+02;
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

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